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(71) Applicant: **THE BROAD INSTITUTE, INC.** [US/US]; 415 Main Street, Cambridge, Massachusetts 02142 (US).

(72) Inventors; and
(71) Applicants: **BARRY, Andrew** [US/US]; c/o 415 Main Street, Cambridge, Massachusetts 02142 (US). **EID, Fatmaelzahraa Sobhy Abdelmouty** [US/US]; c/o 415 Main Street, Cambridge, Massachusetts 02142 (US).

(72) Inventors: **DEVERMAN, Benjamin**; c/o 415 Main Street, Cambridge, Massachusetts 02142 (US). **HUANG, Qin**; c/o 415 Main Street, Cambridge, Massachusetts 02142 (US). **CHAN, Ken**; c/o 415 Main Street, Cambridge, Massachusetts 02142 (US).

(74) Agent: **HARDING, Drew** et al.; Johnson, Marcou, Isaacs & Nix, LLC, PO Box 691, Hoschton, Georgia 30548 (US).

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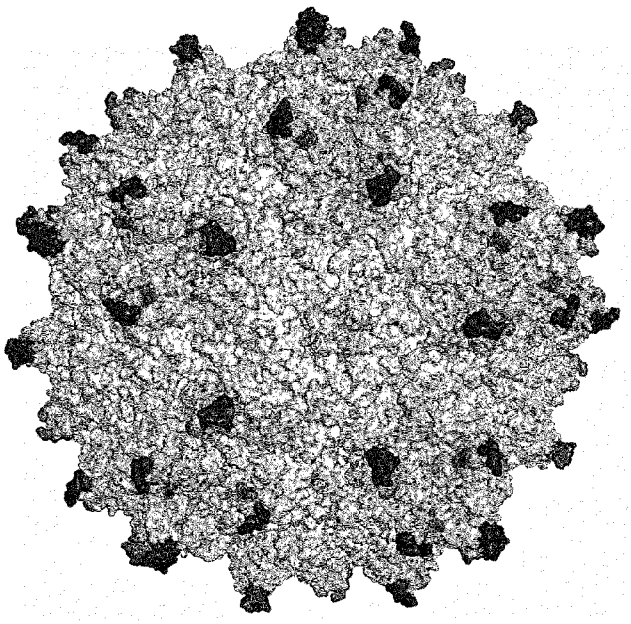

FIG. 1

(57) Abstract: An engineered AAV capsid is provided, in which at least one protein on the capsid is modified to include a n-mer motif, which promotes transduction of the capsid into the central nervous system (CNS) through interaction with the Transferrin receptor. Further embodiments provide a vector system comprising one or more vectors encoding AAV capsids and a method of delivering cargo to the CNS. The method comprises administering, in vivo or in vitro, a AAV capsid according to embodiments described herein and the AVV capsid comprises one or more cargo molecules.

[Continued on next page]

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AAV CAPSIDS THAT ENABLE CNS-WIDE GENE DELIVERY THROUGH INTERACTIONS WITH THE TRANSFERRIN RECEPTOR

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Application No. 63/432,336, filed December 13, 2022 and U.S. Provisional Application No. 63/368,470 filed July 14, 2022. The entire contents of the above-identified applications are hereby fully incorporated herein by reference.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH

[0002] This invention was made with government support under Grant No. NS111689 awarded by the National Institutes of Health and Grant No. MH120096 awarded by the National Institute of Mental Health. The government has certain rights in the invention.

REFERENCE TO AN ELECTRONIC SEQUENCE LISTING

[0003] Reference is made to the electronic sequence listing ("BROD-5515WP_ST26.xml"; Size is 36,487,898 bytes, created on July 14, 2023) is herein incorporated by reference in its entirety.

REFERENCE TO ELECTRONIC TABLES

[0004] Reference is made to electronic Tables 1-20 and 22 filed herewith in the United States Patent and Trademark Office. Reference is also made to Tables 1-13 filed on July 14, 2022, in the United States Patent and Trademark Office, and assigned Serial No. 63/368,470. The Table are herein incorporated by reference in their entirety.

TECHNICAL FIELD

[0005] The subject matter disclosed herein relates generally to enhancing transduction of an engineered AA capsid into the central nervous system (CNS) through interaction with the Transferrin receptor. In particular examples described herein, at least one protein on the capsid is modified to include an n-mer motif. Particular examples relate to a vector system having one or more vectors encoding AAV capsids and a method of delivering cargo to the CNS, in which an

AAV capsid according to the examples described herein is administered *in vivo* or *in vitro*, and the AAV capsid comprises one or more cargo molecules.

BACKGROUND

[0006] The development of gene therapies for neurodevelopmental and neurological disorders has been constrained by the inability to efficiently deliver genes throughout the CNS. Several studies have reported engineered AAV9 capsids, most notably the AAV-PHP.B family, that are capable of highly effective gene transfer throughout the CNS after intravenous administration in adult mice. To date however, none of the engineered AAV capsids that cross the blood-brain barrier (BBB) and transduce the mouse brain with high efficiency have been shown to exhibit their enhanced CNS tropism in primates. In this work, Applicants take a mechanism-first approach and engineer AAV capsids that interact with the Transferrin Receptor (TFRC).

[0007] Citation or identification of any document in this application is not an admission that such a document is available as prior art to the present invention.

SUMMARY

[0008] In one aspect, provided herein is a composition comprises a targeting moiety effective to increase transduction of central nervous system tissues (CNS) via binding to a transferrin receptor (TFRC), optionally further comprising a cargo coupled to or otherwise associated with the targeting moiety. In addition, one aspect provided herein is of a vector system comprising one or more vectors encoding a targeting moiety effective to increase transduction of central nervous system tissues (CNS). Additional embodiments provided herein comprise polypeptides or particles encoded or produced by a vector system herein or a cell comprising the composition, vector, polynucleotide or particle provided herein. In one aspect, provided herein is a method of delivering one or more cargos to the CNS by administering a composition provided herein.

[0009] In an example embodiment, the targeting moiety binds to the extracellular domain of TFRC. In an example embodiment, the targeting moiety binds to one or more of the apical, helical, and/or protease-like domain of the extracellular domain. In an example embodiment, the targeting moiety binds to the apical domain.

[0010] In an example embodiment, the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of X_1-X_2-X_3-X_4-X_5-X_6-X_7 wherein: X_1 comprises of Y, M, F, and L; X_2 comprises of S, H, T, and A; X_3 comprises of K and R; X_4 comprises of A, G, I, L, M, N, Q, S, T, V and H; X_5 comprises of N, G, A, L, M, Q, S, and T; X_6 comprises of A, T, H, N, F, I, P, L, Y, G, S, V, D, E, M, and Q; and X_7 comprises of D and N. In an example embodiment, X_1 comprises of Y, M, and L; X_2 comprises of S, H, T, and A; X_3 comprises of K and R; X_4 comprises of A, G, I, L, M, N, Q, S, T, and V; X_5 comprises N; X_6 comprises of A, T, H, N, F, I, P, L, and Y; and X_7 comprises of D and N; or X_1 comprises of Y, M, and L; X_2 comprises of S, H, T, and A; X_3 comprises of K and R; X_4 comprises of A, G, I, L, M, N, Q, S, T, and V; X_5 comprises G; X_6 comprises of A, G, F, H, I, L, N, P, S, T, V, and Y; and X_7 comprises of D and N; or X_1 comprises of L and Y; X_2 comprises of A, H, and S; X_3 comprises of K and R; X_4 comprises of A, G, H, I, L, M, N, Q, S, T, and V; X_5 comprises G; X_6 comprises P; andX_7 comprises D; or X_1 comprises of L and Y; X_2 comprises of A, H, and S; X_3 comprises of K and R; X_4 comprises of A, G, H, I, L, M, N, Q, S, T, and V; X_5 comprises G; X_6 comprises P; and X_7 comprises N; or X_1 comprises Y;X_2 comprises S; X_3 comprises K; X_4 comprises of A, I, L, M, N, Q, S, T, and V; X_5 comprises G; X_6 comprises of X; and X_7 comprises Y, P, T, Q, V, F, L, H, S, A, E, D, I, and M; or X_1 comprises of L and Y; X_2 comprises S; X_3 comprises of R and K; X_4 comprises of V, I, T, L, and A; X_5 comprises of S and A; X_6 comprises of P, R, Y, F, H, I, K, and W; and X_7 comprises D; or X_1 comprises of F, L, M, and Y; X_2 comprises H; X_3 comprises of K and R; X_4 comprises of A, L, and M; X_5 comprises of A, G, L, M, N, Q, S, and T; X_6 comprises of A, D, E, F, H, I, L, M, N, Q, P, S, T, V, and Y; and X_7 comprises of D and N; or X_1 comprises of L, M, and Y; X_2 comprises H; X_3 comprises of K and R; X_4 comprises of A, L, and M; X_5 comprises of A, G, L, M, N, Q, S, and T; X_6 comprises of A, D, E, F, H, I, L, M, N, Q, P, S, T, V, and Y; and X_7 comprises N; or X_1 comprises of L, M, and Y; X_2 comprises H; X_3 comprises of K and R; X_4 comprises of A, L, and M; X_5 comprises of A, G, L, M, N, Q, S, and T; X_6 comprises of A, D, E, F, H, I, L, M, N, Q, P, S, T, V, and Y; and X_7 comprises D; or X_1 comprises of L, M, and Y; X_2 comprises H; X_3 comprises of K and R; X_4 comprises L; X_5 comprises of S, Q, G, T, N, and L; X_6 comprises of P, T, V, I, Q, L, and A; andX_7 comprises D; or X_1 comprises F; X_2 comprises S; X_3 comprises R; X_4 comprises L; X_5 comprises G; X_6 comprises of A, H, N, L, V, S, P, and T; andX_7 comprises N; or X_1 comprises F; X_2 comprises A;

X_3 comprises R; X_4 comprises of T, S, and N; X_5 comprises G; X_6 comprises of Y, F, H, P, and A; andX_7 comprises N; or X_1 comprises F; X_2 comprises H; X_3 comprises of K and R; X_4 comprises L; X_5 comprises G; X_6 comprises of I, P, and S; and X_7 comprises of N and D. In an example embodiment, the n-mer motif is selected from the group consisting of LHRLGPN (SEQ ID NO: 36834), YSRIGPN (SEQ ID NO: 14632), LHRLGPN (SEQ ID NO: 36834), LHRLGPD (SEQ ID NO: 36413), LHRAGPD (SEQ ID NO: 36894), YSRIGPD (SEQ ID NO: 38223), LSRIGPD (SEQ ID NO: 36274), LARSGPD (SEQ ID NO: 18035), YSRNSDN (SEQ ID NO: 16626), LHKAGPN (SEQ ID NO: 36305), LSRIGPN (SEQ ID NO: 36347), LAKSGPN (SEQ ID NO: 36287), YARNGPN (SEQ ID NO: 14048) and YSRNSDN (SEQ ID NO: 16626). In an example embodiment, the n-mer motif is YSRIGPN (SEQ ID NO: 14632).

[0011] In an example embodiment, the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of X_1-X_2-X_3-X_4-X_5-X_6-X_7 wherein: X_1 comprises of Y or L; X_2 comprises H; X_3 comprises A; X_4 comprises of K, R, N, and A; X_5 comprises of G, Q, L, and S;X_6 comprises of P, L, I, N, D, and T; andX_7 comprises N. In the example embodiment, the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of X_1-X_2-X_3-X_4-X_5-X_6-X_7 wherein: X_1 comprises of A, F, H, I, L, N, P, R, S, T, V, and Y; X_2 comprises of A, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, W, and Y; X_3 comprises S; X_4 comprises of S and T; X_5 comprises N; X_6 comprises G; and X_7 comprises of I, R, and V. In an example embodiment, X_1 comprises of F, L, and Y; X_2 comprises of D, E, H, N, Q, S, and T; X_3 comprises S; X_4 comprises of S and T; X_5 comprises N; X_6 comprises G; and X_7 comprises of I and V; or X_1 comprises of V, P, I, S, T, H, and A; X_2 comprises of A, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, and Y; X_3 comprises of S; X_4 comprises of S and T; X_5 comprises N; X_6 comprises G; andX_7 comprises of I and V; or X_1 comprises of A, F, I, L, P, S, T, V, and Y; X_2 comprises of D, E, N, Q, S, and T; X_3 comprises S; X_4 comprises of T and S; X_5 comprises N; X_6 comprises G; and X_7 comprises R; or X_1 comprises R; X_2 comprises of E, D, Q, and T; X_3 comprises S; X_4 comprises of S and T; X_5 comprises N; X_6 comprises G; and X_7 comprises of I and V. In an example embodiment, the n-mer motif is selected from the group consisting of FRSTNGV (SEQ ID NO: 16070), VESTNGR (SEQ ID NO: 36431), VDSTNGV (SEQ ID NO: 12206), VQSTNGV (SEQ ID NO: 36423), VSSTNGV (SEQ ID NO: 12333),

TESTNGR (SEQ ID NO: 17558), VQSTNGI (SEQ ID NO: 11292) and FVSTNGV (SEQ ID NO: 11162).

[0012] In an example embodiment, the wherein the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of X_1-X_2-X_3-X_4-X_5-X_6-X_7 wherein: X_1 comprises of R and T; X_2 comprises of T, L, M, S, G, D, N, E, R, K, Y, and W; X_3 comprises of G, E, D, I, F, H, S, A, M, P, V, Y, W, Q, and T; X_4 comprises of D, T, E, H, N, and G; X_5 comprises of A, V, S, T, and D; X_6 comprises of Y, F, P and A; and X_7 comprises of A and P. In an example embodiment, X_1 comprises R; X_2 comprises of T, M, L, and S; X_3 comprises of Y, S, A, M, I, F, and P; X_4 comprises D; X_5 comprises of A, V, S, and T; X_6 comprises of Y and F; and X_7 comprises P; or X_1 comprises R; X_2 comprises of T, M, L, and S; X_3 comprises of Y, S, A, M, I, F, and P; X_4 comprises D; X_5 comprises of A, V, S, and T; X_6 comprises of Y and F; and X_7 comprises A; or X_1 comprises R; X_2 comprises of G, T, D, S, N, and E; X_3 comprises of E, D, P, S, and G; X_4 comprises of D, T, E, H, and N; X_5 comprises of V, A, and T; X_6 comprises of Y and F; and X_7 comprises P;or X_1 comprises R; X_2 comprises of G, L, T, D, and S; X_3 comprises of D, P, S, and G; X_4 comprises of D, E, H, and N; X_5 comprises of V and T; X_6 comprises of Y and F; and X_7 comprises P; or X_1 comprises T; X_2 comprises of R, K, Y, and W; X_3 comprises of E, W, Y, Q, S, and T; X_4 comprises G; X_5 comprises D; X_6 comprises of P and A; and X_7 comprises of A and P. In an example embodiment, the n-mer motif is selected from the group consisting of RGEDVYP (SEQ ID NO: 36864), RLEDVFP (SEQ ID NO: 36264), RTYDSYP (SEQ ID NO: 37938), RTYDAYP (SEQ ID NO: 38571), RTYDSFP (SEQ ID NO: 37806), RTETVYP (SEQ ID NO: 36486), RTETVFP (SEQ ID NO: 36389), and RTEHVFP (SEQ ID NO: 36603).

[0013] In an example embodiment, the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of X_1-X_2-X_3-X_4-X_5-X_6-X_7 wherein: X_1 comprises L; X_2 comprises C; X_3 comprises of K and R; X_4 comprises P; X_5 comprises C; X_6 comprises of L, S, D, A, N, Q, H, P, and V; and X_7 comprises of E, T, G, A, D, N, and S. In an example embodiment, the n-mer motif is LCKPCLD (SEQ ID NO: 36437) or LCKPCPT (SEQ ID NO: 36438). In an example embodiment, the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of X_1-X_2-X_3-X_4-X_5-X_6-X_7 wherein: X_1 comprises of Y, and F; X_2 comprises of W, F, and Y; X_3 comprises of S, T, H, A and Q; X_4 comprises G; X_5 comprises of I, T, V, Q, M, H, K, and R; X_6 comprises of I, P, H, L, M, A, Q, T,

V, K, and R; andX_7 comprises of A, S, D, E, and N. In an example embodiment, X_1 comprises of Y and F; X_2 comprises of W, F, and Y; X_3 comprises of T and S; X_4 comprises G; X_5 comprises of I, T, V, Q, M, and H; X_6 comprises of I, P, H, L, M, A, Q, T, and V; and X_7 comprises of A, S, D, and E; or X_1 comprises of Y and F; X_2 comprises of W, F, and Y; X_3 comprises of T and S; X_4 comprises G; X_5 comprises of I, T, V, Q, M, and H; X_6 comprises of K and R; and X_7 comprises of A, S, D, and E; or X_1 comprises of Y and F; X_2 comprises of W, F, and Y; X_3 comprises of T and S; X_4 comprises G; X_5 comprises of K and R; X_6 comprises of I, P, H, L, M, A, Q, T, and V; and X_7 comprises of A, S, D, and E; or X_1 comprises Y; X_2 comprises F; X_3 comprises T; X_4 comprises G; X_5 comprises of K, R, Q, M, H, and I; X_6 comprises of T, R, H, K, V, and L; and X_7 comprises E; or X_1 comprises Y; X_2 comprises F; X_3 comprises of T, S, H, and A; X_4 comprises G; X_5 comprises of K, R, and T; X_6 comprises of I, P, H, L, M, A, Q, and T; and X_7 comprises of D and N; or X_1 comprises Y; X_2 comprises W; X_3 comprises T; X_4 comprises G; X_5 comprises of K, M, V, and T; X_6 comprises of P, V, I, H, Q, T, M, and L; and X_7 comprises of E and D; or X_1 comprises of Y and F; X_2 comprises F; X_3 comprises of S, H, A, and Q; X_4 comprises G; X_5 comprises of K, Q, and R; X_6 comprises of I, V, L, K, H, R, Q, and M; and X_7 comprises E;

[0014] In the example embodiment, the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of X_1-X_2-X_3-X_4-X_5-X_6-X_7 wherein: X_1 comprises of K, R, S, G, N, T, M, Q, V, D, I, and E; X_2 comprises of D, S, N, M, L, G, P, E, and A; X_3 comprises of E, D, G, S, A, R, Q, T, P, and N; X_4 comprises of F, Y, T, V, S, N, A, G, and H; X_5 comprises of T, K, S, R, V, and H; X_6 comprises of T, S, G, V, A, K, R, N, D, E, and H; and X_7 comprises of F, W, and Y. In an example embodiment, X_1 comprises of K and R; X_2 comprises of D, S, and N; X_3 comprises E; X_4 comprises F; X_5 comprises of T, K, S, R, and V; X_6 comprises of T, S, G, and V; and X_7 comprises of F, W, and Y; or X_1 comprises of K and R; X_2 comprises D; X_3 comprises D; X_4 comprises of F and Y; X_5 comprises of T, S, V, and H; X_6 comprises of T, S, G, V, and A; and X_7 comprises of F, W, and Y; or X_1 comprises of S, R, G, N, T, M, and Q; X_2 comprises D; X_3 comprises G; X_4 comprises of T, V, S, N, and Y; X_5 comprises S; X_6 comprises of K and R; and X_7 comprises W; or X_1 comprises of R, V, D, I, Q, and K; X_2 comprises of M, L, and G; X_3 comprises of S, E, A, R, and Q; X_4 comprises D; X_5 comprises R; X_6 comprises of T, A, S, G, K, and N; and X_7 comprises W; or X_1 comprises of D, I, E, Q, V, S, and K; X_2 comprises of L, M, G, and P; X_3 comprises of E, A, S, D, Q, and T; X_4 comprises of S and A; X_5 comprises

R; X_6 comprises of D, S, E, T, G, and A; and X_7 comprises W; or X_1 comprises G; X_2 comprises of E, S, P, G, and A; X_3 comprises of D, E, P, and N; X_4 comprises of G, H, T, S, and N; X_5 comprises V; X_6 comprises of R, K, and S; and X_7 comprises of W and Y; or X_1 comprises R; X_2 comprises E; X_3 comprises of D, E, P, and N; X_4 comprises of G, H, T, S, and N; X_5 comprises V; X_6 comprises of R, K, and S; and X_7 comprises of W and Y; or X_1 comprises G; X_2 comprises of G and S; X_3 comprises of G, E, S, A, P, and D; X_4 comprises of T, G, and S; X_5 comprises S; X_6 comprises of S, T, H, K, R, A, and N; and X_7 comprises W. In an example embodiment, the n-mer motif is selected from the group consisting of KDEFTTF (SEQ ID NO: 36308), KDDFTTY (SEQ ID NO: 36336), RDEFTTY (SEQ ID NO: 36615), KDEFSTY (SEQ ID NO: 36390), RDEFTSF (SEQ ID NO: 36701), and REDHVSW (SEQ ID NO: 37067).

[0015] In an example embodiment, the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of X_1-X_2-X_3-X_4-X_5-X_6-X_7 wherein: X_1 comprises of V, I, R, N and D; X_2 comprises of A, G, and S; X_3 comprises of L, T, S, H, and G; X_4 comprises of K, R, and E; X_5 comprises G; X_6 comprises of W, R, A, and I; and X_7 comprises of D and G. In an example embodiment the n-mer motif is selected from the group consisiting of IALKGWD (SEQ ID NO: 36248), NALEGRD (SEQ ID NO: 36407), VALEGRD (SEQ ID NO: 36604), and VALKGWD (SEQ ID NO: 17701). In an example embodiment the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of X_1-X_2-X_3-X_4-X_5-X_6-X_7 wherein: X_1 comprises of L, M, and W; X_2 comprises of F, R, W, K, T, and Y; X_3 comprises of D and S; X_4 comprises G; X_5 comprises T; X_6 comprises of P, G, S, N, A, and R; and X_7 comprises of A, P, S, and Y.

[0016] In an example embodiment, the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of X_1-X_2-X_3-X_4-X_5-X_6-X_7 wherein: X_1 comprises of P, N, and K; X_2 comprises of Y and F; X_3 comprises of A; X_4 comprises of R and K; X_5 comprises of S; X_6 comprises of P, V, A, R, I, L, S, E; and X_7 comprises of E, D, M, and L.

[0017] In an example embodiment, a composition comprising a targeting moiety effective to increase transduction of CNS tissues comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of Z_1-X_1-Z_2-X_2-X_3-X_4-X_5 wherein Z_1 comprises Y, F, or L, Z_2 comprises S, R, or K, X_1 – X_5 are independently selected amino acids. In an example embodiment, X_1 optionally comprises of A, S, or H; X_2 optionally comprises of S, T, L, or I; X_3

optionally comprises N or G; X_4 optionally comprises G; X_5 optionally comprises of N, D, I, V, or R. In an example embodiment, the n-mer motif is selected from the group consisting of YSRIGPN (SEQ ID NO: 14632), YSRLNMN (SEQ ID NO: 14301), YSRLNKD (SEQ ID NO: 16577), and YHRLSNN (SEQ ID NO: 16636). In an example embodiment, the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of is X_1-H-X_2-L-X_3-X_4-X_5 wherein X_1 – X_5 are independently selected amino acids. In an example embodiment, the n-mer motif is VHRLQDK (SEQ ID NO: 16602) or LHALSHN (SEQ ID NO: 16608).

[0018] In an example embodiment, the n-mer motif is PSATNGV (SEQ ID NO: 20486), QVSTNGI (SEQ ID NO: 16021), SYSSNGV (SEQ ID NO: 16234), HQSSNGV (SEQ ID NO: 15978), VGSINGI (SEQ ID NO: 16200), AMSTNGR (SEQ ID NO: 16000), SASTNGV (SEQ ID NO: 16127), YMSTNGV (SEQ ID NO: 16042), YYSSNGV (SEQ ID NO: 16206), VHSTNGI (SEQ ID NO: 16134), PLSTNGV (SEQ ID NO: 16233), VYSTNGI (SEQ ID NO: 16059), IISTNGV (SEQ ID NO: 16054), RSVSSNGV (SEQ ID NO: 20502), YKSSNGV (SEQ ID NO: 16123), FRSTNGV (SEQ ID NO: 16070, and/or FVSTNGV (SEQ ID NO: 11162). In an example embodiment, the n-mer is selected from any one of the amino acid sequences of Tables 1-22, or any combination thereof. In an example embodiment, the n-mer motif is selected from the amino acid sequences of SEQ ID NO: 10952-20481 and 36241-42428. In an example embodiment, the targeting moiety is part of a viral capsid protein, including an AAV capsid.

[0019] In an example embodiment, the targeting moiety is inserted or substituted in loop IV, loop VIII, or both of an AAV capsid protein. In an example embodiment, the targeting moiety is IPFSRVNPDT (SEQ ID NO: 20285), LGFARTGAAD (SEQ ID NO: 20274), LGFTKSSGSD (SEQ ID NO: 20270), LRYSKTQGES (SEQ ID NO: 20266), SPYARSSAGV (SEQ ID NO: 20271), VGWSRLDLTT (SEQ ID NO: 20262). In an example embodiment, the n-mer is inserted between two amino acids of the one or more capsid proteins such that the n-mer is external to the AAV capsid when the protein comprising the n-mer is incorporated into the AAV capsid. In an example embodiment, the viral capsid protein is an AAV viral capsid protein. In an example embodiment, the n-mer is inserted between amino acids 588 and 589 of a capsid protein of AAV9, or in an analogous position of a capsid protein from AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAVrh8, AAV rh.74, or AAV rh. 10. In an example embodiment, the targeting

moiety is inserted between two consecutive amino acids within amino acids 451-460 of a capsid protein of AAV9, or in an analogous position of a capsid protein from AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAVrh8, AAV rh.74, or AAV rh. 10. In an example embodiment, the capsid protein is VP1, VP2, VP3, or a combination thereof.

[0020] In an example embodiment, the cargo is a polynucleotide, one or more polypeptides, a ribonucleoprotein complex. In an example embodiment, the polynucleotide encodes one or more polypeptides and/or a RNAi oligonucleotide. In an example embodiment, the polynucleotide encodes one or more polypeptides. In an example embodiment, the one or more polypeptides comprise an enzyme or an antibody, including therapeutically useful enzyme or antibody (or antigen-binding form thereof). In an example embodiment, the polynucleotide encodes a CRISPR-Cas system. In an exemplary embodiment, the cargo is a recombinant AAV genome that is incorporated into a capsid comprising the n-mer and the recombinant AAV genome encodes a therapeutic protein or nucleic acid, including being operably linked to an appropriate regulatory sequence that directs expression of the protein or nucleic acid in the target tissue. In an example embodiment, the polynucleotide is operably linked to a regulatory sequences that promotes expression in the CNS.

[0021] In one aspect, A viral capsid or viral particle, comprising any composition as described herein. In an example embodiment, the viral capsid or viral particle further comprises a recombinant viral genome, wherein the recombinant viral genome encodes a therapeutic protein or nucleic acid, control polypeptide or nucleic acid, and/or selectable marker polypeptide or nucleic acid. In an example embodiment, the therapeutic protein or nucleic acid, control polypeptide or nucleic acid, and/or selectable marker polypeptide or nucleic acid is operably linked to a regulatory sequence that promotes expression in the CNS. In an example embodiment, the viral capsid or viral particle is an AAV viral capsid or AAV viral particle. In an example embodiment, the recombinant viral genome is a recombinant AAV viral genome. In an example embodiment, the targeting moiety is inserted between amino acids of 588 and 589 of a capsid protein of AAV9, or in an analogous position of a capsid protein from AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAVrh8, AAV rh.74, or AAV rh. 10.

[0022] In one aspect, provided herein is a composition comprising one or more vectors encoding a targeting moiety effective to increase transduction of central nervous system tissues

(CNS). In an example embodiment, a vector system comprising one or more vectors, wherein at least one of the one or more vectors encodes a targeting moiety effective to increase transduction of central nervous system tissues (CNS) via binding to a transferrin receptor (TFRC), and optionally wherein at least one of the one or more vectors encodes a recombinant AAV genome comprising a transgene encoding a protein or a polypeptide Also provided is a composition comprising a polypeptide or viral capsid comprising the targeting moiety, *e.g.*, the n-mer that is effective to increase transduction of CNS tissues as described herein optionally further comprising a cargo, such as a recombinant AAV genome encoding a therapeutic protein or nucleic acid incorporated within, coupled to or otherwise associated with the targeting moiety containing polypeptide. In an example embodiment, the targeting moiety binds to the extracellular domain of TFRC. In an example embodiment, the targeting moiety binds to one or more of the apical, helical, and/or protease-like domain of the extracellular domain. In an example embodiment, the targeting moiety binds the apical domain. In an example embodiment, the targeting moiety comprises any n-mer motif described herein. In an example embodiment, the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of Z_1-X_1-Z_2-X_2-X_3-X_4-X_5 wherein Z_1 comprises of Y, F, and L, Z_2 comprises of S, R, and K, X_1 – X_5 are independently selected amino acids. In an example embodiment, X_1 optionally comprises of A, S, or H; X_2 optionally comprises of S, T, L, or I; X_3 optionally comprises N or G; X_4 optionally comprises G; X_5 optionally comprises of N, D, I, V, or R. In an example embodiment, the n-mer motif is selected from the group consisting of YSRIGPN (SEQ ID NO: 14632), YSRLNMN (SEQ ID NO: 14301), YSRLNKD (SEQ ID NO: 16577), and YHRLSNN (SEQ ID NO: 16636).

[0023] In an example embodiment, the targeting moiety encoded by a vector system or incorporated into a viral vector, including an AAV capsid, comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of is X_1-H-X_2-L-X_3-X_4-X_5 wherein X_1 – X_5 are independently selected amino acids. In an example embodiment, the n-mer motif is VHRLQDK (SEQ ID NO: 16602) or LHALSHN (SEQ ID NO: 16608). In an example embodiment, the n-mer motif is comprises PSATNGV (SEQ ID NO: 20486), QVSTNGI (SEQ ID NO: 16021), SYSSNGV (SEQ ID NO: 16234), HQSSNGV (SEQ ID NO: 15978), VGSINGI (SEQ ID NO: 16199), AMSTNGR (SEQ ID NO: 16000), SASTNGV (SEQ ID NO: 16127), YMSTNGV (SEQ ID NO: 16042), YYSSNGV (SEQ ID NO: 16206), VHSTNGI (SEQ ID NO:

16134), PLSTNGV (SEQ ID NO: 16233), VYSTNGI (SEQ ID NO: 16059), IISTNGV (SEQ ID NO: 16054), RSVSSNGV (SEQ ID NO: 20502), YKSSNGV (SEQ ID NO: 16123), FRSTNGV (SEQ ID NO: 16070), and/or FVSTNGV (SEQ ID NO: 11162). In an example embodiment, provided herein are vectors or recombinant polypeptides, including, engineered AAV capsids wherein the n-mer is selected from any one as listed in any of Tables 1-22, or any combination thereof. In an example embodiment, provided herein are vectors wherein the n-mer motif is selected from SEQ ID NOS: 10952-20481 and 36241-42428. In an example embodiment, provided herein are vectors which encode the targeting moiety is part of a viral capsid protein.

[0024] In an example embodiment, the targeting moiety is inserted or substituted in loop IV and/or loop VIII of an AAV capsid protein. In an example embodiment, the targeting moiety is IPFSRVNPDT (SEQ ID NO: 20285), LGFARTGAAD (SEQ ID NO: 20274), LGFTKSSGSD (SEQ ID NO: 20270), LRYSKTQGES (SEQ ID NO: 20266), SPYARSSAGV (SEQ ID NO: 20271), VGWSRLDLTT (SEQ ID NO: 20262). In an example embodiment, provided herein are vectors wherein the n-mer is inserted between two amino acids of the one or more capsid proteins such that the n-mer is external to the AAV capsid. In an example embodiment, provided herein are vectors wherein the viral capsid protein is an AAV viral capsid protein. In an example embodiment, provided herein are vectors wherein the n-mer is inserted between amino acids 588 and 589 of a capsid protein of AAV9, or in an analogous position of a capsid protein from AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAVrh8, AAV rh.74, or AAV rh. 10. In an example embodiment, the targeting moiety is inserted between two amino acids within amino acids 451-460 of a capsid protein of AAV9, or in an analogous position of a capsid protein from AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAVrh8, AAV rh.74, or AAV rh. 10. In an example embodiment, provided herein are vectors wherein the capsid protein is VP1, VP2, VP3, or a combination thereof.

[0025] In an example embodiment, provided herein are vectors wherein the cargo is a polynucleotide, one or more polypeptides, a ribonucleoprotein complex. In an example embodiment, provided herein are vectors wherein the polynucleotide encodes one or more polypeptides and/or a RNAi oligonucleotide. In an example embodiment, provided herein are vectors wherein the polynucleotide encodes one or more polypeptides. In an example embodiment, provided herein are vectors wherein the one or more polypeptides comprise enzymes or antibodies.

In an example embodiment, the polynucleotide encodes a CRISPR-Cas system. In an example embodiment, the polynucleotide is operably linked to a regulatory sequence that promotes expression in the CNS.

[0026] In one aspect, provided herein is a composition comprising a polypeptide encoded or produced by the vector systems described herein. In an example embodiment, the polypide is a capsid protein, optionally an AAV capsid polypeptide. In one aspect, provided herein is a composition comprising a particle produced by the vector systems described herein. In an example embodiment, the particle is a viral particle, optionally an AAV particle. In one aspect, provided herein is a composition comprising a cell comprising the composition, vector, polypeptide, or particle described herein.

[0027] In one aspect, provided herein is a method of delivering one or more cargos to the CNS, comprising: administering, in vivo or in vitro, the engineered AAV capsid as described herein, or the vector as described herein. In an example embodiment, provided herein a method of delivery wherein the cargo is a recombinant AAV genome which encodes an RNAi oligonucleotide, a polynucleotide encoding a polypeptide, or a polypeptide, optionally operably linked to regulatory sequences that promote expression in the target tissue (such as the CNS). In an example embodiment, provided herein a method of delivery wherein the polypeptide includes an enzyme or antibody. In an example embodiment, provided herein a method of delivery wherein the cargo encodes a Cas polypeptide, a guide molecule, or both. In an example embodiment, provided herein a method of delivery wherein the cargo encodes a nuclease or a nucleic acid component of a RNA-guided nuclease. In an example embodiment, provided herein a method of delivery wherein the cargo is one or more polynucleotides encoding the nuclease and nucleic acid component of a RNA-guided nuclease.

[0028] In one aspect, a method of creating humanized transgenic non-human animals comprising: delivering to one or more cells of a non-human animal a vector system or a recombinant viral particle comprising a recombinant viral genome, wherein the vector system or recombinant viral genome encodes a human transferrin polypeptide, wherein the encoded human transferrin polypeptide is under the control of a tissue-specific promoter or miRNA binding element that has selective activity in the desired cell, tissue, or organ.

[0029] In example embodiments, the one or more cells are endothelial cells. In an example embodiment, the one or more cells are CNS cells. In example embodiments, the one or more cells are of the CNS vasculature, lungs, kidneys, liver, or any combination thereof. In example embodiments, the endothelial cells are of the CNS vasculature. In an example embodiment, the recombinant viral particle, optionally an AAV viral particle, comprises a capsid polypeptide, optionally an AAV capsid polypeptide, wherein the capsid polypeptide comprises a CNS specific n-mer motif. In an example embodiment, the CNS-specific n-mer motif comprises X1-N-X3-X4-X5-X6-X7, wherein X5 is independently selected from K or R, and X1, X3, X4, X6 and X7 are independently selected from any amino acid, optionally wherein the overall charge of the n-mer motif at neutral pH is between 0 and + 2. In an example embodiment, the CNS-specific n-mer motif comprises or consists of NNSTRGG (SEQ ID NO: 42429), GNSARNI (SEQ ID NO: 42430), and GNSVRDF (SEQ ID NO: 42431). In an example embodiment, the transgenic non-human animal is a rodent, optionally a mouse.

[0030] In one aspect, provided herein is a humanized transgenic non-human animal comprising: one or more cells expressing a human transferrin polypeptide, optionally wherein the one or more cells are CNS cells. In an example embodiment, the transgenic non-human animal is a rodent, optionally a mouse. A humanized transgenic non-human animal produced by any method described herein. In an example embodiment, the humanized non-human animal has a suppressed immune system.

[0031] In one aspect, provided herein is a method of screening n-mer motifs capable of conferring transduction of central nervous system (CNS) tissues via binding to a transferrin receptor (TFRC) in humanized transgenic non-human animals comprising: introducing one or more compositions comprising a candidate n-mer motif to humanized non-human transgenic animal described herein; and detecting binding of the compositions that bind to a transferrin receptor (TFRC) and/or detecting transduction or uptake by one or more CNS cells of the humanized transgenic non-human animal. In an example embodiment, the candidate n-mer motif comprises or consists of X1-N-X3-X4-X5-X6-X7, wherein X5 is independently selected from K or R, and X1, X3, X4, X6 and X7 are independently selected from any amino acid, optionally wherein the overall charge of the n-mer motif at neutral pH is between 0 and + 2. In an example

embodiment, the composition is a viral particle comprising one or more capsid proteins each comprising the candidate n-mer motif.

[0032] In an example embodiment, the viral particle is an AAV viral particle and the one or more capsid proteins is an AAV capsid protein, optionally wherein the candidate n-mer motif is inserted in between amino acids 588-589 of an AAV9 capsid polypeptide or in an analogous position of a capsid protein from AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAVrh8, AAV rh.74, or AAV rh. 10. In an example embodiment, at least one of the one or more compositions furthers comprises a cargo. In an example embodiment, the cargo is or encodes a therapeutic nucleic acid or polypeptide, a selectable marker, or a control polypeptide or nucleic acid.

[0033] In one aspect, a method of *in vivo* modeling comprising introducing a second vector system capable of targeting a transgenic polypeptide in a transgenic non-human animal as described herein. In example embodiments, the non-human animal has a suppressed immune system.

[0034] The method of screening vector systems capable of transduction of central nervous system (CNS) tissues via binding to a transferrin receptor (TFRC) in humanized transgenic non-human animals comprising: (a) introducing a plurality of vector systems to one or more humanized transgenic non-human animal and (b) detecting the vector systems that bind to a transferrin receptor (TFRC).

[0035] These and other aspects, objects, features, and advantages of the example embodiments will become apparent to those having ordinary skill in the art upon consideration of the following detailed description of example embodiments.

BRIEF DESCRIPTION OF THE DRAWINGS

[0036] An understanding of the features and advantages of the present invention will be obtained by reference to the following detailed description that sets forth illustrative embodiments, in which the principles of the invention may be utilized, and the accompanying drawings of which:

[0037] **FIG. 1** – Structural model of AAV9 highlighting the regions modified. The model highlights the loop IV residues where substitution mutagenesis was performed in some examples

(blue) and the residues (AA588-589) between which loop VIII insertions were made (magenta) in other examples. The K449R mutation is shown in green.

[0038] **FIG. 2A-2B** – Capsids that bind human TFRC are capable of dramatically enhanced binding and transduction of CHO cells expressing human TFRC. The indicated AAVs packaging an AAV-CAG-GFP-2A-Luciferase-WPRE-pA genome were administered to control CHO cells or CHO cells expressing human TFRC (hTFRC) at 10K vg/cell. (A). The graph shows binding to the indicated CHO cells with the indicated AAV. (B) The graph shows the transduction efficiency normalized to AAV for the indicated AAV. Transduction was measured 24 hours after virus administration with a luciferase reporter assay.

[0039] **FIG. 3** – Surface human TFRC protein levels on hCMEC/D3 cells with a lentivirus expressing TFRC. Cells transduced with the indicated MOI of VSV-G pseudotyped lentivirus expressing human TFRC were incubated at 4C with an antibody that binds TFRC. The cells were then fixed without membrane permeabilization and immunostained with anti-TFRC (ThermoFisher, cat# 14-0719-82) to assess the levels of cell surface exposed TFRC. Images show immunostaining (green) and cell nuclei (blue).

[0040] **FIG. 4** – TFRC binding capsids more efficiently transduce hCMEC/D3 cells, and binding and transduction of hCMEC/D3 cells are further increased by elevating TFRC expression by lentiviral delivery of TFRC. The indicated AAVs were administered to both control and human TFRC expressing hCMEC/D3 cells at 5,000 vg/cell. Binding and transduction were assessed as described in Figure 2.

[0041] **FIG. 5A-5B** – The enhanced transduction of hCMEC/D3 cells by AAV-BI19 relative to AAV9 is blocked by a human TFRC antibody. The AAV9 or AAV-BI19 were used to package AAV-CAG-GFP-2A-Luciferase-WPRE-pA genome. The indicated AAVs were administered to hCMEC/D3 cells at 2,000K vg/cell in the absence or presence of the indicated concentration of monoclonal anti-TFRC antibody. Transduction (A) was assessed 24 hours after virus administration, and binding (B) was assessed at 1 hour.

[0042] **FIG. 6** – Expression of human TFRC in mouse brain endothelial cells *in vivo* increases CNS transduction by AAV-BI19. (Left) The schematic shows the experimental design. In the 2-step transduction assay, step one is the delivery of the target receptor gene to brain endothelial cells in NSG mice using intravenous administration of AAV-BI30 (Krolak *et al. Nature*

Cardiovascular Research 2022). In this experiment, the target receptor is human TFRC or mouse LY6A, which is used as a positive control (LY6A is required for efficient entry of AAV-PHP.eB to the CNS and is deficient in NSG mice. 7 Days later, the second virus (either AAV-BI19:CAG-mScarlet, which binds hTFRC, or AAV-PHP.eB:CAG-mScarlet, which binds LY6A) or is delivered. Delivering AAV-BI19 to animals that received the non-target receptor, AAV-BI30:LY6A (upper right), and AAV-PHP.eB to animals that received hTFRC serve as negative controls (lower left). CNS transduction by AAV-BI19 is enhanced in animals that previously received the AAV-BI19 receptor hTFRC (lower right). Images show transduction in the brains of mice 3 weeks after delivery of the second virus. All AAVs were delivered at 1e11 vg/animal.

[0043] **FIG. 7** – Representative SDS-PAGE showing Fc-control (Fc-ctrl), human TFRC-Fc (hTFRC), mouse TFRC-Fc (mTFRC), and marmoset TFRC-Fc (marTFRC). The indicated proteins were produced in HEK293 cells and pulled down with ProA-magnetic beads. The proteins were then separated by SDS-PAGE and stained for total protein using SyPro Ruby.

[0044] **FIG. 8A-8B** – Clustering analysis of 7-mer sequences that bind human TFRC. AAV 7-mer insertions found to interact with human TFRC were found to form distinct sequence clusters. (A) Sequences were one-hot encoded, projected with UMAP, and clustered with a Gaussian mixture model (k = 30). (B) Cluster sequence logos show the AA frequency in each cluster, the cluster number (k) and the number (n) of sequences per cluster. A list of sequences in each cluster is provided in Table 12.

[0045] **FIG. 9** – Individual binding to CHO cells stably expressing TFRC.

[0046] **FIG. 10** – The enhanced transduction of hCMEC/D3 cells by BI-19 relative to AAV9 is blocked by an anti-human TFRC antibody.

[0047] **FIG. 11** – Overexpression of TFRC on mouse brain vasculature in vivo increases BI-19 transduction in the CNS.

[0048] **FIG. 12A-12B** – BI19 is actively transported across a human brain vascular layer in vitro. hCMEC cells were cultured until confluent on a Transwell insert. A pool of viruses was added to the top chamber, and the fraction of the vector found in the bottom chamber was assessed at the indicated time by qPCR. Virus was added to cells at 37C or at 4C. The 4C control demonstrates the amount of the viral particles that enter the bottom chamber without being actively

transported. (B) The graphs provide the fraction of AAV genomes found in the bottom chamber at 37C divided by the fraction of the AAV genomes found in the bottom chamber at 4C.

[0049] **FIG. 13A-13C** – Expression of human TFRC in mouse brain endothelial cells in vivo increases CNS transduction by AAV-BI19. (A) The schematic shows the experimental design. In the 2-step transduction assay, step one is the delivery of the target receptor gene to brain endothelial cells in NSG mice using intravenous administration of AAV-BI30 (Krolak et al. Nature Cardiovascular Research 2022). In this experiment, the target receptor is human TFRC or mouse LY6A, which is used as a positive control (LY6A is required for efficient entry of AAV-PHP.eB to the CNS and is deficient in NSG mice). (B) Images show sagittal sections of the mouse brain transduced by AAV-PHP.eB (left) or AAV-BI19 (right) in mice made to express mouse LY6A or human TFRC through delivery of the genes encoding these proteins by AAV-BI30. AAV-BI30:CAG-human TFRC or AAV-BI30:CAG-mouse LY6A vectors were administered intravenously to adult NSG mice at 1e11 vg/animal. 28 days later, the second virus, either AAV-BI19, which binds hTFRC or AAV-PHP.eB, which binds mouse LY6A, was delivered at a dose of 5e11 vg/animal. Both vectors packaged the same AAV genome (AAV-CAG-NLS-mScarlet-2A-Luciferase-pA). CNS transduction by AAV-BI19 is enhanced in animals that previously received the AAV-BI19 receptor hTFRC (lower right). Delivering AAV-BI19 to animals that received the non-target receptor, AAV-BI30:LY6A (upper right), and AAV-PHP.eB to animals that received hTFRC serve as negative controls (lower left). Images show transduction (assessed by imaging native mScarlet fluorescence) in the brains of mice three weeks after delivery of AAV-PHP.eB or AAV-BI19.

[0050] **FIG. 14A-14D** – AAV-BI19 more efficiently crosses the BBB and transduces neurons throughout the brain in mice where the extracellular domain of human TFRC was knocked into the mouse Tfrc gene. (A-B) 8e11 vg/mouse of AAV-BI19 or AAV9 packaging CAG-NLS-mScarlet-2A-Luciferase-pA was systemically administered (injection into the retro-orbital sinus) to adult huTFRC KI mice (B-hTFRC, CytoBiogen). Expression was assessed seven days after AAV administration. (A-B) The images show matched exposures of native nuclear mScarlet expression in whole sagittal brain sections from homozygous B-hTFRC mice after transduction with AAV-BI19 (A) or AAV9 (B). (C-D) AAV-BI19 (C) or AAV9 (D) transduction of neurons (NeuN immunostaining) in the brain of huTFRC KI mice. The mScarlet exposures in C and D

were not matched. The mScarlet exposures in D were longer in order to show transduction by AAV9.

[0051] **FIG. 15** – AAV-BI19 transduces human brain endothelial cells in the presence of human holo-Transferrin. Cells from the hCMEC human brain endothelial cell line were preincubated with or without human Transferrin at the indicated concentration and then transduced by AAV-BI19 or AAV9 packaging CAG-GFP-2A-Luciferase (5000 vg/cell) and assessed for transduction 24 hours later by measuring Luciferase activity. The graph shows transduction normalized relative to AAV9 in the absence of human Transferrin.

[0052] **FIG. 16A-16E** – AAV9 can be reprogrammed to bind human TfR1. (16A) AAV9-based 7-mer NNK capsid libraries (random 7-mer insertion between residues 588–589 in VP1) were screened for selective binding of huTfR1 as an Fc fusion protein or when transiently overexpressed on HEK293 and CHO cells. (16B) Four huTfR1-binding variants that shared a common motif were identified. Each variant was individually produced to carry a CAG-NLS-mScarlet-p2A-Luc-WPRE construct. They exhibited enhanced species-specific binding (16C) and transduction (16D) of CHO cells stably expressing *TFRC* from human but not macaque, marmoset, or mouse . For the binding assay, each cell line was seeded at 30,000 cells per well and, 24 hours later, each well was subjected to a media change with the fresh media that contained each AAV9 variant carrying CAG-NLS-mScarlet-P2A-Luciferase-SV40-WPRE at 3,000 vg/cell. The cells were maintained at 4°C with gentle rocking for one hour and washes with PBS. Then, DNA was extracted and subjected to qPCR targeting mScarlet. For the transduction assay, each cell line was seeded at 100,000 cells per well and, 24 hours later, each well was subjected to a media change with the fresh media that contained each AAV9 variant carrying CAG-NLS-mScarlet-P2A-Luciferase-SV40-WPRE at 3,000 vg/cell. The cells were maintained at 37°C with 5% CO_2 for 24 hours. Then, transduction was measured using the britelite Plus reporter gene assay system. A one-way ANOVA test was performed to assess significant differences; **** indicates $P < 0.0001$. (16E) Characterization of the binding kinetics between AAV-BI19 and TfR1 in the presence or absence of Holo-Tf. Fitting of Bio-Layer Interferometry (BLI) traces of immobilized AAV-BI19 capsids incubated at 30°C with 6.25–200 nM of Peptidisc-reconstituted huTfR1 showed a strong binding between the variant and the receptor (top left), whereas AAV9 capsids demonstrated no significant association with huTfR1 (top right). The effect of Holo-Transferrin (Holo-Tf) on AAV-

BI19 binding was tested by incubation of AAV-BI19 capsids with 6.25–200 nM of Peptidisc-reconstituted huTfR1 in the presence of a molar excess of 200 nM Holo-Tf (bottom left). AAV-BI19 binds to huTfR1-in the presence of Holo-Tf. AAV9 showed no significant binding to huTfR1 regardless of the presence of Holo-Tf (bottom right).

[0053] **FIG. 17A-17B** – TfR1 expression in CHO cells. Applicants established stable CHO cell lines expressing human, macaque, marmoset, or mouse TFRC via random lentiviral integration of each exogenous construct under the control of an EF-1 alpha promoter. (17A) RNA was extracted from each cell line, reverse transcribed, and the cDNA was subjected to qPCR using species-specific primers (Table 23). (17B) Each cell line was immunostained with anti-TfR1 antibodies: abcam ab84036, polyclonal, targeting the N-terminal (mostly intracellular) domain of huTfR1, or OKT9, monoclonal, targeting the apical domain of huTfR1.

[0054] **FIG. 18A-18D** – TfR1-targeted capsids transduce human brain endothelial cells via interactions with huTfR1. The TfR1-targeted variants exhibited enhanced binding (18A) and transduction (18B) of human brain microvascular endothelial cells (hBMVEC) and hCMEC/D3 cells. For the binding assay, hBMVEC or hCMEC/D3 cells were seeded at 15,000 or 30,000 cells per well, respectively, and, 24 hours later, each well was subjected to a media change with the fresh media that contained each AAV9 variant carrying CAG-NLS-mScarlet-P2A-Luciferase-SV40-WPRE at 12,000 or 6,000 vg/cell for hBMVEC or hCMEC/D3 cells, respectively. The cells were maintained at 4°C with gentle rocking for one hour. Then, DNA was extracted and subjected to qPCR targeting mScarlet. For the transduction assay, hBMVEC or hCMEC/D3 cells were seeded at 5,000 or 10,000 cells per well, respectively, and, 24 hours later, each well was subjected to a media change with the fresh media that contained each AAV9 variant carrying CAG-NLS-mScarlet-P2A-Luciferase-SV40-WPRE at 12,000 or 6,000 vg/cell for hBMVEC or hCMEC/D3 cells, respectively. Transduction was measured using the britelite Plus reporter gene assay system 24 hours after AAV addition. A two-tailed t-test was performed to assess significant differences; ****, ***, **, and * indicate $P < 0.0001$, < 0.001, < 0.01, and < 0.05 respectively. (18C) AAV-BI19 transduction of hCMEC/D3 cells was inhibited by the OKT9 antibody that targets the huTfR1 apical domain but not an antibody that targets the Transferrin binding domain of huTfR1. The hCMEC/D3 cells were seeded at 7,500 cells per well. Two days later, 100 µL of media with 3e8 vg/mL of the indicated AAV and the specified concentration of OKT9 or R&D AF2474 antibody

was transferred to each well. Transduction was measured 24 hours later using the britelite Plus reporter gene assay system. A two-way ANOVA test was performed to assess significant differences; **** indicates $P < 0.0001$. (18D) AAV-BI19 is actively transported across an endothelial cell barrier. Transwell inserts were seeded with hCMEC cells and grown to confluence. Barcoded AAV-BI19, AAV9, and AAV2 were pooled and applied to the upper chamber of the transwell at 25,000 vg/cell/AAV in media heated to 37°C or chilled to 4°C as indicated. The amount of virus transported across the transwell at three hours at the indicated temperatures was quantified by qPCR and normalized to the corresponding starting titer. Data is represented as four replicates ± SEM. An unpaired t-test was performed to assess significant differences; * indicates $P < 0.05$ and ns indicates no statistical difference. A dashed line is drawn at 10,000 vg, below which there is reduced ability to accurately quantify the amount of virus.

[0055] **FIG. 19A-19D** – AAV-BI19 binding to the TfR1 apical domain depends on Y247 and T248 residues present in the human protein but not macaque or mouse. (19A) Alignment of the human, macaque, and marmoset TfR1 apical domain amino acid sequences from residue 200-380. The differences from the human sequence are highlighted in blue. Amino acid differences between human and macaque proteins are highlighted in four groups (colored outlines, 19A) and on Alphafold2 structural models (19B). (19C) CHO cells were transiently transfected to express the wild type human TfR1 (huTfR1) or variants with the indicated substitutions where the human residue was replaced by the corresponding macaque residue or (19D) the wild type macaque TfR1 (macTfR1) or a variant with D247Y and S248T substitutions (n=4 replicate transfections per plasmid ± SEM shown). Cells were maintained at 37°C with 5% CO_2. At 24 hours post-transfection, AAV-BI19 or AAV9 encoding ssCAG-NLS-mScarlet-P2A-Lucierase-pA was applied at 10,000 vg/cell. After 24 hours, viral transduction was measured using the britelite Plus reporter gene assay system. For (19C), a one-way ANOVA was performed to determine significant differences in transduction among the groups using the wild type huTfR1 as the control. To account for multiple comparisons, a Dunnett's correction was applied. Only those comparisons with a $P \leq 0.05$ are reported with an asterisk (* or **** indicate $P \leq 0.05$ or ≤ 0.0001, respectively). For (19D), an unpaired two-tailed t-test was performed between the two groups (** indicates $P \leq 0.01$).

[0056] **FIG. 20** – TfR1 expression in B-hTFR1 mice. RNA was extracted from the cortex and spinal cord regions of C57BL/6J or B-hTFR1 mice that had been treated with either AAV9 or

AAV-BI19. The RNA was reversed transcribed and the cDNA was subjected to qPCR using primers spanning exon 1 and exon 2 of the mouse *Tfrc* gene (Table 23). Note that, in B-hTFR1 mice, exons 4–19 of the mouse *Tfrc* gene that encode the extracellular region have been replaced by the corresponding human exons. TfR1 expression was not found to be significantly different between C57BL/6J and B-hTFR1 mice (two-way ANOVA).

[0057] FIG. 21A-21I – AAV-BI19 efficiently delivers genes to the CNS in knock-in mice expressing the huTfR1 extracellular domain. AAV-BI19 or AAV9 encoding ssCAG-NLS-mScarlet-P2A-Luciferase-pA was intravenously injected into adult female C57BL/6J or C57BL/6-Tfr1tm1TFR1/Bcgen (B-hTFR1) mice at 5 x 10^{11} vg/mouse. After three weeks, the (21A) biodistribution of vector genomes per mouse genome, (21B) mScarlet transcript levels relative to AAV9 in C57BL/6J mice, and (21C) luciferase activity relative to AAV9 in C57BL/6J were measured within different organs. For AAV9 in C57BL/6J and AAV-BI19 in B-hTFR1, n = 4 mice per group, ± SEM shown. For AAV9 in B-hTFR1 and AAV-BI19 in C57BL/6J n = 3 mice per group, ± SEM shown. A two-way ANOVA was performed to determine significant differences within organs among the four groups of mice with AAV-BI19 in B-hTFR1 as the main comparison group and using a Bonferroni multiple comparison correction; ****, ***, **, and * indicate $P \leq 0.0001$, $P \leq 0.001$, $P \leq 0.01$, and $P \leq 0.05$, respectively, between AAV-BI19 in B-hTFR1 and each of the other groups of mice. Representative (21D) whole brain and (21E) spinal cord images of the C57BL/6J and B-hTFR1 mice treated with AAV-BI19 or AAV9 encoding ssCAG-NLS-mScarlet-P2A-Luciferase-pA are shown at a dose of 5e11 vg per mouse. Native mScarlet fluorescence was assessed three weeks post injection. Images show the cells transduced by AAV-BI19 overlaid with (21F) $NeuN^+$ neurons or (21G) $SOX9^+$ stained cells in the cortex, thalamus, and striatum of B-hTFR1 mice. The percentage of (21H) $NeuN^+$ neurons or (21I) $SOX9^+$ astrocytes that expressed mScarlet in the cortex, striatum, and thalamus were assessed (n = 3 mice for AAV9 in B-hTFR1 and AAV-BI19 in C57BL/6J mice, n = 4 mice for AAV9 in C57BL/6J and AAV-BI19 in B-hTFR1 mice; error bars indicate ± SEM). A two-way ANOVA was performed to determine significant differences in transduction within specific brain regions among the four groups of mice across the two capsids with AAV-BI19 in B-hTFR1 as the main comparison group and using a Bonferroni multiple comparison correction. The **** indicates $P \leq 0.0001$ between AAV-BI19 in B-hTFR1

and each of the three other groups of mice (AAV9 in C57BL/6J, AAV9 in B-hTFR1, and AAV-BI19 in C57BL/6J).

[0058] **FIG. 22A-22B** – AAV-BI19 exhibits similar transduction to AAV9 in the liver and dorsal root ganglion in B-hTFR1 mice. ssAAV-BI19:CAG-NLS-mScarlet-P2A-Lucierase-pA or ssAAV9:CAG-NLS-mScarlet-P2A-Luciferase-pA was intravenously injected into adult female C57BL/6J or B-hTFR1 mice at a dose of 5 x 10^{11} vg/mouse. At three weeks post-injection, native fluorescence was assessed in the (22A) liver and (22B) dorsal root ganglion.

[0059] **FIG. 23** – Expression of huTfR1 in mouse brain endothelial cells *in vivo* increases CNS transduction by AAV-BI19. In the 2-step transduction assay, step one is the delivery of the target receptor gene to brain endothelial cells in NSG mice using intravenous administration of AAV-BI30 (Krolak, T., et al. (2022). A high-efficiency AAV for endothelial cell transduction throughout the central nervous system. Nature Cardiovascular Research *1*, 389–400.). In this experiment, the target receptors were human TfR1 (huTfR1, encoded by the *TFRC* gene) or mouse LY6A, which was used as a positive control as LY6A is required for the efficient entry of AAV-PHP.eB into the CNS and is deficient in NSG mice. AAV-BI30 was systemically administered at 1e11 vg/mouse to deliver AAV-CAG-hTFRC-WPRE-3x-miR122-pA (top) or AAV-CAG-LY6A-WPRE-3x-miR122-pA (bottom). At 28 days post-injection, the second virus (5e11 vg/mL of either AAV-BI19:CAG-mScarlet, which binds huTfR1 (left), or AAV-PHP.eB:CAG-mScarlet, which binds LY6A (right) was systemically administered. This experiment was performed with three mice per condition. Representative images show the AAV transduction in sagittal mouse brain sections of mice three weeks after the delivery of the second virus. CNS transduction by AAV-PHP.eB and AAV-BI19 was enhanced in the animals that were previously treated with AAV-BI30:LY6A (bottom right) or AAV-BI30:hTFRC (top left), respectively. AAV-BI19 did not exhibit enhanced CNS transduction in the animals that had received the non-target receptor, AAV-BI30:LY6A (bottom left). As a negative control, AAV-PHP.eB also did not exhibit enhanced CNS transduction in the animals that had received AAV-BI30:hTFRC (top right).

[0060] **FIG. 24** – The vast majority of capsids with 7-mer sequences conforming to the motif families and genera defined in Table 21 bind human TFR1-Fc fusion proteins. For each family/genus, the percentage of sequences contained within the motif that were measured in the library is provided within the x-axis label.

[0061] **FIG. 25** – Extensive functional characterization of capsids that bind human TFR1. Capsids were selected based on human TFR1-Fc binding and enhanced transduction activity in one or more of the following in vivo assays: transduction of the B-hTFR1 KI mouse brain or spinal cord transduction or the 2-step assay with BI30:CAG-humanTFRC. The capsids with enhanced in vivo tropisms in human TFRC expressing mice, were then assessed for additional functions relevant to the selection of top capsid candidates. Note the vast majority of selected sequences showed elevated enrichment relative to AAV9 for the following assays: B-hTFR1 KI (brain and spinal cord), 2-step hTFRC brain, human TFR1-Fc binding, binding to CHO cells expressing human TFRC (CHO-hTFRC), and binding to hCMEC and hCMEC-hTFRC cells. In contrast these capsids were not positively enriched for transduction of control mice (2-step mice transduced with AAV-BI30-CAG-LY6A). Left, AAV was encoded into the library with 5 nucleotide sequences at 1x, 10x, 100x copies relative to other capsid sequences in the library to facilitate accurate comparisons in assays where AAV9 at 1x performs poorly, e.g., in vivo CNS transduction.

[0062] The figures herein are for illustrative purposes only and are not necessarily drawn to scale.

DETAILED DESCRIPTION OF THE EXAMPLE EMBODIMENTS

General Definitions

[0063] Unless defined otherwise, technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure pertains. Definitions of common terms and techniques in molecular biology may be found in Molecular Cloning: A Laboratory Manual, 2nd edition (1989) (Sambrook, Fritsch, and Maniatis); Molecular Cloning: A Laboratory Manual, 4th edition (2012) (Green and Sambrook); Current Protocols in Molecular Biology (1987) (F.M. Ausubel et al. eds.); the series Methods in Enzymology (Academic Press, Inc.): PCR 2: A Practical Approach (1995) (M.J. MacPherson, B.D. Hames, and G.R. Taylor eds.): Antibodies, A Laboratory Manual (1988) (Harlow and Lane, eds.): Antibodies A Laboratory Manual, 2nd edition 2013 (E.A. Greenfield ed.); Animal Cell Culture (1987) (R.I. Freshney, ed.); Benjamin Lewin, Genes IX, published by Jones and Bartlet, 2008 (ISBN 0763752223); Kendrew *et al.* (eds.), The Encyclopedia of Molecular Biology, published by Blackwell Science Ltd., 1994 (ISBN 0632021829); Robert A. Meyers (ed.), Molecular Biology

and Biotechnology: a Comprehensive Desk Reference, published by VCH Publishers, Inc., 1995 (ISBN 9780471185710); Singleton *et al.*, Dictionary of Microbiology and Molecular Biology 2nd ed., J. Wiley & Sons (New York, N.Y. 1994), March, Advanced Organic Chemistry Reactions, Mechanisms and Structure 4th ed., John Wiley & Sons (New York, N.Y. 1992); and Marten H. Hofker and Jan van Deursen, Transgenic Mouse Methods and Protocols, 2nd edition (2011).

[0064] As used herein, the singular forms "a", "an", and "the" include both singular and plural referents unless the context clearly dictates otherwise.

[0065] The term "optional" or "optionally" means that the subsequent described event, circumstance or substituent may or may not occur, and that the description includes instances where the event or circumstance occurs and instances where it does not.

[0066] The recitation of numerical ranges by endpoints includes all numbers and fractions subsumed within the respective ranges, as well as the recited endpoints.

[0067] The terms "about" or "approximately" as used herein when referring to a measurable value such as a parameter, an amount, a temporal duration, and the like, are meant to encompass variations of and from the specified value, such as variations of +/-10% or less, +/-5% or less, +/-1% or less, and +/-0.1% or less of and from the specified value, insofar such variations are appropriate to perform in the disclosed invention. It is to be understood that the value to which the modifier "about" or "approximately" refers is itself also specifically, and preferably, disclosed.

[0068] As used herein, a "biological sample" may contain whole cells and/or live cells and/or cell debris. The biological sample may contain (or be derived from) a "bodily fluid". The present invention encompasses embodiments wherein the bodily fluid is selected from amniotic fluid, aqueous humour, vitreous humour, bile, blood serum, breast milk, cerebrospinal fluid, cerumen (earwax), chyle, chyme, endolymph, perilymph, exudates, feces, female ejaculate, gastric acid, gastric juice, lymph, mucus (including nasal drainage and phlegm), pericardial fluid, peritoneal fluid, pleural fluid, pus, rheum, saliva, sebum (skin oil), semen, sputum, synovial fluid, sweat, tears, urine, vaginal secretion, vomit and mixtures of one or more thereof. Biological samples include cell cultures, bodily fluids, cell cultures from bodily fluids. Bodily fluids may be obtained from a mammal organism, for example by puncture, or other collecting or sampling procedures.

[0069] The terms "subject," "individual," and "patient" are used interchangeably herein to refer to a vertebrate, preferably a mammal, more preferably a human. Mammals include, but are

not limited to, murines, simians, humans, farm animals, sport animals, and pets. Tissues, cells and their progeny of a biological entity obtained in vivo or cultured in vitro are also encompassed.

[0070] Various embodiments are described hereinafter. It should be noted that the specific embodiments are not intended as an exhaustive description or as a limitation to the broader aspects discussed herein. One aspect described in conjunction with a particular embodiment is not necessarily limited to that embodiment and can be practiced with any other embodiment(s). Reference throughout this specification to "one embodiment", "an embodiment", "an example embodiment," means that a particular feature, structure or characteristic described in connection with the embodiment is included in at least one embodiment of the present invention. Thus, appearances of the phrases "in one embodiment," "in an embodiment," or "an example embodiment" in various places throughout this specification are not necessarily all referring to the same embodiment, but may. Furthermore, the particular features, structures or characteristics may be combined in any suitable manner, as would be apparent to a person skilled in the art from this disclosure, in one or more embodiments. Furthermore, while some embodiments described herein include some but not other features included in other embodiments, combinations of features of different embodiments are meant to be within the scope of the invention. For example, in the appended claims, any of the claimed embodiments can be used in any combination.

[0071] All publications, published patent documents, and patent applications cited herein are hereby incorporated by reference to the same extent as though each individual publication, published patent document, or patent application was specifically and individually indicated as being incorporated by reference.

OVERVIEW

[0072] Embodiments disclosed herein provide targeting moieties which promote transduction into the CNS through interaction with the Transferrin receptor. These targeting moieties may be incorporated into particles, such as viral capsid delivery particles, to confer tropism on the delivery particles and promote transduction of CNS. Example CNS tissue include brain and spinal cord tissue. Example CNS cell types include neurons and glial cells. Further embodiments disclosed herein provide a vector system comprising one or more vectors encoding AAV capsids according to embodiments described herein. Accordingly, embodiments disclosed herein provide compositions capable of delivering cargos with enhanced selectivity and efficiency to the CNS

vasculature. Embodiments disclosed herein also provide vector systems for the generation and loading of such delivery particles with a cargo. Likewise, embodiments disclosed herein provide methods for use of such compositions to target CNS endothelial cells, in vitro and in vivo, with implications for both therapeutic and research purposes.

[0073] Additional feature and advantages of the aforementioned embodiments are further described below.

Targeting Moieties and Compositions Thereof

[0074] In example embodiments, compositions are provided herein comprising a targeting moiety with an enhanced tropism for endothelial cells of the CNS. A target moiety with an enhanced tropism for endothelial cells of the CNS promotes, increases, or otherwise improves binding to, and in some cases, transduction of the CNS as compared to a natural or wild-type target moiety. This targeting moiety may be coupled directly to a cargo to be delivered such as an oligonucleotide or polypeptide. Alternatively, the targeting molecule may be incorporated into a delivery particle to confer tropism for endothelial cells of the CNS on the delivery particle. A non-limiting example of delivery particle is a viral capsid particle. In such embodiments, the targeting moiety may be incorporated into a viral capsid polypeptide such that the targeting moiety is incorporated into the assembled viral capsid. However, other particle delivery systems where the targeting moiety may be incorporated or attached, for example on exosomes or liposomes, are also envisioned and encompassed as alternative embodiments herein.

[0075] In a preferred embodiment, provided herein is a composition comprising a targeting moiety effective to increase transduction of central nervous system (CNS) tissues via binding to a transferrin receptor (TFRC), optionally further comprising a cargo coupled to or otherwise associated with the targeting moiety. A target moiety with an increased transduction promotes, enhances, or otherwise improves binding to, and in some cases, transduction of the CNS as compared to a natural or wild-type target moiety. In an example embodiment, the targeting moiety binds to the extracellular domain of TFRC. In an example embodiment, the targeting moiety binds to one or more of the apical, helical, and/or protease-like domain of the extracellular domain. In an example embodiment, the targeting moiety binds to the apical domain. In an example embodiment, the n-mer is an animo acid sequence of length n. The length of the n-mer may be any necessary length to transduce the CNS. In example embodiments, the n-mer is 1, 2, 3, 4, 5, 6, 7, 8,

9, 10, 11, or 12 amino acids in length. In an example embodiment, the n-mer motif has a length of at least 7 amino acids. In an example embodiment, a composition comprising a targeting moiety effective to increase transduction of CNS tissues comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of Z_1-X_1-Z_2-X_2-X_3-X_4-X_5 wherein Z_1 is Y, F, or L, Z_2 is S, R, or K, X_1 – X_5 are independently selected amino acids. In an example embodiment, X_1 optionally comprises of A, S, or H; X_2 optionally comprises of S, T, L, or I; X_3 optionally comprises N or G; X_4 optionally comprises G; X_5 optionally comprises of N, D, I, V, or R. In an example embodiment, the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of is X_1-H-X_2-L-X_3-X_4-X_5 wherein X_1 – X_5 are independently selected amino acids.

[0076] In example embodiments, the n-mer can be used to increase transduction in target cells i.e., CNS cells and tissues. The increase in transduction efficiency (which may correspond to the tropism efficiency) of the n-mer to a cell may be compared to a composition that does not contain the targeting moiety for example inclusion of one or more targeting moieties in a composition can result in an increase in transduction and or transduction efficiency by 10%, 20%, 30%, 40%, 50%, 60% 70% 80% 90% a 100% or more. In an exemplary embodiment the increase in transduction and or transduction efficiency is one and a half fold, two-fold, three-fold, four-fold, five-fold, six-fold, seven-fold, eight-fold, nine-fold, ten-fold, 20-fold, 30-fold, 40-fold, 50-fold, 60-fold, 70-fold, 80-fold or more relative to a composition lacking the n-mer. In one embodiment the transduction and/or transduction efficiency is increased or enhanced in endothelial cells, in one embodiment increase in endothelial cells of the vasculature, for example, the central nervous system vasculature. In embodiments, the transduction and /or transduction efficiency is increased or enhanced in cells of the central nervous system. In embodiments, the transduction and /or transduction efficiency is increased or enhanced in neurons and glial cells. In an embodiment, the composition comprising a n-mer is selective to a target cell as compared to other cell types and/or other virus particles. As used herein, 'selective' and 'cell-selective' refers to preferential targeting for cells as compared to other cell types. Preferably, the targeting moiety is selective for a desired target (e.g. cell, organ, system e.g. CNS tissues) or set of targets by at least 2:1, 3:1, 4:1, 5:1, 6:1 7:1, 8:1, 9:1. 10:1 or more; or 10%, 20%, 30%, 40%, 50%, 60%, 70%, 75% 80%, 85% 90% or more, relative to other targets or cells (e.g. CNS). In an example embodiment, the composition

comprising a targeting moiety described herein can have an increased uptake, delivery rate, transduction rate, efficiency, amount, or a combination thereof in a target cell (e.g., endothelial cells across the CNS e.g., brain endothelium, arterio-venous axis in brain, retina, and spinal cord vasculature) as compared to other cells types (e.g. muscle cells) and/or other virus particles (e.g., AAVs not containing the targeting moiety) and other compositions that do not contain the cell-selective n-mer motif of the present invention.

[0077] In an example embodiment, the n-mer motif is selected from the group consisting of YSRIGPN (SEQ ID NO: 14632), YSRLNMN (SEQ ID NO: 14301), YSRLNKD (SEQ ID NO: 16577), and YHRLSNN (SEQ ID NO: 16636). In an example embodiment, the n-mer motif is VHRLQDK (SEQ ID NO: 16602) or LHALSHN (SEQ ID NO: 16608). In an example embodiment, the n-mer motif is comprises PSATNGV (SEQ ID NO: 20486), QVSTNGI (SEQ ID NO: 16021), SYSSNGV (SEQ ID NO: 16234), HQSSNGV (SEQ ID NO: 15978), VGSINGI (SEQ ID NO: 16199), AMSTNGR (SEQ ID NO: 16000), SASTNGV (SEQ ID NO: 16127), YMSTNGV (SEQ ID NO: 16042), YYSSNGV (SEQ ID NO: 16206), VHSTNGI (SEQ ID NO: 16134), PLSTNGV (SEQ ID NO: 16233), VYSTNGI (SEQ ID NO: 16059), IISTNGV (SEQ ID NO: 16054), RSVSSNGV (SEQ ID NO: 20502), YKSSNGV (SEQ ID NO: 16123), FRSTNGV (SEQ ID NO: 16070, and/or FVSTNGV (SEQ ID NO: 11162). In an example embodiment, the n-mer is selected from any of the amino acid sequences in Tables 1-13, or any combination thereof. In an example embodiment, the n-mer motif is selected from a peptide having an amino acid sequence of one of SEQ ID NO:10952-20481. In an example embodiment, the targeting moiety is part of (e.g., inserted between consecutive amino acids of) a viral capsid protein, including an AAV capsid protein.

Transferrin Receptor (TFRC) Binding

[0078] In a preferred embodiment, the targeting moiety binds to a Transferrin receptor. The TFRC (i.e., TfR1 protein encoded by the *TFRC* gene, or CD71) comprises of two types of receptors: TFRC1 (or cluster of differentiation 71 (CD71)) and TFRC2. TFRC2 is less common than TFRC1 and is predominantly expressed in hepatocytes. TFRC1 binds transferrin (TF) with high affinity and is commonly expressed. TFRC1 is a type II transmembrane glycoprotein of around 90 kDa and comprises of around 760 amino acids. TFRC1 is typically found as a dimer linked by disulfide bonds on the cell surface, see FIG. 4.

[0079] The TFRC1 domain contains an extracellular C-terminal domain (around 671 amino acids) and comprises of the TF binding site. The extracellular C-terminal domain comprises of three subdomains: apical, helical, and protease-like domain, see FIG. 4. Furthermore, the extracellular C-terminal domain comprises of three N-linked glycosylation sites at asparagine residues 251, 317, and 727 and one *O*-linked glycosylation site at threonine 104, which contribute to adequate function of the receptor. TFRC1 additionally comprises of a transmembrane domain (around 29 amino acids), and an intracellular N-terminal domain (around 61 amino acids). Alternative to the delivery of iron through TF with TFRC1, uptake of iron can also occur through H-ferritin binding through the apical domain. See also Candelaria, P. V.; *et al.* Antibodies Targeting the Transferrin Receptor 1 (TfR1) as Direct Anti-Cancer Agents. Frontiers in Immunology, 2021, 12, hereby incorporated by reference.

[0080] In an example embodiment, the targeting moiety binds to the extracellular domain of TFRC. In an example embodiment, the targeting moiety binds to one or more of the apical, helical, and/or protease-like domain. In an example embodiment, the targeting moiety binds to the apical domain.

Engineered Viral Capsids

[0081] Described herein are various embodiments of engineered viral capsids, such as adeno-associated virus (AAV) capsids, that can be engineered to confer cell-selective tropism, such as CNS tissue- and cell-specific tropism, to an engineered viral particle. Engineered viral capsids can be lentiviral, retroviral, adenoviral, or AAV capsids. The engineered capsids can be included in an engineered virus particle (e.g., an engineered lentiviral, retroviral, adenoviral, or AAV virus particle), and can confer cell-selective tropism to the engineered viral particle. The engineered viral capsids described herein can include one or more engineered viral capsid proteins described herein. The engineered viral capsids described herein can include one or more engineered viral capsid proteins described herein that can contain one or more target moiety as described elsewhere herein.

[0082] The engineered viral capsids can be variants of wild-type viral capsid. For example, in some embodiments, the engineered AAV capsids can be variants of wild-type AAV capsids. In some embodiments, the wild-type AAV capsids can be composed of VP1, VP2, VP3 capsid proteins or a combination thereof. In other words, the engineered AAV capsids can include one or

more variants of a wild-type VP1, wild-type VP2, and/or wild-type VP3 capsid proteins. In some embodiments, the serotype of the reference wild-type AAV capsid can be AAV-1, AAV-2, AAV-3, AAV-4, AAV-5, AAV-6, AAV-8, AAV-9 or any combination thereof. In some embodiments, the serotype of the wild-type AAV capsid can be AAV-9. The engineered AAV capsids can have a different tropism than that of the reference wild-type AAV capsid.

[0083] In some embodiments, the target moiety is incorporated into a viral protein, such as a capsid protein, including but not limited to lentiviral, adenoviral, AAV, bacteriophage, retroviral proteins. In some embodiments, the target moiety is located between two amino acids of the viral protein such that the target moiety is external (i.e., is presented on the surface of) to a viral capsid. In an example embodiment, the target moiety disclosed herein can be inserted between two consecutive amino acids in the wild-type viral protein (VP) (or capsid protein), including in regions that are surface exposed when incorporated into a viral capsid. In some embodiments, the target moiety can be inserted between two consecutive amino acids in a variable amino acid region in a viral capsid protein.

[0084] In some embodiments, the target moiety can be inserted between two consecutive amino acids in a variable amino acid region in an AAV capsid protein. The core of each wild-type AAV viral protein contains an eight-stranded beta-barrel motif (betaB to betaI) and an alpha-helix (alphaA) that are conserved in autonomous parvovirus capsids (see e.g., DiMattia et al. 2012. J. Virol. 86(12):6947-6958). Structural variable regions (VRs), also referred to as "loops", occur in the surface loops that connect the beta-strands, which cluster to produce local variations in the capsid surface. AAVs have 12 variable regions (also referred to as hypervariable regions) (see e.g., Weitzman and Linden. 2011. "Adeno-Associated Virus Biology." In Snyder, R.O., Moullier, P. (eds.) Totowa, NJ: Humana Press). In one example embodiment, one or more target moiety can be inserted between two amino acids in one or more of the 12 variable regions in the wild-type AVV capsid proteins. In one example embodiment, the one or more target moieties can be each be inserted between two amino acids in VR-I, VR-II, VR-III, VR-IV, VR-V, VR-VI, VR-VII, VR-III, VR-IX, VR-X, VR-XI, VR-XII, or a combination thereof. In an example embodiment, the targeting moiety is inserted or substituted in loop IV and/or loop VIII. In an example embodiment, the targeting moiety is IPFSRVNPDT (SEQ ID NO: 20285), LGFARTGAAD (SEQ ID NO:

20274), LGFTKSSGSD (SEQ ID NO: 20270), LRYSKTQGES (SEQ ID NO: 20266), SPYARSSAGV (SEQ ID NO: 20271), VGWSRLDLTT (SEQ ID NO: 20262).

[0085] In one example embodiment, the engineered capsid is a modified AAV1 capsid and can have a target moiety motif inserted after or a neighbor of amino acid 590 (i.e., between amino acid 590 and 591). In one example embodiment, the engineered capsid is a modified AAV3 capsid and can have a target moiety motif inserted after or a neighbor of amino acid 586. In one example embodiment, the engineered capsid is a modified AAV4 capsid and can have a target moiety motif inserted after or a neighbor of amino acid 586. In one example embodiment, the engineered capsid is a modified AAV5 capsid and can have a target moiety motif inserted after or a neighbor of amino acid 575. In one example embodiment, the engineered capsid is a modified AAV6 capsid and can have a target moiety inserted at or a neighbor of amino acid 585 and optionally Y705-731, T492V, K531E. In one example embodiment, the engineered capsid is a modified AAV8 capsid and can have a target moiety inserted after or a neighbor of amino acid 585 and 590. In one example embodiment, the engineered capsid is a modified AAV9 capsid and can have a target moiety inserted in between amino acid 588 and 589. (Büning, H.; Srivastava, A. Capsid Modifications for Targeting and Improving the Efficacy of AAV Vectors. Molecular Therapy - Methods & Clinical Development 2019, 12, 248–265). In one example embodiment, the engineered capsid can have a 7-mer motif inserted between amino acids 588 and 589 of an AAV9 viral protein. SEQ ID NO: 20506 is a reference AAV9 capsid sequence for at least referencing the insertion sites discussed above. In an example embodiment, the engineered capsid can have a 7-mer motif inserted between two consecutive amino acids within amino acids 451-460 of a capsid protein of AAV9 viral protein. SEQ ID NO: 20506 is a reference AAV9 capsid sequence for at least referencing the insertion sites discussed above. It will be appreciated that target moieties can be inserted in analogous positions in AAV viral proteins of other serotypes, such as but not limited to, AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV rh.74, AAV rh.10 capsid polypeptide. In some embodiments as previously discussed, the target moiety(s) can be inserted between any two contiguous amino acids within the AAV viral protein and in some embodiments the insertion is made in a variable region.

[0086] In one example embodiment, the first 1, 2, 3, or 4 amino acids of a target moiety can replace 1, 2, 3, or 4 amino acids of a polypeptide into which it is inserted and preceding the

insertion site. Using an AAV as another non-limiting example, one or more of the target moieties can be inserted into e.g., an AAV9 capsid polypeptide between amino acids 588 and 589 and the insert can replace amino acids 586, 587, and 588 such that the amino acid immediately preceding the target moiety after insertion is residue 585. It will be appreciated that this principle can apply in any other insertion context and is not necessarily limited to insertion between residues 588 and 589 of an AAV9 capsid or equivalent position in another AAV capsid. It will further be appreciated that in some embodiments, no amino acids in the polypeptide into which the target moiety is inserted are replaced by the target moiety. In an example embodiment, the AAV capsid protein is selected from SEQ ID NO: 20506.

[0087] In some embodiments, in addition to the n-mer motif(s) the targeting moiety can include a polypeptide, a polynucleotide, a lipid, a polymer, a sugar, or a combination thereof.

[0088] The engineered viral capsid and/or capsid proteins can be encoded by one or more engineered viral capsid polynucleotides. In some embodiments, the engineered viral capsid polynucleotide is an engineered AAV capsid polynucleotide, engineered lentiviral capsid polynucleotide, engineered retroviral capsid polynucleotide, or engineered adenovirus capsid polynucleotide. In some embodiments, an engineered viral capsid polynucleotide (e.g., an engineered AAV capsid polynucleotide, engineered lentiviral capsid polynucleotide, engineered retroviral capsid polynucleotide, or engineered adenovirus capsid polynucleotide) can include a 3' polyadenylation signal. The polyadenylation signal can be an SV40 polyadenylation signal.

[0089] In some embodiments, the engineered polynucleotide can be included in a polynucleotide that is configured to express the engineered capsid in a host cell system for production of viral particles. The host cell system may also include a construct that expresses a recombinant viral genome that comprises a transgene encoding a polypeptide or nucleic acid operably linked to one or more regulatory sequences that promote expression of the transgene in a target cell, including a recombinant AAV genome where the transgene and regulatory sequences are flanked by AAV ITR sequences.

[0090] In some embodiments, the engineered AAV capsid encoding polynucleotide can be included in a polynucleotide that is configured to be an express the engineered capsid in a host cell system for production of AAV viral particles. The host cell system may also include a construct that expresses a recombinant AAV viral genome that comprises a transgene encoding a

polypeptide or nucleic acid operably linked to one or more regulatory sequences that promote expression of the transgene in a target cell, including a recombinant AAV genome where the transgene and regulatory sequences are flanked by AAV ITR sequences. In some embodiments, the engineered AAV capsid encoding polynucleotide can be operably coupled to a poly adenylation tail. In some embodiments, the poly adenylation tail can be an SV40 poly adenylation tail. In some embodiments, the AAV capsid encoding polynucleotide can be operably coupled to a promoter. In some embodiments, the regulatory sequence that regulates expression of the transgene is a promoter and can be a tissue specific promoter. In some embodiments, the tissue specific promoter is specific for muscle (e.g., cardiac, skeletal, and/or smooth muscle), neurons and supporting cells (e.g., astrocytes, glial cells, Schwann cells, etc.), fat, spleen, liver, kidney, immune cells, spinal fluid cells, synovial fluid cells, skin cells, cartilage, tendons, connective tissue, bone, pancreas, adrenal gland, blood cell, bone marrow cells, placenta, endothelial cells, and combinations thereof. In some embodiments, the promoter can be a constitutive promoter. Suitable tissue specific promoters and constitutive promoters are discussed elsewhere herein and are generally known in the art and can be commercially available. Suitable neuronal tissue/cell specific promoters include, but are not limited to, GFAP promoter (astrocytes), SYN1 promoter (neurons), and NSE/RU5' (mature neurons).

Further Capsid Modifications

[0091] In one example embodiment, the viral capsid protein may comprise one or more mutations relative to wild type. In an example embodiment, the one or more mutations comprise a K449R substitution in a capsid polypeptide of AAV 9 20507, or a substitution in an analogous position of a capsid polypeptide from AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAVrh8, AAV rh.74, or AAV rh. 10. In an example embodiment, the K449R substituted AAV capsid is selected from SEQ ID NO: 20507.

[0092] In example embodiments, the viral capsid protein may comprise additional targeting motifs that are in addition to the n-mer motifs of the present disclosure. Without being bound by theory the additional targeting moieties can be antibodies or fragments thereof, In some embodiments, the additional targeting moiety can be any molecule or composition capable of recognizing, binding, attaching to, or otherwise interacting with a binding partner that can be present on the surface of a target cell. Binding partners include, but are not limited to nucleic acids,

proteins, peptides, sugars, fats, or any combination thereof or any other molecule or molecules that are present on the surface of a target cell. In some embodiments, the binding partner is unique to a cell type or cell state or a to a group of related cell types or cell states. In some embodiments, the binding partner is a receptor, channel, or other complex present on the surface of a target cell. These additional targeting moieties can be used to target, e.g., specific cell types or cell states within those the set of target cells targeted by the n-mer motif. As used herein, "cell state" is used to describe transient elements of a cell's identity. Cell state can be thought of as the transient characteristic profile or phenotype of a cell. Cell states arise transiently during time-dependent processes, either in a temporal progression that is unidirectional (e.g., during differentiation, or following an environmental stimulus) or in a state vacillation that is not necessarily unidirectional and in which the cell may return to the origin state. Vacillating processes can be oscillatory (e.g., cell-cycle or circadian rhythm) or can transition between states with no predefined order (e.g., due to stochastic, or environmentally controlled, molecular events). These time-dependent processes may occur transiently within a stable cell type (as in a transient environmental response), or may lead to a new, distinct type (as in differentiation). See e.g., Wagner et al., 2016. Nat Biotechnol. 34(11): 1145-1160.

[0093] In some embodiments, the additional targeting moiety is or includes a peptide or a polypeptide. In some embodiments, the additional targeting moiety is or includes an antibody or fragment thereof. Exemplary antibodies and fragments thereof are described in greater detail elsewhere herein, see e.g., discussion on exemplary cargos. In some embodiments, the additional targeting moiety is or includes an aptamer. In some embodiments, the additional targeting moiety is or includes a small molecule. In some embodiments, the additional targeting moiety is or includes a nucleic acid (e.g., DNA or RNA). In some embodiments, the additional targeting moiety is or includes a receptor. In some embodiments, the additional targeting moiety is or includes a receptor ligand. In some embodiments, the additional targeting moiety is or includes a carbohydrate (e.g., a sugar). In some embodiments, the additional targeting moiety is or includes a lipid. In some embodiments, the additional targeting moiety is an engineered protein scaffold. In some embodiments, the additional targeting moiety is an affibody. In some embodiments, the additional targeting moiety is an antibody mimetic. In some embodiments, the additional targeting moiety is an engineered binding protein, such as a designed ankyrin repeat proteins (DARPins)

(see e.g., Plückthun et al., Annu. Rev. Pharmacol. Toxicol. (2015) 55(1): 489-511) , avimers (Silverman et al., Nat. Biotechnol. (2005) 23 (12): 1556–1561 and Jeong et al. Nat. Biotechnol. (2005) 23(12): 1493-1494), or affibodies (see e.g., Nord et al., Nat. Biotechnol. (1997) 15(8):772-777). In example embodiments, the additional targeting moiety is a receptor ligand or binding protein. In some embodiments, the additional targeting moiety is attached or otherwise coupled to the capsid surface. In some embodiments, the additional targeting moiety is encoded by a vector that produces a capsid of the present invention described herein.

Engineered Vectors and Vector Systems

[0094] Also provided herein are vectors and vector systems that can contain one or more of the engineered polynucleotides described herein that can encode one or more of the target moieties of the present invention, including but not limited to engineered viral polynucleotides (e.g., polynucleotides encoding engineered AAV capsid proteins). In a preferred embodiment, provided herein is a vector system comprising one or more vectors encoding a targeting moiety effective to increase transduction of central nervous system tissues (CNS), optionally further comprising a cargo coupled to or otherwise associated with the targeting moiety or further comprising a construct which encodes the cargo, including a recombinant viral genome comprising a transgene. In preferred embodiment, the targeting moiety encoded in the vector system binds to Transferrin Receptor (TFRC). As used in this context, engineered viral capsid polynucleotides refers to any one or more of the polynucleotides described herein capable of encoding an engineered viral capsid as described elsewhere herein and/or polynucleotide(s) capable of encoding one or more engineered viral capsid proteins described elsewhere herein. Further, where the vector includes an engineered viral capsid polynucleotide described herein, the vector can also be referred to and considered an engineered vector or system thereof although not specifically noted as such. In embodiments, the vector can contain one or more polynucleotides encoding one or more elements of an engineered viral capsid described herein. The vectors and systems thereof can be useful in producing bacterial, fungal, yeast, plant cells, animal cells, and transgenic animals that can express one or more components of the engineered viral capsid, particle, or other compositions described herein. Within the scope of this disclosure are vectors containing one or more of the polynucleotide sequences described herein. One or more of the polynucleotides that are part of the engineered viral capsid and system thereof described herein can be included in a vector or vector system.

[0095] In example embodiments, a vector used in the production of the rAAVs disclosed herein comprises a rep gene and cap gene). The rep gene typically encodes Rep78, Rep68, Rep52 and Rep40 from a single ORF. These replication factors aid AAV genome replication and virion assembly. The cap gene typically encodes the three capsid proteins (i.e., virion protein 1 (VP1), VP2 and VP3) from a single ORF as well. In addition, the three capsid proteins are regulated by transcription from a start codon (ACG) and alternative splicing. The cap gene also encodes, from an in-frameshifted ORF, an assembly-activating protein (AAP). The AAP is essential for capsid assembly.

[0096] In some embodiments, the vector can include an engineered viral (e.g., AAV) capsid polynucleotide having a 3' polyadenylation signal. In some embodiments, the 3' polyadenylation is an SV40 polyadenylation signal. In some embodiments the vector does not have splice regulatory elements. In some embodiments, the vector includes one or more minimal splice regulatory elements. In some embodiments, the vector can further include a modified splice regulatory element, wherein the modification inactivates the splice regulatory element. In some embodiments, the modified splice regulatory element is a polynucleotide sequence sufficient to induce splicing, between a rep protein polynucleotide and the engineered viral (e.g., AAV) capsid protein variant polynucleotide. In some embodiments, the polynucleotide sequence can be sufficient to induce splicing is a splice acceptor or a splice donor. In some embodiments, the viral (e.g., AAV) capsid polynucleotide is an engineered viral (e.g., AAV) capsid polynucleotide as described elsewhere herein. It some embodiments, the vector does not include one or more minimal splice regulatory elements, modified splice regulatory agent, splice acceptor, and/or splice donor.

[0097] The vectors and/or vector systems can be used, for example, to express one or more of the engineered viral (e.g., AAV) capsid and/or other polynucleotides in a cell, such as a producer cell, to produce engineered viral (e.g., AAV) particles and/or other compositions (e.g., polypeptides, particles, etc.) containing an engineered viral (e.g., AAV) capsid or other composition containing an n-mer motif of the present invention described elsewhere herein. Other uses for the vectors and vector systems described herein are also within the scope of this disclosure. In general, and throughout this specification, the term is a tool that allows or facilitates the transfer of an entity from one environment to another. In some contexts which will be appreciated by those

of ordinary skill in the art, "vector" can be a term of art to refer to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. A vector can be a replicon, such as a plasmid, phage, or cosmid, into which another DNA segment may be inserted so as to bring about the replication of the inserted segment. Generally, a vector is capable of replication when associated with the proper control elements.

[0098] Vectors include, but are not limited to, nucleic acid molecules that are single-stranded, double-stranded, or partially double-stranded; nucleic acid molecules that comprise one or more free ends, no free ends (e.g., circular); nucleic acid molecules that comprise DNA, RNA, or both; and other varieties of polynucleotides known in the art. One type of vector is a "plasmid," which refers to a circular double stranded DNA loop into which additional DNA segments can be inserted, such as by standard molecular cloning techniques. Another type of vector is a viral vector, wherein virally derived DNA or RNA sequences are present in the vector for packaging into a virus (e.g., retroviruses, replication defective retroviruses, adenoviruses, replication defective adenoviruses, and adeno-associated viruses (AAVs)). Viral vectors also include polynucleotides carried by a virus for transfection into a host cell. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors." Common expression vectors of utility in recombinant DNA techniques are often in the form of plasmids.

[0099] Recombinant expression vectors can be composed of a nucleic acid (e.g., a polynucleotide) of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory elements, which can be selected on the basis of the host cells to be used for expression, that is operatively-linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" and "operatively-linked" are used interchangeably herein and further defined elsewhere herein. In the context of a vector, the term "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory element(s) in a manner that allows

for expression of the nucleotide sequence (e.g., in an in vitro transcription/translation system or in a host cell when the vector is introduced into the host cell).

[0100] In some embodiments, the vector can be a bicistronic vector. In some embodiments, a bicistronic vector can be used for one or more elements of the engineered viral (e.g., AAV) capsid system described herein. In some embodiments, expression of elements of the engineered viral (e.g., AAV) capsid system described herein can be driven by a suitable constitutive or tissue specific promoter. Where the element of the engineered viral (e.g., AAV) capsid system is an RNA, its expression can be driven by a Pol III promoter, such as a U6 promoter. In some embodiments, the two are combined.

Cell-based Vector Amplification and Expression

Vectors can be designed for expression of one or more elements of the engineered viral (e.g., AAV) capsid system or other compositions containing an n-mer motif of the present invention described herein (e.g., nucleic acid transcripts, proteins, enzymes, and combinations thereof) in a suitable host cell. In an example embodiment, a composition comprising a targeting moiety effective to increase transduction of CNS tissues comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of Z_1-X_1-Z_2-X_2-X_3-X_4-X_5 wherein Z_1 is Y, F, or L, Z_2 is S, R, or K, X_1 – X_5 are independently selected amino acids. In an example embodiment, X_1 optionally comprises of A, S, or H; X_2 optionally comprises of S, T, L, or I; X_3 optionally comprises N or G; X_4 optionally comprises G; X_5 optionally comprises of N, D, I, V, or R. The n-mer motif may be selected from the group consisting of YSRIGPN (SEQ ID NO: 14632), YSRLNMN (SEQ ID NO: 14301), YSRLNKD (SEQ ID NO: 16577), and YHRLSNN (SEQ ID NO: 16636). In an example embodiment, the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of is X_1-H-X_2-L-X_3-X_4-X_5 wherein X_1 – X_5 are independently selected amino acids. In an example embodiment, the n-mer motif is VHRLQDK (SEQ ID NO: 16602) or LHALSHN (SEQ ID NO: 16608). In an example embodiment, the n-mer motif is comprises PSATNGV (SEQ ID NO: 20486), QVSTNGI (SEQ ID NO: 16021), SYSSNGV (SEQ ID NO: 16234), HQSSNGV (SEQ ID NO: 15978), VGSINGI (SEQ ID NO: 16200), AMSTNGR (SEQ ID NO: 16000), SASTNGV (SEQ ID NO: 16127), YMSTNGV (SEQ ID NO: 16042), YYSSNGV (SEQ ID NO: 16206), VHSTNGI (SEQ ID NO: 16134), PLSTNGV (SEQ ID NO: 16233), VYSTNGI (SEQ ID NO: 16059), IISTNGV (SEQ ID

NO: 16054), RSVSSNGV (SEQ ID NO: 20502), YKSSNGV (SEQ ID NO: 16123), FRSTNGV (SEQ ID NO: 16070, and/or FVSTNGV (SEQ ID NO: 11162).

[0101] In some embodiments, the suitable host cell is a prokaryotic cell. Suitable host cells include, but are not limited to, bacterial cells, yeast cells, insect cells, and mammalian cells. The vectors can be viral-based or non-viral based. In some embodiments, the suitable host cell is a eukaryotic cell. In some embodiments, the suitable host cell is a suitable bacterial cell. Suitable bacterial cells include, but are not limited to, bacterial cells from the bacteria of the species Escherichia coli. Many suitable strains of E. coli are known in the art for expression of vectors. These include, but are not limited to Pir1, Stbl2, Stbl3, Stbl4, TOP10, XL1 Blue, and XL10 Gold. In some embodiments, the host cell is a suitable insect cell. Suitable insect cells include those from *Spodoptera frugiperda*. Suitable strains of *S. frugiperda* cells include, but are not limited to, Sf9 and Sf21. In some embodiments, the host cell is a suitable yeast cell. In some embodiments, the yeast cell can be from Saccharomyces cerevisiae. In some embodiments, the host cell is a suitable mammalian cell. Many types of mammalian cells have been developed to express vectors. Suitable mammalian cells include, but are not limited to, HEK293, Chinese Hamster Ovary Cells (CHOs), mouse myeloma cells, HeLa, U2OS, A549, HT1080, CAD, P19, NIH 3T3, L929, N2a, MCF-7, Y79, SO-Rb50, HepG G2, DIKX-X11, J558L, Baby hamster kidney cells (BHK), and chicken embryo fibroblasts (CEFs). Suitable host cells are discussed further in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990).

[0102] In some embodiments, the vector can be a yeast expression vector. Examples of vectors for expression in yeast *Saccharomyces cerevisiae* include pYepSec1 (Baldari, et al., 1987. EMBO J. 6: 229-234), pMFa (Kuijan and Herskowitz, 1982. Cell 30: 933-943), pJRY88 (Schultz et al., 1987. Gene 54: 113-123), pYES2 (Invitrogen Corporation, San Diego, Calif.), and picZ (InVitrogen Corp, San Diego, Calif.). As used herein, a "yeast expression vector" refers to a nucleic acid that contains one or more sequences encoding an RNA and/or polypeptide and may further contain any desired elements that control the expression of the nucleic acid(s), as well as any elements that enable the replication and maintenance of the expression vector inside the yeast cell. Many suitable yeast expression vectors and features thereof are known in the art; for example, various vectors and techniques are illustrated in in Yeast Protocols, 2nd edition, Xiao, W., ed.

(Humana Press, New York, 2007) and Buckholz, R.G. and Gleeson, M.A. (1991) Biotechnology (NY) 9(11): 1067-72. Yeast vectors can contain, without limitation, a centromeric (CEN) sequence, an autonomous replication sequence (ARS), a promoter, such as an RNA Polymerase III promoter, operably linked to a sequence or gene of interest, a terminator such as an RNA polymerase III terminator, an origin of replication, and a marker gene (e.g., auxotrophic, antibiotic, or other selectable markers). Examples of expression vectors for use in yeast may include plasmids, yeast artificial chromosomes, 2μ plasmids, yeast integrative plasmids, yeast replicative plasmids, shuttle vectors, and episomal plasmids.

[0103] In some embodiments, the vector is a baculovirus vector or expression vector and can be suitable for expression of polynucleotides and/or proteins in insect cells. Baculovirus vectors available for expression of proteins in cultured insect cells (e.g., SF9 cells) include the pAc series (Smith, et al., 1983. Mol. Cell. Biol. 3: 2156-2165) and the pVL series (Lucklow and Summers, 1989. Virology 170: 31-39). rAAV (recombinant Adeno-associated viral) vectors are preferably produced in insect cells, e.g., Spodoptera frugiperda Sf9 insect cells, grown in serum-free suspension culture. Serum-free insect cells can be purchased from commercial vendors, e.g., Sigma Aldrich (EX-CELL 405).

[0104] In some embodiments, the vector is a mammalian expression vector. In some embodiments, the mammalian expression vector is capable of expressing one or more polynucleotides and/or polypeptides in a mammalian cell. Examples of mammalian expression vectors include, but are not limited to, pCDM8 (Seed, 1987. Nature 329: 840) and pMT2PC (Kaufman, et al., 1987. EMBO J. 6: 187-195). The mammalian expression vector can include one or more suitable regulatory elements capable of controlling expression of the one or more polynucleotides and/or proteins in the mammalian cell. For example, commonly used promoters are derived from polyoma, adenovirus 2, cytomegalovirus, simian virus 40, and others disclosed herein and known in the art. More detail on suitable regulatory elements are described elsewhere herein.

[0105] For other suitable expression vectors and vector systems for both prokaryotic and eukaryotic cells see, e.g., Chapters 16 and 17 of Sambrook, et al., MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

[0106] In some embodiments, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert, et al., 1987. *Genes Dev.* 1: 268-277), lymphoid-specific promoters (Calame and Eaton, 1988. *Adv. Immunol.* 43: 235-275), in particular promoters of T cell receptors (Winoto and Baltimore, 1989. *EMBO J.* 8: 729-733) and immunoglobulins (Baneiji, et al., 1983. *Cell* 33: 729-740; Queen and Baltimore, 1983. *Cell* 33: 741-748), neuron-specific promoters (e.g., the neurofilament promoter; Byrne and Ruddle, 1989. *Proc. Natl. Acad. Sci. USA* 86: 5473-5477), pancreas-specific promoters (Edlund, et al., 1985. *Science* 230: 912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, e.g., the murine hox promoters (Kessel and Gruss, 1990. *Science* 249: 374-379) and the α-fetoprotein promoter (Campes and Tilghman, 1989. *Genes Dev.* 3: 537-546). With regards to these prokaryotic and eukaryotic vectors, mention is made of U.S. Patent 6,750,059, the contents of which are incorporated by reference herein in their entirety. Other embodiments can utilize viral vectors, with regards to which mention is made of U.S. Patent application 13/092,085, the contents of which are incorporated by reference herein in their entirety. Tissue-specific regulatory elements are known in the art and in this regard, mention is made of U.S. Patent 7,776,321, the contents of which are incorporated by reference herein in their entirety. In some embodiments, a regulatory element can be operably linked to a transgene in a recombinant genome packaged by the engineered AAV capsid system so as to drive expression of the one or more elements of the transgene delivered by the viral vector as described herein in a tissue specific manner.

[0107] Vectors may be introduced and propagated in a prokaryote or prokaryotic cell. In some embodiments, a prokaryote is used to amplify copies of a vector to be introduced into a eukaryotic cell or as an intermediate vector in the production of a vector to be introduced into a eukaryotic cell (e.g., amplifying a plasmid as part of a viral vector packaging system). In some embodiments, a prokaryote is used to amplify copies of a vector and express one or more nucleic acids, such as to provide a source of one or more proteins for delivery to a host cell or host organism.

[0108] In some embodiments, the vector can be a fusion vector or fusion expression vector. In some embodiments, fusion vectors add a number of amino acids to a protein encoded therein, such as to the amino terminus, carboxy terminus, or both of a recombinant protein. Such fusion vectors can serve one or more purposes, such as: (i) to increase expression of recombinant protein; (ii) to increase the solubility of the recombinant protein; and (iii) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. In some embodiments, expression of polynucleotides (such as non-coding polynucleotides) and proteins in prokaryotes can be carried out in Escherichia coli with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion polynucleotides and/or proteins. In some embodiments, the fusion expression vector can include a proteolytic cleavage site, which can be introduced at the junction of the fusion vector backbone or other fusion moiety and the recombinant polynucleotide or protein to enable separation of the recombinant polynucleotide or protein from the fusion vector backbone or other fusion moiety subsequent to purification of the fusion polynucleotide or protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Example fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson, 1988. *Gene* 67: 31-40), pMAL (New England Biolabs, Beverly, Mass.) and pRIT5 (Pharmacia, Piscataway, N.J.) that fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. Examples of suitable inducible non-fusion E. coli expression vectors include pTrc (Amrann et al., (1988) Gene 69:301-315) and pET 11d (Studier et al., GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 60-89).

[0109] In some embodiments, one or more vectors driving expression of one or more elements of an engineered viral (e.g., AAV) capsid system or other composition containing an n-mer motif described herein are introduced into a host cell such that expression of the elements of the engineered delivery system described herein direct formation of an engineered viral (e.g., AAV) capsid system or other composition containing an n-mer motif described herein (including but not limited to an engineered gene transfer agent particle, which is described in greater detail elsewhere herein). For example, different elements of the engineered viral (e.g., AAV) capsid system or other composition containing an n-mer motif described herein can each be operably linked to separate regulatory elements on separate vectors. RNA(s) of different elements of the engineered delivery

system described herein can be delivered to an animal or mammal or cell thereof to produce an animal or mammal or cell thereof that constitutively or inducibly or conditionally expresses different elements of the engineered viral (e.g., AAV) capsid system or other composition containing an n-mer motif described herein that incorporates one or more elements of the engineered viral (e.g., AAV) capsid system or other composition containing an n-mer motif described herein or contains one or more cells that incorporates and/or expresses one or more elements of the engineered viral (e.g., AAV) capsid system or other composition containing an n-mer motif described herein.

[0110] In some embodiments, two or more of the elements expressed from the same or different regulatory element(s) can be combined in a single vector, with one or more additional vectors providing any components of the system not included in the first vector. Engineered polynucleotides of the present invention that are combined in a single vector may be arranged in any suitable orientation, such as one element located 5' with respect to ("upstream" of) or 3' with respect to ("downstream" of) a second element. The coding sequence of one element may be located on the same or opposite strand of the coding sequence of a second element, and oriented in the same or opposite direction. In some embodiments, a single promoter drives expression of a transcript encoding one or more engineered viral (e.g., AAV) capsid proteins or other composition containing an n-mer motif described herein, embedded within one or more intron sequences (e.g., each in a different intron, two or more in at least one intron, or all in a single intron). In some embodiments, the engineered polynucleotides of the present invention (including but not limited to engineered viral polynucleotides) can be operably linked to and expressed from the same promoter.

Vector Features

[0111] The vectors can include additional features that can confer one or more functionalities to the vector, the polynucleotide to be delivered, a virus particle produced there from, or polypeptide expressed thereof. Such features include, but are not limited to, regulatory elements, selectable markers, molecular identifiers (e.g., molecular barcodes), stabilizing elements, and the like. It will be appreciated by those skilled in the art that the design of the expression vector and additional features included can depend on such factors as the choice of the host cell to be transformed, the level of expression desired, etc.

Regulatory Elements

[0112] In embodiments, the polynucleotides and/or vectors thereof described herein (including, but not limited to, the engineered AAV capsid polynucleotides of the present invention) can include one or more regulatory elements that can be operatively linked to the polynucleotide. The term "regulatory element" is intended to include promoters, enhancers, internal ribosomal entry sites (IRES), and other expression control elements (e.g., transcription termination signals, such as polyadenylation signals and poly-U sequences). Such regulatory elements are described, for example, in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Regulatory elements include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the nucleotide sequence only in certain host cells (e.g., tissue-specific regulatory sequences). A tissue-specific promoter can direct expression primarily in a desired tissue of interest, such as muscle, neuron, bone, skin, blood, specific organs (e.g., liver, brain), or particular cell types (e.g., lymphocytes). Regulatory elements may also direct expression in a temporal-dependent manner, such as in a cell-cycle dependent or developmental stage-dependent manner, which may or may not also be tissue or cell-type specific. In some embodiments, a vector comprises one or more pol III promoter (e.g., 1, 2, 3, 4, 5, or more pol III promoters), one or more pol II promoters (e.g., 1, 2, 3, 4, 5, or more pol II promoters), one or more pol I promoters (e.g., 1, 2, 3, 4, 5, or more pol I promoters), or combinations thereof. Examples of pol III promoters include, but are not limited to, U6 and H1 promoters. Examples of pol II promoters include, but are not limited to, the retroviral Rous sarcoma virus (RSV) LTR promoter (optionally with the RSV enhancer), the cytomegalovirus (CMV) promoter (optionally with the CMV enhancer) (see, e.g., Boshart et al, Cell, 41:521-530 (1985)), the SV40 promoter, the dihydrofolate reductase promoter, the β-actin promoter, the phosphoglycerol kinase (PGK) promoter, and the EF1α promoter. Also encompassed by the term "regulatory element" are enhancer elements, such as WPRE; CMV enhancers; the R-U5' segment in LTR of HTLV-I (Mol. Cell. Biol., Vol. 8(1), p. 466-472, 1988); SV40 enhancer; and the intron sequence between exons 2 and 3 of rabbit β-globin (Proc. Natl. Acad. Sci. USA., Vol. 78(3), p. 1527-31, 1981).

[0113] In some embodiments, the regulatory sequence can be a regulatory sequence described in U.S. Pat. No. 7,776,321, U.S. Pat. Pub. No. 2011/0027239, and PCT publication WO

2011/028929, the contents of which are incorporated by reference herein in their entirety. In some embodiments, the vector can contain a minimal promoter. In some embodiments, the minimal promoter is the Mecp2 promoter, tRNA promoter, or U6. In a further embodiment, the minimal promoter is tissue specific. In some embodiments, the length of the vector polynucleotide the minimal promoters and polynucleotide sequences is less than 4.4Kb.

[0114] To express a polynucleotide, the vector can include one or more transcriptional and/or translational initiation regulatory sequences, e.g., promoters, that direct the transcription of the gene and/or translation of the encoded protein in a cell. In some embodiments a constitutive promoter may be employed. Suitable constitutive promoters for mammalian cells are generally known in the art and include, but are not limited to SV40, CAG, CMV, EF-1α, β-actin, RSV, and PGK. Suitable constitutive promoters for bacterial cells, yeast cells, and fungal cells are generally known in the art, such as a T-7 promoter for bacterial expression and an alcohol dehydrogenase promoter for expression in yeast.

[0115] In some embodiments, the regulatory element can be a regulated promoter. "Regulated promoter" refers to promoters that direct gene expression not constitutively, but in a temporally- and/or spatially-regulated manner, and includes tissue-specific, tissue-preferred and inducible promoters. In some embodiments, the regulated promoter is a tissue specific promoter as previously discussed elsewhere herein. Regulated promoters include conditional promoters and inducible promoters. In some embodiments, conditional promoters can be employed to direct expression of a polynucleotide in a specific cell type, under certain environmental conditions, and/or during a specific state of development. Suitable tissue specific promoters can include, but are not limited to, liver specific promoters (e.g. APOA2, SERPIN A1 (hAAT), CYP3A4, and MIR122), pancreatic cell promoters (e.g. INS, IRS2, Pdx1, Alx3, Ppy), cardiac specific promoters (e.g. Myh6 (alpha MHC), MYL2 (MLC-2v), TNI3 (cTnl), NPPA (ANF), Slc8a1 (Ncx1)), central nervous system cell promoters (SYN1, GFAP, INA, NES, MOBP, MBP, TH, FOXA2 (HNF3 beta)), skin cell specific promoters (e.g. FLG, K14, TGM3), immune cell specific promoters, (e.g. ITGAM, CD43 promoter, CD14 promoter, CD45 promoter, CD68 promoter), urogenital cell specific promoters (e.g. Pbsn, Upk2, Sbp, Fer1l4), endothelial cell specific promoters (e.g. ENG), pluripotent and embryonic germ layer cell specific promoters (e.g. Oct4, NANOG, Synthetic Oct4, T brachyury, NES, SOX17, FOXA2, MIR122), and muscle cell specific promoter (e.g. Desmin).

Other tissue and/or cell specific promoters are discussed elsewhere herein and can be generally known in the art and are within the scope of this disclosure.

[0116] Inducible/conditional promoters can be positively inducible/conditional promoters (e.g. a promoter that activates transcription of the polynucleotide upon appropriate interaction with an activated activator, or an inducer (compound, environmental condition, or other stimulus) or a negative/conditional inducible promoter (e.g. a promoter that is repressed (e.g. bound by a repressor) until the repressor condition of the promotor is removed (e.g. inducer binds a repressor bound to the promoter stimulating release of the promoter by the repressor or removal of a chemical repressor from the promoter environment). The inducer can be a compound, environmental condition, or other stimulus. Thus, inducible/conditional promoters can be responsive to any suitable stimuli such as chemical, biological, or other molecular agents, temperature, light, and/or pH. Suitable inducible/conditional promoters include, but are not limited to, Tet-On, Tet-Off, Lac promoter, pBad, AlcA, LexA, Hsp70 promoter, Hsp90 promoter, pDawn, XVE/OlexA, GVG, and pOp/LhGR.

[0117] In some embodiments, the vector or system thereof can include one or more elements capable of translocating and/or expressing an engineered polynucleotide of the present invention (e.g., an engineered viral (e.g., AAV) capsid polynucleotide) to/in a specific cell component or organelle. Such organelles can include, but are not limited to, nucleus, ribosome, endoplasmic reticulum, Golgi apparatus, chloroplast, mitochondria, vacuole, lysosome, cytoskeleton, plasma membrane, cell wall, peroxisome, centrioles, etc.

Selectable Markers and Tags

[0118] One or more of the engineered polynucleotides of the present invention (e.g., an engineered viral (e.g., AAV) capsid polynucleotide) can be operably linked, fused to, or otherwise modified to include a polynucleotide that encodes or is a selectable marker or tag, which can be a polynucleotide or polypeptide. In some embodiments, the polypeptide encoding a polypeptide selectable marker can be incorporated in the engineered polynucleotide of the present invention (e.g., an engineered viral (e.g., AAV) capsid polynucleotide) such that the selectable marker polypeptide, when translated, is inserted between two amino acids between the N- and C- terminus of an engineered polypeptide (e.g., the engineered AAV capsid polypeptide) or at the N- and/or C-terminus of the engineered polypeptide (e.g., an engineered AAV capsid polypeptide). In some

embodiments, the selectable marker or tag is a polynucleotide barcode or unique molecular identifier (UMI).

[0119] It will be appreciated that the polynucleotide encoding such selectable markers or tags can be incorporated into a polynucleotide encoding one or more components of the engineered AAV capsid system described herein in an appropriate manner to allow expression of the selectable marker or tag. Such techniques and methods are described elsewhere herein and will be instantly appreciated by one of ordinary skill in the art in view of this disclosure. Many such selectable markers and tags are generally known in the art and are intended to be within the scope of this disclosure.

[0120] Suitable selectable markers and tags include, but are not limited to, affinity tags, such as chitin binding protein (CBP), maltose binding protein (MBP), glutathione-S-transferase (GST), poly(His) tag; solubilization tags such as thioredoxin (TRX) and poly(NANP), MBP, and GST; chromatography tags such as those consisting of polyanionic amino acids, such as FLAG-tag; epitope tags such as V5-tag, Myc-tag, HA-tag and NE-tag; protein tags that can allow specific enzymatic modification (such as biotinylation by biotin ligase) or chemical modification (such as reaction with FlAsH-EDT2 for fluorescence imaging), DNA and/or RNA segments that contain restriction enzyme or other enzyme cleavage sites; DNA segments that encode products that provide resistance against otherwise toxic compounds including antibiotics, such as, spectinomycin, ampicillin, kanamycin, tetracycline, Basta, neomycin phosphotransferase II (NEO), hygromycin phosphotransferase (HPT)) and the like; DNA and/or RNA segments that encode products that are otherwise lacking in the recipient cell (e.g., tRNA genes, auxotrophic markers); DNA and/or RNA segments that encode products which can be readily identified (e.g., phenotypic markers such as β-galactosidase, GUS; fluorescent proteins such as green fluorescent protein (GFP), cyan (CFP), yellow (YFP), red (RFP), luciferase, and cell surface proteins); polynucleotides that can generate one or more new primer sites for PCR (e.g., the juxtaposition of two DNA sequences not previously juxtaposed), DNA sequences not acted upon or acted upon by a restriction endonuclease or other DNA modifying enzyme, chemical, etc.; epitope tags (e.g. GFP, FLAG- and His-tags), and, DNA sequences that make a molecular barcode or unique molecular identifier (UMI), DNA sequences required for a specific modification (e.g., methylation) that allows its identification. Other suitable markers will be appreciated by those of skill in the art.

[0121] Selectable markers and tags can be operably linked to one or more components of the engineered AAV capsid system or other compositions and/or systems described herein via suitable linker, such as a glycine or glycine serine linkers as short as GS or GG up to $(GGGGG)_3$ (SEQ ID NO: 20482) or $(GGGGS)_3$ (SEQ ID NO: 20483). Other suitable linkers are described elsewhere herein.

[0122] The vector or vector system can include one or more polynucleotides encoding one or more n-mers. In some embodiments, the n-mer encoding polynucleotides can be included in the vector or vector system, such as a viral vector system, such that they are expressed within and/or on the virus particle(s) produced such that the virus particles can be targeted to specific cells, tissues, organs, etc. In some embodiments, the n-mer encoding polynucleotides can be included in the vector or vector system such that the engineered polynucleotide(s) of the present invention (e.g., an engineered viral (e.g., AAV) capsid polynucleotide(s)) and/or products expressed therefrom include the n-mer and can be targeted to specific cells, tissues, organs, etc. In some embodiments, such as non-viral carriers, the n-mer can be attached to the carrier (e.g., polymer, lipid, inorganic molecule etc.) and can be capable of targeting the carrier and any attached or associated engineered polynucleotide(s) of the present invention, the engineered polypeptides, or other compositions of the present invention described herein, to specific cells, tissues, organs, etc. In some embodiments, the specific cells are CNS cells.

Cell-free Vector and Polynucleotide Expression

[0123] In some embodiments, the polynucleotide(s) encoding an n-mer motif of the present invention can be expressed from a vector or suitable polynucleotide in a cell-free in vitro system. In some embodiments, the polynucleotide encoding one or more features of the engineered AAV capsid system can be expressed from a vector or suitable polynucleotide in a cell-free in vitro system. In other words, the polynucleotide can be transcribed and optionally translated in vitro. In vitro transcription/translation systems and appropriate vectors are generally known in the art and commercially available. Generally, in vitro transcription and in vitro translation systems replicate the processes of RNA and protein synthesis, respectively, outside of the cellular environment. Vectors and suitable polynucleotides for in vitro transcription can include T7, SP6, T3, promoter regulatory sequences that can be recognized and acted upon by an appropriate polymerase to transcribe the polynucleotide or vector.

[0124] *In vitro* translation can be stand-alone (e.g., translation of a purified polyribonucleotide) or linked/coupled to transcription. In some embodiments, the cell-free (or in vitro) translation system can include extracts from rabbit reticulocytes, wheat germ, and/or E. coli. The extracts can include various macromolecular components that are needed for translation of exogenous RNA (e.g., 70S or 80S ribosomes, tRNAs, aminoacyl-tRNA, synthetases, initiation, elongation factors, termination factors, etc.). Other components can be included or added during the translation reaction, including but not limited to, amino acids, energy sources (ATP, GTP), energy regenerating systems (creatine phosphate and creatine phosphokinase (eukaryotic systems)) (phosphoenol pyruvate and pyruvate kinase for bacterial systems), and other co-factors (Mg2+, K+, etc.). As previously mentioned, in vitro translation can be based on RNA or DNA starting material. Some translation systems can utilize an RNA template as starting material (e.g., reticulocyte lysates and wheat germ extracts). Some translation systems can utilize a DNA template as a starting material (e.g., E coli-based systems). In these systems transcription and translation are coupled and DNA is first transcribed into RNA, which is subsequently translated. Suitable standard and coupled cell-free translation systems are generally known in the art and are commercially available.

Codon Optimization of Vector Polynucleotides

[0125] As described elsewhere herein, the polynucleotide encoding an n-mer motif of the present invention and/or other polynucleotides described herein or the transgene contained within the recombinant AAV genome can be codon optimized. In some embodiments, polynucleotides of the engineered AAV capsid system described herein can be codon optimized. In some embodiments, one or more polynucleotides contained in a vector ("vector polynucleotides") described herein that are in addition to an optionally codon optimized polynucleotide encoding an n-mer motif, including but not limited to, embodiments of the engineered AAV capsid system described herein, can be codon optimized. In general, codon optimization refers to a process of modifying a nucleic acid sequence for enhanced expression in the host cells of interest by replacing at least one codon (e.g., about or more than about 1, 2, 3, 4, 5, 10, 15, 20, 25, 50, or more codons) of the native sequence with codons that are more frequently or most frequently used in the genes of that host cell while maintaining the native amino acid sequence. Various species exhibit particular bias for certain codons of a particular amino acid. Codon bias (differences in codon

usage between organisms) often correlates with the efficiency of translation of messenger RNA (mRNA), which is in turn believed to be dependent on, among other things, the properties of the codons being translated and the availability of particular transfer RNA (tRNA) molecules. The predominance of selected tRNAs in a cell is generally a reflection of the codons used most frequently in peptide synthesis. Accordingly, genes can be tailored for optimal gene expression in a given organism based on codon optimization. Codon usage tables are readily available, for example, at the "Codon Usage Database" available at www.kazusa.or.jp/codon/ and these tables can be adapted in a number of ways. See Nakamura, Y., et al. "Codon usage tabulated from the international DNA sequence databases: status for the year 2000" Nucl. Acids Res. 28:292 (2000). Computer algorithms for codon optimizing a particular sequence for expression in a particular host cell are also available, such as Gene Forge (Aptagen; Jacobus, PA), are also available. In some embodiments, one or more codons (e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 50, or more, or all codons) in a sequence encoding a DNA/RNA-targeting Cas protein corresponds to the most frequently used codon for a particular amino acid. As to codon usage in yeast, reference is made to the online Yeast Genome database available at www.yeastgenome.org/community/codon_usage.shtml, or *Codon selection in yeast*, Bennetzen and Hall, J Biol Chem. 1982 Mar 25;257(6):3026-31. As to codon usage in plants including algae, reference is made to *Codon usage in higher plants, green algae, and cyanobacteria*, Campbell and Gowri, Plant Physiol. 1990 Jan; 92(1): 1–11.; as well as *Codon usage in plant genes*, Murray et al, Nucleic Acids Res. 1989 Jan 25;17(2):477-98; or *Selection on the codon bias of chloroplast and cyanelle genes in different plant and algal lineages*, Morton BR, J Mol Evol. 1998 Apr;46(4):449-59.

[0126] The vector polynucleotide can be codon optimized for expression in a specific cell-type, tissue type, organ type, and/or subject type. In some embodiments, a codon optimized sequence is a sequence optimized for expression in a eukaryote, e.g., humans (i.e., being optimized for expression in a human or human cell), or for another eukaryote, such as another animal (e.g., a mammal or avian) as is described elsewhere herein. Such codon optimized sequences are within the ambit of the ordinary skilled artisan in view of the description herein. In some embodiments, the polynucleotide is codon optimized for a specific cell type. Such cell types can include, but are not limited to, epithelial cells (including skin cells, cells lining the gastrointestinal tract, cells lining other hollow organs), nerve cells (nerves, brain cells, spinal column cells, nerve support cells (e.g.,

astrocytes, glial cells, Schwann cells etc.) , muscle cells (e.g., cardiac muscle, smooth muscle cells, and skeletal muscle cells), connective tissue cells (fat and other soft tissue padding cells, bone cells, tendon cells, cartilage cells), blood cells, stem cells and other progenitor cells, immune system cells, germ cells, and combinations thereof. Such codon optimized sequences are within the ambit of the ordinary skilled artisan in view of the description herein. In some embodiments, the polynucleotide is codon optimized for a specific tissue type. Such tissue types can include, but are not limited to, muscle tissue, connective tissue, nervous tissue, and epithelial tissue. Such codon optimized sequences are within the ambit of the ordinary skilled artisan in view of the description herein. In some embodiments, the polynucleotide is codon optimized for a specific organ. Such organs include, but are not limited to, muscles, skin, intestines, liver, spleen, brain, lungs, stomach, heart, kidneys, gallbladder, pancreas, bladder, thyroid, bone, blood vessels, blood, and combinations thereof. Such codon optimized sequences are within the ambit of the ordinary skilled artisan in view of the description herein.

[0127] In some embodiments, a vector polynucleotide is codon optimized for expression in particular cells, such as prokaryotic or eukaryotic cells. The eukaryotic cells may be those of or derived from a particular organism, such as a plant or a mammal, including but not limited to human, or non-human eukaryote or animal or mammal as discussed herein, e.g., mouse, rat, rabbit, dog, livestock, or non-human mammal or primate.

Non-Viral Vectors and Carriers

[0128] In some embodiments, the vector is a non-viral vector or carrier. In some embodiments, non-viral vectors can have the advantage(s) of reduced toxicity and/or immunogenicity and/or increased bio-safety as compared to viral vectors The terms of art "Non-viral vectors and carriers" and as used herein in this context refers to molecules and/or compositions that are not based on one or more component of a virus or virus genome (excluding any nucleotide to be delivered and/or expressed by the non-viral vector) that can be capable of attaching to, incorporating, coupling, and/or otherwise interacting with an engineered capsid polynucleotide (e.g., an engineered AAV capsid polynucleotide) or other composition of the present invention described herein and can be capable of ferrying the polynucleotide to a cell and/or expressing the polynucleotide. It will be appreciated that this does not exclude the inclusion of a virus-based polynucleotide that is to be delivered. For example, if a gRNA to be delivered is directed against a virus component and it is

inserted or otherwise coupled to an otherwise non-viral vector or carrier, this would not make said vector a "viral vector". Non-viral vectors and carriers include naked polynucleotides, chemical-based carriers, polynucleotide (non-viral) based vectors, and particle-based carriers. It will be appreciated that the term "vector" as used in the context of non-viral vectors and carriers refers to polynucleotide vectors and "carriers" used in this context refers to a non-nucleic acid or polynucleotide molecule or composition that be attached to or otherwise interact with a polynucleotide to be delivered, such as an engineered AAV capsid polynucleotide of the present invention.

Naked Polynucleotides

[0129] In some embodiments one or more engineered AAV capsid polynucleotides or other polynucleotides of the present invention described elsewhere herein can be included in a naked polynucleotide. The term of art "naked polynucleotide" as used herein refers to polynucleotides that are not associated with another molecule (e.g., proteins, lipids, and/or other molecules) that can often help protect it from environmental factors and/or degradation. As used herein, associated with includes, but is not limited to, linked to, adhered to, adsorbed to, enclosed in, enclosed in or within, mixed with, and the like. Naked polynucleotides that include one or more of the engineered AAV capsid polynucleotides or other polynucleotides of the present invention described herein can be delivered directly to a host cell and optionally expressed therein. The naked polynucleotides can have any suitable two- and three-dimensional configurations. By way of non-limiting examples, naked polynucleotides can be single-stranded molecules, double stranded molecules, circular molecules (e.g., plasmids and artificial chromosomes), molecules that contain portions that are single stranded and portions that are double stranded (e.g., ribozymes), and the like. In some embodiments, the naked polynucleotide contains only the engineered AAV capsid polynucleotide(s) or other polynucleotides of the present invention. In some embodiments, the naked polynucleotide can contain other nucleic acids and/or polynucleotides in addition to the engineered AAV capsid polynucleotide(s) or other polynucleotides of the present invention described elsewhere herein. The naked polynucleotides can include one or more elements of a transposon system. Transposons and system thereof are described in greater detail elsewhere herein.

Non-Viral Polynucleotide Vectors

[0130] In some embodiments, one or more of the engineered AAV capsid polynucleotides or other polynucleotides of the present invention can be included in a non-viral polynucleotide vector. Suitable non-viral polynucleotide vectors include, but are not limited to, transposon vectors and vector systems, plasmids, bacterial artificial chromosomes, yeast artificial chromosomes, AR(antibiotic resistance)-free plasmids and miniplasmids, circular covalently closed vectors (e.g., minicircles, minivectors, miniknots,), linear covalently closed vectors ("dumbbell shaped"), MIDGE (minimalistic immunologically defined gene expression) vectors, MiLV (micro-linear vector) vectors, Ministrings, mini-intronic plasmids, PSK systems (post-segregationally killing systems), ORT (operator repressor titration) plasmids, and the like. See e.g., Hardee et al. 2017. Genes. 8(2):65.

[0131] In some embodiments, the non-viral polynucleotide vector can have a conditional origin of replication. In some embodiments, the non-viral polynucleotide vector can be an ORT plasmid. In some embodiments, the non-viral polynucleotide vector can have a minimalistic immunologically defined gene expression. In some embodiments, the non-viral polynucleotide vector can have one or more post-segregationally killing system genes. In some embodiments, the non-viral polynucleotide vector is AR-free. In some embodiments, the non-viral polynucleotide vector is a minivector. In some embodiments, the non-viral polynucleotide vector includes a nuclear localization signal. In some embodiments, the non-viral polynucleotide vector can include one or more CpG motifs. In some embodiments, the non-viral polynucleotide vectors can include one or more scaffold/matrix attachment regions (S/MARs). See e.g., Mirkovitch et al. 1984. Cell. 39:223-232, Wong et al. 2015. Adv. Genet. 89:113-152, whose techniques and vectors can be adapted for use in the present invention. S/MARs are AT-rich sequences that play a role in the spatial organization of chromosomes through DNA loop base attachment to the nuclear matrix. S/MARs are often found close to regulatory elements such as promoters, enhancers, and origins of DNA replication. Inclusion of one or S/MARs can facilitate a once-per-cell-cycle replication to maintain the non-viral polynucleotide vector as an episome in daughter cells. In embodiments, the S/MAR sequence is located downstream of an actively transcribed polynucleotide (e.g., one or more engineered AAV capsid polynucleotides or other polynucleotides or molecules of the present invention) included in the non-viral polynucleotide vector. In some embodiments, the S/MAR can

be a S/MAR from the beta-interferon gene cluster. See e.g., Verghese et al. 2014. Nucleic Acid Res. 42:e53; Xu et al. 2016. Sci. China Life Sci. 59:1024-1033; Jin et al. 2016. 8:702-711; Koirala et al. 2014. Adv. Exp. Med. Biol. 801:703-709; and Nehlsen et al. 2006. Gene Ther. Mol. Biol. 10:233-244, whose techniques and vectors can be adapted for use in the present invention.

[0132] In some embodiments, the non-viral vector is a transposon vector or system thereof. As used herein, "transposon" (also referred to as transposable element) refers to a polynucleotide sequence that is capable of moving form location in a genome to another. There are several classes of transposons. Transposons include retrotransposons and DNA transposons. Retrotransposons require the transcription of the polynucleotide that is moved (or transposed) in order to transpose the polynucleotide to a new genome or polynucleotide. DNA transposons are those that do not require reverse transcription of the polynucleotide that is moved (or transposed) in order to transpose the polynucleotide to a new genome or polynucleotide. In some embodiments, the non-viral polynucleotide vector can be a retrotransposon vector. In some embodiments, the retrotransposon vector includes long terminal repeats. In some embodiments, the retrotransposon vector does not include long terminal repeats. In some embodiments, the non-viral polynucleotide vector can be a DNA transposon vector. DNA transposon vectors can include a polynucleotide sequence encoding a transposase. In some embodiments, the transposon vector is configured as a non-autonomous transposon vector, meaning that the transposition does not occur spontaneously on its own. In some of these embodiments, the transposon vector lacks one or more polynucleotide sequences encoding proteins required for transposition. In some embodiments, the non-autonomous transposon vectors lack one or more Ac elements.

[0133] In some embodiments, a non-viral polynucleotide transposon vector system can include a first polynucleotide vector that contains the engineered AAV capsid polynucleotide(s) or other polynucleotides, or molecules of the present invention described herein flanked on the 5' and 3' ends by transposon terminal inverted repeats (TIRs) and a second polynucleotide vector that includes a polynucleotide capable of encoding a transposase coupled to a promoter to drive expression of the transposase. When both are expressed in the same cell the transposase can be expressed from the second vector and can transpose the material between the TIRs on the first vector (e.g., the engineered AAV capsid polynucleotide(s) or other polynucleotides or molecules of the present invention) and integrate it into one or more positions in the host cell's genome. In

some embodiments the transposon vector or system thereof can be configured as a gene trap. In some embodiments, the TIRs can be configured to flank a strong splice acceptor site followed by a reporter and/or other gene (e.g., one or more of the engineered AAV capsid polynucleotide(s) or other polynucleotides or molecules of the present invention) and a strong poly A tail. When transposition occurs while using this vector or system thereof, the transposon can insert into an intron of a gene and the inserted reporter or other gene can provoke a mis-splicing process and as a result it in activates the trapped gene.

[0134] Any suitable transposon system can be used. Suitable transposon and systems thereof can include Sleeping Beauty transposon system (Tc1/mariner superfamily) (see e.g., Ivics et al. 1997. Cell. 91(4): 501-510), piggyBac (piggyBac superfamily) (see e.g., Li et al. 2013 110(25): E2279-E2287 and Yusa et al. 2011. PNAS. 108(4): 1531-1536), Tol2 (superfamily hAT), Frog Prince (Tc1/mariner superfamily) (see e.g., Miskey et al. 2003 Nucleic Acid Res. 31(23):6873-6881) and variants thereof.

Chemical Carriers

[0135] In some embodiments, the engineered AAV capsid polynucleotide(s) or other polynucleotides or other molecules of the present invention described herein can be coupled to a chemical carrier. Chemical carriers that can be suitable for delivery of polynucleotides can be broadly classified into the following classes: (i) inorganic particles, (ii) lipid-based, (iii) polymer-based, and (iv) peptide based. They can be categorized as (1) those that can form condensed complexes with a polynucleotide (such as the engineered AAV capsid polynucleotide(s) of the present invention), (2) those capable of targeting specific cells, (3) those capable of increasing delivery of the polynucleotide or other molecules (such as the engineered AAV capsid polynucleotide(s))of the present invention to the nucleus or cytosol of a host cell, (4) those capable of disintegrating from DNA/RNA in the cytosol of a host cell, and (5) those capable of sustained or controlled release. It will be appreciated that any one given chemical carrier can include features from multiple categories. The term "particle" as used herein, refers to any suitable sized particles for delivery of the compositions (including particles, polypeptides, polynucleotides, and other compositions described herein) present invention described herein. Suitable sizes include macro-, micro-, and nano-sized particles.

[0136] In some embodiments, the non-viral carrier can be an inorganic particle. In some embodiments, the inorganic particle, can be a nanoparticle. The inorganic particles can be configured and optimized by varying size, shape, and/or porosity. In some embodiments, the inorganic particles are optimized to escape from the reticulo endothelial system. In some embodiments, the inorganic particles can be optimized to protect an entrapped molecule from degradation. The suitable inorganic particles that can be used as non-viral carriers in this context can include, but are not limited to, calcium phosphate, silica, metals (e.g., gold, platinum, silver, palladium, rhodium, osmium, iridium, ruthenium, mercury, copper, rhenium, titanium, niobium, tantalum, and combinations thereof), magnetic compounds, particles, and materials, (e.g., supermagnetic iron oxide and magnetite), quantum dots, fullerenes (e.g., carbon nanoparticles, nanotubes, nanostrings, and the like), and combinations thereof. Other suitable inorganic non-viral carriers are discussed elsewhere herein.

[0137] In some embodiments, the non-viral carrier can be lipid-based. Suitable lipid-based carriers are also described in greater detail herein. In some embodiments, the lipid-based carrier includes a cationic lipid or an amphiphilic lipid that is capable of binding or otherwise interacting with a negative charge on the polynucleotide to be delivered (e.g., such as an engineered AAV capsid polynucleotide of the present invention). In some embodiments, chemical non-viral carrier systems can include a polynucleotide (such as the engineered AAV capsid polynucleotide(s)) or other composition or molecule of the present invention) and a lipid (such as a cationic lipid). These are also referred to in the art as lipoplexes. Other embodiments of lipoplexes are described elsewhere herein. In some embodiments, the non-viral lipid-based carrier can be a lipid nano emulsion. Lipid nano emulsions can be formed by the dispersion of an immiscible liquid in another stabilized emulsifying agent and can have particles of about 200 nm that are composed of the lipid, water, and surfactant that can contain the polynucleotide to be delivered (e.g., the engineered AAV capsid polynucleotide(s) of the present invention). In some embodiments, the lipid-based non-viral carrier can be a solid lipid particle or nanoparticle.

[0138] In some embodiments, the non-viral carrier can be peptide-based. In some embodiments, the peptide-based non-viral carrier can include one or more cationic amino acids. In some embodiments, 35 to 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 99 or 100 % of the amino acids are cationic. In some embodiments, peptide carriers can be used in conjunction with other

types of carriers (e.g., polymer-based carriers and lipid-based carriers to functionalize these carriers). In some embodiments, the functionalization is targeting a host cell. Suitable polymers that can be included in the polymer-based non-viral carrier can include, but are not limited to, polyethylenimine (PEI), chitosan, poly (DL-lactide) (PLA), poly (DL-Lactide-co-glycoside) (PLGA), dendrimers (see e.g., US Pat. Pub. 2017/0079916 whose techniques and compositions can be adapted for use with the engineered AAV capsid polynucleotides of the present invention), polymethacrylate, and combinations thereof.

[0139] In some embodiments, the non-viral carrier can be configured to release an engineered delivery system polynucleotide that is associated with or attached to the non-viral carrier in response to an external stimulus, such as pH, temperature, osmolarity, concentration of a specific molecule or composition (e.g., calcium, NaCl, and the like), pressure and the like. In some embodiments, the non-viral carrier can be a particle that is configured includes one or more of the engineered AAV capsid polynucleotides or other compositions of the present invention describe herein and an environmental triggering agent response element, and optionally a triggering agent. In some embodiments, the particle can include a polymer that can be selected from the group of polymethacrylates and polyacrylates. In some embodiments, the non-viral particle can include one or more embodiments of the compositions microparticles described in US Pat. Pubs. 20150232883 and 20050123596, whose techniques and compositions can be adapted for use in the present invention.

[0140] In some embodiments, the non-viral carrier can be a polymer-based carrier. In some embodiments, the polymer is cationic or is predominantly cationic such that it can interact in a charge-dependent manner with the negatively charged polynucleotide to be delivered (such as the engineered AAV capsid polynucleotide(s) of the present invention). Polymer-based systems are described in greater detail elsewhere herein.

Viral Vectors

[0141] In some embodiments, the vector is a viral vector. The term of art "viral vector" and as used herein in this context refers to polynucleotide based vectors that contain one or more elements from or based upon one or more elements of a virus that can be capable of expressing and packaging a polynucleotide, such as an engineered AAV capsid polynucleotide, cargo, or other composition or molecule of the present invention, into a virus particle and producing said virus

particle when used alone or with one or more other viral vectors (such as in a viral vector system). Viral vectors and systems thereof can be used for producing viral particles for delivery of and/or expression and/or generation of one or more compositions of the present invention described herein (including, but not limited to, any viral particle and associated cargo). The viral vector can be part of a viral vector system involving multiple vectors. In some embodiments, systems incorporating multiple viral vectors can increase the safety of these systems. Suitable viral vectors can include adenoviral-based vectors, adeno associated vectors, helper-dependent adenoviral (HdAd) vectors, hybrid adenoviral vectors, and the like. Other embodiments of viral vectors and viral particles produce therefrom are described elsewhere herein. In some embodiments, the viral vectors are configured to produce replication incompetent viral particles for improved safety of these systems.

Adenoviral vectors, Helper-dependent Adenoviral vectors, and Hybrid Adenoviral Vectors

[0142] In some embodiments, the vector can be an adenoviral vector. In some embodiments, the adenoviral vector can include elements such that the virus particle produced using the vector or system thereof can be serotype 2, 5, or 9. In some embodiments, the polynucleotide to be delivered via the adenoviral particle can be up to about 8 kb. Thus, in some embodiments, an adenoviral vector can include a DNA polynucleotide to be delivered that can range in size from about 0.001 kb to about 8 kb. Adenoviral vectors have been used successfully in several contexts (see e.g., Teramato et al. 2000. Lancet. 355:1911-1912; Lai et al. 2002. DNA Cell. Biol. 21:895-913; Flotte et al., 1996. Hum. Gene. Ther. 7:1145-1159; and Kay et al. 2000. Nat. Genet. 24:257-261. The vector can encode the engineered AAV capsids, said capsids forming adenoviral particles.

[0143] In some embodiments the vector can be a helper-dependent adenoviral vector or system thereof. These are also referred to in the field as "gutless" or "gutted" vectors and are a modified generation of adenoviral vectors (see e.g., Thrasher et al. 2006. Nature. 443:E5-7). In embodiments of the helper-dependent adenoviral vector system one vector (the helper) can contain all the viral genes required for replication but contains a conditional gene defect in the packaging domain. The second vector of the system can contain only the ends of the viral genome, one or more engineered AAV capsid polynucleotides, and the native packaging recognition signal, which can allow selective packaged release from the cells (see e.g., Cideciyan et al. 2009. N Engl J Med. 361:725-

727). Helper-dependent Adenoviral vector systems have been successful for gene delivery in several contexts (see e.g., Simonelli et al. 2010. J Am Soc Gene Ther. 18:643-650; Cideciyan et al. 2009. N Engl J Med. 361:725-727; Crane et al. 2012. Gene Ther. 19(4):443-452; Alba et al. 2005. Gene Ther. 12:18-S27; Croyle et al. 2005. Gene Ther. 12:579-587; Amalfitano et al. 1998. J. Virol. 72:926-933; and Morral et al. 1999. PNAS. 96:12816-12821). The techniques and vectors described in these publications can be adapted for inclusion and delivery of the engineered AAV capsid polynucleotides described herein. In some embodiments, the polynucleotide to be delivered via the viral particle produced from a helper-dependent adenoviral vector or system thereof can be up to about 38 kb. Thus, in some embodiments, a adenoviral vector can include a DNA polynucleotide to be delivered that can range in size from about 0.001 kb to about 37 kb (see e.g., Rosewell et al. 2011. J. Genet. Syndr. Gene Ther. Suppl. 5:001).

[0144] In some embodiments, the vector is a hybrid-adenoviral vector or system thereof. Hybrid adenoviral vectors are composed of the high transduction efficiency of a gene-deleted adenoviral vector and the long-term genome-integrating potential of adeno-associated, retroviruses, lentivirus, and transposon based-gene transfer. In some embodiments, such hybrid vector systems can result in stable transduction and limited integration site. See e.g., Balague et al. 2000. Blood. 95:820-828; Morral et al. 1998. Hum. Gene Ther. 9:2709-2716; Kubo and Mitani. 2003. J. Virol. 77(5): 2964-2971; Zhang et al. 2013. PloS One. 8(10) e76771; and Cooney et al. 2015. Mol. Ther. 23(4):667-674), whose techniques and vectors described therein can be modified and adapted for use in the engineered AAV capsid system of the present invention. In some embodiments, a hybrid-adenoviral vector can include one or more features of a retrovirus and/or an adeno-associated virus. In some embodiments the hybrid-adenoviral vector can include one or more features of a spuma retrovirus or foamy virus (FV). See e.g., Ehrhardt et al. 2007. Mol. Ther. 15:146-156 and Liu et al. 2007. Mol. Ther. 15:1834-1841, whose techniques and vectors described therein can be modified and adapted for use in the engineered AAV capsid system of the present invention. Advantages of using one or more features from the FVs in the hybrid-adenoviral vector or system thereof can include the ability of the viral particles produced therefrom to infect a broad range of cells, a large packaging capacity as compared to other retroviruses, and the ability to persist in quiescent (non-dividing) cells. See also e.g., Ehrhardt et al. 2007. Mol. Ther. 156:146-

156 and Shuji et al. 2011. Mol. Ther. 19:76-82, whose techniques and vectors described therein can be modified and adapted for use in the engineered AAV capsid system of the present invention.

Adeno Associated Vectors

[0145] In an embodiment, the engineered vector or system thereof can be an adeno-associated vector (AAV). See, e.g., West et al., Virology 160:38-47 (1987); U.S. Pat. No. 4,797,368; WO 93/24641; Kotin, Human Gene Therapy 5:793-801 (1994); and Muzyczka, J. Clin. Invest. 94:1351 (1994). Although similar to adenoviral vectors in some of their features, AAVs have some deficiency in their replication and/or pathogenicity and thus can be safer that adenoviral vectors. In some embodiments the AAV can integrate into a specific site on chromosome 19 of a human cell with no observable side effects. In some embodiments, the capacity of the AAV vector, system thereof, and/or AAV particles can be up to about 4.7 kb. The AAV vector or system thereof can include one or more engineered capsid polynucleotides described herein.

[0146] The AAV vector or system thereof can be operably linked to a regulatory sequence, said regulatory sequence encoding one or more regulatory molecules. In some embodiments the regulatory molecules can be promoters, enhancers, repressors and the like, which are described in greater detail elsewhere herein. In some embodiments, the AAV vector or system thereof can include one or more polynucleotides that can encode one or more regulatory proteins. In some embodiments, the promoter can be a tissue specific promoter as previously discussed. In some embodiments, the tissue specific promoter can drive expression of an engineered capsid AAV capsid polynucleotide described herein.

[0147] The AAV vector or system thereof can include one or more polynucleotides that can encode one or more capsid proteins, such as the engineered AAV capsid proteins described elsewhere herein. The engineered capsid proteins can be capable of assembling into a protein shell (an engineered capsid) of the AAV virus particle. The engineered capsid can have a cell-, tissue-, and/or organ-specific tropism.

[0148] In some embodiments, the AAV vector or system thereof can include one or more adenovirus helper factors or polynucleotides that can encode one or more adenovirus helper factors. Such adenovirus helper factors can include, but are not limited, E1A, E1B, E2A, E4ORF6, and VA RNAs. In some embodiments, a producing host cell line expresses one or more of the adenovirus helper factors.

[0149] The AAV vector or system thereof can be configured to produce AAV particles having a specific serotype. In some embodiments, the serotype can be AAV-1, AAV-2, AAV-3, AAV-4, AAV-5, AAV-6, AAV-8, AAV-9 or any combinations thereof. In some embodiments, the AAV can be AAV1, AAV-2, AAV-5, AAV-9 or any combination thereof. One can select the AAV of the AAV with regard to the cells to be targeted; e.g., one can select AAV serotypes 1, 2, 5, 9 or a hybrid capsid AAV-1, AAV-2, AAV-5, AAV-9 or any combination thereof for targeting brain and/or neuronal cells; and one can select AAV-4 for targeting cardiac tissue; and one can select AAV-8 for delivery to the liver. Thus, in some embodiments, an AAV vector or system thereof capable of producing AAV particles capable of targeting the brain and/or neuronal cells can be configured to generate AAV particles having serotypes 1, 2, 5 or a hybrid capsid AAV-1, AAV-2, AAV-5 or any combination thereof. In some embodiments, an AAV vector or system thereof capable of producing AAV particles capable of targeting cardiac tissue can be configured to generate an AAV particle having an AAV-4 serotype. In some embodiments, an AAV vector or system thereof capable of producing AAV particles capable of targeting the liver can be configured to generate an AAV having an AAV-8 serotype. See also Srivastava. 2017. Curr. Opin. Virol. 21:75-80.

[0150] It will be appreciated that while the different serotypes can provide some level of cell, tissue, and/or organ specificity, each serotype still is multi-tropic and thus can result in tissue-toxicity if using that serotype to target a tissue that the serotype is less efficient in transducing. Thus, in addition to achieving some tissue targeting capacity via selecting an AAV of a particular serotype, it will be appreciated that the tropism of the AAV serotype can be modified by an engineered AAV capsid described herein. As described elsewhere herein, variants of wild-type AAV of any serotype can be generated via a method described herein and determined to have a particular cell-specific tropism, which can be the same or different as that of the reference wild-type AAV serotype. In some embodiments, the cell, tissue, and/or specificity of the wild-type serotype can be enhanced (e.g., made more selective or specific for a particular cell type that the serotype is already biased towards). For example, wild-type AAV-9 is biased towards muscle and brain in humans (see e.g., Srivastava. 2017. Curr. Opin. Virol. 21:75-80.) By including an engineered AAV capsid and/or capsid protein variant of wild-type AAV-9 as described herein, the bias for e.g., brain can be reduced or eliminated and/or the septicity increased such that the brain

specificity appears reduced in comparison, thus enhancing the specificity for the muscle as compared to the wild-type AAV-9. As previously mentioned, inclusion of an engineered capsid and/or capsid protein variant of a wild-type AAV serotype can have a different tropism than the wild-type reference AAV serotype. For example, an engineered AAV capsid and/or capsid protein variant of AAV-9 can have specificity for a tissue other than muscle or brain in humans.

[0151] In some embodiments, the AAV vector is a hybrid AAV vector or system thereof. Hybrid AAVs are AAVs that include genomes with elements from one serotype that are packaged into a capsid derived from at least one different serotype. For example, if it is the rAAV2/5 that is to be produced, and if the production method is based on the helper-free, transient transfection method discussed below, the 1st plasmid and the 3rd plasmid (the adeno helper plasmid) will be the same as discussed for rAAV2 production. However, the 2nd plasmid, the pRepCap will be different. In this plasmid, called pRep2/Cap5, the Rep gene is still derived from AAV2, while the Cap gene is derived from AAV5. The production scheme is the same as the above-mentioned approach for AAV2 production. The resulting rAAV is called rAAV2/5, in which the genome is based on recombinant AAV2, while the capsid is based on AAV5. It is assumed the cell or tissue-tropism displayed by this AAV2/5 hybrid virus should be the same as that of AAV5. It will be appreciated that wild-type hybrid AAV particles suffer the same specificity issues as with the non-hybrid wild-type serotypes previously discussed.

[0152] Advantages achieved by the wild-type based hybrid AAV systems can be combined with the increased and customizable cell-specificity that can be achieved with the engineered AAV capsids can be combined by generating a hybrid AAV that can include an engineered AAV capsid described elsewhere herein. It will be appreciated that hybrid AAVs can contain an engineered AAV capsid containing a genome with elements from a different serotype than the reference wild-type serotype that the engineered AAV capsid is a variant of. For example, a hybrid AAV can be produced that includes an engineered AAV capsid that is a variant of an AAV-9 serotype that is used to package a genome that contains components (e.g., AAV2 ITRs) from an AAV-2 serotype. As with wild-type based hybrid AAVs previously discussed, the tropism of the resulting AAV particle will be that of the engineered AAV capsid.

[0153] A tabulation of certain wild-type AAV serotypes as to these cells can be found in Grimm, D. et al, J. Virol. 82: 5887-5911 (2008) reproduced below as **Table A**. Further tropism details can be found in Srivastava. 2017. Curr. Opin. Virol. 21:75-80 as previously discussed.

Table A

Cell Line	AAV-1	AAV-2	AAV-3	AAV-4	AAV-5	AAV-6	AAV-8	AAV-9
Huh-7	13	100	2.5	0.0	0.1	10	0.7	0.0
HEK293	25	100	2.5	0.1	0.1	5	0.7	0.1
HeLa	3	100	2.0	0.1	6.7	1	0.2	0.1
HepG2	3	100	16.7	0.3	1.7	5	0.3	ND
Hep1A	20	100	0.2	1.0	0.1	1	0.2	0.0
911	17	100	11	0.2	0.1	17	0.1	ND
CHO	100	100	14	1.4	333	50	10	1.0
COS	33	100	33	3.3	5.0	14	2.0	0.5
MeWo	10	100	20	0.3	6.7	10	1.0	0.2
NIH3T3	10	100	2.9	2.9	0.3	10	0.3	ND
A549	14	100	20	ND	0.5	10	0.5	0.1
HT1180	20	100	10	0.1	0.3	33	0.5	0.1
Monocytes	1111	100	ND	ND	125	1429	ND	ND
Immature DC	2500	100	ND	ND	222	2857	ND	ND
Mature DC	2222	100	ND	ND	333	3333	ND	ND

[0154] In example embodiments, the AAV vector or system thereof is AAV rh.74 or AAV rh.10.

[0155] In example embodiments, the AAV vector or system thereof is configured as a "gutless" vector, similar to that described in connection with a retroviral vector. In some embodiments, the "gutless" AAV vector or system thereof can have the cis-acting viral DNA elements involved in genome amplification and packaging in linkage with the heterologous sequences of interest (e.g., a transgene encoding a therapeutic protein or nucleic acid of interest)).

Vectors Encoding the Transgene

[0156] In one example embodiment, the vector encoding the transgene (also referred to as "an artificial genome") comprises the transgene to be delivered flanked on either side by AAV ITRs. Only ~145 bp AAV ITRs are required for recombinant AAV (rAAV) propagation because they participate in vector production, induce transgene expression, and ensure continual cell transduction. Accordingly, ~96% of the AAV genome can be removed for gene therapy. For

example, the rep and cap genes can be substituted for the expression cassette containing a promoter (such as those described herein), a therapeutic transgene (for example, IDS) and a poly(A) tail forms the essence of all AAV vectors.

[0157] In example embodiments, additional modifications may be implemented to further increase the efficacy of the AAV. For example, the AAV ITRs may be modified to increase the expression of the rAAV vector upon transduction, which may allow the transgene to be expressed without second-strand DNA synthesis; the promoter may be modifyed to increase transcription; and the codons in the transgene may be engineered to modify mRNA production and/or translation.

[0158] In example embodiments, the ITRs are modified to overcome second-strand synthesis after infection. The AAV transduction rate is restricted by the synthesis of dsDNA from the single-stranded AAV genome. ITRs initiate second-strand synthesis. In an example embodiment, modified ITRs are no longer suitable substrates for the Rep68 and Rep78 proteins. As a result, the terminal resolution of replication is obviated and specific self-complementary AAV (scAAV) replication intermediates are produced. The scAAV intermediates comprise plus and minus strands of DNA fused by the modified ITRs encapsulated into the virion shell. Wild-type AAVs package either a single plus-strand or minus-strand DNA. The modified scAAV intermediates are delivered to the nucleus, these plus and minus strands instantaneously anneal to form dsDNA.

[0159] In example embodiments, the cis-elements are optimized for targeted delivery. The cis-elements are optimized because the packaging capacity of AAVs is restricted. In an example embodiment, small cis-elements replace long promoter sequences for the delivery of large therapeutic transgenes (e.g., 4.4–4.5 kbs).

[0160] In example embodiments, several strategies may be used to deliver transgenes using AAV vectors. Example approach 1 takes advantage of an AAV genome concatemerized via the homologous recombination of ITR sequences. In this approach, transgene cassettes may be split into two or more vectors, which are then delivered to the same cells. After the virus is uncoated, an intact transgene is formed by the homologous recombination between the two or more fragments.

[0161] In example approach 2, truncated transgene fragments of different lengths are packaged into different AAV virions at undefined locations on the vector genome. Either homologous recombination of the overlapping regions of the different AAV vector genomes or annealing of

different AAV vector genomes at complementary regions via single-stranded templates produces the transgene cassette. In example embodiments, overlapping fragments may be added to the end of the individual AAV vectors to encourage homologous recombination.

[0162] In example approach 3, a hybrid dual-vector incorporates an overlapping region with intron splice sites in the split vector transgenes. Approach 3 uses concatemerization activity of AAV genomes to bring independent AAV vector genomes together. Recombination (for example, the starting vectors are segregated into a two halves each carrying the 5′ and 3′ splicing elements, respectively), and splicing provide the appropriate transgene protein. This strategy may increase the expression of full functional protein.

[0163] In example approach 4, an AAV genome is cross-packaged into the capsids of other parvoviruses thus creating chimeric vectros. In example approach 5, intein-mediated protein trans-splicing is used. Intein catalyzes protein splicing thereby causing the ligation of two polypeptides via trans-splicing (this approach is similar to intron-mediated RNA splicing). Multiple AAV vectors are delivered to the same cells. Each of the AAV vectors encode one of the fragments of target proteins, the fragments are flanked by short split inteins. The full-length protein forms after protein trans-splicing. See e.g., Li, C., Samulski, R.J. Engineering adeno-associated virus vectors for gene therapy. Nat Rev Genet 21, 255–272 (2020), herein incorporated by reference.

[0164]

Vector Construction

[0165] The vectors described herein can be constructed using any suitable process or technique. In some embodiments, one or more suitable recombination and/or cloning methods or techniques can be used to the vector(s) described herein. Suitable recombination and/or cloning techniques and/or methods can include, but not limited to, those described in U.S. Application publication No. US 2004-0171156 A1. Other suitable methods and techniques are described elsewhere herein.

[0166] Construction of recombinant AAV vectors are described in a number of publications, including U.S. Pat. No. 5,173,414; Tratschin et al., Mol. Cell. Biol. 5:3251-3260 (1985); Tratschin, et al., Mol. Cell. Biol. 4:2072-2081 (1984); Hermonat & Muzyczka, PNAS 81:6466-6470 (1984); and Samulski et al., J. Virol. 63:03822-3828 (1989). Any of the techniques and/or methods can be

used and/or adapted for constructing an AAV or other vector described herein. AAV vectors are discussed elsewhere herein.

[0167] In some embodiments, the vector can have one or more insertion sites, such as a restriction endonuclease recognition sequence (also referred to as a "cloning site"). In some embodiments, one or more insertion sites (e.g., about or more than about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more insertion sites) are located upstream and/or downstream of one or more sequence elements of one or more vectors.

[0168] Delivery vehicles, vectors, particles, nanoparticles, formulations and components thereof for expression of one or more elements of a engineered AAV capsid system described herein are as used in the foregoing documents, such as International Patent Application Publication WO 2014/093622 (PCT/US2013/074667) and are discussed in greater detail herein.

Virus Particle Production from Viral Vectors

AAV Particle Production

[0169] There are two main strategies for producing AAV particles from AAV vectors and systems thereof, such as those described herein, which depend on how the adenovirus helper factors are provided (helper v. helper free). In some embodiments, a method of producing AAV particles from AAV vectors and systems thereof can include adenovirus infection into cell lines that stably harbor AAV replication and capsid encoding polynucleotides along with AAV vector containing the polynucleotide to be packaged and delivered by the resulting AAV particle (e.g., the engineered AAV capsid polynucleotide(s)). In some embodiments, a method of producing AAV particles from AAV vectors and systems thereof can be a "helper free" method, which includes co-transfection of an appropriate producing cell line with three vectors (e.g., plasmid vectors): (1) an AAV vector that contains a polynucleotide of interest (e.g., a transgene encoding a therapeutic protein or nucleic acid operably linked to a regulatory element that promotes expression in the target tissue) between 2 ITRs; (2) a vector that carries the AAV Rep-Cap encoding polynucleotide, including the engineered capsid protein described herein; and helper polynucleotides. One of skill in the art will appreciate various methods and variations thereof that are both helper and -helper free and as well as the different advantages of each system.

[0170] The engineered AAV vectors and systems thereof described herein can be produced by any of these methods.

Vector and Virus Particle Delivery

[0171] A vector (including non-viral carriers) described herein can be introduced into host cells to thereby produce transcripts, proteins, or peptides, including fusion proteins or peptides encoded by nucleic acids as described herein (e.g., engineered AAV capsid system transcripts, proteins, enzymes, mutant forms thereof, fusion proteins thereof, etc.), and virus particles (such as from viral vectors and systems thereof).

[0172] AAV capsids prepared from one or more engineered AAV capsid polynucleotides can be used to deliver a recombinant AAV genome encoding a therapeutic protein or nucleic acid of interest. Alternatively, adenovirus or other plasmid or viral vector types as previously described, can be used, in particular, using formulations and doses from, for example, US Patents Nos. 8,454,972 (formulations, doses for adenovirus), 8,404,658 (formulations, doses for AAV) and 5,846,946 (formulations, doses for DNA plasmids) and from clinical trials and publications regarding the clinical trials involving lentivirus, AAV and adenovirus. For examples, for AAV, the route of administration, formulation and dose can be as in US Patent No. 8,454,972 and as in clinical trials involving AAV. For Adenovirus, the route of administration, formulation and dose can be as in US Patent No. 8,404,658 and as in clinical trials involving adenovirus.

[0173] For plasmid delivery, the route of administration, formulation and dose can be as in US Patent No 5,846,946 and as in clinical studies involving plasmids. In some embodiments, doses can be based on or extrapolated to an average 70 kg individual (e.g., a male adult human), and can be adjusted for patients, subjects, mammals of different weight and species. Frequency of administration is within the ambit of the medical or veterinary practitioner (e.g., physician, veterinarian), depending on usual factors including the age, sex, general health, other conditions of the patient or subject and the particular condition or symptoms being addressed. The viral vectors can be injected into or otherwise delivered to the tissue or cell of interest.

[0174] In terms of *in vivo* delivery, AAV is advantageous over other viral vectors for a couple of reasons such as low toxicity (this may be due to the purification method not requiring ultra-centrifugation of cell particles that can activate the immune response) and a low probability of causing insertional mutagenesis because it does not integrate into the host genome.

[0175] The vector(s) and virus particles described herein can be delivered into a host cell in vitro, in vivo, and or ex vivo. Delivery can occur by any suitable method including, but not limited

to, physical methods, chemical methods, and biological methods. Physical delivery methods are those methods that employ physical force to counteract the membrane barrier of the cells to facilitate intracellular delivery of the vector. Suitable physical methods include, but are not limited to, needles (e.g., injections), ballistic polynucleotides (e.g., particle bombardment, micro projectile gene transfer, and gene gun), electroporation, sonoporation, photoporation, magnetofection, hydroporation, and mechanical massage. Chemical methods are those methods that employ a chemical to elicit a change in the cells membrane permeability or other characteristic(s) to facilitate entry of the vector into the cell. For example, the environmental pH can be altered which can elicit a change in the permeability of the cell membrane. Biological methods are those that rely and capitalize on the host cell's biological processes or biological characteristics to facilitate transport of the vector (with or without a carrier) into a cell. For example, the vector and/or its carrier can stimulate an endocytosis or similar process in the cell to facilitate uptake of the vector into the cell.

[0176] Delivery of engineered AAV capsid system components (e.g., polynucleotides encoding engineered AAV capsid and/or capsid proteins) to cells via particles. The term "particle" as used herein, refers to any suitable sized particles for delivery of the engineered AAV capsid system components described herein. Suitable sizes include macro-, micro-, and nano-sized particles. In some embodiments, any of the of the engineered AAV capsid system components (e.g., polypeptides, polynucleotides, vectors, and combinations thereof described herein) can be attached to, coupled to, integrated with, otherwise associated with one or more particles or component thereof as described herein. The particles described herein can then be administered to a cell or organism by an appropriate route and/or technique. In some embodiments, particle delivery can be selected and be advantageous for delivery of the polynucleotide or vector components. It will be appreciated that in embodiments, particle delivery can also be advantageous for other engineered capsid system molecules and formulations described elsewhere herein.

Engineered Virus Particles Including an Engineered Viral (e.g., AAV) Capsid

[0177] Also described herein are engineered virus particles (also referred to here and elsewhere herein as "engineered viral particles" that can contain an engineered viral capsid (e.g., AAV capsid, referred to as "engineered AAV particles") as described in detail elsewhere herein. It will be appreciated that the engineered AAV particles can be adenovirus-based particles, helper adenovirus-based particles, AAV-based particles, or hybrid adenovirus-based particles that

contain at least one engineered AAV capsid proteins as previously described. An engineered AAV capsid is one that that contains one or more engineered AAV capsid proteins as are described elsewhere herein. In some embodiments, the engineered AAV particles can include 1-60 engineered AAV capsid proteins described herein. In some embodiments, the engineered AAV particles can contain 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, or 60 engineered capsid proteins. In some embodiments, the engineered AAV particles can contain 0-59 wild-type AAV capsid proteins. In some embodiments, the engineered AAV particles can contain 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, or 59 wild-type AAV capsid proteins. The engineered AAV particles can thus include one or more n-mer motifs as is previously described.

[0178] The engineered AAV particle can include one or more cargo polynucleotides. Cargo polynucleotides are discussed in greater detail elsewhere herein. Methods of making the engineered AAV particles from viral and non-viral vectors are described elsewhere herein. Formulations containing the engineered virus particles are described elsewhere herein.

Example Cargos

[0179] The n-mers can be coupled to or otherwise associated with a cargo. Cargos can include any molecule that is capable of being coupled to or associated with the n-mers described herein. Cargos can include, without limitation, nucleotides, oligonucleotides, polynucleotides, amino acids, peptides, polypeptides, riboproteins, lipids, sugars, pharmaceutically active agents (e.g., drugs, imaging and other diagnostic agents, and the like), chemical compounds, and combinations thereof. In some embodiments, the cargo is DNA, RNA, amino acids, peptides, polypeptides, antibodies, aptamers, ribozymes, guide sequences for ribozymes that inhibit translation or transcription of essential tumor proteins and genes, hormones, immunomodulators, antipyretics, anxiolytics, antipsychotics, analgesics, antispasmodics, anti-inflammatories, anti-histamines, anti-infectives, radiation sensitizers, chemotherapeutics, radioactive compounds, imaging agents, and combinations thereof. In embodiments, the cargo is a recombinant AAV genome comprising a transgene, for example, encoding a therapeutic protein or nucleic acid, operably linked to

regulatory sequences that direct expression of the therapeutic protein or nucleic acid in a target tissue, flanked by AAV ITR sequences.

[0180] In some embodiments, the cargo is capable of treating or preventing a neurological disease or disorder, details of which are described herein.

[0181] In some embodiments, the cargo is a morpholino, a peptide-linked morpholino, an antisense oligonucleotide, a PMO, a therapeutic transgene, a polynucleotide encoding a therapeutic polypeptide or peptide, a PPMO, one or more peptides, one or more polynucleotides encoding a CRISPR-Cas protein, a guide RNA, or both, a ribonucleoprotein, wherein the ribonucleoprotein comprises a CRISPR-Cas system molecule, a therapeutic transgene RNA, or other gene modifying or therapeutic RNA and/or protein, or any combination thereof.

[0182] In some embodiments, one or more n-mers described herein is directly attached to the cargo. In some embodiments, one or more n-mers described herein is indirectly coupled to the cargo, such as via a linker molecule. In some embodiments, one or more one or more n-mers described herein is coupled to associated with a polypeptide or other particle that is coupled to, attached to, encapsulates, and/or contains a cargo.

[0183] Exemplary particles include, without limitation, viral particles (e.g., viral capsids, which is inclusive of bacteriophage capsids), polysomes, liposomes, nanoparticles, microparticles, exosomes, micelles, and the like. The term "nanoparticle" as used herein includes a nanoscale deposit of a homogenous or heterogeneous material. Nanoparticles may be regular or irregular in shape and may be formed from a plurality of co-deposited particles that form a composite nanoscale particle. Nanoparticles may be generally spherical in shape or have a composite shape formed from a plurality of co-deposited generally spherical particles. Exemplary shapes for the nanoparticles include, but are not limited to, spherical, rod, elliptical, cylindrical, disc, and the like. In some embodiments, the nanoparticles have a substantially spherical shape.

Cargo Polynucleotides

[0184] Cargos are also described elsewhere herein. In some embodiments, the cargo is a cargo polynucleotide that can be packaged into an engineered viral particle and subsequently delivered to a cell. In some embodiments, delivery is cell selective, e.g., neurons and glial cells of the central nervous system. In some embodiments, the one or more cargo polynucleotides are part of the engineered viral (e.g., AAV) genome of the viral (e.g., AAV) system and packaged within the

engineered capsid containing a targeting moiety of the present invention. The cargo polynucleotides can be packaged into an engineered viral (e.g., AAV) particle, which can be delivered to, e.g., a cell. In some embodiments, the cargo polynucleotide can be capable of modifying a polynucleotide (e.g., gene or transcript) of a cell to which it is delivered. As used herein, "gene" can refer to a hereditary unit corresponding to a sequence of DNA that occupies a specific location on a chromosome and that contains the genetic instruction for a characteristic(s) or trait(s) in an organism. The term gene can refer to translated and/or untranslated regions of a genome. "Gene" can refer to the specific sequence of DNA that is transcribed into an RNA transcript that can be translated into a polypeptide or be a catalytic RNA molecule, including but not limited to, tRNA, siRNA, piRNA, miRNA, long-non-coding RNA and shRNA. Polynucleotide, gene, transcript, etc. modification includes all genetic engineering techniques including, but not limited to, gene editing as well as conventional recombinational gene modification techniques (e.g., whole or partial gene insertion, deletion, and mutagenesis (e.g., insertional and deletional mutagenesis) techniques.

[0185] In example embodiments, the cargo molecule is a polynucleotide that is or can encode a vaccine. In example embodiments, the cargo molecule is a polynucleotide encoding an antibody.

Interference RNAs

[0186] In certain example embodiments, the one or more polynucleotides may encode one or more interference RNAs. Interference RNAs are RNA molecules capable of suppressing gene expressions. Example types of interference RNAs include small interfering RNA (siRNA), microRNA (miRNA), and short hairpin RNA (shRNA).

[0187] In certain example embodiments, the interference RNA may be a siRNAs. Small interfering RNA (siRNA) molecules are capable of inhibiting target gene expression by interfering RNA. siRNAs may be chemically synthesized, or may be obtained by in vitro transcription, or may be synthesized in vivo in target cell. siRNAs may comprise double-stranded RNA from 15 to 40 nucleotides in length and can contain a protuberant region 3' and/or 5' from 1 to 6 nucleotides in length. Length of protuberant region is independent from total length of siRNA molecule. siRNAs may act by post-transcriptional degradation or silencing of target messenger. In some cases, the exogenous polynucleotides encode shRNAs. In shRNAs, the antiparallel strands that form siRNA are connected by a loop or hairpin region.

[0188] The interference RNA (e.g., siRNA) may suppress expression of genes to promote long term survival and functionality of cells after transplanted to a subject. In some examples, the interference RNAs suppress genes in TGFβ pathway, e.g., TGFβ, TGFβ receptors, and SMAD proteins. In some examples, the interference RNAs suppress genes in colony-stimulating factor 1 (CSF1) pathway, e.g., CSF1 and CSF1 receptors. In certain embodiments, the one or more interference RNAs suppress genes in both the CSF1 pathway and the TGFβ pathway. TGFβ pathway genes may comprise one or more of ACVR1, ACVR1C, ACVR2A, ACVR2B, ACVRL1, AMH, AMHR2, BMP2, BMP4, BMP5, BMP6, BMP7, BMP8A, BMP8B, BMPR1A, BMPR1B, BMPR2, CDKN2B, CHRD, COMP, CREBBP, CUL1, DCN, E2F4, E2F5, EP300, FST, GDF5, GDF6, GDF7, ID1, ID2, ID3, ID4, IFNG, INHBA, INHBB, INHBC, INHBE, LEFTY1, LEFTY2, LOC728622, LTBP1, MAPK1, MAPK3, MYC, NODAL, NOG, PITX2, PPP2CA, PPP2CB, PPP2R1A, PPP2R1B, RBL1, RBL2, RBX1, RHOA, ROCK1, ROCK2, RPS6KB1, RPS6KB2, SKP1, SMAD1, SMAD2, SMAD3, SMAD4, SMAD5, SMAD6, SMAD7, SMAD9, SMURF1, SMURF2, SP1, TFDP1, TGFB1, TGFB2, TGFB3, TGFBR1, TGFBR2, THBS1, THBS2, THBS3, THBS4, TNF, ZFYVE16, and/or ZFYVE9.

[0189] In some embodiments, the cargo polynucleotide is an RNAi molecule, antisense molecule, and/or a gene silencing oligonucleotide or a polynucleotide that encodes an RNAi molecule, antisense molecule, and/or gene silencing oligonucleotide.

[0190] As used herein, "gene silencing oligonucleotide" refers to any oligonucleotide that can alone or with other gene silencing oligonucleotides utilize a cell's endogenous mechanisms, molecules, proteins, enzymes, and/or other cell machinery or exogenous molecule, agent, protein, enzyme, and/or polynucleotide to cause a global or specific reduction or elimination in gene expression, RNA level(s), RNA translation, RNA transcription, that can lead to a reduction or effective loss of a protein expression and/or function of a non-coding RNA as compared to wild-type or a suitable control. This is synonymous with the phrase "gene knockdown" Reduction in gene expression, RNA level(s), RNA translation, RNA transcription, and/or protein expression can range from about 100, 99, 98, 97, 96, 95, 94, 93, 92, 91, 90, 89, 88, 87, 86, 85, 84, 83, 82, 81, 80, 79, 78, 77, 76, 75, 74, 73, 72, 71, 70, 69, 68, 67, 66, 65, 64, 63, 62, 61, 60, 59, 58, 57, 56, 55, 54, 53, 52, 51, 50, 49, 48, 47, 46, 45, 44, 43, 42 41, 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, to 1% or

less reduction. "Gene silencing oligonucleotides" include, but are not limited to, any antisense oligonucleotide, ribozyme, any oligonucleotide (single or double stranded) used to stimulate the RNA interference (RNAi) pathway in a cell (collectively RNAi oligonucleotides), small interfering RNA (siRNA), microRNA, and short-hairpin RNA (shRNA). Commercially available programs and tools are available to design the nucleotide sequence of gene silencing oligonucleotides for a desired gene, based on the gene sequence and other information available to one of ordinary skill in the art.

[0191] In some embodiments, a cargo polynucleotide, such as an encoding polynucleotide, is flanked by at least a retroelement polypeptide encoding polynucleotide 3' UTR or portion thereof, such as the proximal region of about 500 base pairs of the 3' UTR. In some embodiments a cargo polynucleotide, such as an encoding polynucleotide, is flanked by a (e.g., endogenous or engineered) retroelement polypeptide (such as a retroviral gag protein or gag homolog) 5' UTR. In some embodiments a cargo polynucleotide, such as an encoding polynucleotide, is flanked by an (e.g., endogenous or engineered) retroelement polypeptide encoding polynucleotide 5' and 3' UTR. In some embodiments, the flanking retroelement polypeptide encoding polynucleotide UTR(s) are from PNMA, Arc, PEG10 or other Sushi Class polypeptide. In some embodiments, the inclusion of the 3' UTR, the 5'UTR, or both can increase packaging and/or delivery of the cargo that they flank. These and other packaging elements are described in greater detail elsewhere herein.

Gene Modification Cargo Polynucleotides

[0192] In some embodiments, the cargo molecule can be a polynucleotide or polypeptide or polynucleotide encoding a polypeptide that can alone or when delivered as part of a system, whether or not delivered with other components of the system, operate to modify the genome, epigenome, and/or transcriptome of a cell to which it is delivered. Such systems include, but are not limited to, CRISPR-Cas systems. Other gene modification systems, e.g., TALENs, Zinc Finger nucleases, Cre-Lox, morpholinos, etc. are other non-limiting examples of gene modification systems whose one or more components can be delivered by the engineered viral (e.g., AAV) particles described herein.

[0193] In some embodiments, the cargo molecule is or encodes a gene editing system or component thereof. In some embodiments, the cargo molecule is or encodes a CRISPR-Cas system

molecule or a component thereof. In some embodiments, the cargo molecule is a polynucleotide that encodes one or more components of a gene modification system (such as a CRISPR-Cas system). In some embodiments the cargo molecule is or encodes a gRNA. CRISPR-Cas system as used herein is intended to encompass by Class 1 and Class 2 CRISPR-Cas systems and derivatives of CRISPR-Cas systems such as base editors, prime editors, and CRISPR-associated transposases (CAST) systems.

[0194] In some embodiments, the cargo molecule can be a polynucleotide or polypeptide or polynucleotide encoding a polypeptide that can alone or when delivered as part of a system, whether or not delivered with other components of the system, operate to modify the genome, epigenome, and/or transcriptome of a cell to which it is delivered, is such that it treats or prevents a disease, a disorder, or a symptom thereof of a neurologic disease or disorder, and/or viruses (such as single stranded RNA viruses). In some embodiments, the cargo molecule, whether or not delivered with other components of the system, operates to modify the genome, epigenome, and/or transcriptome of a cell to which it is delivered, is such that it treats or prevents a neurological disease or disorder described further herein.

[0195] In some embodiments, the cargo molecule, whether or not delivered with other components of the system, operates to modify the genome, epigenome, and/or transcriptome of a cell to which it is delivered, is such that can modify the GAA gene, such as any of those described in US Pat. App. Pub. 20190284555, the contents of which are incorporated by reference as if expressed in their entirety herein and can be adapted for use with the present invention.

[0196] In some embodiments, the cargo molecule is or encodes an antisense oligomer or RNA molecule, such as those described in U.S. Pat. App. Pub. US20160251398, US20150267202, and US20180216111, the contents of which are incorporated by reference as if expressed in their entirety herein and can be adapted for use with the present invention.

[0197] In some embodiments, the cargo molecule can be a peptide-oligomer, conjugate as described in e.g., International Patent Application Publication WO2017106304A1, the contents of which are incorporated by reference as if expressed in their entirety herein and can be adapted for use with the present invention.

[0198] An embodiment of the invention encompasses methods of modifying a genomic locus of interest to change gene expression in a cell by introducing into the cell any of the compositions described herein.

[0199] An embodiment of the invention is that the above elements are comprised in a single composition or comprised in individual compositions. These compositions may advantageously be applied to a host to elicit a functional effect on the genomic level.

Polypeptides

[0200] In certain example embodiments, the cargo molecule may one or more polypeptides or may be a nucleic acid encoding a polypeptide. The polypeptide may be a full-length protein or a functional fragment or functional domain thereof, that is a fragment or domain that maintains the desired functionality of the full-length protein. As used within this section "protein" is meant to refer to full-length proteins and functional fragments and domains thereof. A wide array of polypeptides may be delivered using the engineered delivery vesicles described herein, including but not limited to, secretory proteins, immunomodulatory proteins, anti-fibrotic proteins, proteins that promote tissue regeneration and/or transplant survival functions, hormones, anti-microbial proteins, anti-fibrillating polypeptides, and antibodies. The one or more polypeptides may also comprise combinations of the aforementioned example classes of polypeptides. It will be appreciated that any of the polypeptides described herein can also be delivered via the engineered delivery vesicles and systems described herein via delivery of the corresponding encoding polynucleotide.

Antibodies

[0201] In certain embodiments, the one or more polypeptides may comprise one or more antibodies. The term "antibody" is used interchangeably with the term "immunoglobulin" herein, and includes intact antibodies, fragments of antibodies, e.g., Fab, F(ab')2 fragments, scFva, and intact antibodies and fragments that have been mutated either in their constant and/or variable region (e.g., mutations to produce chimeric, partially humanized, or fully humanized antibodies, as well as to produce antibodies with a desired trait, e.g., enhanced binding and/or reduced FcR binding). The term "fragment" refers to a part or portion of an antibody or antibody chain comprising fewer amino acid residues than an intact or complete antibody or antibody chain. Fragments can be obtained via chemical or enzymatic' treatment of an intact or complete antibody

or antibody chain. Fragments can also be obtained by recombinant means. Exemplary fragments include Fab, Fab', F(ab')2, Fabc, Fd, dAb, V_{HH} and scF and/or Fv fragments. As used herein, a preparation of antibody protein "having less than about 50% of non-antibody protein (also referred to herein as a "contaminating protein"), or of chemical precursors, is considered to be "substantially free." 40%, 30%, 20%, 10% and more preferably 5% (by dry weight), of non-antibody protein, or of chemical precursors is considered to be substantially free. When the antibody protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, i.e., culture medium represents less than about 30%, preferably less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume or mass of the protein preparation.

[0202] In example embodiments, the antibody is a fragment or portion thereof. In an example embodiment, the antibody is an epitope binding protein or portion thereof. The term "binding portion" of an antibody (or "antibody portion") includes one or more complete domains, e.g., a pair of complete domains, as well as fragments of an antibody that retain the ability to specifically bind to a target molecule. It has been shown that the binding function of an antibody can be performed by fragments of a full-length antibody. Binding fragments are produced by recombinant DNA techniques, or by enzymatic or chemical cleavage of intact immunoglobulins. Binding fragments include Fab, Fab', F(ab')2, Fabc, Fd, dAb, Fv, single chains, single-chain antibodies, e.g., scFv, and single domain antibodies.

[0203] In some embodiments, the cargo or antibody is an antibody fragment or portion. In some embodiments, the cargo is an epitope binding protein. Examples of portions of antibodies or epitope-binding proteins encompassed by the present definition include: (i) the Fab fragment, having V_L, C_L, V_H and C_H1 domains; (ii) the Fab' fragment, which' is a Fab fragment having one or more cysteine residues at the C-terminus of the C_H1 domain; (iii) the Fd fragment having V_H and C_H1 domains; (iv) the Fd' fragment having V_H and C_H1 domains and one or more cysteine residues at the C-terminus of the CHI domain; (v) the Fv fragment having the V_L and V_H domains of a single arm of an antibody; (vi) the dAb fragment (Ward et al., 341 Nature 544 (1989)) which consists of a V_H domain or a V_L domain that binds antigen; (vii)'isolated CDR regions or isolated CDR regions presented in a functional framework; (viii) $F(ab')_2$ fragments which are bivalent fragments including two Fab' fragments linked by a disulphide bridge at the hinge region; (ix)

single chain antibody molecules (e.g., single chain Fv; scFv) (Bird et al., 242 Science 423 (1988); and Huston et al., 85 PNAS 5879 (1988)); (x) "diabodies" with two antigen binding sites, comprising a heavy chain variable domain (V_H) connected to a light chain variable domain (V_L) in the same polypeptide chain (see, e.g., EP 404,097; WO 93/11161; Hollinger et al., 90 PNAS 6444 (1993)); (xi) "linear antibodies" comprising a pair of tandem Fd segments (V_H-C_h1-V_H-C_h1) which, together with complementary light chain oligopeptides, form a pair of "antigen binding regions" (Zapata et al., Protein Eng. 8(10):1057-62 (1995); and U.S. Patent No. 5,641,870).

[0204] The term "antigen-binding fragment" refers to a polypeptide fragment of an immunoglobulin or antibody that binds antigen or competes with intact antibody (i.e., with the intact antibody from which they were derived) for antigen binding (i.e., specific binding). As such these antibodies or fragments thereof are included in the scope of the invention, provided that the antibody or fragment binds specifically to a target molecule.

[0205] In some embodiments, the antibody is a single-chain antibody (scFvs). The term "single-chain variable fragment", as used herein refers to a fusion protein containing the variable region(s) of the heavy (V_H) and light (V_L) of an immunoglobulin that are connected via a linker peptide. The linker peptide typically ranges from about 10 to about 25 amino acids. The linker can be flexible and can contain one or more glycine residues for flexibility. The linker can contain one or more serine or threonine residues to increase or modify solubility. The V_H and light (V_L) can be linked via the linker in any order. In some embodiments, N terminus of the V_H and is coupled, via a linker, C terminus of the (V_L). In some embodiments, C terminus of the V_H and is coupled, via a linker, N terminus of the (V_L). In some embodiments, the scFV is a bivalent or trivalent scFvs. In some embodiments bitrivalent or trivalent scFvs are bi or trispecific, menaing that they can target 2 or 3, respectively, different epitopes. See also e.g., Hollinger, Philipp; Prospero, T; Winter, G (July 1993). "Diabodies": small bivalent and bispecific antibody fragments". *Proceedings of the National Academy of Sciences of the United States of America*. **90** (14): 6444–8; incq, S; Bosman, F; Buyse, MA; Degrieck, R; Celis, L; De Boer, M; Van Doorsselaere, V; Sablon, E (2001). "Expression and purification of monospecific and bispecific recombinant antibody fragments derived from antibodies that block the CD80/CD86-CD28 costimulatory pathway". Protein Expression and Purification. 22 (1): 11–24. doi:10.1006/prep.2001.1417; Le Gall, F.; Kipriyanov, SM; Moldenhauer, G; Little, M (1999). "Di-, tri- and tetrameric single chain Fv antibody fragments

against human CD19: effect of valency on cell binding". *FEBS Letters*. **453** (1): 164–168. doi:10.1016/S0014-5793(99)00713-9; Huston, J. S.; Levinson, D.; Mudgett-Hunter, M.; Tai, M. S.; Novotný, J.; Margolies, M. N.; Crea, R. (1988). "Protein engineering of antibody binding sites: recovery of specific activity in an anti-digoxin single-chain Fv analogue produced in Escherichia coli". Proceedings of the National Academy of Sciences of the United States of America. 85 (16): 5879–5883; de Graaf et al., Methods Mol Biol. 2002;178:379-87. doi: 10.1385/1-59259-240-6:379; Zhou, H.X., J Mol Biol. 2003 May 23;329(1):1-8. doi: 10.1016/s0022-2836(03)00372-3; Bird and Walker. Trends Biotechnol. 1991 Apr;9(4):132-7. doi: 10.1016/0167-7799(91)90044-I; Wörn et al., J Mol Biol. 2001 Feb 2;305(5):989-1010. doi: 10.1006/jmbi.2000.4265.

[0206] As used herein, "heavy chain antibody," "VHH" or "single-domain antibodies" (sdAbs) refers to an antibody which is composed only of two heavy chains and lacks the two light chains usually found in antibodies (see, e.g., Henry and MacKenzie, Antigen recognition by single-domain antibodies: structural latitudes and constraints. MAbs. 2018 Aug-Sep; 10(6): 815–826). VHH can refer to an antibody or VHH domain. Single-domain antibodies (sdAb) are also referred to as a "nanobody", which is defined herein as an antibody fragment composed of a single monomeric variable antibody domain. As used herein "VHH" is used interchangeably with "nanobody." The ~12–15 kDa variable domains of these antibodies (VHHs and VNARs) can be produced recombinantly and can recognize antigen in the absence of the remainder of the antibody heavy chain. In common antibodies, the antigen binding region consists of the variable domains of the heavy and light chains (VH and VL). Heavy-chain antibodies can bind antigens despite having only VH domains. In certain embodiments, the heavy chain antibody is an antibody derived from cartilaginous fishes (immunoglobulin new antigen receptor (IgNAR)) or camelid ungulates. Non-limiting examples of camelids include dromedaries, camels, llamas and alpacas.

[0207] It is intended that the term "antibody" encompass any Ig class or any Ig subclass (e.g., the IgG1, IgG2, IgG3, and IgG4 subclasses of IgG) obtained from any source (e.g., humans and non-human primates, and in rodents, lagomorphs, caprines, bovines, equines, ovines, etc.).

[0208] The term "Ig class" or "immunoglobulin class", as used herein, refers to the five classes of immunoglobulin that have been identified in humans and higher mammals, IgG, IgM, IgA, IgD, and IgE. The term "Ig subclass" refers to the two subclasses of IgM (H and L), three subclasses of IgA (IgA1, IgA2, and secretory IgA), and four subclasses of IgG (IgG1, IgG2, IgG3, and IgG4)

that have been identified in humans and higher mammals. The antibodies can exist in monomeric or polymeric form; for example, lgM antibodies exist in pentameric f–rm, and IgA antibodies exist in monomeric, dimeric or multimeric form.

[0209] The term "IgG subclass" refers to the four subclasses of immunoglobulin class IgG - IgG1, IgG2, IgG3, and IgG4 that have "been identified in humans and higher mammals by the heavy chains of the immunoglobulins, V1 - γ4, respectively. The term "single-chain immunoglobulin" or "single-chain antibody" (used interchangeably herein) refers to a protein having a two-polypeptide chain structure consisting of a heavy and a light chain, said chains being stabilized, for example, by interchain peptide linkers, which has the ability to specifically bind antigen. The term "domain" refers to a globular region of a heavy or light chain polypeptide comprising peptide loops (e.g., comprising 3 or 4 peptide loops) stabilized, for example, by β pleated sheet and/or intrachain disulfide bond. Domains are further referred to herein as "constant" or "variable", based on the relative lack of sequence variation within the domains of various class members in the case of "constant" domain, or the significant variation within the domains of various class members in the case of a "variable" domain. Antibody or polypeptide "domains" are often referred to interchangeably in the antibody or polypeptide "regions". The "constant" domains of an antibody light chain are referred to interchangeably as "light chain constant regions", "light chain constant domains", "CL" regions or "CL" domains." The "constant" domains of an antibody heavy chain are referred to interchangeably as "heavy chain constant regions", "heavy chain constant domains", "CH" regions or "CH" domains." The "variable" domains of an antibody light chain are referred to interchangeably as "light chain variable regions", "light chain variable domains", "VL" regions or "VL" domains." The "variable" domains of an antibody heavy chain are referred to interchangeably as "heavy chain constant regions", "heavy chain constant domains", "VH" regions or "VH" domains.

[0210] The term "region" can also refer to a part or portion of an antibody chain or antibody chain domain (e.g., a part or portion of a heavy or light chain or a part or portion of a constant or variable domain, as defined herein), as well as more discrete parts or portions of said chains or domains. For example, light and heavy chains or light and heavy chain variable domains include "complementarity determining regions" or "CDRs" interspersed among "framework regions" or "FRs", as defined herein.

[0211] The term "conformation" refers to the tertiary structure of a protein or polypeptide (e.g., an antibody, antibody chain, domain or region thereof). For example, the phrase "light (or heavy) chain conformation" refers to the tertiary structure of a light (or heavy) chain variable region, and the phrase "antibody conformation" or "antibody fragment conformation" refers to the tertiary structure of an antibody or fragment thereof.

[0212] The term "antibody-like protein scaffolds" or "engineered protein scaffolds" broadly encompasses proteinaceous non-immunoglobulin specific-binding agents, typically obtained by combinatorial engineering (such as site-directed random mutagenesis in combination with phage display or other molecular selection techniques). Usually, such scaffolds are derived from robust and small soluble monomeric proteins (such as Kunitz inhibitors or lipocalins) or from a stably folded extra-membrane domain of a cell surface receptor (such as protein A, fibronectin or the ankyrin repeat).

[0213] Such scaffolds have been extensively reviewed in Binz et al. (Engineering novel binding proteins from non-immunoglobulin domains. Nat Biotechnol 2005, 23:1257-1268), Gebauer and Skerra (Engineered protein scaffolds as next-generation antibody therapeutics. Curr Opin Chem Biol. 2009, 13:245-55), Gill and Damle (Biopharmaceutical drug discovery using novel protein scaffolds. Curr Opin Biotechnol 2006, 17:653-658), Skerra (Engineered protein scaffolds for molecular recognition. J Mol Recognit 2000, 13:167-187), and Skerra (Alternative non-antibody scaffolds for molecular recognition. Curr Opin Biotechnol 2007, 18:295-304), and include without limitation affibodies, based on the Z-domain of staphylococcal protein A, a three-helix bundle of 58 residues providing an interface on two of its alpha-helices (Nygren, Alternative binding proteins: Affibody binding proteins developed from a small three-helix bundle scaffold. FEBS J 2008, 275:2668-2676); engineered Kunitz domains based on small polypeptides of 58 residues) and robust, disulphide-crosslinked serine protease inhibitor, typically of human origin (e.g., LACI-D1), which can be engineered for different protease specificities (Nixon and Wood, Engineered protein inhibitors of proteases. Curr Opin Drug Discov Dev 2006, 9:261-268); monobodies or adnectins based on the 10th extracellular domain of human fibronectin III (10Fn3), which adopts an Ig-like beta-sandwich fold (94 residues) with 2–3 exposed loops but lacks the central disulphide bridge (Koide and Koide, Monobodies: antibody mimics based on the scaffold of the fibronectin type III domain. Methods Mol Biol 2007, 352:95-109); anticalins derived from

the lipocalins, a diverse family of eight-stranded beta-barrel proteins (ca. 180 residues) that naturally form binding sites for small ligands by means of four structurally variable loops at the open end, which are abundant in humans, insects, and many other organisms (Skerra, Alternative binding proteins: Anticalins—harnessing the structural plasticity of the lipocalin ligand pocket to engineer novel binding activities. FEBS J 2008, 275:2677-2683); DARPins, designed ankyrin repeat domains (166 residues), which provide a rigid interface arising from typically three repeated beta-turns (Stumpp et al., DARPins: a new generation of protein therapeutics. Drug Discov Today 2008, 13:695-701); avimers (multimerized LDLR-A module) (Silverman et al., Multivalent avimer proteins evolved by exon shuffling of a family of human receptor domains. Nat Biotechnol 2005, 23:1556-1561); and cysteine-rich knottin peptides (Kolmar" Alternative binding proteins: biological activity and therapeutic potential of cystine-knot miniproteins. FEBS J 2008, 275:2684-2690).

[0214] "Specific binding" of an antibody means that the antibody exhibits appreciable affinity for a particular antigen or epitope and, generally, does not exhibit significant cross reactivity. "Appreciable" binding includes binding with an affinity of at least 25 μM. Antibodies with affinities greater than 1 x 10^7 M^{-1} (or a dissociation coefficient of 1μM or less or a dissociation coefficient of 1nm or less) typically bind with correspondingly greater specificity. Values intermediate of those set forth herein are also intended to be within the scope of the present invention and antibodies of the invention bind with a range of affinities, for example, 100nM or less, 75nM or less, 50nM or less, 25nM or less, for example 10nM or less, 5nM or less, 1nM or less, or in embodiments 500pM or less, 100pM or less, 50pM or less or 25pM or less. An antibody that "does not exhibit significant cross reactivity" is one that will not appreciably bind to an entity other than its target (e.g., a different epitope or a different molecule). For example, an antibody that specifically binds to a target molecule will appreciably bind the target molecule but will not significantly react with non-target molecules or peptides. An antibody specific for a particular epitope will, for example, not significantly cross react with remote epitopes on the same protein or peptide. Specific binding can be determined according to any art-recognized means for determining such binding. Preferably, specific binding is determined according to Scatchard analysis and/or competitive binding assays.

[0215] As used herein, the term "affinity" refers to the strength of the binding of a single antigen-combining site with an antigenic determinant. Affinity depends on the closeness of stereochemical fit between antibody combining sites and antigen determinants, on the size of the area of contact between them, on the distribution of charged and hydrophobic groups, etc. Antibody affinity can be measured by equilibrium dialysis or by the kinetic BIACORE™ method. The dissociation constant, Kd, and the association constant, Ka, are quantitative measures of affinity.

[0216] As used herein, the term "monoclonal antibody" refers to an antibody derived from a clonal population of antibody-producing cells (e.g., B lymphocytes or B cells) which is homogeneous in structure and antigen specificity. The term "polyclonal antibody" refers to a plurality of antibodies originating from different clonal populations of antibody-producing cells which are heterogeneous in their structure and epitope specificity, but which recognize a common antigen. Monoclonal and polyclonal antibodies may exist within bodily fluids, as crude preparations, or may be purified, as described herein."Humanized" forms of non-human (e.g., murine) antibodies are chimeric antibodies that contain minimal sequence derived from non-human immunoglobulin. For the most part, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a hypervariable region of the recipient are replaced by residues from a hypervariable region of a non-human species (donor antibody) such as mouse, rat, rabbit, or nonhuman primate having the desired specificity, affinity, and capacity. In some instances, FR residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, humanized antibodies may comprise residues that are not found in the recipient antibody or in the donor antibody. These modifications are made to further refine antibody performance. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the hypervariable regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin sequence. The humanized antibody optionally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin.

[0217] As used herein, a "blocking" antibody or an antibody "antagonist" is one which inhibits or reduces biological activity of the antigen(s) it binds. In certain embodiments, the blocking

antibodies or antagonist antibodies or portions thereof described herein completely inhibit the biological activity of the antigen(s).

[0218] Antibodies may act as agonists or antagonists of the recognized polypeptides. For example, the present invention includes antibodies which disrupt receptor/ligand interactions either partially or fully. The invention features both receptor-specific antibodies and ligand-specific antibodies. The invention also features receptor-specific antibodies which do not prevent ligand binding but prevent receptor activation. Receptor activation (i.e., signaling) may be determined by techniques described herein or otherwise known in the art. For example, receptor activation can be determined by detecting the phosphorylation (e.g., tyrosine or serine/threonine) of the receptor or of one of its down-stream substrates by immunoprecipitation followed by western blot analysis. In specific embodiments, antibodies are provided that inhibit ligand activity or receptor activity by at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 60%, or at least 50% of the activity in absence of the antibody.

[0219] The invention also features receptor-specific antibodies which both prevent ligand binding and receptor activation as well as antibodies that recognize the receptor-ligand complex. Likewise, encompassed by the invention are neutralizing antibodies which bind the ligand and prevent binding of the ligand to the receptor, as well as antibodies which bind the ligand, thereby preventing receptor activation, but do not prevent the ligand from binding the receptor. Further included in the invention are antibodies which activate the receptor. These antibodies may act as receptor agonists, i.e., potentiate or activate either all or a subset of the biological activities of the ligand-mediated receptor activation, for example, by inducing dimerization of the receptor. The antibodies may be specified as agonists, antagonists or inverse agonists for biological activities comprising the specific biological activities of the peptides disclosed herein. The antibody agonists and antagonists can be made using methods known in the art. See, e.g., PCT publication WO 96/40281; U.S. Pat. No. 5,811,097; Deng et al., Blood 92 (6):1981-1988 (1998); Chen et al., Cancer Res. 58(16):3668-3678 (1998); Harrop et al., J. Immunol. 161(4) :1786-1794 (1998); Zhu et al., Cancer Res. 58(15):3209-3214 (1998); Yoon et al., J. Immunol. 160(7):3170-3179 (1998); Prat et al., J. Cell. Sci. III (Pt2):237-247 (1998); Pitard et al., J. Immunol. Methods 205 (2):177-190 (1997); Liautard et al., Cytokine 9(4):233-241 (1997); Carlson et al., J. Biol. Chem.

272(17):11295-11301 (1997); Taryman et al., Neuron 14(4):755-762 (1995); Muller et al., Structure 6(9):1153-1167 (1998); Bartunek et al., Cytokine 8(1):14-20 (1996).

[0220] The antibodies as defined for the present invention include derivatives that are modified, i.e., by the covalent attachment of any type of molecule to the antibody such that covalent attachment does not prevent the antibody from generating an anti-idiotypic response. For example, but not by way of limitation, the antibody derivatives include antibodies that have been modified, e.g., by glycosylation, acetylation, pegylation, phosphylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to a cellular ligand or other protein, etc. Any of numerous chemical modifications may be carried out by known techniques, including, but not limited to specific chemical cleavage, acetylation, formylation, metabolic synthesis of tunicamycin, etc. Additionally, the derivative may contain one or more non-classical amino acids.

Engineered Cells and Organisms Expressing said Engineered AAV capsids

[0221] Described herein are engineered cells that can include one or more of the engineered AAV capsid polynucleotides, polypeptides, vectors, and/or vector systems. In some embodiments, one or more of the engineered AAV capsid polynucleotides can be expressed in the engineered cells. In some embodiments, the engineered cells can be capable of producing engineered AAV capsid proteins and/or engineered AAV capsid particles that are described elsewhere herein. Also described herein are modified or engineered organisms that can include one or more engineered cells described herein. The engineered cells can be engineered to express a cargo molecule (e.g., a cargo polynucleotide) dependently or independently of an engineered AAV capsid polynucleotide as described elsewhere herein, *e.g.*, packaged within an engineered AAV capsid as described herein.

[0222] A wide variety of animals, plants, algae, fungi, yeast, etc. and animal, plant, algae, fungus, yeast cell or tissue systems may be engineered to express one or more nucleic acid constructs of the engineered AAV capsid system described herein using various transformation methods mentioned elsewhere herein. This can produce organisms that can produce engineered AAV capsid particles, such as for production purposes, engineered AAV capsid design and/or generation, and/or model organisms. In some embodiments, the polynucleotide(s) encoding one or more components of the engineered AAV capsid system described herein can be stably or

transiently incorporated into one or more cells of a plant, animal, algae, fungus, and/or yeast or tissue system. In some embodiments, one or more of engineered AAV capsid system polynucleotides are genomically incorporated into one or more cells of a plant, animal, algae, fungus, and/or yeast or tissue system. Further embodiments of the modified organisms and systems are described elsewhere herein. In some embodiments, one or more components of the engineered AAV capsid system described herein are expressed in one or more cells of the plant, animal, algae, fungus, yeast, or tissue systems.

Engineered Cells

[0223] Described herein are various embodiments of engineered cells that can include one or more of the engineered AAV capsid system polynucleotides, polypeptides, vectors, and/or vector systems described elsewhere herein. In some embodiments, the cells can express one or more of the engineered AAV capsid polynucleotides and can produce one or more engineered AAV capsid particles, which are described in greater detail herein. Such cells are also referred to herein as "producer cells". It will be appreciated that these engineered cells are different from "modified cells" described elsewhere herein in that the modified cells are not necessarily producer cells unless they include one or more of the engineered AAV capsid polynucleotides, engineered AAV capsid vectors or other vectors described herein that render the cells capable of producing an engineered AAV capsid particle. Modified cells can be recipient cells of an engineered AAV capsid particles and can, in some embodiments, be modified by the engineered AAV capsid particle(s) and/or a cargo polynucleotide delivered to the recipient cell. Modified cells are discussed in greater detail elsewhere herein. The term modification can be used in connection with modification of a cell that is not dependent on being a recipient cell. For example, isolated cells can be modified prior to receiving an engineered AAV capsid molecule.

[0224] In an embodiment, the invention provides a non-human eukaryotic organism; for example, a multicellular eukaryotic organism, including a eukaryotic host cell containing one or more components of an engineered delivery system described herein according to any of the described embodiments. In other embodiments, the invention provides a eukaryotic organism; preferably a multicellular eukaryotic organism, comprising a eukaryotic host cell containing one or more components of an engineered delivery system described herein according to any of the described embodiments. In some embodiments, the organism is a host of AAV.

[0225] In particular embodiments, the plants, algae, fungi, yeast, etc., cells or parts obtained are transgenic plants, comprising an exogenous DNA sequence incorporated into the genome of all or part of the cells.

[0226] The engineered cell can be a prokaryotic cell. The prokaryotic cell can be bacterial cell. The prokaryotic cell can be an archaea cell. The bacterial cell can be any suitable bacterial cell. Suitable bacterial cells can be from the genus *Escherichia, Bacillus, Lactobacillus, Rhodococcus, Rodhobacter, Synechococcus, Synechoystis, Pseudomonas, Psedoaltermonas, Stenotrophamonas*, and *Streptomyces* Suitable bacterial cells include, but are not limited to Escherichia coli cells, *Caulobacter crescentus* cells, *Rodhobacter sphaeroides* cells, *Psedoaltermonas haloplanktis* cells. Suitable strains of bacterial include, but are not limited to BL21(DE3), DL21(DE3)-pLysS, BL21 Star-pLysS, BL21-SI, BL21-AI, Tuner, Tuner pLysS, Origami, Origami B pLysS, Rosetta, Rosetta pLysS, Rosetta-gami-pLysS, BL21 CodonPlus, AD494, BL2trxB, HMS174, NovaBlue(DE3), BLR, C41(DE3), C43(DE3), Lemo21(DE3), Shuffle T7, ArcticExpress and ArticExpress (DE3).

[0227] The engineered cell can be a eukaryotic cell. The eukaryotic cells may be those of or derived from a particular organism, such as a plant or a mammal, including but not limited to human, or non-human eukaryote or animal or mammal as herein discussed, e.g., mouse, rat, rabbit, dog, livestock, or non-human mammal or primate. In some embodiments the engineered cell can be a cell line. Examples of cell lines include, but are not limited to, C8161, CCRF-CEM, MOLT, mIMCD-3, NHDF, HeLa-S3, Huh1, Huh4, Huh7, HUVEC, HASMC, HEKn, HEKa, MiaPaCell, Panc1, PC-3, TF1, CTLL-2, C1R, Rat6, CV1, RPTE, A10, T24, J82, A375, ARH-77, Calu1, SW480, SW620, SKOV3, SK-UT, CaCo2, P388D1, SEM-K2, WEHI-231, HB56, TIB55, Jurkat, J45.01, LRMB, Bcl-1, BC-3, IC21, DLD2, Raw264.7, NRK, NRK-52E, MRC5, MEF, Hep G2, HeLa B, HeLa T4, COS, COS-1, COS-6, COS-M6A, BS-C-1 monkey kidney epithelial, BALB/ 3T3 mouse embryo fibroblast, 3T3 Swiss, 3T3-L1, 132-d5 human fetal fibroblasts; 10.1 mouse fibroblasts, 293-T, 3T3, 721, 9L, A2780, A2780ADR, A2780cis, A172, A20, A253, A431, A-549, ALC, B16, B35, BCP-1 cells, BEAS-2B, bEnd.3, BHK-21, BR 293, BxPC3, C3H-10T1/2, C6/36, Cal-27, CHO, CHO-7, CHO-IR, CHO-K1, CHO-K2, CHO-T, CHO Dhfr -/-, COR-L23, COR-L23/CPR, COR-L23/5010, COR-L23/R23, COS-7, COV-434, CML T1, CMT, CT26, D17, DH82, DU145, DuCaP, EL4, EM2, EM3, EMT6/AR1, EMT6/AR10.0, FM3, H1299, H69, HB54, HB55, HCA2, HEK-293, HeLa, Hepa1c1c7, HL-60, HMEC, HT-29, Jurkat, JY cells, K562 cells, Ku812,

KCL22, KG1, KYO1, LNCap, Ma-Mel 1-48, MC-38, MCF-7, MCF-10A, MDA-MB-231, MDA-MB-468, MDA-MB-435, MDCK II, MDCK II, MOR/0.2R, MONO-MAC 6, MTD-1A, MyEnd, NCI-H69/CPR, NCI-H69/LX10, NCI-H69/LX20, NCI-H69/LX4, NIH-3T3, NALM-1, NW-145, OPCN / OPCT cell lines, Peer, PNT-1A / PNT 2, RenCa, RIN-5F, RMA/RMAS, Saos-2 cells, Sf-9, SkBr3, T2, T-47D, T84, THP1 cell line, U373, U87, U937, VCaP, Vero cells, WM39, WT-49, X63, YAC-1, YAR, and transgenic varieties thereof. Cell lines are available from a variety of sources known to those with skill in the art (see, e.g., the American Type Culture Collection (ATCC) (Manassas, Va.)).

[0228] In some embodiments, the engineered cell is a muscle cell (e.g. cardiac muscle, skeletal muscle, and/or smooth muscle), bone cell , blood cell, immune cell (including but not limited to B cells, macrophages, T-cells, CAR-T cells, and the like), kidney cells, bladder cells, lung cells, heart cells, liver cells, brain cells, neurons, skin cells, stomach cells, neuronal support cells, intestinal cells, epithelial cells, endothelial cells, stem or other progenitor cells, adrenal gland cells, cartilage cells, and combinations thereof.

[0229] In some embodiments, the engineered cell can be a fungus cell. As used herein, a "fungal cell" refers to any type of eukaryotic cell within the kingdom of fungi. Phyla within the kingdom of fungi include Ascomycota, Basidiomycota, Blastocladiomycota, Chytridiomycota, Glomeromycota, Microsporidia, and Neocallimastigomycota. Fungal cells may include yeasts, molds, and filamentous fungi. In some embodiments, the fungal cell is a yeast cell.

[0230] As used herein, the term "yeast cell" refers to any fungal cell within the phyla Ascomycota and Basidiomycota. Yeast cells may include budding yeast cells, fission yeast cells, and mold cells. Without being limited to these organisms, many types of yeast used in laboratory and industrial settings are part of the phylum Ascomycota. In some embodiments, the yeast cell is an S. cerevisiae, Kluyveromyces marxianus, or Issatchenkia orientalis cell. Other yeast cells may include without limitation Candida spp. (e.g., Candida albicans), Yarrowia spp. (e.g., Yarrowia lipolytica), Pichia spp. (e.g., Pichia pastoris), Kluyveromyces spp. (e.g., Kluyveromyces lactis and Kluyveromyces marxianus), Neurospora spp. (e.g., Neurospora crassa), Fusarium spp. (e.g., Fusarium oxysporum), and Issatchenkia spp. (e.g., Issatchenkia orientalis, a.k.a. Pichia kudriavzevii and Candida acidothermophilum). In some embodiments, the fungal cell is a filamentous fungal cell. As used herein, the term "filamentous fungal cell" refers to any type of

fungal cell that grows in filaments, i.e., hyphae or mycelia. Examples of filamentous fungal cells may include without limitation Aspergillus spp. (e.g., Aspergillus niger), Trichoderma spp. (e.g., Trichoderma reesei), Rhizopus spp. (e.g., Rhizopus oryzae), and Mortierella spp. (e.g., Mortierella isabellina).

[0231] In some embodiments, the fungal cell is an industrial strain. As used herein, "industrial strain" refers to any strain of fungal cell used in or isolated from an industrial process, e.g., production of a product on a commercial or industrial scale. Industrial strain may refer to a fungal species that is typically used in an industrial process, or it may refer to an isolate of a fungal species that may be also used for non-industrial purposes (e.g., laboratory research). Examples of industrial processes may include fermentation (e.g., in production of food or beverage products), distillation, biofuel production, production of a compound, and production of a polypeptide. Examples of industrial strains can include, without limitation, JAY270 and ATCC4124.

[0232] In some embodiments, the fungal cell is a polyploid cell. As used herein, a "polyploid" cell may refer to any cell whose genome is present in more than one copy. A polyploid cell may refer to a type of cell that is naturally found in a polyploid state, or it may refer to a cell that has been induced to exist in a polyploid state (e.g., through specific regulation, alteration, inactivation, activation, or modification of meiosis, cytokinesis, or DNA replication). A polyploid cell may refer to a cell whose entire genome is polyploid, or it may refer to a cell that is polyploid in a particular genomic locus of interest.

[0233] In some embodiments, the fungal cell is a diploid cell. As used herein, a "diploid" cell may refer to any cell whose genome is present in two copies. A diploid cell may refer to a type of cell that is naturally found in a diploid state, or it may refer to a cell that has been induced to exist in a diploid state (e.g., through specific regulation, alteration, inactivation, activation, or modification of meiosis, cytokinesis, or DNA replication). For example, the S. cerevisiae strain S228C may be maintained in a haploid or diploid state. A diploid cell may refer to a cell whose entire genome is diploid, or it may refer to a cell that is diploid in a particular genomic locus of interest. In some embodiments, the fungal cell is a haploid cell. As used herein, a "haploid" cell may refer to any cell whose genome is present in one copy. A haploid cell may refer to a type of cell that is naturally found in a haploid state, or it may refer to a cell that has been induced to exist in a haploid state (e.g., through specific regulation, alteration, inactivation, activation, or

modification of meiosis, cytokinesis, or DNA replication). For example, the S. cerevisiae strain S228C may be maintained in a haploid or diploid state. A haploid cell may refer to a cell whose entire genome is haploid, or it may refer to a cell that is haploid in a particular genomic locus of interest.

[0234] In some embodiments, the engineered cell is a cell obtained from a subject. In some embodiments, the subject is a healthy or non-diseased subject. In some embodiments, the subject is a subject with a desired physiological and/or biological characteristic such that when a engineered AAV capsid particle is produced it can package one or more cargo polynucleotides that can be related to the desired physiological and/or biological characteristic and/or capable of modifying the desired physiological and/or biological characteristic. Thus, the cargo polynucleotides of the produced engineered AAV capsid particle can be capable of transferring the desired characteristic to a recipient cell. In some embodiments, the cargo polynucleotides are capable of modifying a polynucleotide of the engineered cell such that the engineered cell has a desired physiological and/or biological characteristic.

[0235] In some embodiments, a cell transfected with one or more vectors described herein is used to establish a new cell line comprising one or more vector-derived sequences.

[0236] The engineered cells can be used to produce engineered viral (e.g., AAV) capsid polynucleotides, vectors, and/or particles. In some embodiments, the engineered viral (e.g., AAV) capsid polynucleotides, vectors, and/or particles are produced, harvested, and/or delivered to a subject in need thereof. In some embodiments, the engineered cells are delivered to a subject. Other uses for the engineered cells are described elsewhere herein. In some embodiments, the engineered cells can be included in formulations and/or kits described elsewhere herein.

[0237] The engineered cells can be stored short-term or long-term for use at a later time. Suitable storage methods are generally known in the art. Further, methods of restoring the stored cells for use (such as thawing, reconstitution, and otherwise stimulating metabolism in the engineered cell after storage) at a later time are also generally known in the art.

Formulations

[0238] The compositions, polynucleotides, polypeptides, particles, cells, vector systems and combinations thereof described herein can be contained in a formulation, such as a pharmaceutical formulation. In some embodiments, the formulations can be used to generate polypeptides and

other particles that include one or more CNS-specific n-mers described herein. In some embodiments, the formulations can be delivered to a subject in need thereof. In some embodiments, component(s) of the engineered AAV capsid system, engineered cells, engineered AAV capsid particles, and/or combinations thereof described herein can be included in a formulation that can be delivered to a subject or a cell. In some embodiments, the formulation is a pharmaceutical formulation. One or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein can be provided to a subject in need thereof or a cell alone or as an active ingredient, such as in a pharmaceutical formulation. As such, also described herein are pharmaceutical formulations containing an amount of one or more of the polypeptides, polynucleotides, vectors, cells, or combinations thereof described herein. In some embodiments, the pharmaceutical formulation can contain an effective amount of the one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein. The pharmaceutical formulations described herein can be administered to a subject in need thereof or a cell.

[0239] In some embodiments, the amount of the one or more of the polypeptides, polynucleotides, vectors, cells, virus particles, nanoparticles, other delivery particles, and combinations thereof described herein contained in the pharmaceutical formulation can range from about 1 pg/kg to about 10 mg/kg based upon the bodyweight of the subject in need thereof or average bodyweight of the specific patient population to which the pharmaceutical formulation can be administered. The amount of the one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein in the pharmaceutical formulation can range from about 1 pg to about 10 g, from about 10 nL to about 10 ml. In embodiments where the pharmaceutical formulation contains one or more cells, the amount can range from about 1 cell to 1×10^2, 1×10^3, 1×10^4, 1×10^5, 1×10^6, 1×10^7, 1×10^8, 1×10^9, 1×10^{10} or more cells. In embodiments where the pharmaceutical formulation contains one or more cells, the amount can range from about 1 cell to 1×10^2, 1×10^3, 1×10^4, 1×10^5, 1×10^6, 1×10^7, 1×10^8, 1×10^9, 1×10^{10} or more cells per nL, µL, mL, or L.

[0240] In embodiments, were engineered AAV capsid particles are included in the formulation, the formulation can contain 1 to 1×10^1, 1×10^2, 1×10^3, 1×10^4, 1×10^5, 1×10^6, 1×10^7, 1×10^8, 1×10^9, 1×10^{10}, 1×10^{11}, 1×10^{12}, 1×10^{13}, 1×10^{14}, 1×10^{15}, 1×10^{16}, 1×10^{17}, 1

x 10^{18}, 1 x 10^{19}, or 1 x 10^{20} transducing units (TU)/mL of the engineered AAV capsid particles. In some embodiments, the formulation can be 0.1 to 100 mL in volume and can contain 1 to 1 x 10^{1}, 1 x 10^{2}, 1 x 10^{3}, 1 x 10^{4}, 1 x 10^{5}, 1 x 10^{6}, 1 x 10^{7}, 1 x 10^{8}, 1 x 10^{9}, 1 x 10^{10}, 1 x 10^{11}, 1 x 10^{12}, 1 x 10^{13}, 1 x 10^{14}, 1 x 10^{15}, 1 x 10^{16}, 1 x 10^{17}, 1 x 10^{18}, 1 x 10^{19}, or 1 x 10^{20} transducing units (TU)/mL of the engineered AAV capsid particles.

Pharmaceutically Acceptable Carriers and Auxiliary Ingredients and Agents

[0241] In embodiments, the pharmaceutical formulation containing an amount of one or more of the polypeptides, polynucleotides, vectors, cells, virus particles, nanoparticles, other delivery particles, and combinations thereof described herein can further include a pharmaceutically acceptable carrier. Suitable pharmaceutically acceptable carriers include, but are not limited to, water, salt solutions, alcohols, gum arabic, vegetable oils, benzyl alcohols, polyethylene glycols, gelatin, carbohydrates such as lactose, amylose or starch, magnesium stearate, talc, silicic acid, viscous paraffin, perfume oil, fatty acid esters, hydroxy methylcellulose, and polyvinyl pyrrolidone, which do not deleteriously react with the active composition.

[0242] The pharmaceutical formulations can be sterilized, and if desired, mixed with auxiliary agents, such as lubricants, preservatives, stabilizers, wetting agents, emulsifiers, salts for influencing osmotic pressure, buffers, coloring, flavoring and/or aromatic substances, and the like which do not deleteriously react with the active composition.

[0243] In addition to an amount of one or more of the polypeptides, polynucleotides, vectors, cells, engineered AAV capsid particles, nanoparticles, other delivery particles, and combinations thereof described herein, the pharmaceutical formulation can also include an effective amount of an auxiliary active agent, including but not limited to, polynucleotides, amino acids, peptides, polypeptides, antibodies, aptamers, ribozymes, hormones, immunomodulators, antipyretics, anxiolytics, antipsychotics, analgesics, antispasmodics, anti-inflammatories, anti-histamines, anti-infectives, chemotherapeutics, and combinations thereof.

[0244] Suitable hormones include, but are not limited to, amino-acid derived hormones (e.g., melatonin and thyroxine), small peptide hormones and protein hormones (e.g., thyrotropin-releasing hormone, vasopressin, insulin, growth hormone, luteinizing hormone, follicle-stimulating hormone, and thyroid-stimulating hormone), eicosanoids (e.g., arachidonic acid, lipoxins, and prostaglandins), and steroid hormones (e.g., estradiol, testosterone, tetrahydro

testosterone Cortisol). Suitable immunomodulators include, but are not limited to, prednisone, azathioprine, 6-MP, cyclosporine, tacrolimus, methotrexate, interleukins (e.g., IL-2, IL-7, and IL-12) , cytokines (e.g., interferons (e.g., IFN-a, IFN-β, IFN-ε, IFN-K, IFN-ω, and IFN-γ), granulocyte colony-stimulating factor, and imiquimod), chemokines (e.g., CCL3, CCL26 and CXCL7), cytosine phosphate-guanosine, oligodeoxynucleotides, glucans, antibodies, and aptamers).

[0245] Suitable antipyretics include, but are not limited to, non-steroidal anti-inflammatories (e.g., ibuprofen, naproxen, ketoprofen, and nimesulide), aspirin and related salicylates (e.g., choline salicylate, magnesium salicylate, and sodium salicylate), paracetamol/acetaminophen, metamizole, nabumetone, phenazone, and quinine.

[0246] Suitable anxiolytics include, but are not limited to, benzodiazepines (e.g., alprazolam, bromazepam, chlordiazepoxide, clonazepam, clorazepate, diazepam, flurazepam, lorazepam, oxazepam, temazepam, triazolam, and tofisopam), serotonergic antidepressants (e.g., selective serotonin reuptake inhibitors, tricyclic antidepressants, and monoamine oxidase inhibitors), mebicar, fabomotizole, selank, bromantane, emoxypine, azapirones, barbiturates, hydroxyzine, pregabalin, validol, and beta blockers.

[0247] Suitable antipsychotics include, but are not limited to, benperidol, bromoperidol, droperidol, haloperidol, moperone, pipamperone, timiperone, fluspirilene, penfluridol, pimozide, acepromazine, chlorpromazine, cyamemazine, dixyrazine, fluphenazine, levomepromazine, mesoridazine, perazine, pericyazine, perphenazine, pipotiazine, prochlorperazine, promazine, promethazine, prothipendyl, thioproperazine, thioridazine, trifluoperazine, triflupromazine, chlorprothixene, clopenthixol, flupentixol, thiothixene, zuclopenthixol, clotiapine, loxapine, prothipendyl, carpipramine, clocapramine, molindone, mosapramine, sulpiride, veralipride, amisulpride, amoxapine, aripiprazole, asenapine, clozapine, blonanserin, iloperidone, lurasidone, melperone, nemonapride, olanzapine, paliperidone, perospirone, quetiapine, remoxipride, risperidone, sertindole, trimipramine, ziprasidone, zotepine, alstonie, bifeprunox, bitopertin, brexpiprazole, cannabidiol, cariprazine, pimavanserin, pomaglumetad methionil, vabicaserin, xanomeline, and zicronapine.

[0248] Suitable analgesics include, but are not limited to, paracetamol/acetaminophen, nonsteroidal anti-inflammatories (e.g., ibuprofen, naproxen, ketoprofen, and nimesulide), COX-2

inhibitors (e.g., rofecoxib, celecoxib, and etoricoxib), opioids (e.g., morphine, codeine, oxycodone, hydrocodone, dihydromorphine, pethidine, buprenorphine), tramadol, norepinephrine, flupirtine, nefopam, orphenadrine, pregabalin, gabapentin, cyclobenzaprine, scopolamine, methadone, ketobemidone, piritramide, and aspirin and related salicylates (e.g., choline salicylate, magnesium salicylate, and sodium salicylate).

[0249] Suitable antispasmodics include, but are not limited to, mebeverine, papaverine, cyclobenzaprine, carisoprodol, orphenadrine, tizanidine, metaxalone, methocarbamol, chlorzoxazone, baclofen, dantrolene, baclofen, tizanidine, and dantrolene. Suitable anti-inflammatories include, but are not limited to, prednisone, non-steroidal anti-inflammatories (e.g., ibuprofen, naproxen, ketoprofen, and nimesulide), COX-2 inhibitors (e.g., rofecoxib, celecoxib, and etoricoxib), and immune selective anti-inflammatory derivatives (e.g., submandibular gland peptide-T and its derivatives)

[0250] Suitable anti-histamines include, but are not limited to, H1-receptor antagonists (e.g., acrivastine, azelastine, bilastine, brompheniramine, buclizine, bromodiphenhydramine, carbinoxamine, cetirizine, chlorpromazine, cyclizine, chlorpheniramine, clemastine, cyproheptadine, desloratadine, dexbrompheniramine, dexchlorpheniramine, dimenhydrinate, dimetindene, diphenhydramine, doxylamine, ebastine, embramine, fexofenadine, hydroxyzine, levocetirizine, loratadine, meclizine, mirtazapine, olopatadine, orphenadrine, phenindamine, pheniramine, phenyltoloxamine, promethazine, pyrilamine, quetiapine, rupatadine, tripelennamine, and triprolidine), H2-receptor antagonists (e.g., cimetidine, famotidine, lafutidine, nizatidine, ranitidine, and roxatidine), tritoqualine, catechin, cromoglicate, nedocromil, and p2-adrenergic agonists.

[0251] Suitable anti-infectives include, but are not limited to, amebicides (e.g., nitazoxanide, paromomycin, metronidazole, tinidazole, chloroquine, miltefosine, amphotericin b, and iodoquinol), aminoglycosides (e.g., paromomycin, tobramycin, gentamicin, amikacin, kanamycin, and neomycin), anthelmintics (e.g., pyrantel, mebendazole, ivermectin, praziquantel, albendazole, thiabendazole, oxamniquine), antifungals (e.g., azole antifungals (e.g., itraconazole, fluconazole, parconazole, ketoconazole, clotrimazole, miconazole, and voriconazole), echinocandins (e.g., caspofungin, anidulafungin, and micafungin), griseofulvin, terbinafine, flucytosine, and polyenes (e.g., nystatin, and amphotericin b), antimalarial agents (e.g., pyrimethamine/sulfadoxine,

artemether/lumefantrine, atovaquone/proguanil, quinine, hydroxychloroquine, mefloquine, chloroquine, doxycycline, pyrimethamine, and halofantrine), antituberculosis agents (e.g., aminosalicylates (e.g., aminosalicylic acid), isoniazid/rifampin, isoniazid/pyrazinamide/rifampin, bedaquiline, isoniazid, ethambutol, rifampin, rifabutin, rifapentine, capreomycin, and cycloserine), antivirals (e.g., amantadine, rimantadine, abacavir/lamivudine, emtricitabine/tenofovir, cobicistat/elvitegravir/emtricitabine/tenofovir, efavirenz/emtricitabine/tenofovir, abacavir/lamivudine/zidovudine, lamivudine/zidovudine, emtricitabine/tenofovir, emtricitabine/lopinavir/ritonavir/tenofovir, interferon alfa-2v/ribavirin, peginterferon alfa-2b, maraviroc, raltegravir, dolutegravir, enfuvirtide, foscarnet, fomivirsen, oseltamivir, zanamivir, nevirapine, efavirenz, etravirine, rilpivirine, delavirdine, nevirapine, entecavir, lamivudine, adefovir, sofosbuvir, didanosine, tenofovir, abacavir, zidovudine, stavudine, emtricitabine, zalcitabine, telbivudine, simeprevir, boceprevir, telaprevir, lopinavir/ritonavir, boceprevir, darunavir, ritonavir, tipranavir, atazanavir, nelfinavir, amprenavir, indinavir, saquinavir, ribavirin, valacyclovir, acyclovir, famciclovir, ganciclovir, and valganciclovir), carbapenems (e.g., doripenem, meropenem, ertapenem, and cilastatin/imipenem), cephalosporins (e.g., cefadroxil, cephradine, cefazolin, cephalexin, cefepime, cefazoline, loracarbef, cefotetan, cefuroxime, cefprozil, loracarbef, cefoxitin, cefaclor, ceftibuten, ceftriaxone, cefotaxime, cefpodoxime, cefdinir, cefixime, cefditoren, ceftizoxime, and ceftazidime), glycopeptide antibiotics (e.g., vancomycin, dalbavancin, oritavancin, and telavancin), glycylcyclines (e.g., tigecycline), leprostatics (e.g., clofazimine and thalidomide), lincomycin and derivatives thereof (e.g., clindamycin and lincomycin), macrolides and derivatives thereof (e.g., telithromycin, fidaxomicin, erythromycin, azithromycin, clarithromycin, dirithromycin, and troleandomycin), linezolid, sulfamethoxazole/trimethoprim, rifaximin, chloramphenicol, Fosfomycin, metronidazole, aztreonam, bacitracin, penicillin (amoxicillin, ampicillin, bacampicillin, carbenicillin, piperacillin, ticarcillin, amoxicillin/clavulanate, ampicillin/sulbactam, piperacillin/tazobactam, clavulanate/ticarcillin, penicillin, procaine penicillin, oxacillin, dicloxacillin, and nafcillin), quinolones (e.g., lomefloxacin, norfloxacin, ofloxacin, gatifloxacin, moxifloxacin, ciprofloxacin, levofloxacin, gemifloxacin, moxifloxacin, cinoxacin, nalidixic acid, enoxacin, grepafloxacin, gatifloxacin, trovafloxacin, and sparfloxacin), sulfonamides (e.g., sulfamethoxazole/trimethoprim, sulfasalazine, and sulfisoxazole), tetracyclines (e.g., doxycycline,

demeclocycline, minocycline, doxycycline/salicylic acid, doxycycline/omega-3 polyunsaturated fatty acids, and tetracycline), and urinary anti-infectives (e.g., nitrofurantoin, methenamine, Fosfomycin, cinoxacin, nalidixic acid, trimethoprim, and methylene blue).

[0252] Suitable chemotherapeutics include, but are not limited to, paclitaxel, brentuximab vedotin, doxorubicin, 5-FU (fluorouracil), everolimus, pemetrexed, melphalan, pamidronate, anastrozole, exemestane, nelarabine, ofatumumab, bevacizumab, belinostat, tositumomab, carmustine, bleomycin, bosutinib, busulfan, alemtuzumab, irinotecan, vandetanib, bicalutamide, lomustine, daunorubicin, clofarabine, cabozantinib, dactinomycin, ramucirumab, cytarabine, Cytoxan, cyclophosphamide, decitabine, dexamethasone, docetaxel, hydroxyurea, dacarbazine, leuprolide, epirubicin, oxaliplatin, asparaginase, estramustine, cetuximab, vismodegib, asparaginase Erwinia chrysanthemi, amifostine, etoposide, flutamide, toremifene, fulvestrant, letrozole, degarelix, pralatrexate, methotrexate, floxuridine, obinutuzumab, gemcitabine, afatinib, imatinib mesylate, carmustine, eribulin, trastuzumab, altretamine, topotecan, ponatinib, idarubicin, ifosfamide, ibrutinib, axitinib, interferon alfa-2a, gefitinib, romidepsin, ixabepilone, ruxolitinib, cabazitaxel, ado-trastuzumab emtansine, carfilzomib, chlorambucil, sargramostim, cladribine, mitotane, vincristine, procarbazine, megestrol, trametinib, mesna, strontium-89 chloride, mechlorethamine, mitomycin, busulfan, gemtuzumab ozogamicin, vinorelbine, filgrastim, pegfilgrastim, sorafenib, nilutamide, pentostatin, tamoxifen, mitoxantrone, pegaspargase, denileukin diftitox, alitretinoin, carboplatin, pertuzumab, cisplatin, pomalidomide, prednisone, aldesleukin, mercaptopurine, zoledronic acid, lenalidomide, rituximab, octreotide, dasatinib, regorafenib, histrelin, sunitinib, siltuximab, omacetaxine, thioguanine (tioguanine), dabrafenib, erlotinib, bexarotene, temozolomide, thiotepa, thalidomide, Bacillus Calmette-Guerin (BCG), temsirolimus, bendamustine hydrochloride, triptorelin, arsenic trioxide, lapatinib, valrubicin, panitumumab, vinblastine, bortezomib, tretinoin, azacitidine, pazopanib, teniposide, leucovorin, crizotinib, capecitabine, enzalutamide, ipilimumab, goserelin, vorinostat, idelalisib, ceritinib, abiraterone, epothilone, tafluposide, azathioprine, doxifluridine, vindesine, and all-trans retinoic acid.

[0253] In embodiments where there is an auxiliary active agent contained in the pharmaceutical formulation in addition to the one or more of the polypeptides, polynucleotides, CRISPR-Cas complexes, vectors, cells, virus particles, nanoparticles, other delivery particles, and

combinations thereof described herein, amount, such as an effective amount, of the auxiliary active agent will vary depending on the auxiliary active agent. In some embodiments, the amount of the auxiliary active agent ranges from 0.001 micrograms to about 1 milligram. In other embodiments, the amount of the auxiliary active agent ranges from about 0.01 IU to about 1000 IU. In further embodiments, the amount of the auxiliary active agent ranges from 0.001 mL to about 1 mL. In yet other embodiments, the amount of the auxiliary active agent ranges from about 1 % w/w to about 50% w/w of the total pharmaceutical formulation. In additional embodiments, the amount of the auxiliary active agent ranges from about 1 % v/v to about 50% v/v of the total pharmaceutical formulation. In still other embodiments, the amount of the auxiliary active agent ranges from about 1 % w/v to about 50% w/v of the total pharmaceutical formulation.

Dosage Forms

[0254] In some embodiments, the pharmaceutical formulations described herein may be in a dosage form. The dosage forms can be adapted for administration by any appropriate route. Appropriate routes include, but are not limited to, rectal, epidural, intracranial, intraocular, inhaled, intranasal, topical (including buccal, sublingual, or transdermal), vaginal, intraurethral, parenteral, intracranial, subcutaneous, intramuscular, intravenous, intraperitoneal, intradermal, intraosseous, intracardiac, intraarticular, intracavernous, intrathecal, intravitreal, intracerebral, gingival, subgingival, intracerebroventricular, and intradermal. Such formulations may be prepared by any method known in the art.

[0255] Dosage forms adapted for parenteral administration and/or adapted for any type of injection (e.g. intravenous, intraperitoneal, subcutaneous, intramuscular, intradermal, intraosseous, epidural, intracardiac, intraarticular, intracavernous, gingival, subgingival, intrathecal, intravitreal, intracerebral, and intracerebroventricular) can include aqueous and/or non-aqueous sterile injection solutions, which can contain anti-oxidants, buffers, bacteriostats, solutes that render the composition isotonic with the blood of the subject, and aqueous and non-aqueous sterile suspensions, which can include suspending agents and thickening agents. The dosage forms adapted for parenteral administration can be presented in a single- unit dose or multi-unit dose containers, including but not limited to sealed ampoules or vials. The doses can be lyophilized and resuspended in a sterile carrier to reconstitute the dose prior to administration. Extemporaneous injection solutions and suspensions can be prepared in some embodiments, from

sterile powders, granules, and tablets. See e.g., Glascock, J. J., *et al.* Delivery of Therapeutic Agents Through Intracerebroventricular (ICV) and Intravenous (IV) Injection in Mice. J. Vis. Exp. (56), e2968 and Foley CP, *et al.* Intra-arterial delivery of AAV vectors to the mouse brain after mannitol mediated blood brain barrier disruption. J Control Release. 2014 Dec 28;196:71-78.

[0256] The dosage form can also be prepared to prolong or sustain the release of any ingredient. In some embodiments, the one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein can be the ingredient whose release is delayed. In other embodiments, the release of an optionally included auxiliary ingredient is delayed. Suitable methods for delaying the release of an ingredient include, but are not limited to, coating or embedding the ingredients in material in polymers, wax, gels, and the like. Delayed release dosage formulations can be prepared as described in standard references such as "Pharmaceutical dosage form tablets," eds. Liberman et. al. (New York, Marcel Dekker, Inc., 1989), "Remington - The science and practice of pharmacy", 20th ed., Lippincott Williams & Wilkins, Baltimore, MD, 2000, and "Pharmaceutical dosage forms and drug delivery systems", 6th Edition, Ansel et al., (Media, PA: Williams and Wilkins, 1995).

[0257] Dosage forms adapted for topical administration can be formulated as ointments, creams, suspensions, lotions, powders, solutions, pastes, gels, sprays, aerosols, or oils. In some embodiments for treatments of the eye or other external tissues, for example the mouth or the skin, the pharmaceutical formulations are applied as a topical ointment or cream. When formulated in an ointment, the one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein can be formulated with a paraffinic or water-miscible ointment base. In some embodiments, the active ingredient can be formulated in a cream with an oil-in-water cream base or a water-in-oil base. Dosage forms adapted for topical administration in the mouth include lozenges, pastilles, and mouth washes.

[0258] Dosage forms adapted for nasal or inhalation administration include aerosols, solutions, suspension drops, gels, or dry powders. In some embodiments, the one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein is contained in a dosage form adapted for inhalation is in a particle-size-reduced form that is obtained or obtainable by micronization. In some embodiments, the particle size of the size reduced (e.g., micronized) compound or salt or solvate thereof, is defined by a D50 value of about 0.5 to about 10 microns as

measured by an appropriate method known in the art. Dosage forms adapted for administration by inhalation also include particle dusts or mists. Suitable dosage forms wherein the carrier or excipient is a liquid for administration as a nasal spray or drops include aqueous or oil solutions/suspensions of an active ingredient (e.g., the one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein and/or auxiliary active agent), which may be generated by various types of metered dose pressurized aerosols, nebulizers, or insufflators.

[0259] In some embodiments, the dosage forms can be aerosol formulations suitable for administration by inhalation. In some of these embodiments, the aerosol formulation can contain a solution or fine suspension of the one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein and a pharmaceutically acceptable aqueous or non-aqueous solvent. Aerosol formulations can be presented in single or multi-dose quantities in sterile form in a sealed container. For some of these embodiments, the sealed container is a single dose or multi-dose nasal, or an aerosol dispenser fitted with a metering valve (e.g., metered dose inhaler), which is intended for disposal once the contents of the container have been exhausted.

[0260] Where the aerosol dosage form is contained in an aerosol dispenser, the dispenser contains a suitable propellant under pressure, such as compressed air, carbon dioxide, or an organic propellant, including but not limited to a hydrofluorocarbon. The aerosol formulation dosage forms in other embodiments are contained in a pump-atomizer. The pressurized aerosol formulation can also contain a solution or a suspension of one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein. In further embodiments, the aerosol formulation can also contain co-solvents and/or modifiers incorporated to improve, for example, the stability and/or taste and/or fine particle mass characteristics (amount and/or profile) of the formulation. Administration of the aerosol formulation can be once daily or several times daily, for example 2, 3, 4, or 8 times daily, in which 1, 2, or 3 doses are delivered each time.

[0261] For some dosage forms suitable and/or adapted for inhaled administration, the pharmaceutical formulation is a dry powder inhalable formulation. In addition to the one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein, an auxiliary active ingredient, and/or pharmaceutically acceptable salt thereof, such a dosage form can contain a powder base such as lactose, glucose, trehalose, mannitol, and/or starch. In some of

these embodiments, the one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein is in a particle-size reduced form. In further embodiments, a performance modifier, such as L-leucine or another amino acid, cellobiose octaacetate, and/or metals salts of stearic acid, such as magnesium or calcium stearate.

[0262] In some embodiments, the aerosol dosage forms can be arranged so that each metered dose of aerosol contains a predetermined amount of an active ingredient, such as the one or more of the one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein.

[0263] Dosage forms adapted for ocular administration can include aqueous and/or nonaqueous sterile solutions that can optionally be adapted for injection, and which can optionally contain anti-oxidants, buffers, bacteriostats, solutes that render the composition isotonic with the eye or fluid contained therein or around the eye of the subject, and aqueous and nonaqueous sterile suspensions, which can include suspending agents and thickening agents.

[0264] For some embodiments, the dosage form contains a predetermined amount of the one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein per unit dose. In some embodiments, the predetermined amount of the Such unit doses may therefore be administered once or more than once a day. Such pharmaceutical formulations may be prepared by any of the methods well known in the art.

Effective Amounts

[0265] In some embodiments, the amount of the primary active agent and/or optional secondary agent can be an effective amount, least effective amount, and/or therapeutically effective amount. As used herein, “effective amount”, “effective concentration”, and/or the like refers to the amount, concentration, etc. of the primary and/or optional secondary agent included in the pharmaceutical formulation that achieve one or more therapeutic effects or desired effect. As used herein, “least effective”, “least effective concentration”, and/or the like amount refers to the lowest amount, concentration, etc. of the primary and/or optional secondary agent that achieves the one or more therapeutic or other desired effects. As used herein, “therapeutically effective amount”, “therapeutically effective concentration” and/or the like refers to the amount, concentration, etc. of the primary and/or optional secondary agent included in the pharmaceutical

formulation that achieves one or more therapeutic effects.In some embodiments, the one or more therapeutic effects comprise transducing the CNS.

[0266] In some embodiments, the amount or effective amount, particularly where an infective particle is being delivered (e.g., a virus particle having the primary or secondary agent as a cargo), the effective amount of virus particles can be expressed as a titer (plaque forming units per unit of volume) or as a MOI (multiplicity of infection). In some embodiments, the effective amount can be about $1X10^{1}$ particles per pL, nL, μL, mL, or L to $1X10^{20}$/ particles per pL, nL, μL, mL, or L or more, such as about $1x10^{1}$, $1x10^{2}$, $1x10^{3}$, $1x10^{4}$, $1x10^{5}$, $1x10^{6}$, $1x10^{7}$, $1x10^{8}$, $1x10^{9}$, $1x10^{10}$, $1x10^{11}$, $1x10^{12}$, $1x10^{13}$, $1x10^{14}$, $1x10^{15}$, $1x10^{16}$, $1x10^{17}$, $1x10^{18}$, $1x10^{19}$, to/or about $1x10^{20}$ particles per pL, nL, μL, mL, or L. In some embodiments, the effective titer can be about $1X10^{1}$ transforming units per pL, nL, μL, mL, or L to $1X10^{20}$/ transforming units per pL, nL, μL, mL, or L or more, such as about $1x10^{1}$, $1x10^{2}$, $1x10^{3}$, $1x10^{4}$, $1x10^{5}$, $1x10^{6}$, $1x10^{7}$, $1x10^{8}$, $1x10^{9}$, $1x10^{10}$, $1x10^{11}$, $1x10^{12}$, $1x0^{13}$, $1x10^{14}$, $1x10^{15}$, $1x10^{16}$, $1x10^{17}$, $1x10^{18}$, $1x10^{19}$, to/or about $1x10^{20}$ transforming units per pL, nL, μL, mL, or L or any numerical value or subrange within these ranges. In some embodiments, the MOI of the pharmaceutical formulation can range from about 0.1 to 10 or more, such as 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3, 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, 8, 8.1, 8.2, 8.3, 8.4, 8.5, 8.6, 8.7, 8.8, 8.9, 9, 9.1, 9.2, 9.3, 9.4, 9.5, 9.6, 9.7, 9.8, 9.9, 10 or more or any numerical value or subrange within these ranges.

[0267] In some embodiments, the effective amount, least effective amount, and/or therapeutically effective amount can be an effective concentration, least effective concentration, and/or therapeutically effective concentration, which can each be any non-zero amount ranging from about 0 to 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, 920, 930, 940,

950, 960, 970, 980, 990, 1000 pM, nM, μM, mM, or M or be any numerical value or subrange within any of these ranges.

[0268] In some embodiments, the primary and/or the optional secondary active agent present in the pharmaceutical formulation can be any non-zero amount ranging from about 0 to 0.001, 0.002, 0.003, 0.004, 0.005, 0.006, 0.007, 0.008, 0.009, 0.01, 0.02, 0.03, 0.04, 0.05, 0.06, 0.07, 0.08, 0.09, 0.1, 0.11, 0.12, 0.13, 0.14, 0.15, 0.16, 0.17, 0.18, 0.19, 0.2, 0.21, 0.22, 0.23, 0.24, 0.25, 0.26, 0.27, 0.28, 0.29, 0.3, 0.31, 0.32, 0.33, 0.34, 0.35, 0.36, 0.37, 0.38, 0.39, 0.4, 0.41, 0.42, 0.43, 0.44, 0.45, 0.46, 0.47, 0.48, 0.49, 0.5, 0.51, 0.52, 0.53, 0.54, 0.55, 0.56, 0.57, 0.58, 0.59, 0.6, 0.61, 0.62, 0.63, 0.64, 0.65, 0.66, 0.67, 0.68, 0.69, 0.7, 0.71, 0.72, 0.73, 0.74, 0.75, 0.76, 0.77, 0.78, 0.79, 0.8, 0.81, 0.82, 0.83, 0.84, 0.85, 0.86, 0.87, 0.88, 0.89, 0.9, 0.91, 0.92, 0.93, 0.94, 0.95, 0.96, 0.97, 0.98, 0.9, to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 99.1, 99.2, 99.3, 99.4, 99.5, 99.6, 99.7, 99.8, 99.9 % w/w, v/v, or w/v of the pharmaceutical formulation or be any numerical value or subrange within any of these ranges.

[0269] In some embodiments, the amount or effective amount of the one or more of the active agent(s) described herein contained in the pharmaceutical formulation can range from about 1 pg/kg to about 10 mg/kg based upon the bodyweight of the subject in need thereof or average bodyweight of the specific patient population to which the pharmaceutical formulation can be administered.

[0270] In embodiments where there is a secondary agent contained in the pharmaceutical formulation, the effective amount of the secondary active agent will vary depending on the secondary agent, the primary agent, the administration route, subject age, disease, stage of disease, among other things, which will be one of ordinary skill in the art.

[0271] When optionally present in the pharmaceutical formulation, the secondary active agent can be included in the pharmaceutical formulation or can exist as a stand-alone compound or pharmaceutical formulation that can be administered contemporaneously or sequentially with the compound, derivative thereof, or pharmaceutical formulation thereof.

[0272] In some embodiments, the effective amount of the secondary active agent, when optionally present, is any non-zero amount ranging from about 0 to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 99.1, 99.2, 99.3, 99.4, 99.5, 99.6, 99.7, 99.8, 99.9 % w/w, v/v, or w/v of the total active agents present in the pharmaceutical formulation or any numerical value or subrange within these ranges. In additional embodiments, the effective amount of the secondary active agent is any non-zero amount ranging from about 0 to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 99.1, 99.2, 99.3, 99.4, 99.5, 99.6, 99.7, 99.8, 99.9 % w/w, v/v, or w/v of the total pharmaceutical formulation or any numerical value or subrange within these ranges.

Kits

[0273] Also described herein are kits that contain one or more of the one or more of the compositions, polypeptides, polynucleotides, vectors, cells, or other components described herein and combinations thereof and pharmaceutical formulations described herein. In embodiments, one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein can be presented as a combination kit. As used herein, the terms "combination kit" or "kit of parts" refers to the compounds, or formulations and additional components that are used to package, screen, test, sell, market, deliver, and/or administer the combination of elements or a single element, such as the active ingredient, contained therein. Such additional components include but are not limited to, packaging, syringes, blister packages, bottles, and the like. The combination kit can contain one or more of the components (e.g., one or more of the one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof) or formulation thereof can be provided in a single formulation (e.g., a liquid, lyophilized powder, etc.), or in separate formulations. The separate components or formulations can be contained in a single package or in separate packages within the kit. The kit can also include instructions in a tangible

medium of expression that can contain information and/or directions regarding the content of the components and/or formulations contained therein, safety information regarding the content of the components(s) and/or formulation(s) contained therein, information regarding the amounts, dosages, indications for use, screening methods, component design recommendations and/or information, recommended treatment regimen(s) for the components(s) and/or formulations contained therein. As used herein, "tangible medium of expression" refers to a medium that is physically tangible or accessible and is not a mere abstract thought or an unrecorded spoken word. "Tangible medium of expression" includes, but is not limited to, words on a cellulosic or plastic material, or data stored in a suitable computer readable memory form. The data can be stored on a unit device, such as a flash memory drive or CD-ROM or on a server that can be accessed by a user via, e.g., a web interface.

[0274] In one embodiment, the invention provides a kit comprising one or more of the components described herein. In some embodiments, the kit comprises a vector system and instructions for using the kit. In some embodiments, the vector system includes a regulatory element operably linked to one or more engineered polynucleotides, such as those containing a selective n-mer, as described elsewhere herein and, optionally, a cargo molecule, which can optionally be operably linked to a regulatory element. The one or more engineered polynucleotides such as those containing a selective n-mer, as described elsewhere herein and, can be included on the same or different vectors as the cargo molecule in embodiments containing a cargo molecule within the kit.

[0275] In some embodiments, the kit comprises a vector system and instructions for using the kit. In some embodiments, the vector system comprises (a) a first regulatory element operably linked to a direct repeat sequence and one or more insertion sites for inserting one or more guide sequences up- or downstream (whichever applicable) of the direct repeat sequence, wherein when expressed, the guide sequence directs sequence-specific binding of a Cas9 CRISPR complex to a target sequence in a eukaryotic cell, wherein the Cas9 CRISPR complex comprises a Cas9 enzyme complexed with the guide sequence that is hybridized to the target sequence; and/or (b) a second regulatory element operably linked to an enzyme-coding sequence encoding said Cas9 enzyme comprising a nuclear localization sequence. Where applicable, a tracr sequence may also be provided. In some embodiments, the kit comprises components (a) and (b) located on the same or

different vectors of the system. In some embodiments, component (a) further comprises two or more guide sequences operably linked to the first regulatory element, wherein when expressed, each of the two or more guide sequences direct sequence specific binding of a CRISPR complex to a different target sequence in a eukaryotic cell. In some embodiments, the Cas9 enzyme comprises one or more nuclear localization sequences of sufficient strength to drive accumulation of said CRISPR enzyme in a detectable amount in the nucleus of a eukaryotic cell. In some embodiments, the CRISPR enzyme is a type V or VI CRISPR system enzyme. In some embodiments, the CRISPR enzyme is a Cas9 enzyme. In some embodiments, the Cas9 enzyme is derived from Francisella tularensis 1, Francisella tularensis subsp. novicida, Prevotella albensis, Lachnospiraceae bacterium MC2017 1, Butyrivibrio proteoclasticus, Peregrinibacteria bacterium GW2011_GWA2_33_10, Parcubacteria bacterium GW2011_GWC2_44_17, Smithella sp. SCADC, Acidaminococcus sp. BV3L6, Lachnospiraceae bacterium MA2020, Candidatus Methanoplasma termitum, Eubacterium eligens, Moraxella bovoculi 237, Leptospira inadai, Lachnospiraceae bacterium ND2006, Porphyromonas crevioricanis 3, Prevotella disiens, or Porphyromonas macacae Cas9 (e.g., modified to have or be associated with at least one DD), and may include further alteration or mutation of the Cas9, and can be a chimeric Cas9. In some embodiments, the DD-CRISPR enzyme is codon-optimized for expression in a eukaryotic cell. In some embodiments, the DD-CRISPR enzyme directs cleavage of one or two strands at the location of the target sequence. In some embodiments, the DD-CRISPR enzyme lacks or substantially DNA strand cleavage activity (e.g., no more than 5% nuclease activity as compared with a wild-type enzyme or enzyme not having the mutation or alteration that decreases nuclease activity). In some embodiments, the first regulatory element is a polymerase III promoter. In some embodiments, the second regulatory element is a polymerase II promoter. In some embodiments, the guide sequence is at least 16, 17, 18, 19, 20, 25 nucleotides, or between 16-30, or between 16-25, or between 16-20 nucleotides in length.

METHODS OF USE FOR DELIVERY OF CARGO TO CNS

[0276] The compositions including one or more of the cell-selective targeting moieties, engineered AAV capsid system polynucleotides, polypeptides, vector(s), engineered cells, engineered AAV capsid particles can be used generally to package and/or deliver one or more cargos to neuron and glial cells of the CNS. In some embodiments, delivery is done in cell-selective

manner based upon the selectivity of the targeting moiety. In some embodiments this is conferred by the tropism of the engineered AAV capsid, which can be influenced at least in part by the inclusion of one or n-mer motifs described elsewhere herein. In some embodiments, compositions including one or more of the CNS targeting moieties, including engineered AAV capsid particles where the capsids incorporate the targeting moiety, can be administered to a subject or a cell, tissue, and/or organ and facilitate the transfer and/or integration of the cargo to the recipient cell. In other embodiments, engineered cells capable of producing compositions, such as polypeptides and other particles (e.g., engineered AAV capsids and viral particles), containing one or more of the targeting moieties can be generated from the polynucleotides, vectors, and vector systems etc., described herein. This includes without limitation, the engineered AAV capsid system molecules (e.g., polynucleotides, vectors, and vector systems, etc.). In some embodiments, the polynucleotides, vectors, and vector systems etc., described herein capable of generating the compositions, such as polypeptides and other particles (e.g., engineered AAV capsids and viral particles), containing one or more of the targeting moieties can be delivered to a cell or tissue, in vivo, ex vivo, or in vitro. In some embodiments, when delivered to a subject, the composition can transform a subject's cell in vivo or ex vivo to produce an engineered cell that can be capable of making a composition described herein that contains one or more of the cell-selective targeting moieties described herein, including but not limited to the engineered AAV capsid particles, which can be released from the engineered cell and deliver cargo molecule(s) to a recipient cell in vivo or produce personalized engineered compositions (e.g., AAV capsid particles) for reintroduction into the subject from which the recipient cell was obtained.

[0277] In some embodiments, an engineered cell can be delivered to a subject, where it can release produced compositions of the present invention (including but not limited to engineered AAV capsid particles) such that they can then deliver a cargo (e.g., a cargo polynucleotide(s)) to a recipient cell. These general processes can be used in a variety of ways to treat and/or prevent disease or a symptom thereof in a subject, generate model cells, generate modified organisms, provide cell selection and screening assays, in bioproduction, and in other various applications.

[0278] In some embodiments, the compositions, such as polypeptides and other particles (e.g., engineered AAV capsids and viral particles), containing one or more of the targeting moieties can

be delivered to neural cells of the CNS. In another example embodiment, the compositions containing one or more targeting moieties can be delivered to glial cells of the CNS.

[0279] In some embodiments, the engineered AAV capsid polynucleotides, vectors, and systems thereof can be used to generate engineered AAV capsid variant libraries that can be mined for variants with a desired cell-selectivity. The description provided herein as supported by the various Examples can demonstrate that one having a desired cell-selectivity in mind could utilize the present invention as described herein to obtain a capsid with the desired cell-selectivity.

Methods of treatment

[0280] Provided herein are methods for treating a disease or disorder, the method comprising administering to a subject in need thereof, a composition as disclosed herein to cells of the CNS. In an aspect, the compositions used in methods disclosed herein are capable of increasing transduction of neurons and/or glial cells of the CNS, allowing for delivery of cargo and therapeutics directly to such cell types. In embodiments, a method is disclosed wherein the cargo is one or more polypeptides.

Diseases or Disorders

[0281] In embodiments, a method is disclosed wherein the disease or disorder is a cancer, neurological disorder, or infection.

[0282] In an embodiment, methods of treatment comprise administering a composition as detailed herein to a subject in need thereof. In an example embodiment, the cancer is a neuroepithelial cancer. In an embodiment, the cancer is a neuroepithelial tumor, for example, Astrocytic tumors, e.g., Diffuse Astrocytoma (fibrillary, protoplasmic, gemistocytic, mixed), Anaplastic (malignant) astrocytoma, Glioblastoma (giant cell, gliosarcoma variants), Pilocytic astrocytoma, Pleomorphic xanthoastrocytoma, or Subependymal giant cell astrocytoma; Oligodendroglial tumors, e.g., Oligodendroglioma, Anaplastic (malignant) Oligodendroglioma, Ependymal tumors, Ependymoma (cellular, papillary, clear cell, tanycytic), Anaplastic (malignant) ependymoma, ependymoma, Subependymoma; Mixed tumors, e.g., Oligoastrocytomaor Anaplastic (malignant) oligoastrocytoma; Choroid plexus tumors, e.g., Choroid Plexus papilloma or Choroid Plexus carcinoma; Neuronal and mixed neuronal-glial tumors, e.g., Gangliocytoma, Ganglioglioma, Dysembryoplastic neuroepithelial tumor (DNET), Dysplastic gangliocytoma of the cerebellum (Lhermitte-Duclos), Desmoplastic infantile

astrocytoma/ganglioglioma, Central neurocytoma, Anaplastic ganglioglioma, Cerebellar liponeurocytoma, Paraganglioma of the filum terminale; Pineal tumors, e.g., Pineocytoma, Pineoblastoma, Pineal parenchymal tumor of intermediate differentiation; Embryonal tumors, e.g., Medulloblastoma (desmoplastic, large cell, melanotic, medullomyoblastoma), Medulloepithelioma, Supratentorial primitive neuroectodermal tumors, PNETs such as Neuroblastoma, Ganglioneuroblastoma, Ependymoblastoma, or Atypical teratoid/rhabdoid tumor; Neuroblastic tumors, e.g., Olfactory (esthesioneuroblastoma), Olfactory neuroepithelioma, Neuroblastomas of the adrenal gland and sympathetic nervous system; Glial tumors of uncertain etiology, e.g., Astroblastoma, Gliomatosis cerebri, Chordoid glioma of the third ventricle.

[0283] In an embodiment, the cancer is a primary cancer metastasized to brain or other region of the central nervous system.

[0284] In an example embodiment, the neurological disorder is caused by a neurodegenerative or a neurodevelopmental disease. Example neurodegenerative diseases include, but are not limited to, Alzheimer's disease and other memory disorders, amyotrophic lateral sclerosis (ALS), ataxia, Huntington's disease, Parkinson's disease, motor neuron disease, multiple system atrophy, progressive supranuclear palsy. Examples of neurodevelopmental diseases include, but are not limited to, attention-deficit/hyperactivity disorder (ADHD), autism, learning disabilities, intellectual disability (also known as mental retardation), conduct disorders, cerebral palsy, speech and language disorders, Tourette syndrome, Schizophrenia, Fragile X syndrome, and impairments in vision and hearing.

NON-HUMAN TRANSGENIC ANIMALS

[0285] In one aspect, as provided herein a method of creating humanized transgenic non-human animals comprising: delivering to one or more cells of a non-human animal a vector system or a recombinant viral particle comprising a recombinant viral genome, wherein: the vector system or recombinant viral genome encodes a human transferrin polypeptide, wherein the encoded human transferrin polypeptide is under the control of a tissue-specific promoter or miRNA binding element that has selective activity in the desired cell, tissue, or organ. In an example embodiment, the one or more cells are endothelial cells. In an example embodiment, the one or more cells are CNS cells. In an example embodiment, the one or more cells are of the CNS vasculature, lungs, kidneys, liver, or any combination thereof. In an example embodiment, the endothelial cells are of

the CNS vasculature. In an example embodiment, the recombinant viral particle, optionally an AAV viral particle, comprises a capsid polypeptide, optionally an AAV capsid polypeptide, wherein the capsid polypeptide comprises a CNS specific n-mer motif. In an example embodiment, the CNS-specific n-mer motif comprises X1-N-X3-X4-X5-X6-X7, wherein X5 is independently selected from K or R, and X1, X3, X4, X6 and X7 are independently selected from any amino acid, optionally wherein the overall charge of the n-mer motif at neutral pH is between 0 and + 2. In an example embodiment, the CNS-specific n-mer motif comprises or consists of NNSTRGG (SEQ ID NO: 42429), GNSARNI (SEQ ID NO: 42430), and GNSVRDF (SEQ ID NO: 42431). In an example embodiment, the transgenic non-human animal is a rodent, optionally a mouse.

[0286] In one aspect, provided herein a humanized transgenic non-human animal comprising: one or more cells expressing a human transferrin polypeptide, optionally wherein the one or more cells are CNS cells. In an example embodiment, the transgenic non-human animal is a rodent, optionally a mouse. In one aspect, provided herein a humanized transgenic non-human animal produced by the methods described herein. In an example embodiment, the humanized non-human animal has a suppressed immune system.

[0287] It will be appreciated that in the present methods, where the non-human transgenic organism is multicellular, e.g., an animal or plant, the modification may occur *ex vivo* or *in vitro*, for instance in a cell culture and in some instances not *in vivo*. In other embodiments, it may occur *in vivo*. In an aspect, the invention provides a method of modifying an organism or a non-human organism by manipulation of a target sequence in a genomic locus of interest comprising: Delivering, e.g., via particle(s) or nanoparticle(s) or vector(s) (e.g., viral vector, e.g., AAV, adenovirus, lentivirus) a non-naturally occurring or engineered composition.

[0288] A single cell or a population of cells may preferably be modified *ex vivo* and then re-introduced, e.g., transplanted to make transgenic organisms that express TFRC in certain cells. The invention in some embodiments comprehends a method of modifying a eukaryote, such as a transgenic eukaryote comprising delivering, e.g., via vector(s) and/or particle(s) and/or nanoparticles a non-naturally occurring or engineered composition. The system may comprise one, two, three or four different vectors; and the system may comprise one, two, three or four different nanoparticle complex(es) delivering the component(s) of the system. Components I, II, III and IV may thus be located on one, two, three or four different vectors, and may be delivered by one, two,

three or four different particle or nanoparticle complex(es) or AAVs or components I, II, III and IV can be located on same or different vector(s) / particle(s) / nanoparticle(s), with all combinations of locations envisaged. And complexes that target the CNS or CNS tissue or CNS cells are advantageous.

[0289] In some embodiments, vectors are delivered to the eukaryotic cell in a transgenic eukaryote. In some embodiments, said modifying takes place in said eukaryotic cell in a cell culture. In one aspect, the invention provides a method of generating a model eukaryotic cell or a model transgenic eukaryote comprising one or more human proteins.

[0290] In one aspect, the present invention provides a transgenic eukaryote, e.g., mouse. In one aspect, the present invention provides a constitutive transgenic eukaryote, e.g., mouse line obtained by crossing of the transgenic mouse with another mouse line. In certain embodiments, progeny (or progenies) derived from said transgenic eukaryote, e.g., mouse line, may be successfully bred over at least five generations without exhibiting increased levels of genome instability or cellular toxicity. In one aspect, the present invention provides a method for simultaneously introducing multiple mutations *ex vivo* in a tissue, organ or a cell line (of the CNS), or in vivo in the same. It can be appreciated that using the novel targeting moiety tools disclosed herein, may produce a transgenic non-human eukaryote, e.g., animal model with multiple mutations in any number of loci can be envisioned and are within the scope of the present invention. It will be appreciated that such a transgenic non-human eukaryote, e.g., animal model provides a valuable tool for research purposes, e.g., viral transduction, and opens the door for developing and testing new therapeutic interventions for targeting specific tissue involving mutations at multiple loci. Such uses are within the scope of the present invention.

[0291] The eukaryotic cell can comprise a constitutive promoter, or a tissue specific promoter, or an inducible promoter; and, the eukaryotic cell can be part of a non-human transgenic eukaryote, e.g., a non-human mammal, primate, rodent, mouse, rat, rabbit, canine, dog, cow, bovine, sheep, ovine, goat, pig, fowl, poultry, chicken, fish, insect or arthropod; advantageously a mouse. The isolated eukaryotic cell or the non-human transgenic eukaryote can express an additional protein or enzyme, such as TfR1; and, the expression of TfR1 can be driven by coding therefor functionally or operatively linked to a constitutive promoter, or a tissue specific promoter, or an inducible promoter.

[0292] The eukaryotic cell can be a mammalian cell, e.g., a mouse cell, such as a mouse cell that is part of a transgenic mouse having cells that express TfR1.

[0293] Transgenic non-human eukaryotic organisms, e.g., animals are also provided in an aspect of practice of the instant invention. Preferred examples include animals comprising TfR1, in terms of polynucleotides encoding TfR1or the protein itself. In certain aspects, the invention involves a constitutive or conditional or inducible TfR1 non-human eukaryotic organism, such as an animal, e.g., a primate, rodent, e.g., mouse, rat and rabbit, are preferred; and can include a canine or dog, livestock (cow / bovine, sheep / ovine, goat or pig), fish, fowl or poultry, e.g., chicken, and an insect or arthropod, with it mentioned that it is advantageous if the animal is a model as to a human or animal protein, cell, or tissue, as use of the non-human eukaryotic organisms in condition modeling, e.g., via inducing a plurality, are preferred. To generate transgenic mice with the constructs, as exemplified herein one may inject pure, linear DNA into the pronucleus of a zygote from a pseudo pregnant female, e.g. a CB56 female. Founders may then be identified, genotyped, and backcrossed to CB57 mice. The constructs may then be cloned and optionally verified, for instance by Sanger sequencing. Knock ins are envisaged (alone or in combination

[0294] Accordingly, the invention involves a non-human eukaryote, animal, mammal, primate, rodent, etc. or cell thereof or tissue thereof that may be used as a model. For example, a method of the invention may be used to create a non-human eukaryote, e.g., an animal, mammal, primate, rodent or cell that comprises a modification in one or more nucleic acid sequences associated or correlated with a cell or tissue of such (such as the CNS). The cell may be *in vivo* or *ex vivo* in the cases of multicellular organisms. In the instance where the cell is in cultured, a cell line may be established if appropriate culturing conditions are met and preferably if the cell is suitably adapted for this purpose (for instance a stem cell). Hence, cell lines are also envisaged.

[0295] In an aspect the invention can involve cells, e.g., non-human eukaryotic, e.g., animal, such as mammal, e.g., primate, rodent, mouse, rat, rabbit, etc., or even human cells, transformed to contain TfR1, e.g., such cells as to which a vector that contains nucleic acid molecule(s) encoding a TfR1, e.g., with nucleic acid(s) encoding a promoter and at least one NLS, advantageously two or more NLSs, or such cells that have had their genome altered, e.g., through the vector being an integrating virus or through such cells being stem cells or cells that give rise

to a cell line or a living organism (but wherein such an organism is advantageously non-human), that contains and expresses nucleic acid molecule(s) encoding TfR1. Such cells are then transplanted into or onto an animal suitable for expressing a cell or tissue. The cells proliferate on or in the non-human eukaryote, e.g., animal model. The non-human eukaryote, e.g., animal model, having the proliferated heterologous transplanted TfR1-containing cells, is then administered RNA(s) or vector(s), e.g., AAV, adenovirus, lentivirus containing or providing RNA(s), e.g., under the control of a promoter such as a U6 promoter and/or particle(s) and/or nanoparticle(s). The non-human eukaryote, e.g., animal model can then be used for testing, e.g., as to potential therapy and/or putative treatment via a possibly pharmaceutically active compound. The administering can be at or to or for body delivery to the proliferated heterologous transplanted TfR1-containing cells, e.g., direct injection at or near such proliferated heterologous transplanted TfR1-containing cells, or injection or other administration in such a way that the RNA(s) are delivered into the proliferated heterologous transplanted TfR1-containing cells, e.g., injection into the bloodstream whereby bodily functions transport to the proliferated heterologous transplanted TfR1-containing cells. In an aspect of the invention, barcoding techniques of WO/2013/138585 A1 can be adapted or integrated into the practice of the invention. WO/2013/138585 A1 provides methods for simultaneously determining the effect of a test condition on viability or proliferation of each of a plurality of genetically heterogeneous cell types. The number of living cells in the sample after exposure to the test condition as compared to the reference number of cells indicates the effect of the test condition on viability or proliferation of each cell type. WO/2013/138585 A1 also provides methods for simultaneously determining the effect of a test condition on viability or proliferation of each of a plurality of genetically heterogeneous cell types. Referenced patent applications are hereby incorporated by reference.

[0296] The practice of the present invention employs, unless otherwise indicated, conventional techniques for generation of genetically modified mice. See Marten H. Hofker and Jan van Deursen, TRANSGENIC MOUSE METHODS AND PROTOCOLS, 2nd edition (2011).

SCREENING AND CELL SELECTION

[0297] In one aspect, as provided herein a method of screening n-mer motifs capable of conferring transduction of central nervous system (CNS) tissues via binding to a transferrin receptor (TFRC) in humanized transgenic non-human animals comprising: introducing one or

more compositions comprising a candidate n-mer motif to humanized non-human transgenic animal of any one of claims 101-113; and detecting binding of the compositions that bind to a transferrin receptor (TFRC) and/or detecting transduction or uptake by one or more CNS cells of the humanized transgenic non-human animal. In an example embodiment, the candidate n-mer motif comprises or consists of X1-N-X3-X4-X5-X6-X7, wherein X5 is independently selected from K or R, and X1, X3, X4, X6 and X7 are independently selected from any amino acid, optionally wherein the overall charge of the n-mer motif at neutral pH is between 0 and + 2. In an example embodiment, the composition is a viral particle comprising one or more capsid proteins each comprising the candidate n-mer motif. In an example embodiment, the viral particle is an AAV viral particle and the one or more capsid proteins is an AAV capsid protein, optionally wherein the candidate n-mer motif is inserted in between amino acids 588-589 of an AAV9 capsid polypeptide or in an analogous position of a capsid protein from AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAVrh8, AAV rh.74, or AAV rh. 10. In an example embodiment, at least one of the one or more compositions furthers comprises a cargo. In an example embodiment, the cargo is or encodes a therapeutic nucleic acid or polypeptide, a selectable marker, or a control polypeptide or nucleic acid.

[0298] In one aspect, a method of screening targeting moieties, including incorporated within an AAV, capable of transduction of central nervous system (CNS) tissues via binding to a transferrin receptor (TFRC) in humanized transgenic non-human animals comprising: (a) introducing a plurality of vector systems to one or more humanized transgenic non-human animal that express the human TFRC and (b) detecting the targeting moiety that binds to a transferrin receptor (TFRC).

[0299] The engineered AAV capsid system vectors, engineered cells, and/or engineered AAV capsid particles described herein can be used in a screening assay and/or cell selection assay. The engineered delivery system vectors, engineered cells, and/or engineered AAV capsid particles can be delivered to a subject and/or cell. In some embodiments, the cell is a eukaryotic cell. The cell can be in vitro, ex vivo, in situ, or in vivo. The engineered AAV capsid system molecules, vectors, engineered cells, and/or engineered AAV capsid particles described herein can introduce an exogenous molecule or compound to subject or cell to which they are delivered. The presence of an exogenous molecule or compound can be detected which can allow for identification of a cell

and/or attribute thereof. In some embodiments, the delivered molecules or particles can impart a gene or other nucleotide modification (e.g., mutations, gene or polynucleotide insertion and/or deletion, etc.). In some embodiments the nucleotide modification can be detected in a cell by sequencing. In some embodiments, the nucleotide modification can result in a physiological and/or biological modification to the cell that results in a detectable phenotypic change in the cell, which can allow for detection, identification, and/or selection of the cell. In some embodiments, the phenotypic change can be cell death, such as embodiments where binding of a CRISPR complex to a target polynucleotide results in cell death. Embodiments of the invention allow for selection of specific cells without requiring a selection marker or a two-step process that may include a counter-selection system. The cell(s) may be prokaryotic or eukaryotic cells.

[0300] In one embodiment the invention provides for a method of selecting one or more cell(s) by introducing one or more mutations in a gene in the one or more cell (s), the method comprising: introducing one or more vectors, which can include one or more engineered delivery system molecules or vectors described elsewhere herein, into the cell (s), wherein the one or more vectors can include a CRISPR enzyme and/or drive expression of one or more of: a guide sequence linked to a tracr mate sequence, a tracr sequence, and an editing template; or other polynucleotide to be inserted into the cell and/or genome thereof; wherein, for example that which is being expressed is within and expressed in vivo by the CRISPR enzyme and/or the editing template, when included, comprises the one or more mutations that abolish CRISPR enzyme cleavage; allowing homologous recombination of the editing template with the target polynucleotide in the cell(s) to be selected; allowing a CRISPR complex to bind to a target polynucleotide to effect cleavage of the target polynucleotide within said gene, wherein the CRISPR complex comprises the CRISPR enzyme complexed with (1) the guide sequence that is hybridized to the target sequence within the target polynucleotide, and (2) the tracr mate sequence that is hybridized to the tracr sequence, wherein binding of the CRISPR complex to the target polynucleotide induces cell death, thereby allowing one or more cell(s) in which one or more mutations have been introduced to be selected. In a preferred embodiment, the CRISPR enzyme is a Cas protein. In another embodiment of the invention the cell to be selected may be a eukaryotic cell.

[0301] The screening methods involving the engineered AAV capsid system molecules, vectors, engineered cells, and/or engineered AAV capsid particles, including but not limited to

those that deliver one more CRISPR-Cas system molecules to cell, can be used in detection methods such as fluorescence in situ hybridization (FISH). In some embodiments, one or more components of an engineered CRISPR-Cas system that includes a catalytically inactive Cas protein, can be delivered by an engineered AAV capsid system molecule, engineered cell, and/or engineered AAV capsid particle described elsewhere herein to a cell and used in a FISH method. The CRISPR-Cas system can include an inactivated Cas protein (dCas) (e.g., a dCas9), which lacks the ability to produce DNA double-strand breaks may be fused with a marker, such as fluorescent protein, such as the enhanced green fluorescent protein (eEGFP) and co-expressed with small guide RNAs to target pericentric, centric and teleomeric repeats in vivo. The dCas system can be used to visualize both repetitive sequences and individual genes in the human genome. Such new applications of labelled dCas, dCas CRISPR-Cas systems, engineered AAV capsid system molecules, engineered cells, and/or engineered AAV capsid particles can be used in imaging cells and studying the functional nuclear architecture, especially in cases with a small nucleus volume or complex 3-D structures. (Chen B, Gilbert LA, Cimini BA, Schnitzbauer J, Zhang W, Li GW, Park J, Blackburn EH, Weissman JS, Qi LS, Huang B. 2013. Dynamic imaging of genomic loci in living human cells by an optimized CRISPR/Cas system. Cell 155(7):1479-91. doi: 10.1016/j.cell.2013.12.001., the teachings of which can be applied and/or adapted to the CRISPR systems described herein. A similar approach involving a polynucleotide fused to a marker (e.g., a fluorescent marker) can be delivered to a cell via an engineered AAV capsid system molecule, vector, engineered cell, and/or engineered AAV capsid particle described herein and integrated into the genome of the cell and/or otherwise interact with a region of the genome of a cell for FISH analysis.

[0302] Similar approaches for studying other cell organelles and other cell structures can be accomplished by delivering to the cell (e.g., via an engineered delivery AAV capsid molecule, engineered cell, and/or engineered AAV capsid particle described herein) one or more molecules fused to a marker (such as a fluorescent marker), wherein the molecules fused to the marker are capable of targeting one or more cell structures. By analyzing the presence of the markers, one can identify and/or image specific cell structures.

[0303] In some embodiments, the engineered AAV capsid system molecules and/or engineered AAV capsid particles can be used in a screening assay inside or outside of a cell. In

some embodiments, the screening assay can include delivering a CRISPR-Cas cargo molecule(s) via an engineered AAV capsid particle.

[0304] Use of the present system in screening is also provided by the present invention, e.g., gain of function screens. Cells which are artificially forced to overexpress a gene are able to down regulate the gene over time (re-establishing equilibrium) e.g., by negative feedback loops. By the time the screen starts the unregulated gene might be reduced again. Other screening assays are discussed elsewhere herein.

[0305] In an embodiment, the invention provides a cell from or of an *in vitro* method of delivery, wherein the method comprises contacting the delivery system with a cell, optionally a eukaryotic cell, whereby there is delivery into the cell of constituents of the delivery system, and optionally obtaining data or results from the contacting, and transmitting the data or results.

[0306] In an embodiment, the invention provides a cell from or of an in vitro method of delivery, wherein the method comprises contacting the delivery system with a cell, optionally a eukaryotic cell, whereby there is delivery into the cell of constituents of the delivery system, and optionally obtaining data or results from the contacting, and transmitting the data or results; and wherein the cell product is altered compared to the cell not contacted with the delivery system, for example altered from that which would have been wild type of the cell but for the contacting. In an embodiment, the cell product is non-human or animal. In some embodiments, the cell product is human.

[0307] In some embodiments, a host cell is transiently or non-transiently transfected with one or more vectors described herein. In some embodiments, a cell is transfected as it naturally occurs in a subject optionally to be reintroduced therein. In some embodiments, a cell that is transfected is taken from a subject. In some embodiments, the cell obtained from or is derived from cells taken from a subject, such as a cell line. Delivery mechanisms and techniques of the engineered AAV capsid system, engineered AAV capsid particles are described elsewhere herein.

[0308] In some embodiments it is envisaged to introduce the engineered AAV capsid system molecule(s) and/or engineered AAV capsid particle(s) directly to the host cell. For instance, the engineered AAV capsid system molecule(s) can be delivered together with one or more cargo molecules to be packaged into an engineered AAV capsid particle.

[0309] The invention is further described in the following examples, which do not limit the scope of the invention described in the claims.

EXAMPLES

Example 1 – Screening for 7-mer modified AAV capsids that bind selectively to cells expressing human TFRC (hTFRC).

[0310] A library of capsids with a 7-mer insertion between AA588 and 589 of AAV9 K449R was screened for capsids that bind to HEK293 or CHO cells transiently transfected with human TFRC (hTFRC) more efficiently than cells expressing a control protein (GFP). Sequences that bind more efficiently to cells expressing hTFRC were identified by NGS. Analysis of these sequences identified several motifs present in a subset of sequences: [YFL][AS][RK]X[NG]X[N] (SEQ ID NO: 20484) and XXS[ST]NG[IVR] (SEQ ID NO: 20485), where X = any amino acid.

[0311] Applicants generated a second round library comprising sequences identified in the cell-based screen for hTFRC binding and all of the sequences conforming to the above two motifs using oligo pool synthesis. The oligo pool was used to generate a capsid library. The second round library was screened on HEK293 cells with or without transient expression of hTFRC (5,000 vg/cell) as performed in the first round (Table 1). In addition, the second round library was screened to identify capsids that more efficiently transduced (1) hCMEC/D3 cells, which express endogenous hTFRC, (2) mouse brain microvascular endothelial cells (BMVECs) (Table 2) as well as (3) mixed culture spheroids consisting of hCMEC/D3 cells, and primary human astrocytes and pericytes (Cho et al, Nature Communications 2017).

[0312] Applicants chose several novel TFRC binding caspids for further study: AAV-BI19: YSRIGPN (SEQ ID NO: 14632); AAV-BI98: YSRLNMN (SEQ ID NO: 14301); AAV-BI99: YSRLNKD (SEQ ID NO: 16577); AAV-BI100: VHRLQDK (SEQ ID NO: 16602); AAV-BI101: YHRLSNN (SEQ ID NO: 16636); and AAV-BI102: LHALSHN (SEQ ID NO: 16608). Applicants used these capsids to package a reporter transgene and transduced CHO cells or CHO cells expressing human TFRC (Figure 2), as well as hCMEC cells or hCMEC cells overexpressing human TFRC (Figure 3). In both cell types, each of the TFRC binding capsids showed enhanced ability to bind and transduce cells expressing human TFRC relative to AAV9. Notably, the enhanced transduction by these engineered capsids was absent in CHO cells, which lack expression of human TFRC. In contrast, the engineered AAVs each showed enhanced transduction

of unmodified hCMEC cells relative to AAV9, which is fitting with the known expression of human TFRC in these cells. The role of TFRC for the enhanced hCMEC transduction of these capsid variants is supported by the finding that transduction was further enhanced in cells with greater cell surface exposed TFRC (Figures 3 and 4).

[0313] To assess whether the enhanced transduction of hCMEC cells by AAV-BI19 requires endogenous TFRC, Applicants attempted to block the interaction of the AAV with TFRC using several anti-TFRC antibodies: OKT9 (Thermo) and AF2474 (R&D Systems). Applicants found that OKT9, which binds to the TFRC apical domain (Ferrero et al J. of Virology https://doi.org/10.1128/JVI .01868-20) blocked transduction by AAV-BI19 in a dose-dependent manner (Figure 5). In contrast, AF2474, which blocks binding of Transferrin to TFRC, did not inhibit transduction by AAV-BI19. Together these results suggest that the enhanced tropism of AAV-BI19 for human brain endothelial cells is mediated through binding to the human TFRC apical domain.

Example 2 - Screening for 7-mer modified AAV capsids that bind selectively to hTFRC-Fc

[0314] In a second experiment, Applicants screened a separately produced AAV9 K499R 7-mer 588 insertion library for variants capable of selectively binding hTFRC when produced as an Fc fusion protein. To perform this assay, Applicants expressed the human or marmoset TFRC-Fc fusions in HEK293 cells and pulled down the Fc fusion proteins from the cell culture media using ProA-magentic beads (Figure 7).

[0315] The recovered 7-mers found to bind hTFRC-Fc were synthesized as an oligo pool and used to generate a second-round library. Applicants screened the second-round library for variants that bind hTFRC using the same hTFRC-Fc assay (Table 4), variants that bind to CHO cells stably expressing hTFRC (Table 5), variants that bind and transduce CHO cells expressing hTFRC (Table 6), and variants that bind HEK293 cells overexpressing hTFRC (Table 7). A subset of sequences bound HEK293 cells expressing either human TFRC or marmoset TFRC (Table 8).

Example 3 - Multiple regions of the AAV capsid can be engineered to enable TFRC binding.

[0316] To determine whether other regions of the AAV capsid could be engineered to bind to TFRC, Applicants generated libraries where a stretch of 10 AA in loop IV of AAV9 were substituted with a random string of AAs of seven or 10 AAs in length. Applicants also repeated

the screen using a new loop VIII 7-mer insertion library as a positive control. Applicants screened these libraries for capsids that gained the ability to bind selectively to human TFRC (Tabel 9 and Table 10) or human TFRC where the apical domain was replaced with the corresponding domain from mouse TFRC (Table 11). Notably, several of the 10 AA sequences recovered in the loop IV substitution library (IP**FSR**VNPDT (SEQ ID NO: 20285), LG**FART**GAAD (SEQ ID NO: 20274), LG**FTK**SSGSD (SEQ ID NO: 20270), LR**YSK**TQGES (SEQ ID NO: 20266), SP**YARS**SAGV (SEQ ID NO: 20271), and VG**WSR**LDLTT (SEQ ID NO: 20262)) contain the partial [YWFL][AST][RK] (SEQ ID NO: 20492) motif like that observed in human TFRC binding 7-mer insertions at loop VIII, suggesting that this binding motif is functional in multiple structural contexts.

Example 4 - Toward a systematic mapping of the relationship between AAV 7-mer sequence and hTFRC binding.

[0317] Applicants have generated a novel type of library (Fit4Function) composed of AAV capsids that uniformly samples only the high production fitness sequence space (International Patent Application WO 2021222636 A1). When used to screen for novel functions (e.g., new receptor binding), the Fit4Function libraries can generate highly reproducible quantitative data suitable for training ML models that predict the function of previously untested sequences within the theoretical sequence space. Applicants screened a Fit4Function library for capsids that selectively bind to TFRC-Fc. Binding was measured at both pH7.4 and pH5.5 and is reported in Table 12. Notably, even within this smaller library (240K unique sequences), several examples of sequences conforming to previously identified motifs were identified (e.g., YAKGGSN (SEQ ID NO: 11535) and YSKSGPG (SEQ ID NO: 20422), [YFL][AS][RK]X[NG]X[N] (SEQ ID NO: 20484); VKSSNGV (SEQ ID NO: 11671), XXS[ST]NG[IVR] (SEQ ID NO: 20485)).

Clustering and motif analyses

[0318] Applicants compiled sequences from all experiments run using human TFRC and the 588 site 7-mer libraries and performed clustering using UMAP. Sequences generated by mutagenesis of the motifs [YFL][AS][RK]X[NG]X[N] (SEQ ID NO: 20484) and XXS[ST]NG[IVR] (SEQ ID NO: 20485) were not included in the clustering analysis (Figure 8 and Table 13) but were considered when defining core sequence motifs shown below.

Motif analysis

[0319] $X_1X_2S[TS]NGX_3$ (SEQ ID NO: 20487), where X1 is any residue other than D, K, R; X2 is any residue other than P; and X3 is a V, I, or R.

[0320] $X_1X_2X_3X_4X_5X_6X_7$, where X1 and X2 are aromatic residues (F, W, or Y); X3 is an S, T, A, H, X4 is a G, N, H; X4 is any residue; X5 is any residue; X6 is any residue; and X7 is D, E, A, S, N, H, or P.

[0321] $X_1CX_2X_3CX_4X_5$, where X1 is L,P,R,A,H,E,S,N, or W; X_2 is G,P,S,T,K,Y,R; X3 is P,K,D,E,L,G, or S; X4 is any residue, and X5 is any residue.

[0322] $FAKX_1X_2X_3X_4$, where X1 is any residue, X2 is a G or an N, X3 is any residue, and X4 is preferably a N or a D.

[0323] $FARX_1X_2X_3X_4$ where X1 is any residue, X2 is a G or an N, X3 is any residue, and X4 is preferably a N or a D.

[0324] $FSKX_1X_2X_3X_4$ where X1 is any residue, X2 is a G or an N, X3 is any residue, and X4 is preferably a N or a D.

[0325] $FSRX_1X_2X_3X_4$ where X1 is any residue, X2 is a G or an N, X3 is any residue, and X4 is preferably a N or a D.

[0326] $LAKX_1X_2X_3X_4$ where X1 is any residue, X2 is a G or an N, X3 is any residue, and X4 is preferably a N or a D.

[0327] $LARX_1X_2X_3X_4$ where X1 is any residue, X2 is a G or an N, X3 is any residue, and X4 is preferably a N or a D.

[0328] $LHKX_1X_2X_3X_4$ where X1 is any residue, X2 is a G or an N, X3 is any residue, and X4 is preferably a N or a D.

[0329] $LHRX_1X_2X_3X_4$ where X1 is any residue, X2 is a G or an N, X3 is any residue, and X4 is preferably a N or a D.

[0330] $LSKX_1X_2X_3X_4$ where X1 is any residue, X2 is a G or an N, X3 is any residue, and X4 is preferably a N or a D.

[0331] $LSRX_1X_2X_3X_4$ where X1 is any residue, X2 is a G or an N, X3 is any residue, and X4 is preferably a N or a D.

[0332] $YAKX_1X_2X_3X_4$ where X1 is any residue, X2 is a G or an N, X3 is any residue, and X4 is preferably a N or a D.

[0333] $YARX_1X_2X_3X_4$ where X1 is any residue, X2 is a G or an N, X3 is any residue, and X4 is preferably a N or a D.

[0334] $YHKX_1X_2X_3X_4$ where X1 is any residue, X2 is a G or an N, X3 is any residue, and X4 is preferably a N or a D.

[0335] $YHRX_1X_2X_3X_4$ where X1 is any residue, X2 is a G or an N, X3 is any residue, and X4 is preferably a N or a D.

[0336] $YMKX_1X_2X_3X_4$ where X1 is any residue, X2 is a G or an N, X3 is any residue, and X4 is preferably a N or a D.

[0337] $YMRX_1X_2X_3X_4$ where X1 is any residue, X2 is a G or an N, X3 is any residue, and X4 is preferably a N or a D.

[0338] $YSKX_1X_2X_3X_4$ where X1 is any residue, X2 is a G or an N, X3 is any residue, and X4 is preferably a N or a D.

[0339] $YVKSX_1X_2X_3$ (SEQ ID NO: 20488), where X1 is a D, E, Q, N, or A; X2 is N, V, T, P, G, S, M, or A; and X3 is a C, G, I, A, N, R, K, S, or T.

[0340] $YVRSX_1X_2X_3$ (SEQ ID NO: 20504), where X1 is a D, E, Q, N, or A; X2 is N, V, T, P, G, S, M, or A; and X3 is a C, G, I, A, N, R, K, S, or T.

[0341] $YVKTX_1X_2X_3$ (SEQ ID NO: 20489), where X1 is a D, E, Q, N, or A; X2 is N, V, T, P, G, S, M, or A; and X3 is a C, G, I, A, N, R, K, S, or T.

[0342] $YVRTX_1X_2X_3$ (SEQ ID NO: 20490), where X1 is a D, E, Q, N, or A; X2 is N, V, T, P, G, S, M, or A; and X3 is a C, G, I, A, N, R, K, S, or T.

[0343] $X_1X_2X_3X_4X_5WP$, where X1 is a R, K, F, I, L, T, Y; and X2, X3 and X4 are any residue; and X5 is D or E.

[0344] $RX_1X_2X_3X_4X_5P$, where X1 and X2 are any residue; X3 is D; X4 is Y, F, V, A, T, S, I, L; and X4 is Y, F, V, or M.

[0345] $RX_1X_2DX_3YP$ (SEQ ID NO: 20491), where X1 and X are any residues; and X3 is A, V, F, T, or S.

[0346] $X_1YAKSX_2X_3$ (SEQ ID NO: 20501), where X1 is an S,Y,D,N, or A; X2 is an L, Y, V, A, Q, or E; and X3 is an L, A, P, D, N, or I.

[0347] $X_1KSSX_2X_3W$ (SEQ ID NO: 20503), where X1 is V, P, D, S, L; X2 is N, G, V, S, H, A, or R; X3 is V, N, S, H, D, or R.

Tables

[0348] Table 1. Capsids that demonstrate preferential binding to hTFRC expressed in HEK293 cells. The second round 7-mer 588 insertion library was screened for binding HEK293 cells transiently transfected with hTFRC (HEK-hTFRC) or control (GFP) HEK293 (HEK-Control). The table provides enrichment scores for each sequence, where enrichment is the log2 assay reads per million (RPM)/RPM in the virus library before screening. "-" <=0; "+" >0 to <=1; "++" >1 to <=2; "+++" >2.

[0349] Table 2. Capsids that transduce hCMECs in vitro. Capsids with the indicated 21-mer NT sequences and 7-mer AA sequences inserted between AA588 and 589 of AAV9 K449R were evaluated for their ability to transduce hCMEC/D3 and mouse brain microvascular endothelial cells (mBMVEC). The table provides enrichment scores for each sequence, where enrichment is the log2 assay reads per million (RPM)/RPM in the virus library before screening. "-" <=0; "+" >0 to <=1; "++" >1 to <=2; "+++" >2.

[0350] Table 3. Capsids that transduce multicellular BBB model cultures containing endothelial cells, astrocytes, and pericytes. The table provides enrichment scores for each sequence, where enrichment is the log2 assay reads per million (RPM)/RPM in the virus library before screening. "-" <=0; "+" >0 to <=1; "++" >1 to <=4; "+++" >4.

[0351] Table 4. Capsids that selectively bind human TFRC-Fc fusion protein. The second round 7-mer 588 insertion library was screened for binding to hTFRC-Fc fusion proteins in a pull-down assay. The table provides enrichment scores for each sequence, where enrichment is the log2 assay reads per million (RPM)/RPM in the virus library before screening. "-" <=0; "+" >0 to <=1; "++" >1 to <=2; "+++" >2.

[0352] Table 5. Capsids that selectively bind human TFRC-Fc fusion protein and bind CHO cells expressing TFRC. The second round 7-mer 588 insertion library was screened for capsids that bind CHO cells stably expressing human TFRC (hTFRC), untransduced control CHO cells (Untransduced), or control transduced CHO cells (Lenti-control). The table provides enrichment scores for each sequence, where enrichment is the log2 assay reads per million (RPM)/RPM in the virus library before screening. "-" <=0; "+" >0 to <=1; "++" >1 to <=5; "+++" >5.

[0353] Table 6. Capsids that selectively bind human TFRC-Fc fusion protein and bind and transduce CHO cells expressing TFRC. The second round 7-mer 588 insertion library was screened for capsids that bind and transduce CHO cells stably expressing human TFRC (hTFRC), untransduced control CHO cells (Untransduced), or control transduced CHO cells (Lenti-control). The table provides enrichment scores for each sequence, where enrichment is the log2 assay reads per million (RPM)/RPM in the virus library before screening. "-" <=0; "+" >0 to <=1; "++" >1 to <=5; "+++" >5.

[0354] Table 7. Capsids that selectively bind human TFRC-Fc fusion protein and bind HEK cells expressing TFRC. The second round 7-mer 588 insertion library was screened for capsids that bind HEK293 cells transiently expressing human TFRC (HEK-hTFRC) or control transduced HEK293 cells (HEK-GFP). The table provides enrichment scores for each sequence, where enrichment is the log2 assay reads per million (RPM)/RPM in the virus library before screening. "-" <=0; "+" >0 to <=1; "++" >1 to <=2; "+++" >2.

[0355] Table 8. Capsids that selectively bind human TFRC-Fc fusion protein and bind marmoset TFRC-Fc fusions. The second round 7-mer 588 insertion library was screened for capsids that bind human and marmoset TFRC-Fc fusion proteins (hTFRC and marTFRC, respectively). The capsids were also evaluated for their ability to bind HEK293 cells transiently expressing human TFRC (HEK-hTFRC) or control transduced HEK293 cells (HEK-GFP). The table provides enrichment scores for each sequence, where enrichment is the log2 assay reads per million (RPM)/RPM in the virus library before screening. "-" <=0; "+" >0 to <=1; "++" >1 to <=23; "+++" >2.

[0356] Table 9. Capsids that selectively bind human and marmoset TFRC-Fc fusion proteins. A 7-mer 588 insertion library was screened for binding to human or marmoset TFRC-Fc fusion proteins (hTFRC and marTFRC, respectively). Binding was performed at pH7.4. Washes were performed at pH7.4 or at pH5.5, as indicated. The table provides enrichment scores for each sequence, where enrichment is the log2 assay reads per million (RPM)/RPM in the virus library before screening. "-" <=0; "+" >0 to <=1; "++" >1 to <=5; "+++" >5.

[0357] Table 10. Capsids that selectively bind human TFRC-Fc fusion protein. A 7-mer or 10-mer loop IV substitution library was screened for binding to human TFRC-Fc fusion proteins. Binding was performed at pH7.4. Washes were performed at pH7.4 or at pH5.5, as

indicated. The table provides enrichment scores for each sequence, where enrichment is the log2 assay reads per million (RPM)/RPM in the virus library before screening. "-" <=0; "+" >0 to <=1; "++" >1 to <=3; "+++" >3.

[0358] Table 11. Capsids that selectively bind human TFRC-Fc fusion protein where the apical domain was replaced by the corresponding region of mouse TFRC. A 7-mer or 10-mer loop IV substitution library was screened for binding to human TFRC-Fc fusion proteins. Binding was performed at pH7.4. Washes were performed at pH7.4 or at pH5.5, as indicated. The table provides enrichment scores for each sequence, where enrichment is the log2 assay reads per million (RPM)/RPM in the virus library before screening. "-" <=0; "+" >0 to <=2; "++" >2 to <=4; "+++" >4.

[0359] Table 12. Capsids that selectively bind human TFRC-Fc fusion protein. A 7-mer 588 insertion Fit4Function library was screened for binding to human TFRC-Fc fusion protein. Binding was performed at pH7.4 or pH5.5, as indicated. The table provides enrichment scores for each sequence, where enrichment is the log2 assay reads per million (RPM)/RPM in the virus library before screening. "-" <=0; "+" >0 to <=2; "++" >2 to <=4; "+++" >4.

[0360] Table 13. The table provides sequence listing of 7-mers that impart TFRC binding when inserted with AAV9 between AA 588-589 and their cluster assignment (Figure 7). The table provides the AA SEQ ID, AA sequence, UMAP coordinates, and cluster number.

[0361] Table B. Individual capsid AA sequences TFRC.

>AAV9	MAADGYLPDWLEDNLSEGIREWWALKPGAPQPKANQQHQDN ARGLVLPGYKYLGPGNGLDKGEPVNAADAAALEHDKAYDQQ LKAGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKR LLEPLGLVEEAAKTAPGKKRPVEQSPQEPDSSAGIGKSGAQPAK KRLNFGQTGDTESVPDPQPIGEPPAAPSGVGSLTMASGGGAPV ADNNEGADGVGSSSGNWHCDSQWLGDRVITTSTRTWALPTYN NHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDFNRFHCHFSPR DWQRLINNNWGFRPKRLNFKLFNIQVKEVTDNNGVKTIANNLT STVQVFTDSDYQLPYVLGSAHEGCLPPFPADVFMIPQYGYLTLN DGSQAVGRSSFYCLEYFPSQMLRTGNNFQFSYEFENVPFHSSYA HSQSLDRLMNPLIDQYLYYLSKTINGSGQNQQTLKFSVAGPSN MAVQGRNYIPGPSYRQQRVSTTVTQNNNSEFAWPGASSWALN GRNSLMNPGPAMASHKEGEDRFFPLSGSLIFGKQGTGRDNVDA DKVMITNEEEIKTTNPVATESYGQVATNHQSAQAQAQTGWVQ NQGILPGMVWQDRDVYLQGPIWAKIPHTDGNFHPSPLMGGFG MKHPPPQILIKNTPVPADPPTAFNKDKLNSFITQYSTGQVSVEIE

	WELQKENSKRWNPEIQYTSNYYKSNNVEFAVNTEGVYSEPRPI GTRYLTRNL* (SEQ ID NO: 20506)
>AAV9 K449R	MAADGYLPDWLEDNLSEGIREWWALKPGAPQPKANQQHQDN ARGLVLPGYKYLGPGNGLDKGEPVNAADAAALEHDKAYDQQ LKAGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKR LLEPLGLVEEAAKTAPGKKRPVEQSPQEPDSSAGIGKSGAQPAK KRLNFGQTGDTESVPDPQPIGEPPAAPSGVGSLTMASGGGAPV ADNNEGADGVGSSSGNWHCDSQWLGDRVITTSTRTWALPTYN NHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDFNRFHCHFSPR DWQRLINNNWGFRPKRLNFKLFNIQVKEVTDNNGVKTIANNLT STVQVFTDSDYQLPYVLGSAHEGCLPPFPADVFMIPQYGYLTLN DGSQAVGRSSFYCLEYFPSQMLRTGNNFQFSYEFENVPFHSSYA HSQSLDRLMNPLIDQYLYYLSRTINGSGQNQQTLKFSVAGPSN MAVQGRNYIPGPSYRQQRVSTTVTQNNNSEFAWPGASSWALN GRNSLMNPGPAMASHKEGEDRFFPLSGSLIFGKQGTGRDNVDA DKVMITNEEEIKTTNPVATESYGQVATNHQSAQAQAQTGWVQ NQGILPGMVWQDRDVYLQGPIWAKIPHTDGNFHPSPLMGGFG MKHPPPQILIKNTPVPADPPTAFNKDKLNSFITQYSTGQVSVEIE WELQKENSKRWNPEIQYTSNYYKSNNVEFAVNTEGVYSEPRPI GTRYLTRNL* (SEQ ID NO: 20507)
>AAV-BI19	MAADGYLPDWLEDNLSEGIREWWALKPGAPQPKANQQHQDN ARGLVLPGYKYLGPGNGLDKGEPVNAADAAALEHDKAYDQQ LKAGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKR LLEPLGLVEEAAKTAPGKKRPVEQSPQEPDSSAGIGKSGAQPAK KRLNFGQTGDTESVPDPQPIGEPPAAPSGVGSLTMASGGGAPV ADNNEGADGVGSSSGNWHCDSQWLGDRVITTSTRTWALPTYN NHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDFNRFHCHFSPR DWQRLINNNWGFRPKRLNFKLFNIQVKEVTDNNGVKTIANNLT STVQVFTDSDYQLPYVLGSAHEGCLPPFPADVFMIPQYGYLTLN DGSQAVGRSSFYCLEYFPSQMLRTGNNFQFSYEFENVPFHSSYA HSQSLDRLMNPLIDQYLYYLSRTINGSGQNQQTLKFSVAGPSN MAVQGRNYIPGPSYRQQRVSTTVTQNNNSEFAWPGASSWALN GRNSLMNPGPAMASHKEGEDRFFPLSGSLIFGKQGTGRDNVDA DKVMITNEEEIKTTNPVATESYGQVATNHQSAQ**YSRIGPN**AQA QTGWVQNQGILPGMVWQDRDVYLQGPIWAKIPHTDGNFHPSP LMGGFGMKHPPPQILIKNTPVPADPPTAFNKDKLNSFITQYSTG QVSVEIEWELQKENSKRWNPEIQYTSNYYKSNNVEFAVNTEGV YSEPRPIGTRYLTRNL* (SEQ ID NO: 20508)
>AAV-BI98	MAADGYLPDWLEDNLSEGIREWWALKPGAPQPKANQQHQDN ARGLVLPGYKYLGPGNGLDKGEPVNAADAAALEHDKAYDQQ LKAGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKR LLEPLGLVEEAAKTAPGKKRPVEQSPQEPDSSAGIGKSGAQPAK KRLNFGQTGDTESVPDPQPIGEPPAAPSGVGSLTMASGGGAPV ADNNEGADGVGSSSGNWHCDSQWLGDRVITTSTRTWALPTYN

	NHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDFNRFHCHFSPR DWQRLINNNWGFRPKRLNFKLFNIQVKEVTDNNGVKTIANNLT STVQVFTDSDYQLPYVLGSAHEGCLPPFPADVFMIPQYGYLTLN DGSQAVGRSSFYCLEYFPSQMLRTGNNFQFSYEFENVPFHSSYA HSQSLDRLMNPLIDQYLYYLSRTINGSGQNQQTLKFSVAGPSN MAVQGRNYIPGPSYRQQRVSTTVTQNNNSEFAWPGASSWALN GRNSLMNPGPAMASHKEGEDRFFPLSGSLIFGKQGTGRDNVDA DKVMITNEEEIKTTNPVATESYGQVATNHQSAQ**YSRLNMN**AQ AQTGWVQNQGILPGMVWQDRDVYLQGPIWAKIPHTDGNFHPS PLMGGFGMKHPPPQILIKNTPVPADPPTAFNKDKLNSFITQYST GQVSVEIEWELQKENSKRWNPEIQYTSNYYKSNNVEFAVNTEG VYSEPRPIGTRYLTRNL* (SEQ ID NO: 20509)
>AAV-BI99	MAADGYLPDWLEDNLSEGIREWWALKPGAPQPKANQQHQDN ARGLVLPGYKYLGPGNGLDKGEPVNAADAAALEHDKAYDQQ LKAGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKR LLEPLGLVEEAAKTAPGKKRPVEQSPQEPDSSAGIGKSGAQPAK KRLNFGQTGDTESVPDPQPIGEPPAAPSGVGSLTMASGGGAPV ADNNEGADGVGSSSGNWHCDSQWLGDRVITTSTRTWALPTYN NHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDFNRFHCHFSPR DWQRLINNNWGFRPKRLNFKLFNIQVKEVTDNNGVKTIANNLT STVQVFTDSDYQLPYVLGSAHEGCLPPFPADVFMIPQYGYLTLN DGSQAVGRSSFYCLEYFPSQMLRTGNNFQFSYEFENVPFHSSYA HSQSLDRLMNPLIDQYLYYLSRTINGSGQNQQTLKFSVAGPSN MAVQGRNYIPGPSYRQQRVSTTVTQNNNSEFAWPGASSWALN GRNSLMNPGPAMASHKEGEDRFFPLSGSLIFGKQGTGRDNVDA DKVMITNEEEIKTTNPVATESYGQVATNHQSAQ**YSRLNKD**AQ AQTGWVQNQGILPGMVWQDRDVYLQGPIWAKIPHTDGNFHPS PLMGGFGMKHPPPQILIKNTPVPADPPTAFNKDKLNSFITQYST GQVSVEIEWELQKENSKRWNPEIQYTSNYYKSNNVEFAVNTEG VYSEPRPIGTRYLTRNL* (SEQ ID NO: 20510)
>AAV-BI100	MAADGYLPDWLEDNLSEGIREWWALKPGAPQPKANQQHQDN ARGLVLPGYKYLGPGNGLDKGEPVNAADAAALEHDKAYDQQ LKAGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKR LLEPLGLVEEAAKTAPGKKRPVEQSPQEPDSSAGIGKSGAQPAK KRLNFGQTGDTESVPDPQPIGEPPAAPSGVGSLTMASGGGAPV ADNNEGADGVGSSSGNWHCDSQWLGDRVITTSTRTWALPTYN NHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDFNRFHCHFSPR DWQRLINNNWGFRPKRLNFKLFNIQVKEVTDNNGVKTIANNLT STVQVFTDSDYQLPYVLGSAHEGCLPPFPADVFMIPQYGYLTLN DGSQAVGRSSFYCLEYFPSQMLRTGNNFQFSYEFENVPFHSSYA HSQSLDRLMNPLIDQYLYYLSRTINGSGQNQQTLKFSVAGPSN MAVQGRNYIPGPSYRQQRVSTTVTQNNNSEFAWPGASSWALN GRNSLMNPGPAMASHKEGEDRFFPLSGSLIFGKQGTGRDNVDA DKVMITNEEEIKTTNPVATESYGQVATNHQSAQ**VHRLQDK**AQ

	AQTGWVQNQGILPGMVWQDRDVYLQGPIWAKIPHTDGNFHPS PLMGGFGMKHPPPQILIKNTPVPADPPTAFNKDKLNSFITQYST GQVSVEIEWELQKENSKRWNPEIQYTSNYYKSNNVEFAVNTEG VYSEPRPIGTRYLTRNL* (SEQ ID NO: 20511)
>AAV-BI101	MAADGYLPDWLEDNLSEGIREWWALKPGAPQPKANQQHQDN ARGLVLPGYKYLGPGNGLDKGEPVNAADAAALEHDKAYDQQ LKAGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKR LLEPLGLVEEAAKTAPGKKRPVEQSPQEPDSSAGIGKSGAQPAK KRLNFGQTGDTESVPDPQPIGEPPAAPSGVGSLTMASGGGAPV ADNNEGADGVGSSSGNWHCDSQWLGDRVITTSTRTWALPTYN NHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDFNRFHCHFSPR DWQRLINNNWGFRPKRLNFKLFNIQVKEVTDNNGVKTIANNLT STVQVFTDSDYQLPYVLGSAHEGCLPPFPADVFMIPQYGYLTLN DGSQAVGRSSFYCLEYFPSQMLRTGNNFQFSYEFENVPFHSSYA HSQSLDRLMNPLIDQYLYYLSRTINGSGQNQQTLKFSVAGPSN MAVQGRNYIPGPSYRQQRVSTTVTQNNNSEFAWPGASSWALN GRNSLMNPGPAMASHKEGEDRFFPLSGSLIFGKQGTGRDNVDA DKVMITNEEEIKTTNPVATESYGQVATNHQSAQ**YHRLSNN**AQ AQTGWVQNQGILPGMVWQDRDVYLQGPIWAKIPHTDGNFHPS PLMGGFGMKHPPPQILIKNTPVPADPPTAFNKDKLNSFITQYST GQVSVEIEWELQKENSKRWNPEIQYTSNYYKSNNVEFAVNTEG VYSEPRPIGTRYLTRNL* (SEQ ID NO: 20512)
>AAV-BI102	MAADGYLPDWLEDNLSEGIREWWALKPGAPQPKANQQHQDN ARGLVLPGYKYLGPGNGLDKGEPVNAADAAALEHDKAYDQQ LKAGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKR LLEPLGLVEEAAKTAPGKKRPVEQSPQEPDSSAGIGKSGAQPAK KRLNFGQTGDTESVPDPQPIGEPPAAPSGVGSLTMASGGGAPV ADNNEGADGVGSSSGNWHCDSQWLGDRVITTSTRTWALPTYN NHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDFNRFHCHFSPR DWQRLINNNWGFRPKRLNFKLFNIQVKEVTDNNGVKTIANNLT STVQVFTDSDYQLPYVLGSAHEGCLPPFPADVFMIPQYGYLTLN DGSQAVGRSSFYCLEYFPSQMLRTGNNFQFSYEFENVPFHSSYA HSQSLDRLMNPLIDQYLYYLSRTINGSGQNQQTLKFSVAGPSN MAVQGRNYIPGPSYRQQRVSTTVTQNNNSEFAWPGASSWALN GRNSLMNPGPAMASHKEGEDRFFPLSGSLIFGKQGTGRDNVDA DKVMITNEEEIKTTNPVATESYGQVATNHQSAQ**LHALSHN**AQ AQTGWVQNQGILPGMVWQDRDVYLQGPIWAKIPHTDGNFHPS PLMGGFGMKHPPPQILIKNTPVPADPPTAFNKDKLNSFITQYST GQVSVEIEWELQKENSKRWNPEIQYTSNYYKSNNVEFAVNTEG VYSEPRPIGTRYLTRNL* (SEQ ID NO: 20513)

Methods for Examples 1 - 4

Plasmids

[0362] The AAV9, AAV-BI18, BI19, BI98-BI102 and AAV-BI159-165 Rep-Cap plasmids were generated by gene synthesis (GenScript). The CAG-WPRE-hGH pA backbone was obtained from Viviana Gradinaru through Addgene (#99122). GFP, GFP-2A-luciferase, and mScarlet cDNAs were synthesized as gBlocks (IDT) or synthesized and cloned (GenScript).

[0363] Full length TFRC cDNA expression and lentiviral plasmids were cloned by inserting the open reading frames of TFRC (human: NM_003234.4; mouse TFRC: NM_011638.4; marmoset TFRC: NM_001301847.1) into the lentiviral backbone pLenti-EF-FH-TAZ-ires-blast (Addgene #52083) with EcoRI/SalI sites.

[0364] For Fc fusion proteins, the coding sequence of the extracellular regions of TFRC (human: 89-760aa; mouse: 89-763aa; marmoset: 89-760aa) were amplified by PCR and inserted into pCMV6-XL4 FLAG-NGRN-Fc (Addgene #115773) with EcoRV and XbaI sites. Signal peptide H7 (ATGGAGTTTGGGCTGAGCTGGGTTTTCCTCGTTGCTCTTTTTAGAGGTGTCCAGTGT (SEQ ID NO: 20493)) was introduced to N terminal of TFRC sequences to direct protein secretion. hTFRC-mApical construct was made by replacing the human TFRC apical domain (AA188-384) by mouse TFRC apical domain (AA 190-386).

Cell lines and primary cultures

[0365] HEK293T/17 (CRL-11268), Pro5 (CRL-1781) and CHO-K1 (CCL-61) were obtained from ATCC. mBMVEC cells (C57-6023) and hBMVECs cells (H-6023) were obtained from Cell Biologics and cultured as directed by the manufacturer. hCMEC/D3 cells were from Millipore-Sigma (SCC066).

Expression and purification of Fc-tagged protein in HEK293-FT cells

[0366] 26 million HEK293-FT cells were seated per 150mm plate the day before transfection. The next day, complete media was changed to Pro293TMa-CDMTM media with two brief rinses with Pro293TMa-CDMTM media to remove serum. Cells were transduced with PEI and 40ug DNA per plate a few hours after media change. The media was replaced 18 hours after transfection. At the second day post-transfection, cell supernatants containing secreted recombinant protein were passed through a 0.45-mm pore size filter and purified on Protein A-Sepharose. 200ul Protein

A-Sepharose were incubated with 100 ml cell culture supernatant overnight at 4C with shaking. The next day, the beads were collected and washed 3 times with 10 ml of PBS, and the proteins were eluted in 200 ul of 100 mM glycine (pH2.7). Then 1/10 volume of 1M Tris (pH8.8) was added to the eluted protein fractions to neutralize the pH.

Lentivirus production

[0367] Lentivirus was produced with a third-generation lentivirus system by cotransfection of three packaging plasmids (pMDLg-RRE, pRSV-Rev and pVSV-G) and vector plasmid encoding hTFRC at a ratio of 4:1:1:6 in HEK cells. Lentivirus was harvested 3 days after transfection, filtered with 0.45um PES to remove the cell debris.

HEK293 and CHO stable cell line generation

[0368] CHO cells were seeded 150,000/well in 12 well plates and transduced with lentivirus containing media for 48 hrs, then transferred to 10 cm dishes for selection with 10 ug/mL blasticidin for about a week. Once all cells had died in the control plate, the selected CHO cells were maintained in media with 1 ug/mL blasticidin. The expression of hTFRC was validated with immunostaining with OKT9 antibody from ThermoFisher (Catalog # 14-0719-82).

Library cloning

[0369] The oligo pool or NNK PCR products were assembled into the RNA expression plasmid with previously described methods in Deverman et al. Nature Biotechnology 2016. For generating the 7-mer 588 site insertion capsid libraries, the hand-mixed (IDT) primer 5′-GTATTCCTTGGTTTTGAACCCAACCGGTCTGCGCCTGTGCMNNMNNMNNMNNMNNMNNMNNTTGGGCACTCTGGTGGTTTGTG-3′ (SEQ ID NO: 20494) primer was used with forward primer 5'-CACTCATCGACCAATACTTGTACTATCTCT (SEQ ID NO: 20495) to PCR amplify a modified AAV9 template (K449R) 10ng pUC57-wtAAV9-X/A plasmid (as in Deverman et al Nature Biotechnology 2016) using Q5 Hot Start High-Fidelity 2× Master Mix (NEB, M0494S) following the manufacturer's protocol.

[0370] To generate the loop IV libraries the forward primers (10merNNK) 5'-ATCGACCAATACTTGTACTATCTCTCTAGAACTNNKNNKNNKNNKNNKNNKNNKNNKNNKCTAAAATTCAGTGTGGCCGGACC (SEQ ID NO: 20496) or (7merNNK) 5'-ATCGACCAATACTTGTACTATCTCTCTAGAACTNNKNNKNNKNNKNNKNNKNNKCTAAAATTCAGTGTGGCCGGACC (SEQ ID NO: 20497) were used with the reverse primer 5-

TTGTCCTTGTTGAAGGCCGTTGGAG (SEQ ID NO: 20498) to amplify the same modified AAV9 template (K449) as described above.

[0371] To assemble an oligonucleotide Library Synthesis (OLS) Pool (Agilent) into an AAV genome, 5 pM of the OLS pool was used as an initial reverse primer along with 0.5 µM of the forward primer to amplified and extended 10 ng of DNA plasmid containing a fragment of AAV9 (pUC57-wtAAV9-X/A) for 5 cycles using Q5® High-Fidelity 2X Master Mix (NEB #M0492S) following the manufacturer's protocol. After the 5-cycle amplification and extension of the oligo pool, the reactions were spiked with 0.5 µM of primer 5'-GTATTCCTTGGTTTTGAACCCAACCG (SEQ ID NO: 20499) (588 site insertion libraries) or 5'-CACTCATCGACCAATACTTGTACTATCTCT (SEQ ID NO: 20495) (loop IV libraries) and amplified for an additional 25 cycles. The PCR product was then purified using Agencourt AMPure XP SPRI paramagnetic beads (Beckman Coulter #A63880) or column purified using a Zymo Research DNA Clean & Concentrator-5 kit (Zymo Research #D4013) following the manufacturer's protocol.

[0372] All library PCR products were cleaned up using AMPure XP beads (Beckman, A63881) following the manufacturer's protocol. The NNK PCR insert was assembled into a linearized mRNA selection vector (AAV9-CMV-Express, described below) with NEBuilder HiFi DNA Assembly Master Mix (NEB, E2621L). Afterwards, Quick CIP (NEB, M0508S) was spiked into the reaction and incubated at 37 °C for 30 min to dephosphorylate unincorporated dNTPs. Finally, T5 Exonuclease (NEB M0663S) was added to the reaction mixture and incubated at 37 °C for 30 min to remove unassembled products. The final assembled product was cleaned up using AMPure XP beads (Beckman, A63881) following the manufacturer's protocol quantified using the Qubit dsDNA HS Assay Kit (Thermo Fisher Scientific, Q32851).

Synthetic round 2 library design

[0373] The library oligo pool consisted of 7-mer insertion sequences recovered from the Round 1 binding assays. In addition, the Experiment 1, round 2 library contained all possible sequences conforming to the following 7-mer motifs [FLY][AS][KR]X[GN]XN (SEQ ID NO: 20500) and XXS[ST]NG[VIR] (SEQ ID NO: 20505), where X is any residue. In experiment 2, the round 2 library comprised only those sequences recovered through binding to Fc-target proteins including TFRC, control sequences including those containing stop codons (to aid in the

assessment of cross packaging), and WT and other reference sequences. All sequences were encoded by two distinct nucleotide sequences designed to serve as biological replicates. In Experiment 4, the F4F "Hammerhead" library was generated as described in Published Patent Application US 20210403946 A1.

RNA selection plasmids

[0374] The mRNA selection vector (AAV9-CMV-Express) was designed to enrich for functional AAV capsid sequences by recovering capsid mRNA from transduced cells. AAV9-CMV-Express uses a ubiquitous CMV enhancer and AAV5 p41 gene regulatory elements to drive AAV9 Cap expression. The AAV9-CMV-Express plasmid was constructed by cloning the following elements into an AAV genome plasmid in the listed order: a cytomegalovirus (CMV) enhancer-promoter, a synthetic intron and the AAV5 P41 promoter along with the 3′ end of the AAV2 Rep gene, which includes the splice donor sequences for the capsid RNA. The capsid gene splice donor sequence in AAV2 Rep was modified from CAGGTACCA to a consensus donor sequence CAGGTAAGT. The AAV9 capsid gene sequence was synthesized with nucleotide changes at 1,344, 1,346 and 1,347 (which introduces a K449R mutation) and at 1,782 (which is a silent mutation) to introduce restriction enzyme recognition sites for NNK library PCR insert fragment cloning. The AAV2 polyadenylation sequence was replaced with a simian virus 40 (SV40) late polyadenylation signal. A previously described cap-deficient Rep-AAP AAV helper plasmid1 was supplied in trans to generate virus with the AAV9-CMV-Express vector.

Virus production and purification

[0375] Recombinant AAVs were generated following a previously published protocol (Challis et al 2019) with minor modifications as described below. HEK293T/17 cells (ATCC, CRL-11268) were seeded at 22 million cells per 15-cm plate the day before transfection and grown in DMEM with GlutaMAX (Gibco, 10569010) supplemented with 5% FBS and 1× non-essential amino acid solution (NEAA) (Gibco, 11140050). The next day, the cells were triple transfected with 39.93 μg of total plasmid DNA encoding rep-cap, pHelper and an ITR-flanked transgene at a plasmid ratio of 4:2:1, respectively, using polyethylenimine (PEI) MAX (Polyscience, 24765-1) at a DNA:PEI ratio of 1:3.5. Twenty hours after transfection, the medium was changed to fresh DMEM with GlutaMAX supplemented with 5% FBS and 1× NEAA. Seventy-two hours after transfection, cells were scraped and pelleted at 2,000 RCF for 10 min. The pellets were resuspended in 7 ml of Salt

Active Nuclease (SAN) digestion buffer (500 mM NaCl, 40 mM Tris-base, 10 mM MgCl2, SAN enzyme (ArcticZymes, 70920-202) at 100 U/ml) for every ten plates and incubated at 37 °C for 1.5 h. Afterwards, the lysate was clarified at 2,000 RCF for 10 min and loaded onto a density step gradient containing OptiPrep (Cosmo Bio, AXS-1114542) at 60%, 40%, 25% and 15% at a volume of 5, 5, 6, and 6 ml, respectively in OptiSeal tubes (Beckman, 361625). The step gradients were spun in a Beckman Type 70ti rotor (Beckman, 337922) in a Sorvall WX+ ultracentrifuge (Thermo Fisher Scientific, 75000090) at 69,000 r.p.m. for 1 h at 18 °C. Afterwards, 4–4.5 ml of the 40–60% interface was extracted using a 16-gauge needle, filtered through a 0.22-μm PES filter and then buffer exchanged with 100 K MWCO protein concentrators (Thermo Fisher Scientific, 88532) into PBS containing 0.001% Pluronic F-68 and concentrated down to a volume of 500 μl. The concentrated virus was then filtered through a 0.22-μm PES filter and stored at 4°C or −80°C.

[0376] The AAV capsid library was produced similarly as above with following exceptions: each plate was triple transfected with 39.93 μg of total plasmid DNA encoding pHelper, RepStop encoding the AAV2 Rep genes, pUC19 at a ratio of 2:1:1, respectively, and with 10 ng of assembled library DNA; the media and cell lysates were harvested 60 hours post transfection and purified following the published protocol (Deverman *et al. Nature Biotechnology* 2016).

ddPCR titering

[0377] Vector aliquots were treated with Turbonuclease (Cat #) at 37C for 1 hour and then deactivated by adding 5 uL EDTA and heated at 70C for 10 minutes. Afterwards, the samples were treated with proteinase K for 2 hours and heated inactivated diluted to within the dynamic range of the ddPCR assay (1 to 10^4 vector genomes) per reaction.

SDS page

[0378] Briefly, proteins in HEK293 cell media pre- or post-pull down with ProA magnetic beads were separated on Bolt 4-12% Bis-Tris Plus gels and stained with SYPRO Ruby (Thermofisher).

Animals

[0379] All procedures were performed as approved by the Broad Institute IACUC. BALB/cJ (000651), C57Bl/6J (000664), and NSG (00557) were obtained from The Jackson Laboratory (JAX). Recombinant AAV vectors were administered intravenously via the retro-orbital sinus in

young adult male or female mice. Mice were randomly assigned to groups based on predetermined sample sizes.

Tissue processing, immunohistochemistry and imaging

[0380] Mice were anesthetized with Euthasol and transcardially perfused with phosphate buffered saline (PBS) at room temperature followed by 4% paraformaldehyde (PFA) in ice cold PBS. Tissues were post-fixed overnight in 4% PFA in PBS and sectioned by vibratome. IHC was performed on floating sections with antibodies diluted in PBS containing 10% donkey serum, 0.1% Triton X-100, and 0.05% sodium azide. Primary antibodies were incubated at room temperature overnight. The sections were then washed and stained with secondary (Alexa-conjugated antibodies, 1:1000) for 4 hours or overnight.

In vivo vector and capsid biodistribution

[0381] 5- to 6-week-old C57Bl/6J mice or BALB/cJ mice were injected intravenously with 10e11 vg of AAV vector packaged into the indicated capsid. One or two hours after injection, the mice were perfused with PBS and tissues were collected and frozen at -80°C. Samples were processed for AAV genome biodistribution analysis and normalized to the number of copies of mouse genomes using qPCR for the GFP element and mouse glucagon by qPCR as previously described (2). NSG mice were used for experiments involving sequential injection of AAV-BI30 carrying human *TFRC* or *Ly6a* (1e11 vg/mouse) followed by AAV-BI19:CAG-mScarlet or AAV-PHP.eB:CAG-mScarlet (3e11 vg/mouse) 1 week after the initial injection.

Luciferase transduction assay

[0382] Human, mouse, or marmoset TFRC (0.1 µg/well) was transfected into the indicated cells (HEK293/17: 4x105/well; CHO: 2.5x104/well, BMVECs: 5x103/well) in 96-well plates (PerkinElmer, 6005680) in triplicate. 48 hours later, cells were transduced with AAV-CAG-GFP-2A-Luciferase-WPRE packaged into AAV9 or the indicated AAV-BI# capsid. Luciferase assays were performed with Britelite plus Reporter Gene Assay System (PerkinElmer, 6066766). Luciferase activity was reported as relative light units (RLU) as raw data or normalized to non-transfected control wells transduced with AAV9.

Cell binding assays

[0383] TFRC family members or GFP control (0.5 µg/well) were transfected into HEK293T cells (3e5/well) using PEI or into CHO cells (1.5e5/well) with lipofectamine 3000 reagent

(ThermoFisher, L3000001) in 24-well plates. 48 hours later, the cells were chilled to 4°C and the media was exchanged with fresh cold media containing the indicated recombinant AAV (1e5 copies per cell). One hour later, cells were washed with cold PBS for 3 times, then fixed with 4%PFA for IHC or lysed for genomic DNA extraction and qPCR analyses or NGS sequencing. For mouse and human BMVECs, 2e4 cells/well were seeded in 12 well plates the day before exposure to the AAVs. The assay was performed as above except AAV vectors were added at 106 copies/cell. HEK293T/17 cells were seeded at 2E7 per T75 flask 12-24 hours prior to being transfected with 20 µg of cDNA encoding eGFP, human TFRC, mouse TFRC or marmoset TFRC. At 24-48 hours post transfection, the cells were incubated with an AAV9 K449R library (7-mer insertion between amino acids 588 and 589) at 1e11 vg/T75 at 4°C for 2 hours. Afterwards, the media was exchanged with PBS for 3 times in order to wash away unbound viruses. The AAVs that remained bound to the cells were extracted with TRIzol (Invitrogen) or with whole genomic DNA isolation reagents (DNeasy, Qiagen) to isolate their viral genomes. The viral genomes were then prepared for NGS to quantify the enrichment of peptides that conferred increased capsid ability to bind cells expressing the target protein.

Transduction screening in vitro

[0384] For *in vitro* screening on cells in 2D culture, 1e11 vg of the AAV capsid library was added to HEK293, CHO, or confluent BMVECs or hCMEC/D3 cells and cellular mRNA was collected 60 hours after administration. BBB spheroids were obtained by co-culture of hCMEC/D3, primary human astrocytes and human pericytes as described (Bergmann *et al. Nature Protocols* 2018). For *in vitro* screening on spheroids, 1e4 vg/cell was used for binding and 2e5 vg/cell was used for transduction in human serum free media.

[0385] mRNA from in vitro assays were recovered using TRIzol (Invitrogen, 15596026) followed by RNA cleanup with RNeasy Mini kit (QIAGEN, 74104). The recovered mRNA was next converted to complementary DNA using an oligonucleotide dT primer using Maxima H Minus Reverse Transcriptase (Thermo Fisher, EP0751).

Fc-protein fusion cloning and protein purification

[0386] The extracellular portion together with signal peptide of protein targets are cloned into Fc-tag backbone (Addgene plasmid # 115773) using XbaI/EcoRV. To generate Fc-fusion proteins the N terminal cytoplasmic and transmembrane domains were replaced with an H7 signal peptide

(Haryadi et al 2015, PLoS One. 2015; 10(2): e0116878; MEFGLSWVFLVALFRGVQC). The C terminal stop codon was replaced with the Fc tag coding sequence containing intron sequences. Also, there is a HRV 3C site and a linker sequence between TFRC and Fc. The Fc-receptor plasmid was transfected into HEK293 cells (40ug per 150mm dish with PEI) in complete DMEM media with 5% FBS. 12-16 hours after transfection, the transfected plate was rinsed with PBS, and 15ml of serum free media (Lonza, BEBP12-764Q) was added. Media containing the secreted Fc-fusion proteins was collected at 48 and 96 hours, filtered (Millipore SE1M003M00) and stored at 4C until use. 35 ul protein A beads (ThermoFisher, 10001D) and Tween 20 (0.05% final concentration) were added to 30 ml of media and incubated at 4C with end to end rotation. The next day, the beads were washed 3 times with cold PBS containing 0.05% Tween-20. Expression was assessed by running a 5 ul aliquot of protein bound beads on a 4-12% protein gel; the remaining fraction was used for pulldown assay.

[0387] Protein A-conjugated beads were used to pull down the LY6A-Fc, LY6C1-Fc, or Fc-only control, which were then washed and incubated with an AAV capsid library.

Fc-fusion pulldown assay

[0388] 10 ul Fc-fusion protein bound protein A beads were mixed with 1e10 vg AAV capsid library in PBS with 0.05% Tween-20 and 1% BSA and incubated overnight at 4C. The next day, beads were washed 3 times with PBS with 0.05% Tween-20 at the indicated pH and then treated with proteinase K to extract the viral genome for NGS preparation after purification with AMPure XP beads following the manufacturer's protocol.

PCR recovery of library sequences

[0389] The AAV genome samples (binding assays) or cDNA (transduction assays) were prepared for next-generation sequencing (NGS) with two rounds of polymerase chain reaction (PCR). In the first round of PCR (PCR1), a set of forward primers and reverse primers containing gene specific priming regions and an overhang sequence containing a portion of the Illumina Read 1 sequence (forward primers) or Illumina Read 2 sequence (reverse primers) were used to selectively amplify AAV genomes from the cDNA with Q5® High-Fidelity 2X Master Mix (NEB #M0492S), with 0.5 μM of each primer.

[0390] The forward and reverse primers contain zero or up to eight N nucleotides inserted in between the gene specific priming region and the partial Illumina Read 1 (forward primers) or

Read 2 (reverse primers) overhang sequence. The forward and reverse primers were paired to produce amplicons of the same size.

[0391] The number of cycles performed in PCR1 using 1uL of cDNA input was chosen to stop before the exponential amplification phase and was determined with qPCR using FastStart Universal SYBR Green Master (Millipore Sigma #4913850001) or Q5® High-Fidelity 2X Master Mix (NEB #M0492S) with SYBR® Green I nucleic acid stain (VWR #12001-798) diluted from 10,000X to 8X per reaction.

[0392] Following PCR1, the amplified DNA was cleaned up using Agencourt AMPure XP SPRI paramagnetic beads (Beckman Coulter #A63880) or column purified using a Zymo Research DNA Clean & Concentrator-5 kit (Zymo Research #D4013) following the manufacturer's protocol. PCR1 samples were then barcoded for Illumina NGS with NEBNext Multiplex Oligos for Illumina Dual Index Primers Set 1 and 2 (NEB #E7600S and #E7780S) with 2 µL PCR1 input and amplified for 5 cycles to generate PCR2 products. The PCR2 products were again purified using Agencourt AMPure XP SPRI paramagnetic beads or column purified using a Zymo Research DNA Clean & Concentrator-5 kit (Zymo Research #D4013) following the manufacturer's protocol.

Preparation of amplified sequences for NGS

[0393] The concentrations of purified PCR2 samples were determined using a Qubit™ dsDNA HS Assay Kit (Invitrogen™ #Q32854) then diluted and pooled according to the Illumina Nextseq System Denature and Dilute Libraries Guide or MiSeq System Denature and Dilute Libraries Guide along with 10-15% PhiX Control v3 (Illumina #FC-110-3001) spiked in. The pooled samples were quantified and checked for correct sizes using an Agilent High Sensitivity DNA Kit (Agilent #5067-4626) on an Agilent 2100 Electrophoresis Bioanalyzer.

[0394] Then samples were either sequenced on an Illumina NextSeq or Miseq machine using a NextSeq 500/550 High Output Kit v2.5 (150 Cycles) (Illumina #20024907), NextSeq 500/550 Mid Output Kit v2.5 (150 Cycles) (Illumina #20024904) or MiSeq Reagent Kit v3 (150-cycle) (Illumina #MS-102-3001) with the indexes read from both ends after 150 read cycles.

NGS analysis

[0395] Following NGS, sequences were aligned to an AAV9 template with 21 N nucleotides insertion between amino acid 588 and 589 to represent the 7-mer insertion using Bowtie 2. Further post processing was performed using SAMtools, Python 3, NumPy and Pandas. Briefly, the

flanking regions up to the 7mer (prefix) and after the 7mer (suffix) region were clipped. The resulting sequence was checked to be 21bp in length. The nucleotide sequences were converted to amino acid sequences and exported using Pandas. Read counts associated with each nucleotide sequence were converted to normalized read counts (reads per million) to adjust for sequencing depth differences between samples. Enrichment scores for each sequence are calculated by log2(normalized read count post screening/normalized read count in the initial virus library).

Clustering analysis

[0396] Capsid sequences were one-hot encoded into vectors of length 20 x 7 = 140, and projected with UMAP with the following parameters: n_neighbors = 8, min_dist = 0.01, metric = Euclidean. Capsid sequences were then clustered using their UMAP projection values (Xx1, Xx2) with the GaussianMixture model from scikit-learn with parameters n_components=30, random_state=1, n_init=10, max_iter=1000.

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Example 5 – Additional Examples

[0429] AAV capsids engineered to bind human TFRC transduce human brain endothelial cells more efficiently than AAV9, an effect that is further enhanced by increasing the surface expression of TFRC. Applicants also showed that transduction of human brain endothelial cells by one of the TFRC binding AAVs, BI-19, is blocked in a dose-dependent manner by an antibody against TFRC. Furthermore, in mice made to express human TFRC on the brain vasculature, Applicants observed increased targeting of BI-19 to the brain, indicating that BI-19 can target human TFRC *in vivo* and suggesting that the engagement of TFRC can increase both endothelial transduction and crossing of the BBB. Together, the data support further exploration of TFRC targeted AAVs as delivery vehicles for CNS gene therapy.

[0430] TFRC binding capsids and sequence space exploration by mutagenesis identifies capsids for individual evaluation.

Capsid ID	Nucleic Acid Sequence	Amino Acid Sequence

BI-19	TACTCACGCATCGGCCCCAAC (SEQ ID NO: 3681)	YSRIGPN (SEQ ID NO: 14632)

[0431] Individually validated human TFRC binding AAV 588 7-mer sequences identified through binding a Fc-TFRC fusion protein.

Capsid ID	Nucleic Acid Sequence	Amino Acid Sequence
BI-98	TATTCTCGCTTAAACATG AAT (SEQ ID NO: 5678)	YSRLNMN (SEQ ID NO: 14301)
BI-99	TACTCACGCCTTAATAA GGAT (SEQ ID NO: 6495)	YSRLNKD (SEQ ID NO: 16577)
BI-100	GTACATCGCCTGCAAGA TAAG (SEQ ID NO: 6626)	VHRLQDK (SEQ ID NO: 16602)
BI-101	TACCATCGTTTGTCCAAT AAC (SEQ ID NO: 5787)	YHRLSNN (SEQ ID NO: 16636)
BI-102	TTACACGCTTTGTCACAC AAT (SEQ ID NO: 6528)	LHALSHN (SEQ ID NO: 16608)

Example 6 – Conclusions

[0432] Antibody blocking experiments (FIG. 10) indicate that the enhanced transduction activity of BI-19 requires TFRC binding. BI-19 appears to bind TFRC through the apical domain, see FIG. 10. TFRC binding contributes minimally to BI-19 hCMEC binding. BI-19 can mediate increased transduction of brain cells following expression of human TFRC on brain vasculature, see FIG. 11.

Example 7

[0433] Here Applicants present new evidence that AAV-BI19 can efficiently cross a human brain vascular barrier model and the mouse blood brain barrier (BBB) and transduce cells throughout the mouse CNS when the mice are made to express human TFRC. In the first experiment, Applicants evaluated the ability of BI19 to cross a brain endothelial barrier made from a human brain endothelial cell line (hCMEC-D3) grown on a transwell insert. After establishing a monolayer of hCMEC-D3 cells, which express TFRC, AAV-BI19 was added to the upper well of the chamber (which models the luminal/blood side), and the fraction of virus that crossed the endothelial barrier and entered the lower chamber (brain side) was assessed. The assay was performed at 37°C or at 4°C, which serves as a control to distinguish passive crossing (occurs at 37°C and 4°C) from active transport (occurs only at 37°C). AAV-BI19 showed temperature- and

time-dependent entry into the lower chamber (FIG. 13A). In contrast, other AAV capsids including AAV9, AAV8, and AAV-BI30 were detected at similar levels in the lower chamber at 37°C and 4°C suggesting that the crossing detected with these AAVs occurred primarily from passive leakage through the endothelial cell barrier. Taking the ratio of the fraction detected in the lower chamber at 37°C vs 4°C demonstrated that the crossing of AAV-BI19 through the endothelial barrier is more temperature-dependent than the other viruses (FIG. 13B).

[0434] Next Applicants sought to assess whether AAV-BI19 could cross the BBB *in vivo*. Because AAV-BI19 binds to human TFR1 but not the TFRC from mouse, marmosets, or macaques, on target *in vivo* validation necessitates expression of human TFRC on mouse brain vasculature. Applicants therefore performed a "two-step BBB crossing experiment" where Applicants used the brain endothelial targeted capsid AAV-BI30 (Krolack et al. Nature Cardiovascular Research 2022) to express the target receptor (human *TFRC* or mouse *Ly6a*) in mice prior to delivery of the capsid to be tested (AAV-BI19 or positive control AAV-PHP.eB) (FIG. 13A). Applicants performed the experiment in adult immunocompromised NGS mice to prevent an acquired immune response from blocking transduction by the second AAV. NSG mice were injected with 1e11 vg/mouse of AAV-BI30 expressing human *TFRC*, or mouse *Ly6a* cDNA as a control. Four weeks later the mice were injected with AAV-BI19 or AAV-PHP.eB carrying an mScarlet reporter driven by the strong, ubiquitous CAG promoter. mScarlet expression was observed throughout the CNS 3 weeks after IV administration of the second AAV (FIG. 13B). Applicants found that AAV-BI19 efficiently crosses the BBB and transduces cells in the mouse brain of animals that were previously injected with AAV-BI30 carrying human *TFRC* but not in animals that were previously injected with AAV-BI30 carrying *Ly6a*. In contrast, AAV-PHP.eB efficiently transduced the brains of mice that expressed AAV-BI30 carrying mouse *Ly6a*. Importantly, AAV-BI19 crossed the BBB and transduced neurons (FIG. 13C). These results demonstrate that AAV-BI19 is capable of crossing the hu*TFRC* expressing BBB in vivo.

[0435] One possible caveat to the experiment above is that transduction by AAV-BI30 may cause huTFRC to be expressed at levels that exceed the normal expression of the protein and expression by AAV-BI30 may cause ectopic huTFRC expression in other cell types where TFRC is normally low. Therefore, Applicants next evaluated AAV-BI19 transduction in mice that have had the exons encoding the extracellular domain of mouse TFRC replaced with the corresponding

exons encoding the ECD of human TFRC (referred to as huTFRC KI mice). In huTFRC KI mice, TFRC is expressed under control of the mouse TFRC gene regulatory elements at levels comparable with endogenous mouse Tfrc (BioCytogen). Confirming the results with the 2-step assay, Applicants find that AAV-BI19, but not AAV9, efficiently transduces the brain of huTFRC KI mice (FIG. 14), providing strong evidence in support of the use of AAV-BI19 for gene delivery across the human BBB. As Applicants observed in the two-step assay, AAV-BI19 efficiently transduced neurons throughout the CNS (FIG. 14C). Finally, Applicants also demonstrate that AAV-BI19 is capable of enhanced transduction of hCMEC cells as compared to AAV9 even in the presence of human Transferrin (FIG. 15), although the extent of transduction relative to AAV9 is slightly reduced. These data suggest that AAV-BI19 has the potential to transduce human brain endothelial cells by engaging human TFR1 or TFR1-Transferrin complexes.

Example 8 - AAV capsids reprogrammed to bind human transferrin receptor mediate brain-wide gene delivery

Abstract

[0436] Developing the means to efficiently deliver genes throughout the human central nervous system (CNS) could provide opportunities to treat a wide range of genetic diseases. Here, Applicants reprogrammed a suite of peptide-modified AAV9 capsids to bind to the human Transferrin Receptor (TfR1) protein, which is highly expressed on the brain endothelium, and demonstrated that this approach could drive blood-brain barrier (BBB)-crossing ability *in vitro* and *in vivo*. The strategy circumvented a key limitation of traditional *in vivo* screens that select for enhanced CNS-wide transduction without specifying a known mechanism of action and therefore identify capsids with unpredictable species specificity and translational potential. The huTfR1-binding capsids transduced human brain endothelial cells through interactions with TfR1. Applicants chose one capsid, AAV-BI19 for further characterization in mice that express a chimeric *TFRC* gene with a humanized extracellular domain. Relative to AAV9, AAV-BI19 efficiently transduced neurons and astrocytes across the brain and spinal cord after intravenous delivery and mediated a 50-fold increase in reporter gene expression in the brain; this enhanced tropism of AAV-BI19 was not observed in other organs evaluated. These results support the further assessment of AAVs programmed to target TfR1 to cross the BBB for human CNS gene therapy.

Introduction

[0437] The field of gene therapy has benefitted from a range of AAV serotypes identified from nature. Most notably, the discovery of AAV9, which can transduce motor neurons as well as neurons and glia within the neonatal CNS, led to the development of an FDA-approved gene therapy for spinal muscular atrophy type 1 (SMA1) (Foust, K. D.; *et al.* Intravascular AAV9 Preferentially Targets Neonatal Neurons and Adult Astrocytes. Nature Biotechnology, 2008, 27, 59–65, Waldrop, M. A.; *et al.* Gene Therapy for Spinal Muscular Atrophy: Safety and Early Outcomes. Pediatrics, 2020, 146.). However, numerous neurodevelopmental, neurodegenerative, and metabolic monogenic CNS diseases still have no available treatments. There is an urgent need for AAV capsids that are engineered to cross the blood-brain barrier (BBB), particularly in adult patients, and more effectively deliver genes to disease-relevant cells at a lower dose. Developing capsids that can effectively deliver gene therapies across the adult BBB will significantly broaden the scope of treatable indications.

[0438] Applicants recently demonstrated that AAV capsids can be reprogrammed to deliver genes across the mouse BBB through a mechanism-focused approach that selects for interactions between capsids and receptor proteins expressed on host cells (Huang, Q.; *et al.* Targeting AAV Vectors to the CNS viade NovoEngineered Capsid-Receptor Interactions, 2022). This receptor-targeting approach solves a key challenge faced in conventional AAV capsid screens, which can identify rare functional capsids without an understanding of their mechanism that determines their tropism and translatability across species. In this work, Applicants extended the receptor-targeting approach to a human target protein and directly engineered a suite of capsids that cross the blood-brain barrier (BBB) by leveraging the human Transferrin Receptor (huTfR1). TfR1 was chosen as a target because of its high expression on the human BBB; its ability to mediate constitutive, ligand-independent endocytosis and transcytosis across the CNS vasculature (Ajioka, R. S.; Kaplan, J. Intracellular Pools of Transferrin Receptors Result from Constitutive Internalization of Unoccupied Receptors. Proceedings of the National Academy of Sciences, 1986, 83, 6445–6449, Maxfield, F. R.; McGraw, T. E. Endocytic Recycling. Nature Reviews Molecular Cell Biology, 2004, 5, 121–132, Moos, T.; Morgan, E. H. Cellular and Molecular Neurobiology, 2000, 20, 77–95, Pardridge, W. M.; *et al.* Human Blood-Brain Barrier Transferrin Receptor. Metabolism, 1987, 36, 892–895, Jefferies, W. A.; *et al.* Transferrin Receptor on Endothelium of Brain Capillaries.

Nature, 1984, 312, 162–163); its history as a receptor for viruses including arenaviruses and canine and feline parvoviruses (Goodman, L. B.; *et al.* Binding Site on the Transferrin Receptor for the Parvovirus Capsid and Effects of Altered Affinity on Cell Uptake and Infection. Journal of Virology, 2010, 84, 4969–4978, Flanagan, M. L.; *et al.* New World Clade B Arenaviruses Can Use Transferrin Receptor 1 (TfR1)-Dependent and -Independent Entry Pathways, and Glycoproteins from Human Pathogenic Strains Are Associated with the Use of TfR1. Journal of Virology, 2008, 82, 938–948.); and its track record as a target to increase the delivery of biologics into the CNS of mice, nonhuman primates (NHPs) (Kariolis, M. S.; *et al.* Brain Delivery of Therapeutic Proteins Using an Fc Fragment Blood-Brain Barrier Transport Vehicle in Mice and Monkeys. Science Translational Medicine, 2020, 12.), and humans as an approved antibody-based therapeutic for Mucopolysaccharidosis type II (MPS II) (Okuyama, T.; *et al.* A Phase 2/3 Trial of Pabinafusp Alfa, IDS Fused with Anti-Human Transferrin Receptor Antibody, Targeting Neurodegeneration in MPS-II. Molecular Therapy, 2021, 29, 671–679).

[0439] Applicants first screened peptide-modified AAV9 capsid libraries for their ability to bind to huTfR1 *in vitro*. The top-performing capsid, AAV-BI19, was then validated and found to exhibit enhanced gene delivery to human brain endothelial cells and to the majority of neurons and glia in human *TFRC* knock-in mice. From *in vivo* biodistribution and mRNA reporter transduction data, the enhanced tropism of AAV-BI19 was found to be specific to the CNS in the huTfR1 knock-in mice. This finding is consistent with the high level of expression of *TFRC* on CNS vasculature relative to the vasculature in other organs (Jefferies, W. A.; *et al.* Transferrin Receptor on Endothelium of Brain Capillaries. Nature, 1984, 312, 162–163). These huTfR1-binding capsids represent promising vectors for CNS gene therapy applications.

Results

[0440] Applicants screened AAV9-based 7-mer NNK capsid libraries (random 7-mer insertion between residues 588–589 in VP1) for selective binding to huTfR1 as an Fc fusion protein and for selective binding to HEK293 and CHO cells overexpressing human *TFRC* as previously described (Huang, Q.; *et al.* Targeting AAV Vectors to the CNS viade NovoEngineered Capsid-Receptor Interactions, 2022) (FIG. 16A). Based on the screen results, Applicants focused on a set of four capsids, AAV-BI19, BI98, BI99, and BI101 that share a common sequence motif (FIG. 16B). These capsids, alongside AAV9, were individually tested for their ability to bind to TfR1 from

human, rhesus macaque, marmoset, or mouse when stably expressed on CHO cells (FIG. 16C,D and FIG. 17). Each capsid packaged a genome that expresses nuclear localized mScarlet and Luciferase under the control of the ubiquitous CAG promoter (AAV-CAG-NLS-mScarlet-P2A-Luciferase-SV40-WPRE). The four capsids exhibited selectively elevated binding to CHO cells expressing human *TFRC* but not the control cells or those expressing mouse or NHP *Tfrc* (FIG. 16C,D).

[0441] The four huTfR1-binding capsids exhibited enhanced binding and transduction of human brain endothelial cells (FIG. 18A,B). The best-performing capsid, AAV-BI19 was chosen for more in-depth analysis. It exhibited comparable post-purification production yields to AAV9. Its enhanced transduction of hCMEC/D3 cells was found to be inhibited by the OKT9 antibody that binds the apical domain of TfR1 but not a polyclonal antibody AF2474 that competes with Tf for binding to TfR1 (FIG. 18C). AAV-BI19 partially colocalized with huTfR1 as puncta on the surface of hCMEC/D3s following incubation at 4°C. The number of AAV-BI19 puncta and the colocalization of AAV-BI19 with huTfR1 was dramatically reduced in the presence of OKT9 (1 μg/mL) but not Transferrin (1 μg/mL) (FIG. 18D). In contrast to AAV-BI19, AAV2 puncta were not found to colocalize with huTfR1 nor were AAV2 puncta affected by OKT9 Transferrin. To assess internalization, AAV-BI19 or AAV2 were added to hCMEC/D3 cells at 25,000 vg/cell for one hour at 37°C. Immunostaining for the AAV capsid and endosomal markers showed partial overlap with both Rab5 and Rab7 proteins, which mark early and late endosomes, respectively. Minimal overlap between AAV2 capsids and Rab5 or Rab7 was observed.

[0442] TFRC is thought to be expressed in virtually all nucleated human cells. Therefore, Applicants next asked whether the introduction of binding to human TFRC rendered AAV-BI19 independent of AAVR for transduction. AAV9 or AAV-BI19 expressing a nuclear GFP was added to hCMEC/D3 or hCMEC/D3 AAVR KO cells at 20,000 vg/cell. 24 hours later the cells were fixed and stained with a pan-AAV antibody (B1). While AAV-BI19 capsids could be detected on or within the hCMEC/D3 AAVR KO cells at a level that was as high or higher than the hCMEC/D3 control cells, transduction in the AAVR KO cells was nearly undetectable for AAV-BI19. In contrast a large fraction of cells were marked with GFP+ nuclei in the control hCMEC/D3 cells. This result suggests that AAV-BI19 remains dependent on AAVR for transduction of hCMEC/D3 cells.

[0443] Applicants next assessed transport across a human endothelial cell barrier in a BBB transwell model established using the hCMEC/D3 cell line. To minimize variance between wells, Applicants mixed AAV-BI19, AAV9, and AAV2 carrying barcoded genomes that were individually identifiable by qPCR. AAV-BI19 D). Of the three capsids, only AAV-BI19 had a statistically significantly higher amount of virus that crossed the hCMEC/D3 cell barrier and transwell membrane at the biological temperature of 37°C as compared to at 4°C, a temperature at which ATP-dependent transcytosis is suppressed, albeit passive crossing can occur (FIG. 18D). Applicants detected more AAV9 in the bottom chamber relative to AAV2, as previously reported in the literature (Merkel, S. F.; *et al.* Trafficking of Adeno-Associated Virus Vectors across a Model of the Blood-Brain Barrier; a Comparative Study of Transcytosis and Transduction Using Primary Human Brain Endothelial Cells. Journal of Neurochemistry, 2016, 140, 216–230, Di Pasquale, G.; Chiorini, J. A. AAV Transcytosis through Barrier Epithelia and Endothelium. Molecular Therapy, 2006, 13, 506–516, Song, R.; *et al.* Selection of rAAV Vectors That Cross the Human Blood-Brain Barrier and Target the Central Nervous System Using a Transwell Model. Molecular Therapy - Methods & Clinical Development, 2022, 27, 73–88), although there was no statistically significant difference between the amount of virus that crossed the hCMEC/D3 cell barrier and transwell membrane at 37°C versus 4°C (FIG. 18D).

[0444] To determine key residues that facilitate the species-specific binding of AAV-BI19 to huTfR1, Applicants identified surface exposed residues that differ between the human versus macaque TfR1 apical domain and created four huTfR1 mutants each containing a different set of closely positioned substitutions such that macaque residues replaced the corresponding human residues at specific positions across the apical domain of huTfR1 (FIG. 19A). CHO cells were transiently transfected to express each mutant and the ability of AAV-BI19 to transduce these cells was assessed. The huTfR1 mutant carrying Y247D and T248S was no longer able to mediate the enhanced transduction phenotype by AAV-BI19 (FIG. 19A). Fitting with this finding, introducing the human amino acid substitutions D247Y and S248T into the macaque TfR1 was sufficient to mediate the enhanced transduction phenotype by AAV-BI19 (FIG. 19B).

[0445] Due to its species-specific mechanism of action, Applicants tested AAV-BI19 in a knock-in mouse model where the huTfR1 extracellular domain had replaced the endogenous mouse TfR1 extracellular domain (FIG. 4) (Liu, C.; *et al.* Abstract 377: Evaluating Delivery of

TFR1-Targeting Therapies to the CNS in a Novel Humanized TFR1 Mouse Model. Cancer Research, 2022, 82, 377–377). Either AAV-BI19 or AAV9 carrying a CAG-NLS-mScarlet-P2A-Luciferase-pA construct was intravenously injected (5e11 vg/mouse) into adult female C57BL/6J or C57BL/6-Tfr1tm1TFR1/Bcgen (B-hTFR1) mice. At three weeks post-injection, relative to AAV9, AAV-BI19 exhibited enhanced biodistribution to and transduction of the brain and spinal cord in B-hTFR1 but not C57BL/6J mice (FIG. 21A-E). This enhancement was not observed in other organs that were assessed. Compared to the C57BL/6J mice that received AAV9, B-hTFR1 mice that received AAV-BI19 showed a 6 and 12-fold increase in viral genomes recovered in the brain and spinal cord, respectively (FIG. 21A); a 54 and 43-fold increase in viral mRNA transcript levels in the brain and spinal cord, respectively (FIG. 19B); and a 132 and 58-fold in the luciferase reporter enzymatic activity in the brain and spinal cord, respectively (FIG. 19C). In addition, relative to AAV9, AAV-BI19 transduced a significant portion of the neurons and astrocytes in the cortex, striatum, and thalamus in B-hTFR1 but not C57BL/6J mice (FIG. 21F-I). In B-hTFR1 mice, AAV-BI19 transduced 54%, 32%, and 67% of $NeuN^+$ cells, a marker for neurons, in the cortex, striatum, and thalamus, respectively (FIG. 21F and 21H). In contrast, in C57BL/6J, AAV-BI19 transduced less than 1% of $NeuN^+$ cells in the cortex and striatum and only 5% of $NeuN^+$ cells in the thalamus. AAV9 transduced only 1–6% of $NeuN^+$ cells in these same brain regions regardless of the mouse strain. More than 80% of $SOX9^+$ cells were transduced by AAV-BI19 in B-hTFR1 mice, as compared to 20% or fewer $SOX9^+$ cells transduced in the cortex, striatum, and thalamus by AAV9 in C57BL/6J mice (FIG. 21G and 21I). The mScarlet reporter expression in the liver was comparable between AAV9 and AAV-BI19 in both C57BL/6J and B-hTFR1 mice (FIG. 22A) in alignment with the biodistribution and transduction data. In C57BL/6J mice, AAV-BI19 was less efficient at transducing the CNS and cells within the dorsal root ganglion (DRG) compared to AAV9; however, DRG cell transduction was comparable between AAV9 and AAV-BI19 in B-hTFR1 mice (FIG. 22B).

[0446] Applicants next sought to determine whether the improved uptake and transport across the brain endothelium mediated by huTfR1 is sufficient to explain the enhanced tropism of AAV-BI19. To test this, Applicants established a two-step BBB-crossing experiment (FIG. 23). In this experiment, NSG mice were first intravenously injected with AAV-BI30, a capsid that targets CNS endothelial cells (Krolak, T.; *et al.* A High-Efficiency AAV for Endothelial Cell Transduction

throughout the Central Nervous System. Nature Cardiovascular Research, 2022, 1, 389–400), carrying either human *TFRC* or mouse *Ly6a*; LY6A is the receptor that mediates the enhanced CNS tropism of AAV-PHP.eB in some strains of mice (Huang Q, *et al.* Delivering genes across the blood-brain barrier: LY6A, a novel cellular receptor for AAV-PHP.B capsids. PLoS One. 2019 Nov 14;14(11):e0225206) and serves as a positive control in this experiment (NSG wild type mice have the non-permissive *Ly6a* allele). Next, at 28 days post-injection, the mice were either intravenously injected with AAV-BI19 or AAV-PHP.eB carrying a CAG-mScarlet reporter. As predicted, AAV-BI19 effectively transduced the CNS of mice that had received AAV-BI30:CAG-hTFRC but not AAV-BI30:CAG-LY6A, and AAV-PHP.eB effectively transduced the CNS of mice that had received AAV-BI30:CAG-LY6A but not AAV-BI30:CAG-hTFRC (FIG. 23). These results show that endothelial expression of human *TFRC* is sufficient to explain much if not all of the enhanced CNS tropism of AAV-BI19. This experiment does rule out the possibility that interactions with TfR1 on brain parenchymal cells in the B-hTfR1 KI mice also impact the tropism of AAV-BI19.

Discussion

[0447] In this work, Applicants demonstrated that AAV capsids can be reprogrammed to target a human cell surface protein in order to more efficiently cross the BBB *in vivo*. This builds on prior work by Applicants' group that successfully yielded suites of LY6A and LY6C1-targeting AAV capsids that cross the BBB in mice. Collectively, these efforts show that it is feasible to target AAV capsids to specific host proteins, including human proteins, to generate potent gene delivery vectors with known mechanisms of action and predictable tropisms. Furthermore, this approach which begins with *in vitro* receptor-binding screens produces reproducible and quantitative data that enables downstream saturation mutagenesis and machine learning-guided exploration of the capsid sequence space (Huang et al 2022).

[0448] While the approach results in greater confidence that the capsids are leveraging a mechanism that exists in humans, the capsids Applicants have reprogrammed to date including those that bind LY6A, LY6C1, and TFR1 have led to species-specific tropism enhancements. Therefore, to leverage In this study, Applicants validated the huTfR1-binding capsids in a knock-in mouse model, C57BL/6-Tfr1tm1TFR1/Bcgen (B-hTFR1) mice (FIG. 21), as well as in a two-step experiment where mice were first made to express hTfR1 on their CNS endothelium (FIG.

23). Given the highly specificity binding of AAV-BI19 for human TfR1, with minimal detected binding to the TfR1 from new world or old world monkeys, it may be worthwhile to establish new standards where gene therapy vectors do not need to be validated in NHP when they have a known mechanism of action that is human-specific.

[0449] In future work, it may be possible to reprogram capsids such that they bind to the same receptor across host species. However, enforcing cross-species receptor-targeting within a single capsid will require a focus on only the most highly conserved surface proteins, which may eliminate well characterized and validated candidate receptors like TfR1 thereby constraining the impact of this receptor-focused retargeting approach. Alternatively, dual efforts to identify human protein-targeted capsids and surrogates with matched affinities and tropism characteristics in one or more pre-clinical species can be undertaken, but this requires significant additional resources. In this context, gene therapy developers will need to weigh the importance of having a capsid that is highly optimized across human-specific assays versus capsids that can be used to demonstrate preclinical.

Methods

Plasmids

[0450] AAV9, AAV-BI19 and BI98-BI101 Rep-Cap plasmids were generated by gene synthesis (GenScript). The CAG-WPRE-hGH pA backbone was obtained from Viviana Gradinaru through Addgene (#99122). GFP, GFP-2A-luciferase, and mScarlet cDNAs were synthesized as gBlocks (IDT) or synthesized and cloned (GenScript).

[0451] Full length *TFRC* cDNA expression and lentiviral plasmids were cloned by inserting the open reading frames of *TFRC* (human: NM_003234.4; mouse: NM_011638.4; marmoset: NM_001301847.1, macaque: NM_001257303.1) into the lentiviral backbone pLenti-EF-FH-TAZ-ires-blast (Addgene #52083) with EcoRI/SalI sites.

[0452] For Fc fusion proteins, the coding sequence of the extracellular regions of TfR1 (human, marmoset, or macaque: 89-760aa; mouse: 89-763aa) were amplified by PCR and inserted into pCMV6-XL4 FLAG-NGRN-Fc (Addgene #115773) with EcoRV and XbaI sites. Signal peptide H7 (ATGGAGTTTGGGCTGAGCTGGGTTTTCCTCGTTGCTCTTTTTAGAGGTGTCCAGTGT (SEQ ID NO: 20493)) was introduced to N terminal of *TFRC* sequences to direct protein secretion.

Cell lines and primary cultures

[0453] HEK293T/17 (CRL-11268), Pro5 (CRL-1781) and CHO-K1 (CCL-61) were obtained from ATCC. mBMVEC cells (C57-6023) and hBMVECs cells (H-6023) were obtained from Cell Biologics and cultured as directed by the manufacturer. hCMEC/D3 cells were from Millipore-Sigma (SCC066).

Reconstitution of full-length TfR1 into Peptidiscs

[0454] Peptidisc peptide with the sequence N-FAEKFKEAVKDYFAKFWDPAAEKLKEAVKDYFAKLWD-C (SEQ ID NO: 42434) was purchased from PEPTIDISC LAB (peptidisc.com) and was dissolved at 2 mg/mL in buffer containing 20 mM TrisHCl, pH=8. TfR1 was reconstituted into Peptidiscs using the 'on-bead' method. Briefly, HEK293 cells expressing C-terminally tagged full length huTfR1 were harvested by centrifugation at 300×g. Cells were lysed by sonication and fractionated by centrifugation at 15,000×g to remove nuclei and cell debris and at 100,000×g to pellet the cell membrane. Membrane was resuspended in TrisHCl, pH=7.5, 50 mM NaCl, 10% glycerol to 10 mg/mL and solubilized with 0.8% DDM at 4°C with gentle agitation. Anti-FLAG M2 magnetic beads (Sigma-Aldrich) were incubated with the solubilized membrane and washed with a buffer of TrisHCl, pH=7.5, 50 mM NaCl, 10% glycerol, 0.02% DDM. Beads were incubated for five minutes at room temperature in a solution of 1 mg/mL Peptidisc peptide and then thoroughly washed in buffer without detergent. Peptidisc-TfR1 was eluted with 0.1 mg/mL 3XFLAG peptide and analyzed by SDS-PAGE.

Bio-Layer Interferometry

[0455] For characterization of the binding dynamics between huTfR1 and AAV capsids, a GatorPrime instrument was used (Gator Bio). Purified AAV-BI19 or AAV9 capsids were diluted in Q buffer (1X PBS, 0.02% Tween 20, and 0.2% BSA) and immobilized on AAVX probes. Probes without capsids were used as a control for nonspecific binding. Peptidisc-reconstituted huTfR1 was similarly prepared in a dilution range from 200 nM to 6.125 nM in Q buffer. Alternatively, this Peptidisc-huTfR1 dilution range was prepared with 200 nM Holo-Tf in each dilution to ensure a complex of huTfR1 with Holo-Tf. Probes were incubated in Q buffer to establish a baseline for 120 seconds, then incubated with AAV-BI19 or AAV9 capsids to reach a loading height of approximately 10 nm before reestablishing a baseline for 120 seconds. Association with Peptidisc-

huTfR1 or Peptidisc-huTfR1-Holo-Tf was performed over 120 seconds and dissociation into Q buffer occurred over 180 seconds.

Lentivirus production

[0456] Lentivirus was produced with a third-generation lentivirus system by cotransfection of three packaging plasmids (pMDLg-RRE, pRSV-Rev, and pVSV-G) and vector plasmid encoding human *TFRC* at a ratio of 4:1:1:6 in HEK293T/17 cells. Lentivirus was harvested three days after transfection and filtered with 0.45 μm PES to remove the cell debris.

Exogenous TfR1 expression in CHO cell lines

[0457] CHO cell lines overexpressing human, macaque, marmoset, or mouse TfR1 were established via random lentiviral integration of exogenous constructs under the control of an EF-1 alpha promoter. Briefly, CHO cells were seeded at 150,000 cells/well in 12 well plates and transduced with lentivirus-containing media for 48 hours, then transferred to 10 cm dishes for selection with 10 μg/mL blasticidin for one week. Once all cells had died in the control plate, the selected CHO cells were maintained in media with 1 μg/mL blasticidin. For validation, RNA was extracted from cells using the Qiagen RNeasy Kit. Maxima H Minus Reverse Transcriptase (ThermoFisher, EP0753) and oligo dT were used for cDNA synthesis. Species-specific primers were used for qPCR (Table 23). The CHO cells expressing TfR1 from each species were immunostained with two anti-TfR1 antibodies: Abcam ab84036, polyclonal, or eBioscienceTM OKT9, monoclonal (FIG. 17).

AAV production and titering

[0458] The AAV9 variant capsids carrying CAG-NLS-mScarlet-P2A-Luciferase-SV40-WPRE were either produced in suspension followed by iodixanol purification and titered as previously described (Eid, F.-E.; *et al.* Systematic Multi-Trait AAV Capsid Engineering for Efficient Gene Delivery, 2022) or produced using adherent cells as previously described (Challis, R.C., *et al.* Systemic AAV vectors for widespread and targeted gene delivery in rodents. *Nat Protoc* **14**, 379–414 (2019)).

Binding assays

[0459] CHO cells stably expressing TfR1 from human, macaque, marmoset, or mouse were seeded at 30,000 cells per well; hCMEC/D3 cells were seeded at 30,000 cells per well; and hBMVEC cells were seeded at 15,000 cells per well. At 24 hours post-seeding, each well was

subjected to a media change with the fresh cold media that contained each AAV9 variant carrying CAG-NLS-mScarlet-P2A-Luciferase-SV40-WPRE at 3,000, 6,000, or 12,000 vg/cell for CHO, hCMEC/D3, or hBMVEC cells, respectively. The plate was then maintained at 4°C with gentle rocking for one hour, followed by five phosphate buffered saline (PBS) washes. Cells were treated with Proteinase K at 56°C for one hour, followed by deactivation at 95°C for 10 minutes. Total DNA extraction was performed using the DNeasy kit (Qiagen). The DNA was diluted 1:20 and subjected to qPCR with the following mScarlet primers: forward primer 5'-CCGTGACCCAGGACACCTC-3' (SEQ ID NO: 42432) and reverse primer 5'-GCCATCTTAATGTCGCCCTTCAG-3' (SEQ ID NO: 42433).

Transduction assays

[0460] CHO cells stably expressing TfR1 from human, macaque, marmoset, or mouse were seeded at 100,000 cells per well; hCMEC/D3 cells were seeded at 10,000 cells per well; and hBMVEC cells were seeded at 5,000 cells per well. At 24 hours post-seeding, each well was subjected to a media change with the fresh media that contained each AAV9 variant carrying CAG-NLS-mScarlet-P2A-Luciferase-SV40-WPRE at 3,000, 6,000, or 12,000 vg/cell for CHO, hCMEC/D3, or hBMVEC cells, respectively, and the plate was maintained at 37°C with 5% CO_2 for 24 hours. Transduction was measured using the britelite plus reporter gene assay system (PerkinElmer, 6066766). Luciferase activity was reported as relative light units (RLU) as raw data or normalized to control wells transduced with AAV9.

Antibody inhibition assay

[0461] The hCMEC/D3 cells were seeded at 7,500 cells per well. Two days later, 100 µL of media with 3e8 vg/mL virus and the specified concentration of OKT9 or R&D AF2474 antibody was transferred to each well. The plate was maintained at 37°C with 5% CO_2 for 24 hours. Transduction was measured using the britelite Plus reporter gene assay system (Revvity).

Transwell assay

[0462] The hCMEC/D3 cell line (Millipore Sigma, Cat. No. SCC066), under 9 passages, was maintained in EGM2-MV media (CC4147 Lonza) to reach confluency. Falcon® Permeable Support for 24-well Plate with 1.0 µm Transparent PET Membrane (353104 Corning) were prepared by coating with collagen type I (08-115 Millipore) diluted 1:50 in PBS and incubated at 37°C for two hours. On Day 0, 3e4/cm^2 of cells were plated on the transmembrane and grown for

two days in 200 µL of EGM2-MV media with VEGF on the top of the transmembrane and 600 µL of media at the bottom of the membrane. On Day 4, the media at both the top and bottom of the transwell was changed to EGM2-MV media without VEGF. Starting from Day 4, TEER values were measured using the EVOM2 meter (World Precision Instruments). TEER values were calculated as the ohmmeter readout in wells with cells minus the ohmmeter readout in wells without cells, multiplied by the surface area in cm^2 units. Transwell permeabilities using this process were previously validated by measuring the permeability of Dextran FITC 4k (46944 Sigma), 40k (76221-470 biotium), and 70k (76221-460 biotium). TEER peaked on Day 6, reaching values >10 Ω/cm^2, which is when AAVs were added to the transwells. AAV-BI19, AAV2, and AAV9 with serotype-specific barcoded transgenes were pooled and added to the top well of the transwell at 25,000 vg/cell (each AAV). After 180 minutes of incubation at 37°C or 4°C, 22 µL of media was extracted from the bottom of the transwell. To detect the amount of virus in the media, extracts were treated with DNAseI (M0303S NEB) for 15 minutes at room temperature, then diluted in TE buffer (5 mM EDTA) and denatured at 70°C for 10 minutes to deactivate DNAseI. DNA extracts were then diluted in 5% Tween 20 with random DNA filler (UltraPure™ Salmon Sperm DNA Solution, ThermoFisher, Cat. No. 15632011). The amount of virus that had passed through the transwell was measured by qPCR using a standard curve of known virus quantities.

Immunofluorescence staining and colocalization

[0463] For huTfR1 colocalization, AAV-BI19 and AAV2 were added to monocultured HCMEC/D3 cells in optical plates (PhenoPlate 96-well, black, optically clear flat-bottom, tissue-culture treated plates, Perkinelmer 6055302) at 25,000 vg/cell, while Transferrin-647 (Transferrin From Human Serum, Alexa Fluor™ 647 Conjugate, T23366, ThermoFisher) and purified TfR1 antibody (Purified Anti-human CD71 Antibody OKT-9, 1:200 dilution, 10713000, AAT Bioquest) were added to wells to reach a final concentration of 1 µg/mL each. Cells were incubated for one hour at 37°C or 4°C accordingly, followed by rinse and fixation with 4% paraformaldehyde.

[0464] To visualize AAV particles, fixed cells were blocked by endogenous biotin (Avidin/Biotin Blocking Kit, SP-2001, Vector Laboratories) and then applying Anti-AAV9 (CaptureSelect™ Biotin Anti-AAV9 Conjugate, 1:200 dilution, 7103332100, ThermoFisher) to the wells treated with AAV-BI19 or wells with no virus, or Anti-AAVX (CaptureSelect™ Biotin Anti-AAVX Conjugate, 1:200 dilution, 7103522100, ThermoFisher) to the wells treated with

AAV2. After 3 PBS washes to clean away unused primary antibodies, Neutravidin 488 (NeutrAvidin Protein, DyLight™ 488, 1:500 dilution, 22832, Thermofisher) was applied for visualization of the primary antibodies.

[0465] To visualize human TfR1, fixed cells were stained with huTfR1 antibody (Purified Anti-human CD71 Antibody OKT-9, 1:200 dilution, 10713000, AAT Bioquest), followed by Alexa-anti-mouse (Cy™3 AffiniPure Goat Anti-Mouse IgG (H+L), 1:500 dilution, 115-165-003, Jackson ImmunoResearch) were used for detection.

[0466] For organelle colocalization, the following stainings were applied: golgi (RCAS1 (D2B6N) XP® Rabbit mAb, 1:200 dilution, 12290, Cell Signaling Technology), early endosome (Rab 5 Antibody (D-11), 1:100 dilution, sc-46692, Santa Cruz Biotechnology), late endosome (Recombinant Alexa Fluor® 647 Anti-RAB7 antibody [EPR7589] (ab198337), 1:400 dilution, ab198337, abcam), and endoplasmic reticulum (Recombinant Alexa Fluor® 488 Anti-KDEL antibody, 1:500 dilution, ab184819, abcam). The following secondary antibodies were used: Streptavidin-555 nm (Streptavidin, AlexaFluor 555, 1:500 dilution, S21381, ThermoFisher), Goat anti mouse 647 nm (Alexa Fluor® 647 AffiniPure Goat Anti-Mouse IgG (H+L), 1:500 dilution, 115-605-062, Jackson ImmunoResearch), Goat anti mouse 488 nm (Alexa Fluor™ 488 Goat Anti-Mouse IgG (H+L) Cross-Adsorbed Secondary Antibody, 1:500 dilution, A-11001, ThermoFisher), Goat anti rabbit 488 nm (Alexa Fluor® 488 AffiniPure Goat Anti-Rabbit IgG (H+L), 1:500 dilution, 111-545-144, Jackson ImmunoResearch)

[0467] For wells requiring additional mouse antibodies, cells were blocked for 60 minutes with mouse-on-mouse blocking reagent (ReadyProbes™ Mouse-on-Mouse IgG Blocking Reagent, 1:30 dilution, R37621, ThermoFisher).

[0468] Images were obtained with a 60X oil objective on a Nikon Ti-e inverted spinning disc confocal microscope using predetermined, optimized and fixed exposure time to allow image comparisons.

TfR1 substitution transduction assay

[0469] CHO cells were transiently transfected with Mirus *Trans*IT-LT1 (Mirus, MIR 2300) plasmids encoding a CAG promoter that drives expression of human TfR1, macaque TfR1, or variants with the indicated amino acid substitutions. Cells were maintained at 37°C with 5% CO_2. At 24 hours post-transfection, AAV-BI19 or AAV9 encoding ssCAG-NLS-mScarlet-P2A-

Lucierase-pA was applied at 10,000 vg/cell. After 24 hours, viral transduction was measured using the britelite Plus reporter gene assay system.

Animals

[0470] All procedures were performed as approved by the Broad Institute IACUC. C57BL/6J (000664) and NOD.Cg-*Prkdcscid Il2rgtm1Wjl*/SzJ (NSG) mice (005557) were obtained from The Jackson Laboratory (JAX). C57BL/6-Tfr1tm1TFR1/Bcgen (B-hTFR1, 110861) were obtained from Biocytogen. Recombinant AAV vectors were administered intravenously via the retro-orbital sinus in young adult male or female mice. Mice were randomly assigned to groups based on predetermined sample sizes. Transgenic animals were genotyped using DNeasy Blood & Tissue Kit (Qiagen, 69504) using primers listed in Table 23. Two mice were excluded from analysis in FIG. 21and FIG. 20. The first mouse was assigned to the AAV9 in B-hTFR1 group but was determined to be negative for huTfR1 on Western blot and by genotyping. The second mouse in the AAV-BI19 in C57BL/6J group displayed no evidence of transduction in the biodistribution, transduction, or luciferase assays, and showed no fluorescent reporter signal in the liver or the brain.

[0471] Mice were anesthetized with Euthasol and transcardially perfused with PBS at room temperature followed by 4% paraformaldehyde (PFA) in ice cold PBS. Tissues were post-fixed overnight in 4% PFA in PBS and sectioned by vibratome. Immunohistochemistry (IHC) was performed on floating sections with antibodies diluted in PBS containing 5% donkey serum, 0.1% Triton X-100, and 0.05% sodium azide. Primary antibodies NeuN 1:500 (Invitrogen, MA5-33103), SOX9 1:250 (abcam, ab185966) were incubated at room temperature overnight. The sections were then washed and stained with secondary Alexa-conjugated antibodies Alexa Fluor 647 (Invitrogen, A-31573) and Alexa Fluor 555 (Invitrogen, A-21427) at 1:1000 for four hours or overnight.

In vivo capsid biodistribution, transduction, and luciferase measurement

[0472] AAV-BI19 or AAV9 encoding ssCAG-NLS-mScarlet-P2A-Luciferase-pA was intravenously injected into adult female C57BL/6J or C57BL/6-Tfr1tm1TFR1/Bcgen (B-hTFR1) mice at a dose of 5×10^{11} vg/mouse. After three weeks, the mice were perfused with PBS. Parts of the mouse brain, liver, spinal cord, and dorsal root ganglions were dropped fixed into 4% PFA. Remaining tissues were collected and frozen at −80°C. For biodistribution, samples were processed for AAV genomes using a DNeasy 96 Blood & Tissue Kit (Qiagen, 69581) and qPCR

was performed targeting mScarlet and mouse glucagon as previously described (see primer sequences in Table 23) (Deverman, B. E.; *et al.* Cre-Dependent Selection Yields AAV Variants for Widespread Gene Transfer to the Adult Brain. Nature Biotechnology, 2016, 34, 204–209). For the mRNA transduction assessment, RNA was isolated using TRIzol (Invitrogen, 15596026) and purified using an RNeasy 96 Kit (Qiagen, 74171); cDNA synthesis was performed using Maxima H Minus Reverse Transcriptase (Thermo Scientific, EP0753); qPCR targeting mScarlet and mouse GAPDH was performed. For the luciferase measurements, protein was extracted from the mice tissues using the lysis buffer T-Per with 1X Halt protease inhibitor (Invitrogen, 78430); 10 µg of total protein was used to assess the reporter gene using the britelite Plus reporter gene assay system (Perkin Elmer, 6066761).

[0473] For the two-step mouse BBB-crossing experiments, NSG mice were first intravenously injected with AAV-BI30 (Krolak, T.; *et al.* A High-Efficiency AAV for Endothelial Cell Transduction throughout the Central Nervous System. Nature Cardiovascular Research, 2022, 1, 389–400) at 1e11 vg/mouse to deliver AAV-CAG-hTFRC-WPRE-3x-miR122-pA or AAV-CAG-LY6A-WPRE-3x-miR122-pA. At 28 days post-injection, 5e11 vg of AAV-BI19:CAG-mScarlet or AAV-PHP.eB:CAG-mScarlet was systemically administered to each mouse. Transduction was assessed three weeks later.

Experiment 1: Screening for 7-mer modified AAV capsids that bind selectively to cells expressing human TFRC (hTFRC).

[0474] A library of capsids with a 7-mer insertion between AA588 and 589 of AAV9 K449R was screened for capsids that more efficiently bind to HEK293 or CHO cells transiently transfected with human TFRC (hTFRC) than cells expressing a control protein (GFP). Sequences that bind more efficiently to cells expressing hTFRC were identified by amplicon NGS. Analysis of these sequences identified several motifs present in a subset of sequences: [YFL][AS][RK]X[NG]X[N] and XXS[ST]NG[IVR], where X = any amino acid.

[0475] Applicants generated a second round library comprising sequences identified in the cell-based screen for hTFRC binding and all of the sequences conforming to the above two motifs using oligo pool synthesis. The oligo pool was used to generate a capsid library. The second round library was screened on HEK293 cells with or without transient expression of hTFRC (5,000 vg/cell) as performed in the first round (Table 1). In addition, the second round library was

screened to identify capsids that more efficiently transduced (1) hCMEC/D3 cells, which express endogenous hTFRC, (2) mouse brain microvascular endothelial cells (BMVEC)s (Table 2) as well as (3) mixed culture spheroids consisting of hCMEC/D3 cells, and primary human astrocytes and pericytes (Cho et al, Nature Communications 2017).

[0476] Applicants chose several novel TFRC binding capsids for further study: AAV-BI19: YSRIGPN (SEQ ID NO: 14632); AAV-BI98: YSRLNMN (SEQ ID NO: 14301); AAV-BI99: YSRLNKD SEQ ID NO: 16577); AAV-BI100: VHRLQDK (SEQ ID NO: 16602); AAV-BI101: YHRLSNN (SEQ ID NO: 16636); and AAV-BI102: LHALSHN (SEQ ID NO: 16608). Applicants used these capsids to package a reporter transgene and transduced CHO cells or CHO cells expressing human TFRC (FIG. 2), as well as hCMEC cells or hCMEC cells overexpressing human TFRC (FIG. 3). In both cell types, each of the TFRC binding capsids showed enhanced ability to bind and transduce cells expressing human TFRC relative to AAV9. Notably, the enhanced transduction by these engineered capsids was absent in CHO cells, which lack expression of human TFRC. In contrast, the engineered AAVs each showed enhanced transduction of unmodified hCMEC cells relative to AAV9, which is fitting with the known expression of human TFRC in these cells. The role of TFRC for the enhanced hCMEC transduction of these capsid variants is supported by the finding that transduction was further enhanced in cells with greater cell surface exposed TFRC (FIG. 3 and 4).

[0477] To assess whether the enhanced transduction of hCMEC cells by AAV-BI19 requires endogenous TFRC, applicants attempted to block the interaction of the AAV with TFRC using several anti-TFRC antibodies: OKT9 (Thermo) and AF2474 (R&D Systems). Applicants found that OKT9, which binds to the TFRC apical domain (Ferrero et al J. of Virology doi.org/10.1128/JVI .01868-20) blocked transduction by AAV-BI19 in a dose-dependent manner (FIG. 5). In contrast, AF2474, which blocks binding of Transferrin to TFRC, did not inhibit transduction by AAV-BI19. Together these results suggest that the enhanced tropism of AAV-BI19 for human brain endothelial cells is mediated through binding to the human TFRC apical domain.

Experiment 2: Screening for 7-mer modified AAV capsids that bind selectively to hTFRC-Fc

[0478] In a second experiment, applicants screened a separately produced AAV9 K499R 7-mer 588 insertion library for variants capable of selectively binding hTFRC when produced as an

Fc fusion protein. To perform this assay, applicants expressed the human or marmoset TFRC-Fc fusions in HEK293 cells, and pulled down the Fc fusion proteins from the cell culture media using ProA-magentic beads (FIG. 7).

[0479] The recovered 7-mers found to bind hTFRC-Fc were synthesized as an oligo pool and used to generate a second-round library. Applicants screened the second-round library for variants that bind hTFRC using the same hTFRC-Fc assay (Table 4), variants that bind to CHO cells stably expressing hTFRC (Table 5), variants that bind and transduce CHO cells expressing hTFRC (Table 6), and variants that bind HEK293 cells overexpressing hTFRC (Table 7). A subset of sequences bound HEK293 cells expressing either human TFRC or marmoset TFRC (Table 8).

Experiment 3: Multiple regions of the AAV capsid can be engineered to enable TFRC binding.

[0480] To determine whether other regions of the AAV capsid could be engineered to bind to TFRC, applicants generated libraries where a stretch of 10 AA in loop IV of AAV9 were substituted with a random string of AAs of seven or 10 AAs in length. Applicants also repeated the screen using a new loop VIII 7-mer insertion library as a positive control. Applicants screened these libraries for capsids that gained the ability to bind selectively to human TFRC (Table 9 and Table 10) or human TFRC where the apical domain was replaced with the corresponding domain from mouse TFRC (Table 11). Notably, several of the 10 AA sequences recovered in the loop IV substitution library (IPFSRVNPDT (SEQ ID NO: 20285), LGFARTGAAD (SEQ ID NO: 20274), LGFTKSSGSD (SEQ ID NO: 20270), LRYSKTQGES (SEQ ID NO: 20266), SPYARSSAGV (SEQ ID NO: 20271), and VGWSRLDLTT (SEQ ID NO: 20262)) contain the partial [YWFL][AST][RK] (SEQ ID NO: 20492) motif like that observed in human TFRC binding 7-mer insertions at loop VIII, suggesting that this binding motif is functional in multiple structural contexts.

Experiment 4: Toward a systematic mapping of the relationship between AAV 7-mer sequence and hTFRC binding.

[0481] Applicants have generated a novel type of library (Fit4Function) composed of AAV capsids that uniformly samples only the high production fitness sequence space (cite WO2021222636A1). When used to screen for novel functions (e.g, new receptor binding), the Fit4Function libraries can generate highly reproducible quantitative data suitable for training ML models that predict the function of previously untested sequences within the theoretical sequence

space. Applicants screened a Fit4Function library for capsids that selectively bind to TFRC-Fc. Binding was measured at both pH7.4 and pH5.5 and is reported in Table 12. Notably, even within this smaller library (240K unique sequences), several examples of sequences conforming to previously identified motifs were identified (e.g., YAKGGSN (SEQ ID NO: 11535) and YSKSGPG (SEQ ID NO: 20422), [YFL][AS][RK]X[NG]X[N] (SEQ ID NO: 20484); VKSSNGV (SEQ ID NO: 11671), XXS[ST]NG[IVR] (SEQ ID NO: 20485)).

Experiment 5: Secondary evaluation of recovered variants from previous assays and use of those sequences to train generative models to predict additional high performing sequences.

[0482] To assess the function of AAV capsids discovered from Experiments 1-4 relative to each other and identify the top performing capsids across several relevant in vitro and in vivo assays, applicants generated a pooled oligo library containing loop VIII 7-mer insertion variants from Experiments 1-4 (>9K unique sequences). Applicants also used a subset of these 7-mer sequences with activity observed across multiple readouts to train a machine learning model (Wavenet that has been previously adapted for use in protein design) to generate additional sequences predicted to bind human TFR1 (>24K unique sequences). All sequences in the library were encoded by at least two unique nucleotide sequences, providing internal replicates for each 7-mer sequence. The pooled oligo library was then produced in two batches, one for in vitro studies. The library was then screened for binding to human, macaque, marmoset and mouse TFR1-Fc fusion proteins, for binding and transduction of control CHO cells or CHO cells stably expressing human, macaque, marmoset or mouse TFRC, for binding and transduction of hCMEC, for binding and transduction of hCMEC cells expressing exogenous human TFRC (hCMEC+hTFRC) in the presence or absence of holo-, total-, or apo-Transferrin (Tf), and for transduction in the brain, spinal cord, liver, muscle, kidney, and heart in mice expressing a chimeric form of TFRC where the extracellular domain of mouse Tfrc (Exons 4-19) have been replaced by the corresponding coding sequence for the extracellular domain of human TFRC (B-hTFR1 mice, Biocytogen). In addition, applicants also developed a two-step assay where AAV-BI30, a capsid that selectively transduces CNS endothelial cells (Krolak et al 2022) was first administered intravenously to immunodeficient NSG mice to express human TFRC, or mouse LY6A as a control, in the CNS vasculature. Subsequently, following expression (4 weeks) from AAV-BI30, the capsid library was administered intravenously and tissue samples were collected 4 weeks later.

Capsid sequences are provided that were found to (1) bind TFR1-Fc fusion proteins with and without an additional 10 minute wash step in dPBS (pH5.5) (Table 14), (2) bind CHO cells expressing human TFRC (Table 15), (3) bind hCMEC and hCMEC+hTFRC (Table 16), (4) transduce hCMEC and hCMEC+hTFRC cells (Table 17), express Cap in the CNS of KI and/or 2-step TFRC mice (Table 18), bind hCMEC+hTFRC cells in the absence of Tf or in the presence of holo-, apo-, or total-Tf (Table 19).

Experiment 6: Screening for capsids that bind human, macaque, marmoset TFR1-Fc fusion proteins

[0483] A new AAV9 K499R 7-mer 588 insertion library was screened for variants capable of selectively binding human, macaque, and mouse TFRC when produced as an Fc fusion protein. Top variants that were found to be enriched through binding human TFR1-Fc are provided (Table 20).

Selection of top functional variants based on convergence across multiple functional assays

[0484] To identify top candidate capsids that engage TFR1 through specific motifs, applicants grouped the recovered sequences from Experiment 5 into 10 families and genera based on common sequence elements (Table 21). The motif definitions were used to extract all of the capsid sequences within the library that conformed to each family or genus definition regardless of activity. Values are reported as the log2 enrichment (human TFR1-Fc binding assay RPM/AAV library RPM) for all sequences within the library for each motif (FIG. 24). Data for AAV9 and a set of negative control sequences (previously determined not to bind human TFRC-Fc) were included to facilitate interpretation of the enrichment scores relative to the parental vector and non-binding capsid sequences. Individual 7-mer AA sequences were encoded by two or more nucleotide references. Note that for each family and genus definition, the vast majority of the tested sequences were found to bind human TFR1-Fc better than AAV9 or the control capsid set (FIG. 24).

[0485] Next, top candidate capsids representing many of the families described above were chosen based on several functional attributes including production fitness (manufacturability), binding enrichment at pH 7 and following a low pH wash (pH 5.5), binding and transduction of hCMEC cells, binding in the presence of Tf (the preferred states are moderate or insensitive), CNS transduction in the humanized mouse models (B-hTFR1 KI mice and 2-step TFRC mice), and liver

transduction in the B-hTFR1 mice (Table 22). Exemplary choices from several families include, but are not limited to, LHRLGPN (SEQ ID NO: 36834), YSRIGPN (SEQ ID NO: 14632) or YARTGPN (SEQ ID NO: 14269) in Family 1; LHAKLPN (SEQ ID NO: 36316) in Family 2; VESTNGR (SEQ ID NO: 36431), VQSTNGV (SEQ ID NO: 36423), and TESTNGR (SEQ ID NO: 17558) in Family 3; RMEDAYP (SEQ ID NO: 36895), RGEDVYP (SEQ ID NO: 36864), and RTYDSFP (SEQ ID NO: 37806) in Family 4; LCKPCLN (SEQ ID NO: 36936) or LCKPCLD (SEQ ID NO: 36437) in Family 5; KDDFTHF (SEQ ID NO: 36464), KDDFTTY (SEQ ID NO: 36336), and REDYVKW (SEQ ID NO: 37652) in Family 7; and NALEGRD (SEQ ID NO: 36407) and IALKGWD (SEQ ID NO: 36248) in Family 8.

Tables Cont.

[0486] Table 14. Capsid that selectively bind to TFR1-Fc fusion proteins. A second round 7-mer 588 insertion library was screened for capsids that bind human, macaque, marmoset, or mouse TFR1-Fc fusion proteins in a pull-down assay. The binding assays were performed at pH7. In some assays the pulled down fusion protein-capsid complexes were washed with pH 5.5 buffer for 10 minutes (+ pH5.5 wash). The table provides an assessment of the enrichment of capsids as assessed by Illumina sequencing where the enrichment is the log2 assay reads per million (RPM)/RPM in the virus library before screening. Enrichment scores are listed within the following ranges: "-" <=0; "+" >0 to <=2; "++" >2 to <=3; "+++" >3.

[0487] Table 15. Capsids that selectively bind human TFR1-Fc fusion protein and CHO cells cells expressing TFRC. A second round 7-mer 588 insertion library was screened for capsids that bind (b) and transduce (t) control CHO cells or CHO cells stabling expressing human, macaque, marmoset, or mouse *TFRC*. The table provides an assessment of the enrichment of capsids as assessed by Illumina sequencing where the enrichment is the log2 assay reads per million (RPM)/RPM of each variant in the virus library. Enrichment scores are listed within the following ranges: "-" <=0; "+" >0 to <=2; "++" >2 to <=3; "+++" >3.

[0488] Table 16. Capsids that bind hCMEC/D3s. A second round 7-mer 588 insertion library was screened for capsids that bind the hCMEC/D3 human brain endothelial cell line, which endogenously expresses TFRC (hCMEC binding) or hCMEC/D3 cells made to stably express human TFRC via transduction with a human TFRC expressing lentivirus (hCMEC-hTFRC binding). The table provides an assessment of the enrichment of capsids as assessed by Illumina

sequencing where the enrichment is the log2 assay reads per million (RPM)/RPM of each variant in the virus library. Enrichment scores are listed within the following ranges: "-" <=0; "+" >0 to <=1; "++" >1 to <=2; "+++" >2.

[0489] Table 17. Capsids that transduce hCMEC/D3s. A second round 7-mer 588 insertion library was screened for capsids that transduce the hCMEC/D3 human brain endothelial cell line, which endogenously expresses TFRC (hCMEC binding) or hCMEC/D3 cells made to stably express human TFRC via transduction with a human TFRC expressing lentivirus (hCMEC-hTFRC binding). The table provides an assessment of the enrichment of capsids as assessed by RT-PCR followed by Illumina sequencing where the enrichment is the log2 assay reads per million (RPM)/RPM of each variant in the virus library. Enrichment scores are listed within the following ranges: "-" <=0; "+" >0 to <=1; "++" >1 to <=3; "+++" >3.

[0490] Table 18. Capsids that transduced cells *in vivo* following intravenous administration of a second round AAV library to mice engineered to express human TFRC or Ly6a as a control. A second round 7-mer 588 insertion library was screened for capsids that transduce cells in the CNS of B-hTFR1mice. The same library was also administered to NGS mice made to express human TFRC (2-step assay) via an AAV-BI30 packaging AAV-CAG-hTFRC or AAV-CMV-CBA-hTFRC. As controls, the same library was also administered to separate cohorts of mice injected with AAV-CAG-Ly6a or AAV-CMV-CBA-Ly6a. The table provides an assessment of the enrichment of capsids as assessed by RT-PCR in the indicated *in vivo* assays followed by Illumina sequencing. Enrichment is the log2 assay reads per million (RPM)/RPM of each variant in the virus library. Enrichment scores are listed within the following ranges: "-" <=0; "+" >0 to <=1; "++" >1 to <=3; "+++" >3.

[0491] Table 19. Capsid binding to hCMEC-hTFRC cells in the presence or absence of human Transferrin (Tf). A second round 7-mer 588 insertion library was screened for capsids that bind hCMEC/D3 human brain endothelial cells made to stably express human TFRC via transduction with a human TFRC expressing lentivirus (hCMEC-hTFRC binding) in the absence of Tf (no Tf) or in the presence of total-Tf, holo-Tf, or apo-Tf (2ug/ul). The table provides an assessment of the enrichment of capsids as assessed by PCR followed by Illumina sequencing where the enrichment is the log2 assay reads per million (RPM)/RPM of each variant in the virus

library. Enrichment scores are listed within the following ranges: "-" <=0; "+" >0 to <=1; "++" >1 to <=3; "+++" >3.

[0492] Table 20. Capsid binding to human or macaque TFR1-Fc fusion proteins and transduction *in vivo* following intravenous administration to mice expressing human or macaque TFRC. A new second round 7-mer 588 insertion library was screened for capsids that bind human, macaque, or mouse TFR1-Fc fusion proteins. The same library was also administered to NGS mice made to express human TFRC (2-step assay) via AAV-BI30 packaging AAV-CAG-hTFRC or AAV-CAG-macaque-TFRC. As controls, a separate group of mice wasleft uninjected with a receptor encoding AAV (2-step, control). The table provides an assessment of the enrichment of capsids as assessed by RT-PCR followed by Illumina sequencing where the enrichment is the log2 assay reads per million (RPM)/RPM of each variant in the virus library. Enrichment scores are listed within the following ranges: "-" <=0; "+" >0 to <=1; "++" >1 to <=3; "+++" >3.

[0493] Table 21. Sequence motif families. The table provides sequence motifs that define specific capsid families and genera, the total number of possible sequence species within the motif, the number of unique 7-mer sequences within each family or genus, and number and fraction of possible sequences from each motif that were tested in the library. Amino acids presented in brackets indicate amino acids acceptable at the specific position. For example, Genus 1.11 FSRLG[AHNLVSPT]N (SEQ ID NO: 42435) has the sequence F-S-R-L-G-X1-N (SEQ ID NO: 42436), where X1 can be any amino acid with the brackets (AHNLVSPT (SEQ ID NO: 42437)).

T21

Family	Genus	Defining sequence motif (SEQ ID NOS: 42384-42428)	Sequences with the motif family/genus	Assayed	Fraction assayed
Family1		[YMFL][SHTA][KR][AGILMNQSTV][NG][ATHNFIPLY][DN]	11520	1608	13.96%
Family1	Genus1.1	[YML][SHTA][KR][AGILMNQSTV][N][ATHNFIPLY][DN]	4320	399	9.24%
Family1	Genus1.2	[YML][SHTA][KR][AGILMNQSTV][G][AGFHILNPSTVY][DN]	5760	825	14.32%
Family1	Genus1.3	[LY][AHS][KR][AGHILMNQSTV]GPD	132	23	17.42%
Family1	Genus1.4	[LY][AHS][KR][AGHILMNQSTV]GPN	132	71	53.79%
Family1	Genus1.5	YSK[AILMNQSTV]G[YPTQVFLHSAEDIM]N	126	122	96.83%
Family1	Genus1.6	[LY]S[RK][VITLA][SA][PRYFHIKW]D	320	42	13.13%
Family1	Genus1.7	[FLMY]H[KR][ALM][AGLMNQST][ADEFHILMNQPSTVY][DN]	4224	172	4.07%
Family1	Genus1.8	[LMY]H[KR][ALM][AGLMNQST][ADEFHILMNQPSTVY]N	1584	61	3.85%
Family1	Genus1.9	[LMY]H[KR][ALM][AGLMNQST][ADEFHILMNQPSTVY]D	1584	87	5.49%
Family1	Genus1.10	[LMY]H[KR]L[SQGTNL][PTVIQLA]D	252	38	15.08%
Family1	Genus1.11	FSRLG[AHNLVSPT]N	8	8	100.00%
Family1	Genus1.12	FAR[TSN]G[YFHPA]N	15	15	100.00%
Family1	Genus1.13	FH[KR]LG[IPS][ND]	12	5	41.67%
Family2	Genus2.1	[YL]HA[KRNA][GQLS][PLINDT]N	192	17	8.85%
Family3		[AFHILNPRSTVY][ADEFGHIKLMNQRSTWY]S[ST]NG[IRV]	1224	657	53.68%
Family3	Genus3.1	[FLY][DEHNQST]S[ST]NG[IV]	84	63	75.00%
Family3	Genus3.2	[VPISTHA][ADEFGHIKLMNQRSTY]S[ST]NG[IV]	448	315	70.31%
Family3	Genus3.3	[AFILPSTVY][DENQST]S[TS]NGR	90	35	38.89%
Family3	Genus3.4	R[EDQT]S[ST]NG[IV]	16	9	56.25%
Family4		R[TLMSGDNE][GEDIFHSAMPVY]D[AVST][YF][AP]	1536	184	11.98%
Family4	Genus4.1	R[TMLS][YSAMIFP]D[AVST][YF]P	224	69	30.80%
Family4	Genus4.2	R[TMLS][YSAMIFP]D[AVST][YF]A	224	13	5.80%
Family4	Genus4.3	R[GTDSNE][EDPSG][DTEHN][VAT][YF]P	900	132	14.67%
Family4	Genus4.4	R[GLTDS][DPSG][DEHN][VT][YF]P	320	53	16.56%
Family4	Genus4.5	T[RKYW][EWYQST]GD[PA][AP]	96	11	11.46%

Family5		LC[KR]PC[LSDANQHPV][ETGADNS]	126	32	25.40%
Family6	Genus6.1	[YF][WFY][TS]G[ITVQMH][IPHLMAQTV][ASDE]	2592	445	17.17%
Family6	Genus6.2	[YF][WFY][TS]G[ITVQMH][KR][ASDE]	576	89	15.45%
Family6	Genus6.3	[YF][WFY][TS]G[KR][IPHLMAQTV][ASDE]	864	201	23.26%
Family6	Genus6.4	YFTG[KRQMHI][TRHKVL]E	36	27	75.00%
Family6	Genus6.5	YF[TSHA]G[KRT][IPHLMAQT][DN]	192	58	30.21%
Family6	Genus6.6	YWTG[KMVT][PVIHQTML][ED]	64	37	57.81%
Family6	Genus6.7	[YF]F[SHAQ]G[KQR][IVLKHRQM]E	192	60	31.25%
Family7	Genus7.1	[KR][DSN]EF[TKSRV][TSGV][FWY]	360	77	21.39%
Family7	Genus7.2	[KR]DD[FY][TSVH][TSGVA][FWY]	240	68	28.33%
Family7	Genus7.3	[SRGNTMQ]DG[TVSNY]S[KR]W	70	32	45.71%
Family7	Genus7.4	[RVDIQK][MLG][SEARQ]DR[TASGKN]W	540	44	8.15%
Family7	Genus7.5	[DIEQVSK][LMGP][EASDQT][SA]R[DSETGA]W	2016	194	9.62%
Family7	Genus7.6	G[ESPGA][DEPN][GHTSN]V[RKS][WY]	600	60	10.00%
Family7	Genus7.7	RE[DEPN][GHTSN]V[RKS][WY]	120	17	14.17%
Family7	Genus7.8	G[GS][GESAPD][TGS]S[STHKRAN]W	252	74	29.37%
Family8		[VIRND][AGS][LTSHG][KRE]G[WRAI][DG]	1800	50	2.78%
Family9		[LMW][FRWKTY][DS]GT[PGSNAR][APSY]	864	56	6.48%
Family10		[PNK][YF]A[RK]S[PVARILSE][EDML]	384	23	5.99%

[0494] Table 22. Top performing capsids across multiple measures relevant to traits important for a CNS gene therapy vector. Data from a second-round library was used to identify capsid sequences with in vivo BBB crossing activity in either or both B-hTFR1 KI mice or in NSG mice made to express human TFRC in brain vascular endothelial cells using AAV-BI30:CAG-human TFRC. Production fitness was assessed as log2 enrichment for each sequence in the AAV library AAV RPM/plasmid library DNA RPM in two separate library batches, one used for in vivo studies and one used for in vitro studies. pH sensitive binding was assessed as log2 enrichment(Fc-hTFR1 binding and washing at pH 7) minus log2 enrichment(Fc-hTFR1 binding pH 7 and washing at pH 7 plus a final pH 5.5 rinse (dPBS) and incubation for 10 min). Capsids were screened to assess whether they are sensitive to competition for binding to TFR1 from human Transferrin (Tf) by assessing binding to hCMEC-hTFRC expressing cells at 4C in the presence of holo-Tf or no-Tf. Insensitive, moderate, and sensitive scores were defined as log2(enrichment score, hCMEC-hTFR+holo-Tf) minus log2(enrichment score, hCMEC-hTFR noTf > -0.4, <= -0.4 to -1, and <-1, respectively).

[0495] Table 23. Primers used for qPCR in this study.

Primer name	Primer sequence
huTfR1-qPCR-F	GCTATGGGACTATTGCTGTGATCGTC (SEQ ID NO: 42438)
huTfR1-qPCR-R	CCAATATAAGCGACGTGCTGCAG (SEQ ID NO: 42439)
msTfR1-qPCR-F	TGTGGAGATGAAACTGGCTGC (SEQ ID NO: 42440)
msTfR1-qPCR-R	AGTGCAATAGCTGCAAAGCAGAG (SEQ ID NO: 42441)
marTfR1-qPCR-F	AACAAGAGCGTGAAGCTCTCTG (SEQ ID NO: 42442)
marTfR1-qPCR-R	CTCCAGGACCCCAGGAGTC (SEQ ID NO: 42443)
macTfR1-qPCR-F	GGAAAACAAGAGTGTGAAGCTCACG (SEQ ID NO: 42444)
macTfR1-qPCR-R	GGAGAGCTGTCCCCACACTG (SEQ ID NO: 42445)
MSCARLET-QPCR-F	CCGTGACCCAGGACACCTC (SEQ ID NO: 42432)
mScarlet-qPCR-R	CTTCTTCTGCATTACGGGGC (SEQ ID NO: 42446)
GAPDH-qPCR-F	ACCACAGTCCATGCCATCAC (SEQ ID NO: 42447)
GAPDH-qPCR-R	TCCACCACCCTGTTGCTGTA (SEQ ID NO: 42448)

mGlucagon-qPCR-F	AAGGGACCTTTACCAGTGATGTG (SEQ ID NO: 42449)
mGlucagon-qPCR-R	ACTTACTCTCGCCTTCCTCGG (SEQ ID NO: 42450)
msTfR1-exon1and2-F	CTAACTTGTTTGGTGGGGAAC (SEQ ID NO: 42451)
msTfR1-exon1and2-R	CTTCATCTGCAGCCAGTTTCAT (SEQ ID NO: 42452)
genotyping-h&mTFRC-F	CTCGTGAGGCTGGATCTCAAAAAGATG (SEQ ID NO: 42453)
genotyping-hTFRC-R	CACCAGGTAAACAAGTCTACCGTTCTTATC (SEQ ID NO: 42454)
genotyping-mTFRC-R	ACTGGGTCTAAGTTACCATTTGACTGC (SEQ ID NO: 42455)

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[0496] Various modifications and variations of the described methods, pharmaceutical compositions, and kits of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific embodiments, it will be understood that it is capable of further modifications and that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention that are obvious to those skilled in the art are intended to be within the scope of the invention. This application is intended to cover any variations, uses, or adaptations of the invention following, in general, the principles of the invention and including such departures from the present disclosure come within known customary practice within the art to which the invention pertains and may be applied to the essential features herein before set forth.

NT SEQ ID#	AA SEQ ID#	NT sequence	AA_sequence	HEK-hTFRC
1	10952	TATTCCAAATCCAATAATAAT	YSKSNNN	++−
2	10953	GATCACGGGATAAATAAATGG	DHGINKW	++−
3	10954	TCCACGGGGGTGAATAAATGG	STGVNKW	++−
4	10955	TATGCGAAAGGGAATATAAAT	YAKGNIN	++−
5	10956	TTGCACAGGCAGAATATAGAT	LHRQNID	++−
6	10957	CACTCCAAAGTGAATATAAAT	HSKVNIN	++−
7	10958	TATGCGAAATTGAATATAAAT	YAKLNIN	++−
8	10959	TATTCCAAAGTGAATATAAAT	YSKVNIN	++−
9	10960	TATGCGAAAGCGAATTATAAT	YAKANYN	++−
10	10961	TTCTCCAAACAGAATTATAAT	FSKQNYN	++−
11	10962	TATGCGAAATCCAATAATAAT	YAKSNNN	++−
12	10963	TATTCCAAATCCAATATAAAT	YSKSNIN	++−
13	10964	ATCGACGAATGGCATCATTTT	IDEWHHF	++−
14	10965	TATGCGAAAGCGAATATAAAT	YAKANIN	++−
15	10966	TATTCCAAAGCGAATTGTAAT	YSKANCN	++−
16	10967	TTCTCCAGGATGAATGATAAT	FSRMNDN	++−
17	10968	TATGCGAAAATAGGGTATAAT	YAKIGYN	++−
18	10969	GGGAATGATTATCAGTCCTAT	GNDYQSY	++−
19	10970	TATGCGAAATCCAATATAAAT	YAKSNIN	++−
20	10971	TTCTCCAAAGCGAATATAAAT	FSKANIN	++−
21	10972	TATTCCAGGGAGAATTATAAT	YSRENYN	++−
22	10973	TATGCGAGGTTGAATATGAAT	YARLNMN	++−
23	10974	TATGCGAAAGGGAATAATAAT	YAKGNNN	++−
24	10975	ACGGAGGAGACGTATTATAAA	TEETYYK	++−
25	10976	TTCGCGAAAGGGAATATAAAT	FAKGNIN	++−
26	10977	TATGCGAAACAGGGGAATAAT	YAKQGNN	++−
27	10978	TTCTCCAAATTGGGGTATAAT	FSKLGYN	++−
28	10979	TTCGCGAAAGCGGGGTATAAT	FAKAGYN	++−
29	10980	TATTCCAGGTTCAATGATAAT	YSRFNDN	++−
30	10981	TACTCAAAGGCCGGCTGCAAC	YSKAGCN	++−
31	10982	TATGCGAAACAGAATATAAAT	YAKQNIN	++−
32	10983	GATAATCACTCCAATAAATGG	DNHSNKW	++−
33	10984	TATGCGAAACACGGGTATAAT	YAKHGYN	++−
34	10985	GATGGGTTGTCCAATAAATGG	DGLSNKW	++−
35	10986	TTCGCGAAAACGGGGTATAAT	FAKTGYN	++−
36	10987	TCCAATGATACGGTGTATAGG	SNDTVYR	++−
37	10988	AATGGGACGTCCTATTCCTGG	NGTSYSW	++−
38	10989	TTTTCACGCATGAACCATAAC	FSRMNHN	++−
39	10990	TATTCCAAACAGGGGATAAAT	YSKQGIN	++−
40	10991	ACGAATAATACGGTGTATAAA	TNNTVYK	++−
41	10992	GATGTGAATGGGAATTATGCG	DVNGNYA	++−
42	10993	TATTCCAGGCACAATGATAAT	YSRHNDN	++−
43	10994	TACGCCAAGGCCAACTGCAAC	YAKANCN	++−
44	10995	TTGTCCAGGACGTCCGATAAT	LSRTSDN	++−

45	10996	TACTCACGCTACGGCGACAAC	YSRYGDN	++−
46	10997	TATGCGAAACCGGGGTATAAT	YAKPGYN	++−
47	10998	TATGCGAAAGCGGGGAATAAT	YAKAGNN	++−
48	10999	TATGCGAAAGCGAATAATAAT	YAKANNN	++−
49	11000	TATTCCAAACAGAATATGAAT	YSKQNMN	++−
50	11001	TATGCGAAACAGAATATGAAT	YAKQNMN	++−
51	11002	ATAGTGTCCACGAATGGGGTG	IVSTNGV	++−
52	11003	TTGGCGAAAACGGGGATAAAT	LAKTGIN	++−
53	11004	TATGCGAAAGCGGGGATAAAT	YAKAGIN	++−
54	11005	TTGTCCAGGTTGAATATAATA	LSRLNII	++−
55	11006	TTCGCGAAATCCGGGATAAAT	FAKSGIN	++−
56	11007	GACGACGTATCACGCAAGTGG	DDVSRKW	++−
57	11008	TATGTGAAATCCGATAATGGG	YVKSDNG	++−
58	11009	GTGGCGCACGCGGGGATAGGG	VAHAGIG	++−
59	11010	TTTTCAAAGCTGGGCTTTAAC	FSKLGFN	++−
60	11011	TATGCGAAATCCGGGATAAAT	YAKSGIN	++−
61	11012	TATGCGAAATTGGGGAATAAT	YAKLGNN	++−
62	11013	TATTCCAAAACGAATATAAAT	YSKTNIN	++−
63	11014	TTCTCCAGGTTGTCCGATAAT	FSRLSDN	++−
64	11015	TTGTCCAAATTGAATGATAAT	LSKLNDN	++−
65	11016	TATGCGAGGACGGGGTCCTCC	YARTGSS	++−
66	11017	TATTCCAAAGCGGGGATAAAT	YSKAGIN	++−
67	11018	TTGCACAAATTGTCCAATCAG	LHKLSNQ	++−
68	11019	TATCACAAATTGAATTTGGTG	YHKLNLV	++−
69	11020	TATTCCAGGTTGGATAGGGAT	YSRLDRD	++−
70	11021	TATGCGAGGATAGGGGATAAT	YARIGDN	++−
71	11022	GTGGAGTCCTCCTCCAAATGG	VESSSKW	++−
72	11023	TATGCGAGGCCGGGGTATAAT	YARPGYN	++−
73	11024	TTGGCGAAATTGGGGCCGAAT	LAKLGPN	++−
74	11025	TATTCCAAACACAATATGAAT	YSKHNMN	++−
75	11026	TATGCGAAAACGGGGATAAAT	YAKTGIN	++−
76	11027	TATGCGAAAAATGGGATAAAT	YAKNGIN	++−
77	11028	TTGTCCAGGACGGGGGATAAT	LSRTGDN	++−
78	11029	AATGATGGGGAGTCCCAGTGG	NDGESQW	++−
79	11030	TATCACGCGTCCTCCTATAAT	YHASSYN	++−
80	11031	GAGGCGTATTCCGATAGGGAT	EAYSDRD	++−
81	11032	TACTCAAAGACCAACTGCAAC	YSKTNCN	++−
82	11033	TATTCCAAATCCGGGCAGAAT	YSKSGQN	++−
83	11034	TTGGCGAGGGGGGCGGATAAT	LARGADN	++−
84	11035	TATGCGAGGTTGGGGCAGAAT	YARLGQN	++−
85	11036	TATTTCGCGGGGAAATATGAT	YFAGKYD	++−
86	11037	TTGTCCAAAACGGGGAATAAT	LSKTGNN	++−
87	11038	TTGTCCAGGTCCTCCATAGAT	LSRSSID	++−
88	11039	GGCCGCTTTTACTCAGACGGC	GRFYSDG	++−
89	11040	TACTCACGCCATAACCATAAC	YSRHNHN	++−

90	11041	GATAAATTCGATAATTATGCG	DKFDNYA	++−
91	11042	TATGCGAAAGAGAATAGGAAT	YAKENRN	++−
92	11043	TTGTCCAAATTGAATTCCAAT	LSKLNSN	++−
93	11044	TTGGCGAAAGCGGGGATAAAT	LAKAGIN	++−
94	11045	CTGGCCAAGAACGGCATCAAC	LAKNGIN	++−
95	11046	GCCTCAGGCTCATCATCATGG	ASGSSSW	++−
96	11047	TACGCCCGCCTGGGCTCAAAC	YARLGSN	++−
97	11048	CTGTCACGCATGAACTTTAAC	LSRMNFN	++−
98	11049	TTGTCCAGGTCCGGGGATAAT	LSRSGDN	++−
99	11050	ATGACGAGGATAGAGAATAAT	MTRIENN	++−
100	11051	CGCATCACCCATCCCTACTCA	RITHPYS	++−
101	11052	ACCTCAGACTACATGTCATTT	TSDYMSF	++−
102	11053	TACGCCAAGACCGGCTGCAAC	YAKTGCN	++−
103	11054	TATTCCAAAGTGAATATGAAT	YSKVNMN	++−
104	11055	GAGCACGCGACGTCCAATTGG	EHATSNW	++−
105	11056	ATGATATCCACGAATGGGAGG	MISTNGR	++−
106	11057	TTGTCCAGGGCGGGGGATAAT	LSRAGDN	++−
107	11058	TTCTCCAAAATAAATTATAAT	FSKINYN	++−
108	11059	TATGCGAGGGTGGGGGATAAT	YARVGDN	++−
109	11060	TTCTCCAGGATAGGGGATAAT	FSRIGDN	++−
110	11061	TTCTCCAAAGCGGGGAATAAT	FSKAGNN	++−
111	11062	CATGAAGGCCATTCACATTGG	HEGHSHW	++−
112	11063	ACGGTGTCCACGAATGGGATA	TVSTNGI	++−
113	11064	AGGTCCGATACGGTGTATATA	RSDTVYI	++−
114	11065	TATTCCAAAGCGAATGATAAT	YSKANDN	++−
115	11066	TACTCAAAGAACAACTACAAC	YSKNNYN	++−
116	11067	TATTCCGCGAGGAATGATAAT	YSARNDN	++−
117	11068	GTACCCTCATCACAAGTATGG	VPSSQVW	++−
118	11069	TTCGCGTATGAGAATAGGAAT	FAYENRN	++−
119	11070	TTTTCAAAGCTGAACCCCAAC	FSKLNPN	++−
120	11071	TATTCCAGGAATGGGGATAAT	YSRNGDN	++−
121	11072	TATTCCAGGGCGTCCGATCAG	YSRASDQ	++−
122	11073	TATTTGAAATCCACGAATAAT	YLKSTNN	++−
123	11074	TTCTCCAAATTGAATCAGAAT	FSKLNQN	++−
124	11075	CAGCACAAATTGCAGCCGTTG	QHKLQPL	++−
125	11076	AATGCGGATTATAATAGGAAT	NADYNRN	++−
126	11077	TTGTCCAGGATAGGGGATAAT	LSRIGDN	++−
127	11078	TACGCCAAGCTGGGCCCCAAC	YAKLGPN	++
128	11079	TTGTCCAGGTTGGGGGATAAT	LSRLGDN	++
129	11080	TATGCGAGGGAGGGGTATAAT	YAREGYN	++
130	11081	CACCCGCCGGCGTATTCCTCC	HPPAYSS	++
131	11082	TATTCCAGGACGAATGATAAT	YSRTNDN	++
132	11083	TATGCGAGGTTGGGGGATAAT	YARLGDN	++
133	11084	TTTGCCAAGTCAGGCTTTAAC	FAKSGFN	++
134	11085	TATGCGAGGATGGGGCAGAAT	YARMGQN	++

135	11086	TTCGCGAGGACGTCCGATAAT	FARTSDN	++
136	11087	TTGTCCAAAATAGGGTTGAAT	LSKIGLN	++
137	11088	TTCACGTCCTCCAATGGGGTG	FTSSNGV	++
138	11089	TATGCGAGGGCGAATTTGAAT	YARANLN	++
139	11090	TTGTCCAAAATAGGGCAGAAT	LSKIGQN	++
140	11091	TTCGCGAGGACGGGGGATAAT	FARTGDN	++
141	11092	TTCGCGAAAACGGGGAATAAT	FAKTGNN	++
142	11093	TTCTCCAGGATAAATTTGAAT	FSRINLN	++
143	11094	GCGTCCGAGTTCATGACGTTC	ASEFMTF	++
144	11095	TTCTCCAGGGCGGGGGATAAT	FSRAGDN	++
145	11096	TATTCCAAAGCGGGGCAGAAT	YSKAGQN	++
146	11097	TTCTCCAGGGCGGGGTTCAAT	FSRAGFN	++
147	11098	TTTTCACGCTACGGCTCAAAC	FSRYGSN	++
148	11099	TATGCGAGGCAGAATACGAAT	YARQNTN	++
149	11100	ATGGTGTCCACGAATGGGGTG	MVSTNGV	++
150	11101	GCCAAGTCAACCAACGGCATC	AKSTNGI	++
151	11102	GTAGGCTCAGCCCATAACTGG	VGSAHNW	++
152	11103	TATTCCAAACAGAATACGAAT	YSKQNTN	++
153	11104	TTGGCGAGGTCCGGGGATAAT	LARSGDN	++
154	11105	ATATTGTCCACGAATGGGATA	ILSTNGI	++
155	11106	GTATTTTCAACCAACGGCATC	VFSTNGI	++
156	11107	TTGTTGTCCACGAATGGGAGG	LLSTNGR	++
157	11108	TATGCGAGGCAGGGGCAGAAT	YARQGQN	++
158	11109	TACTCACGCTCAGGCATCAAC	YSRSGIN	++
159	11110	TTGTCCAAAGTGGGGGATAAT	LSKVGDN	++
160	11111	TATTCCAAAGCGAATACGAAT	YSKANTN	++
161	11112	GGCGAATCAGACCGCAAGTGG	GESDRKW	++
162	11113	CTGTCAAAGATCGGCGTAAAC	LSKIGVN	++
163	11114	TTGGCGAAATCCGGGCAGAAT	LAKSGQN	++
164	11115	TATGCGAAATCCGGGCAGAAT	YAKSGQN	++
165	11116	TTCTCCAAATTGGGGCACAAT	FSKLGHN	++
166	11117	TATTCCAGGGTGAATGAGAAT	YSRVNEN	++
167	11118	TACTCAAAGAACAACCATAAC	YSKNNHN	++
168	11119	TTGTATTCCACGAATGGGATA	LYSTNGI	++
169	11120	TATGCGAGGCAGGGGATGAAT	YARQGMN	++
170	11121	TTGTCCAAAGTGGGGTCCAAT	LSKVGSN	++
171	11122	GAAATGGGCGGCGGCTCATGG	EMGGGSW	++
172	11123	TTCGCGAAATCCGGGCACAAT	FAKSGHN	++
173	11124	TATGCGAAATCCAATATGAAT	YAKSNMN	++
174	11125	TATGCGAAAGCGAATATGAAT	YAKANMN	++
175	11126	GACCTGTCACATGCCAAGTGG	DLSHAKW	++
176	11127	GGGGAGGGGATAGTGAGGTGG	GEGIVRW	++
177	11128	TATTCCAAAGGGAATGATAAT	YSKGNDN	++
178	11129	TATGCGAGGGTGGGGCAGAAT	YARVGQN	++
179	11130	TTGGCGAGGACGGGGGATAAT	LARTGDN	++

180	11131	TTGTCCAGGTCCAATGATAAT	LSRSNDN	++
181	11132	TCCGTGTCCACGAATGGGAGG	SVSTNGR	++
182	11133	TATTCCAAACACAATGTGAAT	YSKHNVN	++
183	11134	TATGCGAGGGCGAATGTGAAT	YARANVN	++
184	11135	TTGGCGAAAAATGGGAATAAT	LAKNGNN	++
185	11136	TTGCACAAATTGACGGTGTCC	LHKLTVS	++
186	11137	TTGGCGAAACAGGGGTTCAAT	LAKQGFN	++
187	11138	GGGAATGATATGTCCACGTGG	GNDMSTW	++
188	11139	TTTGTATCAACCAACGGCATC	FVSTNGI	++
189	11140	TTCTCCAGGATAAATGATAAT	FSRINDN	++
190	11141	TTTGCCCGCGCCGGCATGAAC	FARAGMN	++
191	11142	GGGTCCGGGATACAGAATTGG	GSGIQNW	++
192	11143	TATGTGTCCACGAATGGGGTG	YVSTNGV	++
193	11144	TTGTCCAAAGCGGGGTTCAAT	LSKAGFN	++
194	11145	TACTCAAAGGGCAACATGAAC	YSKGNMN	++
195	11146	TATGCGAGGCAGGGGGATAAT	YARQGDN	++
196	11147	TATGCGAAAACGGGGCAGAAT	YAKTGQN	++
197	11148	ACGAGGAATGGGAATATAGCG	TRNGNIA	++
198	11149	CAGGTGTCCACGAATGGGGTG	QVSTNGV	++
199	11150	TTTCATTCAACCAACGGCATC	FHSTNGI	++
200	11151	ACGAGGATAGGGAATAATGCG	TRIGNNA	++
201	11152	TTTGTACGCTCAGACATCAAG	FVRSDIK	++
202	11153	TTCTCCAAAACGGGGCCGAAT	FSKTGPN	++
203	11154	TTGTCCAAATTGGGGCCGAAT	LSKLGPN	++
204	11155	GTGAAATCCATGAATGGGGTG	VKSMNGV	++
205	11156	TTGTTCTCCACGAATGGGGTG	LFSTNGV	++
206	11157	TATGCGAGGTCCGGGGATAAT	YARSGDN	++
207	11158	TACTCAAAGCAAGGCTCAAAC	YSKQGSN	++
208	11159	TATGCGAAATTGAATTTCAAT	YAKLNFN	++
209	11160	ATAGAGTCCACGAATGGGGTG	IESTNGV	++
210	11161	TTGCACAGGGCGACGTATGAT	LHRATYD	++
211	11162	TTCGTGTCCACGAATGGGGTG	FVSTNGV	++
212	11163	TATGCGAAAGATAATTGGAAT	YAKDNWN	++
213	11164	CCGCAGTCCACGAATGGGGTG	PQSTNGV	++
214	11165	TATTCCAAATGGAATGATAAT	YSKWNDN	++
215	11166	CTGGCCAAGCAAGGCCATAAC	LAKQGHN	++
216	11167	TCCATATCCACGAATGGGAGG	SISTNGR	++
217	11168	TATGCGAAATTGGGGTTCAAT	YAKLGFN	++
218	11169	TTGCACAAAGCGTCCCCGACG	LHKASPT	++
219	11170	TATTCCTCCTTGAATCCGAAA	YSSLNPK	++
220	11171	TATGCGAGGACGAATGATAAT	YARTNDN	++
221	11172	TTGGCGAAAAATGGGTTCAAT	LAKNGFN	++
222	11173	TTGGCGAAATCCGGGATGAAT	LAKSGMN	++
223	11174	TTCTCCAAAGCGGGGATAAAT	FSKAGIN	++
224	11175	TTGTCCAAACAGGGGAATAAT	LSKQGNN	++

225	11176	TTCTCCAAAACGGGGTTCAAT	FSKTGFN	++
226	11177	TATTCCAAACAGGGGATGAAT	YSKQGMN	++
227	11178	TTGTCCAAAATGGGGCCGAAT	LSKMGPN	++
228	11179	TATGCGAGGTTGAATGATAAT	YARLNDN	++
229	11180	TATTCCAGGATGGGGGATAAT	YSRMGDN	++
230	11181	CGCAACGAAGGCTCATCATGG	RNEGSSW	++
231	11182	TACTCAAAGTCAGGCTACAAC	YSKSGYN	++
232	11183	TTGGCGAAACAGGGGTTGAAT	LAKQGLN	++
233	11184	CACAAATCCACGAATGGGTAT	HKSTNGY	++
234	11185	TTGTCCAAATTGGGGTTGAAT	LSKLGLN	++
235	11186	CAGGATGGGAATTCCAGGTAT	QDGNSRY	++
236	11187	TTGTCCAGGATGAATGATAAT	LSRMNDN	++
237	11188	CTGGCCAAGGGCGGCTTTAAC	LAKGGFN	++
238	11189	TTGTCCAAATCCGGGCCGAAT	LSKSGPN	++
239	11190	TTCATGTCCACGAATGGGGTG	FMSTNGV	++
240	11191	TATGGGTCCACGAATGGGGTG	YGSTNGV	++
241	11192	ATGTCCAAATTGAATGCGAAT	MSKLNAN	++
242	11193	AAATTGCCGGATTATGGGAAT	KLPDYGN	++
243	11194	TATGCGAAACAGGGGTTCAAT	YAKQGFN	++
244	11195	ACGCACTCCGGGAAATCCGCG	THSGKSA	++
245	11196	TTCTCCAGGACGGGGGATAAT	FSRTGDN	++
246	11197	TTGGCGAAATCCGGGTTGAAT	LAKSGLN	++
247	11198	TTTGCCCGCGCCGGCCCCAAC	FARAGPN	++
248	11199	TACTCAAAGATGAACACCAAC	YSKMNTN	++
249	11200	TTGCAGTCCACGAATGGGATA	LQSTNGI	++
250	11201	ATGACGTCCACGAATGGGGTG	MTSTNGV	++
251	11202	TATGCGAGGCCGGGGATAAAT	YARPGIN	++
252	11203	TATGCGAAAACGGGGTTCAAT	YAKTGFN	++
253	11204	TATGCGAAAAATGGGCACAAT	YAKNGHN	++
254	11205	TTCTCCAAAGTGGGGATGAAT	FSKVGMN	++
255	11206	TTGGCGAAAACGGGGATGAAT	LAKTGMN	++
256	11207	TTGTCCAAAACGGGGCCGAAT	LSKTGPN	++
257	11208	ATGTCCTCCACGAATGGGGTG	MSSTNGV	++
258	11209	TTGTCCAGGCAGAATGATAAT	LSRQNDN	++
259	11210	TATGCGAAATCCGGGGGGAAT	YAKSGGN	++
260	11211	TTGGCGAAAGCGGGGCACAAT	LAKAGHN	++
261	11212	TATTCCAAAACGGGGCACAAT	YSKTGHN	++
262	11213	TGGGCGTCCACGAATGGGGTG	WASTNGV	++
263	11214	ATAGTGTCCACGAATGGGATA	IVSTNGI	++
264	11215	TATGCGAAAGGGGGGCAGAAT	YAKGGQN	++
265	11216	TTCGCGAAAACGGGGCACAAT	FAKTGHN	++
266	11217	TTCGCGAAAGGGGGGATAAAT	FAKGGIN	++
267	11218	TATTCCAAACACAATGATAAT	YSKHNDN	++
268	11219	TTCTCCAAAGTGGGGGCGAAT	FSKVGAN	++
269	11220	TACGCCAAGAACGGCTACAAC	YAKNGYN	++

270	11221	TTCTCCAAAATAGGGCCGAAT	FSKIGPN	++
271	11222	TTTGCCAAGTCAGGCAACAAC	FAKSGNN	++
272	11223	TATTCCAGGCAGGGGACGAAT	YSRQGTN	++
273	11224	CACATATCCACGAATGGGGTG	HISTNGV	++
274	11225	TATGCGAGGGCGGGGCAGAAT	YARAGQN	++
275	11226	TACTCAAAGATGGGCATGAAC	YSKMGMN	++
276	11227	TTGGCGAAAACGGGGCACAAT	LAKTGHN	++
277	11228	TATTCCAAACAGAATCCGAAT	YSKQNPN	++
278	11229	TACGCCCGCGCCGGCAAGGAC	YARAGKD	++
279	11230	TATTCCAAAGTGGGGGATAAT	YSKVGDN	++
280	11231	TTTATCTCAACCAACGGCATC	FISTNGI	++
281	11232	TTCGCGTCCACGAATGGGATA	FASTNGI	++
282	11233	TTCTGGTCCGGGGAGGTGTCC	FWSGEVS	++
283	11234	TGCTCAGGCCGCCCCCAAGAA	CSGRPQE	++
284	11235	TTTGCCTCAACCAACGGCGTA	FASTNGV	++
285	11236	TTGTCCAAATCCTCCGTGAAT	LSKSSVN	++
286	11237	TTTGCCAAGGGCGGCTGGAAC	FAKGGWN	++
287	11238	TACTCAAAGCTGGGCATCAAC	YSKLGIN	++
288	11239	TTGTCCAAAGTGGGGATGAAT	LSKVGMN	++
289	11240	ACGTATTCCGGGAATAATGCG	TYSGNNA	++
290	11241	AGGTCCCCGGTGACGTTCCCG	RSPVTFP	++
291	11242	TTGGCGAGGCCGGGGCCGAAT	LARPGPN	++
292	11243	CTGGCCAAGGGCGGCATCAAC	LAKGGIN	++
293	11244	ATAGTGTCCACGAATGGGAGG	IVSTNGR	++
294	11245	TGGGAGTCCACGAATGGGGTG	WESTNGV	++
295	11246	TACGCCAAGAACGGCGTAAAC	YAKNGVN	++
296	11247	TTGTCCAGGACGGGGGAGAAT	LSRTGEN	++
297	11248	ACGAAATTGGGGGATAATGCG	TKLGDNA	++
298	11249	TTCTCCAAACAGGGGTATAAT	FSKQGYN	++
299	11250	TTCGATTCCACGAATGGGATA	FDSTNGI	++
300	11251	TATGCGAGGAATGGGGATAAT	YARNGDN	++
301	11252	TTGTCCAAAGTGGGGGAGAAT	LSKVGEN	++
302	11253	CTGTCAAAGCTGGGCATCAAC	LSKLGIN	++
303	11254	TATGCGAGGCAGGGGGAGAAT	YARQGEN	++
304	11255	TACGTATCAACCAACGGCATC	YVSTNGI	++
305	11256	CAGGAGTCCACGAATGGGGTG	QESTNGV	++
306	11257	TTGCACGCGAGGGGGTTGGAT	LHARGLD	++
307	11258	TATGCGAGGTTGAATGTGAAT	YARLNVN	++
308	11259	CCGTATGCGGTGTCCATGAAA	PYAVSMK	++
309	11260	TATTCCAAAGTGAATTTCAAT	YSKVNFN	++
310	11261	CTGTCAAAGACCGGCCATAAC	LSKTGHN	++
311	11262	GTGATGTCCACGAATGGGATA	VMSTNGI	++
312	11263	TTGGCGAAAACGGGGCAGAAT	LAKTGQN	++
313	11264	TATGCGAAAGGGGGGTTCAAT	YAKGGFN	++
314	11265	TTGTCCAAAGCGGGGCCGAAT	LSKAGPN	++

315	11266	TTTGCCAAGACCGGCATGAAC	FAKTGMN	++
316	11267	TTGTCCAAAGCGGGGATGAAT	LSKAGMN	++
317	11268	TATTCCAAACAGGGGGATAAT	YSKQGDN	++
318	11269	TATGCGAGGGATGGGTATAAT	YARDGYN	++
319	11270	TATTCCAGGCAGGGGATGAAT	YSRQGMN	++
320	11271	TTGGCGAAAACGGGGTTCAAT	LAKTGFN	++
321	11272	ACGTTGTCCACGAATGGGATA	TLSTNGI	++
322	11273	GCGATATCCACGAATGGGAGG	AISTNGR	++
323	11274	TATGCGAGGAATGGGCAGAAT	YARNGQN	++
324	11275	TATGCGAAACCGGGGAATAAT	YAKPGNN	++
325	11276	TTCTCCAAATTGAATACGAAT	FSKLNTN	++
326	11277	ATAAAATCCACGAATGGGGTG	IKSTNGV	++
327	11278	ACGTTGTCCGCGAATGGGAGG	TLSANGR	++
328	11279	AGGGAGTCCACGAATGGGGTG	RESTNGV	++
329	11280	TACGCCAAGCCCGGCTTTAAC	YAKPGFN	++
330	11281	TACGCCCGCGCCGGCATCAAC	YARAGIN	++
331	11282	GCGAAATCCACGAATGGGGTG	AKSTNGV	++
332	11283	GTGAAATATGATTGGTCCGAT	VKYDWSD	++
333	11284	TATCACAAAACGTCCTTGAAT	YHKTSLN	++
334	11285	TATGCGAAAGGGAATCCGAAT	YAKGNPN	++
335	11286	GAGTGGTCCACGAATGGGAGG	EWSTNGR	++
336	11287	TTGAAATCCACGAATGGGATA	LKSTNGI	++
337	11288	GTGGGGTCCACGAATGGGATA	VGSTNGI	++
338	11289	AGGGATGAGACGAGGTTGTGG	RDETRLW	++
339	11290	CTGGCCAAGCAAGGCATCAAC	LAKQGIN	++
340	11291	TATTCCAGGATGGGGGAGAAT	YSRMGEN	++
341	11292	GTGCAGTCCACGAATGGGATA	VQSTNGI	++
342	11293	TATTCCAAAACGGGGTTGAAT	YSKTGLN	++
343	11294	TACTCAAAGCAAGGCGTAAAC	YSKQGVN	++
344	11295	TTCTCCAAATTGAATTTGAAT	FSKLNLN	++
345	11296	TACGCCAAGTCAGGCCTGAAC	YAKSGLN	++
346	11297	TCAGAAACCTCATCACGCTGG	SETSSRW	++
347	11298	ATACCGCAGACGAATTATGCG	IPQTNYA	++
348	11299	GGCAACATGAACCGCTACGAC	GNMNRYD	++
349	11300	TTGTTGTCCACGAATGGGATA	LLSTNGI	++
350	11301	CACGGGGGGGCGTCCGCGTAT	HGGASAY	++
351	11302	GAGAAATCCACGAATGGGAGG	EKSTNGR	++
352	11303	TTGTCCAGGATGGGGGATAAT	LSRMGDN	++
353	11304	GGGAATGATGGGTCCAAATAT	GNDGSKY	++
354	11305	TATTCCAAAGGGAATACGAAT	YSKGNTN	++
355	11306	TTCGCGAAAACGGGGCCGAAT	FAKTGPN	++
356	11307	TATGCGAGGTTGGGGGTGAAT	YARLGVN	++
357	11308	TATTCCAAAGGGAATGTGAAT	YSKGNVN	++
358	11309	TACATGTCAACCAACGGCATC	YMSTNGI	++
359	11310	TCCTATTCCACGAATGGGATA	SYSTNGI	++

360	11311	TACTCAAAGTCAAACGTAAAC	YSKSNVN	++
361	11312	TCCTTGTCCACGAATGGGAGG	SLSTNGR	++
362	11313	TACTCACGCCATGGCACCAAC	YSRHGTN	++
363	11314	TATTCCAAAACGGGGGGGAAT	YSKTGGN	++
364	11315	TATTCCAAAGCGAATGCGAAT	YSKANAN	++
365	11316	CTGGCCAAGTCAGGCATCAAC	LAKSGIN	++
366	11317	CTGGCCAAGGGCGGCCAAAAC	LAKGGQN	++
367	11318	TACTCAAAGGGCAACCAAAAC	YSKGNQN	++
368	11319	TTGTCCAAAGCGGGGCAGAAT	LSKAGQN	++
369	11320	TGGGATTCCTCCAATGGGGTG	WDSSNGV	++
370	11321	TTGGCGAAATCCGGGTCCAAT	LAKSGSN	++
371	11322	TACTCAAAGTACGGCCCCAAC	YSKYGPN	++
372	11323	TTGTCCAAAGCGGGGCACAAT	LSKAGHN	++
373	11324	TTGTCCAAAATGAATTTGAAT	LSKMNLN	++
374	11325	TTGGCGAAAGGGGGGTTGAAT	LAKGGLN	++
375	11326	CTGTCAAAGGTAGGCCTGAAC	LSKVGLN	++
376	11327	TTTGCCAAGGGCGGCCATAAC	FAKGGHN	++
377	11328	GAGCAGTCCACGAATGGGAGG	EQSTNGR	++
378	11329	GGGGAGGTGAATGTGAGGTGG	GEVNVRW	++
379	11330	CCGATGTCCACGAATGGGAGG	PMSTNGR	++
380	11331	AATGTGTCCACGAATGGGAGG	NVSTNGR	++
381	11332	TATGCGAGGTTGAATGCGAAT	YARLNAN	++
382	11333	TTGGCGAAAAATGGGCACAAT	LAKNGHN	++
383	11334	AATACGTCCACGAATGGGGTG	NTSTNGV	++
384	11335	TTGGCGAGGAATGGGGATAAT	LARNGDN	++
385	11336	TACGCCAAGATCGGCCTGAAC	YAKIGLN	++
386	11337	TATTCCAAAACGGGGGATAAT	YSKTGDN	++
387	11338	ATCACCTCAACCAACGGCATC	ITSTNGI	++
388	11339	TACTCAAAGAACAACTTTAAC	YSKNNFN	++
389	11340	ACGTATTCCACGAATGGGATA	TYSTNGI	++
390	11341	GGGATGGATGGGAATAAATAT	GMDGNKY	++
391	11342	TTGATGTCCACGAATGGGATA	LMSTNGI	++
392	11343	ATGCAGTCCACGAATGGGGTG	MQSTNGV	++
393	11344	TATGCGAAAGCGGGGGCGAAT	YAKAGAN	++
394	11345	TTGGCGAAAACGGGGTCCAAT	LAKTGSN	++
395	11346	CTGTCAAAGATCGGCATGAAC	LSKIGMN	++
396	11347	TTCTCCAAAACGGGGAATAAT	FSKTGNN	++
397	11348	TATTCCAAAACGGGGGCGAAT	YSKTGAN	++
398	11349	GCGAATGGGAGGTCCTTGTAT	ANGRSLY	++
399	11350	TATGCGAAATCCGGGGTGAAT	YAKSGVN	++
400	11351	TACTCACGCATCAACATCAAC	YSRININ	++
401	11352	TATTCCAAAATAGGGGAGAAT	YSKIGEN	++
402	11353	CACATGTCCACGAATGGGGTG	HMSTNGV	++
403	11354	GCGCAGTCCACGAATGGGGTG	AQSTNGV	++
404	11355	CTGGCCAAGTCAGGCCATAAC	LAKSGHN	++

405	11356	TTGGCGAAAATGGGGTTCAAT	LAKMGFN	++
406	11357	AGGTCCGAGACGGTGTATCAG	RSETVYQ	++
407	11358	TATTCCAAATCCGGGACGAAT	YSKSGTN	++
408	11359	TACTCAAAGGGCAACGCCAAC	YSKGNAN	++
409	11360	GGGGGGTCCAATTCCTCCTGG	GGSNSSW	++
410	11361	GCGCACTCCACGAATGGGGTG	AHSTNGV	++
411	11362	TTGTCCAAAGCGGGGGTGAAT	LSKAGVN	++
412	11363	ATAGCGTCCACGAATGGGATA	IASTNGI	++
413	11364	AGGGAGCCGAATGTGCAGTGG	REPNVQW	++
414	11365	TATGCGTCCTCCGGGTATAAT	YASSGYN	++
415	11366	GTGTCCTCCTCCAATGGGGTG	VSSSNGV	++
416	11367	TTTGCCCGCTCAGGCGTAAAC	FARSGVN	++
417	11368	TATGCGAAAACGGGGTTGAAT	YAKTGLN	++
418	11369	TATGCGAGGTCCAATGATAAT	YARSNDN	++
419	11370	TTCGCGAGGAATGGGCAGAAT	FARNGQN	++
420	11371	TTGGCGAAACAGGGGCCGAAT	LAKQGPN	++
421	11372	AATCAGGCGGATTTGAGGTGG	NQADLRW	++
422	11373	GATCCGTCCGATAAAAGGTGG	DPSDKRW	++
423	11374	TTGTCCTCCACGAATGGGATA	LSSTNGI	++
424	11375	CACAAATCCACGAATGGGATA	HKSTNGI	++
425	11376	TATGCGAAAACGGGGGATAAT	YAKTGDN	++
426	11377	TACTCAAAGAACGGCCTGAAC	YSKNGLN	++
427	11378	TTCGCGAGGAATGGGATGAAT	FARNGMN	++
428	11379	GAAAAGTCAACCAACGGCATC	EKSTNGI	++
429	11380	ATAGGGGGGACGTCCAATTAT	IGGTSNY	++
430	11381	TACTCACGCGCCAACAACAAC	YSRANNN	++
431	11382	CTGTCAAAGCAAGGCTACAAC	LSKQGYN	++
432	11383	TTGGCGAAAACGGGGGTGAAT	LAKTGVN	++
433	11384	TATTCCAAAATAGGGACGAAT	YSKIGTN	++
434	11385	TATTCCAGGTTGGGGTTCAAT	YSRLGFN	++
435	11386	ATACACTCCTCCAATGGGGTG	IHSSNGV	++
436	11387	ATGTCAGAATCATCACGCTGG	MSESSRW	++
437	11388	TATTCCAGGAATGGGTTGAAT	YSRNGLN	++
438	11389	TTGGCGAAAACGGGGGCGAAT	LAKTGAN	++
439	11390	TTGGCGAGGGGGGGGGATAAT	LARGGDN	++
440	11391	TTTTCAAAGCTGAACATGAAC	FSKLNMN	++
441	11392	ACGAGGTCCGGGTCCTCCGCG	TRSGSSA	++
442	11393	TATGCGAAAGCGAATTTGAAT	YAKANLN	++
443	11394	TACGCCAAGCATGGCTTTAAC	YAKHGFN	++
444	11395	TCCGTGTCCACGAATGGGATA	SVSTNGI	++
445	11396	ATAGGGTCCACGAATGGGATA	IGSTNGI	++
446	11397	TTGTCCAAATTGAATCCGAAT	LSKLNPN	++
447	11398	TACTCAAAGACCGGCAACAAC	YSKTGNN	++
448	11399	TATTCCAAACACAATTCCAAT	YSKHNSN	++
449	11400	TTCGTGTCCACGAATGGGAGG	FVSTNGR	++

450	11401	TATGCGAAAGCGAATGTGAAT	YAKANVN	++
451	11402	ACGAATTCCACGCACGGGATA	TNSTHGI	++
452	11403	TTGTCCAAATCCGGGTTGAAT	LSKSGLN	++
453	11404	AGGGATGAGTTCAGGGCGTAT	RDEFRAY	++
454	11405	TTGGGGTCCACGAATGGGAGG	LGSTNGR	++
455	11406	CAGAAATCCACGAATGGGGTG	QKSTNGV	++
456	11407	TACTCAAAGGCCGGCGGCAAC	YSKAGGN	++
457	11408	GTGGTGTCCACGAATGGGGTG	VVSTNGV	++
458	11409	CCGAAATCCACGAATGGGGTG	PKSTNGV	++
459	11410	TCCGATTCCTCCAATGGGAGG	SDSSNGR	++
460	11411	TATTCCAAAGCGAATTCCAAT	YSKANSN	++
461	11412	CTGTCAAAGTCAGGCTTTAAC	LSKSGFN	++
462	11413	GCGACGTCCACGAATGGGGTG	ATSTNGV	++
463	11414	AGGGAGGGGACGTCCTATTAT	REGTSYY	++
464	11415	TTCTCCTCCACGAATGGGATA	FSSTNGI	++
465	11416	TATCAGTCCACGAATGGGATA	YQSTNGI	++
466	11417	TATGCGAGGTCCAATGAGAAT	YARSNEN	++
467	11418	CACGAGTCCACGAATGGGGTG	HESTNGV	++
468	11419	TCCACGTCCACGAATGGGATA	STSTNGI	++
469	11420	GTGTATTCCTCCAATGGGGTG	VYSSNGV	++
470	11421	GAGTCCTCCACGAATGGGAGG	ESSTNGR	++
471	11422	CTGGCCAAGATGGGCATGAAC	LAKMGMN	++
472	11423	ACGAAATCCACGAATGGGGTG	TKSTNGV	++
473	11424	TATGCGAAAGTGGGGCCGAAT	YAKVGPN	++
474	11425	AATGCGTCCACGAATGGGAGG	NASTNGR	++
475	11426	TACGCCCGCCTGGGCTTTAAC	YARLGFN	++
476	11427	ATGTCCGAGGCGTCCACGTGG	MSEASTW	++
477	11428	TTGGCGAAAATAGGGCCGAAT	LAKIGPN	++
478	11429	AATTCCGGGACGGCGAAATAT	NSGTAKY	++
479	11430	TTCTCCAAAGCGGGGCCGAAT	FSKAGPN	++
480	11431	TATGCGAAAGGGGGGGATAAT	YAKGGDN	++
481	11432	TTGGCGAAATCCGGGACGAAT	LAKSGTN	++
482	11433	CTGTCAAAGATGGGCCATAAC	LSKMGHN	++
483	11434	ACGACGTCCCAGAATGGGAGG	TTSQNGR	++
484	11435	TACTCACGCATCAACTTTAAC	YSRINFN	++
485	11436	TACGCCAAGGGCGGCAACAAC	YAKGGNN	++
486	11437	TTCTCCAGGCAGAATGATAAT	FSRQNDN	++
487	11438	ACGTATTCCACGAATGGGGTG	TYSTNGV	++
488	11439	TTCGCGAAAACGGGGTTCAAT	FAKTGFN	++
489	11440	GACGGCGGCACCTCACGCTAC	DGGTSRY	++
490	11441	CTGTCAAAGGGCAACTACAAC	LSKGNYN	++
491	11442	CACGATTCCTCCAATGGGGTG	HDSSNGV	++
492	11443	TTGAAAAATGGGCAGTCCGCG	LKNGQSA	++
493	11444	CAGGATACGTCCTCCAGGTGG	QDTSSRW	++
494	11445	TATGCGAAAGCGGGGTTGAAT	YAKAGLN	++

495	11446	CTGTCAAAGCAAAACATCAAC	LSKQNIN	++
496	11447	TTGCACTCCACGAATGGGGTG	LHSTNGV	++
497	11448	TATGAGTCCTCCAATGGGGTG	YESSNGV	++
498	11449	TATGCGAAATCCAATTTCAAT	YAKSNFN	++
499	11450	ACGGGGTCCACGAATGGGATA	TGSTNGI	++
500	11451	ACGCAGTCCACGAATGGGGTG	TQSTNGV	++
501	11452	TATGAGTCCACGAATGGGATA	YESTNGI	++
502	11453	ATGAAATCCACGAATGGGGTG	MKSTNGV	++
503	11454	TATTCCAAAGATAATTGGAAT	YSKDNWN	++
504	11455	CACGTGTCCACGAATGGGGTG	HVSTNGV	++
505	11456	TTGGTGTCCACGAATGGGGTG	LVSTNGV	++
506	11457	TTCTCCAAAGTGGGGACGAAT	FSKVGTN	++
507	11458	TACTCAAAGGCCGGCGTAAAC	YSKAGVN	++
508	11459	TTCGGGTCCACGAATGGGGTG	FGSTNGV	++
509	11460	TTGGCGAAAGGGGGGCACAAT	LAKGGHN	++
510	11461	GTGGCGTCCTCCAATGGGGTG	VASSNGV	++
511	11462	ATCAAGTCAACCAACGGCATC	IKSTNGI	++
512	11463	ACGAGGTCCGGGGATATAGCG	TRSGDIA	++
513	11464	TACTCAAAGGGCAACCTGAAC	YSKGNLN	++
514	11465	TTTGCCAAGCAAGGCTGGAAC	FAKQGWN	++
515	11466	TTGTCCAAAGCGGGGTTGAAT	LSKAGLN	++
516	11467	TCATTTTCAACCAACGGCATC	SFSTNGI	++
517	11468	TACTCACGCCCCGGCCATAAC	YSRPGHN	++
518	11469	ACGAGGGATACGAATGGGAGG	TRDTNGR	++
519	11470	TATGCGAAAACGGGGGGGAAT	YAKTGGN	++
520	11471	TATGCGAGGGGGAATGATAAT	YARGNDN	++
521	11472	GTGGCGTCCACGAATGGGATA	VASTNGI	++
522	11473	GCGCAGTCCACGAATGGGATA	AQSTNGI	++
523	11474	TTCGCGAAAACGGGGATAAAT	FAKTGIN	++
524	11475	AGGGCGTCCGATGTGTATCCG	RASDVYP	++
525	11476	CGCGGCTCAGACGTATTTCCC	RGSDVFP	++
526	11477	TTGGCGAAAGGGGGGCCGAAT	LAKGGPN	++
527	11478	TTGTCCAAAGCGGGGGCGAAT	LSKAGAN	++
528	11479	TACGCCAAGGGCAACTTTAAC	YAKGNFN	++
529	11480	GCGGATTCCACGAATGGGAGG	ADSTNGR	++
530	11481	CTGGCCAAGGCCGGCTACAAC	LAKAGYN	++
531	11482	CTGTCAAAGGTAGGCGTAAAC	LSKVGVN	++
532	11483	TACTCAAAGGGCAACATCAAC	YSKGNIN	++
533	11484	TGGTCCTCCTCCAATGGGGTG	WSSSNGV	++
534	11485	GCGGTGTCCACGAATGGGAGG	AVSTNGR	++
535	11486	CTGTCAAAGATCGGCAACAAC	LSKIGNN	++
536	11487	ATAGATTCCACGAATGGGGTG	IDSTNGV	++
537	11488	TCATCAGACTACAAGATCTAC	SSDYKIY	++
538	11489	TTCTCCAAAGCGGGGTTCAAT	FSKAGFN	++
539	11490	TTCGAGTCCACGAATGGGGTG	FESTNGV	++

540	11491	TCAAACTCACGCGAAGGCATC	SNSREGI	++
541	11492	TATTCCAAAGCGAATGTGAAT	YSKANVN	++
542	11493	TCCCACTCCACGAATGGGGTG	SHSTNGV	++
543	11494	TATTCCAGGGGGAATGAGAAT	YSRGNEN	++
544	11495	CTGTCAAAGACCGGCATCAAC	LSKTGIN	++
545	11496	TATTCCAAATCCAATGATAAT	YSKSNDN	++
546	11497	TATTCCAGGCACGGGTTCAAT	YSRHGFN	++
547	11498	TATGCGAGGTATGGGGATAAT	YARYGDN	++
548	11499	TATTCCAGGCAGAATGATAAT	YSRQNDN	++
549	11500	TTGTCCAAAGGGAATTTCAAT	LSKGNFN	++
550	11501	CAGAAATCCACGAATGGGATA	QKSTNGI	++
551	11502	TTCGCGAGGAATGGGGCGAAT	FARNGAN	++
552	11503	TTCATATCCACGAATGGGGTG	FISTNGV	++
553	11504	TACGCCAAGCAAGGCCTGAAC	YAKQGLN	++
554	11505	GATTATACGGGGAGGATAGCG	DYTGRIA	++
555	11506	ACGTATTCCTCCAATGGGGTG	TYSSNGV	++
556	11507	TCCAGGTCCACGAATGGGGCG	SRSTNGA	++
557	11508	TACTCAAAGCATAACGCCAAC	YSKHNAN	++
558	11509	TTGGCGAGGCCGGGGATAAAT	LARPGIN	++
559	11510	GTGCCGTATACGTCCTCCAAT	VPYTSSN	++
560	11511	TATCACTCCTCCAATGGGGTG	YHSSNGV	++
561	11512	TACCATAAGAACGGCTACAAC	YHKNGYN	++
562	11513	ATATTCTCCACGAATGGGGTG	IFSTNGV	++
563	11514	TTCTCCAAAGCGAATGTGAAT	FSKANVN	++
564	11515	TATGCGAAAAATGGGTCCAAT	YAKNGSN	++
565	11516	GCGGAGTCCACGAATGGGAGG	AESTNGR	++
566	11517	TATGCGAAAGCGGGGACGAAT	YAKAGTN	++
567	11518	CATATCTCAACCAACGGCATC	HISTNGI	++
568	11519	TATGCGAAAGCGGGGGTGAAT	YAKAGVN	++
569	11520	TTTTCAAAGACCGGCTACAAC	FSKTGYN	++
570	11521	TATGCGAGGGGGGGGGATAAT	YARGGDN	++
571	11522	GTGGAGTCCACGAATGGGGTG	VESTNGV	++
572	11523	TTCCAGTCCTCCAATGGGGTG	FQSSNGV	++
573	11524	TCACATTCATCAAACGGCGTA	SHSSNGV	++
574	11525	TATGCGAAATCCAATCACAAT	YAKSNHN	++
575	11526	TTGGCGAGGTTGGGGGATAAT	LARLGDN	++
576	11527	TTGCAGTCCACGAATGGGGTG	LQSTNGV	++
577	11528	TACTCAAAGGCCAACATCAAC	YSKANIN	++
578	11529	CACAATTCCTCCAATGGGGTG	HNSSNGV	++
579	11530	TTGTCCAAACAGGGGCCGAAT	LSKQGPN	++
580	11531	GTAATCTCAACCAACGGCATC	VISTNGI	++
581	11532	TTTGCCAAGTCAGGCCTGAAC	FAKSGLN	++
582	11533	TATGCGAAAGTGGGGGCGAAT	YAKVGAN	++
583	11534	TTGTCCTCCACGAATGGGGTG	LSSTNGV	++
584	11535	TATGCGAAAGGGGGGTCCAAT	YAKGGSN	++

585	11536	TTCTCCAAAGCGAATCACAAT	FSKANHN	++
586	11537	TTTATCTCAACCAACGGCCGC	FISTNGR	++
587	11538	TTGTCCAGGTTGTCCGAGACG	LSRLSET	++
588	11539	TGGCAGTCCTCCAATGGGATA	WQSSNGI	++
589	11540	TACTACTCAACCAACGGCGTA	YYSTNGV	++
590	11541	AATTGGTCCACGAATGGGGTG	NWSTNGV	++
591	11542	TACTCAAAGACCGGCATGAAC	YSKTGMN	++
592	11543	TTGTCCAAAGTGGGGACGAAT	LSKVGTN	++
593	11544	ACGCACTATGATAATGGGAGG	THYDNGR	++
594	11545	TATAGGTCCTCCAATGGGGTG	YRSSNGV	++
595	11546	AGGGAGTCCGATTTGAAATGG	RESDLKW	++
596	11547	TACGCCAAGTCAGGCTCAAAC	YAKSGSN	++
597	11548	TACGCCAAGGGCAACCTGAAC	YAKGNLN	++
598	11549	TATGCGAAATCCGGGACGAAT	YAKSGTN	++
599	11550	TACATCTCAACCAACGGCATC	YISTNGI	++
600	11551	GAGGATGGGTCCCCGAGGTGG	EDGSPRW	++
601	11552	TTGTCCAGGCAGGGGGATAAT	LSRQGDN	++
602	11553	CTGTCAAAGGTAGGCATCAAC	LSKVGIN	++
603	11554	TGGGGGTCCACGAATGGGGTG	WGSTNGV	++
604	11555	CTGTCAAAGCTGGGCAACAAC	LSKLGNN	++
605	11556	TATGCGTCCACGAATGGGGTG	YASTNGV	++
606	11557	TACTCAAAGATCGGCGTAAAC	YSKIGVN	++
607	11558	TACTCACGCAACGGCGTAAAC	YSRNGVN	++
608	11559	TACTCAAAGGTAGGCATCAAC	YSKVGIN	++
609	11560	TACTCACGCATCAACGACAAC	YSRINDN	++
610	11561	CTGTCAAAGATCGGCATCAAC	LSKIGIN	++
611	11562	GTGGGGTCCTCCAATGGGGTG	VGSSNGV	++
612	11563	ACGATATCCACGAATGGGATA	TISTNGI	++
613	11564	TACTCAAAGAAGAACGAAAAC	YSKKNEN	++
614	11565	TTGGCGAGGTCCGGGGAGAAT	LARSGEN	++
615	11566	GTGAGGTCCACGAATGGGGAG	VRSTNGE	++
616	11567	TATGCGAAAGGGAATACGAAT	YAKGNTN	++
617	11568	CAGGGGTCCACGAATGGGAGG	QGSTNGR	++
618	11569	TTCTCCAAAGTGGGGTTGAAT	FSKVGLN	++
619	11570	CTGGCCAAGGGCGGCATGAAC	LAKGGMN	++
620	11571	TTGGTGTCCACGAATGGGAGG	LVSTNGR	++
621	11572	TTGGCGAAATCCGGGGTGAAT	LAKSGVN	++
622	11573	TACTCAAAGCCCGGCCCCAAC	YSKPGPN	++
623	11574	TATTCCAAAACGGGGACGAAT	YSKTGTN	++
624	11575	CGCAAGGACGGCACCGCCTCA	RKDGTAS	++
625	11576	ACGCAGTCCTCCAATGGGGTG	TQSSNGV	++
626	11577	TACTCAAAGCATAACAACAAC	YSKHNNN	++
627	11578	TACTCAAAGGTAAACTACAAC	YSKVNYN	++
628	11579	CTGTCAAAGCTGAACCAAAAC	LSKLNQN	++
629	11580	CTGGCCAAGCTGGGCATCAAC	LAKLGIN	++

630	11581	TATGCGAGGGTGGGGTTCAAT	YARVGFN	++
631	11582	CAAAACGGCCATTCATCATGG	QNGHSSW	++
632	11583	TACTCAAAGTCAGGCGTAAAC	YSKSGVN	++
633	11584	GGCGGCGACGGCAACGCCTAC	GGDGNAY	++
634	11585	TATGCGAGGGCGAATGATAAT	YARANDN	++
635	11586	GTGTTGTCCACGAATGGGGTG	VLSTNGV	++
636	11587	ACGGATGAGACGGTGTATTCC	TDETVYS	++
637	11588	ATAACGTCCTCCAATGGGGTG	ITSSNGV	++
638	11589	ATGATGTCCACGAATGGGGTG	MMSTNGV	++
639	11590	TTGTCCAAAATAGGGACGAAT	LSKIGTN	++
640	11591	AGGTCCGATACGTCCATATGG	RSDTSIW	++
641	11592	TCCTTCTCCACGAATGGGGTG	SFSTNGV	++
642	11593	TTCTCCAAATTGGGGGCGAAT	FSKLGAN	++
643	11594	TCAGAATCAACCAACGGCATC	SESTNGI	++
644	11595	TATGCGAAAGCGGGGTCCAAT	YAKAGSN	++
645	11596	ATCGAATCAACCAACGGCATC	IESTNGI	++
646	11597	CAGTCCTCCACGAATGGGGTG	QSSTNGV	++
647	11598	TTTTCATCATCAAACGGCGTA	FSSSNGV	++
648	11599	TATGCGAAAGGGGGGATGAAT	YAKGGMN	++
649	11600	TACGCCCGCGCCAACATGAAC	YARANMN	++
650	11601	TATGCGAAAGGGGGGGCGAAT	YAKGGAN	++
651	11602	TATGCGAAAAATGGGCAGAAT	YAKNGQN	++
652	11603	GGGACGTCCACGAATGGGAGG	GTSTNGR	++
653	11604	TACGCCAAGACCAACTACAAC	YAKTNYN	++
654	11605	AGGGCGGAGTCCAAAACGTGG	RAESKTW	++
655	11606	TCCACGTCCCAGAATGGGAGG	STSQNGR	++
656	11607	CCGAATTCCACGAATGGGGTG	PNSTNGV	++
657	11608	TTCGCGAGGAATGGGACGAAT	FARNGTN	++
658	11609	CTGTCAAAGGTAGGCAACAAC	LSKVGNN	++
659	11610	TTTGCCCGCAACGGCGTAAAC	FARNGVN	++
660	11611	TTTTCACGCGTAGGCGACAAC	FSRVGDN	++
661	11612	TATGCGAAAATAGGGGCGAAT	YAKIGAN	++
662	11613	AATGAGGATTTCGTGAGGTAT	NEDFVRY	++
663	11614	GTGGATGAGTTCAGGACGTAT	VDEFRTY	++
664	11615	ACGGATTCCACGAATGGGATA	TDSTNGI	++
665	11616	AGGCACGATCAGGTGTATCCG	RHDQVYP	++
666	11617	TATAGGTCCACGAATGGGTAT	YRSTNGY	++
667	11618	CATTCACGCCTGAACGTAGAA	HSRLNVE	++
668	11619	GAGAGGTCCACGAATGGGGTG	ERSTNGV	++
669	11620	CTGTCAAAGTCAGGCCATAAC	LSKSGHN	++
670	11621	TTTTCACGCACCGGCGAAAAC	FSRTGEN	++
671	11622	GGCTCATCAACCAACGGCCGC	GSSTNGR	++
672	11623	TACTCACGCAACGGCATGAAC	YSRNGMN	++
673	11624	TTGTCCAAAGCGAATTTCAAT	LSKANFN	++
674	11625	TGGGAGTCCTCCAATGGGGTG	WESSNGV	++

675	11626	ATAGAGTCCTCCAATGGGGTG	IESSNGV	++
676	11627	TTCGCGAGGAATGGGTTCAAT	FARNGFN	++
677	11628	GTGATGTCCTCCAATGGGGTG	VMSSNGV	++
678	11629	TACTCAAAGCATAACTTTAAC	YSKHNFN	++
679	11630	TACTCAAAGAACGGCTTTAAC	YSKNGFN	++
680	11631	TATGCGAAAGAGGGGAGGAAT	YAKEGRN	++
681	11632	TATTCCAAAAATGGGTCCAAT	YSKNGSN	++
682	11633	GCGTCCTCCACGAATGGGGTG	ASSTNGV	++
683	11634	TACGCCAAGCTGGGCATGAAC	YAKLGMN	++
684	11635	TCCTGGTCCTCCAATGGGGTG	SWSSNGV	++
685	11636	AGGAATTTGGATGTGACGTGG	RNLDVTW	++
686	11637	CCGCAGTCCTCCAATGGGGTG	PQSSNGV	++
687	11638	TACTTTACCGGCACCTCATCA	YFTGTSS	++
688	11639	TTGATGTCCACGAATGGGGTG	LMSTNGV	++
689	11640	TACTCAAAGTCAGGCAACAAC	YSKSGNN	++
690	11641	GGGTGGTCCACGAATGGGGTG	GWSTNGV	++
691	11642	ACGAAATCCGGGATGAATGCG	TKSGMNA	++
692	11643	TACTCACGCCAAGGCAACAAC	YSRQGNN	++
693	11644	ACCGAATCAACCAACGGCATC	TESTNGI	++
694	11645	GTGCCGTATACGGGGTATGAT	VPYTGYD	++
695	11646	TTGTCCGCGAGGTCCGATAAT	LSARSDN	++
696	11647	CAGGATTCCACGAATGGGATA	QDSTNGI	++
697	11648	TACTCAAAGTCAGGCATGAAC	YSKSGMN	++
698	11649	ACCCAATCATCATCAGGCCGC	TQSSSGR	++
699	11650	TTGTCCAGGAATAATGATAAT	LSRNNDN	++
700	11651	TATGCGAGGTCCGGGGAGAAT	YARSGEN	++
701	11652	CAGGTGTCCACGAATGGGAGG	QVSTNGR	++
702	11653	TTGTCCAAATTGGGGACGAAT	LSKLGTN	++
703	11654	TACTCACGCAACAACAACAAC	YSRNNNN	++
704	11655	TTGTCCAAAGCGGGGTCCAAT	LSKAGSN	++
705	11656	TTGCACGTGCAGGGGCCGAAT	LHVQGPN	++
706	11657	CACTTCTCCTCCAATGGGGTG	HFSSNGV	++
707	11658	TACTCAAAGTCAAACCATAAC	YSKSNHN	++
708	11659	ACGTTCTCCTCCAATGGGGTG	TFSSNGV	++
709	11660	TACTCAAAGATGGGCCTGAAC	YSKMGLN	++
710	11661	TACTCAAAGGTAGGCGGCAAC	YSKVGGN	++
711	11662	TTGTCCAAAATAGGGGATAAT	LSKIGDN	++
712	11663	GTGGCGTCCACGAATGGGGTG	VASTNGV	++
713	11664	TCCGATTCCACGAATGGGGTG	SDSTNGV	++
714	11665	TTGATATCCACGAATGGGGTG	LISTNGV	++
715	11666	TACTCAAAGTCAGGCGGCAAC	YSKSGGN	++
716	11667	TACTCAAAGACCGGCTCAAAC	YSKTGSN	++
717	11668	TTGGCGAGGAATGGGTGGAAT	LARNGWN	++
718	11669	ATGGCGTCCACGAATGGGGTG	MASTNGV	++
719	11670	TTCTCCAGGCAGAATGTGAAT	FSRQNVN	++

720	11671	GTGAAATCCTCCAATGGGGTG	VKSSNGV	++
721	11672	TATGCGAGGTCCAATTTCAAT	YARSNFN	++
722	11673	TTGGCGAAAGGGGGGGCGAAT	LAKGGAN	++
723	11674	TTTGCCAAGAACGGCTACAAC	FAKNGYN	++
724	11675	TTCGATTCCACGAATGGGGTG	FDSTNGV	++
725	11676	TTGTCCAAATCCGGGGCGAAT	LSKSGAN	++
726	11677	TATGCGAAAGCGGGGATGAAT	YAKAGMN	++
727	11678	TTCTCCAAACAGGGGCCGAAT	FSKQGPN	++
728	11679	ATGGTGTCCACGAATGGGAGG	MVSTNGR	++
729	11680	GTGATATCCTCCAATGGGGTG	VISSNGV	++
730	11681	TTCTCCAGGATGAATGAGAAT	FSRMNEN	++
731	11682	TATGCGAGGATGGGGGATAAT	YARMGDN	++
732	11683	TACTCAAAGCAAAACGCCAAC	YSKQNAN	++
733	11684	CGCGAATCAACCAACGGCATC	RESTNGI	++
734	11685	TTGTCCAAAGGGAATGTGAAT	LSKGNVN	++
735	11686	TTGTCCAAATTGGGGTCCAAT	LSKLGSN	++
736	11687	TATGCGAAATTGGGGTTGAAT	YAKLGLN	++
737	11688	TACTCAAAGCAAAACCTGAAC	YSKQNLN	++
738	11689	TTGTCCAAAGCGAATCACAAT	LSKANHN	++
739	11690	GTACTGTCAACCAACGGCATC	VLSTNGI	++
740	11691	CATCGCTCAACCAACGGCCAA	HRSTNGQ	++
741	11692	ACGACGTCCACGAATGGGGTG	TTSTNGV	++
742	11693	TTCTCCAAAATGAATGTGAAT	FSKMNVN	++
743	11694	GGGGCGGATGGGTCCAGGTGG	GADGSRW	++
744	11695	GCGGCGTCCACGAATGGGATA	AASTNGI	++
745	11696	TTGGCGAAAGGGGGGGTGAAT	LAKGGVN	++
746	11697	GGCATGAAGAACGTAATGTTT	GMKNVMF	++
747	11698	CATGAATCAACCAACGGCATC	HESTNGI	++
748	11699	TACTCAAAGATGGGCTCAAAC	YSKMGSN	++
749	11700	AATAATGGGGGGTCCTTGTGG	NNGGSLW	++
750	11701	CTGATGTCAACCAACGGCCGC	LMSTNGR	++
751	11702	GCGGTGTCCACGAATGGGGTG	AVSTNGV	++
752	11703	TATTCCAGGCAGAATACGAAT	YSRQNTN	++
753	11704	TTCTCCAAAGTGGGGCACAAT	FSKVGHN	++
754	11705	TATCACAGGCAGGGGGGGGAT	YHRQGGD	++
755	11706	TTCGCGAGGACGGGGGAGAAT	FARTGEN	++
756	11707	AGGGCGTTGGAGGGGGCGGAT	RALEGAD	++
757	11708	TATGCGAAATCCAATGATAAT	YAKSNDN	++
758	11709	TTGAGGAATGGGAATTCCGCG	LRNGNSA	++
759	11710	TTGTTGTCCACGAATGGGGTG	LLSTNGV	++
760	11711	TTGGCGAAATCCGGGGAGAAT	LAKSGEN	++
761	11712	TATGCGAAAACGAATATGAAT	YAKTNMN	++
762	11713	CGCCGCGACGGCACCGCCTAC	RRDGTAY	++
763	11714	TCCACGTCCACGAATGGGGTG	STSTNGV	++
764	11715	TACTCAAAGTACAACCTGAAC	YSKYNLN	++

765	11716	GATGGGGGGACGTCCCACTAT	DGGTSHY	++
766	11717	ATGGAGTCCACGAATGGGAGG	MESTNGR	++
767	11718	CATCAATCAACCAACGGCATC	HQSTNGI	++
768	11719	CTGGCCAAGGGCGGCAACAAC	LAKGGNN	++
769	11720	TCCGAGTCCACGAATGGGAGG	SESTNGR	++
770	11721	TACTCAAAGCATGGCAACAAC	YSKHGNN	++
771	11722	TTGCCGAGGGAGGTGTATGCG	LPREVYA	++
772	11723	CAAATGTCAACCAACGGCCGC	QMSTNGR	++
773	11724	TATTCCAAACAGAATGTGAAT	YSKQNVN	++
774	11725	TATGCGAGGGAGGGGCCGAAT	YAREGPN	++
775	11726	AAGGACGGCGAATCATCATGG	KDGESSW	++
776	11727	TATGCGAGGGCGGGGGATAAT	YARAGDN	++
777	11728	TTCTCCAAAGTGGGGGATAAT	FSKVGDN	++
778	11729	GCGGCGTCCACGAATGGGGTG	AASTNGV	++
779	11730	CTGTCAAAGATGGGCTTTAAC	LSKMGFN	++
780	11731	CAACGCTACGACGCCTACGAA	QRYDAYE	++
781	11732	ACGATATCCACGAATGGGGTG	TISTNGV	++
782	11733	GAGGGGTCCACGAATGGGAGG	EGSTNGR	++
783	11734	TATGCGAAATCCGGGGAGAAT	YAKSGEN	++
784	11735	CTGGCCAAGACCGGCAACAAC	LAKTGNN	++
785	11736	AACTTTTCAACCAACGGCATC	NFSTNGI	++
786	11737	CTGGCCAAGGTAGGCTACAAC	LAKVGYN	++
787	11738	ATAGCGTCCACGAATGGGGTG	IASTNGV	++
788	11739	CGCGGCGCCGACGTACATTGG	RGADVHW	++
789	11740	TTTTCAAAGCTGAACGAAAAC	FSKLNEN	++
790	11741	TATTTCTCCGGGACGACGGAT	YFSGTTD	++
791	11742	TTGGCGAAAATGGGGCCGAAT	LAKMGPN	++
792	11743	TACTCAAAGATCAACCATAAC	YSKINHN	++
793	11744	GTGGAGTTCGAGTGGTCCGAT	VEFEWSD	++
794	11745	TACGCCCGCCTGAACTTTAAC	YARLNFN	++
795	11746	TACTCAAAGCATAACATCAAC	YSKHNIN	++
796	11747	GCGATGTCCACGAATGGGGTG	AMSTNGV	++
797	11748	TTGGCGAAATTGGGGTTGAAT	LAKLGLN	++
798	11749	CTGGCCAAGTCAGGCAACAAC	LAKSGNN	++
799	11750	CACTTCTCCACGAATGGGATA	HFSTNGI	++
800	11751	CACGCGTCCTCCAATGGGGTG	HASSNGV	++
801	11752	CAACAATCAACCAACGGCATC	QQSTNGI	++
802	11753	TACTCACGCTCAAACATCAAC	YSRSNIN	++
803	11754	TCCAATGAGTCCTCCACGTGG	SNESSTW	++
804	11755	TATGCGAAACAGGGGGCGAAT	YAKQGAN	++
805	11756	CCGGCGTCCACGAATGGGAGG	PASTNGR	++
806	11757	GTGTTCTCCACGAATGGGGTG	VFSTNGV	++
807	11758	TATTCCAAAATGGGGGATAAT	YSKMGDN	++
808	11759	TACTCAAAGTGGGGCGCCAAC	YSKWGAN	++
809	11760	TACTCAAAGACCGGCGTAAAC	YSKTGVN	++

810	11761	TTGGCGAAAGCGGGGGTGAAT	LAKAGVN	++
811	11762	TTGTCCAGGATAGGGGAGAAT	LSRIGEN	++
812	11763	TACTCAAAGTCAAACCTGAAC	YSKSNLN	++
813	11764	TATTCCAGGACGAATGAGAAT	YSRTNEN	++
814	11765	GTGGGGTCCACGAATGGGGTG	VGSTNGV	++
815	11766	TATGCGAAAACGGGGGCGAAT	YAKTGAN	++
816	11767	GGGTCCGAGAGGTCCTCCTGG	GSERSSW	++
817	11768	TTGTCCAAAATGAATGATAAT	LSKMNDN	++
818	11769	CAGCAGTCCACGAATGGGGTG	QQSTNGV	++
819	11770	TATGCGAGGCAGAATGATAAT	YARQNDN	++
820	11771	CACAATTCCACGAATGGGATA	HNSTNGI	++
821	11772	TTTTCACGCACCGGCCAAAAC	FSRTGQN	++
822	11773	CCGCAGTCCACGAATGGGATA	PQSTNGI	++
823	11774	TCCCAGTCCACGAATGGGGTG	SQSTNGV	++
824	11775	CCGTGGTCCTCCAATGGGGTG	PWSSNGV	++
825	11776	ATAATGTCCACGAATGGGGTG	IMSTNGV	++
826	11777	TCCAAATCCACGAATGGGATA	SKSTNGI	++
827	11778	TGGAATTCCTCCAATGGGGTG	WNSSNGV	++
828	11779	TATGCGAGGATAGGGGAGAAT	YARIGEN	++
829	11780	TTGTCCGGGGAGTCCAGGTAT	LSGESRY	++
830	11781	TATGCGAGGAATGGGGGGAAT	YARNGGN	++
831	11782	GATAATAGGGGGAATAATGCG	DNRGNNA	++
832	11783	TTGGAGTCCACGAATGGGAGG	LESTNGR	++
833	11784	TTGGCGAAACAGGGGATGAAT	LAKQGMN	++
834	11785	TTCACGTCCACGAATGGGGTG	FTSTNGV	++
835	11786	AATGAGTCCACGAATGGGGTG	NESTNGV	++
836	11787	ACGCACTCCACGAATGGGATA	THSTNGI	++
837	11788	TACGTACATTCACAAAACTAC	YVHSQNY	++
838	11789	AATGATGGGAGGTCCAATTAT	NDGRSNY	++
839	11790	TATGCGAAAGTGGGGATGAAT	YAKVGMN	++
840	11791	TTGGCGAAATCCGGGGCGAAT	LAKSGAN	++
841	11792	TATTCCAGGCACAATGAGAAT	YSRHNEN	++
842	11793	TATGCGAAAGCGAATCCGAAT	YAKANPN	++
843	11794	AGGTCCGAGGCGACGTATCCG	RSEATYP	++
844	11795	TTGTCCAGGTCCGGGGAGAAT	LSRSGEN	++
845	11796	TACTCAAAGATGAACCTGAAC	YSKMNLN	++
846	11797	TATGCGAAAAATGGGATGAAT	YAKNGMN	++
847	11798	TTCCACTCCTCCAATGGGGTG	FHSSNGV	++
848	11799	TTGTCCAGGGCGGGGGAGAAT	LSRAGEN	++
849	11800	TTGGGGTCCACGAATGGGATA	LGSTNGI	++
850	11801	TATTCCTCCTCCAATGGGGTG	YSSSNGV	++
851	11802	TTGGCGAAACAGGGGGTGAAT	LAKQGVN	++
852	11803	TTCTCCAGGCAGGGGATGAAT	FSRQGMN	++
853	11804	TCAGCCTCAACCAACGGCATC	SASTNGI	++
854	11805	CAGATGTCCACGAATGGGGTG	QMSTNGV	++

855	11806	TTGTCCAAAAATAATGTGAAT	LSKNNVN	++
856	11807	CACGCGTCCACGAATGGGATA	HASTNGI	++
857	11808	ACGCCGGATCACGTGCAGTGG	TPDHVQW	++
858	11809	AGGTTGGAGACGCACGATTGG	RLETHDW	++
859	11810	GGCACCTCAACCGCCTCATGG	GTSTASW	++
860	11811	TACTCAAAGAACGGCCATAAC	YSKNGHN	++
861	11812	TATTCCAAACACAATACGAAT	YSKHNTN	++
862	11813	TATTCCAGGCACGGGGAGAAT	YSRHGEN	++
863	11814	TTGGCGAGGCAGGGGGATAAT	LARQGDN	++
864	11815	TTTTCAAAGATCGGCATCAAC	FSKIGIN	++
865	11816	TACTCAAAGCTGGGCGACAAC	YSKLGDN	++
866	11817	TACTCAAAGCTGAACGGCAAC	YSKLNGN	++
867	11818	TACTCACGCAACGGCCAAAAC	YSRNGQN	++
868	11819	ATATCCTCCACGAATGGGGTG	ISSTNGV	++
869	11820	TACGCCCTGTCAGGCTTTAAC	YALSGFN	++
870	11821	CCGATATCCACGAATGGGAGG	PISTNGR	++
871	11822	ATGTTTTCAACCAACGGCATC	MFSTNGI	++
872	11823	CTGTCAAAGATGAACCATAAC	LSKMNHN	++
873	11824	ACCGACGGCCAATCAGGCTGG	TDGQSGW	++
874	11825	GCGATATCCACGAATGGGGTG	AISTNGV	++
875	11826	GTGACGTCCACGAATGGGATA	VTSTNGI	++
876	11827	TTGGCGAAAACGGGGGATAAT	LAKTGDN	++
877	11828	TACTCAAAGGGCGGCTTTAAC	YSKGGFN	++
878	11829	CTGTCAAAGCTGAACATGAAC	LSKLNMN	++
879	11830	TACCAATCATCAAACGGCGTA	YQSSNGV	++
880	11831	TTGACGTCCACGAATGGGGTG	LTSTNGV	++
881	11832	CTGTCAAAGCAAAACGTAAAC	LSKQNVN	++
882	11833	CTGTCAAAGCAAGGCCATAAC	LSKQGHN	++
883	11834	GATGCGTTGCACGGGAGGAAT	DALHGRN	++
884	11835	TATTCCAAAGTGAATTCCAAT	YSKVNSN	++
885	11836	TTCGAGTCCTCCAATGGGGTG	FESSNGV	++
886	11837	TATTCCAAAGTGAATGTGAAT	YSKVNVN	++
887	11838	TTCTCCAAAGTGGGGGTGAAT	FSKVGVN	++
888	11839	ACGTCCGGGTCCTCCTCCTGG	TSGSSSW	++
889	11840	ACGATGTCCACGAATGGGGTG	TMSTNGV	++
890	11841	CACAATTCCACGAATGGGGTG	HNSTNGV	++
891	11842	ATGCACTCCACGAATGGGATA	MHSTNGI	++
892	11843	TATGCGAAAGGGAATCAGAAT	YAKGNQN	++
893	11844	TCAAACTCAACCAACGGCATC	SNSTNGI	++
894	11845	TACTCAAAGGCCGGCACCAAC	YSKAGTN	++
895	11846	ACGGAGTCCACGAATGGGGTG	TESTNGV	++
896	11847	AATGTGGATCACGTGTCCTGG	NVDHVSW	++
897	11848	ACGGATTCCACGAATGGGGTG	TDSTNGV	++
898	11849	TTTTCAAAGTCAGGCCATAAC	FSKSGHN	++
899	11850	TCAATCTCAACCAACGGCATC	SISTNGI	++

900	11851	TCCATGTCCACGAATGGGATA	SMSTNGI	++
901	11852	TCCATGTCCACGAATGGGGTG	SMSTNGV	++
902	11853	CACCAGTCCACGAATGGGGTG	HQSTNGV	++
903	11854	CAGGCGTCCACGAATGGGGTG	QASTNGV	++
904	11855	CCGCACTCCACGAATGGGGTG	PHSTNGV	++
905	11856	AGGTTGTCCGAGTCCAATTGG	RLSESNW	++
906	11857	GAGCACTCCACGAATGGGAGG	EHSTNGR	++
907	11858	ATGCACTCCACGAATGGGGTG	MHSTNGV	++
908	11859	GTGACGTCCTCCATGGGGAGG	VTSSMGR	++
909	11860	TACTCAAAGTCAGGCATCAAC	YSKSGIN	++
910	11861	TTTTCAAAGGACAACTTTAAC	FSKDNFN	++
911	11862	TACTCAAAGGGCAACAACAAC	YSKGNNN	++
912	11863	ACGAAATCCTCCAATGGGGTG	TKSSNGV	++
913	11864	ACGGCGTCCACGAATGGGATA	TASTNGI	++
914	11865	TACTCAAAGATCGGCCAAAAC	YSKIGQN	++
915	11866	CACACGTCCACGAATGGGATA	HTSTNGI	++
916	11867	TCCGATTCCACGAATGGGATA	SDSTNGI	++
917	11868	TTGGCGAAACACGGGGCGAAT	LAKHGAN	++
918	11869	GCGGAGTCCACGAATGGGGTG	AESTNGV	++
919	11870	TACCTGTCAACCAACGGCGTA	YLSTNGV	++
920	11871	TTGGCGAAAATGGGGGTGAAT	LAKMGVN	++
921	11872	TCCGCGTCCTCCAATGGGGTG	SASSNGV	++
922	11873	GTAGTATCATCAAACGGCGTA	VVSSNGV	++
923	11874	GCGATATCCACGAATGGGATA	AISTNGI	++
924	11875	CACACGTCCACGAATGGGGTG	HTSTNGV	++
925	11876	TTTGCCAAGGGCGGCATGAAC	FAKGGMN	++
926	11877	GGGGGGGGGACGAATGCGTGG	GGGTNAW	++
927	11878	ACGAATTCCACGAATGGGGTG	TNSTNGV	++
928	11879	TATGCGAAAAATGGGTTGAAT	YAKNGLN	++
929	11880	TACTCAAAGGCCAACCAAAAC	YSKANQN	++
930	11881	GTGGAGTATGGGCAGAGGAAT	VEYGQRN	++
931	11882	GCGTCCTCCACGAATGGGATA	ASSTNGI	++
932	11883	CTGTCAAAGATGGGCAACAAC	LSKMGNN	++
933	11884	TATGCGAAACAGGGGGTGAAT	YAKQGVN	++
934	11885	CCGGAGTCCACGAATGGGGTG	PESTNGV	++
935	11886	CATTACTCAACCAACGGCATC	HYSTNGI	++
936	11887	CTGTCAAAGGTAGGCCCCAAC	LSKVGPN	++
937	11888	ACGGCGTCCTCCAATGGGGTG	TASSNGV	++
938	11889	ATAAATTCCACGAATGGGATA	INSTNGI	++
939	11890	TATGCGAGGGATGGGCCGAAT	YARDGPN	++
940	11891	TACTCAAAGATGAACATCAAC	YSKMNIN	++
941	11892	TTGAATTCCACGAATGGGGTG	LNSTNGV	++
942	11893	TATTCCAAACAGAATGAGAAT	YSKQNEN	++
943	11894	TATGCGAAAGGGAATCACAAT	YAKGNHN	++
944	11895	GAGGTGTCCACGAATGGGAGG	EVSTNGR	++

945	11896	TATGCGAAAGGGAATGATAAT	YAKGNDN	++
946	11897	TCAGACGGCTCATCACTGTGG	SDGSSLW	++
947	11898	ACGTTCTCCACGAATGGGGTG	TFSTNGV	++
948	11899	CTGTCAAAGACCGGCGTAAAC	LSKTGVN	++
949	11900	TACTCACGCAACGGCTACAAC	YSRNGYN	++
950	11901	TATGCGAGGACGTCCACGGAT	YARTSTD	++
951	11902	TTGTCCAAAGCGGGGACGAAT	LSKAGTN	++
952	11903	TATTCCAAACAGGGGGAGAAT	YSKQGEN	++
953	11904	TTCGCGAAATCCGGGGCGAAT	FAKSGAN	++
954	11905	TTGGCGAGGCAGGGGGAGAAT	LARQGEN	++
955	11906	CAGACGTCCACGAATGGGGTG	QTSTNGV	++
956	11907	TTGTCCAAAGCGAATATGAAT	LSKANMN	++
957	11908	TATGAGTCCACGAATGGGGTG	YESTNGV	++
958	11909	TTGTCCAAAGCGGGGGATAAT	LSKAGDN	++
959	11910	TACTCAAAGATGGGCAACAAC	YSKMGNN	++
960	11911	TATTCCAGGGCGAATGAGAAT	YSRANEN	++
961	11912	ACGAGGAATGGGGCGAATGCG	TRNGANA	++
962	11913	GAGACGTCCACGAATGGGAGG	ETSTNGR	++
963	11914	TGGCAGGAGACGAATGGGAAA	WQETNGK	++
964	11915	ATAACGTCCACGAATGGGGTG	ITSTNGV	++
965	11916	TCCGGGTCCACGAATGGGGTG	SGSTNGV	++
966	11917	TTCAATTCCTCCAATGGGGTG	FNSSNGV	++
967	11918	TTCTCCAGGGCGGGGACGAAT	FSRAGTN	++
968	11919	CAGACGTCCTCCAATGGGGTG	QTSSNGV	++
969	11920	CCGGAGTCCACGAATGGGAGG	PESTNGR	++
970	11921	ATCATGTCAACCAACGGCATC	IMSTNGI	++
971	11922	GAGAATTCCACGAATGGGAGG	ENSTNGR	++
972	11923	CGCCCCAACGGCCATTCAGCC	RPNGHSA	++
973	11924	ATACACTCCACGAATGGGATA	IHSTNGI	++
974	11925	CCGAGGTCCTCCAATGGGGTG	PRSSNGV	++
975	11926	TTGCAGTCCTCCAATGGGGTG	LQSSNGV	++
976	11927	TACTCAAAGGTAGGCGTAAAC	YSKVGVN	++
977	11928	TACTCAAAGCAAAACCATAAC	YSKQNHN	++
978	11929	TTGTCCAAAGGGGGGCCGAAT	LSKGGPN	++
979	11930	ATCCAATCAACCAACGGCATC	IQSTNGI	++
980	11931	ACGAATAGGGTGCCGCACTCC	TNRVPHS	++
981	11932	CATCATGGCGTATCAGCCTAC	HHGVSAY	++
982	11933	GTATGGTCATCAAACGGCGTA	VWSSNGV	++
983	11934	TATTCCAAACAGGGGACGAAT	YSKQGTN	++
984	11935	GCGGATTCCACGAATGGGGTG	ADSTNGV	++
985	11936	GGGGAGGGGTATTCCACGTGG	GEGYSTW	++
986	11937	CTGTCACGCATCAACTTTAAC	LSRINFN	++
987	11938	CACATGTCCACGAATGGGATA	HMSTNGI	++
988	11939	TATGCGAAAGCGAATGATAAT	YAKANDN	++
989	11940	ATAATATCCACGAATGGGATA	IISTNGI	++

990	11941	CACTATTCCACGAATGGGGTG	HYSTNGV	++
991	11942	ATCATCTCAACCAACGGCCGC	IISTNGR	++
992	11943	TATGCGAGGTATAATGATAAT	YARYNDN	++
993	11944	TTGATATCCACGAATGGGATA	LISTNGI	++
994	11945	TACTCAAAGTCAGGCCTGAAC	YSKSGLN	++
995	11946	CATTGGTCAACCAACGGCATC	HWSTNGI	++
996	11947	CTGTCAAAGCTGAACCTGAAC	LSKLNLN	++
997	11948	TATTCCAAATCCAATCCGAAT	YSKSNPN	++
998	11949	TATTCCAGGAATGGGACGAAT	YSRNGTN	++
999	11950	TATGCGAAAATAGGGATGAAT	YAKIGMN	++
1000	11951	TTGACGTCCACGAATGGGATA	LTSTNGI	++
1001	11952	TCAGTATCAACCAACGGCGTA	SVSTNGV	++
1002	11953	ATGGAGTCCTCCAATGGGGTG	MESSNGV	++
1003	11954	TCCAATTCCTCCAATGGGGTG	SNSSNGV	++
1004	11955	GTGTATTCCACGAATGGGGTG	VYSTNGV	++
1005	11956	TCACATTCAACCAACGGCATC	SHSTNGI	++
1006	11957	CAGCACTCCACGAATGGGGTG	QHSTNGV	++
1007	11958	TTGTCCAAAACGGGGATGAAT	LSKTGMN	++
1008	11959	TTGTCCAAACAGGGGATGAAT	LSKQGMN	++
1009	11960	CTGTCAAAGTCATCAAACAAC	LSKSSNN	++
1010	11961	TTCGGGTCCACGAATGGGATA	FGSTNGI	++
1011	11962	TATGCGAGGGTGGGGGAGAAT	YARVGEN	++
1012	11963	TTCTCCAAAGCGGGGCAGAAT	FSKAGQN	++
1013	11964	CACACGTCCTCCAATGGGGTG	HTSSNGV	++
1014	11965	TATTCCAAAACGGGGGAGAAT	YSKTGEN	++
1015	11966	TACTTTTCACATGTAGTAGAA	YFSHVVE	++
1016	11967	CTGGCCAAGAACGGCCCCAAC	LAKNGPN	++
1017	11968	ATATCCGAGTCCTCCAGGTGG	ISESSRW	++
1018	11969	CTGTCACGCTACAACGAAAAC	LSRYNEN	++
1019	11970	TTGTCCAGGTTGTCCGATACG	LSRLSDT	++
1020	11971	CTGGCCTCAACCAACGGCCGC	LASTNGR	++
1021	11972	TATGCGAAAGCGGGGGATAAT	YAKAGDN	++
1022	11973	CACGGGTCCACGAATGGGGTG	HGSTNGV	++
1023	11974	GTGTCCTCCACGAATGGGATA	VSSTNGI	++
1024	11975	TTCTCCAAATCCGGGCCGAAT	FSKSGPN	++
1025	11976	GCGTGGTCCACGAATGGGGTG	AWSTNGV	++
1026	11977	CTGTCAAAGATGGGCATCAAC	LSKMGIN	++
1027	11978	TTGGCGAAAGCGGGGTTGAAT	LAKAGLN	++
1028	11979	GTGACGTCCTCCAATGGGGTG	VTSSNGV	++
1029	11980	TATTCCAAAGCGAATCCGAAT	YSKANPN	++
1030	11981	TTGTCCAAAGGGAATCACAAT	LSKGNHN	++
1031	11982	ACGGCGGCGCACGTGACGTGG	TAAHVTW	++
1032	11983	CAGGAGTCCACGAATGGGAGG	QESTNGR	++
1033	11984	TTGTCCAAAATGGGGTTGAAT	LSKMGLN	++
1034	11985	ATATCCTCCTCCAATGGGATG	ISSSNGM	++

1035	11986	CTGCATTCAACCAACGGCATC	LHSTNGI	++
1036	11987	TTGGCGAAAAATGGGATGAAT	LAKNGMN	++
1037	11988	TATTCCAAATCCAATGCGAAT	YSKSNAN	++
1038	11989	TTGGCGAAAACGGGGACGAAT	LAKTGTN	++
1039	11990	ATGATGTCCACGAATGGGATA	MMSTNGI	++
1040	11991	TATTCCAGGGATGGGTATAAT	YSRDGYN	++
1041	11992	TATACGTCCTCCAATGGGGTG	YTSSNGV	++
1042	11993	GAGGCGTCCACGAATGGGAGG	EASTNGR	++
1043	11994	AATTCCTCCACGTCCACGTGG	NSSTSTW	++
1044	11995	TACTCAAAGGCCAACAACAAC	YSKANNN	++
1045	11996	ACGTCCTCCACGAATGGGGTG	TSSTNGV	++
1046	11997	CCGTATGCGGCGTCCAGGGAT	PYAASRD	++
1047	11998	GCGAATGGGTCCTCCAAATAT	ANGSSKY	++
1048	11999	AATCACTCCACGAATGGGAGG	NHSTNGR	++
1049	12000	TATTCCAGGCAGAATCCGAAT	YSRQNPN	++
1050	12001	TACGCCAAGTCACAAATGAAC	YAKSQMN	++
1051	12002	CAGATATCCACGAATGGGATA	QISTNGI	++
1052	12003	TATCACGTGCACGGGGATAAT	YHVHGDN	++
1053	12004	TATGCGAAACCGGGGGCGAAT	YAKPGAN	++
1054	12005	TACTCAAAGTCAGGCTCAAAC	YSKSGSN	++
1055	12006	TACGCCAAGTCAGGCGCCAAC	YAKSGAN	++
1056	12007	TACAACTCATCAAACGGCGTA	YNSSNGV	++
1057	12008	TACCGCACCGACGGCTTTTCA	YRTDGFS	++
1058	12009	TCCTCCTCCACGAATGGGATA	SSSTNGI	++
1059	12010	TACGCCAAGATGGGCCTGAAC	YAKMGLN	++
1060	12011	TACTCAGCCTCAGGCCCCAAC	YSASGPN	++
1061	12012	CTGTCAAAGCAAGGCTTTAAC	LSKQGFN	++
1062	12013	CACGATTCCACGAATGGGGTG	HDSTNGV	++
1063	12014	GTGTCCTCCCAGAATGGGGTG	VSSQNGV	++
1064	12015	TACTCAAAGATGGGCCAAAAC	YSKMGQN	++
1065	12016	AACTTTTCAACCAACGGCCGC	NFSTNGR	++
1066	12017	TACTCACGCGGCAACGACAAC	YSRGNDN	++
1067	12018	GCGTCCGATACGAATGGGAGG	ASDTNGR	++
1068	12019	ACGCAGTCCTTGAATGGGAGG	TQSLNGR	++
1069	12020	CCGTCCTCCACGAATGGGGTG	PSSTNGV	++
1070	12021	AAGGACGGCAACTCATCATGG	KDGNSSW	++
1071	12022	TTCGCGAAAGCGGGGTGGAAT	FAKAGWN	++
1072	12023	TACTACTCAGGCAAGATCGAC	YYSGKID	++
1073	12024	TTGTCCAGGATAAATGATAAT	LSRINDN	++
1074	12025	ACGACGTCCACGAATGGGATA	TTSTNGI	++
1075	12026	GAAGCCTCAACCAACGGCATC	EASTNGI	++
1076	12027	TTCTCCTCCACGAATGGGGTG	FSSTNGV	++
1077	12028	TTCGCGAAAGCGGGGTTCAAT	FAKAGFN	++
1078	12029	TTGGCGAGGGGGGGGGAGAAT	LARGGEN	++
1079	12030	GTGGAGTCCTCCAATGGGGTG	VESSNGV	++

1080	12031	TATGCGAAAAATGGGGGGAAT	YAKNGGN	++
1081	12032	TCCGGGTCCACGAATGGGATA	SGSTNGI	++
1082	12033	TATGCGAAAAATGGGACGAAT	YAKNGTN	++
1083	12034	TTGCACAAAAATACGGAGAAT	LHKNTEN	++
1084	12035	TTCAGGTCCTCCAATGGGGTG	FRSSNGV	++
1085	12036	AAAGGGGCGGATCACTCCTGG	KGADHSW	++
1086	12037	GTGAATTCCACGAATGGGGTG	VNSTNGV	++
1087	12038	GTAAACTCAACCAACGGCATC	VNSTNGI	++
1088	12039	AACCATGCCTCACATGCCTGG	NHASHAW	++
1089	12040	TTGGCGAAAATGGGGTTGAAT	LAKMGLN	++
1090	12041	TACTCAAAGTACAACATCAAC	YSKYNIN	++
1091	12042	TATTTCACGCACCAGTCCGAG	YFTHQSE	++
1092	12043	TACGCCAAGACCGGCAACAAC	YAKTGNN	++
1093	12044	TTGATATCCACGAATGGGAGG	LISTNGR	++
1094	12045	TCACGCTCATCAAACGGCGTA	SRSSNGV	++
1095	12046	TTGGCGTCCACGAATGGGATA	LASTNGI	++
1096	12047	GCGGGGTCCACGAATGGGGTG	AGSTNGV	++
1097	12048	AGGACGTCCTCCAATGGGCAG	RTSSNGQ	++
1098	12049	GAACGCTCAACCAACGGCATC	ERSTNGI	++
1099	12050	CCGGGGTCCACGAATGGGGTG	PGSTNGV	++
1100	12051	TTGGCGAGGAATGGGGAGAAT	LARNGEN	++
1101	12052	TCACAATCAACCAACGGCATC	SQSTNGI	++
1102	12053	TATGCGAAAATGGGGCAGAAT	YAKMGQN	++
1103	12054	AAGTTTCCCTCACATGACTGG	KFPSHDW	++
1104	12055	GTAGAATCAACCAACGGCATC	VESTNGI	++
1105	12056	CTGTCAAAGATGAACATCAAC	LSKMNIN	++
1106	12057	AGGAATGAGGGGGTGGCGTGG	RNEGVAW	++
1107	12058	TATGCGAAAGGGGGGGTGAAT	YAKGGVN	++
1108	12059	TACTCAAAGATGGGCGGCAAC	YSKMGGN	++
1109	12060	TTCATATCCTCCAATGGGGTG	FISSNGV	++
1110	12061	TACTCAAAGGGCAACCCCAAC	YSKGNPN	++
1111	12062	GCGTTGTCCACGAATGGGAGG	ALSTNGR	++
1112	12063	AAAGAGTCCTCCTATGCGTGG	KESSYAW	++
1113	12064	ACGGGGTCCACGAATGGGGTG	TGSTNGV	++
1114	12065	TTGTCCAAAACGGGGGCGAAT	LSKTGAN	++
1115	12066	AGGGAGTCCTCCAATGGGTAT	RESSNGY	++
1116	12067	TTGGCGAAAGGGGGGTCCAAT	LAKGGSN	++
1117	12068	GGGACGGGGAAACAGCAGTGG	GTGKQQW	++
1118	12069	TCCTCCTCCACGAATGGGGTG	SSSTNGV	++
1119	12070	AGGGATTCCACGAATGGGATA	RDSTNGI	++
1120	12071	TTGAAAGATGGGACGGCGTCC	LKDGTAS	++
1121	12072	ATGGATTCCACGAATGGGAGG	MDSTNGR	++
1122	12073	CATGCCTCAACCAACGGCGTA	HASTNGV	++
1123	12074	CAATGGGACGGCTCACCCTCA	QWDGSPS	++
1124	12075	ATGGGGTCCACGAATGGGGTG	MGSTNGV	++

1125	12076	AATGATTCCACGAATGGGAGG	NDSTNGR	++
1126	12077	ACGCCGGAGCCGGTGAGGTGG	TPEPVRW	++
1127	12078	ACGACGTCCTCCAATGGGGTG	TTSSNGV	++
1128	12079	AATTTCTCCACGAATGGGGTG	NFSTNGV	++
1129	12080	CTGGCCCGCAACGGCGGCAAC	LARNGGN	++
1130	12081	ACGGGGTCCTCCAATGGGGTG	TGSSNGV	++
1131	12082	TACGCCAAGCCCGGCCATAAC	YAKPGHN	++
1132	12083	TATGCGAAACACGGGGCGAAT	YAKHGAN	++
1133	12084	GCCCGCTCATCAAACGGCGTA	ARSSNGV	++
1134	12085	TACTCAAAGACCAACTACAAC	YSKTNYN	++
1135	12086	TCCTCCTCCACGAATGGGTTG	SSSTNGL	++
1136	12087	TTTCAATCAACCAACGGCATC	FQSTNGI	++
1137	12088	ATAGGGTCCACGAATGGGGTG	IGSTNGV	++
1138	12089	AATGAGTCCACGAATGGGAGG	NESTNGR	++
1139	12090	CCGTTGTCCACGAATGGGAGG	PLSTNGR	++
1140	12091	TACTCAAAGGGCAACTCAAAC	YSKGNSN	++
1141	12092	TTGTCCAAAGCGGGGGAGAAT	LSKAGEN	++
1142	12093	AAAAAAGATGGGACGAATGCG	KKDGTNA	++
1143	12094	TACTCACGCTCAGGCGAAAAC	YSRSGEN	++
1144	12095	TATGCGAGGTATAATCCGAAT	YARYNPN	++
1145	12096	GTGAATGAGACGAATGGGGTG	VNETNGV	++
1146	12097	ACGATGTCCACGAATGGGATA	TMSTNGI	++
1147	12098	AGGGATTCCACGAATGGGGTG	RDSTNGV	++
1148	12099	TATTATTCCACGAATGGGATA	YYSTNGI	++
1149	12100	GTACATTCATCAAACGGCGTA	VHSSNGV	++
1150	12101	TACTCAAAGATGGGCGCCAAC	YSKMGAN	++
1151	12102	TTGTCCAAATCCAATGTGAAT	LSKSNVN	++
1152	12103	TACAACAACGGCTCACGCTAC	YNNGSRY	++
1153	12104	TGGATATCCACGAATGGGGTG	WISTNGV	++
1154	12105	CACGGGTCCACGAATGGGATA	HGSTNGI	++
1155	12106	TACGCCCGCGGCGGCGGCAAC	YARGGGN	++
1156	12107	TTGGATTCCACGAATGGGATA	LDSTNGI	++
1157	12108	TATTCCAGGGAGGGGCCGAAT	YSREGPN	++
1158	12109	CTGTCAAAGATGAACTACAAC	LSKMNYN	++
1159	12110	TACTCACGCTCAAACGAAAAC	YSRSNEN	++
1160	12111	TATGCGAGGCCGGGGTTGAAT	YARPGLN	++
1161	12112	CTGGCCAAGGCCGGCAACAAC	LAKAGNN	++
1162	12113	TCCGATTCCACGAATGGGAGG	SDSTNGR	++
1163	12114	TACTCAAAGACCAACTTTAAC	YSKTNFN	++
1164	12115	TTGGCGAGGGCGGGGACGAAT	LARAGTN	++
1165	12116	AGGTATGATGGGTCCTCCGCG	RYDGSSA	++
1166	12117	ACGAATTCCTCCAATGGGGTG	TNSSNGV	++
1167	12118	CAGAATTCCACGAATGGGATA	QNSTNGI	++
1168	12119	TACTCAAAGAACGGCATCAAC	YSKNGIN	++
1169	12120	TTCACGTCCACGAATGGGATA	FTSTNGI	++

1170	12121	ACCGCCGACAACTACACCGTA	TADNYTV	++
1171	12122	TCCATATCCACGAATGGGGTG	SISTNGV	++
1172	12123	GGGAATAATGGGAATGTGTGG	GNNGNVW	++
1173	12124	TCCTTGTCCACGAATGGGGTG	SLSTNGV	++
1174	12125	TATTCCAAATCCGGGTGTAAT	YSKSGCN	++
1175	12126	GAGTCCTCCACGAATGGGATA	ESSTNGI	++
1176	12127	CTGTCAAAGGGCAACATCAAC	LSKGNIN	++
1177	12128	ACCTGGTCAACCAACGGCATC	TWSTNGI	++
1178	12129	CAGAATTCCACGAATGGGGTG	QNSTNGV	++
1179	12130	GAAAACTCAACCAACGGCAAG	ENSTNGK	++
1180	12131	TTGGTGTCCACGAATGGGATA	LVSTNGI	++
1181	12132	TTCTATTCCACGAATGGGGTG	FYSTNGV	++
1182	12133	ATGAACTCAACCAACGGCATC	MNSTNGI	++
1183	12134	CCGGATTCCACGAATGGGAGG	PDSTNGR	++
1184	12135	TATGCGAAAGCGGGGTGTAAT	YAKAGCN	++
1185	12136	TATTCCAAACAGAATCAGAAT	YSKQNQN	++
1186	12137	TTGAGGTCCTCCAATGGGGTG	LRSSNGV	++
1187	12138	TATTCCAAAGTGAATGATAAT	YSKVNDN	++
1188	12139	AGGGATGGGAATTCCACGTAT	RDGNSTY	++
1189	12140	TCATCAGGCTCATCATCATGG	SSGSSSW	++
1190	12141	ATGGAATCAACCAACGGCATC	MESTNGI	++
1191	12142	TACTCACGCCAAGGCGACAAC	YSRQGDN	++
1192	12143	TATGCGAGGACGAATGAGAAT	YARTNEN	++
1193	12144	ACGGCGTCCACGAATGGGGTG	TASTNGV	++
1194	12145	ATCCTGTCAACCAACGGCGTA	ILSTNGV	++
1195	12146	TTGTCCAGGTTGGGGGAGAAT	LSRLGEN	++
1196	12147	TTGGCGTCCACGAATGGGGTG	LASTNGV	++
1197	12148	TATTCCAAAGTGGGGGAGAAT	YSKVGEN	++
1198	12149	TACGCCCGCTCAAACCAAAAC	YARSNQN	++
1199	12150	AACCAATCAACCAACGGCCGC	NQSTNGR	++
1200	12151	TACGCCCGCGGCGGCGAAAAC	YARGGEN	++
1201	12152	TACTCAAAGCATAACCTGAAC	YSKHNLN	++
1202	12153	CATAAGTCATCAAACGGCGTA	HKSSNGV	++
1203	12154	CTGGCCAAGATGGGCATCAAC	LAKMGIN	++
1204	12155	GGGCAGGGGAATTCCGCGTGG	GQGNSAW	++
1205	12156	TATGCGAAAGATGGGCCGAAT	YAKDGPN	++
1206	12157	AACAAGTACGGCTCAGACGTA	NKYGSDV	++
1207	12158	TATGCGAGGGGGAATGAGAAT	YARGNEN	++
1208	12159	GGGCAGTCCACGAATGGGAGG	GQSTNGR	++
1209	12160	CACTTCTCCACGAATGGGGTG	HFSTNGV	++
1210	12161	AATGCGTCCACGAATGGGGTG	NASTNGV	++
1211	12162	TCAGCCTCAACCAACGGCCGC	SASTNGR	++
1212	12163	AGGGAGAATAATGTGACGTGG	RENNVTW	++
1213	12164	CAGCACTCCACGAATGGGATA	QHSTNGI	++
1214	12165	CTGTCAAAGATCGGCCCCAAC	LSKIGPN	++

1215	12166	CCGATGTCCACGAATGGGGTG	PMSTNGV	++
1216	12167	TTGTCCAGGGCGAATGAGAAT	LSRANEN	++
1217	12168	TATTCCAAAATAAATGATAAT	YSKINDN	++
1218	12169	TTGGCGAAAAATGGGGCGAAT	LAKNGAN	++
1219	12170	TATTCCAAAAATGGGGCGAAT	YSKNGAN	++
1220	12171	GCGTATTCCACGAATGGGGTG	AYSTNGV	++
1221	12172	TACTCAAAGCAAAACAACAAC	YSKQNNN	++
1222	12173	TATAATTCCACGAATGGGATA	YNSTNGI	++
1223	12174	TTGGCGAAAGCGGGGCAGAAT	LAKAGQN	++
1224	12175	TTGTCCAAAGAGAATTATAAT	LSKENYN	++
1225	12176	ACCTCATCAACCAACGGCATC	TSSTNGI	++
1226	12177	TTCTCCAAAATACAGACGGAG	FSKIQTE	++
1227	12178	GAGGATTCCACGAATGGGAGG	EDSTNGR	++
1228	12179	TCCAATTCCACGAATGGGGTG	SNSTNGV	++
1229	12180	AGGGATTCCAATGTGTATCCG	RDSNVYP	++
1230	12181	AGGCCGGATGGGACGCCGTCC	RPDGTPS	++
1231	12182	TATGCGAAACAGAATCCGAAT	YAKQNPN	++
1232	12183	TTGGCGAAAGGGGGGACGAAT	LAKGGTN	++
1233	12184	CTGTCAAAGAACAACTACAAC	LSKNNYN	++
1234	12185	TTCAATTCCACGAATGGGGTG	FNSTNGV	++
1235	12186	AACAACTCAACCAACGGCGTA	NNSTNGV	++
1236	12187	GGGTCCTCCACGAATGGGGTG	GSSTNGV	++
1237	12188	GAGGAGTCCACGAATGGGAGG	EESTNGR	++
1238	12189	TACTCAAAGAACGGCAACAAC	YSKNGNN	++
1239	12190	GTGACGTCCACGAATGGGGTG	VTSTNGV	++
1240	12191	TTGGCGAAAAATGGGACGAAT	LAKNGTN	++
1241	12192	TTGTATTCCACGAATGGGGTG	LYSTNGV	++
1242	12193	AATTATAGGGGGGATAATGCG	NYRGDNA	++
1243	12194	ATCTCATACGACTACGGCAAC	ISYDYGN	++
1244	12195	TTGGCGAAAAATGGGGTGAAT	LAKNGVN	++
1245	12196	TTGCACGCGTCCTCCATGAAT	LHASSMN	++
1246	12197	CAGATATCCACGAATGGGGTG	QISTNGV	++
1247	12198	GTGCACAAACAGTTGCCGAAT	VHKQLPN	++
1248	12199	TATGAGTCCATAAATGGGAGG	YESINGR	++
1249	12200	GGCATGAAGAACAAGTTTGAC	GMKNKFD	++
1250	12201	AATCAGTCCACGAATGGGGTG	NQSTNGV	++
1251	12202	CAGGATTCCACGAATGGGAGG	QDSTNGR	++
1252	12203	TTTTCACGCCAAGGCAACAAC	FSRQGNN	++
1253	12204	TTGGCGAAACAGGGGGCGAAT	LAKQGAN	++
1254	12205	TTTCAATCAACCAACGGCGTA	FQSTNGV	++
1255	12206	GTGGATTCCACGAATGGGGTG	VDSTNGV	++
1256	12207	CTGGCCAAGCAAGGCAACAAC	LAKQGNN	++
1257	12208	AAGGACGGCGTATCAGTATGG	KDGVSVW	++
1258	12209	GGCGAATCAACCAACGGCCGC	GESTNGR	++
1259	12210	TGGGTGTCCACGAATGGGGTG	WVSTNGV	++

1260	12211	TTGTCCAAATCCGGGCAGAAT	LSKSGQN	++
1261	12212	ACGGGGGGGGAGTCCAGGTGG	TGGESRW	++
1262	12213	TTCGCGAGGTCCGGGGAGAAT	FARSGEN	++
1263	12214	CGCCTGTCAACCAACGGCGTA	RLSTNGV	++
1264	12215	ACGTGGTCCTCCAATGGGGTG	TWSSNGV	++
1265	12216	ATGAACTCAACCAACGGCGTA	MNSTNGV	++
1266	12217	AAGACCTCACGCGAAGGCGTA	KTSREGV	++
1267	12218	ATGTTCTCCACGAATGGGGTG	MFSTNGV	++
1268	12219	TTGGCGAAACCGGGGCCGAAT	LAKPGPN	++
1269	12220	TACTCAAAGCTGCAAGACAAC	YSKLQDN	++
1270	12221	GACCTGGACTCAACCAAGTGG	DLDSTKW	++
1271	12222	CATGAATCATCAAACGGCGTA	HESSNGV	++
1272	12223	TCCGGGTCCTCCAATGGGAGG	SGSSNGR	++
1273	12224	TATGCGAAAACGGGGGAGAAT	YAKTGEN	++
1274	12225	TATGCGAAACAGGGGACGAAT	YAKQGTN	++
1275	12226	TATACGAGGTCCGATACGTCC	YTRSDTS	++
1276	12227	CTGTCAAAGGCCGGCATCAAC	LSKAGIN	++
1277	12228	CCGCACTCCACGAATGGGATA	PHSTNGI	++
1278	12229	ATCTCATCAACCAACGGCATC	ISSTNGI	++
1279	12230	AAACAGTCCGATTTGACGTGG	KQSDLTW	++
1280	12231	CTGTCAAAGCAAGGCATCAAC	LSKQGIN	++
1281	12232	TTGGAGTCCTCCAATGGGGTG	LESSNGV	++
1282	12233	CATTGGTCATCAAACGGCGTA	HWSSNGV	++
1283	12234	AGGGAGGGGGCGGGGTCCTGG	REGAGSW	++
1284	12235	AGGTTGGATTCCAATGGGTGG	RLDSNGW	++
1285	12236	TATGCGAGGCCGGGGACGAAT	YARPGTN	++
1286	12237	AACTACAACAACGTATACTCA	NYNNVYS	++
1287	12238	CTGTCAAAGGTAGGCGGCAAC	LSKVGGN	++
1288	12239	CACTCCTCCACGAATGGGGTG	HSSTNGV	++
1289	12240	TTGTCCAAAATGAATACGAAT	LSKMNTN	++
1290	12241	TTGTCCAAATCCGGGACGAAT	LSKSGTN	++
1291	12242	ACGATATCCTCCAATGGGGTG	TISSNGV	++
1292	12243	CCCGTATCAACCAACGGCGTA	PVSTNGV	++
1293	12244	TACTCAAAGATGGGCGAAAAC	YSKMGEN	++
1294	12245	AGGGGGGAGAATCACGCGTGG	RGENHAW	++
1295	12246	AATTCCTCCACGAATGGGGTG	NSSTNGV	++
1296	12247	GTGGATTCCAGGGAGGGGAGG	VDSREGR	++
1297	12248	TTCTCCAGGGCGAATGAGAAT	FSRANEN	++
1298	12249	CAAGGCTCAGGCCTGTTTATC	QGSGLFI	++
1299	12250	CTGTCAAAGTCAGCCAACAAC	LSKSANN	++
1300	12251	TGGACCTCATCAAACGGCGTA	WTSSNGV	++
1301	12252	TTGCACTCCTCCAATGGGGTG	LHSSNGV	++
1302	12253	TATTCCAAAGTGAATGAGAAT	YSKVNEN	++
1303	12254	ACGATGTCCTCCAATGGGGTG	TMSSNGV	++
1304	12255	CATGACTCAACCAACGGCCGC	HDSTNGR	++

1305	12256	TTGGCGAAACAGGGGCAGAAT	LAKQGQN	++
1306	12257	GAGAAATCCACGAATGGGGTG	EKSTNGV	++
1307	12258	TTGTCCAGGATGGGGGAGAAT	LSRMGEN	++
1308	12259	TTCGCGAAAATGGGGCCGAAT	FAKMGPN	++
1309	12260	CCGTATTCCACGAATGGGGTG	PYSTNGV	++
1310	12261	TGGCATTCATCAAACGGCGTA	WHSSNGV	++
1311	12262	AATGAGTCCACGAATGGGATA	NESTNGI	++
1312	12263	TCAAACGCCTCATCAAACTGG	SNASSNW	++
1313	12264	TACTCAAAGTCAAACATGAAC	YSKSNMN	++
1314	12265	TTGCACAAAAATTTGCCGGAT	LHKNLPD	++
1315	12266	GCGCAGTCCTCCAATGGGGTG	AQSSNGV	++
1316	12267	AACCATTCAGGCCGCTCAGCC	NHSGRSA	++
1317	12268	TTTTCAAAGTTTAACCCCAAC	FSKFNPN	++
1318	12269	AATACGTCCACGAATGGGATA	NTSTNGI	++
1319	12270	AGGCAGGATCACGTGATGTAT	RQDHVMY	++
1320	12271	AACACCGGCAACTCACATTGG	NTGNSHW	++
1321	12272	CCGTGGGAGGGGGGGCCGAGG	PWEGGPR	++
1322	12273	ATACAGTCCTCCAATGGGGTG	IQSSNGV	++
1323	12274	TTGTCCAGGCACAATGAGAAT	LSRHNEN	++
1324	12275	ATGTCAGACAACAAGCATTGG	MSDNKHW	++
1325	12276	CTGTCAAAGTCAAACATCAAC	LSKSNIN	++
1326	12277	TACTCACGCCAAGGCGAAAAC	YSRQGEN	++
1327	12278	TACGCCCGCCTGAACATCAAC	YARLNIN	++
1328	12279	ATAGATGGGAATTCCCCGTAT	IDGNSPY	++
1329	12280	ATGGATTCCACGAATGGGGTG	MDSTNGV	++
1330	12281	TTGTCCAAATCCGGGTCCAAT	LSKSGSN	++
1331	12282	GCGTCCTCCTCCAATGGGGTG	ASSSNGV	++
1332	12283	ATGTTGTCCACGAATGGGGTG	MLSTNGV	++
1333	12284	TTCTCCAGGACGAATGTGAAT	FSRTNVN	++
1334	12285	TTGGATTCCACGAATGGGGTG	LDSTNGV	++
1335	12286	TACTCACGCATCAACATGAAC	YSRINMN	++
1336	12287	TTCTCCAGGTTGGGGGAGAAT	FSRLGEN	++
1337	12288	TACTACACCGGCATCAACGAC	YYTGIND	++
1338	12289	CACTCCTCCACGAATGGGATA	HSSTNGI	++
1339	12290	ATGACCTCAACCAACGGCATC	MTSTNGI	++
1340	12291	CCCGGCTCAACCAACGGCCGC	PGSTNGR	++
1341	12292	TATGCGTCCTCCAATGGGGTG	YASSNGV	++
1342	12293	ATGGTGTCCACGAATGGGATA	MVSTNGI	++
1343	12294	CTGGAATCAACCAACGGCATC	LESTNGI	++
1344	12295	ATATCCTCCTCCAATGGGGTG	ISSSNGV	++
1345	12296	TATTCCAAAAATGGGGTGAAT	YSKNGVN	++
1346	12297	TGGCAGTCCTCCAATGGGGTG	WQSSNGV	++
1347	12298	TTTTCAAAGCTGGGCCTGAAC	FSKLGLN	++
1348	12299	AATAAATCCACGAATGGGGTG	NKSTNGV	++
1349	12300	TATTTCACGGGGACGAATAAT	YFTGTNN	++

1350	12301	CCGAAATCCACGAATGGGATA	PKSTNGI	++
1351	12302	TGGGCGTCCACGAATGGGATA	WASTNGI	++
1352	12303	ATGGGGGGGTCCTCCAATTGG	MGGSSNW	++
1353	12304	GCGACGGATTATATGGCGTAT	ATDYMAY	++
1354	12305	TTCTCCAGGGCGGGGGAGAAT	FSRAGEN	++
1355	12306	AGGAATGATGGGACGTCCTGG	RNDGTSW	++
1356	12307	TTGTCCAAAACGGGGCAGAAT	LSKTGQN	++
1357	12308	TATGCGAAACAGAATCACAAT	YAKQNHN	++
1358	12309	TTCTATTCCACGAATGGGATA	FYSTNGI	++
1359	12310	TGGGCGTCCTCCAATGGGGTG	WASSNGV	++
1360	12311	ACGGTGTCCTCCAATGGGGTG	TVSSNGV	++
1361	12312	GTGGATTCCACGAATGGGATA	VDSTNGI	++
1362	12313	TTGGCGAAAATAGGGTTCAAT	LAKIGFN	++
1363	12314	AGGTCCGGGGAGTCCGCGTGG	RSGESAW	++
1364	12315	ATGAGGACGGGGATGGGGCCG	MRTGMGP	++
1365	12316	TTTATGTCAACCAACGGCATC	FMSTNGI	++
1366	12317	TATGCGAAAGGGAATTCCAAT	YAKGNSN	++
1367	12318	CACGTGTCCTCCAATGGGGTG	HVSSNGV	++
1368	12319	AATTTGAAAGGGACGGGGGCG	NLKGTGA	++
1369	12320	GGGCACGCGGGGTCCACGTGG	GHAGSTW	++
1370	12321	GTGGCGGGGAGGGGGTATGAT	VAGRGYD	++
1371	12322	AATCACTCCACGAATGGGATA	NHSTNGI	++
1372	12323	TACTCACGCTACAACGAAAAC	YSRYNEN	++
1373	12324	AATCAGTCCACGAATGGGATA	NQSTNGI	++
1374	12325	ACGTCCGATTATGAGTCCTAT	TSDYESY	++
1375	12326	TACTCAAAGCAAGGCGGCAAC	YSKQGGN	++
1376	12327	TTGGCGAAATCCGGGTGTAAT	LAKSGCN	++
1377	12328	CACTCCTCCACGCACGGGCAG	HSSTHGQ	++
1378	12329	TCCTTCTCCTCCAATGGGGTG	SFSSNGV	++
1379	12330	TATTATACGGGGACGACGATG	YYTGTTM	++
1380	12331	GCGTTCTCCACGAATGGGGTG	AFSTNGV	++
1381	12332	ATCATCTCATCAAACGGCGTA	IISSNGV	++
1382	12333	GTATCATCAACCAACGGCGTA	VSSTNGV	++
1383	12334	TTGTCCAAAATGAATGCGAAT	LSKMNAN	++
1384	12335	AGGGCGAATGGGGATAATGCG	RANGDNA	++
1385	12336	TACTCAAAGCATGGCTCAAAC	YSKHGSN	++
1386	12337	TTGTCCAAACACAATGATAAT	LSKHNDN	++
1387	12338	GCGGATGGGATATCCACGTAT	ADGISTY	++
1388	12339	TATTCCAAAAATGGGGATAAT	YSKNGDN	++
1389	12340	TCCACGTCCTCCAATGGGGTG	STSSNGV	++
1390	12341	CTGGCCAAGGGCAACTACAAC	LAKGNYN	++
1391	12342	GTAAACTCATCAAACGGCGTA	VNSSNGV	++
1392	12343	ATCTACTCAACCAACGGCGTA	IYSTNGV	++
1393	12344	TATTCCGATTTCAATGGGAGG	YSDFNGR	++
1394	12345	CACGATTCCACGAATGGGATA	HDSTNGI	++

1395	12346	TATGCGAAACACGGGTTGAAT	YAKHGLN	++
1396	12347	TATGCGAAATTGGGGGTGAAT	YAKLGVN	++
1397	12348	AAGAACGACGGCAACCCCTGG	KNDGNPW	++
1398	12349	CTGGCCAAGAACGGCCAAAAC	LAKNGQN	++
1399	12350	GCCCATTCAACCAACGGCATC	AHSTNGI	++
1400	12351	AATACGGATGGGTGGAGGGAT	NTDGWRD	++
1401	12352	AGGGATGGGGCGTCCGTGTAT	RDGASVY	++
1402	12353	TGGATCTCATCAAACGGCGTA	WISSNGV	++
1403	12354	AGGGATTCCTCCAATGGGGTG	RDSSNGV	++
1404	12355	TACGCCAAGCCCGGCGTAAAC	YAKPGVN	++
1405	12356	TCCCAGTCCTCCAATGGGGTG	SQSSNGV	++
1406	12357	GCGTGGTCCACGAATGGGATA	AWSTNGI	++
1407	12358	GCCAACTCAACCAACGGCATC	ANSTNGI	++
1408	12359	CCGACGTCCACGAATGGGATA	PTSTNGI	++
1409	12360	ATCTACTCAACCAACGGCATC	IYSTNGI	++
1410	12361	TTTGAATCAACCAACGGCCGC	FESTNGR	++
1411	12362	TTGATGTCCTCCAATGGGGTG	LMSSNGV	++
1412	12363	CAAATGTCAACCAACGGCATC	QMSTNGI	++
1413	12364	TTCTCCAAAATAGGGCAGAAT	FSKIGQN	++
1414	12365	TACTCAAAGAACGGCCAAAAC	YSKNGQN	++
1415	12366	TACTCAAAGGGCGGCAACAAC	YSKGGNN	++
1416	12367	ACCCATTCAGGCTTTGGCCCC	THSGFGP	++
1417	12368	AATGCGTCCCAGGGGTGGGAT	NASQGWD	++
1418	12369	GCGGGGGGGGCGAATGTGTGG	AGGANVW	++
1419	12370	TATTCCAAAATAAATTTCAAT	YSKINFN	++
1420	12371	GAATGGTCAACCAACGGCGTA	EWSTNGV	++
1421	12372	AATGTGTCCACGAATGGGGTG	NVSTNGV	++
1422	12373	TACTCACGCAACGGCGAAAAC	YSRNGEN	++
1423	12374	TGGGTGTCCTCCAATGGGGTG	WVSSNGV	++
1424	12375	ATGTACGACGGCACCCGCTCA	MYDGTRS	++
1425	12376	TTTTCAAAGGGCAACATCAAC	FSKGNIN	++
1426	12377	GGGGATTCCACGAATGGGAGG	GDSTNGR	++
1427	12378	TACTCAAAGATCAACGTAAAC	YSKINVN	++
1428	12379	TATTCCAAAGCGGGGGAGAAT	YSKAGEN	++
1429	12380	TTTCATTCAACCAACGGCGTA	FHSTNGV	++
1430	12381	TCAGAATCAACCAACGGCGTA	SESTNGV	++
1431	12382	TTGTCCAAAAATGGGCACAAT	LSKNGHN	++
1432	12383	ATGGACTCAACCAACGGCATC	MDSTNGI	++
1433	12384	TATGCGAAAATGGGGTCCAAT	YAKMGSN	++
1434	12385	TACTCACGCCAAAACGAAAAC	YSRQNEN	++
1435	12386	GATTCCTCCACGTGGAGGGAT	DSSTWRD	++
1436	12387	TACTCACGCTCAGGCGACAAC	YSRSGDN	++
1437	12388	TGGGAATCAACCAACGGCATC	WESTNGI	++
1438	12389	AATTCCTCCTCCAATGGGGTG	NSSSNGV	++
1439	12390	TTGTCCAAACAGGGGGTGAAT	LSKQGVN	++

1440	12391	ATAGATTCCACGAATGGGAGG	IDSTNGR	++
1441	12392	ACCTCATCATCAAACGGCGTA	TSSSNGV	++
1442	12393	TGGGATTCCACGAATGGGATA	WDSTNGI	++
1443	12394	CAGGAGTCCACGAATGGGATA	QESTNGI	++
1444	12395	TACGCCAAGATGGGCGTAAAC	YAKMGVN	++
1445	12396	CTGTCATCATCAAACGGCGTA	LSSSNGV	++
1446	12397	CTGTCAAAGTCAGGCAACAAC	LSKSGNN	++
1447	12398	AGGACGAATACGAATGGGATA	RTNTNGI	++
1448	12399	TGGAACTCAACCAACGGCATC	WNSTNGI	++
1449	12400	GATACGAATGCGATGAAATAT	DTNAMKY	++
1450	12401	GCGGTGTCCACGAATGGGATA	AVSTNGI	++
1451	12402	TCCGGGTCCTCCAATCCGTGG	SGSSNPW	++
1452	12403	ATAGCGTCCTCCAATGGGGTG	IASSNGV	++
1453	12404	AAGAACGGCGGCTCAGCCTGG	KNGGSAW	++
1454	12405	CAGTGGTCCTCCAATGGGGTG	QWSSNGV	++
1455	12406	TACTCAAAGTCAGGCGAAAAC	YSKSGEN	++
1456	12407	ATAGTGTCCTCCAATGGGGTG	IVSSNGV	++
1457	12408	CACTTGTCCACGAATGGGGTG	HLSTNGV	++
1458	12409	TTCGCGAAAGGGGGGTTGAAT	FAKGGLN	+
1459	12410	TACTCAAAGAACGGCACCAAC	YSKNGTN	+
1460	12411	CACCACTCCACGAATGGGATA	HHSTNGI	+
1461	12412	AAATTGCCGGAGTATGGGCAC	KLPEYGH	+
1462	12413	AATTCCAAAGGGACGGGGGCG	NSKGTGA	+
1463	12414	ACGGATTCCACGTCCGGGAGG	TDSTSGR	+
1464	12415	TACGGCTCAACCAACGGCATC	YGSTNGI	+
1465	12416	TTGGGGGGGGCGTCCTTGTAT	LGGASLY	+
1466	12417	CTGAACTCAACCAACGGCATC	LNSTNGI	+
1467	12418	TTGTCCAGGCAGGGGGAGAAT	LSRQGEN	+
1468	12419	TATGCGAAATTGAATCCGAAT	YAKLNPN	+
1469	12420	CAAGCCTCAACCAACGGCATC	QASTNGI	+
1470	12421	GGGGTGAAAGGGACGATGTTC	GVKGTMF	+
1471	12422	TATGCGAAACAGAATGTGAAT	YAKQNVN	+
1472	12423	TCCTCCTCCACGACGGGGAGG	SSSTTGR	+
1473	12424	CATGGCGGCAACTCACATTAC	HGGNSHY	+
1474	12425	AGGGATGAGAGGACGACGTAT	RDERTTY	+
1475	12426	AGGTTGTCCGATGCGTATCCG	RLSDAYP	+
1476	12427	ATAGCGAGGACGGGGCACGAT	IARTGHD	+
1477	12428	TCCGATTCCTCCAATGGGGTG	SDSSNGV	+
1478	12429	AATGATTCCACGAATGGGGTG	NDSTNGV	+
1479	12430	AGGTCCAATGAGACGTTCCCG	RSNETFP	+
1480	12431	TCACTGTCAACCAACGGCATC	SLSTNGI	+
1481	12432	AGGGATTCCACGCCGCACTGG	RDSTPHW	+
1482	12433	GTGAATGCGACGAATGGGGTG	VNATNGV	+
1483	12434	GTAGTATCAACCAACGGCATC	VVSTNGI	+
1484	12435	TATGCGAAAACGAATGTGAAT	YAKTNVN	+

1485	12436	CACATATCCTCCAATGGGGTG	HISSNGV	+
1486	12437	GGCAACTCAACCAACGGCATC	GNSTNGI	+
1487	12438	TATGCGAGGAATGGGGAGAAT	YARNGEN	+
1488	12439	TATTCCAAAAATAATCCGAAT	YSKNNPN	+
1489	12440	AAAAATGGGCAGTCCACGTAT	KNGQSTY	+
1490	12441	GTAGTATCAACCAACGGCCGC	VVSTNGR	+
1491	12442	TTGGCGAAATCCGGGGATAAT	LAKSGDN	+
1492	12443	TTGGCGAAATTGGGGGCGAAT	LAKLGAN	+
1493	12444	CTGTTTTCAACCAACGGCATC	LFSTNGI	+
1494	12445	GATACGTCCACGAATGGGAGG	DTSTNGR	+
1495	12446	TTGGGGTCCACGAATGGGGTG	LGSTNGV	+
1496	12447	ATGATATCCACGAATGGGGTG	MISTNGV	+
1497	12448	TACTCAAAGACCAACAACAAC	YSKTNNN	+
1498	12449	GAGTTGAATGATGTGAAATGG	ELNDVKW	+
1499	12450	GCGGAGTCCACGAATGGGATA	AESTNGI	+
1500	12451	AGGGGGGCGACGATAATGCCG	RGATIMP	+
1501	12452	GTGAGGGATACGAATGGGATG	VRDTNGM	+
1502	12453	CTGCGCTCAGGCGCCGCCCCC	LRSGAAP	+
1503	12454	TGGAATTCCACGAATGGGGTG	WNSTNGV	+
1504	12455	GAGTGGTCCACGAATGGGATA	EWSTNGI	+
1505	12456	TGGCAGAGGGGGGAGATAAAT	WQRGEIN	+
1506	12457	TTGGCGAGGGGGAATGTGAAT	LARGNVN	+
1507	12458	TCATGGTCAACCAACGGCGTA	SWSTNGV	+
1508	12459	TTCATGTCCTCCAATGGGGTG	FMSSNGV	+
1509	12460	CCGATATCCACGAATGGGGTG	PISTNGV	+
1510	12461	TCACGCTTTGGCGACTCAGCC	SRFGDSA	+
1511	12462	TCCGGGGATGGGTCCAGGTAT	SGDGSRY	+
1512	12463	TATTCCAAATATGGGGATAAT	YSKYGDN	+
1513	12464	TTGTCCAAAAATGGGATAAAT	LSKNGIN	+
1514	12465	TCCGGGTCCTCCAATGGGGTG	SGSSNGV	+
1515	12466	AATATATCCACGAATGGGGTG	NISTNGV	+
1516	12467	AATGCGGGGACGTCCAATTGG	NAGTSNW	+
1517	12468	AGGAGGGAGGATTCCTATTCC	RREDSYS	+
1518	12469	AACAAGTCAACCAACGGCATC	NKSTNGI	+
1519	12470	TTGTCCAGGGTGAATGAGAAT	LSRVNEN	+
1520	12471	CGCATCTCATCAAACGGCGTA	RISSNGV	+
1521	12472	ACGCACTCCTCCAATGGGGTG	THSSNGV	+
1522	12473	TATATATCCACGAATGGGGTG	YISTNGV	+
1523	12474	TTGGCGAGGATGGGGGATAAT	LARMGDN	+
1524	12475	ACGGCGTATGGGCAGAATGCG	TAYGQNA	+
1525	12476	TATTCCAGGCCGGGGTTGAAT	YSRPGLN	+
1526	12477	ATGATCTCAACCAACGGCATC	MISTNGI	+
1527	12478	TTTTCAAAGAACGGCCCCAAC	FSKNGPN	+
1528	12479	TTGTCCAAAGCGAATACGAAT	LSKANTN	+
1529	12480	CTGGCCAAGGGCAACTTTAAC	LAKGNFN	+

1530	12481	GTACAATCATCAAACGGCGTA	VQSSNGV	+
1531	12482	TATTCCAAAGCGAATGAGAAT	YSKANEN	+
1532	12483	TATGCGAGGGCGGGGGAGAAT	YARAGEN	+
1533	12484	CTGAACTCATCAAACGGCGTA	LNSSNGV	+
1534	12485	TACATCTCAACCAACGGCCGC	YISTNGR	+
1535	12486	ATCAACTCATCAAACGGCGTA	INSSNGV	+
1536	12487	TACTCAAAGAACAACAACAAC	YSKNNNN	+
1537	12488	GGGGGGCACATGTCCACGTAT	GGHMSTY	+
1538	12489	CCGTGGTCCACGAATGGGGTG	PWSTNGV	+
1539	12490	CAGGAGTCCTCCAATGGGGTG	QESSNGV	+
1540	12491	TTGAGGGATGGGACGGGGTCC	LRDGTGS	+
1541	12492	ATCAAGTCATCAAACGGCGTA	IKSSNGV	+
1542	12493	ATAAAATGGGAGTCCGGGGAT	IKWESGD	+
1543	12494	TACTCAAAGAACAACGCCAAC	YSKNNAN	+
1544	12495	CCGAATTCCTCCAATGGGGTG	PNSSNGV	+
1545	12496	TTGTCCAGGCAGAATGAGAAT	LSRQNEN	+
1546	12497	TATGCGAGGATGGGGGGGAAT	YARMGGN	+
1547	12498	CAAAACTCAACCAACGGCCGC	QNSTNGR	+
1548	12499	AAAAATGAGTCCACGTTGTGG	KNESTLW	+
1549	12500	TACCATAAGTCAGACTTTAAC	YHKSDFN	+
1550	12501	ATAGATTCCACGAATGGGATA	IDSTNGI	+
1551	12502	TTTGAATCAACCAACGGCATC	FESTNGI	+
1552	12503	TACTCAAAGATGAACTCAAAC	YSKMNSN	+
1553	12504	GTGCCGTCCACGAATGGGAGG	VPSTNGR	+
1554	12505	TTGGCGAAAACGGGGGAGAAT	LAKTGEN	+
1555	12506	CATAACAACTCATCATCATGG	HNNSSSW	+
1556	12507	TTGACGTCCTCCAATGGGGTG	LTSSNGV	+
1557	12508	TACGCCAAGGGCAACTGCAAC	YAKGNCN	+
1558	12509	GCGGGGGGGGGGTCCACGTAT	AGGGSTY	+
1559	12510	TTCTTGTCCACGAATGGGGTG	FLSTNGV	+
1560	12511	ACGGAGTCCTCCGAGGGGAGG	TESSEGR	+
1561	12512	GCGACGGAGACGGGGCCGAAA	ATETGPK	+
1562	12513	GTGGATTCCTCCAATGGGGTG	VDSSNGV	+
1563	12514	TATGCGAGGGCGAATGAGAAT	YARANEN	+
1564	12515	TACTCACGCGGCGGCGACAAC	YSRGGDN	+
1565	12516	CAGTCCTCCACGAATGGGATA	QSSTNGI	+
1566	12517	TACTCAAAGATGAACGAAAAC	YSKMNEN	+
1567	12518	TACTCACGCCATGGCCCCAAC	YSRHGPN	+
1568	12519	CCCTCATCATCAAACGGCGTA	PSSSNGV	+
1569	12520	GAGAATTCCACGAATGGGGTG	ENSTNGV	+
1570	12521	GCGAATTCCACGAATGGGGTG	ANSTNGV	+
1571	12522	GACAACGGCCTGTCAAAGTAC	DNGLSKY	+
1572	12523	CATGAATCAACCAACGGCCGC	HESTNGR	+
1573	12524	CAGACGTCCAGGGAGGGGATA	QTSREGI	+
1574	12525	TTTTACACCGGCCATGCCGAC	FYTGHAD	+

1575	12526	CGCAACGACCTGACCTTTCCC	RNDLTFP	+
1576	12527	GATACGGGGACGTCCAGGTAT	DTGTSRY	+
1577	12528	ATGGCCTCAACCAACGGCATC	MASTNGI	+
1578	12529	TATTCCAAAGTGAATCCGAAT	YSKVNPN	+
1579	12530	TATTCCAAAGAGAATTATAAT	YSKENYN	+
1580	12531	GTAGCCTACACCTCATCAGAC	VAYTSSD	+
1581	12532	TACTCAAAGCATGGCGACAAC	YSKHGDN	+
1582	12533	CAGACGTCCACGAATGGGATA	QTSTNGI	+
1583	12534	TACTCAAAGCATAACCAAAAC	YSKHNQN	+
1584	12535	ATCCGCTCATCAAACGGCGTA	IRSSNGV	+
1585	12536	TATTCCAAATCCAATGAGAAT	YSKSNEN	+
1586	12537	AGGGTGACGGAGAATTGGTTG	RVTENWL	+
1587	12538	AAGGAATCAACCTCAAAGTGG	KESTSKW	+
1588	12539	TATGATTCCACGAATGGGATA	YDSTNGI	+
1589	12540	TACGCCAAGCATGGCGTAAAC	YAKHGVN	+
1590	12541	GTGAATGAGTCCGTGGCGTGG	VNESVAW	+
1591	12542	TTTTCAAAGCAAAACATCAAC	FSKQNIN	+
1592	12543	TACTCAAAGCAAAACGACAAC	YSKQNDN	+
1593	12544	ATGCGCTCATCAAACGGCGTA	MRSSNGV	+
1594	12545	GTGCCGCACAAAGGGTCCGGG	VPHKGSG	+
1595	12546	ACCTTTTCAGGCACCATGGCC	TFSGTMA	+
1596	12547	TACGACTCATCAAACGGCGTA	YDSSNGV	+
1597	12548	TTCTCCAAACAGGGGCACAAT	FSKQGHN	+
1598	12549	ATGAAAGATGGGACGGCGTCC	MKDGTAS	+
1599	12550	GCGTGGTCCTCCAATGGGGTG	AWSSNGV	+
1600	12551	TTGTCCAAACAGGGGGCGAAT	LSKQGAN	+
1601	12552	TATTCCAGGGTGAATGGGAAT	YSRVNGN	+
1602	12553	CTGGCCCGCATGGGCTACAAC	LARMGYN	+
1603	12554	TATGTGTCCTCCAATGGGGTG	YVSSNGV	+
1604	12555	TTGGCGAGGTTGGGGGAGAAT	LARLGEN	+
1605	12556	TTGGCGAAAATGGGGCAGAAT	LAKMGQN	+
1606	12557	CTGTCAAAGATGAACAACAAC	LSKMNNN	+
1607	12558	TTCGCGTCCTCCAATGGGGTG	FASSNGV	+
1608	12559	TTTTCACGCCAAGGCTTTAAC	FSRQGFN	+
1609	12560	AATCAGTCCTCCGTGACGTGG	NQSSVTW	+
1610	12561	GAGATGTCCACGAATGGGAGG	EMSTNGR	+
1611	12562	TTGATATCCTCCAATGGGGTG	LISSNGV	+
1612	12563	TATTCCAAAGTGAATCAGAAT	YSKVNQN	+
1613	12564	TTGGCGAAACACGGGTTGAAT	LAKHGLN	+
1614	12565	CTGGCCAAGTCAGGCGGCAAC	LAKSGGN	+
1615	12566	TATGCGAGGATGAATGATAAT	YARMNDN	+
1616	12567	TACACCCATGGCACCAACCAT	YTHGTNH	+
1617	12568	GTGGAGAGGTCCGGGTGGGAT	VERSGWD	+
1618	12569	GAATCATACAACGGCCGCAAC	ESYNGRN	+
1619	12570	TACTCATCAACCAACGGCGTA	YSSTNGV	+

1620	12571	TACTCAAAGAACAACATCAAC	YSKNNIN	+
1621	12572	CTGTCAAAGAACAACATCAAC	LSKNNIN	+
1622	12573	GAAATGGCCCATAAGAACTGG	EMAHKNW	+
1623	12574	TATGCGAAATATAATCCGAAT	YAKYNPN	+
1624	12575	TCATCATCATCAAACGGCGTA	SSSSNGV	+
1625	12576	TTCGCGAGGAATGGGGATAAT	FARNGDN	+
1626	12577	TACGACTCAACCAACGGCGTA	YDSTNGV	+
1627	12578	ACGGGGTCCTCCCACGGGTGG	TGSSHGW	+
1628	12579	TTCTCCAGGGTGAATGATAAT	FSRVNDN	+
1629	12580	ACGTATTCCGGGGATCCGGCG	TYSGDPA	+
1630	12581	GGCGACATGGTAGTACGCTAC	GDMVVRY	+
1631	12582	TTCGCGAAATCCGGGACGAAT	FAKSGTN	+
1632	12583	AATTCCGGGGTGTCCATATAT	NSGVSIY	+
1633	12584	GATGGGGGGCACTCCCACTAT	DGGHSHY	+
1634	12585	TGGACGGATACGAATGGGGCG	WTDTNGA	+
1635	12586	TTGTCCAGGTCCGGGAATGAT	LSRSGND	+
1636	12587	TTGGCGAAACAGGGGACGAAT	LAKQGTN	+
1637	12588	GGCGACGACTTTACCAAGTTT	GDDFTKF	+
1638	12589	GGCCATTCAACCAACGGCATC	GHSTNGI	+
1639	12590	TACTTTCAAGGCGTAATCAAC	YFQGVIN	+
1640	12591	CAGGGGTCCACGAATGGGATA	QGSTNGI	+
1641	12592	GCGGGGTCCACGAATGGGATA	AGSTNGI	+
1642	12593	TTTGCCAAGGGCAACGTAAAC	FAKGNVN	+
1643	12594	TTGTCCAAAGGGAATTTGAAT	LSKGNLN	+
1644	12595	GGCGACTACCCCGTAAAGTAC	GDYPVKY	+
1645	12596	ATGGAGTCCACGAATGGGGTG	MESTNGV	+
1646	12597	ATGTCATCAACCAACGGCATC	MSSTNGI	+
1647	12598	AACCTGGGCTCAAACACCTGG	NLGSNTW	+
1648	12599	CACTCCAGGGCGAATACGGAT	HSRANTD	+
1649	12600	GGGAGGAATGGGAATCCGGCG	GRNGNPA	+
1650	12601	TACTCAAAGCATGGCCAAAAC	YSKHGQN	+
1651	12602	TATTCCAAAATGGGGACGAAT	YSKMGTN	+
1652	12603	TTGGATTCCACGAATGGGAGG	LDSTNGR	+
1653	12604	GATAGGTATGGGAGGTCCCCG	DRYGRSP	+
1654	12605	AATTCCTCCACGAATGGGATA	NSSTNGI	+
1655	12606	TTCTCCAAAATGAATACGAAT	FSKMNTN	+
1656	12607	TATTCCAGGTTCAATGAGAAT	YSRFNEN	+
1657	12608	GGGGGGTCCGGGACGACGTGG	GGSGTTW	+
1658	12609	ACCGTAGGCTACTCAACCTAC	TVGYSTY	+
1659	12610	TCAGAATCATCAAACGGCGTA	SESSNGV	+
1660	12611	CGCGGCCCCGCCGAATACCCC	RGPAEYP	+
1661	12612	TATGCGAAAACGAATCCGAAT	YAKTNPN	+
1662	12613	AACCATTCAACCAACGGCGTA	NHSTNGV	+
1663	12614	TTGTATTCCTCCAATGGGGTG	LYSSNGV	+
1664	12615	CAGAATCAGTCCCACACGTGG	QNQSHTW	+

1665	12616	TACTCAAAGCCCGGCCTGAAC	YSKPGLN	+
1666	12617	TTGGCGAGGGCGGGGGATAAT	LARAGDN	+
1667	12618	TCAAACTCATCACATGGCTGG	SNSSHGW	+
1668	12619	TATTCCAAAACGAATGATAAT	YSKTNDN	+
1669	12620	AATATGTCCACGAATGGGAGG	NMSTNGR	+
1670	12621	TATGCGAAAATAGGGACGAAT	YAKIGTN	+
1671	12622	TACTCAAAGACCAACCATAAC	YSKTNHN	+
1672	12623	TATGCGAAATTGGGGGATAAT	YAKLGDN	+
1673	12624	TACACCAAGTCAGGCTCAAAC	YTKSGSN	+
1674	12625	TTGTCCAAAATGAATGAGAAT	LSKMNEN	+
1675	12626	TCATACTCAACCAACGGCGTA	SYSTNGV	+
1676	12627	GATTCCCACTCCCACACGTGG	DSHSHTW	+
1677	12628	TTGACGAGGTCCTCCTATGAT	LTRSSYD	+
1678	12629	TTCTCCAAAACGGGGTTGAAT	FSKTGLN	+
1679	12630	CACGGGTCCTCCAATGGGGTG	HGSSNGV	+
1680	12631	CTGGCCAAGCTGGGCAACAAC	LAKLGNN	+
1681	12632	TATGCGAAAACGAATCACAAT	YAKTNHN	+
1682	12633	CAGGAGCACACGGTGTATAGG	QEHTVYR	+
1683	12634	GCGAATTCCTCCAATGGGGTG	ANSSNGV	+
1684	12635	TTTGAATCAAAGGTAGCCTAC	FESKVAY	+
1685	12636	TCCGCGTCCTCCAATGGGATA	SASSNGI	+
1686	12637	TATTCCAAAGATGGGCCGAAT	YSKDGPN	+
1687	12638	GGCCAAGGCTCATCAACCTGG	GQGSSTW	+
1688	12639	CAACAATCAACCAACGGCCGC	QQSTNGR	+
1689	12640	CGCAACGACTCAAACGGCGTA	RNDSNGV	+
1690	12641	TATTCCAGGCACGGGGATAAT	YSRHGDN	+
1691	12642	TACTTTTCATCAAACGGCGTA	YFSSNGV	+
1692	12643	CACATGTCCTCCAATGGGGTG	HMSSNGV	+
1693	12644	TTGTCCAAAATGGGGTCCAAT	LSKMGSN	+
1694	12645	AACAACTCATCAAACGGCGTA	NNSSNGV	+
1695	12646	TTGGCGTCCTCCAATGGGGTG	LASSNGV	+
1696	12647	CAACATTCACGCGAAGGCGTA	QHSREGV	+
1697	12648	TTGTCCAAAATGGGGACGAAT	LSKMGTN	+
1698	12649	TTTGACGGCAAGTCACCCTAC	FDGKSPY	+
1699	12650	TATTCCGTGAAAAATACGAAT	YSVKNTN	+
1700	12651	TTGTCCAAACAGAATTTGAAT	LSKQNLN	+
1701	12652	GGGGCGAATCAGTCCTCCTGG	GANQSSW	+
1702	12653	TTGGCGAGGGATGGGCCGAAT	LARDGPN	+
1703	12654	ATAACGTCCGATAATGGGAGG	ITSDNGR	+
1704	12655	ATGCACTCCTCCAATGGGGTG	MHSSNGV	+
1705	12656	TATGCGAAACAGAATTTGAAT	YAKQNLN	+
1706	12657	ACGAGGAATGGGACGCCGGCG	TRNGTPA	+
1707	12658	TACTCAAAGGGCGGCATCAAC	YSKGGIN	+
1708	12659	ACCAACGACGCCGTAAAGTGG	TNDAVKW	+
1709	12660	ACGAAATCCGGGGATTTGCCG	TKSGDLP	+

1710	12661	TACTCACGCAACAACCAAAAC	YSRNNQN	+
1711	12662	GGGCAGTCCACGAATGGGGTG	GQSTNGV	+
1712	12663	GACTCATACTCAGGCCAAGAC	DSYSGQD	+
1713	12664	TTCTCCAAAGCGAATACGAAT	FSKANTN	+
1714	12665	ACCCTGTCATCAAACGGCGTA	TLSSNGV	+
1715	12666	TATTCCAGGGAGGGGTTCAAT	YSREGFN	+
1716	12667	TACCTGAAGTCACAAACCGTA	YLKSQTV	+
1717	12668	TTCGATTCCTCCAATGGGGTG	FDSSNGV	+
1718	12669	CAGGAGTCCCAGAATGGGAGG	QESQNGR	+
1719	12670	ATGACGTCCTCCAATGGGGTG	MTSSNGV	+
1720	12671	AGGGGGAATGAGTCCGGGTGG	RGNESGW	+
1721	12672	TATGCGAAAGAGGGGTATAAT	YAKEGYN	+
1722	12673	TACGCCAAGTCAAACCAAAAC	YAKSNQN	+
1723	12674	GCGATGTCCACGAATGGGATA	AMSTNGI	+
1724	12675	TACGCCCGCTACGGCGAAAAC	YARYGEN	+
1725	12676	GTGGCGTCCTCCGGGGCGGGG	VASSGAG	+
1726	12677	AACATCTCAACCAACGGCATC	NISTNGI	+
1727	12678	TTCTCCAGGGTGAATGAGAAT	FSRVNEN	+
1728	12679	TTGTCCAAATTGGGGGAGAAT	LSKLGEN	+
1729	12680	GATCACAAAGGGCAGATAGCG	DHKGQIA	+
1730	12681	TATGCGAAATTGAATGCGAAT	YAKLNAN	+
1731	12682	TATGCGAAAGCGAATCAGAAT	YAKANQN	+
1732	12683	GGGGAGTCCACGAATGGGGTG	GESTNGV	+
1733	12684	TATGCGAAACAGAATACGAAT	YAKQNTN	+
1734	12685	TACTCAAAGGCCAACGGCAAC	YSKANGN	+
1735	12686	ATCGACTCATCAAACGGCGTA	IDSSNGV	+
1736	12687	TTCTTCTCCACGAATGGGATA	FFSTNGI	+
1737	12688	TACTCAAAGATCAACACCAAC	YSKINTN	+
1738	12689	GATAATTCCACGAATGGGAGG	DNSTNGR	+
1739	12690	GTGGAGTATTCCTTCGGGGAT	VEYSFGD	+
1740	12691	TTCGCGAAAACGGGGGTGAAT	FAKTGVN	+
1741	12692	ACCGAATCATCAAACGGCGTA	TESSNGV	+
1742	12693	AACTACTCAACCAACGGCATC	NYSTNGI	+
1743	12694	ATAATGTCCTCCAATGGGGTG	IMSSNGV	+
1744	12695	CTGGCCCGCATCGGCTCAAAC	LARIGSN	+
1745	12696	AATGATTCCACGAATGGGATA	NDSTNGI	+
1746	12697	TTTTCAAAGGTAGGCGAAAAC	FSKVGEN	+
1747	12698	TTGTCCAAATTGGGGGATAAT	LSKLGDN	+
1748	12699	GTAACCGACTTTAACGGCAAG	VTDFNGK	+
1749	12700	TATTCCAAACCGAATTTCAAT	YSKPNFN	+
1750	12701	CAGGGGTCCACGAATGGGGTG	QGSTNGV	+
1751	12702	TTTTCAAAGATGGGCCATAAC	FSKMGHN	+
1752	12703	GATTTCAGGGGGAATGATGCG	DFRGNDA	+
1753	12704	TTCGCGAAAAATGGGTTGAAT	FAKNGLN	+
1754	12705	TACTCAAAGGGCAACGAAAAC	YSKGNEN	+

1755	12706	TATTCCAAAACGAATGTGAAT	YSKTNVN	+
1756	12707	GTAGACTCAACCAACGGCCGC	VDSTNGR	+
1757	12708	CGCGGCGGCTACGAAACCTTT	RGGYETF	+
1758	12709	GTACCCCAACGCGGCGACTTT	VPQRGDF	+
1759	12710	CCGTGGTCCACGAATGGGATA	PWSTNGI	+
1760	12711	CACGCGAATACGTCCAATTGG	HANTSNW	+
1761	12712	GCGTTCTCCACGAATGGGATA	AFSTNGI	+
1762	12713	ATGCTGTCAACCAACGGCATC	MLSTNGI	+
1763	12714	GAACAATCAACCAACGGCATC	EQSTNGI	+
1764	12715	TCAAAGTCATCAAACGGCGTA	SKSSNGV	+
1765	12716	TACGCCAAGCTGAACAACAAC	YAKLNNN	+
1766	12717	TACTCAAAGAACAACATGAAC	YSKNNMN	+
1767	12718	TATGCGCACGCGGGGATAGGG	YAHAGIG	+
1768	12719	GGGCCGCAGTCCTCCACGTGG	GPQSSTW	+
1769	12720	AACCAAGACTACGTAAAGTAC	NQDYVKY	+
1770	12721	TACTTTGACGGCAAGGTATCA	YFDGKVS	+
1771	12722	TTCGCGAGGTTCGGGCCGAAT	FARFGPN	+
1772	12723	TCCAATGGGAATTCCTCCTAT	SNGNSSY	+
1773	12724	GGGAATTCCACGAATGGGGTG	GNSTNGV	+
1774	12725	GATAATAGGGGGAGGGCGGCG	DNRGRAA	+
1775	12726	TACTCAAAGTCAAACTCAAAC	YSKSNSN	+
1776	12727	TTGGCGAGGGCGGGGTCCAAT	LARAGSN	+
1777	12728	TATGCGAAATTCGGGTTCAAT	YAKFGFN	+
1778	12729	TATGCGAGGCCGGGGATGAAT	YARPGMN	+
1779	12730	TATGCGAAAGCGGGGGGGAAT	YAKAGGN	+
1780	12731	CAGAATTCCTCCAATGGGGTG	QNSSNGV	+
1781	12732	ACGGATTCCTCCAATGGGGTG	TDSSNGV	+
1782	12733	TTTTCACGCTCAGGCCAAAAC	FSRSGQN	+
1783	12734	TATGCGAAAGGGAATGAGAAT	YAKGNEN	+
1784	12735	TATTCCAGGGATAATTTCAAT	YSRDNFN	+
1785	12736	TATTCCGCGGCGAATGCGAAT	YSAANAN	+
1786	12737	ATCGAATCAACCAACGGCCGC	IESTNGR	+
1787	12738	AATGATGGGGGGTCCGCGTGG	NDGGSAW	+
1788	12739	TACTCAAAGTACGGCGAAAAC	YSKYGEN	+
1789	12740	TACGCCAAGCAAGGCGAAAAC	YAKQGEN	+
1790	12741	CTGTCAAAGAACGGCGTAAAC	LSKNGVN	+
1791	12742	TTGGCGAAAGCGGGGACGAAT	LAKAGTN	+
1792	12743	AATGCGTCCACGAATGGGATA	NASTNGI	+
1793	12744	TATGCGAAAACGAATACGAAT	YAKTNTN	+
1794	12745	TTGTCCAAAGCGAATCAGAAT	LSKANQN	+
1795	12746	GAGGTGTCCACGAATGGGGTG	EVSTNGV	+
1796	12747	TTGGCGAAAGTGGGGCCGAAT	LAKVGPN	+
1797	12748	TCACGCGACACCAACGGCCGC	SRDTNGR	+
1798	12749	TATTCCAAAGGGGGGGTGAAT	YSKGGVN	+
1799	12750	TACGCCAAGCTGAACGTAAAC	YAKLNVN	+

1800	12751	ACGTATTCCGGGGATTCCGCG	TYSGDSA	+
1801	12752	CTGTCACGCTACAACGACAAC	LSRYNDN	+
1802	12753	CCGAATGGGAGGTCCGCGTAT	PNGRSAY	+
1803	12754	TATTCCAGGGAGAATTTCAAT	YSRENFN	+
1804	12755	GGGTGGAGGGGGGAGCCGTCC	GWRGEPS	+
1805	12756	TATGCGAAATCCAATGCGAAT	YAKSNAN	+
1806	12757	CTGTCACGCTTTAACGACAAC	LSRFNDN	+
1807	12758	CGCGGCGACCGCACCTTTCCC	RGDRTFP	+
1808	12759	GCGTATTCCACGAATGGGATA	AYSTNGI	+
1809	12760	TCATCAGGCGCCTCAACCTGG	SSGASTW	+
1810	12761	TATGCGAAACAGAATGCGAAT	YAKQNAN	+
1811	12762	GATGGGAATGGGTCCCACTGG	DGNGSHW	+
1812	12763	TTTTCACGCAACGGCATGAAC	FSRNGMN	+
1813	12764	GCGGATTCCACGAATGGGATA	ADSTNGI	+
1814	12765	GGGACGGGGGCGAATCCGTGG	GTGANPW	+
1815	12766	ACGAAAAATGGGAATTCCGCG	TKNGNSA	+
1816	12767	TTCTCCAAAGCGGGGGATAAT	FSKAGDN	+
1817	12768	GGGCAGAAAGGGATACCGTAT	GQKGIPY	+
1818	12769	GCCACCTCATCAAACGGCGTA	ATSSNGV	+
1819	12770	AGGCCGGATACGGTGCAGTGG	RPDTVQW	+
1820	12771	CCGGATTCCACGAATGGGGTG	PDSTNGV	+
1821	12772	TTGGCGAGGATAGGGGAGAAT	LARIGEN	+
1822	12773	TTGGATTCCTCCAATGGGGTG	LDSSNGV	+
1823	12774	GGCTCATCAACCAACGGCATC	GSSTNGI	+
1824	12775	TATGCGAAAGGGGGGGCGGGG	YAKGGAG	+
1825	12776	TTCTCCAGGTCCAATGATAAT	FSRSNDN	+
1826	12777	TATGCGAAAGCGGGGGAGAAT	YAKAGEN	+
1827	12778	TATGCGAGGGATGGGTGGAAT	YARDGWN	+
1828	12779	TACTCAAAGGTAGGCGGCGAC	YSKVGGD	+
1829	12780	AATGATAGGAAAACGGGGGAG	NDRKTGE	+
1830	12781	GCCCCCTCAACCCATACCTGG	APSTHTW	+
1831	12782	AACGTATCAACCAACGGCATC	NVSTNGI	+
1832	12783	CCGACGTCCTCCAATGGGGTG	PTSSNGV	+
1833	12784	TTCGTGTCCTCCAATGGGGTG	FVSSNGV	+
1834	12785	TTTTCAAAGATGAACGACAAC	FSKMNDN	+
1835	12786	CAGTCCGGGTCCTCCCCGTAT	QSGSSPY	+
1836	12787	TTGGCGAAAGGGGGGGAGAAT	LAKGGEN	+
1837	12788	TTCGCGAGGGGGGGGGATAAT	FARGGDN	+
1838	12789	CTGGCCCGCGAAGGCCCCAAC	LAREGPN	+
1839	12790	GCCTCAGGCAACTCAATGTGG	ASGNSMW	+
1840	12791	GGCCATGCCGACCAAAAGTGG	GHADQKW	+
1841	12792	ATAGATTCCGTGAATGGGAGG	IDSVNGR	+
1842	12793	TTGGCGAAAGTGGGGCACAAT	LAKVGHN	+
1843	12794	TTCTCCAGGTATAATGAGAAT	FSRYNEN	+
1844	12795	TACTCACGCCATGGCTACAAC	YSRHGYN	+

1845	12796	TTTGACTCAACCAACGGCCGC	FDSTNGR	+
1846	12797	GGCGGCTCATCAACCGTATGG	GGSSTVW	+
1847	12798	TACCTGTCAACCAACGGCATC	YLSTNGI	+
1848	12799	TTCTCCAGGCAGAATGAGAAT	FSRQNEN	+
1849	12800	TATGCGAGGCCGAATTTCAAT	YARPNFN	+
1850	12801	TACTCAAAGATCAACCTGAAC	YSKINLN	+
1851	12802	TATGCGAAAGGGGGGGAGAAT	YAKGGEN	+
1852	12803	TTGGCGAGGGCGGGGGAGAAT	LARAGEN	+
1853	12804	GTGACGGATGGGATGAGGTAT	VTDGMRY	+
1854	12805	CAATCATCATCAAACGGCGTA	QSSSNGV	+
1855	12806	GACGGCGGCTCAGCCTCATGG	DGGSASW	+
1856	12807	CTGGCCAAGATCGGCATCAAC	LAKIGIN	+
1857	12808	CAGCAGTCCTCCAATGGGGTG	QQSSNGV	+
1858	12809	GGGAATGGGAAATCCTCCTAT	GNGKSSY	+
1859	12810	TTGGCGAAAGTGGGGATAAAT	LAKVGIN	+
1860	12811	GGCGTACCCGGCACCATGTTT	GVPGTMF	+
1861	12812	TTGTCCAGGTCCTCCCAGGAT	LSRSSQD	+
1862	12813	TACTCAAAGATCAACGAAAAC	YSKINEN	+
1863	12814	GGCTACTCAACCAACGGCCGC	GYSTNGR	+
1864	12815	ATCCGCTCAGGCTCAGCCGGC	IRSGSAG	+
1865	12816	TATGCGAGGCACGGGGAGAAT	YARHGEN	+
1866	12817	TTGTCCAGGTCCAATGAGAAT	LSRSNEN	+
1867	12818	ACGGATGCGCAGTCCAGGTAT	TDAQSRY	+
1868	12819	TACTCAAAGAACAACACCAAC	YSKNNTN	+
1869	12820	AAAAATGGGGAGTCCAATTGG	KNGESNW	+
1870	12821	TTGGCGAGGATAGGGGATAAT	LARIGDN	+
1871	12822	GGCCATTCAACCAACGGCGTA	GHSTNGV	+
1872	12823	TACTCAAAGATGAACGGCAAC	YSKMNGN	+
1873	12824	TTTTCAAAGTCAGGCCTGAAC	FSKSGLN	+
1874	12825	CGCGAAACCAACGTAGGCTGG	RETNVGW	+
1875	12826	GGGGCGTCCACGAATGGGAGG	GASTNGR	+
1876	12827	TACTCAAAGACCGGCTGCAAC	YSKTGCN	+
1877	12828	TTTGCCCGCGGCGGCGAAAAC	FARGGEN	+
1878	12829	TACGCCAAGCTGGGCATCAAC	YAKLGIN	+
1879	12830	GACTCAACCGGCATGAAGTAC	DSTGMKY	+
1880	12831	ATGAATTCCTCCAATGGGGTG	MNSSNGV	+
1881	12832	TTCTCCAAAACGGGGATGAAT	FSKTGMN	+
1882	12833	TTCGCGAGGAATGGGGAGAAT	FARNGEN	+
1883	12834	ACGTGGACGGGGGTGGGGCCG	TWTGVGP	+
1884	12835	TCACATGGCGCCTCAACCTGG	SHGASTW	+
1885	12836	TCCATATCCTCCAATGGGGTG	SISSNGV	+
1886	12837	AAGAACGACTCAATCCTGTGG	KNDSILW	+
1887	12838	TATGCGAAAGAGGGGTGGAAT	YAKEGWN	+
1888	12839	AAGTCATCAACCAACGGCGTA	KSSTNGV	+
1889	12840	TTCGCGAAAACGGGGCAGAAT	FAKTGQN	+

1890	12841	TATTCCAAAGAGGGGCCGAAT	YSKEGPN	+
1891	12842	GGCTGGTCAACCAACGGCATC	GWSTNGI	+
1892	12843	AACCCCTCATCATCAGCCTGG	NPSSSAW	+
1893	12844	GCGTTGTCCACGAATGGGGTG	ALSTNGV	+
1894	12845	TATTTCGCGGGGGTGCCGGCG	YFAGVPA	+
1895	12846	TATCACGCGTCCACGCCGAAT	YHASTPN	+
1896	12847	TACTCAAAGAACAACGACAAC	YSKNNDN	+
1897	12848	TTTTACTCATCAAACGGCGTA	FYSSNGV	+
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1900	12851	ACGGAGGGGCAGTCCAAATGG	TEGQSKW	+
1901	12852	CTGGCCAAGATCGGCCTGAAC	LAKIGLN	+
1902	12853	TTGTCCAAACAGAATGCGAAT	LSKQNAN	+
1903	12854	TTTGCCAAGAACGGCATGAAC	FAKNGMN	+
1904	12855	GAATCATCAACCAACGGCGTA	ESSTNGV	+
1905	12856	TCCAATGCGACGACGGGGTGG	SNATTGW	+
1906	12857	CTGCGCAACGGCGTAAACGCC	LRNGVNA	+
1907	12858	TTGTCCAGGACGAATGAGAAT	LSRTNEN	+
1908	12859	TGGATGTCCTCCAATGGGGTG	WMSSNGV	+
1909	12860	CCGCACTCCTCCAATGGGGTG	PHSSNGV	+
1910	12861	TTCTCCAGGGATAATTATAAT	FSRDNYN	+
1911	12862	CCGTATTCCACGAATGGGATA	PYSTNGI	+
1912	12863	TACGCCAAGGGCGGCGGCAAC	YAKGGGN	+
1913	12864	TTGGCGTTGAGGGGGATGGAT	LALRGMD	+
1914	12865	CTGTCAAAGGCCAACAACAAC	LSKANNN	+
1915	12866	TACTCAAAGATCAACATGAAC	YSKINMN	+
1916	12867	ATGGGGTCCACGAATGGGATA	MGSTNGI	+
1917	12868	CAAACCTCAACCAACGGCCGC	QTSTNGR	+
1918	12869	TATGCGAGGCCGGGGTTCAAT	YARPGFN	+
1919	12870	GTACCCCCCTACCATCATTCA	VPPYHHS	+
1920	12871	TATGCGAAATTGAATACGAAT	YAKLNTN	+
1921	12872	AAAGATTCCCACGTGGCGTGG	KDSHVAW	+
1922	12873	ATGTATTCCACGAATGGGATA	MYSTNGI	+
1923	12874	GGCGGCGCCGGCGTAGGCTGG	GGAGVGW	+
1924	12875	ACGGGGGGGACGTCCGCGTAT	TGGTSAY	+
1925	12876	TTCTCCAGGTCCGGGGATAAT	FSRSGDN	+
1926	12877	AAAAGGTCCGGGGAGAATGCG	KRSGENA	+
1927	12878	TTGAATGGGAGGGGGTATGAT	LNGRGYD	+
1928	12879	GCGGGGTCCGGGAATGCGTGG	AGSGNAW	+
1929	12880	CCGTTCTCCACGAATGGGATA	PFSTNGI	+
1930	12881	CTGGCCAAGATCGGCGTAAAC	LAKIGVN	+
1931	12882	TTGGCGAGGCACGGGGAGAAT	LARHGEN	+
1932	12883	ATAGGGTTGTCCGGGTTCGAT	IGLSGFD	+
1933	12884	TTGTCCAAAGCGAATGATAAT	LSKANDN	+
1934	12885	CTGAAGCTGAACCCCAACTCA	LKLNPNS	+

1935	12886	TTGGCGAGGGTGGGGGAGAAT	LARVGEN	+
1936	12887	TTCGCGAGGCCGGGGCCGAAT	FARPGPN	+
1937	12888	TACGCCAAGCAAGGCGGCAAC	YAKQGGN	+
1938	12889	TATGCGAAAGATGGGTGGAAT	YAKDGWN	+
1939	12890	TACTACTCAGGCCATGTAACC	YYSGHVT	+
1940	12891	ATGGAATCAAACGTACGCTGG	MESNVRW	+
1941	12892	TACGCCAAGGTAGGCCAAAAC	YAKVGQN	+
1942	12893	TTGGCGAAACACGGGATGAAT	LAKHGMN	+
1943	12894	GGGACGTCCACGAATGGGGTG	GTSTNGV	+
1944	12895	AATAATAGGGGGAGGGATGCG	NNRGRDA	+
1945	12896	TCCACGTCCACGGATGGGAGG	STSTDGR	+
1946	12897	TATGCGAAACACGGGGATAAT	YAKHGDN	+
1947	12898	ATGTCCTCCTCCAATGGGGTG	MSSSNGV	+
1948	12899	GAGTTCTCCACGAATGGGAGG	EFSTNGR	+
1949	12900	TCCGTGTCCTCCAATGGGGTG	SVSSNGV	+
1950	12901	TTGGCGAAAACGGGGGGGAAT	LAKTGGN	+
1951	12902	CCGGATTCCACGAATGGGATA	PDSTNGI	+
1952	12903	TTCGCGAAAAATGGGGTGAAT	FAKNGVN	+
1953	12904	TTGGCGAGGCCGGGGGTGAAT	LARPGVN	+
1954	12905	GGGTCCGTGCAGGTGAAATAT	GSVQVKY	+
1955	12906	TATTCCAGGGAGGGGTGGAAT	YSREGWN	+
1956	12907	GGGAATACGGTGGTGTCCTGG	GNTVVSW	+
1957	12908	GAGTATTCCACGAATGGGAGG	EYSTNGR	+
1958	12909	TTGTCCAGGTTCAATGAGAAT	LSRFNEN	+
1959	12910	TACTGGAACAACAACGAATCA	YWNNNES	+
1960	12911	TTTTCAAAGTCAGGCATGAAC	FSKSGMN	+
1961	12912	TTGGCGAGGGAGGGGTATAAT	LAREGYN	+
1962	12913	CTGGAATCAACCAACGGCGTA	LESTNGV	+
1963	12914	TACTCACGCCCCGGCATCAAC	YSRPGIN	+
1964	12915	TTCTCCAGGATAAATGAGAAT	FSRINEN	+
1965	12916	AACATCTCAACCAACGGCCGC	NISTNGR	+
1966	12917	TTGGTGAGGTCCGTGAATGAG	LVRSVNE	+
1967	12918	TACTCACGCTTTGGCTCAAAC	YSRFGSN	+
1968	12919	TTCTCCAGGTTGGGGTATAAT	FSRLGYN	+
1969	12920	TATTCCAGGTATGGGATGAAT	YSRYGMN	+
1970	12921	TACTCAAAGTACAACGAAAAC	YSKYNEN	+
1971	12922	TTCTTCTCCGGGGAGACGTTG	FFSGETL	+
1972	12923	TTCTCCAAAATGGGGTTGAAT	FSKMGLN	+
1973	12924	GATAATCACGGGAATAGGTAT	DNHGNRY	+
1974	12925	TACGCCAAGATGGGCGACAAC	YAKMGDN	+
1975	12926	GTACCCAACAAGGGCGACTTT	VPNKGDF	+
1976	12927	TCAACCGGCTCATCAAACTGG	STGSSNW	+
1977	12928	TACTCACGCGGCGGCGAAAAC	YSRGGEN	+
1978	12929	TACTCAAAGAACGGCGAAAAC	YSKNGEN	+
1979	12930	TTCTCCAGGCAGGGGGATAAT	FSRQGDN	+

1980	12931	TTGGTGTCCTCCAATGGGGTG	LVSSNGV	+
1981	12932	AACTCATCAGGCCGCTCAGCC	NSSGRSA	+
1982	12933	AATCCGAAAGGGTCCGGGGAG	NPKGSGE	+
1983	12934	TTCGCGAAAGGGGGGGTGAAT	FAKGGVN	+
1984	12935	TACGCCAAGCTGGGCGAAAAC	YAKLGEN	+
1985	12936	TACTCAAAGCATGGCGAAAAC	YSKHGEN	+
1986	12937	AATGAGAAAAGGATGTATGAG	NEKRMYE	+
1987	12938	TTGGCGAAAGAGGGGAGGAAT	LAKEGRN	+
1988	12939	TATGAGTATGGGTATGGGAAT	YEYGYGN	+
1989	12940	TTGGCGAGGTATGGGGAGAAT	LARYGEN	+
1990	12941	TTCACGAGGTTGGATGATAGG	FTRLDDR	+
1991	12942	TATAATAGGTTGGGGTATGAT	YNRLGYD	+
1992	12943	ACGAGGGAGGGGGATGTGCCG	TREGDVP	+
1993	12944	GAGGCGTCCACGAATGGGGTG	EASTNGV	+
1994	12945	CACAATGCGATGTCCTCCTAT	HNAMSSY	+
1995	12946	TTGCACAAAGTGTTGTATGAT	LHKVLYD	+
1996	12947	TTTTCAAAGGCCAACAACAAC	FSKANNN	+
1997	12948	ATGTCCGAGACGTCCGGGTGG	MSETSGW	+
1998	12949	ACGTGGAATGGGCAGAATGCG	TWNGQNA	+
1999	12950	CTGGCCAAGCATGGCTCAAAC	LAKHGSN	+
2000	12951	CCGGGGTCCTCCAATGGGGTG	PGSSNGV	+
2001	12952	TTCTCCAAAACGGGGGCGAAT	FSKTGAN	+
2002	12953	AATGGGATGAATGGGAGGGAT	NGMNGRD	+
2003	12954	GATGCGAGGACGGATAGGAAT	DARTDRN	+
2004	12955	TCATCATCATCAAACGGCATG	SSSSNGM	+
2005	12956	CAGCACTCCTCCAATGGGGTG	QHSSNGV	+
2006	12957	TTCTCCAAAATAGGGGATAAT	FSKIGDN	+
2007	12958	TTCTCCAAATCCGGGGTGAAT	FSKSGVN	+
2008	12959	GAGACGTCCACGAATGGGATA	ETSTNGI	+
2009	12960	GAGTCCTCCTCCAATGGGGTG	ESSSNGV	+
2010	12961	AATAAATATGGGATGGATACG	NKYGMDT	+
2011	12962	TATGCGAAAATAGGGGATAAT	YAKIGDN	+
2012	12963	TCCAATGGGAGGAATCCGTAT	SNGRNPY	+
2013	12964	CTGGCCAAGGGCGGCGACAAC	LAKGGDN	+
2014	12965	ACGCCGTCCACGAATGGGAGG	TPSTNGR	+
2015	12966	GGCGAAGGCATCCATAAGTGG	GEGIHKW	+
2016	12967	AATCACAGGTTGGCGGAGAAT	NHRLAEN	+
2017	12968	CTGTCACGCGGCAACGACAAC	LSRGNDN	+
2018	12969	TACGTACGCACCGACACCTCA	YVRTDTS	+
2019	12970	TACGCCAAGTCAAACTCAAAC	YAKSNSN	+
2020	12971	TTGGCGAGGGGGTCCAATGAT	LARGSND	+
2021	12972	CCGTTCTCCTCCAATGGGGTG	PFSSNGV	+
2022	12973	TATTCCAGGGATGGGCCGAAT	YSRDGPN	+
2023	12974	TTGGCGAAAGGGAATCCGAAT	LAKGNPN	+
2024	12975	TACGCCAAGGTAGGCGTAAAC	YAKVGVN	+

2025	12976	GACTCATCAACCAACGGCCGC	DSSTNGR	+
2026	12977	GCGAAATCCTCCAATGGGGTG	AKSSNGV	+
2027	12978	GAGAAAGGGTATAATGTGTAT	EKGYNVY	+
2028	12979	GAGGCGCCGGATATAAGGTAT	EAPDIRY	+
2029	12980	CATTCAGCCACCTCAAAGTAC	HSATSKY	+
2030	12981	CTGTCACGCAACGGCGAAAAC	LSRNGEN	+
2031	12982	TTCGCGAAAACGGGGGATAAT	FAKTGDN	+
2032	12983	GGGCCGACGGAGGTGAGGTAT	GPTEVRY	+
2033	12984	TTGGCGAAATTGGGGCAGAAT	LAKLGQN	+
2034	12985	ACGCAGTCCACGCACGGGAAT	TQSTHGN	+
2035	12986	AATGGGTCCACGAATGGGGTG	NGSTNGV	+
2036	12987	CTGTCACGCCATGGCGACAAC	LSRHGDN	+
2037	12988	GAAGGCTCAACCAACGGCGTA	EGSTNGV	+
2038	12989	GAGGAGGCGAGGGGGAGGTTG	EEARGRL	+
2039	12990	TTCTCCAGGCACAATGATAAT	FSRHNDN	+
2040	12991	AGGCAGTCCTCCAATGGGGAG	RQSSNGE	+
2041	12992	AATGCGAGGACGGGGCACGAT	NARTGHD	+
2042	12993	TATTCCAGGGAGGGGCACAAT	YSREGHN	+
2043	12994	ACGTCCTCCACGGTGGGGAGG	TSSTVGR	+
2044	12995	TACGCCAAGGAAAACTGGAAC	YAKENWN	+
2045	12996	TCCACGAATGGGATGTCCTAT	STNGMSY	+
2046	12997	CCCAACGCCGGCGTATCATGG	PNAGVSW	+
2047	12998	GAGAATGGGAAAGGGATGAAT	ENGKGMN	+
2048	12999	TACGCCGCCGCCTCACTGTAC	YAAASLY	+
2049	13000	GGCGTATCAGGCTCATCATGG	GVSGSSW	+
2050	13001	CTGTCAAAGATGGGCCAAAAC	LSKMGQN	+
2051	13002	AAGGAATCAACCAACGGCGTA	KESTNGV	+
2052	13003	AATATGTCCACGAATGGGGTG	NMSTNGV	+
2053	13004	TTTTCAAAGTCAGGCGCCAAC	FSKSGAN	+
2054	13005	TACTCAAAGAACAACCAAAAC	YSKNNQN	+
2055	13006	TACTCAAAGAACAACGAAAAC	YSKNNEN	+
2056	13007	TACGCCAAGCTGAACATGAAC	YAKLNMN	+
2057	13008	TCCGGGACGACGGGGTGGGAT	SGTTGWD	+
2058	13009	CAGTATTCCACGAATGGGGTG	QYSTNGV	+
2059	13010	TTCTCCAAAGCGAATGATAAT	FSKANDN	+
2060	13011	TACGCCCGCCATAACCCCAAC	YARHNPN	+
2061	13012	TATTCCAGGAGGGGGGATAAT	YSRRGDN	+
2062	13013	CTGTCAAAGATGAACTCAAAC	LSKMNSN	+
2063	13014	TTCTCCAGGACGAATGATAAT	FSRTNDN	+
2064	13015	AATCACACGGGGAAAATGGCG	NHTGKMA	+
2065	13016	GTACCCTACAAGGGCGACTTT	VPYKGDF	+
2066	13017	CTGTTTTCATCAAACGGCGTA	LFSSNGV	+
2067	13018	GTAAACTCAAACTCATCATGG	VNSNSSW	+
2068	13019	CCGGTGTCCACGAATGGGAGG	PVSTNGR	+
2069	13020	CTGCATGCCTCAACCGTAAAC	LHASTVN	+

2070	13021	TTGTCCAGGAATGGGGATAAT	LSRNGDN	+
2071	13022	TTCTCCAGGATGGGGTTCAAT	FSRMGFN	+
2072	13023	ACGTCCCCGAATTTGTCCTGG	TSPNLSW	+
2073	13024	GACGCCTACCGCGGCTCAGAC	DAYRGSD	+
2074	13025	TCCGGGCAGTCCACGGGGTGG	SGQSTGW	+
2075	13026	TTGTCCAAACAGGGGACGAAT	LSKQGTN	+
2076	13027	TACGCCAAGCCCGGCACCAAC	YAKPGTN	+
2077	13028	TCCTCCTCCTCCGCGACGTGG	SSSSATW	+
2078	13029	CCCGCCTCAACCAACGGCATC	PASTNGI	+
2079	13030	CAGTTCTCCACGAATGGGGTG	QFSTNGV	+
2080	13031	CTGTCAAAGGCCTCAGGCAAC	LSKASGN	+
2081	13032	TTGGATGGGAATTCCATGTAT	LDGNSMY	+
2082	13033	TACGCCAAGATGGGCGAAAAC	YAKMGEN	+
2083	13034	TCCATGTCCTCCAATGGGGTG	SMSSNGV	+
2084	13035	TGGTCATCAGCCTACCCCGTA	WSSAYPV	+
2085	13036	TACTCACGCCATAACTCAAAC	YSRHNSN	+
2086	13037	TTGGCGAAAATAGGGGCGAAT	LAKIGAN	+
2087	13038	ACCGGCCAAACCACCTCATGG	TGQTTSW	+
2088	13039	GATCACTCCACGAATGGGAGG	DHSTNGR	+
2089	13040	GGGGATTCCACGAATGGGGTG	GDSTNGV	+
2090	13041	GAGAGGTCCTCCAATGGGGTG	ERSSNGV	+
2091	13042	TACTCAAAGACCAACCTGAAC	YSKTNLN	+
2092	13043	TCAAACGGCGCCTCATCATAC	SNGASSY	+
2093	13044	TACGCCAAGCTGAACCTGAAC	YAKLNLN	+
2094	13045	TTGTCCAAAAATGGGTTGAAT	LSKNGLN	+
2095	13046	GAAGGCGGCGGCGGCCGCTAC	EGGGGRY	+
2096	13047	TGGAGGTCCGATGGGTATGCG	WRSDGYA	+
2097	13048	TATTCCAAATTCAATGAGAAT	YSKFNEN	+
2098	13049	TCATCAACCGGCATGTCATTT	SSTGMSF	+
2099	13050	ATGACGGATGGGACGAAATAT	MTDGTKY	+
2100	13051	GTGCAGGATTATGATAGGAAT	VQDYDRN	+
2101	13052	AATCAGGATGGGTATATGGTG	NQDGYMV	+
2102	13053	AATACGGCGACGAATGGGAGG	NTATNGR	+
2103	13054	CTGTCAAAGTCAAACCTGAAC	LSKSNLN	+
2104	13055	GTGCCGTCCACGAATGGGGTG	VPSTNGV	+
2105	13056	AACTTTCAAGGCTACGGCCAA	NFQGYGQ	+
2106	13057	AATGCGTATGAGGCGAGGAAT	NAYEARN	+
2107	13058	AAAGAGTCCTCCAATGGGGTG	KESSNGV	+
2108	13059	GATAGGGGGAATTCCACGTAT	DRGNSTY	+
2109	13060	TATGCGAAAGCGAATGAGAAT	YAKANEN	+
2110	13061	GATTTGAGGGGGACGGGGGCG	DLRGTGA	+
2111	13062	TACGCCCGCCCCAACGAAAAC	YARPNEN	+
2112	13063	TACTCAAAGTGGGGCGACAAC	YSKWGDN	+
2113	13064	TACTCACGCTTTAACCCCAAC	YSRFNPN	+
2114	13065	CTGGCCAAGGCCGGCGAAAAC	LAKAGEN	+

2115	13066	CATCTGTCAACCAACGGCCGC	HLSTNGR	+
2116	13067	AATCACTCCTCCAATGGGGTG	NHSSNGV	+
2117	13068	GGCCCCCCCGACTTTATGCGC	GPPDFMR	+
2118	13069	ACCGGCTCATCACATGACTGG	TGSSHDW	+
2119	13070	GAGATATCCACGAATGGGAGG	EISTNGR	+
2120	13071	TTCTCCAGGTCCGGGGAGAAT	FSRSGEN	+
2121	13072	CTGTCAAAGCAAAACACCAAC	LSKQNTN	+
2122	13073	TATTCCAGGGATGGGCACAAT	YSRDGHN	+
2123	13074	TTGTCCAGGGGGAATGAGAAT	LSRGNEN	+
2124	13075	GGGTCCGGGGAGGTGAGGTAT	GSGEVRY	+
2125	13076	CCGTATTCCTCCAATGGGGTG	PYSSNGV	+
2126	13077	TACTCACGCCCCGGCGTAAAC	YSRPGVN	+
2127	13078	GGCCTGGGCTCAGTAACCTGG	GLGSVTW	+
2128	13079	CGCCAATCAGACTCATTTGAA	RQSDSFE	+
2129	13080	TACTTTTCAGGCGCCAACGTA	YFSGANV	+
2130	13081	GATTCCGAGGGGACGAGGAAT	DSEGTRN	+
2131	13082	TCAGGCTCACCCAACCGCTAC	SGSPNRY	+
2132	13083	CGCGAATCAGTAAACGGCTGG	RESVNGW	+
2133	13084	TTGGCGAAATTGGGGACGAAT	LAKLGTN	+
2134	13085	ATGATGTCCTCCAATGGGGTG	MMSSNGV	+
2135	13086	GGGGGGCCGCAGGTGTTGTAT	GGPQVLY	+
2136	13087	TATTTCGCGTCCCAGAGGGAG	YFASQRE	+
2137	13088	GGGAGGGGGGAGAATCACTAT	GRGENHY	+
2138	13089	TACTCACGCGAAGGCAAGAAC	YSREGKN	+
2139	13090	GAAGGCCTGATCGGCAAGGAC	EGLIGKD	+
2140	13091	CTGTCAAAGGCCGGCGGCAAC	LSKAGGN	+
2141	13092	CCCGAATCAACCAACGGCATC	PESTNGI	+
2142	13093	TACTCACGCGAAGGCGCCAAC	YSREGAN	+
2143	13094	GGCATCGGCAACTCAGCCTGG	GIGNSAW	+
2144	13095	TATGCGAAAGTGGGGGATAAT	YAKVGDN	+
2145	13096	CCGATGTCCACGAATGGGATA	PMSTNGI	+
2146	13097	GGGAATGAGATGGAGTCCTGG	GNEMESW	+
2147	13098	CCCGAATCATCAAACGGCGTA	PESSNGV	+
2148	13099	CGCACCTCATCAACCGGCGTA	RTSSTGV	+
2149	13100	ATAAAATATACGTCCTCCGAT	IKYTSSD	+
2150	13101	ACGAGGTCCGATCCGAATTCC	TRSDPNS	+
2151	13102	TCAGACGGCATCTCACCCTAC	SDGISPY	+
2152	13103	TACTCACGCACCAACGGCAAC	YSRTNGN	+
2153	13104	TACTCAAAGACCAACATGAAC	YSKTNMN	+
2154	13105	TGCTCAGTACCCTCACTGCCC	CSVPSLP	+
2155	13106	TACGCCAAGTCAAACGAAAAC	YAKSNEN	+
2156	13107	ACCGGCGGCCATTCAACCTGG	TGGHSTW	+
2157	13108	TACGGCGGCCATACCATGTAC	YGGHTMY	+
2158	13109	TTTTCAAAGATGAACGAAAAC	FSKMNEN	-
2159	13110	TTCTCCAAATTGGGGGATAAT	FSKLGDN	-

2160	13111	ACCCCCCGCGGCGCCGCCGCC	TPRGAAA	-
2161	13112	CATCATGAACATGGCCCCCGC	HHEHGPR	-
2162	13113	TATTCCAGGGAGGGGATGAAT	YSREGMN	-
2163	13114	GACTACCGCGGCACCCTGCCC	DYRGTLP	-
2164	13115	TATGCGAAACCGGGGATGAAT	YAKPGMN	-
2165	13116	ATAGGGGGGTCCTCCACGTAT	IGGSSTY	-
2166	13117	GACCATGCCAACTCACGCTAC	DHANSRY	-
2167	13118	TACGCCCGCGACGGCATGAAC	YARDGMN	-
2168	13119	TACGCCCGCGAAGGCCATAAC	YAREGHN	-
2169	13120	TTTAACGGCCGCACCTCATAC	FNGRTSY	-
2170	13121	TATAATAGGTTGTCCGATAAT	YNRLSDN	-
2171	13122	TTCGCGAAAGGGGGGACGAAT	FAKGGTN	-
2172	13123	GCCTCAGGCACCTCACCCTGG	ASGTSPW	-
2173	13124	TTTTCACGCTCAAACGAAAAC	FSRSNEN	-
2174	13125	GGGAGGTCCGGGAATGCGGCG	GRSGNAA	-
2175	13126	TTTTCACGCCATGGCTTTAAC	FSRHGFN	-
2176	13127	TACAACTCAACCGAAGGCCGC	YNSTEGR	-
2177	13128	CAGCAGCCGTCCCACTTGTGG	QQPSHLW	-
2178	13129	GATGGGGATAGGGGGGGGTGG	DGDRGGW	-
2179	13130	TTCGCGAAATCCGGGGATAAT	FAKSGDN	-
2180	13131	TACGCCAAGGAAGGCTGCAAC	YAKEGCN	-
2181	13132	ATGAGGAATGATGGGTATGGG	MRNDGYG	-
2182	13133	GTGAATGGGGGGTCCAAATAT	VNGGSKY	-
2183	13134	ATAACGGAGGGGTTGAAATGG	ITEGLKW	-
2184	13135	TGGTTGGCGGGGCCGTCCGCG	WLAGPSA	-
2185	13136	AATGGGCAGGGGTCCACGTGG	NGQGSTW	-
2186	13137	TTCGCGAGGACGAATGATAAT	FARTNDN	-
2187	13138	AGGTATCACGATTCCTATGCG	RYHDSYA	-
2188	13139	AGGCAGTCCATAAATGGGTAT	RQSINGY	-
2189	13140	CAGGCGGAGAGGGGGTATGAT	QAERGYD	-
2190	13141	TTCGCGAGGTTCGGGGCGAAT	FARFGAN	-
2191	13142	ACCCGCCAAGGCATCTCAGCC	TRQGISA	-
2192	13143	TATGTGAGGAATGATCACTCC	YVRNDHS	-
2193	13144	GACATGAACAACAACAAGTGG	DMNNNKW	-
2194	13145	TTCGTGAGGTCCGATTCCAAT	FVRSDSN	-
2195	13146	TACTCACGCGACGGCTTTAAC	YSRDGFN	-
2196	13147	TACGCCCGCGACGGCCATAAC	YARDGHN	-
2197	13148	TTTTCAAAGGCCGGCGAAAAC	FSKAGEN	-
2198	13149	GGGAATGAGGGGTATTGGGAT	GNEGYWD	-
2199	13150	AATTCCTTGGGGACGGGGGCG	NSLGTGA	-
2200	13151	TACGCCAAGCATGGCGAAAAC	YAKHGEN	-
2201	13152	TGGGGGTCCTCCTCCTCCTAT	WGSSSSY	-
2202	13153	TATTCCAGGGAGGGGTTGAAT	YSREGLN	-
2203	13154	TATTCCAGGGAGAATTGGAAT	YSRENWN	-
2204	13155	TTGACGTCCACGCACGGGATG	LTSTHGM	-

2205	13156	AATACGGGGACGTCCTCCTAT	NTGTSSY	-
2206	13157	TACGCCAAGGACGGCTTTAAC	YAKDGFN	-
2207	13158	CAGCCGTTGGGGGGGTATGAT	QPLGGYD	-
2208	13159	GAGTATGGGGGGGGGAAATAT	EYGGGKY	-
2209	13160	TTCTCCAGGCAGGGGGAGAAT	FSRQGEN	-
2210	13161	CTGTGGAACGCCACCGCCCCC	LWNATAP	-
2211	13162	TATGCGAAACAGAATGAGAAT	YAKQNEN	-
2212	13163	AATTTCTCCGGGCAGAATGCG	NFSGQNA	-
2213	13164	AATAATGGGCACATGGCGTAT	NNGHMAY	-
2214	13165	TTCTCCAAAATAGGGGAGAAT	FSKIGEN	-
2215	13166	TTTTCAAAGATCAACCCCAAC	FSKINPN	-
2216	13167	GGGGGGGGGACGTCCCCGTAT	GGGTSPY	-
2217	13168	GGCAACGGCGGCACCCATTGG	GNGGTHW	-
2218	13169	TACTCACGCGACAACTGGAAC	YSRDNWN	-
2219	13170	ATAGGGTCCGCGAATGGGGTG	IGSANGV	-
2220	13171	TGGTCACGCCTGGAAAACAAC	WSRLENN	-
2221	13172	GGGTCCTCCAATGAGAAATGG	GSSNEKW	-
2222	13173	TACTCACGCGAAAACCATAAC	YSRENHN	-
2223	13174	TATGCGAGGCCGGGGCAGAAT	YARPGQN	-
2224	13175	AACGAAGGCCGCGGCTACGCC	NEGRGYA	-
2225	13176	TTGTCCAAATCCTCCTTGGAT	LSKSSLD	-
2226	13177	TATTCCAAAGAGGGGTGGAAT	YSKEGWN	-
2227	13178	GAGTCCTCCGGGTCCTCCTGG	ESSGSSW	-
2228	13179	TACGCCCGCGACGGCGCCAAC	YARDGAN	-
2229	13180	TTCGCGAAAGAGGGGTGGAAT	FAKEGWN	-
2230	13181	TACTCACGCCTGGGCGAAAAC	YSRLGEN	-
2231	13182	TTTGCCCGCGAAGGCTTTAAC	FAREGFN	-
2232	13183	GGCATCTACGACACCATGCCC	GIYDTMP	-
2233	13184	GAGGCGTTGTCCGATAGGGGG	EALSDRG	-
2234	13185	TACTTTGAACTGCGCTCAAAC	YFELRSN	-
2235	13186	CATGGCACCGGCACCCATTTT	HGTGTHF	-
2236	13187	ATCCAAGGCACCACCTACGCC	IQGTTYA	-
2237	13188	TTTTCAAAGCATAACGACAAC	FSKHNDN	-
2238	13189	GGCTCAGCCTCAACCCAATGG	GSASTQW	-
2239	13190	TACTCAAAGACCAACGAAAAC	YSKTNEN	-
2240	13191	ATGCCCTCACCCAACTTTGGC	MPSPNFG	-
2241	13192	TATAAAACGGGGACGATGTAT	YKTGTMY	-
2242	13193	TTCTCCAAATTGGGGGAGAAT	FSKLGEN	-
2243	13194	GTATCAGGCACCCATGGCGTA	VSGTHGV	-
2244	13195	TATGTGCACTCCAATTCCAAT	YVHSNSN	-
2245	13196	TATTCCAGGTTGGATGAGACG	YSRLDET	-
2246	13197	TATGCGAAATTGGGGACGAAT	YAKLGTN	-
2247	13198	AACATGAACGGCTACGGCCAA	NMNGYGQ	-
2248	13199	TACGCCCGCATGGGCACCAAC	YARMGTN	-
2249	13200	TACGCCCGCGACGGCAACAAC	YARDGNN	-

2250	13201	GGCGAAGAACGCTCAAAGTGG	GEERSKW	-
2251	13202	ATGGCGAATCACGTGACGTAT	MANHVTY	-
2252	13203	TATGCGTCCGGGTCCAATGGG	YASGSNG	-
2253	13204	AGGGATCACACGTCCACGTAT	RDHTSTY	-
2254	13205	GTAGGCGGCAACTCAACCTAC	VGGNSTY	-
2255	13206	TACGCCCGCGAAGGCATGAAC	YAREGMN	-
2256	13207	AATTCCGGGAATTCCTCCTAT	NSGNSSY	-
2257	13208	GTATCAAACAAGTCAGCCGGC	VSNKSAG	-
2258	13209	ATCAACGGCGTACATATGGTA	INGVHMV	-
2259	13210	TACCATGGCGGCGCCCCCGTA	YHGGAPV	-
2260	13211	TATCACAGGTCCTTCGATCCG	YHRSFDP	-
2261	13212	TACTACACCGGCCTGCAAGCC	YYTGLQA	-
2262	13213	TTTGACGGCACCCGCCCCTAC	FDGTRPY	-
2263	13214	AAATCCGAGTATTATTCCGAT	KSEYYSD	-
2264	13215	AACGTAGACTACGCCCGCAAC	NVDYARN	-
2265	13216	AACGCCATCGGCGTAACCTGG	NAIGVTW	-
2266	13217	ATAAATGGGCACTCCAATTAT	INGHSNY	-
2267	13218	ATCACCGGCTACGCCCAATTT	ITGYAQF	-
2268	13219	TTCTCCAGGTATAATGATAAT	FSRYNDN	-
2269	13220	TTTGCCAAGTTTGGCACCAAC	FAKFGTN	-
2270	13221	TATTCCAGGTTCGGGCCGAAT	YSRFGPN	-
2271	13222	TACTCACGCTACAACCCCAAC	YSRYNPN	-
2272	13223	TTTGCCCGCTACGGCCCCAAC	FARYGPN	-
2273	13224	TATGCGAGGTTCGGGATGAAT	YARFGMN	-
2274	13225	GGCTCATACAACACCACCTAC	GSYNTTY	-
2275	13226	CTGGCCCAATCAGGCCCCAAC	LAQSGPN	-
2276	13227	ACGTCCGGGAATTCCACGTAT	TSGNSTY	-
2277	13228	CGCGAAAACAACGGCTCATGG	RENNGSW	-
2278	13229	ATGCAATACGACTCAGGCGAC	MQYDSGD	-
2279	13230	TACGCCAAGTACGGCGAAAAC	YAKYGEN	-
2280	13231	ATCGACGGCCGCAACTACGCC	IDGRNYA	-
2281	13232	CTGTGGAACGGCGAACAAGCC	LWNGEQA	-
2282	13233	CAGGAGGGGGGGTCCAGGTAT	QEGGSRY	-
2283	13234	TACTTTACCCATACCGGCGAA	YFTHTGE	-
2284	13235	TTCTCCAGGATGGGGGAGAAT	FSRMGEN	-
2285	13236	CACGATAATCAGTCCAAATAT	HDNQSKY	-
2286	13237	TACGTATCAGGCACCATGAAC	YVSGTMN	-
2287	13238	TGGTACGCCGGCACCCATGAA	WYAGTHE	-
2288	13239	GCGGGGTCCTCCGTGGGGTGG	AGSSVGW	-
2289	13240	CTGCCCCGCGCCGGCGACTTT	LPRAGDF	-
2290	13241	GAAGCCCAAGGCATGCGCAAC	EAQGMRN	-
2291	13242	GAGGGGTCCATGACGAAATGG	EGSMTKW	-
2292	13243	TACGCCAAGACCAACGAAAAC	YAKTNEN	-
2293	13244	TACGCCCGCGAAGGCCTGAAC	YAREGLN	-
2294	13245	TCCCAGGGGAATACGAATTGG	SQGNTNW	-

2295	13246	TTGGATTCCTCCGTGAGGTAT	LDSSVRY	-
2296	13247	TTTGCCCGCCTGGGCTACAAC	FARLGYN	-
2297	13248	AATATAAAATGGGATCCGCAC	NIKWDPH	-
2298	13249	GAAGGCAACGGCACCCGCAAC	EGNGTRN	-
2299	13250	AATATACCGGGGTTGATATAT	NIPGLIY	-
2300	13251	TACGCCCGCATGAACGAAAAC	YARMNEN	-
2301	13252	GCCGACGCCTACAAGACCTAC	ADAYKTY	-
2302	13253	TTCTCCAAAAATGGGTGGAAT	FSKNGWN	-
2303	13254	GGCATCTCAACCAACGGCCGC	GISTNGR	-
2304	13255	TACTCACGCTTTGGCGACAAC	YSRFGDN	-
2305	13256	TACTCACGCTTTGGCGGCAAC	YSRFGGN	-
2306	13257	TTTTCAAAGAACAACTGGAAC	FSKNNWN	-
2307	13258	TATTCCAAATTCGGGTATAAT	YSKFGYN	-
2308	13259	TACGCCCGCTGGGGCGAAAAC	YARWGEN	-
2309	13260	TTTGCCCGCTTTGGCTCAAAC	FARFGSN	-
2310	13261	CAGACGGGGACGTCCCCGTAT	QTGTSPY	-
2311	13262	AATAATATAGATGTGAGGTGG	NNIDVRW	-
2312	13263	TACTCACGCGAAAACATCAAC	YSRENIN	-
2313	13264	CAGAATAATGGGTCCCCGTAT	QNNGSPY	-
2314	13265	CTGAACTCACTGGCCGCCTAC	LNSLAAY	-
2315	13266	TCAAACGGCGGCACCACCTGG	SNGGTTW	-
2316	13267	TATTCCAATATAGGGCCGAAT	YSNIGPN	-
2317	13268	TCAGGCGGCACCGCCCTGTAC	SGGTALY	-
2318	13269	CGCGCCGGCATGCCCGGCGCC	RAGMPGA	-
2319	13270	TACTCAAAGGAAAACTGGAAC	YSKENWN	-
2320	13271	ACCCGCGCCGGCAACGGCGCC	TRAGNGA	-
2321	13272	AACCAAGGCAACAACACCTGG	NQGNNTW	-
2322	13273	ATAGAGTATCACTCCGGGAAT	IEYHSGN	-
2323	13274	GTATCAGGCTCATCAGCCTAC	VSGSSAY	-
2324	13275	TACGCCCGCGAAAACTACAAC	YARENYN	-
2325	13276	AGGCAGGCGGATACGTATCCG	RQADTYP	-
2326	13277	GACTCATCAGGCCAACGCTAC	DSSGQRY	-
2327	13278	GGCATCCAAAACCAATCATGG	GIQNQSW	-
2328	13279	GTAGGCGGCAACTCAGGCTAC	VGGNSGY	-
2329	13280	GTGGGGAATGGGTCCTTGTAT	VGNGSLY	-
2330	13281	GGCGGCGGCGTAGCCCATTAC	GGGVAHY	-
2331	13282	ACCGGCTCATCAACCTCATGG	TGSSTSW	-
2332	13283	TATTCCAGGGATAATCACAAT	YSRDNHN	-
2333	13284	GTGCAGTATGAGTCCAGGGAT	VQYESRD	-
2334	13285	TCCGGGAATGGGTCCTTCATA	SGNGSFI	-
2335	13286	TACACCTCAAACACCAAGTAC	YTSNTKY	-
2336	13287	TACTCAAAGGGCGGCGACAAC	YSKGGDN	-
2337	13288	TACCATGACAACGGCCGCAAC	YHDNGRN	-
2338	13289	TCAGCCGGCAACTCAACCTAC	SAGNSTY	-
2339	13290	TCAGGCACCGGCAACGGCTGG	SGTGNGW	-

2340	13291	TACTCACGCCCCAACGAAAAC	YSRPNEN	-
2341	13292	ACCAACGAATGGGGCGGCCAT	TNEWGGH	-
2342	13293	AGGCCGCCGGAGTATAATTCC	RPPEYNS	-
2343	13294	ATAACGAATTATCACCACGAG	ITNYHHE	-
2344	13295	AACGGCACCTCATCAGGCTGG	NGTSSGW	-
2345	13296	ACCATGTCAAACACCTACTCA	TMSNTYS	-
2346	13297	TATTCCGGGTCCCAGCACTAT	YSGSQHY	-
2347	13298	TACTCACGCGAAGGCATCAAC	YSREGIN	-
2348	13299	CGCAACGAAACCTCAGCCTAC	RNETSAY	-
2349	13300	AGGGATGGGTATAATGGGTTC	RDGYNGF	-
2350	13301	TACGCCCGCGAAGGCATCAAC	YAREGIN	-
2351	13302	GGCCTGGGCGGCAACCCCTAC	GLGGNPY	-
2352	13303	GTGAATATAAATACGGCGTGG	VNINTAW	-
2353	13304	TACTGGGACTCAACCCATTCA	YWDSTHS	-
2354	13305	TATTCCAAAGATAATATGAAT	YSKDNMN	-
2355	13306	GACAAGAACACCTCAAACTGG	DKNTSNW	-
2356	13307	TTCTCCAAACACAATGAGAAT	FSKHNEN	-
2357	13308	TTTTCATCAACCAACGGCACC	FSSTNGT	-
2358	13309	TACGCCAAGGTAGGCGAAAAC	YAKVGEN	-
2359	13310	TTTTCACGCCTGGGCGCCAAC	FSRLGAN	-
2360	13311	TCAACCGGCATCTCATCATAC	STGISSY	-
2361	13312	TATTCCAAAGAGAATTGTAAT	YSKENCN	-
2362	13313	AACTCAGGCGCCGCCTCATGG	NSGAASW	-
2363	13314	TACGCCCGCGACGGCCTGAAC	YARDGLN	-
2364	13315	TTGTTGTCCAATCAGACGTGG	LLSNQTW	-
2365	13316	TACTCACGCGACGGCAACAAC	YSRDGNN	-
2366	13317	TACTCAAAGGAAGGCTTTAAC	YSKEGFN	-
2367	13318	TATGCGAAAGAGGGGTTCAAT	YAKEGFN	-
2368	13319	TACTCACGCACCAACTCAGAC	YSRTNSD	-
2369	13320	GTGGCGTCCGATCACGGGAGG	VASDHGR	-
2370	13321	ACCAACGAAGGCTCAGCCTGG	TNEGSAW	-
2371	13322	AATGATAAAGGGTATGGGTCC	NDKGYGS	-
2372	13323	AATAATTATGGGACGCCGTTC	NNYGTPF	-
2373	13324	GAGATATCCAGGGGGCACATG	EISRGHM	-
2374	13325	GAAGAATTTGGCCAACGCAAC	EEFGQRN	-
2375	13326	ACCATGACCGGCTTTGGCGCC	TMTGFGA	-
2376	13327	AACATCAACGGCACCGGCCGC	NINGTGR	-
2377	13328	GGCGCCGGCTCATCATCATAC	GAGSSSY	-
2378	13329	CGCAACGACGAAGCCAAGTGG	RNDEAKW	-
2379	13330	CTGCATGCCACCCAACCCAAC	LHATQPN	-
2380	13331	TGGAACACCGGCGTACATTAC	WNTGVHY	-
2381	13332	TCAGCCGGCACCTCATCATAC	SAGTSSY	-
2382	13333	ACCGGCGAAGCCCCCCGCAAC	TGEAPRN	-
2383	13334	GACTACCAAGGCACCAACCCC	DYQGTNP	-
2384	13335	GGGATATCCATGATAATGCCG	GISMIMP	-

2385	13336	GAGAAAAATACGGGGTGGGAT	EKNTGWD	-
2386	13337	TATTCCAAATTCGGGAATAAT	YSKFGNN	-
2387	13338	TATTCCAGGGAGAATGTGAAT	YSRENVN	-
2388	13339	TCATCAGAAGGCACCCGCTAC	SSEGTRY	-
2389	13340	ACCCCCAAGTCAAACTACGCC	TPKSNYA	-
2390	13341	GATAATAGGGGGACGGGGTCC	DNRGTGS	-
2391	13342	TTGGCGAATTCCCACTGGGAT	LANSHWD	-
2392	13343	GAAGGCGGCAAGTCACCCTAC	EGGKSPY	-
2393	13344	CATGGCGAATCAGCCGGCTGG	HGESAGW	-
2394	13345	ATCTCACAAGAACGCTACGGC	ISQERYG	-
2395	13346	TATTCCAAAGATAATTATAAT	YSKDNYN	-
2396	13347	TTCTCCAGGGATAATCCGAAT	FSRDNPN	-
2397	13348	TTTGCCCGCGACAACTTTAAC	FARDNFN	-
2398	13349	TTTGCCAAGTTTGGCGCCAAC	FAKFGAN	-
2399	13350	AACATGTACCCCACCCCCGGC	NMYPTPG	-
2400	13351	TACTCACGCTTTGGCGCCAAC	YSRFGAN	-
2401	13352	TTCTCCAGGTTCGGGAATAAT	FSRFGNN	-
2402	13353	TATTCCAAATGGGGGACGAAT	YSKWGTN	-
2403	13354	TATTCCAGGTGGGGGGAGAAT	YSRWGEN	-
2404	13355	TTTGCCAAGTGGGGCCAAAAC	FAKWGQN	-
2405	13356	AACCAATCACCCATCCCCGTA	NQSPIPV	-
2406	13357	GGCGGCAACACCTCAACCTAC	GGNTSTY	-
2407	13358	AGGGCGGTGGATGCGTATTCC	RAVDAYS	-
2408	13359	ACCATGGGCACCAACCCCTAC	TMGTNPY	-
2409	13360	GACAACCGCAACGTAGCCTGG	DNRNVAW	-
2410	13361	AAGTCAGTAGACTACGGCTCA	KSVDYGS	-
2411	13362	GGCAACTCAGGCGCCAACTGG	GNSGANW	-
2412	13363	TACGAACAAGGCTGGCGCGAC	YEQGWRD	-
2413	13364	GATAATGGGAATGCGAGGTAT	DNGNARY	-
2414	13365	TACATGGGCGGCGAAATGGTA	YMGGEMV	-
2415	13366	GACTTTGGCTCAAACGGCCGC	DFGSNGR	-
2416	13367	GGCCAAGACTACTCAACCTAC	GQDYSTY	-
2417	13368	AACGCCTACGGCGTACCCCGC	NAYGVPR	-
2418	13369	TCAGCCGAATCATACCGCAAC	SAESYRN	-
2419	13370	TATACGCACTTCGAGTTCGAT	YTHFEFD	-
2420	13371	CGCTCACAAGACACCGCCTGG	RSQDTAW	-
2421	13372	ATCTCAGGCGCCACCGCCGGC	ISGATAG	-
2422	13373	TACTCACGCGACGGCGCCAAC	YSRDGAN	-
2423	13374	TACGCCAAGTGGGGCCAAAAC	YAKWGQN	-
2424	13375	GGGGGGGGGGCGACGGCGTAT	GGGATAY	-
2425	13376	TTTTCACGCGAAAACCCCAAC	FSRENPN	-
2426	13377	CTGAAGTACGAACATGCCGAC	LKYEHAD	-
2427	13378	AACGTATCAGAACTGCGCTGG	NVSELRW	-
2428	13379	TACCAATCAGGCGAAATGAAC	YQSGEMN	-
2429	13380	TACTCACGCGAAAACGACAAC	YSRENDN	-

2430	13381	ACCCGCACCGGCGACGGCGCC	TRTGDGA	-
2431	13382	TGGCGCCAAGGCGAAATGGAA	WRQGEME	-
2432	13383	GTAGGCACCATCGGCCGCGAC	VGTIGRD	-
2433	13384	TCATCAACCGGCAACGGCTGG	SSTGNGW	-
2434	13385	CGCGGCGAAACCTCAACCTAC	RGETSTY	-
2435	13386	TATTCCAAATGGGGGGAGAAT	YSKWGEN	-
2436	13387	CACGATGCGAAATCCATGTAT	HDAKSMY	-
2437	13388	GACACCGACCATATGCGCTTT	DTDHMRF	-
2438	13389	CGCTCAGACGGCGGCTACGGC	RSDGGYG	-
2439	13390	TTTTCACGCGACGGCCCCAAC	FSRDGPN	-
2440	13391	ACCACCGGCTCAAACCCCTTT	TTGSNPF	-
2441	13392	TTTGCCCGCGCCGGCGAAAAC	FARAGEN	-
2442	13393	CATTCAAAGAACAACGACAAC	HSKNNDN	-
2443	13394	TACATCCGCCATGAAACCCAA	YIRHETQ	-
2444	13395	AACGGCTCACAATCATCATAC	NGSQSSY	-
2445	13396	TACTCAGGCGGCGGCATGCCC	YSGGGMP	-
2446	13397	ATGGGCTCATCAAACGCCTGG	MGSSNAW	-
2447	13398	AACCTGCAAGCCTCATCATGG	NLQASSW	-
2448	13399	TTCTCCAGGTATAATGCGAAT	FSRYNAN	-
2449	13400	AAGGGCGCCGACGTATACCCC	KGADVYP	-
2450	13401	GTAGACTCAACCTCAGGCCGC	VDSTSGR	-
2451	13402	AACATGCATGGCATCCCCATG	NMHGIPM	-
2452	13403	TTGGCGACGACGACGAATTGG	LATTTNW	-
2453	13404	TACGTAATGGAAAACCGCAAC	YVMENRN	-
2454	13405	TACTCACGCGACGGCTGGAAC	YSRDGWN	-
2455	13406	TACTCACGCGACGGCGACAAC	YSRDGDN	-
2456	13407	GTACATGACTCAGGCGGCCGC	VHDSGGR	-
2457	13408	TTCGCGAGGGATGGGCCGAAT	FARDGPN	-
2458	13409	TTTTCACGCGAAAACATCAAC	FSRENIN	-
2459	13410	GGCCTGAAGAACTACCCCGCC	GLKNYPA	-
2460	13411	TACTCACGCGAAGGCACCAAC	YSREGTN	-
2461	13412	GTGTCCCCGTCCTCCGTGTGG	VSPSSVW	-
2462	13413	GGCATCCCCAACATCGCCTAC	GIPNIAY	-
2463	13414	GAAGGCCATAACGGCCGCGAC	EGHNGRD	-
2464	13415	GACTCAACCTCAGTAACCTGG	DSTSVTW	-
2465	13416	GGCTCAGGCCTGGTAGCCTAC	GSGLVAY	-
2466	13417	ATGTCAGGCCAAGGCGCCGGC	MSGQGAG	-
2467	13418	ATGAAAAATGGGGATGCGTCC	MKNGDAS	-
2468	13419	AGGGATGATGTGTCCGCGTAT	RDDVSAY	-
2469	13420	CACTGGGCGTCCAATGGGATG	HWASNGM	-
2470	13421	TACGCCGTATCAGGCGCCGGC	YAVSGAG	-
2471	13422	CTGGACGGCTTTTCAGCCCGC	LDGFSAR	-
2472	13423	GAACAATGGGGCAACGGCGAC	EQWGNGD	-
2473	13424	TACGCCAAGTTTGGCCATAAC	YAKFGHN	-
2474	13425	AATGTGGATGGGATGGCGTGG	NVDGMAW	-

2475	13426	TCAAACCCCGGCTCAGTATAC	SNPGSVY	-
2476	13427	TACTCAAACCTGTCAATGCCC	YSNLSMP	-
2477	13428	CGCCAAGTAGACGTATACGCC	RQVDVYA	-
2478	13429	ATAGATGGGACGAATGGGAGG	IDGTNGR	-
2479	13430	TTGCACGGGGGGCCGGCGCCG	LHGGPAP	-
2480	13431	TACGCCAAGGACGGCATGAAC	YAKDGMN	-
2481	13432	TCCTCCGGGGAGTCCTTGTAT	SSGESLY	-
2482	13433	CGCGACCCCGGCTACGTAGTA	RDPGYVV	-
2483	13434	CAGGGGGGGACGACGTCCTAT	QGGTTSY	-
2484	13435	TTTTCACGCGAAGGCTGGAAC	FSREGWN	-
2485	13436	TATGCGAGGTTCGGGGCGAAT	YARFGAN	-
2486	13437	ACCTCAGCCTCAAACGGCGTA	TSASNGV	-
2487	13438	ACGAATCCGAATGTGGCGTGG	TNPNVAW	-
2488	13439	TACGCCCGCGACAACTACAAC	YARDNYN	-
2489	13440	TTCTCCAGGTTCGGGCAGAAT	FSRFGQN	-
2490	13441	GGCGAACGCCTGGTAACCTAC	GERLVTY	-
2491	13442	ACGCCGTTGTCCCCGTCCTGG	TPLSPSW	-
2492	13443	TTCTCCAGGTATGGGGAGAAT	FSRYGEN	-
2493	13444	TTTGCCCGCCTGGGCGACAAC	FARLGDN	-
2494	13445	TATTCCAGGGAGAATGAGAAT	YSRENEN	-
2495	13446	TTTGCCCGCGACAACATGAAC	FARDNMN	-
2496	13447	GTAGGCGAAGCCGGCTACTTT	VGEAGYF	-
2497	13448	TATGCGAGGTTCGGGCAGAAT	YARFGQN	-
2498	13449	TTTTCACGCTTTGGCGAAAAC	FSRFGEN	-
2499	13450	TTGAAAGATGGGAGGTCCGCG	LKDGRSA	-
2500	13451	ATCGCCACCCGCGGCATCGAC	IATRGID	-
2501	13452	GCGGATTCCGCGTCCTCCTGG	ADSASSW	-
2502	13453	AACCAACCCGGCTCACATATG	NQPGSHM	-
2503	13454	TTTGCCCGCCCCGGCCATAAC	FARPGHN	-
2504	13455	TTTTCACGCTACGGCGACAAC	FSRYGDN	-
2505	13456	TACGCCCGCGACGGCGGCAAC	YARDGGN	-
2506	13457	TCAGGCTCATCAACCGGCTAC	SGSSTGY	-
2507	13458	GGCAACGGCGCCGGCTACTCA	GNGAGYS	-
2508	13459	AACCATTCAGGCGACCCCTCA	NHSGDPS	-
2509	13460	GAGGATGGGAAAGGGGGGTGG	EDGKGGW	-
2510	13461	TATTCCAAAGATAATGGGAAT	YSKDNGN	-
2511	13462	TACTCACGCTTTGGCGTAAAC	YSRFGVN	-
2512	13463	AACACCTACGGCACCGGCGAA	NTYGTGE	-
2513	13464	TTCTCCCCGAATGTGGTGTTC	FSPNVVF	-
2514	13465	TACTCAAAGGAAGGCATGAAC	YSKEGMN	-
2515	13466	AACGGCGAAGCCGGCCGCTAC	NGEAGRY	-
2516	13467	TTGGAGGGGCAGTATGGGAAT	LEGQYGN	-
2517	13468	TTTTCAAAGGAAAACGGCAAC	FSKENGN	-
2518	13469	GCGTTGGAGGGGCACTCCTGG	ALEGHSW	-
2519	13470	TACGCCAAGGAAAACCCCAAC	YAKENPN	-

2520	13471	TACGCCAAGTTTGGCGCCAAC	YAKFGAN	-
2521	13472	TTCTCCAAAGATAATGCGAAT	FSKDNAN	-
2522	13473	GCCAACCATGACGTAGGCTGG	ANHDVGW	-
2523	13474	GAACCCCCCTCACTGCGCTAC	EPPSLRY	-
2524	13475	GGCTCAAACGACTCACGCTAC	GSNDSRY	-
2525	13476	TTCTCCAAATTCGGGTCCAAT	FSKFGSN	-
2526	13477	GGCCTGAAGGACTCAGCCTGG	GLKDSAW	-
2527	13478	TCAAAGGAACATGGCTACGCC	SKEHGYA	-
2528	13479	TATTCCAGGGATAATTTGAAT	YSRDNLN	-
2529	13480	TTTTCAAAGTTTGGCCTGAAC	FSKFGLN	-
2530	13481	ATCCAATACGAAAACGGCGGC	IQYENGG	-
2531	13482	GGCTACAACTACTCAGGCGCC	GYNYSGA	-
2532	13483	ATCATGTCAGCCGACGCCTGG	IMSADAW	-
2533	13484	TACTCACGCTTTGGCGAAAAC	YSRFGEN	-
2534	13485	GATATGAAAGGGAATGTGGCG	DMKGNVA	-
2535	13486	TTTGCCAAGTTTGGCTCAAAC	FAKFGSN	-
2536	13487	ACCTCAGACCGCGACGGCCGC	TSDRDGR	-
2537	13488	AACCATGCCGGCAACGGCGCC	NHAGNGA	-
2538	13489	AACGAAGCCTCAGGCGGCTGG	NEASGGW	-
2539	13490	TTTTCAAAGTTTGGCCAAAAC	FSKFGQN	-
2540	13491	AACATGACCGGCAACGGCGCC	NMTGNGA	-
2541	13492	AACGGCACCGGCGCCACCTAC	NGTGATY	-
2542	13493	TATTCCAAATTCGGGACGAAT	YSKFGTN	-
2543	13494	GCCTCAATCGACGGCCCCAAG	ASIDGPK	-
2544	13495	TCAGACCGCGGCTCAGGCGCC	SDRGSGA	-
2545	13496	TATTCCAAATTCGGGGAGAAT	YSKFGEN	-
2546	13497	TTTATGTCATCAAACGGCGCC	FMSSNGA	-
2547	13498	TTTTCAAAGGAAAACTACAAC	FSKENYN	-
2548	13499	TACACCAACTACAACGGCGCC	YTNYNGA	-
2549	13500	TGGCGCGACTCAAACGGCGCC	WRDSNGA	-
2550	13501	TACGCCAAGTGGGGCACCAAC	YAKWGTN	-
2551	13502	TTTGCCAAGTGGGGCGAAAAC	FAKWGEN	-
2552	13503	TATTTCAGGGATCACGCGCCG	YFRDHAP	-
2553	13504	TACGCCCGCTTTGGCGACAAC	YARFGDN	-
2554	13505	ACCGCCTACGGCGACGGCGCC	TAYGDGA	-

NT SEQ ID#	AA SEQ ID#	NT sequence	AA_sequence		
2555	13506	TATTCCAGGCAGAATTATAAT	YSRQNYN	++	+
2556	13507	TATGCGAGGATGGGGTATAAT	YARMGYN	+++	+
2557	13508	TATGCGAGGGGGAATTATAAT	YARGNYN	++	-
2558	13509	TATTCCAGGTCCAATTATAAT	YSRSNYN	++	++
2559	13510	TATTCCAGGTTGAATTATAAT	YSRLNYN	+++	-
2560	13511	TTCTCCAGGGTGAATATAAAT	FSRVNIN	+	-
2561	13512	TATTCCAGGCACGGGCAGAAT	YSRHGQN	+++	-
2562	13513	TATTCCAGGCAGGGGTATAAT	YSRQGYN	+	-
2563	13514	TTCTCCAGGTTGGGGATAAAT	FSRLGIN	++	+
2564	13515	TATGCGAGGATGAATATAAAT	YARMNIN	++	+
2565	13516	TATTCCAGGGCGAATTATAAT	YSRANYN	++	-
2566	13517	TATTCCAGGTTGAATATAAAT	YSRLNIN	+++	+
2567	13518	TTCGCGAGGGGGGGGTATAAT	FARGGYN	++	++
2568	13519	TTTTCACGCGCCAACCATAAC	FSRANHN	++	+++
2569	13520	TTCTCCAGGGCGGGGTATAAT	FSRAGYN	+	-
2570	13521	TTTTCAAAGATGAACTACAAC	FSKMNYN	+	-
2571	13522	TTCGCGAGGTTGAATATAAAT	FARLNIN	+	-
2572	13523	TATTCCAAACAGAATATAAAT	YSKQNIN	+	-
2573	13524	TTCGCGAGGACGAATTATAAT	FARTNYN	++	+++
2574	13525	TATGCGAGGATAGGGTATAAT	YARIGYN	+	-
2575	13526	TATTCCAAATTGAATAATAAT	YSKLNNN	++	-
2576	13527	TATGCGAAATTCAATTATAAT	YAKFNYN	+	-
2577	13528	TATGCGAGGCAGAATTATAAT	YARQNYN	+++	+++
2578	13529	TTCTCCAGGGCGAATTATAAT	FSRANYN	++	++
2579	13530	TATGCGAAAGCGGGGTATAAT	YAKAGYN	+	+++
2580	13531	TATTCCAGGACGAATATAAAT	YSRTNIN	+	+
2581	13532	TATTCCAAAATGGGGTATAAT	YSKMGYN	+	-
2582	13533	TTCTCCAGGATAAATAATAAT	FSRINNN	++	-
2583	13534	TTCTCCAGGGCGAATATAAAT	FSRANIN	+	+++
2584	13535	TATTCCAGGTTGAATAATAAT	YSRLNNN	+++	-
2585	13536	TATGCGAGGGCGGGGAATAAT	YARAGNN	+	+
2586	13537	TATTCCAAATTGAATATAAAT	YSKLNIN	++	-
2587	13538	TTTTCACGCCTGAACCATAAC	FSRLNHN	++	-
2588	13539	TATTCCAGGCAGAATAATAAT	YSRQNNN	+	-
2589	13540	TTCGCGAGGATAGGGCCGAAT	FARIGPN	+	-
2590	13541	TATTCCAGGGGGAATTATAAT	YSRGNYN	+++	-
2591	13542	TACGCCCGCTACGGCGTAAAC	YARYGVN	++	-
2592	13543	TACTCACGCCTGAACTTTAAC	YSRLNFN	+++	-
2593	13544	TATGCGAAATATGGGTATAAT	YAKYGYN	++	+++
2594	13545	TACGCCCGCATGGGCTTTAAC	YARMGFN	+	-
2595	13546	TATTCCAAAGCGAATATGAAT	YSKANMN	++	-
2596	13547	TTCTCCAAAATAAATATAAAT	FSKININ	+	-
2597	13548	TACTCACGCTACAACGCCAAC	YSRYNAN	+++	-
2598	13549	TATGCGAGGGCGGGGTATAAT	YARAGYN	+++	-

2599	13550	TTCTCCAGGGCGGGGAATAAT	FSRAGNN	+	-
2600	13551	TTCTCCAAAATAGGGTATAAT	FSKIGYN	+	-
2601	13552	TATTCCAAACACAATTATAAT	YSKHNYN	++	-
2602	13553	TATGCGAGGACGGGGTATAAT	YARTGYN	+++	+
2603	13554	TATTCCAGGAATGGGAATAAT	YSRNGNN	+	+
2604	13555	TACGCCCGCGGCGGCTACAAC	YARGGYN	+++	++
2605	13556	TATTCCAGGGCGGGGTATAAT	YSRAGYN	+++	+++
2606	13557	TATGCGAAAACGGGGTATAAT	YAKTGYN	+	-
2607	13558	TATTCCAAAGGGAATTGTAAT	YSKGNCN	+++	-
2608	13559	TATGCGAAAATGGGGTATAAT	YAKMGYN	+	-
2609	13560	TTCGCGAGGAATGGGTATAAT	FARNGYN	+	-
2610	13561	TTCTCCAGGAATAATATGAAT	FSRNNMN	+++	+++
2611	13562	TATTCCAGGCAGAATATGAAT	YSRQNMN	+	-
2612	13563	TATTCCAGGAATAATATGAAT	YSRNNMN	+	-
2613	13564	TATTCCAAAAGGAATGAGAAT	YSKRNEN	++	+
2614	13565	TATTCCAAAGCGGGGTGGAAT	YSKAGWN	+	-
2615	13566	TATGCGAGGCACAATTTCAAT	YARHNFN	+++	-
2616	13567	TATGCGAGGGCGAATTATAAT	YARANYN	++	-
2617	13568	TATGCGAGGTATGGGCCGAAT	YARYGPN	+	-
2618	13569	TTTTCACGCTCAGGCCATAAC	FSRSGHN	+++	++
2619	13570	TACGCCAAGGTAGGCAAGAAC	YAKVGKN	+++	-
2620	13571	TACTCACGCCAAAACCATAAC	YSRQNHN	+++	-
2621	13572	TTCTCCAGGATGAATTTGAAT	FSRMNLN	++	++
2622	13573	TTCGCGAGGTCCGGGTATAAT	FARSGYN	++	-
2623	13574	TACGCCAAGCATGGCCATAAC	YAKHGHN	+++	-
2624	13575	TATGCGAGGGGGGGGATAAAT	YARGGIN	+++	-
2625	13576	TTCTCCAAAGTGGGGTATAAT	FSKVGYN	+	-
2626	13577	TATGCGAGGCAGGGGTATAAT	YARQGYN	++	+
2627	13578	TACGCCAAGTACGGCCCCAAC	YAKYGPN	+++	-
2628	13579	TATTCCAGGCACAATCCGAAT	YSRHNPN	+++	-
2629	13580	TATTCCAGGGTGGGGATAAAT	YSRVGIN	++	++
2630	13581	TCCGGGTCCTATACGAATTAT	SGSYTNY	+	-
2631	13582	TATGCGAGGGGGAATAATAAT	YARGNNN	++	-
2632	13583	TATGCGAGGGTGGGGAATAAT	YARVGNN	+	++
2633	13584	TTCTCCAAATCCGGGTATAAT	FSKSGYN	++	-
2634	13585	TATGCGAAAGTGGGGTATAAT	YAKVGYN	+	+
2635	13586	TTCTCCAGGTTGGGGCACAAT	FSRLGHN	+	+++
2636	13587	TGTGCGCCGGCGGGGAGGGAT	CAPAGRD	++	-
2637	13588	TATTCCAGGTCCGGGTTCAAT	YSRSGFN	++	+++
2638	13589	TTTTCACGCGTAGGCCCCAAC	FSRVGPN	++	++
2639	13590	TTTTCAAAGTTTGGCCCCAAC	FSKFGPN	+	-
2640	13591	TATTCCAGGCACAATTTCAAT	YSRHNFN	+	-
2641	13592	TATGCGAGGCAGGGGATAAAT	YARQGIN	+	-
2642	13593	TATTCCAAAACGGGGTATAAT	YSKTGYN	+	-
2643	13594	TATTCCAGGTCCGGGCACAAT	YSRSGHN	+++	-

2644	13595	TTCTCCAGGATAGGGCACAAT	FSRIGHN	+++	-
2645	13596	TACTCACGCAAGAACGACAAC	YSRKNDN	++	-
2646	13597	TATGCGAGGAATGGGTATAAT	YARNGYN	+	++
2647	13598	AGGGGGGATGGGCACTATAAT	RGDGHYN	++	-
2648	13599	TATTCCAGGACGGGGTATAAT	YSRTGYN	++	+
2649	13600	TATTCCAGGCACGGGATAAAT	YSRHGIN	+	-
2650	13601	TATTCCAGGGCGAATCCGAAT	YSRANPN	+	-
2651	13602	TATTCCAGGACGAATATGAAT	YSRTNMN	+	-
2652	13603	TATGCGAGGTCCGGGATAAAT	YARSGIN	+	-
2653	13604	TTCTCCAGGTTGGGGAATAAT	FSRLGNN	+	-
2654	13605	TATCACAGGTTGGGGATAGAT	YHRLGID	+	-
2655	13606	TATTCCAGGAATGGGATAAAT	YSRNGIN	++	+
2656	13607	TATGCGAGGTTGAATAATAAT	YARLNNN	++	-
2657	13608	TTCTCCAGGGCGAATATGAAT	FSRANMN	+	-
2658	13609	TATGCGAGGGGGAATATGAAT	YARGNMN	+	+
2659	13610	TACGCCCGCTCAAACCCCAAC	YARSNPN	+++	-
2660	13611	TACGCCCGCTACGGCAACAAC	YARYGNN	+++	-
2661	13612	TATTCCAAACACGGGTATAAT	YSKHGYN	+++	-
2662	13613	TTCGCGAGGCAGGGGAATAAT	FARQGNN	++	-
2663	13614	CTGCATAAGCTGCTGGTAGGC	LHKLLVG	++	-
2664	13615	TTCGCGAGGACGGGGATAAAT	FARTGIN	++	+
2665	13616	TTCGCGAGGGCGGGGTATAAT	FARAGYN	++	-
2666	13617	TTTGCCCGCCAAGGCCCCAAC	FARQGPN	+	-
2667	13618	TTCGCGAGGGGGGGGATAAAT	FARGGIN	+	++
2668	13619	TTCTCCAGGAAAAATGAGAAT	FSRKNEN	+++	-
2669	13620	TATGCGAGGTTGGGGAATAAT	YARLGNN	+	-
2670	13621	TTCGCGAGGCAGGGGATAAAT	FARQGIN	+	-
2671	13622	TATTCCAAATTCAATAATAAT	YSKFNNN	+	++
2672	13623	TTCTCCAGGATAGGGCCGAAT	FSRIGPN	+	+
2673	13624	TATTCCAGGGGGGGGCCGAAT	YSRGGPN	++	-
2674	13625	TATGCGAGGTTCGGGCCGAAT	YARFGPN	++	-
2675	13626	TTCTCCAAAATGGGGTATAAT	FSKMGYN	+	-
2676	13627	TATTCCAGGTCCAATCACAAT	YSRSNHN	+++	-
2677	13628	TATGCGAGGCACAATTATAAT	YARHNYN	+++	-
2678	13629	TATTCCAAACACGGGCCGAAT	YSKHGPN	+	-
2679	13630	TTCGCGAGGGTGGGGTATAAT	FARVGYN	++	-
2680	13631	TATGCGAGGTATGGGATAAAT	YARYGIN	++	+
2681	13632	TATTCCAGGATGGGGCACAAT	YSRMGHN	++	-
2682	13633	TATTCCAGGGGGAATGCGAAT	YSRGNAN	+	+
2683	13634	TTTGCCAAGTACGGCCCCAAC	FAKYGPN	+	-
2684	13635	TATTCCAGGGCGGGGATAAAT	YSRAGIN	+	++
2685	13636	TATGCGAGGACGGGGATAAAT	YARTGIN	+	-
2686	13637	TTTTCACGCACCGGCTACAAC	FSRTGYN	+	+
2687	13638	TACTCACGCGCCGGCTTTAAC	YSRAGFN	++	-
2688	13639	TTTTCACGCGCCAACACCAAC	FSRANTN	+	-

2689	13640	TATTCCAGGATAGGGTATAAT	YSRIGYN	++	+
2690	13641	TATGCGAGGATGAATAATAAT	YARMNNN	+	+++
2691	13642	TATTCCAAAAGGAATGATAAT	YSKRNDN	+++	-
2692	13643	TATGCGAAAGTGGGGTGGAAT	YAKVGWN	+	-
2693	13644	TATGCGAGGAATGCGAATAAT	YARNANN	+	-
2694	13645	TACGCCCGCGCCGGCATGAAC	YARAGMN	+	-
2695	13646	TATGCGAAATTGAATTATAAT	YAKLNYN	+	-
2696	13647	TATTCCAGGTATGGGACGAAT	YSRYGTN	++	-
2697	13648	TTTGCCCGCGGCGGCCATAAC	FARGGHN	+++	-
2698	13649	TATTCCAGGGTGAATTATAAT	YSRVNYN	++	-
2699	13650	TTTTCACGCCATGGCTCAAAC	FSRHGSN	+	-
2700	13651	TATATAAAATCCGATAAAATG	YIKSDKM	+	-
2701	13652	TTCGCGAGGTCCGGGAATAAT	FARSGNN	+	-
2702	13653	TTCGCGAGGTCCGGGATAAAT	FARSGIN	+	-
2703	13654	TACTCACGCACCAACTTTAAC	YSRTNFN	+	-
2704	13655	TATGCGAGGATAGGGTCCAAT	YARIGSN	+	-
2705	13656	TTCTCCAAAGGGAATTATAAT	FSKGNYN	+	+
2706	13657	TATTCCAAAGCGGGGGATAAT	YSKAGDN	+++	-
2707	13658	ACCGTAGACCATGTAAAGTGG	TVDHVKW	+	-
2708	13659	TATTCCAGGATGGGGATAAAT	YSRMGIN	+	-
2709	13660	TATTCCAAAGGGGGGGTGGAAT	YSKGGWN	++	-
2710	13661	TATGCGAGGGGGGCGAATAAT	YARGANN	+	+
2711	13662	TATTCCAGGGTGAATATGAAT	YSRVNMN	+	-
2712	13663	TTTGCCCGCCAAGGCCATAAC	FARQGHN	+	-
2713	13664	TATTCCAGGATAGGGATAAAT	YSRIGIN	++	+++
2714	13665	TATTCCAAACACGGGATAAAT	YSKHGIN	+	-
2715	13666	TACGCCCGCGGCAACCATAAC	YARGNHN	+++	++
2716	13667	TATTCCAGGATGAATTATAAT	YSRMNYN	++	-
2717	13668	TACTCACGCCATAACATGAAC	YSRHNMN	+	-
2718	13669	TATGCGAGGCACGGGATAAAT	YARHGIN	+++	+++
2719	13670	TATTCCAGGATGGGGTCCAAT	YSRMGSN	++	+
2720	13671	TATTCCAGGATAAATAATAAT	YSRINNN	++	+++
2721	13672	TTCTCCAAAGTGGGGAATAAT	FSKVGNN	++	-
2722	13673	TATTCCAAACACGGGTTGAAT	YSKHGLN	+	-
2723	13674	TATTCCAGGATGGGGTTCAAT	YSRMGFN	++	-
2724	13675	TATTCCAGGAATAATGTGAAT	YSRNNVN	+	-
2725	13676	TATTCCAGGAATAATATAAAT	YSRNNIN	+	-
2726	13677	TACTCACGCTACGGCGTAAAC	YSRYGVN	+++	++
2727	13678	TTCGCGAGGCACAATATAAAT	FARHNIN	+++	-
2728	13679	TATTCCAGGCACGGGTCCAAT	YSRHGSN	+	-
2729	13680	TTCTCCAAACACAATAATAAT	FSKHNNN	+	-
2730	13681	TATGCGAGGATAGGGATAAAT	YARIGIN	+	-
2731	13682	TACGCCCGCCATGGCCATAAC	YARHGHN	+++	+++
2732	13683	TTCTCCAGGCAGAATAATAAT	FSRQNNN	+	++
2733	13684	TATTCCAGGCACAATGTGAAT	YSRHNVN	+	-

2734	13685	TTCGCGAGGGGGAATAATAAT	FARGNNN	++	-
2735	13686	TTCGCGAAAGGGGGGTATAAT	FAKGGYN	+++	-
2736	13687	TTCGCGAGGCAGAATATAAAT	FARQNIN	+	-
2737	13688	TTCTCCAGGTTGAATGTGAAT	FSRLNVN	+++	+++
2738	13689	TATTCCAGGACGAATCCGAAT	YSRTNPN	+	++
2739	13690	TTCTCCAGGGCGGGGATAAAT	FSRAGIN	+	-
2740	13691	TATTCCAGGATAAATCACAAT	YSRINHN	++	+
2741	13692	TATGCGGCGTCCGGGAGGAAT	YAASGRN	+	-
2742	13693	TTCTCCAGGCAGAATTATAAT	FSRQNYN	++	-
2743	13694	TTCTCCAGGATGAATGTGAAT	FSRMNVN	+	-
2744	13695	TTCGCGAGGTATGGGCAGAAT	FARYGQN	++	+++
2745	13696	TTCTCCAGGTTGAATTCCAAT	FSRLNSN	++	+++
2746	13697	TATTCCAAAGTGAATTGGAAT	YSKVNWN	+	-
2747	13698	TATGCGAAATTCGGGCCGAAT	YAKFGPN	++	+
2748	13699	TATGCGAGGGGGAATTTGAAT	YARGNLN	++	-
2749	13700	TTCTCCAGGACGAATAATAAT	FSRTNNN	+	+
2750	13701	TTTTCACGCTCAGGCTACAAC	FSRSGYN	++	-
2751	13702	TTGCACAGGGCGGCGGGGAAT	LHRAAGN	+	++
2752	13703	TTCGCGAGGCACGGGCCGAAT	FARHGPN	+++	-
2753	13704	TATGCGAAATTCAATAATAAT	YAKFNNN	+	-
2754	13705	AACGTAGCCGAACGCAAGTGG	NVAERKW	+	-
2755	13706	TTCGCGAGGGCGAATAATAAT	FARANNN	++	-
2756	13707	TTCTCCAAAATAGGGAATAAT	FSKIGNN	+	-
2757	13708	TATGCGAGGGCGGGGTCCAAT	YARAGSN	+	-
2758	13709	TATTCCAGGCAGGGGCACAAT	YSRQGHN	+++	-
2759	13710	TTTTCACGCGCCAACTCAAAC	FSRANSN	+	-
2760	13711	TTCGCGAGGTCCGCGAATAAT	FARSANN	+	++
2761	13712	TATTCCAGGCAGAATTTGAAT	YSRQNLN	+	++
2762	13713	TATGCGAAAGGGGGGATAAAT	YAKGGIN	++	-
2763	13714	TATGCGAGGGCGAATCACAAT	YARANHN	+	+++
2764	13715	TATTCCAGGTTGAATCACAAT	YSRLNHN	+++	++
2765	13716	TACTCACGCGCCAACCATAAC	YSRANHN	+++	+
2766	13717	TACGCCCGCCATGGCTCAAAC	YARHGSN	++	-
2767	13718	TACGCCCGCATCGGCGTAAAC	YARIGVN	+	++
2768	13719	TACTCACGCGCCAACTTTAAC	YSRANFN	++	-
2769	13720	TTTTCACGCCTGAACATGAAC	FSRLNMN	++	-
2770	13721	TATTCCAGGTCCAATACGAAT	YSRSNTN	++	-
2771	13722	TATGCGAGGATAGGGCAGAAT	YARIGQN	+	+
2772	13723	TATTCCAGGTCCGGGATGAAT	YSRSGMN	+	-
2773	13724	TATGCGAGGCACGGGTATAAT	YARHGYN	+++	-
2774	13725	TATGCGAAACACGGGATAAAT	YAKHGIN	+++	-
2775	13726	TATGCGAGGTTGGGGTATAAT	YARLGYN	++	++
2776	13727	TTTGCCCGCCATGGCTTTAAC	FARHGFN	+	+++
2777	13728	TATTCCAGGTCCGGGCAGAAT	YSRSGQN	+	+
2778	13729	TATTCCAGGAATGGGCACAAT	YSRNGHN	+	+++

2779	13730	TATTCCAGGATGGGGGTGAAT	YSRMGVN	++	-
2780	13731	TACGCCAAGTCAGGCTGGAAC	YAKSGWN	+	-
2781	13732	TTCTCCAGGGTGGGGACGAAT	FSRVGTN	+	-
2782	13733	TTCGCGAGGTTGGGGATAAAT	FARLGIN	+	-
2783	13734	TTCTCCAAATTGGGGCCGAAT	FSKLGPN	+	-
2784	13735	TTCTCCAGGAATAATCACAAT	FSRNNHN	+++	-
2785	13736	TATGCGAGGAATAATTATAAT	YARNNYN	++	-
2786	13737	TTTTCACGCATCGGCATCAAC	FSRIGIN	+	-
2787	13738	TTTTCACGCCTGAACCAAAAC	FSRLNQN	++	-
2788	13739	TACTCACGCATCGGCATGAAC	YSRIGMN	+++	+++
2789	13740	TACTCACGCAACGGCTTTAAC	YSRNGFN	+	+
2790	13741	TATGCGAGGTTGAATCACAAT	YARLNHN	++	+
2791	13742	TATGCGAGGCAGGGGTCCAAT	YARQGSN	++	-
2792	13743	TATTCCAAATGGAATACGAAT	YSKWNTN	+++	-
2793	13744	TTCGCGAGGTCCAATATGAAT	FARSNMN	+	-
2794	13745	TACTCACGCGTAGGCTACAAC	YSRVGYN	+++	-
2795	13746	TACGTACGCTCACAAAACCTG	YVRSQNL	+	-
2796	13747	TTCTCCAGGATAAATATGAAT	FSRINMN	++	-
2797	13748	TATTCCAAAATGAATCCGAAT	YSKMNPN	+	-
2798	13749	TATTCCAGGGGGAATATGAAT	YSRGNMN	+	-
2799	13750	TTCTCCAAATATAATATAAAT	FSKYNIN	+++	-
2800	13751	TATTCCAGGGTGGGGAATAAT	YSRVGNN	++	+++
2801	13752	TTTGCCAAGTCAGGCCCCAAC	FAKSGPN	+++	-
2802	13753	TTCGCGAGGTCCGGGTTCAAT	FARSGFN	+	+
2803	13754	TATTCCAGGATGAATCAGAAT	YSRMNQN	+	-
2804	13755	TATGCGAGGATGGGGAATAAT	YARMGNN	++	-
2805	13756	TTCTCCAGGGGGGGGATAAAT	FSRGGIN	++	+
2806	13757	TATTCCAGGTCCGGGAATAAT	YSRSGNN	++	+++
2807	13758	TATTCCAGGTCCAATGCGAAT	YSRSNAN	+	-
2808	13759	TACTCACGCGGCAACCCCAAC	YSRGNPN	+	-
2809	13760	TTTTCACGCGCCGGCCTGAAC	FSRAGLN	++	+++
2810	13761	TACGCCCGCGGCGGCATGAAC	YARGGMN	++	-
2811	13762	TTTTCAAAGCTGAACTACAAC	FSKLNYN	+	-
2812	13763	TTTTCACGCATCGGCCAAAAC	FSRIGQN	+	-
2813	13764	TACGCCCGCTCAGGCCTGAAC	YARSGLN	+	-
2814	13765	TACGCCCGCCAAAACCATAAC	YARQNHN	++	-
2815	13766	TACTCACGCGGCAACCATAAC	YSRGNHN	+	-
2816	13767	TTTTCACGCGTAGGCATCAAC	FSRVGIN	+	-
2817	13768	TATTCCAGGGTGAATCACAAT	YSRVNHN	++	++
2818	13769	TTCTCCAGGATGGGGCCGAAT	FSRMGPN	++	-
2819	13770	TATTCCAAAGTGGGGTGGAAT	YSKVGWN	++	-
2820	13771	TATTCCAGGCAGGGGTTCAAT	YSRQGFN	++	-
2821	13772	TATTCCAGGCAGGGGCCGAAT	YSRQGPN	++	-
2822	13773	TTCTCCAGGTTGGGGTTGAAT	FSRLGLN	++	+
2823	13774	TTCTCCAGGACGGGGCACAAT	FSRTGHN	+	++

2824	13775	TACTCAAAGTGGAACGCCAAC	YSKWNAN	++	-
2825	13776	TTCGCGAGGACGGGGTTGAAT	FARTGLN	+	-
2826	13777	TATGCGAAAATAGGGCCGAAT	YAKIGPN	+	-
2827	13778	TTCTCCAGGATAGGGTTGAAT	FSRIGLN	+++	-
2828	13779	TATGCGAAAATAGGGTTCAAT	YAKIGFN	+	-
2829	13780	TATTCCAAAATAGGGGATAAT	YSKIGDN	++	-
2830	13781	TTCGCGAGGTTCAATACGAAT	FARFNTN	+++	-
2831	13782	TATTCCAGGGTGAATTTCAAT	YSRVNFN	+	+
2832	13783	TATGCGAGGACGAATACGAAT	YARTNTN	+	++
2833	13784	TTTGCCCGCAACGGCCTGAAC	FARNGLN	+	-
2834	13785	TATGCGAAATATGGGATAAAT	YAKYGIN	+	-
2835	13786	TATGCGAGGCACGGGATGAAT	YARHGMN	+	-
2836	13787	TACGCCCGCGGCAACTTTAAC	YARGNFN	++	-
2837	13788	TTCTCCAAATTGAATTCCAAT	FSKLNSN	+	-
2838	13789	TATGCGAGGGTGGGGCACAAT	YARVGHN	+	+
2839	13790	ACCAACGCCACCTCAAAGTGG	TNATSKW	++	+
2840	13791	TATTCCAGGGCGAATGTGAAT	YSRANVN	+	+
2841	13792	TATTCCAGGGCGGGGGGGAAT	YSRAGGN	++	+
2842	13793	TATTCCAGGAAAGGGGAGAAT	YSRKGEN	+	-
2843	13794	TTCGCGAGGTTGGGGCACAAT	FARLGHN	++	-
2844	13795	CGCGACGACTTTACCGCCTAC	RDDFTAY	+	-
2845	13796	TTTGCCCGCTCAGGCCCCAAC	FARSGPN	+	-
2846	13797	TTCTCCAAATTGGGGAATAAT	FSKLGNN	+	+
2847	13798	TACGCCCGCACCAACATCAAC	YARTNIN	+	-
2848	13799	TTCTCCAGGTTGGGGGTGAAT	FSRLGVN	+	-
2849	13800	TATGCGAAATCCGGGTGTAAT	YAKSGCN	++	-
2850	13801	TATTCCAGGTATAATCAGAAT	YSRYNQN	+++	-
2851	13802	TATTCCAGGATAGGGCAGAAT	YSRIGQN	++	-
2852	13803	TATTCCAGGATGAATTCCAAT	YSRMNSN	+	+
2853	13804	TATTCCAGGTCCGGGGTGAAT	YSRSGVN	+	-
2854	13805	TATGCGAGGGCGGGGGTGAAT	YARAGVN	+	-
2855	13806	TTCTCCAAAGTGGGGCCGAAT	FSKVGPN	++	-
2856	13807	CTGTCAAAGCTGGGCCATAAC	LSKLGHN	++	-
2857	13808	TACGCCCGCCATGGCCAAAAC	YARHGQN	++	-
2858	13809	TATGCGAGGACGAATTTGAAT	YARTNLN	+	-
2859	13810	TATTCCAGGCACAATACGAAT	YSRHNTN	++	-
2860	13811	AGGTCCGGGAATTCCTCCTAT	RSGNSSY	+	++
2861	13812	TATGCGAGGACGAATGTGAAT	YARTNVN	+	-
2862	13813	TTCGCGAGGTCCGGGTTGAAT	FARSGLN	+	-
2863	13814	TATTCCAAAGCGAATTTCAAT	YSKANFN	+++	+
2864	13815	TATTCCAAACACAATCACAAT	YSKHNHN	++	-
2865	13816	TATTCCAGGTTGAATCCGAAT	YSRLNPN	+++	+
2866	13817	TACTCACGCCAAAACGTAAAC	YSRQNVN	+	-
2867	13818	TATTCCAGGTTGAATGTGAAT	YSRLNVN	+++	-
2868	13819	TTTGCCCGCGCCGGCGCCAAC	FARAGAN	++	-

2869	13820	TATTCCAGGACGAATCACAAT	YSRTNHN	+	+
2870	13821	TATGCGAGGCAGAATGTGAAT	YARQNVN	+	-
2871	13822	TATGCGAGGCAGGGGCACAAT	YARQGHN	+++	-
2872	13823	TACGCCAAGTACAACCATAAC	YAKYNHN	+++	-
2873	13824	TTCTCCAGGGTGGGGTCCAAT	FSRVGSN	+	-
2874	13825	TATTCCAGGCAGAATCAGAAT	YSRQNQN	++	-
2875	13826	TATGCGAGGGTGGGGTTGAAT	YARVGLN	+	-
2876	13827	TTCGCGAGGACGGGGGTGAAT	FARTGVN	+	++
2877	13828	TACGCCCGCTCAGGCTACAAC	YARSGYN	++	+
2878	13829	TACTCAAAGTACGGCAACAAC	YSKYGNN	+	-
2879	13830	TATTCCAGGGTGGGGCACAAT	YSRVGHN	++	++
2880	13831	TTCGCGAAAATGGGGTATAAT	FAKMGYN	+	+
2881	13832	TACGCCAAGTACGGCCATAAC	YAKYGHN	+++	++
2882	13833	TACTCAAAGTCAGGCCATAAC	YSKSGHN	+	-
2883	13834	TATGCGAGGATAGGGATGAAT	YARIGMN	+	+
2884	13835	TACTCACGCATCAACCTGAAC	YSRINLN	++	-
2885	13836	TACGCCCGCATGAACTTTAAC	YARMNFN	+	-
2886	13837	TATTCCAAAGTGGGGTTCAAT	YSKVGFN	+	-
2887	13838	TTTTCACGCATGGGCAACAAC	FSRMGNN	+	-
2888	13839	TATTCCAGGAATAATCACAAT	YSRNNHN	+	+++
2889	13840	TTCTCCAGGGGGAATATAAAT	FSRGNIN	+	+
2890	13841	TTGCACAGGATGACGCCGAAT	LHRMTPN	++	-
2891	13842	TATTCCAGGTCCAATCAGAAT	YSRSNQN	+	+
2892	13843	CTGTCAAAGCTGGGCTTTAAC	LSKLGFN	++	-
2893	13844	TATTCCAGGTTGAATACGAAT	YSRLNTN	+++	-
2894	13845	TACGCCCGCGGCAACTCAAAC	YARGNSN	+	-
2895	13846	TATGCGAGGGCGAATTTCAAT	YARANFN	+	-
2896	13847	TATTCCAGGTCCAATGTGAAT	YSRSNVN	+	-
2897	13848	TACTCACGCCTGAACCTGAAC	YSRLNLN	+++	+
2898	13849	TACGCCCGCATGGGCCATAAC	YARMGHN	+	-
2899	13850	TATTCCAGGGCGAATGATAAT	YSRANDN	+	-
2900	13851	TATGCGAGGACGGGGTTCAAT	YARTGFN	++	+
2901	13852	TTCGCGAGGTCCGGGCAGAAT	FARSGQN	+	++
2902	13853	TTCTCCAGGGCGAATGTGAAT	FSRANVN	+	+
2903	13854	TACTCACGCATGAACGTAAAC	YSRMNVN	+	+
2904	13855	TATGCGAAAGCGGGGCAGAAT	YAKAGQN	+	+
2905	13856	TACTCACGCACCGGCCATAAC	YSRTGHN	+++	-
2906	13857	TATGCGAGGTCCGGGTTCAAT	YARSGFN	++	-
2907	13858	TATGCGAGGACGGGGTCCAAT	YARTGSN	+	-
2908	13859	TATGCGAAACAGGGGTGGAAT	YAKQGWN	+	+
2909	13860	TTCGCGAGGACGGGGTTCAAT	FARTGFN	+	-
2910	13861	TTCTCCAAAGCGAATTTCAAT	FSKANFN	+	++
2911	13862	TACTCACGCCTGAACGGCAAC	YSRLNGN	+	-
2912	13863	TATTCCAGGTTGGGGAAAGAT	YSRLGKD	++	-
2913	13864	TATGCGAGGTCCGGGCCGAAT	YARSGPN	+++	-

2914	13865	TATTCCAGGATAAATCAGAAT	YSRINQN	+	+
2915	13866	TTTGCCAAGCAAGGCTACAAC	FAKQGYN	+	-
2916	13867	TTCTCCAGGACGGGGACGAAT	FSRTGTN	+	-
2917	13868	TATGCGAAAATAGGGCACAAT	YAKIGHN	+	-
2918	13869	CTGTCACGCATGAACTACAAC	LSRMNYN	++	-
2919	13870	TTTTCACGCATGAACACCAAC	FSRMNTN	++	+++
2920	13871	TATTCCAGGGGGAATCAGAAT	YSRGNQN	++	+
2921	13872	TACTCACGCATGAACCCCAAC	YSRMNPN	++	-
2922	13873	TATGCGAGGCAGAATCCGAAT	YARQNPN	+	+
2923	13874	TATTCCAGGTTGGGGTTGAAT	YSRLGLN	++	+
2924	13875	TATGCGAGGGCGGGGTTGAAT	YARAGLN	+	-
2925	13876	TATGCGAGGGGGAATCAGAAT	YARGNQN	+	-
2926	13877	TACTCAAAGATGGGCTTTAAC	YSKMGFN	+	+
2927	13878	TACGCCCGCGTAGGCTACAAC	YARVGYN	+++	-
2928	13879	TTCTCCAGGGCGGGGCAGAAT	FSRAGQN	+	-
2929	13880	CTGGCCAAGCTGGGCCATAAC	LAKLGHN	+	-
2930	13881	ATAAGGTCCATGAATGGGGTG	IRSMNGV	+	-
2931	13882	TATGCGAAAGCGGGGCCGAAT	YAKAGPN	+	-
2932	13883	TACTCAAAGGGCAACTGGAAC	YSKGNWN	+++	-
2933	13884	ACCAACTCAACCAACGGCATC	TNSTNGI	+	-
2934	13885	TATTCCAGGGTGAATACGAAT	YSRVNTN	+	+
2935	13886	TTCCACAAATTGGGGTCCAAT	FHKLGSN	+	-
2936	13887	TATTCCAGGACGGGGCAGAAT	YSRTGQN	+	+
2937	13888	TATTCCAGGTCCGGGTCCAAT	YSRSGSN	+	-
2938	13889	TTCTCCAGGGCGAATTTCAAT	FSRANFN	+++	-
2939	13890	TATGCGAGGATGGGGTCCAAT	YARMGSN	+	+
2940	13891	TTTGCCCGCGTAGGCATCAAC	FARVGIN	+++	-
2941	13892	TACGCCCGCACCGGCATGAAC	YARTGMN	++	-
2942	13893	TTCGCGAGGACGGGGCAGAAT	FARTGQN	+	-
2943	13894	TTTTCACGCGTAGGCCATAAC	FSRVGHN	++	+
2944	13895	TATGCGAAAATGAATATAAAT	YAKMNIN	+	-
2945	13896	TATGCGAGGATGGGGGCGAAT	YARMGAN	++	-
2946	13897	TATGCGAGGATAGGGTTCAAT	YARIGFN	+	-
2947	13898	TATTCCAGGTTGAATCAGAAT	YSRLNQN	+++	-
2948	13899	TACTCAAAGATGAACTACAAC	YSKMNYN	+	-
2949	13900	TACTCACGCCAAGGCGCCAAC	YSRQGAN	+	+
2950	13901	TATTCCAGGGTGGGGATGAAT	YSRVGMN	++	-
2951	13902	TTCTCCAGGACGGGGTTCAAT	FSRTGFN	+	+
2952	13903	TACTCACGCATGAACTTTAAC	YSRMNFN	++	-
2953	13904	TACTCAAAGATCGGCAACAAC	YSKIGNN	+	-
2954	13905	TACGCCCGCGTAGGCATGAAC	YARVGMN	++	+++
2955	13906	TATGCGAGGAAAGGGGAGAAT	YARKGEN	+++	-
2956	13907	TTCTCCAGGATGAATTCCAAT	FSRMNSN	+++	-
2957	13908	TATTCCAAATCCGGGTGGAAT	YSKSGWN	+++	+++
2958	13909	TACGCCAAGCTGGGCTACAAC	YAKLGYN	++	-

2959	13910	TTTGCCCGCATGGGCCTGAAC	FARMGLN	+	-
2960	13911	TTCTCCAGGTTGGGGTCCAAT	FSRLGSN	+	-
2961	13912	TATTCCAGGGTGAATGCGAAT	YSRVNAN	+	+
2962	13913	TACTCAAAGGCCGGCTTTAAC	YSKAGFN	+	++
2963	13914	TATGCGAGGGGGGGGTCCAAT	YARGGSN	+	++
2964	13915	TATGCGAAATCCAATTGGAAT	YAKSNWN	++	-
2965	13916	TACGCCAAGATGGGCTTTAAC	YAKMGFN	+	-
2966	13917	TTCTCCAGGTTGGGGATGAAT	FSRLGMN	+	-
2967	13918	TACTCACGCGCCAACATGAAC	YSRANMN	+	-
2968	13919	TACGCCAAGCAAAACTACAAC	YAKQNYN	+	+
2969	13920	TATTCCAGGCAGGGGCAGAAT	YSRQGQN	+	-
2970	13921	TTCGCGAGGATGGGGCCGAAT	FARMGPN	+	-
2971	13922	TACTCACGCGGCAACCTGAAC	YSRGNLN	+	-
2972	13923	TATTCCAGGACGGGGTTCAAT	YSRTGFN	++	-
2973	13924	TTTGCCAAGAACGGCCCCAAC	FAKNGPN	+	-
2974	13925	TTCGCGAGGCACGGGTATAAT	FARHGYN	+++	-
2975	13926	TTCGCGAGGTTCAATCAGAAT	FARFNQN	+	++
2976	13927	TTCGCGAGGTCCGGGGCGAAT	FARSGAN	+	-
2977	13928	TATGCGAGGATAGGGCCGAAT	YARIGPN	++	-
2978	13929	TTGTCCAGGCACAATGATAAT	LSRHNDN	+	-
2979	13930	TATGCGAGGACGGGGTTGAAT	YARTGLN	+	-
2980	13931	TACTCAAAGCATGGCCATAAC	YSKHGHN	+++	-
2981	13932	TTTTCACGCCAAGGCTACAAC	FSRQGYN	++	-
2982	13933	TATGCGAGGGGGGGGAATAAT	YARGGNN	+	-
2983	13934	TTCGCGAGGACGGGGCCGAAT	FARTGPN	++	+++
2984	13935	TATTCCAGGGTGAATTCCAAT	YSRVNSN	+	+
2985	13936	TTCTCCAGGTTGAATGGGAAT	FSRLNGN	+	-
2986	13937	TACTCACGCATGAACATCAAC	YSRMNIN	+	+
2987	13938	TATTCCAAAATGGGGCCGAAT	YSKMGPN	+	-
2988	13939	TATTCCAGGATAGGGACGAAT	YSRIGTN	++	++
2989	13940	TATGCGAGGATGGGGGTGAAT	YARMGVN	+	++
2990	13941	GTGTCCGGGAGGTCCGCGTAT	VSGRSAY	+	-
2991	13942	TATTCCAGGACGAATACGAAT	YSRTNTN	+	-
2992	13943	TATTCCAGGGTGGGGACGAAT	YSRVGTN	+++	-
2993	13944	TACTCACGCTCAGGCTACAAC	YSRSGYN	+++	-
2994	13945	TATGCGAAAGCGGGGTGGAAT	YAKAGWN	+	-
2995	13946	TACTCACGCACCGGCCTGAAC	YSRTGLN	+	-
2996	13947	TTCGCGAGGACGGGGGCGAAT	FARTGAN	+	++
2997	13948	TTCTCCAGGTTGAATGCGAAT	FSRLNAN	++	-
2998	13949	TATTCCAGGATAGGGGTGAAT	YSRIGVN	++	+
2999	13950	TTCTCCAGGATAGGGGTGAAT	FSRIGVN	+	-
3000	13951	TACGCCAAGGGCGGCTGCAAC	YAKGGCN	+	-
3001	13952	TATGCGAAATCCGGGATGAAT	YAKSGMN	+	-
3002	13953	TATGCGAGGTTGAATTCCAAT	YARLNSN	+++	-
3003	13954	TATTCCAGGGTGAATGTGAAT	YSRVNVN	+	+

3004	13955	TATTCCAGGAATAATCCGAAT	YSRNNPN	++	-
3005	13956	TATTCCAGGATGAATGCGAAT	YSRMNAN	++	+
3006	13957	TATGCGAAAGGGGGGCACAAT	YAKGGHN	+	-
3007	13958	TTCGCGAGGGGGGGGTCCAAT	FARGGSN	+	-
3008	13959	TACTCAAAGCATGGCTTTAAC	YSKHGFN	+++	-
3009	13960	TATGCGAGGTCCGGGATGAAT	YARSGMN	+	-
3010	13961	TTTTCACGCGTAGGCCAAAAC	FSRVGQN	++	+
3011	13962	TTCTCCAGGGCGGGGCACAAT	FSRAGHN	++	-
3012	13963	TATGCGAGGATGAATTATAAT	YARMNYN	++	-
3013	13964	TATTCCAGGTCCGGGGCGAAT	YSRSGAN	++	-
3014	13965	TATGCGAGGCAGGGGGGGAAT	YARQGGN	+	-
3015	13966	TTTTCACGCATCGGCTCAAAC	FSRIGSN	+	-
3016	13967	TACTCACGCGCCAACACCAAC	YSRANTN	+	+
3017	13968	TATGCGAGGGCGGGGACGAAT	YARAGTN	+	+
3018	13969	TATGCGAGGATGAATCACAAT	YARMNHN	++	-
3019	13970	TTCTCCAGGTTGGGGCAGAAT	FSRLGQN	+	+
3020	13971	TTCTCCAAAATAGGGCACAAT	FSKIGHN	+	-
3021	13972	TACTCACGCATCGGCCATAAC	YSRIGHN	+++	++
3022	13973	TATGCGAGGAATGGGTTCAAT	YARNGFN	+	-
3023	13974	TATGCGAGGTTGAATACGAAT	YARLNTN	+	+
3024	13975	TATGCGAGGAATGGGATGAAT	YARNGMN	+	-
3025	13976	TACTCACGCGCCAACATCAAC	YSRANIN	++	-
3026	13977	TTCGCGAGGGTGGGGCCGAAT	FARVGPN	+	+
3027	13978	CTGTCAAAGCTGAACGCCAAC	LSKLNAN	+	+
3028	13979	CTGGCCAAGATCGGCTACAAC	LAKIGYN	+	-
3029	13980	TATTCCAGGATAAATGCGAAT	YSRINAN	+	-
3030	13981	TACTCAAAGATCGGCCTGAAC	YSKIGLN	+	-
3031	13982	TTCTCCAGGTTGAATCCGAAT	FSRLNPN	+	-
3032	13983	TATGCGAAAACGGGGCACAAT	YAKTGHN	+	-
3033	13984	TACTCACGCATGGGCATGAAC	YSRMGMN	+	-
3034	13985	TACTCAAAGCAAGGCTACAAC	YSKQGYN	+	-
3035	13986	TTCGCGAAAGCGGGGCCGAAT	FAKAGPN	+	-
3036	13987	TACTCACGCGCCAACGGCAAC	YSRANGN	++	-
3037	13988	TTCGCGAAAACGGGGTGGAAT	FAKTGWN	++	-
3038	13989	TATGCGAGGGTGGGGGCGAAT	YARVGAN	+	+
3039	13990	TATGCGAGGCAGGGGCCGAAT	YARQGPN	++	-
3040	13991	TATTCCAAAGTGGGGGCGAAT	YSKVGAN	++	-
3041	13992	TATTCCAGGGCGGGGGCGAAT	YSRAGAN	+	+
3042	13993	TTTTCACGCCATGGCAACAAC	FSRHGNN	++	-
3043	13994	TTTGCCCGCTACGGCTCAAAC	FARYGSN	+++	-
3044	13995	TTCTCCAGGTTGAATGATAAT	FSRLNDN	++	-
3045	13996	GTGTTCTCCTCCAATGGGGTG	VFSSNGV	+	-
3046	13997	TACTCACGCGCCAACGCCAAC	YSRANAN	++	-
3047	13998	TACTCAAAGATGAACATGAAC	YSKMNMN	+	++
3048	13999	TATTCCAAAGGGAATTTCAAT	YSKGNFN	+	-

3049	14000	TTTTCACGCGCCGGCTCAAAC	FSRAGSN	+	+
3050	14001	TATTCCAGGGCGGGGCAGAAT	YSRAGQN	+	-
3051	14002	TATTCCAGGTCCGCGACGAAT	YSRSATN	+	-
3052	14003	TATGCGAGGGGGGGGTTGAAT	YARGGLN	++	-
3053	14004	TACGCCAAGACCGGCGTAAAC	YAKTGVN	+++	-
3054	14005	TATTCCAAATTGGGGCCGAAT	YSKLGPN	++	-
3055	14006	TATGCGAGGCAGGGGGTGAAT	YARQGVN	+	-
3056	14007	TACTCAAAGGTAGGCTGCAAC	YSKVGCN	+++	-
3057	14008	TTGTCCAGGTCCGGGACGAAT	LSRSGTN	++	+
3058	14009	TTTGCCCGCCAAGGCCTGAAC	FARQGLN	+	-
3059	14010	TACTCACGCGTAGGCCTGAAC	YSRVGLN	+++	-
3060	14011	TATGCGAGGATGGGGATGAAT	YARMGMN	+	+
3061	14012	TTCGCGAGGGGGGGGGTGAAT	FARGGVN	++	-
3062	14013	TACGCCAAGGCCGGCTTTAAC	YAKAGFN	+	-
3063	14014	TTCAGGTCCACGAATGGGATA	FRSTNGI	++	-
3064	14015	TTTTCACGCGCCAACAACAAC	FSRANNN	++	-
3065	14016	ATAAGGTCCACGAATGGGATA	IRSTNGI	+	-
3066	14017	TTCTCCAAAATGGGGAATAAT	FSKMGNN	+	-
3067	14018	TTTTCAAAGCTGAACGTAAAC	FSKLNVN	+	-
3068	14019	TACTCACGCTCAGGCGGCAAC	YSRSGGN	++	-
3069	14020	TATGCGAGGGGGAATCCGAAT	YARGNPN	+	+
3070	14021	TTCTCCAGGCCGAATAATAAT	FSRPNNN	+	-
3071	14022	TTCGCGAGGACGGGGTCCAAT	FARTGSN	+	++
3072	14023	TATGCGAGGGTGGGGCCGAAT	YARVGPN	++	-
3073	14024	TATTCCAGGAAAAATGAGAAT	YSRKNEN	++	++
3074	14025	TATGCGAGGGGGGGGGCGAAT	YARGGAN	+	+
3075	14026	TACTCAAAGATGAACTTTAAC	YSKMNFN	+	-
3076	14027	CTGTCAAAGCAAAACTTTAAC	LSKQNFN	+	-
3077	14028	ACCAAGTCAACCAACGGCATC	TKSTNGI	+	-
3078	14029	TACTCACGCCATAACATCAAC	YSRHNIN	++	-
3079	14030	TTTGCCCGCACCGGCTACAAC	FARTGYN	+	-
3080	14031	TTCTCCAGGATAAATGTGAAT	FSRINVN	+	-
3081	14032	TATGCGAGGGCGGGGCACAAT	YARAGHN	++	-
3082	14033	TACTCACGCCAAGGCCTGAAC	YSRQGLN	+	-
3083	14034	TATTCCAGGTTGGGGCACAAT	YSRLGHN	++	+
3084	14035	TTTTCAAAGCTGAACAACAAC	FSKLNNN	+	-
3085	14036	TATTCCAAATTGAATCCGAAT	YSKLNPN	++	-
3086	14037	TATTCCAGGACGAATTCCAAT	YSRTNSN	++	-
3087	14038	TACTCACGCGCCGGCACCAAC	YSRAGTN	+	-
3088	14039	ATAACGGGGATGTCCAAATAT	ITGMSKY	+	-
3089	14040	TATTCCAAAGTGGGGCCGAAT	YSKVGPN	++	-
3090	14041	TATGCGAGGGGGAATGTGAAT	YARGNVN	+	+
3091	14042	TACGCCCGCACCGGCGGCAAC	YARTGGN	+	-
3092	14043	TATTCCAGGATGAATCACAAT	YSRMNHN	+++	+
3093	14044	TTTGCCCGCAACGGCATCAAC	FARNGIN	+	+

3094	14045	TATTCCAAACAGGGGTGTAAT	YSKQGCN	+++	-
3095	14046	TATTCCAGGTTGGGGATGAAT	YSRLGMN	+++	-
3096	14047	TTCTCCAGGGCGGGGATGAAT	FSRAGMN	+	-
3097	14048	TATGCGAGGAATGGGCCGAAT	YARNGPN	+++	-
3098	14049	TTCTCCAGGATAGGGGGGAAT	FSRIGGN	++	+
3099	14050	TATTCCAAATTGAATGCGAAT	YSKLNAN	++	-
3100	14051	TTCGCGAGGGGGGGGTTCAAT	FARGGFN	+	-
3101	14052	TACTCAAAGCATGGCGCCAAC	YSKHGAN	+	-
3102	14053	TACGCCCGCTCAGGCCAAAAC	YARSGQN	++	-
3103	14054	CTGGCCAAGACCGGCCCCAAC	LAKTGPN	++	-
3104	14055	TATGCGAAATATGGGATGAAT	YAKYGMN	+	-
3105	14056	TACTCACGCATGAACAACAAC	YSRMNNN	+	-
3106	14057	TTGCACAAAACGACGCACAAT	LHKTTHN	+	-
3107	14058	TTCTCCAGGGTGGGGATGAAT	FSRVGMN	++	-
3108	14059	TATTCCAGGGTGGGGCCGAAT	YSRVGPN	+++	+
3109	14060	TTGCACGCGGCGTTGCCGAAT	LHAALPN	+	-
3110	14061	TACTCACGCGCCGGCCATAAC	YSRAGHN	+++	-
3111	14062	TATGCGAGGACGAATCCGAAT	YARTNPN	+	-
3112	14063	TTTTCAAAGATGAACTTTAAC	FSKMNFN	++	-
3113	14064	TTTGCCCGCAACGGCCATAAC	FARNGHN	+	-
3114	14065	TACTCACGCATCAACCCCAAC	YSRINPN	+	+++
3115	14066	TTCTCCAAATTGAATCACAAT	FSKLNHN	+	-
3116	14067	TATGCGAGGACGAATCAGAAT	YARTNQN	+	-
3117	14068	TATGCGAGGCAGAATCAGAAT	YARQNQN	+	+
3118	14069	TATGCGAGGATAGGGCACAAT	YARIGHN	++	-
3119	14070	TACTCACGCCCCAACTACAAC	YSRPNYN	++	+++
3120	14071	TATTCCAAATGGAATAATAAT	YSKWNNN	+++	++
3121	14072	TTCGCGAGGGGGGGGGCGAAT	FARGGAN	++	-
3122	14073	TTCTCCAGGACGGGGTTGAAT	FSRTGLN	+	-
3123	14074	TACTCACGCATCGGCGGCAAC	YSRIGGN	+++	+++
3124	14075	TACTCAAAGATCGGCATCAAC	YSKIGIN	+	++
3125	14076	TATGCGAGGCCGGGGGCGAAT	YARPGAN	+	+
3126	14077	TTCGCGAGGACGGGGATGAAT	FARTGMN	+	-
3127	14078	TACTCACGCTCAAACATGAAC	YSRSNMN	+	-
3128	14079	TACTCAAAGCTGAACCAAAAC	YSKLNQN	+	+
3129	14080	TACGCCAAGGGCAACTGGAAC	YAKGNWN	+	+
3130	14081	CTGTCAAAGATCGGCCATAAC	LSKIGHN	++	-
3131	14082	TACTCAAAGGCCAACTACAAC	YSKANYN	+	-
3132	14083	TATTCCAGGGTGGGGGTGAAT	YSRVGVN	+	-
3133	14084	TTTGCCCGCGGCGGCCCCAAC	FARGGPN	++	-
3134	14085	TACTCAAAGGTAGGCCATAAC	YSKVGHN	+	-
3135	14086	TATGCGAAACAGGGGTCCAAT	YAKQGSN	++	-
3136	14087	TACGCCCGCTCAGGCACCAAC	YARSGTN	+	-
3137	14088	TTCTCCAGGCAGGGGCCGAAT	FSRQGPN	+	-
3138	14089	TATGCGAGGAATGGGCACAAT	YARNGHN	+	-

3139	14090	TATGCGAGGCAGGGGACGAAT	YARQGTN	+	+++
3140	14091	TACTCACGCGGCGGCATGAAC	YSRGGMN	+	+++
3141	14092	TTTTCACGCGTAGGCGCCAAC	FSRVGAN	++	-
3142	14093	TATTCCAAAATGGGGGTGAAT	YSKMGVN	+	++
3143	14094	TACTCAAAGGTAGGCTCAAAC	YSKVGSN	+	-
3144	14095	TACGCCCGCGCCAACCCCAAC	YARANPN	+	-
3145	14096	TTTGCCCGCGGCAACATCAAC	FARGNIN	+	-
3146	14097	TATTCCAAATTGAATCACAAT	YSKLNHN	+	-
3147	14098	TACTCACGCGTAGGCTTTAAC	YSRVGFN	++	++
3148	14099	TACTCACGCATGAACATGAAC	YSRMNMN	+	-
3149	14100	TATGCGAGGCACAATTCCAAT	YARHNSN	+	-
3150	14101	TATGCGAGGGGGGGGACGAAT	YARGGTN	+	-
3151	14102	TTGTCCAGGCAGGGGCCGAAT	LSRQGPN	+	-
3152	14103	TACTCACGCGCCGGCCTGAAC	YSRAGLN	++	+
3153	14104	TACTCAAAGACCGGCTTTAAC	YSKTGFN	+	-
3154	14105	TACGCCCGCTCAGGCGGCAAC	YARSGGN	++	-
3155	14106	TACTCACGCGGCAACATCAAC	YSRGNIN	++	-
3156	14107	TACGCCCGCGGCGGCTTTAAC	YARGGFN	++	-
3157	14108	TTGAGGTCCACGAATGGGGTG	LRSTNGV	+	-
3158	14109	TATGCGAGGTCCGGGGTGAAT	YARSGVN	+	+
3159	14110	TATTCCAGGTTCAATATGAAT	YSRFNMN	+	+
3160	14111	TACGTAAAGTCAAACAACAAC	YVKSNNN	+	-
3161	14112	TACGCCAAGCTGGGCCATAAC	YAKLGHN	+	-
3162	14113	TATGCGAGGCACGGGTTGAAT	YARHGLN	+	-
3163	14114	TATGCGAGGATAGGGGGGAAT	YARIGGN	++	-
3164	14115	TATTCCAGGGTGGGGTCCAAT	YSRVGSN	++	-
3165	14116	TATTCCAGGCAGGGGGTGAAT	YSRQGVN	+	-
3166	14117	TTCGCGAAATATAATCCGAAT	FAKYNPN	+	-
3167	14118	TATTCCAAATGGAATCAGAAT	YSKWNQN	+	+
3168	14119	TTCTCCAGGATGGGGGCGAAT	FSRMGAN	++	++
3169	14120	TTCTCCAGGTCCGGGTTGAAT	FSRSGLN	+	-
3170	14121	TATTCCAAATCCGGGTTCAAT	YSKSGFN	+++	-
3171	14122	TATGCGAGGACGGGGGTGAAT	YARTGVN	+	+
3172	14123	TACTCAAAGAACGGCTGCAAC	YSKNGCN	+++	-
3173	14124	TATGCGAAAGTGGGGCACAAT	YAKVGHN	+	-
3174	14125	ATCTTTTCAACCAACGGCATC	IFSTNGI	++	-
3175	14126	TACTCACGCATCGGCTTTAAC	YSRIGFN	+++	-
3176	14127	TATTCCAAATATGGGTTGAAT	YSKYGLN	++	-
3177	14128	TACGCCAAGACCAACTGGAAC	YAKTNWN	+	++
3178	14129	CATTCACGCACCGGCTCAAAC	HSRTGSN	+	-
3179	14130	TACTCACGCATGAACCTGAAC	YSRMNLN	+	+
3180	14131	TTCGCGAGGGGGGGGACGAAT	FARGGTN	+	-
3181	14132	TACTCACGCATCAACGTAAAC	YSRINVN	+	-
3182	14133	TATACGAGGTTGAATCAGAAT	YTRLNQN	++	-
3183	14134	CCGAGGTCCACGAATGGGATA	PRSTNGI	++	-

3184	14135	TTCGCGAGGATAGGGAATAAT	FARIGNN	++	-
3185	14136	TATTCCAGGTTGGGGGCGAAT	YSRLGAN	++	++
3186	14137	TACTCACGCGCCGGCGTAAAC	YSRAGVN	+	-
3187	14138	CTGTCAAAGCTGGGCGTAAAC	LSKLGVN	+	-
3188	14139	TACGCCAAGCAAGGCTACAAC	YAKQGYN	+++	++
3189	14140	TACGCCCGCTCAGGCTCAAAC	YARSGSN	+	-
3190	14141	TATTCCAGGACGAATGTGAAT	YSRTNVN	+	+
3191	14142	TATTCCAGGGCGAATTCCAAT	YSRANSN	++	-
3192	14143	TACTCACGCGGCGGCTTTAAC	YSRGGFN	+	-
3193	14144	TACTCACGCGGCGGCTACAAC	YSRGGYN	+	++
3194	14145	TATGCGAGGACGGGGACGAAT	YARTGTN	+	+
3195	14146	TATGCGAGGTTGGGGCACAAT	YARLGHN	++	-
3196	14147	TATGCGAGGACGAATGCGAAT	YARTNAN	++	+
3197	14148	TACTCACGCACCAACAACAAC	YSRTNNN	+	-
3198	14149	TACTCACGCTCAGGCCTGAAC	YSRSGLN	+	++
3199	14150	TATTCCAAACAGGGGTTCAAT	YSKQGFN	++	-
3200	14151	TACGCCCGCGTAGGCACCAAC	YARVGTN	+	-
3201	14152	TACTCACGCCCCAACCATAAC	YSRPNHN	+++	-
3202	14153	CTGGCCAAGGCCGGCATGAAC	LAKAGMN	+	-
3203	14154	TATGCGAGGCACGGGGATAAT	YARHGDN	+	-
3204	14155	TTCTCCAGGATAAATATAAAT	FSRININ	++	-
3205	14156	TATTCCAGGGGGGGGAATAAT	YSRGGNN	+	-
3206	14157	TATGCGAGGATGGGGTTGAAT	YARMGLN	+	+
3207	14158	TACGCCAAGGGCAACGTAAAC	YAKGNVN	+	-
3208	14159	TACGCCAAGACCGGCATGAAC	YAKTGMN	+	-
3209	14160	TATTCCAGGTGGAATGAGAAT	YSRWNEN	+	-
3210	14161	ATAGATGCGTCCTCCAGGTGG	IDASSRW	+++	-
3211	14162	TATGCGAGGCAGAATTTGAAT	YARQNLN	+	++
3212	14163	TTCGCGAGGGGGGGGTTGAAT	FARGGLN	++	-
3213	14164	TTCTCCAAATATGGGCACAAT	FSKYGHN	++	-
3214	14165	TTTGCCAAGTACGGCTACAAC	FAKYGYN	++	-
3215	14166	TATGCGAGGTATGGGTCCAAT	YARYGSN	+++	-
3216	14167	TTTTCACGCGTAGGCAACAAC	FSRVGNN	++	+++
3217	14168	TACTCACGCGTAAACATCAAC	YSRVNIN	+	+++
3218	14169	CTGTCAAAGATGAACGTAAAC	LSKMNVN	+	-
3219	14170	TATGCGAGGCAGGGGTTCAAT	YARQGFN	+++	-
3220	14171	TTCTCCAGGGCGAATCAGAAT	FSRANQN	+	-
3221	14172	TATGCGAGGTTCAATGGGAAT	YARFNGN	+	-
3222	14173	TATGCGAAAAGGGGGGAGAAT	YAKRGEN	+++	-
3223	14174	TATTCCAAATTGGGGGCGAAT	YSKLGAN	+	+
3224	14175	TACTCACGCGCCGGCATGAAC	YSRAGMN	++	-
3225	14176	TATTCCAAAATAGGGCCGAAT	YSKIGPN	++	-
3226	14177	TTTGCCCGCGGCGGCAACAAC	FARGGNN	+	-
3227	14178	TACTCACGCATGGGCCTGAAC	YSRMGLN	+	+++
3228	14179	TTCTCCAGGGTGGGGGTGAAT	FSRVGVN	++	-

3229	14180	TATGCGAAAATAGGGATAAAT	YAKIGIN	+	-
3230	14181	TACTCAAAGATGAACGTAAAC	YSKMNVN	+	+
3231	14182	TATGCGAAAATGGGGCACAAT	YAKMGHN	+	-
3232	14183	TACTCACGCGCCGGCAACAAC	YSRAGNN	++	-
3233	14184	TACTCACGCCCCAACTTTAAC	YSRPNFN	+	-
3234	14185	TATGCGAAAACGGGGTGGAAT	YAKTGWN	+	+
3235	14186	TATGTGAGGTCCGGGGGGAAT	YVRSGGN	+	+
3236	14187	TATGCGAGGTTGGGGGCGAAT	YARLGAN	+	++
3237	14188	TATTCCAAATTCAATATGAAT	YSKFNMN	+	-
3238	14189	CAGGGGGAGGAGAGGAAATGG	QGEERKW	+	-
3239	14190	TATTCCAGGGCGGGGCCGAAT	YSRAGPN	+++	+
3240	14191	TACGCCCGCACCGGCCATAAC	YARTGHN	++	-
3241	14192	TTTTCACGCCTGAACATCAAC	FSRLNIN	+++	-
3242	14193	TATGCGAGGGGGAATACGAAT	YARGNTN	+	-
3243	14194	TACTCACGCCATGGCCTGAAC	YSRHGLN	++	-
3244	14195	TATGCGAGGTTGAATCAGAAT	YARLNQN	+	+
3245	14196	TATTCCAGGATGGGGGCGAAT	YSRMGAN	+	-
3246	14197	TACGCCCGCACCAACTACAAC	YARTNYN	+++	-
3247	14198	TATGCGAAAAATGGGCCGAAT	YAKNGPN	+	-
3248	14199	TACGCCGGCCGCGGCCCCAAC	YAGRGPN	++	-
3249	14200	TACTCAAAGCTGAACTTTAAC	YSKLNFN	+++	+
3250	14201	TTTTCACGCTCAGGCGTAAAC	FSRSGVN	+	+
3251	14202	TTCTCCAAAAATAATTATAAT	FSKNNYN	++	-
3252	14203	TACTCACGCCAAAACGCCAAC	YSRQNAN	++	+
3253	14204	TTCTCCAGGATAGGGACGAAT	FSRIGTN	+	-
3254	14205	CTGGCCAAGCTGGGCTTTAAC	LAKLGFN	+	++
3255	14206	TACTCACGCCAAGGCATCAAC	YSRQGIN	++	+
3256	14207	TATTCCAAATTGAATACGAAT	YSKLNTN	++	-
3257	14208	TACTCAAAGATGAACAACAAC	YSKMNNN	+	-
3258	14209	TTCTCCAGGCAGAATGCGAAT	FSRQNAN	+	-
3259	14210	TTCGCGAAATCCGGGTGGAAT	FAKSGWN	++	+++
3260	14211	TACTCACGCACCGGCTCAAAC	YSRTGSN	+	+
3261	14212	AATTGGTCCTCCAATGGGGTG	NWSSNGV	++	-
3262	14213	TTTGCCCGCATGGGCACCAAC	FARMGTN	+	-
3263	14214	TTCGCGAAACACAATTATAAT	FAKHNYN	+	-
3264	14215	TTCGCGAGGATGGGGCACAAT	FARMGHN	+	-
3265	14216	TATGCGAGGTCCGGGGCGAAT	YARSGAN	+	+
3266	14217	TATGCGAGGGGGGGGCACAAT	YARGGHN	+++	-
3267	14218	TACTCACGCACCGGCATCAAC	YSRTGIN	+	-
3268	14219	TATGCGAGGTTGGGGCCGAAT	YARLGPN	++	++
3269	14220	ATGAAGTCAACCAACGGCATC	MKSTNGI	+	-
3270	14221	TACTCAAAGTACGGCGTAAAC	YSKYGVN	+	-
3271	14222	TATTCCAAATCCGGGCCGAAT	YSKSGPN	+	-
3272	14223	TTCTCCAGGCAGGGGTTGAAT	FSRQGLN	+	-
3273	14224	TACTCAAAGATCGGCTACAAC	YSKIGYN	+	-

3274	14225	TACGCCCGCATCGGCAACAAC	YARIGNN	++	+
3275	14226	TTTTCAAAGCTGAACGCCAAC	FSKLNAN	+	-
3276	14227	CTGGCCAAGGCCGGCCCCAAC	LAKAGPN	++	-
3277	14228	TTTGCCAAGAACGGCTTTAAC	FAKNGFN	+	-
3278	14229	TACTCAAAGCTGGGCGTAAAC	YSKLGVN	+	-
3279	14230	CTGGCCAAGACCGGCCTGAAC	LAKTGLN	++	-
3280	14231	TTCTCCAGGATAGGGATGAAT	FSRIGMN	++	-
3281	14232	TACGCCCGCGCCAACGCCAAC	YARANAN	+	-
3282	14233	TACTCACGCGGCGGCATCAAC	YSRGGIN	+	++
3283	14234	TACTCAAAGCTGGGCATGAAC	YSKLGMN	+	-
3284	14235	TTCGCGAAATCCGGGATGAAT	FAKSGMN	+	-
3285	14236	TACGCCCGCTCAAACACCAAC	YARSNTN	+	-
3286	14237	TATTCCAGGACGAATTTGAAT	YSRTNLN	+	-
3287	14238	TACTCAAAGCTGGGCTCAAAC	YSKLGSN	+	+
3288	14239	TTCGCGAGGGGGAATGTGAAT	FARGNVN	+	+
3289	14240	TGTGGGGGGATAGGGAGGTCC	CGGIGRS	+++	-
3290	14241	TGGATGTCAACCAACGGCGTA	WMSTNGV	+++	-
3291	14242	TATTCCAAAATGGGGCACAAT	YSKMGHN	++	-
3292	14243	TACTCACGCCTGAACTCAAAC	YSRLNSN	+++	-
3293	14244	GAGATGGATAATGTGAGGTGG	EMDNVRW	+	-
3294	14245	TTCTCCAGGCAGAATTTGAAT	FSRQNLN	+	++
3295	14246	CAGTATGGGAAAGTGTATATA	QYGKVYI	++	-
3296	14247	TACTCAAAGCAAGGCCTGAAC	YSKQGLN	++	-
3297	14248	TACGTACGCTCATCACAAAAC	YVRSSQN	+	+
3298	14249	TACTCACGCATGAACACCAAC	YSRMNTN	+	-
3299	14250	TACTCACGCTACGGCGAAAAC	YSRYGEN	+	-
3300	14251	TTCTCCAGGATGAATCAGAAT	FSRMNQN	+	+
3301	14252	TATTCCAAATATGGGGCGAAT	YSKYGAN	+	-
3302	14253	TATTCCAAAACGGGGTGGAAT	YSKTGWN	++	-
3303	14254	TTCTCCAGGTCCAATTATAAT	FSRSNYN	++	-
3304	14255	CGCGGCGGCTCATCACCCTAC	RGGSSPY	+	-
3305	14256	CTGTCAAAGATGAACTTTAAC	LSKMNFN	+	-
3306	14257	TTTTCAAAGGTAAACTACAAC	FSKVNYN	+	-
3307	14258	TTTTCACGCCAAAACATCAAC	FSRQNIN	+	-
3308	14259	TACTCAAAGCTGAACGTAAAC	YSKLNVN	++	-
3309	14260	TATTCCAGGGTGAATCAGAAT	YSRVNQN	+	-
3310	14261	TATTCCAGGTCCGGGACGAAT	YSRSGTN	++	-
3311	14262	TACTCACGCATCGGCGCCAAC	YSRIGAN	+++	-
3312	14263	TATTCCAGGACGGGGGGGAAT	YSRTGGN	++	-
3313	14264	TATGCGAGGACGGGGGCGAAT	YARTGAN	+	++
3314	14265	TATGCGAGGTCCGGGCACAAT	YARSGHN	++	-
3315	14266	CTGTCAAAGATGGGCGTAAAC	LSKMGVN	+	-
3316	14267	TATTCCAGGACGGGGATGAAT	YSRTGMN	+	-
3317	14268	TTTTCAAAGATGGGCCCCAAC	FSKMGPN	+	-
3318	14269	TATGCGAGGACGGGGCCGAAT	YARTGPN	+++	+

3319	14270	TACGCCAAGGGCGGCTACAAC	YAKGGYN	+	-
3320	14271	TTCGCGAGGGCGAATTATAAT	FARANYN	+	++
3321	14272	TATGCGAAAACGAATTTCAAT	YAKTNFN	++	-
3322	14273	TATGCGAGGATGGGGCCGAAT	YARMGPN	+	+
3323	14274	TATGCGAAAACGGGGCCGAAT	YAKTGPN	++	-
3324	14275	TACGTACGCACCGGCGTAAAC	YVRTGVN	+	-
3325	14276	TACGCCCGCACCTCAGGCAAC	YARTSGN	++	-
3326	14277	TATGCGAGGAAAGGGGATAAT	YARKGDN	+++	-
3327	14278	ATGCACAATGGGACGAATGCG	MHNGTNA	+	-
3328	14279	TATGCGAGGGGGAATGCGAAT	YARGNAN	+	-
3329	14280	TATGCGAAAATGGGGGCGAAT	YAKMGAN	+	+
3330	14281	CTGGCCCGCACCGGCGAAAAC	LARTGEN	+	-
3331	14282	TTTTCACGCCTGAACACCAAC	FSRLNTN	++	++
3332	14283	TATTCCAGGAATAATTCCAAT	YSRNNSN	+	-
3333	14284	CTGAAGTCAACCAACGGCGTA	LKSTNGV	+	-
3334	14285	TACGTACGCTCAAACGTAGGC	YVRSNVG	++	++
3335	14286	TACACCTCAACCAACGGCATC	YTSTNGI	+	-
3336	14287	TATTCCAAAATGAATCACAAT	YSKMNHN	+	-
3337	14288	TATTCCAGGTCCAATTTGAAT	YSRSNLN	+	-
3338	14289	TACTCAAAGCTGAACATGAAC	YSKLNMN	++	-
3339	14290	TACTCAAAGGTAGGCTACAAC	YSKVGYN	+	-
3340	14291	TACTCAAAGCTGGGCACCAAC	YSKLGTN	+	-
3341	14292	TACTCAAAGCGCGGCGACAAC	YSKRGDN	+++	-
3342	14293	TACTCACGCACCGGCAACAAC	YSRTGNN	+	-
3343	14294	TTCTCCAGGGTGAATGTGAAT	FSRVNVN	+	-
3344	14295	TATTTCACGGGGAGGACGTCC	YFTGRTS	+	-
3345	14296	TTCGCGAGGTTGAATAATAAT	FARLNNN	++	+
3346	14297	TTCGCGAAAATAGGGTTCAAT	FAKIGFN	++	-
3347	14298	TATTCCAGGATAGGGTCCAAT	YSRIGSN	+	-
3348	14299	TTCGCGAGGATGGGGAATAAT	FARMGNN	++	+++
3349	14300	TATTCCAGGGGGAATTTCAAT	YSRGNFN	++	-
3350	14301	TACTCACGCCTGAACATGAAC	YSRLNMN	+++	-
3351	14302	TATACGTCCGCGTATCCGAGG	YTSAYPR	+	-
3352	14303	TATTCCAGGTTGAATGAGAAT	YSRLNEN	++	-
3353	14304	TACTCAAAGATCGGCTCAAAC	YSKIGSN	+	-
3354	14305	TTTTCACGCGTAGGCTACAAC	FSRVGYN	+++	++
3355	14306	TACGCCCGCCATGGCGTAAAC	YARHGVN	++	-
3356	14307	TACTCACGCATCAACTCAAAC	YSRINSN	++	-
3357	14308	TACTCACGCAACGGCGCCAAC	YSRNGAN	+	-
3358	14309	TACGCCCGCACCAACATGAAC	YARTNMN	++	-
3359	14310	TACTCACGCCCCAACGTAAAC	YSRPNVN	+	-
3360	14311	TTCGCGAGGCAGGGGATGAAT	FARQGMN	+	-
3361	14312	TACTCACGCACCAACGCCAAC	YSRTNAN	+	+
3362	14313	TATTCCAAACACGGGACGAAT	YSKHGTN	+	+
3363	14314	CTGGCCAAGCTGGGCTACAAC	LAKLGYN	+	-

3364	14315	TTCTCCAGGGCGAATGCGAAT	FSRANAN	+	-
3365	14316	TACTCACGCATCAACTACAAC	YSRINYN	++	-
3366	14317	CTGGCCAAGATGGGCCATAAC	LAKMGHN	+	-
3367	14318	CTGTCAAAGCTGGGCATGAAC	LSKLGMN	+	-
3368	14319	CTGGCCAAGCATGGCATCAAC	LAKHGIN	++	-
3369	14320	TATTCCAAAAAAGGGGATAAT	YSKKGDN	++	-
3370	14321	TTTTCACGCCTGAACAACAAC	FSRLNNN	+++	++
3371	14322	TTTTCACGCCATAACCAAAAC	FSRHNQN	++	-
3372	14323	TTTTCACGCGTAGGCGGCAAC	FSRVGGN	+	-
3373	14324	TACTCACGCGTAAACCCCAAC	YSRVNPN	+	+
3374	14325	TACTCACGCACCGGCGTAAAC	YSRTGVN	+	-
3375	14326	TCCTGGTCCACGAATGGGATA	SWSTNGI	+	-
3376	14327	CTGTCACGCCTGAACGACAAC	LSRLNDN	+	-
3377	14328	TACTCACGCATCAACACCAAC	YSRINTN	+	-
3378	14329	TTGAATACGTCCGTGAAATGG	LNTSVKW	+	-
3379	14330	TACTCAAAGAACGGCTACAAC	YSKNGYN	+	-
3380	14331	TACACCCATTCAAACAAGCAA	YTHSNKQ	+	-
3381	14332	TTCGCGAGGTCCGGGATGAAT	FARSGMN	+	+
3382	14333	TACTCAAAGATCAACTACAAC	YSKINYN	++	+
3383	14334	TTTGCCCGCACCGGCGGCAAC	FARTGGN	+	+
3384	14335	TTCTCCAAAATAGGGATGAAT	FSKIGMN	+	-
3385	14336	TATTCCAGGACGAATCAGAAT	YSRTNQN	+	+
3386	14337	TTCTCCAAAGGGAATTTCAAT	FSKGNFN	+++	-
3387	14338	TATGCGAGGAATGGGACGAAT	YARNGTN	+	-
3388	14339	TATGCGAGGGAGGGGAGGAAT	YAREGRN	+	-
3389	14340	TACTCACGCACCAACTACAAC	YSRTNYN	++	-
3390	14341	ATATTGTCCTCCAATGGGGTG	ILSSNGV	+	-
3391	14342	TACTCAAAGCTGGGCTACAAC	YSKLGYN	+++	+
3392	14343	TACTCAAAGCTGAACTCAAAC	YSKLNSN	+	-
3393	14344	TACTCACGCGTAGGCCAAAAC	YSRVGQN	+	-
3394	14345	TTGTCCAGGCAGAATTTCAAT	LSRQNFN	+	-
3395	14346	TATTCCAGGACGGGGGCGAAT	YSRTGAN	+	-
3396	14347	TACTCACGCATGGGCAACAAC	YSRMGNN	+++	-
3397	14348	CGCGAATCAGGCCTGGCCTGG	RESGLAW	+	-
3398	14349	TTCGCGAGGAATGGGTCCAAT	FARNGSN	+	-
3399	14350	TACTCACGCCTGAACGCCAAC	YSRLNAN	+++	+
3400	14351	TTCTCCAAAATAGGGGCGAAT	FSKIGAN	+	-
3401	14352	TTCGCGAGGGGGAATTATAAT	FARGNYN	++	+++
3402	14353	TTTGCCCGCGTAGGCCTGAAC	FARVGLN	+++	-
3403	14354	TATTCCAAACACAATCCGAAT	YSKHNPN	+	++
3404	14355	TACGCCCGCACCAACTTTAAC	YARTNFN	+	-
3405	14356	TTGGCGAGGGTGGGGTTGAAT	LARVGLN	+++	-
3406	14357	AACCAACGCGGCTACGGCAAC	NQRGYGN	++	+
3407	14358	TACTCAAAGTCAAACACCAAC	YSKSNTN	+	-
3408	14359	TACTCAAAGGCCGGCCATAAC	YSKAGHN	+	-

3409	14360	TACTCACGCCAAAACATCAAC	YSRQNIN	+	+
3410	14361	CACTATTCCTCCAATGGGGTG	HYSSNGV	+	-
3411	14362	TATGCGAGGGCGGGGGGGAAT	YARAGGN	+	+++
3412	14363	TTTGCCCGCTCAGGCACCAAC	FARSGTN	++	-
3413	14364	TTCGCGAAAGTGGGGTATAAT	FAKVGYN	+	-
3414	14365	TATTCCAGGTATGGGATAAAT	YSRYGIN	++	-
3415	14366	TTTTCACGCCTGAACCTGAAC	FSRLNLN	+++	-
3416	14367	TTCTCCAGGTTGGGGCCGAAT	FSRLGPN	+	-
3417	14368	TATGCGAAAAATAATTGGAAT	YAKNNWN	++	+
3418	14369	TATTTCGTGGGGTCCAGGGCG	YFVGSRA	++	-
3419	14370	TACTCAAAGCTGGGCTTTAAC	YSKLGFN	+	++
3420	14371	TTTTCAAAGGCCGGCTACAAC	FSKAGYN	+	+++
3421	14372	TATGCGAGGAAAAATGATAAT	YARKNDN	++	-
3422	14373	TACGCCCGCTCAAACATCAAC	YARSNIN	+	-
3423	14374	TACTCACGCGTAGGCGGCAAC	YSRVGGN	++	-
3424	14375	TTTTCACGCGGCAACGTAAAC	FSRGNVN	++	-
3425	14376	ATGTGGGACGGCACCTCACCC	MWDGTSP	++	-
3426	14377	TTTTCACGCCAAGGCGCCAAC	FSRQGAN	++	-
3427	14378	TATTCCAGGGTGGGGGCGAAT	YSRVGAN	+++	+
3428	14379	TACTCAAAGGCCGGCCCCAAC	YSKAGPN	+	-
3429	14380	TACGCCAAGATGGGCATCAAC	YAKMGIN	+	+
3430	14381	TTTTCAAAGATGAACCATAAC	FSKMNHN	+	+
3431	14382	TTTTCACGCATGGGCATCAAC	FSRMGIN	++	++
3432	14383	TACGCCAAGGTAGGCTTTAAC	YAKVGFN	+++	-
3433	14384	TACTCACGCCTGGGCTCAAAC	YSRLGSN	++	++
3434	14385	AGGTCCGGGTATGGGGCGGGG	RSGYGAG	+	-
3435	14386	TACGCCAAGGGCAACATGAAC	YAKGNMN	+	-
3436	14387	TACTCACGCCATAACGCCAAC	YSRHNAN	+++	-
3437	14388	TACTCAAAGCTGAACCTGAAC	YSKLNLN	++	-
3438	14389	TTCTCCAGGTTGGGGACGAAT	FSRLGTN	+	-
3439	14390	TTTTCACGCACCAACTACAAC	FSRTNYN	+++	-
3440	14391	TTTTCACGCGTAGGCCTGAAC	FSRVGLN	+	-
3441	14392	ATACACTCCACGAATGGGGTG	IHSTNGV	++	-
3442	14393	TACTCAAAGACCGGCCAAAAC	YSKTGQN	++	-
3443	14394	ATAAATTCCACGAATGGGGTG	INSTNGV	+	-
3444	14395	TACTCACGCATGAACGGCAAC	YSRMNGN	+	-
3445	14396	TACTCACGCGGCGGCGCCAAC	YSRGGAN	+	+
3446	14397	TACGCCCGCCATGGCTTTAAC	YARHGFN	+++	-
3447	14398	TACTCACGCCATAACGGCAAC	YSRHNGN	+	-
3448	14399	TACGCCCGCACCGGCAACAAC	YARTGNN	++	-
3449	14400	TACTCAAAGCAAAACTGGAAC	YSKQNWN	+	-
3450	14401	TATTCCAGGGGGGGGTTGAAT	YSRGGLN	+	-
3451	14402	AGGGGGCACGATGTGTCCTGG	RGHDVSW	++	-
3452	14403	TACTCACGCAACAACACCAAC	YSRNNTN	++	+++
3453	14404	TACTCACGCTCAAACAACAAC	YSRSNNN	+++	+

3454	14405	TACGCCCGCATCGGCGCCAAC	YARIGAN	+	-
3455	14406	TTTTCACGCAACGGCCTGAAC	FSRNGLN	+	-
3456	14407	TACTCACGCAACAACTTTAAC	YSRNNFN	++	-
3457	14408	TACTCACGCGGCGGCCAAAAC	YSRGGQN	+++	+
3458	14409	TACTCACGCGGCAACAACAAC	YSRGNNN	++	-
3459	14410	TACTCACGCATGGGCCAAAAC	YSRMGQN	+	++
3460	14411	CTGTCAAAGATCGGCGAAAAC	LSKIGEN	+	-
3461	14412	CTGTCACGCGCCAACTTTAAC	LSRANFN	++	-
3462	14413	TTTGCCCGCGTAGGCGCCAAC	FARVGAN	+	-
3463	14414	TACTCAAAGTACGGCCATAAC	YSKYGHN	++	-
3464	14415	AAAGCGGCGTCCCACGGGTGG	KAASHGW	+	-
3465	14416	TATTCCAAAATAGGGCACAAT	YSKIGHN	+	-
3466	14417	TACTCACGCCATGGCGTAAAC	YSRHGVN	++	-
3467	14418	TACTCAAAGCAAAACTTTAAC	YSKQNFN	++	-
3468	14419	TATGCGAGGGGGGGGGTGAAT	YARGGVN	+	-
3469	14420	TTTTCACGCACCAACATCAAC	FSRTNIN	+	-
3470	14421	TACGCCCGCCAAAACAACAAC	YARQNNN	+	++
3471	14422	TATGCGAGGTATGGGATGAAT	YARYGMN	++	-
3472	14423	CCGTATGCGAAATCCGTGGAT	PYAKSVD	++	-
3473	14424	TACGCCCGCGCCAACTCAAAC	YARANSN	+	-
3474	14425	TTCGCGAGGATGAATAATAAT	FARMNNN	++	+
3475	14426	TTTGCCCGCTCAGGCCATAAC	FARSGHN	++	-
3476	14427	TATGCGAAATGGGGGCCGAAT	YAKWGPN	++	+++
3477	14428	TATACGCACACGCAGAGGAAT	YTHTQRN	+	+++
3478	14429	TATGCGAAATCCAATCCGAAT	YAKSNPN	+	-
3479	14430	AATTGGTCCACGAATGGGATA	NWSTNGI	+	-
3480	14431	TACGCCCGCCAAAACATGAAC	YARQNMN	+	+
3481	14432	TACGCCCGCCAAAACATCAAC	YARQNIN	++	+
3482	14433	TACGCCCGCGCCGGCTTTAAC	YARAGFN	++	+++
3483	14434	TACTCAAAGTACGGCCAAAAC	YSKYGQN	+++	-
3484	14435	TACGCCAAGATCGGCAAGAAC	YAKIGKN	+++	-
3485	14436	TTTTCAAAGATCGGCGTAAAC	FSKIGVN	+	-
3486	14437	TTGTCCAGGGTGAATGATAAT	LSRVNDN	+	-
3487	14438	TTTGCCCGCGAAGGCCGCAAC	FAREGRN	+	-
3488	14439	ACGGCGAGGGGGGATAGGGCG	TARGDRA	++	-
3489	14440	TTTTCACGCATGAACATCAAC	FSRMNIN	+	-
3490	14441	TACGCCAAGTCAGGCCCCAAC	YAKSGPN	++	-
3491	14442	TTTTCAAAGCTGGGCATCAAC	FSKLGIN	+	++
3492	14443	TACTCACGCATCGGCCTGAAC	YSRIGLN	++	-
3493	14444	TACGCCCGCTCAGGCAACAAC	YARSGNN	++	-
3494	14445	TACGCCCGCACCGGCCAAAAC	YARTGQN	++	-
3495	14446	GTGAGGTCCGGGTCCATAGGG	VRSGSIG	+	-
3496	14447	TACTCACGCGCCGGCTCAAAC	YSRAGSN	+	-
3497	14448	TACTCAAAGTACGGCACCAAC	YSKYGTN	++	-
3498	14449	TATGCGAGGCAGAATGAGAAT	YARQNEN	++	-

3499	14450	TATTCCAAATATAATGTGAAT	YSKYNVN	+	-
3500	14451	TATTCCAGGCACAATTTGAAT	YSRHNLN	+++	-
3501	14452	TATTCCAAAATAGGGTTCAAT	YSKIGFN	+	-
3502	14453	TTGTCCAGGGTGGGGGCGTCC	LSRVGAS	+	-
3503	14454	TTCTCCAGGTCCAATGTGAAT	FSRSNVN	+	-
3504	14455	TATTCCAGGTTCAATAATAAT	YSRFNNN	+	++
3505	14456	TTTGCCAAGCAAGGCTTTAAC	FAKQGFN	+	+
3506	14457	TTCTCCAAACACAATTTCAAT	FSKHNFN	++	-
3507	14458	TACGCCCGCCCCGGCCATAAC	YARPGHN	+	-
3508	14459	AACCGCTCAACCAACGGCGTA	NRSTNGV	+	-
3509	14460	TGGATGTCCACGAATGGGATA	WMSTNGI	++	-
3510	14461	TACTCAAAGCTGAACTACAAC	YSKLNYN	+++	-
3511	14462	TTGAGGGGGAAAGGGTATGAT	LRGKGYD	+	-
3512	14463	TACTCAAAGTACGGCTCAAAC	YSKYGSN	++	-
3513	14464	TTTTCACGCGCCGGCCCCAAC	FSRAGPN	+	++
3514	14465	AAGGACAACACCCCCTACTGG	KDNTPYW	++	-
3515	14466	TTCGCGAGGGGGGGGGGGAAT	FARGGGN	+	-
3516	14467	CTGTCAAAGACCGGCCTGAAC	LSKTGLN	+	-
3517	14468	TACTCACGCTCAAACGACAAC	YSRSNDN	+	-
3518	14469	TACTCACGCCCCAACATCAAC	YSRPNIN	+	-
3519	14470	TACGCCAAGCTGAACCATAAC	YAKLNHN	++	-
3520	14471	TATACGAGGATGCACCAGAAT	YTRMHQN	+	-
3521	14472	TTCTCCAGGTCCGGGTTCAAT	FSRSGFN	+	-
3522	14473	TTTGCCCGCAACGGCCCCAAC	FARNGPN	+	-
3523	14474	TATTCCAAAAATAATGTGAAT	YSKNNVN	++	-
3524	14475	CGCGGCTCACAAACCTCATAC	RGSQTSY	+	-
3525	14476	TACGCCCGCGTAGGCGGCAAC	YARVGGN	++	+
3526	14477	TATTCCAGGATAAATGGGAAT	YSRINGN	+	+
3527	14478	TACTCAAAGTGGAACGAAAAC	YSKWNEN	+	-
3528	14479	TACTCACGCATCGGCAACAAC	YSRIGNN	++	-
3529	14480	TACGCCAAGTACGGCTCAAAC	YAKYGSN	+	+++
3530	14481	CCGACGTCCACGAATGGGGTG	PTSTNGV	++	++
3531	14482	TTCGCGAGGGCGGGGCACAAT	FARAGHN	++	-
3532	14483	CTGTCAAAGGTAGGCGCCAAC	LSKVGAN	++	-
3533	14484	TACTCACGCCCCGGCATGAAC	YSRPGMN	++	+++
3534	14485	TACGCCAAGCATGGCTCAAAC	YAKHGSN	+	-
3535	14486	TTCGCGAGGTATAATGGGAAT	FARYNGN	+++	-
3536	14487	TATGCGAGGATAAATAATAAT	YARINNN	+	+++
3537	14488	AAATTGGATAGGTCCAATTGG	KLDRSNW	+	-
3538	14489	TTGCACAGGGCGGGGATATCC	LHRAGIS	+	+++
3539	14490	TTTTCACGCGCCGGCGTAAAC	FSRAGVN	++	-
3540	14491	TTCTCCAGGATGAATGCGAAT	FSRMNAN	++	+
3541	14492	TTTTCACGCATGAACATGAAC	FSRMNMN	+	+++
3542	14493	TTCTCCAGGGTGAATACGAAT	FSRVNTN	+	+
3543	14494	TATAATTCCACGAATGGGGTG	YNSTNGV	+	-

3544	14495	CGCCTGTACGACGCCTACGAA	RLYDAYE	++	-
3545	14496	TACGCCCGCATCGGCACCAAC	YARIGTN	++	-
3546	14497	TACTCAAAGGGCGGCATGAAC	YSKGGMN	+	-
3547	14498	CTGGCCAAGATGGGCAACAAC	LAKMGNN	+	-
3548	14499	GTGATATCCACGAATGGGGTG	VISTNGV	+	-
3549	14500	TATGCGAAACACGGGTGGAAT	YAKHGWN	+	-
3550	14501	TACGCCCGCGGCAACATCAAC	YARGNIN	++	+
3551	14502	GTATGGTCAACCAACGGCATC	VWSTNGI	+	-
3552	14503	TACTCAAAGATCGGCGCCAAC	YSKIGAN	+	-
3553	14504	TACTCACGCTCAAACCCCAAC	YSRSNPN	++	-
3554	14505	TACTCACGCCAAAACTTTAAC	YSRQNFN	++	-
3555	14506	TGGGGCTCAACCAACGGCATC	WGSTNGI	+	-
3556	14507	TACGCCCGCCTGGGCATGAAC	YARLGMN	++	-
3557	14508	TTCTCCAAAGCGGGGGCGAAT	FSKAGAN	++	+
3558	14509	TTTTCAAAGTCAAACTGGAAC	FSKSNWN	++	-
3559	14510	TTGTCCAAAAATAATCACAAT	LSKNNHN	+	-
3560	14511	TACGCCAAGTCAAACCTGAAC	YAKSNLN	+	-
3561	14512	TATGCGAGGAATAATCCGAAT	YARNNPN	++	-
3562	14513	TTTTCAAAGGCCGGCCTGAAC	FSKAGLN	+	+
3563	14514	TACTCACGCGTAAACAACAAC	YSRVNNN	+++	+
3564	14515	TTCTCCAGGACGGGGGCGAAT	FSRTGAN	+	-
3565	14516	TTCGCGAGGACGAATATGAAT	FARTNMN	+	+
3566	14517	AATACGTCCATGAATGGGAGG	NTSMNGR	++	-
3567	14518	TACTCAAAGAACGGCTGGAAC	YSKNGWN	++	+++
3568	14519	TTCTCCAGGTCCAATATGAAT	FSRSNMN	++	+
3569	14520	TTTTCAAAGTCAGGCTTTAAC	FSKSGFN	+	-
3570	14521	TTTTCAAAGCTGAACATCAAC	FSKLNIN	++	+++
3571	14522	TTCGCGAGGGCGGGGTTGAAT	FARAGLN	+	-
3572	14523	CTGAACGCCACCTCATCATGG	LNATSSW	++	-
3573	14524	TACTCAAAGTACAACATGAAC	YSKYNMN	+	+
3574	14525	ACGCACAAATTGTCCGTGAAT	THKLSVN	+	-
3575	14526	TACGCCCGCTCAAACGTAAAC	YARSNVN	+	-
3576	14527	TACGCCCGCAACGGCATCAAC	YARNGIN	+	-
3577	14528	TTCGCGAAATCCGGGGTGAAT	FAKSGVN	+	-
3578	14529	TACGCCCGCAACGGCCTGAAC	YARNGLN	+	-
3579	14530	TACGCCCGCCATGGCGCCAAC	YARHGAN	+++	-
3580	14531	TATTCCAGGAATGGGCCGAAT	YSRNGPN	++	-
3581	14532	TACGCCCGCCTGAACCCCAAC	YARLNPN	++	-
3582	14533	TACGCCAAGAACGGCTGGAAC	YAKNGWN	+	+
3583	14534	CGCGGCGGCTCATCAAACTAC	RGGSSNY	+++	-
3584	14535	TATGCGAAACACGGGCAGAAT	YAKHGQN	++	-
3585	14536	TATGCGAGGTATGGGCAGAAT	YARYGQN	++	+++
3586	14537	TTCTCCAAACAGAATTTCAAT	FSKQNFN	++	-
3587	14538	TTTGCCCGCATCGGCATCAAC	FARIGIN	++	-
3588	14539	TATTCCAAAGGGGGGTTGAAT	YSKGGLN	+	-

3589	14540	CTGTCAAAGATCGGCGCCAAC	LSKIGAN	++	-
3590	14541	TATTCCAAAAATAATTCCAAT	YSKNNSN	+	-
3591	14542	TACGCCCGCCTGGGCCTGAAC	YARLGLN	+++	+++
3592	14543	TTTTCACGCGCCAACCTGAAC	FSRANLN	++	++
3593	14544	TATGCGAAATTGGGGTCCAAT	YAKLGSN	+	+
3594	14545	TACTCACGCGTATCAGACACC	YSRVSDT	+	-
3595	14546	TTCACGGCGGGGACGAGGAAT	FTAGTRN	+	-
3596	14547	TACTCACGCAACGGCTCAAAC	YSRNGSN	+	-
3597	14548	TTGGCGAAATTGGGGGTGAAT	LAKLGVN	+	-
3598	14549	TATTCCAAAAAAAATGATAAT	YSKKNDN	++	-
3599	14550	TTCTCCAGGACGAATACGAAT	FSRTNTN	+	-
3600	14551	ATGTCAGCCCATGTAAAGTAC	MSAHVKY	+++	-
3601	14552	TACTCAAAGGCCGGCTACAAC	YSKAGYN	+	+++
3602	14553	TTCTCCAAAAGGAATGATAAT	FSKRNDN	++	-
3603	14554	TATTCCAAAAAAGGGGAGAAT	YSKKGEN	+	-
3604	14555	TTTGCCCGCGTAGGCATGAAC	FARVGMN	++	++
3605	14556	TACTCACGCCTGGGCTACAAC	YSRLGYN	++	-
3606	14557	TTCTCCAAAACGGGGTGGAAT	FSKTGWN	+++	-
3607	14558	TACTCACGCTACAACGACAAC	YSRYNDN	+	-
3608	14559	TTTGCCAAGAACGGCATCAAC	FAKNGIN	+	-
3609	14560	TTCGCGAAACACGGGCCGAAT	FAKHGPN	+	-
3610	14561	ATCGCCCTGCGCGGCGCCGGC	IALRGAG	+	-
3611	14562	TTTTCACGCGGCGGCTACAAC	FSRGGYN	++	-
3612	14563	TTCTCCAGGATGGGGCACAAT	FSRMGHN	++	-
3613	14564	TACGCCAAGAACGGCGAAAAC	YAKNGEN	+	-
3614	14565	TACGCCCGCCCCGGCGTAAAC	YARPGVN	+++	-
3615	14566	TATGCGAGGTATAATGTGAAT	YARYNVN	+	-
3616	14567	TACTCAAAGGTAAACGCCAAC	YSKVNAN	+	-
3617	14568	TACTCAAAGTACGGCATCAAC	YSKYGIN	+	-
3618	14569	TATTCCAGGGGGGGGTCCAAT	YSRGGSN	++	+
3619	14570	TTCTCCAAATATAATGCGAAT	FSKYNAN	+++	-
3620	14571	TTTTCACGCCAAGGCATCAAC	FSRQGIN	+	-
3621	14572	TATCACAAATTGAATCCGGCG	YHKLNPA	+	-
3622	14573	TTGGCGAGGATGGGGGAGAAT	LARMGEN	+	-
3623	14574	TATTCCAGGTTGGGGCCGAAT	YSRLGPN	+++	-
3624	14575	TACGCCCGCATGGGCATCAAC	YARMGIN	+	-
3625	14576	TACTCACGCATCGGCGACAAC	YSRIGDN	++	-
3626	14577	CTGTCAAAGCTGGGCGCCAAC	LSKLGAN	++	-
3627	14578	TACGCCAAGGCCAACCATAAC	YAKANHN	+	-
3628	14579	TTTTCAAAGGTAAACTTTAAC	FSKVNFN	+	-
3629	14580	TATGCGAGGTCCAATCACAAT	YARSNHN	++	++
3630	14581	TACTCAAAGCTGAACGACAAC	YSKLNDN	+	-
3631	14582	TACGCCAAGGGCGGCTGGAAC	YAKGGWN	+	-
3632	14583	TTGTCCAGGGCGTCCGTGATA	LSRASVI	+	-
3633	14584	TTTAACTCAACCAACGGCATC	FNSTNGI	+	-

3634	14585	TACTCACGCCTGGGCAACAAC	YSRLGNN	+++	-
3635	14586	TACTCAAAGTACAACACCAAC	YSKYNTN	++	+
3636	14587	TACTCAAAGATCAACGCCAAC	YSKINAN	+	-
3637	14588	CACTGGTCCACGAATGGGGTG	HWSTNGV	+	-
3638	14589	TACTCACGCGGCAACTCAAAC	YSRGNSN	+	++
3639	14590	TTCTCCAGGACGGGGATGAAT	FSRTGMN	++	+++
3640	14591	GTACGCTACGAATCAGGCAAC	VRYESGN	+	-
3641	14592	TTCGCGAGGCACGGGAATAAT	FARHGNN	+	+
3642	14593	TATTCCAGGTCCGGGCCGAAT	YSRSGPN	+++	+++
3643	14594	TTCGCGAGGATAGGGGTGAAT	FARIGVN	+	-
3644	14595	TTTTCAAAGGCCGGCGTAAAC	FSKAGVN	+	-
3645	14596	TTGGCGAAAAATGGGTCCAAT	LAKNGSN	+	-
3646	14597	TTTTCACGCATGAACAACAAC	FSRMNNN	+++	+++
3647	14598	TTCTCCAAAGCGGGGTCCAAT	FSKAGSN	+	-
3648	14599	TACTCACGCGGCGGCACCAAC	YSRGGTN	++	-
3649	14600	ATCCAATCAACCAACGGCGTA	IQSTNGV	+++	-
3650	14601	TATGCGAGGTATGGGGCGAAT	YARYGAN	++	++
3651	14602	TACGCCAAGCAAGGCCCCAAC	YAKQGPN	++	-
3652	14603	TTTGCCCGCATGGGCATGAAC	FARMGMN	+	+
3653	14604	TACTCAAAGATCAACAACAAC	YSKINNN	+	-
3654	14605	TTTTCACGCTCAGGCAACAAC	FSRSGNN	+	-
3655	14606	TACCAACCCAACTCATACGGC	YQPNSYG	+++	-
3656	14607	TACTCACGCGCCGGCGACAAC	YSRAGDN	+++	-
3657	14608	TACGCCCGCCGCAACGACAAC	YARRNDN	++	-
3658	14609	TTTTCACGCTCAGGCATCAAC	FSRSGIN	++	+
3659	14610	TTCGCGAGGTTGGGGTCCAAT	FARLGSN	+	-
3660	14611	TTTGCCCGCACCAACACCAAC	FARTNTN	+	++
3661	14612	TTTTCAAAGATGGGCTTTAAC	FSKMGFN	+	-
3662	14613	TACATCCGCACCCAAATCAAC	YIRTQIN	+	-
3663	14614	TACTCACGCACCGGCACCAAC	YSRTGTN	++	-
3664	14615	TTCTCCAAAGCGGGGTGGAAT	FSKAGWN	+	-
3665	14616	TTTGCCCGCGCCGGCTTTAAC	FARAGFN	++	+++
3666	14617	TACTCACGCCATGGCGGCAAC	YSRHGGN	+++	-
3667	14618	TACTCAAAGGTAGGCAAGAAC	YSKVGKN	+++	-
3668	14619	TACTCAAAGGCCGGCGCCAAC	YSKAGAN	++	-
3669	14620	TATTCCAGGATGGGGCCGAAT	YSRMGPN	+++	-
3670	14621	TTCTCCAGGCAGAATTTCAAT	FSRQNFN	+	++
3671	14622	TTTGCCCGCCAAGGCGTAAAC	FARQGVN	+	-
3672	14623	TACGCCAAGATCGGCAACAAC	YAKIGNN	+	-
3673	14624	TTTGCCCGCCAAGGCGCCAAC	FARQGAN	+	-
3674	14625	TTGTCCAAAGCGAATGCGAAT	LSKANAN	+	-
3675	14626	CCGGGGTCCACGAATGGGATA	PGSTNGI	+++	-
3676	14627	TATGCGAGGAATAATTTGAAT	YARNNLN	+	-
3677	14628	TACTCACGCCTGAACGACAAC	YSRLNDN	+++	-
3678	14629	TTCGCGAGGGTGGGGCACAAT	FARVGHN	+	-

3679	14630	TTCTCCAAAATGAATGCGAAT	FSKMNAN	++	+
3680	14631	CTGTCAAAGATGGGCGCCAAC	LSKMGAN	+	-
3681	14632	TACTCACGCATCGGCCCCAAC	YSRIGPN	+++	-
3682	14633	TTCTCCAGGCAGAATCAGAAT	FSRQNQN	+	-
3683	14634	TTTTCACGCTCAGGCTCAAAC	FSRSGSN	++	-
3684	14635	TATTCCAGGTTGGGGGGGAAT	YSRLGGN	+	+
3685	14636	AGGTTCAATGGGTTGAATGCG	RFNGLNA	+++	-
3686	14637	TATGCGAGGTATAATATGAAT	YARYNMN	++	-
3687	14638	TACTCACGCAACAACTACAAC	YSRNNYN	++	+
3688	14639	CCCTTTTCAACCAACGGCGTA	PFSTNGV	+	-
3689	14640	TGGGTAAAGTCATCACCCGGC	WVKSSPG	++	-
3690	14641	TTTGCCAAGGAAGGCCGCAAC	FAKEGRN	+	-
3691	14642	TACTCACGCTTTAACGCCAAC	YSRFNAN	++	-
3692	14643	GAATCATACGTAGGCCGCAAC	ESYVGRN	++	-
3693	14644	TACGCCAAGTACGGCCAAAAC	YAKYGQN	++	++
3694	14645	TTTGCCCGCATCGGCCTGAAC	FARIGLN	+	-
3695	14646	CCGAATTCCACGAATGGGATA	PNSTNGI	+	-
3696	14647	TACTCACGCCAAAACTCAAAC	YSRQNSN	++	-
3697	14648	TTCGCGAAAATGGGGTTCAAT	FAKMGFN	+	+
3698	14649	TTTTCACGCAACAACGCCAAC	FSRNNAN	+	-
3699	14650	TTCTCCAGGCAGGGGCACAAT	FSRQGHN	+	+
3700	14651	TGGTCAAAGCTGCATGCCAAC	WSKLHAN	+	-
3701	14652	AATTATTCCACGAATGGGGTG	NYSTNGV	+++	-
3702	14653	TACTCAAAGTACAACGCCAAC	YSKYNAN	++	-
3703	14654	TACTCACGCAACAACGCCAAC	YSRNNAN	++	-
3704	14655	TACTCAAAGCATAACGAAAAC	YSKHNEN	+	-
3705	14656	TTTTCACGCCAAAACATGAAC	FSRQNMN	+	-
3706	14657	TACGCCAAGATCGGCGTAAAC	YAKIGVN	+	-
3707	14658	CATCATTCATCAAACGGCGTA	HHSSNGV	+	-
3708	14659	TACTCACGCTACAACGTAAAC	YSRYNVN	++	-
3709	14660	TTTTCACGCGGCGGCCCCAAC	FSRGGPN	+	-
3710	14661	TTTTCAAAGGCCAACCCCAAC	FSKANPN	++	-
3711	14662	TACCATTCAACCAACGGCATC	YHSTNGI	+++	-
3712	14663	ACCCGCACCGGCGTATCAGCC	TRTGVSA	+	-
3713	14664	TACTCACGCTCAAACTTTAAC	YSRSNFN	+	-
3714	14665	TATTCCAAACACGGGGGGAAT	YSKHGGN	++	-
3715	14666	TATTCCAGGTATGGGCAGAAT	YSRYGQN	++	-
3716	14667	TTCGCGAGGCACGGGATGAAT	FARHGMN	+++	+
3717	14668	TTTTCACGCTCAAACATCAAC	FSRSNIN	++	-
3718	14669	TTTGCCCGCCAAGGCACCAAC	FARQGTN	++	+
3719	14670	TATGCGAGGTTGGGGACGAAT	YARLGTN	+	-
3720	14671	TACTCAAAGAACAACTGGAAC	YSKNNWN	++	-
3721	14672	TTTGCCCGCGGCAACCTGAAC	FARGNLN	+	+
3722	14673	TTTTCAAAGCTGAACGACAAC	FSKLNDN	+	-
3723	14674	TACTCACGCATCAACGAAAAC	YSRINEN	+	-

3724	14675	TTTTCACGCCATAACGAAAAC	FSRHNEN	+	-
3725	14676	TTTTCAAAGGTAGGCCAAAAC	FSKVGQN	+	+
3726	14677	TTCGCGAGGCACAATAATAAT	FARHNNN	+++	-
3727	14678	TACTCACGCTACAACATGAAC	YSRYNMN	+	-
3728	14679	TACGCCAAGTACGGCGCCAAC	YAKYGAN	++	-
3729	14680	TTTGCCAAGCATGGCTACAAC	FAKHGYN	++	+
3730	14681	TACGCCCGCAACGGCGCCAAC	YARNGAN	++	-
3731	14682	TTTTCAAAGGCCAACCTGAAC	FSKANLN	++	-
3732	14683	GGCGGCGCCTCAAAGGGCTGG	GGASKGW	+	-
3733	14684	TTTTCACGCGTAAACCATAAC	FSRVNHN	++	-
3734	14685	TACGCCCGCACCAACCATAAC	YARTNHN	+++	-
3735	14686	TATTCCAGGCCGAATTTGAAT	YSRPNLN	+	-
3736	14687	CCCTCATCAACCAACGGCATC	PSSTNGI	++	-
3737	14688	CTGGCCCGCGTAGGCCAAAAC	LARVGQN	+	-
3738	14689	TACCATAAGATGTCACTGGGC	YHKMSLG	+	-
3739	14690	TTTTCACGCGGCAACTACAAC	FSRGNYN	+++	++
3740	14691	TACTCACGCTCAAACTCAAAC	YSRSNSN	+	++
3741	14692	TTGTCCAGGTCCGGGTGGAAT	LSRSGWN	++	-
3742	14693	TACGCCCGCATGGGCGAAAAC	YARMGEN	++	-
3743	14694	TACTCAAAGTACAACCAAAAC	YSKYNQN	++	-
3744	14695	TACGCCCGCCTGGGCATCAAC	YARLGIN	++	-
3745	14696	TACTCAAAGTTTAACATCAAC	YSKFNIN	+++	++
3746	14697	TATGCGAGGAATAATCACAAT	YARNNHN	++	-
3747	14698	TTTTCACGCGCCAACGACAAC	FSRANDN	+	+
3748	14699	TTTTCACGCCATAACATCAAC	FSRHNIN	+++	-
3749	14700	TACGCCAAGGGCGGCACCAAC	YAKGGTN	++	-
3750	14701	TATTCCAGGCAGAATGGGAAT	YSRQNGN	+	-
3751	14702	GAGACGTCCACGAATGGGGTG	ETSTNGV	+	-
3752	14703	CGCGACCGCTACTCAGCCGGC	RDRYSAG	+++	-
3753	14704	TACTCACGCCTGGGCCAAAAC	YSRLGQN	++	+++
3754	14705	TACGCCCGCGCCAACCAAAAC	YARANQN	+	-
3755	14706	ATGCAATCATCAAACGGCGTA	MQSSNGV	+	-
3756	14707	CTGTCAAAGCATAACCTGAAC	LSKHNLN	+	-
3757	14708	ATGTCACGCGTATCAGTACTG	MSRVSVL	+	-
3758	14709	CTGTCAAAGCATAACACCAAC	LSKHNTN	+	-
3759	14710	CGCGGCCCCAACTCATACCCC	RGPNSYP	+	-
3760	14711	TTCGCGAAAGCGGGGCACAAT	FAKAGHN	+	-
3761	14712	TTCTCCAGGATGGGGTTGAAT	FSRMGLN	+	-
3762	14713	TTCTCCAAACACGGGAATAAT	FSKHGNN	++	-
3763	14714	TATCACAAATTGCAGAATGGG	YHKLQNG	+	-
3764	14715	TTCTCCAGGTATGGGACGAAT	FSRYGTN	+++	-
3765	14716	GATAAATATGATAGGTATACG	DKYDRYT	+	-
3766	14717	TATTCCAAATTCAATGTGAAT	YSKFNVN	+	+
3767	14718	CTGTCAAAGATGAACCAAAAC	LSKMNQN	++	-
3768	14719	TACTCAAAGTTTAACTACAAC	YSKFNYN	+	++

3769	14720	TTTTCAAAGGCCAACGCCAAC	FSKANAN	+	-
3770	14721	TACGCCCGCGTAGGCGTAAAC	YARVGVN	+	-
3771	14722	TACTCACGCTACAACACCAAC	YSRYNTN	+++	-
3772	14723	TTTGCCCGCGAAGGCTGGAAC	FAREGWN	++	-
3773	14724	ATGTATTCCACGAATGGGGTG	MYSTNGV	+	-
3774	14725	AACTACTCAACCAACGGCCGC	NYSTNGR	++	-
3775	14726	TATGCGAAAGCGAATACGAAT	YAKANTN	+	-
3776	14727	TATGCGAGGGTGAATTATAAT	YARVNYN	+++	-
3777	14728	TATTCCAAATATAATCACAAT	YSKYNHN	+++	++
3778	14729	TACTCACGCAACAACGACAAC	YSRNNDN	+	-
3779	14730	CAAGACTCAACCAACGGCGTA	QDSTNGV	++	-
3780	14731	TACGCCCGCAACAACGTAAAC	YARNNVN	+	-
3781	14732	TTCGCGAGGCACGGGGCGAAT	FARHGAN	+++	-
3782	14733	TTCGTGAAATCCAATTCCGGG	FVKSNSG	++	-
3783	14734	TTTTCAAAGCAAAACTGGAAC	FSKQNWN	+	-
3784	14735	TACGCCAAGCCCAACTGGAAC	YAKPNWN	++	-
3785	14736	TTCTCCAAAGGGAATTGGAAT	FSKGNWN	+++	-
3786	14737	TATTCCAGGTATGGGTCCAAT	YSRYGSN	+	-
3787	14738	TATGCGAAATCCAATACGAAT	YAKSNTN	+	-
3788	14739	GTGGCGTATACGAATGGGTAT	VAYTNGY	+	-
3789	14740	TACTCAAAGTGGAACTCAAAC	YSKWNSN	+++	+++
3790	14741	TTTTCAAAGCATGGCCCCAAC	FSKHGPN	++	-
3791	14742	GGCGCCAACGAATGGCGCGAC	GANEWRD	++	-
3792	14743	TACGCCCGCCCCGGCCCCAAC	YARPGPN	++	-
3793	14744	TACGCCAAGCGCGGCGACAAC	YAKRGDN	++	++
3794	14745	TTGCCGAATCAGTGGAGGGAT	LPNQWRD	+	-
3795	14746	TATTTCTCCCAGAGGACGGAG	YFSQRTE	+	-
3796	14747	TTCGCGAGGACGAATTTCAAT	FARTNFN	++	-
3797	14748	GCGACGTCCACGAATGGGATA	ATSTNGI	+	-
3798	14749	AACACCTCATCAAACGGCGTA	NTSSNGV	++	-
3799	14750	TACGGCCGCGTAACCTCAAAC	YGRVTSN	+	+
3800	14751	TACGCCAAGCTGGGCCAAAAC	YAKLGQN	+	-
3801	14752	TTCTCCAAAGGGGGGTTCAAT	FSKGGFN	+	-
3802	14753	CTGGCCAAGCTGGGCATGAAC	LAKLGMN	++	-
3803	14754	TTCTCCAGGCAGGGGACGAAT	FSRQGTN	+	-
3804	14755	TTTGCCCGCTCAAACACCAAC	FARSNTN	+	-
3805	14756	TTTTCACGCATGGGCTCAAAC	FSRMGSN	+	-
3806	14757	CTGGCCCGCGTAGGCAACAAC	LARVGNN	+	-
3807	14758	TTTGCCCGCCTGGGCAACAAC	FARLGNN	++	-
3808	14759	TACTCACGCTCAAACGGCAAC	YSRSNGN	+	-
3809	14760	TTCTCCAGGCAGAATTCCAAT	FSRQNSN	+	-
3810	14761	TATGCGAGGGATGGGAGGAAT	YARDGRN	++	++
3811	14762	TATGCGAAATATGGGGGGAAT	YAKYGGN	++	-
3812	14763	TACTCACGCAACAACCTGAAC	YSRNNLN	+	-
3813	14764	TTCTCCAAAGCGGGGACGAAT	FSKAGTN	+	-

3814	14765	TACTCACGCCATAACCAAAAC	YSRHNQN	+	-
3815	14766	TTTGCCAAGCATGGCCATAAC	FAKHGHN	++	+
3816	14767	TGGAAGCATCTGTCAATGGGC	WKHLSMG	+	-
3817	14768	TACGCCCGCGCCGGCGCCAAC	YARAGAN	+++	-
3818	14769	GAACGCAACATCGGCCGCCTG	ERNIGRL	++	-
3819	14770	TGCAAGGGCGGCTGCATGGTA	CKGGCMV	+	-
3820	14771	TACGCCAAGCAAGGCGACAAC	YAKQGDN	+	-
3821	14772	TGGTTCTCCGGGACGACGAAT	WFSGTTN	+	-
3822	14773	TTTTCAAAGCGCAACGAAAAC	FSKRNEN	+++	-
3823	14774	TTTTCACGCGGCAACGCCAAC	FSRGNAN	++	++
3824	14775	CTGGCCCGCGTAGGCATCAAC	LARVGIN	++	-
3825	14776	TACTCACGCCTGGGCACCAAC	YSRLGTN	+	-
3826	14777	TTCTCCAGGGTGAATGCGAAT	FSRVNAN	+	-
3827	14778	TTTTCACGCAACGGCTTTAAC	FSRNGFN	+	-
3828	14779	TATGCGAGGCCGGGGTCCAAT	YARPGSN	+++	-
3829	14780	TACTCAAAGAACAACTGCAAC	YSKNNCN	+	-
3830	14781	TACGCCCGCCAAAACTCAAAC	YARQNSN	+	-
3831	14782	TACGCCAAGATCGGCTCAAAC	YAKIGSN	++	++
3832	14783	TTTTCAAAGATCGGCACCAAC	FSKIGTN	+	-
3833	14784	TTTTCACGCGTAAACTACAAC	FSRVNYN	++	-
3834	14785	TTCGCGAGGGGGAATTTCAAT	FARGNFN	+	-
3835	14786	TTCGCGAGGACGAATCACAAT	FARTNHN	+++	-
3836	14787	GATGCGGCGTATGTGAAATAT	DAAYVKY	+	-
3837	14788	TACTCAAAGTACAACGACAAC	YSKYNDN	+	-
3838	14789	TTCGCGAGGCAGAATATGAAT	FARQNMN	+	-
3839	14790	AGGTTGACGGATATAACGTGG	RLTDITW	++	-
3840	14791	TATGCGAGGTATGGGACGAAT	YARYGTN	++	++
3841	14792	TTCAATGGGTCCAATAGGTAT	FNGSNRY	+	-
3842	14793	ACGAATTGGGGGGGGCCGGCG	TNWGGPA	+	+
3843	14794	TTTGCCCGCGCCGGCGGCAAC	FARAGGN	++	-
3844	14795	TATTCCAAATATAATTCCAAT	YSKYNSN	++	-
3845	14796	TTTGCCAAGGTAGGCTTTAAC	FAKVGFN	+	-
3846	14797	TTTTCACGCAACGGCATCAAC	FSRNGIN	+	+
3847	14798	TTTTCAAAGGCCGGCCATAAC	FSKAGHN	+	-
3848	14799	TTGGCGAAAAATGGGTGTAAT	LAKNGCN	++	-
3849	14800	TATGCGAAATATAATATGAAT	YAKYNMN	++	-
3850	14801	GGGGGGGGGTCCGTGAGGTAT	GGGSVRY	+++	-
3851	14802	TTCTCCAGGCAGAATCACAAT	FSRQNHN	+	-
3852	14803	CAGCACTATAATGGGTTGGGG	QHYNGLG	+	-
3853	14804	TACGCCAAGGCCAACTGGAAC	YAKANWN	++	+++
3854	14805	TATGCGAGGCACGGGACGAAT	YARHGTN	+	-
3855	14806	TTTGCCCGCCATGGCCTGAAC	FARHGLN	++	-
3856	14807	TACTCAAAGCAAGGCCCCAAC	YSKQGPN	+	-
3857	14808	TTCGCGAGGTCCGGGGGGAAT	FARSGGN	++	-
3858	14809	TTCTCCAGGAATAATGTGAAT	FSRNNVN	+	++

3859	14810	TTCTCCAGGTTGGGGGGGAAT	FSRLGGN	++	-
3860	14811	TATGCGAGGATGAATACGAAT	YARMNTN	+	+++
3861	14812	GAGCAGTCCACGAATGGGGTG	EQSTNGV	+	-
3862	14813	CGCGCCGCCGAAGTATACCCC	RAAEVYP	+++	-
3863	14814	CTGTCAAAGGGCGGCTTTAAC	LSKGGFN	+	-
3864	14815	AACAAGTGGGGCATGTCACCC	NKWGMSP	+++	-
3865	14816	TATGCGAGGTTCAATCCGAAT	YARFNPN	+	-
3866	14817	TATGCGAGGTCCTCCCAGTCC	YARSSQS	+	++
3867	14818	TACGCCAAGACCAACAACAAC	YAKTNNN	+	-
3868	14819	TATTATCAGGGGACGTCCGCG	YYQGTSA	+	-
3869	14820	TTTTCACGCCATGGCATCAAC	FSRHGIN	+	-
3870	14821	TTTTCACGCGTAAACCTGAAC	FSRVNLN	+	-
3871	14822	TACTCAAAGTTTAACGCCAAC	YSKFNAN	+	-
3872	14823	TACGCCCGCATGAACCCCAAC	YARMNPN	+	-
3873	14824	TATGCGAGGTCCTCCCAGATA	YARSSQI	+	-
3874	14825	TTTGCCAAGGGCGGCGCCAAC	FAKGGAN	+	-
3875	14826	TATTCCAGGTATAATTCCAAT	YSRYNSN	+++	++
3876	14827	TTCGCGAGGATGGGGGTGAAT	FARMGVN	+	-
3877	14828	TTTGCCCGCTCAAACCTGAAC	FARSNLN	+	-
3878	14829	TTTGCCCGCCAAGGCTACAAC	FARQGYN	++	-
3879	14830	TATGCGAAAACGAATTTGAAT	YAKTNLN	+	+
3880	14831	TTTTCACGCTCAAACTTTAAC	FSRSNFN	+	+
3881	14832	TTTGCCAAGAACGGCAACAAC	FAKNGNN	+	-
3882	14833	TACGCCAAGCCCGGCCTGAAC	YAKPGLN	+++	-
3883	14834	ATCTTTTCATCAAACGGCGTA	IFSSNGV	++	-
3884	14835	TTCTCCAGGTCCAATCACAAT	FSRSNHN	++	-
3885	14836	TTTGCCCGCTCAGGCGACAAC	FARSGDN	+	-
3886	14837	TATGCGAGGGAGAATAAAAAT	YARENKN	++	-
3887	14838	TATGCGAAATATGGGACGAAT	YAKYGTN	++	+
3888	14839	TTTTCACGCTCAAACCTGAAC	FSRSNLN	+	-
3889	14840	CGCGAAGTATCACGCTCATAC	REVSRSY	+	-
3890	14841	ATGAACTCATCATCAGGCTGG	MNSSSGW	+	-
3891	14842	TATTCCAGGATGGGGGGGAAT	YSRMGGN	++	+++
3892	14843	TTCTCCAGGCAGGGGCAGAAT	FSRQGQN	+	-
3893	14844	TTCGCGAGGATAGGGCAGAAT	FARIGQN	+	++
3894	14845	TATGCGAAATATGGGGTGAAT	YAKYGVN	+	+
3895	14846	TACTCACGCCCCAACAACAAC	YSRPNNN	+	+
3896	14847	TACTCAAAGATCAACCCCAAC	YSKINPN	+	-
3897	14848	ATAGGGTCCTCCAATGGGGTG	IGSSNGV	+	-
3898	14849	TTCTCCAAACAGGGGTTCAAT	FSKQGFN	+	-
3899	14850	TACTCAAAGTCAAACTGGAAC	YSKSNWN	+++	-
3900	14851	CTGGCCAAGCATGGCACCAAC	LAKHGTN	++	-
3901	14852	TTCTCCAGGATGGGGATGAAT	FSRMGMN	+	-
3902	14853	TTTGCCCGCATGGGCATCAAC	FARMGIN	++	-
3903	14854	TTGTCCAGGCAGGGGTGGAAT	LSRQGWN	+	-

3904	14855	TTTTCACGCACCAACCTGAAC	FSRTNLN	++	++
3905	14856	TATGCGAGGATGAATGCGAAT	YARMNAN	+	+++
3906	14857	TTGTCCAAACACGGGTATAAT	LSKHGYN	+	-
3907	14858	TACGCCCGCGCCGGCCCCAAC	YARAGPN	+	+
3908	14859	GCGCAGGCGGCGAAAAATTGG	AQAAKNW	+++	-
3909	14860	TTGTCCAGGACGTCCACGAAT	LSRTSTN	+++	-
3910	14861	TACTCACGCCTGGGCGTAAAC	YSRLGVN	++	+++
3911	14862	TATTCCAAATATAATTTCAAT	YSKYNFN	+	-
3912	14863	TATACGCACTCCACGTATGGG	YTHSTYG	+	-
3913	14864	TATGCGAGGGTGAATCACAAT	YARVNHN	+++	-
3914	14865	TACTCACGCCCCGGCAACAAC	YSRPGNN	+	-
3915	14866	TACGCCAAGGTAGGCCTGAAC	YAKVGLN	+	-
3916	14867	TACTCACGCCATGGCATGAAC	YSRHGMN	++	-
3917	14868	TATCACAAATTGTTGTCCGGG	YHKLLSG	++	-
3918	14869	TTCGCGAGGCAGGGGCAGAAT	FARQGQN	+	-
3919	14870	TATGCGAGGCACGGGGGGAAT	YARHGGN	+++	-
3920	14871	CTGGCCCGCCTGGGCTCAAAC	LARLGSN	+++	+++
3921	14872	TTCTCCAAATATAATAATAAT	FSKYNNN	+++	+++
3922	14873	TACTCAAAGCTGAACAAGAAC	YSKLNKN	+++	-
3923	14874	TTTTCACGCGGCGGCGCCAAC	FSRGGAN	+	++
3924	14875	TTCGCGAGGATGGGGGCGAAT	FARMGAN	++	+
3925	14876	GAAAACCGCCCCGAACGCAAG	ENRPERK	++	++
3926	14877	TTTTCACGCAACGGCTACAAC	FSRNGYN	+	-
3927	14878	TTCGCGAGGTTGGGGGTGAAT	FARLGVN	+	-
3928	14879	CGCAACGAATCATCATTTCCC	RNESSFP	++	-
3929	14880	TTCTCCAGGCACAATGTGAAT	FSRHNVN	++	-
3930	14881	TACTTTGCCCATGTACAAGAA	YFAHVQE	+++	-
3931	14882	TTGGCGAGGGGGGGGTCCTAT	LARGGSY	+	-
3932	14883	TTCTCCAAACACAATACGAAT	FSKHNTN	+	-
3933	14884	ATCGACGGCCATTCATACTAC	IDGHSYY	+++	-
3934	14885	TATTCCAAATTCAATTCCAAT	YSKFNSN	+	-
3935	14886	TATGCGAAATATAATATAAAT	YAKYNIN	+	+
3936	14887	TACTCAAAGTACAACAACAAC	YSKYNNN	++	++
3937	14888	TACGCCCGCACCAACGGCAAC	YARTNGN	+	-
3938	14889	TTGAATTCCATGTCCAAATAT	LNSMSKY	+	-
3939	14890	ACCGGCGGCACCTCATACTAC	TGGTSYY	++	-
3940	14891	TACGCCCGCAACAACATGAAC	YARNNMN	++	-
3941	14892	TATGCGAAACACGGGGGGAAT	YAKHGGN	+	-
3942	14893	AGGGCGAATGCGGGGGCGGGG	RANAGAG	+	-
3943	14894	TTTTCACGCACCAACGCCAAC	FSRTNAN	+	+
3944	14895	TTCTCCAGGGTGAATATGAAT	FSRVNMN	+	-
3945	14896	TTTGCCAAGCATGGCTTTAAC	FAKHGFN	+	+
3946	14897	TACGCCCGCGCCAACATCAAC	YARANIN	+	-
3947	14898	AATCAGTATGGGTCCGGGAGG	NQYGSGR	++	-
3948	14899	TTCTCCAGGGTGAATCAGAAT	FSRVNQN	+	-

3949	14900	TTTGCCCGCGTAGGCAACAAC	FARVGNN	+	-
3950	14901	TTCTCCAGGTCCAATGCGAAT	FSRSNAN	+	-
3951	14902	TACGCCAAGAAGGGCGACAAC	YAKKGDN	+	-
3952	14903	TTCTCCAGGATAAATTCCAAT	FSRINSN	+++	++
3953	14904	TATTCCAGGTTCAATACGAAT	YSRFNTN	+++	++
3954	14905	TTCGCGAGGTCCAATTATAAT	FARSNYN	++	-
3955	14906	CTGTCACGCATCAACGAAAAC	LSRINEN	+	-
3956	14907	GGGAATACGTCCAAATCCTGG	GNTSKSW	+++	+++
3957	14908	TTCGCGAGGCAGAATAATAAT	FARQNNN	++	-
3958	14909	TTGTCCAAACCGGGGCCGAAT	LSKPGPN	+	-
3959	14910	TATGCGAGGAATAATTTCAAT	YARNNFN	++	-
3960	14911	TTCGCGAGGGTGAATAATAAT	FARVNNN	+	-
3961	14912	TTTGCCCGCACCAACGTAAAC	FARTNVN	+	+
3962	14913	GTAGACGGCCGCTCAATGTAC	VDGRSMY	++	-
3963	14914	TTTTCACGCACCAACCATAAC	FSRTNHN	+++	-
3964	14915	TACTCAAAGATCAACTCAAAC	YSKINSN	++	-
3965	14916	GTACAAGGCCGCTCATCATAC	VQGRSSY	+	-
3966	14917	TTCGCGAAAAGGAATGATAAT	FAKRNDN	+++	-
3967	14918	TTCGCGAGGTTGGGGACGAAT	FARLGTN	+	-
3968	14919	TATTCCAAATTCAATCCGAAT	YSKFNPN	++	+
3969	14920	TTTGCCAAGCAAGGCATGAAC	FAKQGMN	+	-
3970	14921	TTTGCCAAGCTGGGCCCCAAC	FAKLGPN	+	-
3971	14922	TATTCCAAAATAAATCAGAAT	YSKINQN	++	-
3972	14923	TTCGCGAAAATGGGGCACAAT	FAKMGHN	+	+
3973	14924	TATTCCAAAATGGGGAAAAAT	YSKMGKN	+++	-
3974	14925	TTCTCCAGGACGGGGCCGAAT	FSRTGPN	+	-
3975	14926	AATGCGAGGGGGATGGGGAAT	NARGMGN	+	-
3976	14927	TATTATCAGTATAAAACGGCG	YYQYKTA	+	-
3977	14928	TTCTCCAAAGGGAATAATAAT	FSKGNNN	+	+
3978	14929	TACGCCAAGTACAACTTTAAC	YAKYNFN	+	-
3979	14930	CTGGCCAAGCAAGGCTCAAAC	LAKQGSN	+	-
3980	14931	TACTCAAAGCCCAACTGGAAC	YSKPNWN	++	-
3981	14932	TACGCCAAGCCCAACTACAAC	YAKPNYN	+	-
3982	14933	TACTCAAAGTTTAACCATAAC	YSKFNHN	++	++
3983	14934	TTCTCCAGGTCCAATCCGAAT	FSRSNPN	+	-
3984	14935	TTCTCCAGGCCGAATCACAAT	FSRPNHN	+	-
3985	14936	AACCAACTGCCCACCCCCAAG	NQLPTPK	+	-
3986	14937	ATGCCGAGGTCCACGTATGGG	MPRSTYG	++	++
3987	14938	TTCGCGAAATATAATAATAAT	FAKYNNN	+	-
3988	14939	TTTTCACGCTTTAACACCAAC	FSRFNTN	+++	-
3989	14940	TATGCGAAATATAATTATAAT	YAKYNYN	+	++
3990	14941	TATTCCAGGGGGGGGCACAAT	YSRGGHN	+++	-
3991	14942	TATGCGAGGCCGAATCCGAAT	YARPNPN	+	-
3992	14943	TACTCAAAGGGCGGCACCAAC	YSKGGTN	+	-
3993	14944	TTTGCCCGCCATGGCATCAAC	FARHGIN	++	-

3994	14945	TTCGCGAGGGCGGGGCAGAAT	FARAGQN	+	-
3995	14946	TTTTCAAAGATCGGCTCAAAC	FSKIGSN	+	-
3996	14947	CGCAACACCTCAACCAACTGG	RNTSTNW	+	-
3997	14948	TTCGCGAGGATGGGGTCCAAT	FARMGSN	++	-
3998	14949	CTGTCAAAGTGGAACGAAAAC	LSKWNEN	+	-
3999	14950	TTCTCCAGGCCGAATTATAAT	FSRPNYN	+	-
4000	14951	TACGCCAAGACCAACGACAAC	YAKTNDN	++	-
4001	14952	TTTTCACGCGGCAACAACAAC	FSRGNNN	+	-
4002	14953	CTGTCAAAGAACAACCTGAAC	LSKNNLN	+	+
4003	14954	CGCACCTCATCATACGGCGTA	RTSSYGV	+	-
4004	14955	CTGGCCAAGATCGGCATGAAC	LAKIGMN	++	-
4005	14956	TTTGCCCGCGCCGGCGTAAAC	FARAGVN	+	-
4006	14957	TTCGCGAAACCGAATATAAAT	FAKPNIN	+++	-
4007	14958	TATTCCAGGACGGGGCCGAAT	YSRTGPN	+++	-
4008	14959	TATGCGAGGGAGGGGTGGAAT	YAREGWN	+	-
4009	14960	TATAGGCCGAGGGTGCCGGAT	YRPRVPD	+	-
4010	14961	TTGGCGAAAGGGCACTATGGG	LAKGHYG	+	-
4011	14962	GCCGGCAACTCACGCGACTGG	AGNSRDW	+	-
4012	14963	TATGCGAGGCCGAATATGAAT	YARPNMN	+	-
4013	14964	TATGCGAGGGAGGGGTTCAAT	YAREGFN	+	-
4014	14965	TATGCGAAACAGAATCAGAAT	YAKQNQN	+	+
4015	14966	CTGTCACGCATGGGCGGCAAC	LSRMGGN	++	-
4016	14967	CTGTCAAAGTGGAACGACAAC	LSKWNDN	++	-
4017	14968	TTTTCAAAGCGCGGCGACAAC	FSKRGDN	+++	-
4018	14969	TACTCACGCAAGGGCGACAAC	YSRKGDN	+	-
4019	14970	TTTTCAAAGCATGGCTTTAAC	FSKHGFN	+++	-
4020	14971	TTCGCGAGGACGAATCAGAAT	FARTNQN	+	-
4021	14972	TTTGCCCGCTCAAACGTAAAC	FARSNVN	++	-
4022	14973	TTTGCCAAGATCGGCCCCAAC	FAKIGPN	++	-
4023	14974	TTTTCACGCTCAAACTCAAAC	FSRSNSN	++	-
4024	14975	TATGCGAAATTGGGGGGGAAT	YAKLGGN	+	-
4025	14976	TTTTCAAAGCTGGGCCAAAAC	FSKLGQN	++	-
4026	14977	TTCGCGAGGCACAATGCGAAT	FARHNAN	++	-
4027	14978	TTCGCGAGGTCCAATCACAAT	FARSNHN	++	-
4028	14979	TTCGCGAGGATGGGGTATAAT	FARMGYN	+	-
4029	14980	TTTGCCAAGAACGGCTGGAAC	FAKNGWN	+	-
4030	14981	TTCGCGAAATTCGGGCCGAAT	FAKFGPN	+	-
4031	14982	TTCTCCAGGACGAATTCCAAT	FSRTNSN	+	-
4032	14983	TTTGCCCGCGCCAACGCCAAC	FARANAN	+++	-
4033	14984	TACTCAAAGACCAACGCCAAC	YSKTNAN	+	-
4034	14985	TACTCAAAGTTTAACCTGAAC	YSKFNLN	+	-
4035	14986	TATGCGAGGAAAAATGAGAAT	YARKNEN	++	+
4036	14987	AACTACGGCAACATGAAGAAC	NYGNMKN	+	-
4037	14988	TACTCAAAGTTTAACACCAAC	YSKFNTN	+	-
4038	14989	ACCAAGTTTGGCCTGTCAGCC	TKFGLSA	+	-

4039	14990	TACGCCCGCGAAGGCAAGAAC	YAREGKN	+	-
4040	14991	TTCGCGAGGATGAATCACAAT	FARMNHN	+++	++
4041	14992	TTCGCGAAAGGGGGGCAGAAT	FAKGGQN	++	-
4042	14993	TACTCACGCAACAACGGCAAC	YSRNNGN	++	-
4043	14994	TTCGCGAGGTCCAATTCCAAT	FARSNSN	+	+
4044	14995	TACTCACGCGAAGGCCGCAAC	YSREGRN	+	+
4045	14996	TTCGCGAGGCACGGGGTGAAT	FARHGVN	+++	++
4046	14997	TTTGCCCGCATCGGCGCCAAC	FARIGAN	++	-
4047	14998	TATTCCAAAACGAATTGGAAT	YSKTNWN	+	-
4048	14999	ATGTGGTCATCAAACGGCGTA	MWSSNGV	+	-
4049	15000	TATTCCAAATATGGGATGAAT	YSKYGMN	+	-
4050	15001	TTTTCACGCGGCAACCCCAAC	FSRGNPN	++	-
4051	15002	TTTTCAAAGATGGGCGCCAAC	FSKMGAN	++	-
4052	15003	TTCGCGAGGTCCAATTTCAAT	FARSNFN	++	-
4053	15004	TATGCGAAATGGAATGCGAAT	YAKWNAN	++	-
4054	15005	CTGTCAAAGATCAACTTTAAC	LSKINFN	+++	-
4055	15006	TACGCCAAGATCGGCGGCAAC	YAKIGGN	+	++
4056	15007	ATGGGCACCTCACGCGGCTGG	MGTSRGW	+++	+++
4057	15008	TATTTCGGGGGGAAACAGGCG	YFGGKQA	+	-
4058	15009	TACGCCCGCTCATCACAAGAC	YARSSQD	+	-
4059	15010	TGGCTGAAGTCACAAGCCTCA	WLKSQAS	+	-
4060	15011	TTTTCACGCAACAACAACAAC	FSRNNNN	+	-
4061	15012	CGCTCAAACTCAGCCTACCCC	RSNSAYP	+	-
4062	15013	GGCAACTCAACCTCAAAGTTT	GNSTSKF	++	-
4063	15014	TTTGCCAAGCAAGGCATCAAC	FAKQGIN	+	-
4064	15015	CTGTCACGCTACGGCGACAAC	LSRYGDN	+	-
4065	15016	TTTTCACGCATCAACGCCAAC	FSRINAN	+	-
4066	15017	TCAAAGGGCACCTCATACTAC	SKGTSYY	+	-
4067	15018	TTTGCCAAGGGCAACCCCAAC	FAKGNPN	+	-
4068	15019	TTCTCCAGGGGGAATACGAAT	FSRGNTN	+	+
4069	15020	CTGAAGTCATCAAACGGCGTA	LKSSNGV	++	-
4070	15021	AAACACTCCACGAATGGGGTG	KHSTNGV	++	-
4071	15022	TTCTCCAAACCGAATTATAAT	FSKPNYN	++	-
4072	15023	AATAGGTATAAATCCGGGGAG	NRYKSGE	++	++
4073	15024	TTCTCCAGGAATAATTTGAAT	FSRNNLN	++	-
4074	15025	TATCCGGGGAAATCCTCCTTC	YPGKSSF	++	-
4075	15026	TATTCCAAATATAATTATAAT	YSKYNYN	++	-
4076	15027	TACGCCAAGTGGAACCCCAAC	YAKWNPN	+++	-
4077	15028	TATGCGAGGCACAATCACAAT	YARHNHN	+++	-
4078	15029	TTTGCCAAGGGCAACGCCAAC	FAKGNAN	+	-
4079	15030	GGGAGGTTGAAATCCGATCAG	GRLKSDQ	+++	-
4080	15031	TTCGCGAGGACGAATGCGAAT	FARTNAN	+	-
4081	15032	TATGCGAAATTCAATCCGAAT	YAKFNPN	+	-
4082	15033	TTTTCACGCGTAAACTCAAAC	FSRVNSN	+	++
4083	15034	CGCAACAACACCGTATACATG	RNNTVYM	+	-

4084	15035	TTCTCCAAACACGGGCACAAT	FSKHGHN	+++	-
4085	15036	CTGTCAAAGTTTAACTACAAC	LSKFNYN	+	-
4086	15037	TTTTCAAAGCATGGCCTGAAC	FSKHGLN	+	-
4087	15038	TCCAGGTATGGGGATGCGGCG	SRYGDAA	++	-
4088	15039	AACAAGTCATCATCATCATGG	NKSSSSW	+	-
4089	15040	TTTTCACGCGGCGGCGTAAAC	FSRGGVN	+	++
4090	15041	TACGCCCGCTCAAACTACAAC	YARSNYN	++	-
4091	15042	ACCCCCTACGGCAAGATGGCC	TPYGKMA	++	-
4092	15043	TTTTCAAAGAAGAACGACAAC	FSKKNDN	++	-
4093	15044	TTTTCACGCAACAACTCAAAC	FSRNNSN	+	-
4094	15045	TTTGCCCGCACCAACCTGAAC	FARTNLN	++	+++
4095	15046	TTTTCAAAGTCAAACTACAAC	FSKSNYN	++	-
4096	15047	TTCTCCAAATCCGGGTGGAAT	FSKSGWN	++	++
4097	15048	TACGCCAAGCCCAACTTTAAC	YAKPNFN	+	-
4098	15049	TTTGCCCGCGGCAACCCCAAC	FARGNPN	+++	-
4099	15050	TACGCCCGCCCCAACATCAAC	YARPNIN	+++	-
4100	15051	TGTGTGAAAACGGATAGGAAT	CVKTDRN	+	-
4101	15052	TTCGCGAGGCAGAATACGAAT	FARQNTN	+	+++
4102	15053	TACGCCCGCTTTAACATGAAC	YARFNMN	+	-
4103	15054	TTCTCCAAACAGAATGCGAAT	FSKQNAN	+	-
4104	15055	TTCTCCAGGGTGAATTTCAAT	FSRVNFN	++	++
4105	15056	TTCTCCAGGAAAGGGGAGAAT	FSRKGEN	+++	-
4106	15057	TATGCGAAAGATGGGAGGAAT	YAKDGRN	+	-
4107	15058	TTCTCCAGGCACAATACGAAT	FSRHNTN	++	-
4108	15059	CTGTCAAAGCAAGGCTCAAAC	LSKQGSN	+	-
4109	15060	TATGCGAGGAGGAATGAGAAT	YARRNEN	+	-
4110	15061	CTGCGCGGCGGCGCCGACCGC	LRGGADR	+++	-
4111	15062	TATTCCAGGTATAATAATAAT	YSRYNNN	#N/A	-
4112	15063	TTTTCACGCGGCAACCATAAC	FSRGNHN	+++	-
4113	15064	TTTGCCCGCGTAGGCCAAAAC	FARVGQN	+++	-
4114	15065	ACCTCAAACAACGTATACCAT	TSNNVYH	++	-
4115	15066	TACTCAAAGCCCGGCTACAAC	YSKPGYN	+	-
4116	15067	TTTGCCCGCGCCAACCATAAC	FARANHN	+++	-
4117	15068	TTCGCGAGGTATAATCAGAAT	FARYNQN	++	+++
4118	15069	TACGCCAAGATGGGCAAGAAC	YAKMGKN	+++	-
4119	15070	TACGCCAAGATGAACTACAAC	YAKMNYN	+	-
4120	15071	TTTGCCCGCTCAAACGCCAAC	FARSNAN	+	-
4121	15072	TTTTCAAAGATGAACTCAAAC	FSKMNSN	++	+
4122	15073	TTTTCACGCCCCGGCCCCAAC	FSRPGPN	++	-
4123	15074	CTGGCCCGCCATGGCGACAAC	LARHGDN	+	+
4124	15075	CTGTCAAAGTACAACGACAAC	LSKYNDN	+	-
4125	15076	ACGAATGCGAGGTCCTCCTAT	TNARSSY	+	-
4126	15077	TATGCGAGGTATAATGCGAAT	YARYNAN	+	++
4127	15078	TACTCACGCGGCGGCGGCAAC	YSRGGGN	+	++
4128	15079	CGCTACACCGGCACCCCCGCC	RYTGTPA	+	-

4129	15080	TATTCCAGGGATAATAGGAAT	YSRDNRN	+	-
4130	15081	TTCGCGAAATTGAATATGAAT	FAKLNMN	+	-
4131	15082	TATGCGAGGTTCAATAATAAT	YARFNNN	+++	-
4132	15083	AACATCCCCTACTCAATGCCC	NIPYSMP	+	-
4133	15084	TTTTCAAAGCATGGCTACAAC	FSKHGYN	++	-
4134	15085	TTTGCCAAGAACGGCGCCAAC	FAKNGAN	+	++
4135	15086	TTCTCCAAAATGGGGGTGAAT	FSKMGVN	+++	++
4136	15087	TACGCCCGCATCAACTCAAAC	YARINSN	++	-
4137	15088	TTTTCAAAGCATGGCATCAAC	FSKHGIN	++	-
4138	15089	TCCGAGTCCACGCACGGGATG	SESTHGM	+	-
4139	15090	GGGGCGTCCGGGTCCATATAT	GASGSIY	+	-
4140	15091	TACGCCCGCATCAACCTGAAC	YARINLN	++	+
4141	15092	CTGTCAAAGATCGGCGGCAAC	LSKIGGN	+	-
4142	15093	TTTTCAAAGTACGGCATGAAC	FSKYGMN	++	-
4143	15094	TTTTCACGCTCAAACCAAAAC	FSRSNQN	++	++
4144	15095	GTGAGGTCCACGTCCGGGATA	VRSTSGI	++	-
4145	15096	TTTTCACGCGGCAACTCAAAC	FSRGNSN	++	-
4146	15097	TTTGCCCGCATCGGCACCAAC	FARIGTN	+	+++
4147	15098	TACTCAAAGCGCGGCGAAAAC	YSKRGEN	+++	-
4148	15099	TACGCCAAGCATGGCACCAAC	YAKHGTN	+	-
4149	15100	TTCGCGAGGCAGAATGCGAAT	FARQNAN	+	++
4150	15101	TATAGGAATGCGGTGATAGGG	YRNAVIG	++	-
4151	15102	TACTCAAAGCCCGGCAACAAC	YSKPGNN	+	++
4152	15103	TTTGCCAAGTCAAACTTTAAC	FAKSNFN	+	-
4153	15104	TTCGCGAGGCACGGGCAGAAT	FARHGQN	+	-
4154	15105	TTCGCGAGGGCGGGGTCCAAT	FARAGSN	+	+
4155	15106	TTCGCGAGGGTGGGGTCCAAT	FARVGSN	+	-
4156	15107	TTCTCCAAAACGGGGCAGAAT	FSKTGQN	+	-
4157	15108	TTTTCACGCACCAACATGAAC	FSRTNMN	+	+
4158	15109	TATACGTATGGGATAAAAGCG	YTYGIKA	+++	+
4159	15110	TATGCGAGGATGAATTCCAAT	YARMNSN	+	-
4160	15111	TTCGCGAGGATGAATTTGAAT	FARMNLN	+	-
4161	15112	ATGACCGGCCATTCACTGTAC	MTGHSLY	++	-
4162	15113	TTCTCCAGGATAAATCCGAAT	FSRINPN	+	+
4163	15114	TTTTCAAAGTACAACGTAAAC	FSKYNVN	+	-
4164	15115	TATGCGAGGTTGAATGGGAAT	YARLNGN	+	-
4165	15116	GGCATCGTAACCGTACGCCAT	GIVTVRH	+++	-
4166	15117	TTTGCCAAGGCCGGCGCCAAC	FAKAGAN	+	-
4167	15118	TACGCCAAGCAAAACGACAAC	YAKQNDN	+	-
4168	15119	TTCGCGAGGCAGAATCACAAT	FARQNHN	++	-
4169	15120	TTCGCGAGGATAAATAATAAT	FARINNN	++	-
4170	15121	TTCGCGAGGGTGGGGACGAAT	FARVGTN	+	-
4171	15122	TTCGCGAGGTATGGGAATAAT	FARYGNN	++	-
4172	15123	TATGCGAAAATAAATAATAAT	YAKINNN	++	-
4173	15124	TTTTCAAAGCAAAACGTAAAC	FSKQNVN	+	-

4174	15125	TTCGCGAAAAGGGGGGAGAAT	FAKRGEN	++	+++
4175	15126	TATGCGAAATATAATAATAAT	YAKYNNN	+	++
4176	15127	TTCTCCAAATTCAATCACAAT	FSKFNHN	+++	-
4177	15128	TTTGCCAAGCAAAACTGGAAC	FAKQNWN	++	-
4178	15129	TTCTCCAAATCCGGGACGAAT	FSKSGTN	+	+
4179	15130	TCACGCACCGGCCTGAACGCC	SRTGLNA	++	-
4180	15131	TATTCCAGGTTCAATGTGAAT	YSRFNVN	+	-
4181	15132	TTTTCACGCCATGGCCTGAAC	FSRHGLN	++	-
4182	15133	TACGCCCGCTCAAACGGCAAC	YARSNGN	++	+
4183	15134	TATGCGAGGATAAATGCGAAT	YARINAN	+	-
4184	15135	TTTGCCCGCCTGGGCCAAAAC	FARLGQN	+	-
4185	15136	TTTTCACGCGGCGGCTCAAAC	FSRGGSN	++	-
4186	15137	TTTTCACGCTACGGCGTAAAC	FSRYGVN	+	-
4187	15138	TACTCAAAGATCAACAAGAAC	YSKINKN	+++	-
4188	15139	TTTGCCCGCTACGGCGTAAAC	FARYGVN	+++	-
4189	15140	TATGCGAGGATAAATGTGAAT	YARINVN	+	-
4190	15141	TACGCCAAGTGGAACTCAAAC	YAKWNSN	+++	-
4191	15142	GTATACGACCGCAAGGGCACC	VYDRKGT	+++	-
4192	15143	TTTTCACGCGGCAACATGAAC	FSRGNMN	+	+
4193	15144	TTCGCGAGGCAGAATCAGAAT	FARQNQN	++	-
4194	15145	TTTTCAAAGTACAACTCAAAC	FSKYNSN	++	-
4195	15146	TATGCGAGGGTGAATCCGAAT	YARVNPN	++	+
4196	15147	TACGCCCGCCATGGCAACAAC	YARHGNN	+++	-
4197	15148	TACTCACGCTACGGCGGCAAC	YSRYGGN	+	-
4198	15149	TATGCGAAAATGAATAAAAAT	YAKMNKN	+++	-
4199	15150	TTTTCACGCACCAACTTTAAC	FSRTNFN	+	-
4200	15151	GTAGGCCGCTGGGGCTCAGAC	VGRWGSD	++	-
4201	15152	TTCTCCAAATATAATGGGAAT	FSKYNGN	+	+
4202	15153	CAGTATGGGACGGCGAAATTC	QYGTAKF	+	-
4203	15154	TTCGCGAAATATAATCACAAT	FAKYNHN	+++	-
4204	15155	TATAAATCCAATTCCAATTAT	YKSNSNY	+	-
4205	15156	TTTGCCAAGTCAGGCGAAAAC	FAKSGEN	+	-
4206	15157	TTTGCCAAGCATGGCCTGAAC	FAKHGLN	+	++
4207	15158	TATGCGAGGGTGAATTTGAAT	YARVNLN	+++	-
4208	15159	TGCAAGTCAGGCGGCCAAACC	CKSGGQT	+++	-
4209	15160	ACCCGCACCGGCGTAATGGCC	TRTGVMA	+	-
4210	15161	TTCGCGAGGCACAATCAGAAT	FARHNQN	+++	-
4211	15162	TATGCGAGGCACAATGCGAAT	YARHNAN	++	+
4212	15163	TATTCCAAATTGGCGACGAAT	YSKLATN	+	-
4213	15164	TTTGCCCGCGGCAACCAAAAC	FARGNQN	+	-
4214	15165	TTCTCCAGGGGGGGGAATAAT	FSRGGNN	+	++
4215	15166	TTCTCCAAAGTGGGGGGGAAT	FSKVGGN	+	-
4216	15167	TACGCCAAGATGAACCCCAAC	YAKMNPN	++	-
4217	15168	TTCTCCAGGGATAATAGGAAT	FSRDNRN	+	-
4218	15169	TACGCCCGCGACAACCGCAAC	YARDNRN	+	-

4219	15170	TTCGCGAGGATAAATCACAAT	FARINHN	++	++
4220	15171	GTAAAGTACACCGGCTCAAAC	VKYTGSN	+	-
4221	15172	ACCCAATACAACACCTACCAT	TQYNTYH	++	-
4222	15173	TATGCGAGGCCGGGGGGGAAT	YARPGGN	+	-
4223	15174	GTACGCCAACTGTCAGCCGGC	VRQLSAG	+	-
4224	15175	AATGTGAGGAGGAATGGGGAG	NVRRNGE	+	-
4225	15176	TTTTCACGCTCAAACAACAAC	FSRSNNN	+	-
4226	15177	TTCGCGAGGCACGGGCACAAT	FARHGHN	+++	-
4227	15178	TTCTCCAAATATGGGGTGAAT	FSKYGVN	+	-
4228	15179	TTTTCAAAGCATGGCGCCAAC	FSKHGAN	+	-
4229	15180	TACGCCAAGTGGAACACCAAC	YAKWNTN	++	-
4230	15181	TTCGCGAAAGCGAATCACAAT	FAKANHN	+	-
4231	15182	TTTGCCCGCCTGAACTCAAAC	FARLNSN	++	-
4232	15183	TATGCGAAATGGGGGTCCAAT	YAKWGSN	++	-
4233	15184	TTCTCCAAACACAATCCGAAT	FSKHNPN	+	-
4234	15185	ATGCATAAGCTGCAAGTAGCC	MHKLQVA	+	-
4235	15186	TTCTCCAAAGGGGGGCACAAT	FSKGGHN	+	-
4236	15187	TTTTCACGCTTTAACGCCAAC	FSRFNAN	+++	-
4237	15188	ATCCCCTCAAAGTCAGCCGGC	IPSKSAG	+	-
4238	15189	TATGCGAAATGGAATAATAAT	YAKWNNN	++	-
4239	15190	GTATCAGCCTCAACCAAGTGG	VSASTKW	+	-
4240	15191	TACTCACGCGAAGGCAACAAC	YSREGNN	+	-
4241	15192	TTCGCGAGGCAGAATTTCAAT	FARQNFN	++	+
4242	15193	TTCGCGAAACAGAATATGAAT	FAKQNMN	+	-
4243	15194	AGGGCGTCCGGGGTGTCCTAT	RASGVSY	+++	-
4244	15195	TTTTCAAAGGGCGGCTGGAAC	FSKGGWN	++	-
4245	15196	ACGAGGCACGGGGGGTCCCCG	TRHGGSP	++	-
4246	15197	CGCGACCGCCAATCAACCTAC	RDRQSTY	+++	-
4247	15198	TACGCCCGCGTAAACGTAAAC	YARVNVN	+	-
4248	15199	ATGAATGCGAAATCCCACTAT	MNAKSHY	+	-
4249	15200	TTCTCCAAAATAAATAATAAT	FSKINNN	+	-
4250	15201	TTTTCAAAGAACGGCTACAAC	FSKNGYN	+	-
4251	15202	TTTGCCAAGGCCAACTTTAAC	FAKANFN	++	-
4252	15203	CATGCCGGCGACCGCTGGATC	HAGDRWI	++	-
4253	15204	TTCTCCAGGATAGGGTATAAT	FSRIGYN	+++	-
4254	15205	TTTGCCAAGTACAACGCCAAC	FAKYNAN	++	-
4255	15206	TTTTCACGCATCAACCAAAAC	FSRINQN	+	-
4256	15207	TATGCGAGGGTGAATGCGAAT	YARVNAN	+	-
4257	15208	TACTCACGCCCCGGCTTTAAC	YSRPGFN	+	-
4258	15209	TCCAGGGGGTCCGGGTATGCG	SRGSGYA	+	+
4259	15210	AACCTGCGCGGCAACGGCGGC	NLRGNGG	+++	-
4260	15211	TTCGCGAAATATGGGGCGAAT	FAKYGAN	+	-
4261	15212	TTTTCAAAGTTTAACATGAAC	FSKFNMN	++	+
4262	15213	TTTTCACGCCATGGCGTAAAC	FSRHGVN	+	-
4263	15214	TTTTCAAAGACCAACTTTAAC	FSKTNFN	+	-

4264	15215	TATTCCAAATATAATCCGAAT	YSKYNPN	++	-
4265	15216	TTTTCAAAGCTGGGCACCAAC	FSKLGTN	+	-
4266	15217	TTCGCGAGGATAAATACGAAT	FARINTN	+	-
4267	15218	TACGCCCGCCATAACGTAAAC	YARHNVN	+	++
4268	15219	TTTTCACGCGGCGGCATGAAC	FSRGGMN	+	+
4269	15220	TACGTACGCAACATCGCCTCA	YVRNIAS	++	+
4270	15221	ACGAGGTCCGGGGCGTCCTCC	TRSGASS	+	-
4271	15222	TTTGCCCGCCAAAACCTGAAC	FARQNLN	++	-
4272	15223	TTTTCAAAGTCAAACATGAAC	FSKSNMN	+	-
4273	15224	TCAGGCTCACCCACCAAGTGG	SGSPTKW	+	-
4274	15225	TTTGCCCGCCTGGGCGCCAAC	FARLGAN	+	-
4275	15226	AACTCATCAGGCGCCCGCTAC	NSSGARY	+	-
4276	15227	TTTTCAAAGATCAACCATAAC	FSKINHN	+	-
4277	15228	TTTGCCCGCTCAAACAACAAC	FARSNNN	++	+
4278	15229	TTTTCAAAGATGGGCATCAAC	FSKMGIN	+	-
4279	15230	TTCTCCAAATTCAATTCCAAT	FSKFNSN	+	+
4280	15231	TATATGAGGGGGTCCTTGAAT	YMRGSLN	++	-
4281	15232	TTCTCCAAACACAATTCCAAT	FSKHNSN	+	-
4282	15233	TATGCGAGGTTCAATGCGAAT	YARFNAN	++	-
4283	15234	TATTCCAGGGTGTCCGGGTTG	YSRVSGL	+	-
4284	15235	TTTTCACGCGGCGGCCATAAC	FSRGGHN	++	-
4285	15236	TTCGCGAAATATGGGATGAAT	FAKYGMN	+	-
4286	15237	TTCGCGAAACACGGGGTGAAT	FAKHGVN	+	+
4287	15238	TTCAGGATGGGGGGGGCGGGG	FRMGGAG	+	-
4288	15239	CAGGCGTTGTCCGGGAAAAAT	QALSGKN	+	+
4289	15240	ATATCCAATGCGGTGAAATAT	ISNAVKY	+	-
4290	15241	TTTGCCAAGTACGGCACCAAC	FAKYGTN	+	-
4291	15242	TTTGCCCGCAACAACCATAAC	FARNNHN	++	-
4292	15243	TTTTCACGCGCCAACGGCAAC	FSRANGN	+	-
4293	15244	ACGAAAGGGATGTCCTCCTAT	TKGMSSY	+	-
4294	15245	TACGCCAAGCATAACCATAAC	YAKHNHN	+	-
4295	15246	TTTGCCAAGCAAGGCACCAAC	FAKQGTN	+	-
4296	15247	TTCGCGAGGATGGGGCAGAAT	FARMGQN	+	-
4297	15248	TTGCCGAAAGGGAATTATGGG	LPKGNYG	+	-
4298	15249	TTTTCAAAGTACGGCGCCAAC	FSKYGAN	++	-
4299	15250	TACGTAAAGTCAGCCATGTCA	YVKSAMS	+	++
4300	15251	TTTGCCAAGCATGGCAACAAC	FAKHGNN	+	-
4301	15252	ACCTCAACCGGCCGCATGGCC	TSTGRMA	+++	-
4302	15253	TACGCCCGCCCCAACCTGAAC	YARPNLN	+++	-
4303	15254	TTGGCGAGGGTGGCGAAAGAT	LARVAKD	+	+
4304	15255	TTTGCCAAGTGGAACCAAAAC	FAKWNQN	+	+++
4305	15256	TTTTCAAAGTACAACATGAAC	FSKYNMN	+	+
4306	15257	TTTGCCCGCGCCAACATCAAC	FARANIN	+	-
4307	15258	TTGCCGAGGTCCGGGAATGTG	LPRSGNV	++	++
4308	15259	TTCGCGAGGGTGAATCACAAT	FARVNHN	++	-

4309	15260	TACGTACGCAACGGCCAAGGC	YVRNGQG	+	-
4310	15261	TTTTCACGCCATAACGCCAAC	FSRHNAN	+++	+++
4311	15262	TTTTCACGCTTTGGCGGCAAC	FSRFGGN	+++	-
4312	15263	TTCGCGAGGAATAATGCGAAT	FARNNAN	+	-
4313	15264	AGGAATGGGACGAATGGGTAT	RNGTNGY	+	-
4314	15265	TTCTCCAAACACGGGGTGAAT	FSKHGVN	++	-
4315	15266	TTTGCCCGCCTGAACGGCAAC	FARLNGN	+++	-
4316	15267	TTCGCGAAATATGGGCACAAT	FAKYGHN	+++	-
4317	15268	ACCAAGTACGGCCATACCGCC	TKYGHTA	++	-
4318	15269	TTCGCGAAAAGGGGGGATAAT	FAKRGDN	++	-
4319	15270	CGCTCACATAACACCGTAGTA	RSHNTVV	+	-
4320	15271	TTCGCGAAAATGAATAATAAT	FAKMNNN	+	+
4321	15272	TACGCCCGCCTGGGCGGCAAC	YARLGGN	+++	-
4322	15273	ATAATAATGGTGAAAAATGCG	IIMVKNA	++	-
4323	15274	TACGCCCGCCATAACCAAAAC	YARHNQN	+++	-
4324	15275	CTGCATACCCGCACCTACGAC	LHTRTYD	+	++
4325	15276	TTTGCCAAGCATGGCGCCAAC	FAKHGAN	+++	-
4326	15277	TATAAACCGTTCACGACGAAT	YKPFTTN	+	-
4327	15278	TTTTCACGCATGGGCCAAAAC	FSRMGQN	+	-
4328	15279	TACGCCAAGTACAACACCAAC	YAKYNTN	++	-
4329	15280	TTTTCAAAGCAAGGCATCAAC	FSKQGIN	+	-
4330	15281	TATGCGAAATGGAATCAGAAT	YAKWNQN	+	++
4331	15282	TTTTCACGCCCCGGCTACAAC	FSRPGYN	+	-
4332	15283	TTTTCACGCGGCAACTTTAAC	FSRGNFN	+	-
4333	15284	GTAAACATGGCCCGCGCCCTG	VNMARAL	+	-
4334	15285	TTTTCACGCTCAGGCGGCAAC	FSRSGGN	+	-
4335	15286	ACCGGCGCCGGCATGAAGTAC	TGAGMKY	++	+
4336	15287	TTCGCGAGGCACAATTCCAAT	FARHNSN	+++	-
4337	15288	TTCGCGAGGCCGAATATAAAT	FARPNIN	+	-
4338	15289	TTCGCGAAACCGAATAATAAT	FAKPNNN	+	-
4339	15290	CGCCAAATGGACACCTACGGC	RQMDTYG	+	-
4340	15291	ACCGCCCGCGGCGTATCAGCC	TARGVSA	+	+++
4341	15292	TTTGTACGCACCATCAACAAC	FVRTINN	+	-
4342	15293	TTCGCGAGGATAGGGGGGAAT	FARIGGN	++	-
4343	15294	TTTTCAAAGCAAGGCGTAAAC	FSKQGVN	++	-
4344	15295	TTTGCCCGCGCCAACTTTAAC	FARANFN	+	+++
4345	15296	AGGGCGAATCACTCCGGGGGG	RANHSGG	++	-
4346	15297	TTTGCCCGCGGCAACGACAAC	FARGNDN	+	-
4347	15298	TTTGCCCGCTACGGCGCCAAC	FARYGAN	+++	-
4348	15299	TACGCCAAGTGGAACGGCAAC	YAKWNGN	+	++
4349	15300	TTTGCCCGCCTGAACCATAAC	FARLNHN	+	-
4350	15301	TTTGCCCGCCTGGGCCTGAAC	FARLGLN	++	-
4351	15302	TACGCCAAGTGGGGCGCCAAC	YAKWGAN	+	++
4352	15303	TTCTCCAGGCACGGGCAGAAT	FSRHGQN	+	-
4353	15304	TTCTCCAGGCACGGGGCGAAT	FSRHGAN	+++	-

4354	15305	TACTCACGCGAAAACCGCAAC	YSRENRN	++	-
4355	15306	TTCGCGAAACAGGGGGCGAAT	FAKQGAN	+	-
4356	15307	TTCTCCAAAAGGGGGGAGAAT	FSKRGEN	+++	-
4357	15308	TATGCGAGGGAGGGGGCGAAT	YAREGAN	++	-
4358	15309	TTCTCCAAATTCAATGCGAAT	FSKFNAN	++	+
4359	15310	TTCGCGAGGAAAGGGGAGAAT	FARKGEN	+++	-
4360	15311	AACGTACCCTCATCAATGTAC	NVPSSMY	+	+
4361	15312	GGCCTGAAGTACACCCCCCAT	GLKYTPH	+	-
4362	15313	TTCTCCAGGCAGGGGGGGAAT	FSRQGGN	+	-
4363	15314	TTTTCAAAGTACGGCCTGAAC	FSKYGLN	++	-
4364	15315	TTTTCACGCCATGGCATGAAC	FSRHGMN	++	-
4365	15316	TTCGCGAGGTTGGGGGGGAAT	FARLGGN	++	-
4366	15317	TTCGCGAAATATGGGTCCAAT	FAKYGSN	+	+++
4367	15318	TGGTCCAAATTGAATGCGATA	WSKLNAI	+	-
4368	15319	TTTTCAAAGAACGGCATGAAC	FSKNGMN	+	-
4369	15320	TTCGCGAGGATAAATGCGAAT	FARINAN	++	-
4370	15321	TCAGGCAACGGCTACGTACGC	SGNGYVR	+	+
4371	15322	TTTGCCAAGTACGGCATCAAC	FAKYGIN	+	-
4372	15323	TTCGCGAGGATGAATATGAAT	FARMNMN	+++	++
4373	15324	TTCGCGAGGAAAGGGGATAAT	FARKGDN	+++	-
4374	15325	CGCAACTCATCATCAACCTAC	RNSSSTY	+	-
4375	15326	TATTCCAAATATGGGGGGAAT	YSKYGGN	+++	-
4376	15327	TTCGCGAGGATAAATTCCAAT	FARINSN	+	++
4377	15328	TTCTCCAAATATAATACGAAT	FSKYNTN	++	++
4378	15329	TACGCCAAGTACAACTCAAAC	YAKYNSN	++	+
4379	15330	AGGAGGGCGGATTCCGGGGGG	RRADSGG	++	-
4380	15331	TTCGCGAGGCAGAATTCCAAT	FARQNSN	+	-
4381	15332	TACTCAAAGGGCGGCGGCAAC	YSKGGGN	+++	-
4382	15333	TACGCCCGCGACGGCTTTAAC	YARDGFN	+	-
4383	15334	TTCGCGAGGCCGGGGAATAAT	FARPGNN	+	-
4384	15335	TACGCCCGCATCAACCATAAC	YARINHN	+++	-
4385	15336	TTTGCCCGCGAAGGCAAGAAC	FAREGKN	+	+
4386	15337	TTCAGGAATGGGACGGGGGCG	FRNGTGA	+	-
4387	15338	AGGGGGTCCAATTTGTATCCG	RGSNLYP	++	-
4388	15339	TATGCGAGGGTGAATACGAAT	YARVNTN	+	-
4389	15340	GGGAATCAGACGTCCAGGAAT	GNQTSRN	+	+
4390	15341	TTTTCACGCGGCAACCAAAAC	FSRGNQN	+	-
4391	15342	TACTCAAAGCCCGGCGCCAAC	YSKPGAN	++	-
4392	15343	TTTTCAAAGTACGGCCAAAAC	FSKYGQN	+	-
4393	15344	TACTCAAAGCCCGGCATCAAC	YSKPGIN	+	-
4394	15345	TACGCCAAGCCCAACCATAAC	YAKPNHN	+	-
4395	15346	ACCCGCACCCATGACAAGCTG	TRTHDKL	+	-
4396	15347	TTTGCCCGCCGCAACGAAAAC	FARRNEN	+++	-
4397	15348	TTCTCCAGGAGGAATGAGAAT	FSRRNEN	+++	-
4398	15349	TATTCCAGGTATGGGAATAAT	YSRYGNN	++	-

4399	15350	TTCGCGAAAGCGAATTGGAAT	FAKANWN	+	++
4400	15351	TATGCGAAAATAAATAAAAAT	YAKINKN	+	-
4401	15352	TATTCCAAAATAGGGAAAAAT	YSKIGKN	+++	-
4402	15353	TACGCCAAGTGGGGCGGCAAC	YAKWGGN	++	-
4403	15354	TATTCCAAATGGGGGAATAAT	YSKWGNN	+	-
4404	15355	TACGCCAAGTACAACGCCAAC	YAKYNAN	+	+
4405	15356	AAGTCAGGCCTGTCATCATAC	KSGLSSY	++	-
4406	15357	TTTGCCCGCATGAACCAAAAC	FARMNQN	+	-
4407	15358	TTTGCCAAGAACGGCTCAAAC	FAKNGSN	+	-
4408	15359	ATCCCCACCATGAAGTACGCC	IPTMKYA	+	-
4409	15360	TCCAGGACGGGGAGGGAGGCG	SRTGREA	+	-
4410	15361	TTCGCGAGGAATAATGTGAAT	FARNNVN	+	++
4411	15362	TACGCCCGCCAAAACGCCATG	YARQNAM	+	-
4412	15363	TATTCCAAATTCAATGGGAAT	YSKFNGN	+	-
4413	15364	ATCTCAGGCTACGGCGGCGGC	ISGYGGG	++	-
4414	15365	TTCGCGAAATTCAATCCGAAT	FAKFNPN	+	++
4415	15366	AAATCCGAGTATGGGCCGTTC	KSEYGPF	++	-
4416	15367	TACGCCCGCGCCAACGGCAAC	YARANGN	+	-
4417	15368	CTGTCATACTCAGGCCGCGAC	LSYSGRD	+	-
4418	15369	TATTCCAGGCCGAATCAGAAT	YSRPNQN	++	-
4419	15370	TATTATTCCAATACGAAAGTG	YYSNTKV	+	++
4420	15371	TTCGCGAAATCCAATTGGAAT	FAKSNWN	++	-
4421	15372	TTTGCCCGCTCAAACCCCAAC	FARSNPN	++	-
4422	15373	TACTCACGCTCAAACATCCAA	YSRSNIQ	+	+
4423	15374	GAGATAAGGACGGGGCACTTG	EIRTGHL	++	-
4424	15375	GAAAAGGGCATGGGCCGCCTG	EKGMGRL	+	+
4425	15376	TTGTCCAGGGCGGCGGGGATA	LSRAAGI	+	-
4426	15377	GTAGACAAGAAGTACTACGCC	VDKKYYA	+++	-
4427	15378	CGCAACCTGCCCATGCTGAAC	RNLPMLN	+++	-
4428	15379	TATGCGAAACCGGGGCAGAAT	YAKPGQN	+	-
4429	15380	TTCGCGAGGGCGAATACGAAT	FARANTN	++	-
4430	15381	TTGAGGAATGGGTTCTCCCCG	LRNGFSP	+	-
4431	15382	TTCGCGAGGAATAATACGAAT	FARNNTN	+	+
4432	15383	CTGGCCGGCACCTCACGCTTT	LAGTSRF	+++	-
4433	15384	TTTGCCCGCATCAACGTAAAC	FARINVN	+++	-
4434	15385	GTGTTGGGGAGGGGGGTGAAT	VLGRGVN	+	-
4435	15386	CTGCGCGGCGACGGCTACGGC	LRGDGYG	++	+++
4436	15387	TTCGCGAGGGCGAATATGAAT	FARANMN	+	+
4437	15388	TTCTCCAGGCACGGGGGGAAT	FSRHGGN	+++	-
4438	15389	AGGGGGGAGTGGTCCTCCCCG	RGEWSSP	++	-
4439	15390	TTCTCCAAAGCGAATGAGAAT	FSKANEN	+	-
4440	15391	CAACCCATGCGCGGCGGCGGC	QPMRGGG	+++	+
4441	15392	TATGGGCCGCAGCCGAAATTG	YGPQPKL	+	-
4442	15393	TTTTCACGCCATGGCACCAAC	FSRHGTN	+++	-
4443	15394	TACTCAAAGGACGGCTGGAAC	YSKDGWN	+	-

4444	15395	TACTCAAAGTACGGCTTTAAC	YSKYGFN	+	-
4445	15396	TTTGCCAAGTACAACTCAAAC	FAKYNSN	+	-
4446	15397	TTTGCCAAGTACAACATGAAC	FAKYNMN	++	-
4447	15398	GATGTGAGGTTGAGGGGGCAG	DVRLRGQ	+	++
4448	15399	TTCTCCAAATATGGGTCCAAT	FSKYGSN	++	-
4449	15400	TGGTTGAAATCCACGCCGAAT	WLKSTPN	++	-
4450	15401	AATATGTTCGGGTCCGGGATG	NMFGSGM	++	-
4451	15402	AATCACGGGTATATGAGGGAT	NHGYMRD	+	-
4452	15403	TTTGCCAAGTACAACCTGAAC	FAKYNLN	++	+
4453	15404	TACGCCAAGAAGAACGACAAC	YAKKNDN	+	-
4454	15405	TATGCGAAATATAATCAGAAT	YAKYNQN	+	-
4455	15406	TTTTCACGCGCCAACCCCAAC	FSRANPN	+++	-
4456	15407	CGCGGCTCAAACTCAATGCCC	RGSNSMP	+	-
4457	15408	TACAAGGTATCATCAACCTAC	YKVSSTY	+	-
4458	15409	AACTCATCATCAGGCCCCCGC	NSSSGPR	+	-
4459	15410	TTTGCCCGCATGAACGTAAAC	FARMNVN	+	-
4460	15411	TTGTCCAGGTCCGGGACGGAT	LSRSGTD	+	-
4461	15412	TTTGCCCGCTACAACGCCAAC	FARYNAN	+++	-
4462	15413	TATGCGAAATTCAATCAGAAT	YAKFNQN	+	-
4463	15414	ATGAAAAATGGGGGGGCGGCG	MKNGGAA	+	-
4464	15415	ATGGATTATGGGTGGTCCGAT	MDYGWSD	+	-
4465	15416	TTTTCACGCGGCGGCACCAAC	FSRGGTN	+	-
4466	15417	TTCGCGAGGCACGGGGGGAAT	FARHGGN	+++	-
4467	15418	TTCGCGAGGATAGGGGATAAT	FARIGDN	+	-
4468	15419	TATTCCGCGGGGAAAATAAAT	YSAGKIN	+	+++
4469	15420	TATGCGAGGTTCAATACGAAT	YARFNTN	+++	-
4470	15421	TACGCCCGCTACAACACCAAC	YARYNTN	+++	-
4471	15422	TTCTCCAGGCCGGGGCACAAT	FSRPGHN	+	-
4472	15423	TCCTATGCGGTGTCCAGGGAT	SYAVSRD	+	-
4473	15424	TACGCCCGCTACAACAACAAC	YARYNNN	++	-
4474	15425	TATTCCAGGTTCAATGGGAAT	YSRFNGN	+	-
4475	15426	AGGGGGACGACGGGGGCGGGG	RGTTGAG	++	-
4476	15427	AGGTCCCACGCGTCCGCGGGG	RSHASAG	+	-
4477	15428	TTCGCGAAATATGGGGTGAAT	FAKYGVN	++	-
4478	15429	GGCATGGGCTCAACCAAGTAC	GMGSTKY	+	+
4479	15430	TACGCCAAGTTTAACGTAAAC	YAKFNVN	+	-
4480	15431	TACATGAAGTCAGGCCCCAAC	YMKSGPN	++	-
4481	15432	AGGAATTCCGGGTCCGTGTTC	RNSGSVF	+	-
4482	15433	ACGGAGAATACGGTGAGGAAA	TENTVRK	+	-
4483	15434	TACGCCCGCTTTAACGTAAAC	YARFNVN	++	-
4484	15435	TATGCGAGGCCGAATGCGAAT	YARPNAN	+	-
4485	15436	AACTACAACCGCGGCGCCGGC	NYNRGAG	+	+
4486	15437	TATATGAAACACTCCCCGAAT	YMKHSPN	+	-
4487	15438	TTCGCGAAAATAGGGGCGAAT	FAKIGAN	+	-
4488	15439	TTCGCGAGGCCGAATAATAAT	FARPNNN	+	-

4489	15440	TACGCCCGCATCAACCAAAAC	YARINQN	+	-
4490	15441	TTTGCCCGCAACAACTCAAAC	FARNNSN	+	-
4491	15442	TGGAAGGGCGGCACCTCAAAC	WKGGTSN	++	-
4492	15443	TACGCCAAGCGCAACGACAAC	YAKRNDN	++	-
4493	15444	TTCTCCAGGATGAATCCGAAT	FSRMNPN	++	-
4494	15445	AACTCATCAGACGGCCCCCGC	NSSDGPR	+	-
4495	15446	TACGCCAAGTGGGGCAACAAC	YAKWGNN	++	++
4496	15447	TTTGCCAAGTTTAACCATAAC	FAKFNHN	+++	-
4497	15448	TTCTCCAGGATGGGGGGGAAT	FSRMGGN	++	-
4498	15449	TTCGCGAGGATGAATGCGAAT	FARMNAN	++	-
4499	15450	TATTATGCGAAAGTGTTGCCG	YYAKVLP	++	-
4500	15451	TTCTCCAAATTCAATCAGAAT	FSKFNQN	++	-
4501	15452	TTTGCCCGCCTGAACGCCAAC	FARLNAN	+++	-
4502	15453	TTCGCGAGGGTGGGGGGGAAT	FARVGGN	+	-
4503	15454	TACGCCAAGTTTAACTCAAAC	YAKFNSN	+	-
4504	15455	ACCCGCGGCGGCGGCTCAGGC	TRGGGSG	+	-
4505	15456	TTCGCGAGGAATAATTTCAAT	FARNNFN	+	-
4506	15457	TCCGCGCCGCCGACGAAATTC	SAPPTKF	++	-
4507	15458	TGGAATCAGTTCACGGGGAAT	WNQFTGN	+	-
4508	15459	GATGCGAATCACAATAGGAAT	DANHNRN	+	-
4509	15460	TTTTCACGCCTGGGCGACAAC	FSRLGDN	+	-
4510	15461	TATACGAAAGGGACGGTGAAT	YTKGTVN	+	-
4511	15462	TACGCCAAGATGGGCACCAAC	YAKMGTN	+	-
4512	15463	TTCGCGAGGCACAATGGGAAT	FARHNGN	+	-
4513	15464	TTCGCGAGGGTGAATCAGAAT	FARVNQN	+	-
4514	15465	ACGCACGCGTTGGTGAATGCG	THALVNA	+	-
4515	15466	TTTGCCAAGTTTAACGTAAAC	FAKFNVN	+	-
4516	15467	TACATGAAGCGCGAAATCTCA	YMKREIS	+	-
4517	15468	ACGCCGCCGACGTTCAAAGTG	TPPTFKV	+	-
4518	15469	TTTGCCAAGTACGGCAACAAC	FAKYGNN	+	+
4519	15470	TATACGAGGTATGGGTTGGAT	YTRYGLD	+	-
4520	15471	TACGCCCGCGTAAACAACAAC	YARVNNN	+	+
4521	15472	ACCCCCACCGGCCGCCCCGCC	TPTGRPA	+	-
4522	15473	TTCTCCAAATATGGGAATAAT	FSKYGNN	++	-
4523	15474	TTCGCGAAACACGGGCAGAAT	FAKHGQN	+	-
4524	15475	TGGAGGGGGAATGGGGTGAAT	WRGNGVN	+	-
4525	15476	TATGCGAAATTCAATCACAAT	YAKFNHN	++	-
4526	15477	TTTTCAAAGCAAGGCTGGAAC	FSKQGWN	++	-
4527	15478	TTCTCCAAATTCAATGTGAAT	FSKFNVN	++	-
4528	15479	TTTTCAAAGTACGGCGGCAAC	FSKYGGN	+++	+
4529	15480	TACTCAAAGTTTGGCCCCAAC	YSKFGPN	++	-
4530	15481	TTCTCCAAATATAATTTGAAT	FSKYNLN	++	-
4531	15482	TTCGCGAAATATAATACGAAT	FAKYNTN	+++	-
4532	15483	GGGAATAGGAATTATTCCGAG	GNRNYSE	+	-
4533	15484	TTCGCGAGGATGAATCCGAAT	FARMNPN	+++	-

4534	15485	TACGCCAAGGTATCATCAAAC	YAKVSSN	+	-
4535	15486	TTCTCCAAAGGGGGGTCCAAT	FSKGGSN	+	-
4536	15487	TTTGCCAAGTACGGCCTGAAC	FAKYGLN	+	-
4537	15488	TTCGCGAGGATGAATACGAAT	FARMNTN	++	-
4538	15489	TTCGCGAAAGCGGGGTCCAAT	FAKAGSN	+	++
4539	15490	TACGCCCGCGTAAACTCAAAC	YARVNSN	+	-
4540	15491	TACGCCCGCCATGGCCCCAAC	YARHGPN	+++	-
4541	15492	ATCGTACATCTGAAGAACTCA	IVHLKNS	+	-
4542	15493	GGGAGGGCGAATCACTCCGGG	GRANHSG	++	-
4543	15494	TTTTCAAAGAACAACTTTAAC	FSKNNFN	++	-
4544	15495	TATGCGAAATATAATGTGAAT	YAKYNVN	+	-
4545	15496	TTTGCCCGCGTAGGCGACAAC	FARVGDN	+	-
4546	15497	TTCTCCAGGCCGAATCCGAAT	FSRPNPN	+	-
4547	15498	TTTGCCAAGTACAACGTAAAC	FAKYNVN	++	-
4548	15499	AACAACCGCGGCACCTCAGAA	NNRGTSE	+	-
4549	15500	CATCGCTCAGGCGGCTACGAC	HRSGGYD	+	-
4550	15501	TTCGCGAGGCACAATGTGAAT	FARHNVN	+	-
4551	15502	TACGCCCGCCATAACGACAAC	YARHNDN	+	-
4552	15503	ACCCTGACCGGCCGCAACTCA	TLTGRNS	+	-
4553	15504	TTCGCGAAAATGGGGTCCAAT	FAKMGSN	+	-
4554	15505	TTCGCGAGGGTGAATTCCAAT	FARVNSN	++	-
4555	15506	GTGTATAGGCCGGTGACGAAT	VYRPVTN	+	-
4556	15507	TTTTCACGCAACAACCAAAAC	FSRNNQN	++	-
4557	15508	ATGAAGTCATACGGCGTAGGC	MKSYGVG	+	+
4558	15509	TTTTCAAAGTACGGCATCAAC	FSKYGIN	++	-
4559	15510	TTTGCCCGCGCCAACCAAAAC	FARANQN	++	-
4560	15511	TTTGCCCGCCATGGCTCAAAC	FARHGSN	++	-
4561	15512	AGGTCCAATGGGTCCGGGCCG	RSNGSGP	++	-
4562	15513	AACAACTCACGCGGCTCATAC	NNSRGSY	+++	-
4563	15514	TACACCAAGCTGACCGGCAAC	YTKLTGN	+	-
4564	15515	TTCGCGAAACACAATCAGAAT	FAKHNQN	+	-
4565	15516	TACTCACGCTTTAACTCAAAC	YSRFNSN	+++	-
4566	15517	TTCTCCAAAAAAGGGGATAAT	FSKKGDN	+	+
4567	15518	TATGCGAGGCCGAATCAGAAT	YARPNQN	+	-
4568	15519	TTTGCCCGCGTAAACTACAAC	FARVNYN	++	++
4569	15520	CGCACCGAATACCAAGTAGGC	RTEYQVG	+++	-
4570	15521	TTCGCGAGGTATAATAATAAT	FARYNNN	++	-
4571	15522	TTCTCCAGGTATAATGGGAAT	FSRYNGN	+++	-
4572	15523	TTCGCGAGGTTCGGGGGGAAT	FARFGGN	+	-
4573	15524	TTTTCAAAGGAAAACTGCAAC	FSKENCN	++	-
4574	15525	GACTCAGGCTACAACCGCAAC	DSGYNRN	++	-
4575	15526	TTCGCGAAAATAGGGGTGAAT	FAKIGVN	+	-
4576	15527	TATGCGAGGCCGAATGGGAAT	YARPNGN	+	-
4577	15528	AACCGCTCAGGCACCTCAGCC	NRSGTSA	++	-
4578	15529	TTTGCCAAGTACAACATCAAC	FAKYNIN	+	+

4579	15530	TTCGCGAAATTGGGGATGAAT	FAKLGMN	+	-
4580	15531	TATGCGAGGTTCAATTCCAAT	YARFNSN	++	-
4581	15532	TTTGCCAAGAAGGGCGAAAAC	FAKKGEN	+	-
4582	15533	TTTGCCAAGCTGGGCCTGAAC	FAKLGLN	+	-
4583	15534	TTTGCCAAGGTAGGCCCCAAC	FAKVGPN	+	-
4584	15535	CGCGGCTCATCACGCGACTCA	RGSSRDS	++	-
4585	15536	TTTGCCCGCGTAAACGTAAAC	FARVNVN	+	-
4586	15537	TCCGGGTATGGGATGATGAAT	SGYGMMN	+	-
4587	15538	TTCGCGAAATTGGGGGCGAAT	FAKLGAN	+	-
4588	15539	GACCGCAACACCCGCATGGTA	DRNTRMV	+++	+
4589	15540	GCCCAAAAGGACACCATGTAC	AQKDTMY	++	-
4590	15541	TATTCCAGGTTCAATCAGAAT	YSRFNQN	+	+
4591	15542	TTCTCCAAATATGGGACGAAT	FSKYGTN	+	-
4592	15543	TATGCGAGGCCGAATACGAAT	YARPNTN	+	-
4593	15544	TTCAAAGGGACGACGCCGTAT	FKGTTPY	++	-
4594	15545	CGCTGGGCCAAGGAAGTAGGC	RWAKEVG	++	+
4595	15546	TGGTACCAAAACCAAAAGGAC	WYQNQKD	++	-
4596	15547	ACCATGCTGGGCGCCCGCAAC	TMLGARN	++	+
4597	15548	TTTGCCAAGTACGGCCAAAAC	FAKYGQN	+	-
4598	15549	GATAGGGGGGATAGGTTCTCC	DRGDRFS	+	-
4599	15550	TATGCGAAATTCAATACGAAT	YAKFNTN	+	-
4600	15551	TTTTCAAAGGGCGGCGCCAAC	FSKGGAN	++	+++
4601	15552	TTTGCCCGCAAGAACGACAAC	FARKNDN	+++	+
4602	15553	TTCGCGAGGGTGAATTTGAAT	FARVNLN	+	+
4603	15554	GGGCCGCCGGCGTTCAAAGCG	GPPAFKA	+	-
4604	15555	CAGCCGAGGAGGATAGAGGTG	QPRRIEV	++	++
4605	15556	AGGTCCAGGAATGAGTCCGGG	RSRNESG	++	-
4606	15557	CTGCGCACCGCCGGCGCCGGC	LRTAGAG	+	-
4607	15558	TTTGCCCGCGTAAACATGAAC	FARVNMN	+	-
4608	15559	TTTGCCAAGCGCAACGAAAAC	FAKRNEN	++	+
4609	15560	TTCGCGAAACACGGGGGGAAT	FAKHGGN	+	-
4610	15561	TCCTGGACGGGGGCGACGGCG	SWTGATA	++	-
4611	15562	TTCTCCAAATATAATCAGAAT	FSKYNQN	++	+
4612	15563	TTCGCGAGGGTGAATGCGAAT	FARVNAN	+	-
4613	15564	TACGCCAAGATCAACACCAAC	YAKINTN	+	+
4614	15565	TTTGCCAAGACCAACGCCAAC	FAKTNAN	+	-
4615	15566	ACGAGGACGGGGATAGCGTCC	TRTGIAS	+	-
4616	15567	TTCGCGAAAGCGAATCCGAAT	FAKANPN	+	-
4617	15568	TACATGAAGCGCGGCGTAGAC	YMKRGVD	+	-
4618	15569	TTCGCGAGGAGGAATGATAAT	FARRNDN	+++	-
4619	15570	ATCAACCTGTCAAAGCTGCAA	INLSKLQ	+	-
4620	15571	TTCTCCAGGTATGGGCAGAAT	FSRYGQN	+++	-
4621	15572	CTGTGGAAGAACGCCATGGAC	LWKNAMD	+	-
4622	15573	TTCGCGAGGAATAATTTGAAT	FARNNLN	+	-
4623	15574	TTTGCCAAGCATAACCATAAC	FAKHNHN	+++	-

4624	15575	TATGCGAAAAATAATTCCAAT	YAKNNSN	+	-
4625	15576	TGGCATTCACCCAACGGCATC	WHSPNGI	+	-
4626	15577	TATGCGAGGCCGGGGGAGAAT	YARPGEN	+	-
4627	15578	GAGAAATATAAAGGGCACATG	EKYKGHM	+	-
4628	15579	TATCAGAGGAATAATATGGTG	YQRNNMV	+	-
4629	15580	TTTTCAAAGATCGGCGGCAAC	FSKIGGN	+	-
4630	15581	TTCGCGAGGATGAATTCCAAT	FARMNSN	+++	+
4631	15582	TTCGCGAAAATAGGGTCCAAT	FAKIGSN	++	-
4632	15583	AGGTCCTCCAATTCCGCGTAT	RSSNSAY	+	-
4633	15584	TTCGCGAAATCCAATTCCAAT	FAKSNSN	+	-
4634	15585	TTTTCAAAGCAAAACCAAAAC	FSKQNQN	++	-
4635	15586	TACGCCAAGAACTCAAACATC	YAKNSNI	+	-
4636	15587	CGCTCAGGCACCATCTACCCC	RSGTIYP	+	-
4637	15588	TTTGCCCGCATCAACCAAAAC	FARINQN	+	-
4638	15589	ACCTCACATGGCCGCTCAGCC	TSHGRSA	+	-
4639	15590	TTCGCGAGGTATAATTCCAAT	FARYNSN	++	-
4640	15591	AATAATAGGGGGACGCAGGCG	NNRGTQA	+	-
4641	15592	TTCGCGAGGATGGGGGGGAAT	FARMGGN	+	-
4642	15593	TTTGCCCGCGCCAACTCAAAC	FARANSN	+	-
4643	15594	TTCGCGAGGGAGAATAAAAAT	FARENKN	+	-
4644	15595	TTCTCCAGGGGGGGGCAGAAT	FSRGGQN	+	-
4645	15596	TTCTCCAGGTCCAATGGGAAT	FSRSNGN	+	-
4646	15597	TTTTCACGCGGCAACGGCAAC	FSRGNGN	+	-
4647	15598	TACGCCCGCATGAACGGCAAC	YARMNGN	+	+
4648	15599	GGGATAATAAGGTCCCCGGTG	GIIRSPV	+	-
4649	15600	TGGAAAGAGCACGCGAAAAAT	WKEHAKN	++	-
4650	15601	TATTCCAAACCGAATACGAAT	YSKPNTN	+	-
4651	15602	TACGCCAAGCCCAACATCAAC	YAKPNIN	++	-
4652	15603	TTCGCGAAATTGGGGTCCAAT	FAKLGSN	+	-
4653	15604	GGCAAGGGCAACACCCTGTAC	GKGNTLY	+++	-
4654	15605	TTTTCACGCCCCGGCACCAAC	FSRPGTN	+	-
4655	15606	TTTGCCAAGGCCAACATGAAC	FAKANMN	++	-
4656	15607	TTCTCCAGGGCGGGGAATGAG	FSRAGNE	+	-
4657	15608	TTTAACGGCCGCGGCATCAAC	FNGRGIN	+	+
4658	15609	ACGCAGTATTCCTCCGGGTAT	TQYSSGY	+++	-
4659	15610	AATTTGAGGTCCAGGGGGGAG	NLRSRGE	+	++
4660	15611	CTGCATCGCAACATGACCGAC	LHRNMTD	+	-
4661	15612	GGGATAAGGAGGCAGGTGGAT	GIRRQVD	+	-
4662	15613	TTCGCGAAATATGGGGGGAAT	FAKYGGN	++	+
4663	15614	GCGGGGTCCACGTCCAGGGCG	AGSTSRA	+	-
4664	15615	AAAAGGTCCGCGGGGTTGGAT	KRSAGLD	+++	-
4665	15616	TTTTCAAAGTTTAACACCAAC	FSKFNTN	+	-
4666	15617	CACAAAAATGGGTCCGGGCAG	HKNGSGQ	++	-
4667	15618	TATGCGAAAATAAATCCGAAT	YAKINPN	++	-
4668	15619	AACCCCCGCAAGAACGAAATG	NPRKNEM	++	-

4669	15620	TTTGCCAAGCTGAACATCAAC	FAKLNIN	+	-
4670	15621	CAAGACACCAACAAGTACTGG	QDTNKYW	+	-
4671	15622	CATTCAATGAAGGTATCATAC	HSMKVSY	+	-
4672	15623	TGGTCCCCGGGGAGGCCGAAT	WSPGRPN	++	-
4673	15624	TTTTCAAAGAAGGGCGAAAAC	FSKKGEN	+	++
4674	15625	TTCTCCAAAGTGAATTCCAAT	FSKVNSN	+	+
4675	15626	ACCTACATCGGCAACAAGGCC	TYIGNKA	+	-
4676	15627	GAGGGGTCCTCCTGGAAAAAT	EGSSWKN	+	-
4677	15628	TACGCCCGCCATAACAACAAC	YARHNNN	+	-
4678	15629	AACTCAGGCAAGACCATGTAC	NSGKTMY	+	+
4679	15630	TTCGCGAAATTGAATCACAAT	FAKLNHN	+	++
4680	15631	TACGCCAAGTTTAACCTGAAC	YAKFNLN	+	-
4681	15632	TTTTCACGCGAAAACCGCAAC	FSRENRN	+	+++
4682	15633	ATGGGGCACTTGTCCTCCTAT	MGHLSSY	+	-
4683	15634	CGCGGCGGCATGTACACCGGC	RGGMYTG	++	++
4684	15635	TATGCGAAAGTGAATGTGAAT	YAKVNVN	++	-
4685	15636	ACCCGCGACGGCCGCGTAGCC	TRDGRVA	+	-
4686	15637	GCGAGGCAGGTGAAAGAGTTG	ARQVKEL	+	-
4687	15638	TTTGCCAAGTTTAACAACAAC	FAKFNNN	+	+
4688	15639	ACCAACGGCCATGGCCGCAAC	TNGHGRN	+++	-
4689	15640	TTTGCCAAGTACAACCAAAAC	FAKYNQN	+	-
4690	15641	TATGCGAGGTTCGGGGGGAAT	YARFGGN	+++	-
4691	15642	TACGCCAAGTTTGGCGGCAAC	YAKFGGN	+	-
4692	15643	TTTTCAAAGATCAACCTGAAC	FSKINLN	+	-
4693	15644	TACGCCCGCCATAACACCAAC	YARHNTN	++	-
4694	15645	TTCGCGAGGCCGAATGCGAAT	FARPNAN	+++	-
4695	15646	TATGCGAGGCACAATGGGAAT	YARHNGN	++	-
4696	15647	TTCGCGAAAGAGGGGTGTAAT	FAKEGCN	+	-
4697	15648	TTTGCCAAGCATAACAACAAC	FAKHNNN	++	-
4698	15649	TTTGCCAAGCATAACCTGAAC	FAKHNLN	+	-
4699	15650	TACAACAAGGGCATCCCCTAC	YNKGIPY	+	-
4700	15651	TTTTCAAAGTTTAACAACAAC	FSKFNNN	+	-
4701	15652	ACCGACAAGTACTCAACCTTT	TDKYSTF	+++	-
4702	15653	TTTGCCCGCGTAAACATCAAC	FARVNIN	+	-
4703	15654	TATATGTCCGAGACGTGGTCC	YMSETWS	++	-
4704	15655	TATATAAAAAATCAGAGGGAT	YIKNQRD	++	-
4705	15656	AACCAAGGCACCGTACGCTTT	NQGTVRF	+	-
4706	15657	TTTGCCCGCCCCAACGGCAAC	FARPNGN	+	-
4707	15658	TGGCAGGCGAAAGTGATGTCC	WQAKVMS	+	-
4708	15659	ATCCATGCCAAGCAACTGAAC	IHAKQLN	+	-
4709	15660	GTATCAGCCACCCGCTTTGGC	VSATRFG	+	-
4710	15661	TATTTGAAAAAAGATTTGTCC	YLKKDLS	+	-
4711	15662	GTGCACCCGGAGTATCACGCG	VHPEYHA	+	-
4712	15663	AAGGGCGGCGGCCATCCCTTT	KGGGHPF	+	-
4713	15664	TTCGCGAAACAGGGGGGGAAT	FAKQGGN	+	-

4714	15665	TTTTCAAAGATCAACGCCAAC	FSKINAN	+++	-
4715	15666	ATGAGGGGGCCGGTGTCCCCG	MRGPVSP	+	-
4716	15667	TTTGCCCGCATCAACCCCAAC	FARINPN	++	-
4717	15668	TTTGCCAAGTTTAACACCAAC	FAKFNTN	++	-
4718	15669	TCCATGAGGTCCCCGAATTCC	SMRSPNS	+	-
4719	15670	TTTGCCCGCATGGGCGAAAAC	FARMGEN	++	+++
4720	15671	TATACGAAAACGTCCCCGTCC	YTKTSPS	+	-
4721	15672	TTCTTGAAATCCAATACGGGG	FLKSNTG	+	+
4722	15673	AAGGCCAACGGCTCATACGCC	KANGSYA	+	-
4723	15674	TTCGCGAAAGATAATTATAAT	FAKDNYN	+	-
4724	15675	AAGGGCGACCCCCCCTGGGGC	KGDPPWG	+++	-
4725	15676	TTTGCCCGCAACAACATGAAC	FARNNMN	+	-
4726	15677	TACGCCGCCAAGTCAAACAAC	YAAKSNN	+++	-
4727	15678	TATAGGCCGGGGAAAAATGAG	YRPGKNE	++	-
4728	15679	TTTGCCCGCATGAACGGCAAC	FARMNGN	++	-
4729	15680	TTTGCCAAGGTAGGCGGCAAC	FAKVGGN	+	-
4730	15681	TTTGCCAAGATGAACGCCAAC	FAKMNAN	+	+
4731	15682	TACGCCAAGTACAACGACAAC	YAKYNDN	+	-
4732	15683	TTTGCCAAGTTTGGCGGCAAC	FAKFGGN	+	-
4733	15684	TTTTCAAAGCATGGCGGCAAC	FSKHGGN	+	-
4734	15685	AAGCCCTACCATAACGACATC	KPYHNDI	+	-
4735	15686	GTACAAGGCGTAGGCAAGAAC	VQGVGKN	++	-
4736	15687	TTTGCCCGCGTAAACTTTAAC	FARVNFN	++	-
4737	15688	TTCGCGAAATTGGGGGGGAAT	FAKLGGN	+	+
4738	15689	TTCGCGAAATATAATGGGAAT	FAKYNGN	++	-
4739	15690	CAGAAACAGAGGGAGATAGGG	QKQREIG	+	-
4740	15691	TTCGCGAAAATAGGGACGAAT	FAKIGTN	+	-
4741	15692	TTTGCCAAGGCCAACGTAAAC	FAKANVN	+	+
4742	15693	TTTGCCCGCCAAAACCCCAAC	FARQNPN	++	-
4743	15694	ACCAACCGCAACGACATCCGC	TNRNDIR	+	-
4744	15695	TATAAACACGGGCCGTTGGCG	YKHGPLA	+	-
4745	15696	ACCTCAGTAGGCACCCGCAAC	TSVGTRN	+	-
4746	15697	TTTGCCCGCGTAAACACCAAC	FARVNTN	++	-
4747	15698	GTAGCCAACTACGGCCGCGAC	VANYGRD	+	-
4748	15699	CACTCCAAAGGGACGAGGGAT	HSKGTRD	++	-
4749	15700	TTTTCACGCGTAAACCCCAAC	FSRVNPN	+	-
4750	15701	TTTGCCAAGACCAACGTAAAC	FAKTNVN	+	-
4751	15702	CGCGACGCCACCAACTACCCC	RDATNYP	++	-
4752	15703	AAATCCGGGGGGGTGGGGTAT	KSGGVGY	+	-
4753	15704	TTTGCCCGCATCAACGGCAAC	FARINGN	+++	-
4754	15705	TTTGCCAAGTTTAACGGCAAC	FAKFNGN	+	+
4755	15706	TGGAACAAGAACATCCATTCA	WNKNIHS	+	-
4756	15707	TTTGCCCGCCCCGGCGGCAAC	FARPGGN	+	-
4757	15708	TTCGCGAAAATAAATCACAAT	FAKINHN	+	-
4758	15709	GGGTTCACGAATTCCGTGTAT	GFTNSVY	+	-

4759	15710	TTTTCACGCCATAACTCAAAC	FSRHNSN	+++	-
4760	15711	TTTGCCAAGTTTAACATCAAC	FAKFNIN	+	-
4761	15712	TACAAGGGCTGGACCGCCGCC	YKGWTAA	++	-
4762	15713	AGGCCGTATACGGATATGGAT	RPYTDMD	+	-
4763	15714	TACGCCAAGATCAACTCAAAC	YAKINSN	+	-
4764	15715	TTTGCCAAGATCAACATGAAC	FAKINMN	+	-
4765	15716	TTCGCGAGGCCGGGGTCCAAT	FARPGSN	++	-
4766	15717	TACGCCAAGATCAACCATAAC	YAKINHN	++	-
4767	15718	AACGGCGACGGCGGCTCATAC	NGDGGSY	++	-
4768	15719	TTCGCGAGGCACAATCCGAAT	FARHNPN	++	-
4769	15720	TTTTCAAAGGGCGGCCAAAAC	FSKGGQN	++	+++
4770	15721	CGCGCCGGCGGCGCCTCAGGC	RAGGASG	+	-
4771	15722	CCGATAAAATCCCAGTCCGGG	PIKSQSG	+	-
4772	15723	TTCGCGAGGTATGGGGGGAAT	FARYGGN	+	-
4773	15724	TTTTCAAAGCCCGGCTTTAAC	FSKPGFN	+	-
4774	15725	CACTGGTCCGGGGCGAATCCG	HWSGANP	+	-
4775	15726	TTTTCAAAGTTTAACATCAAC	FSKFNIN	+	-
4776	15727	AATTGGGGGAATAAATCCGAT	NWGNKSD	+	-
4777	15728	TTTGCCCGCTTTAACTCAAAC	FARFNSN	+++	-
4778	15729	TACCAAGCCTCAATGGCCAAC	YQASMAN	+	-
4779	15730	TTTGCCAAGATCAACTTTAAC	FAKINFN	+	+
4780	15731	TACTCACGCCCCAACGGCAAC	YSRPNGN	+++	-
4781	15732	ATAAAAGGGTATGGGTTGGAT	IKGYGLD	+	-
4782	15733	TTTTCAAAGCTGTCACAACAA	FSKLSQQ	+	-
4783	15734	TTCGCGAAAATAGGGGATAAT	FAKIGDN	+++	-
4784	15735	TTCGCGAGGCACAATTTCAAT	FARHNFN	++	-
4785	15736	TTCTCCAAAATAAATTCCAAT	FSKINSN	++	-
4786	15737	TTCGCGAAACCGGGGATAAAT	FAKPGIN	++	-
4787	15738	TATTCCAAATGGAATCCGAAT	YSKWNPN	+	+++
4788	15739	TTTTCAAAGTGGAACCAAAAC	FSKWNQN	++	+++
4789	15740	TGGACGCCGTCCGCGTATTCC	WTPSAYS	+	-
4790	15741	GACCCCCGCTCACGCGCCTCA	DPRSRAS	++	+
4791	15742	TTCGCGAGGAAAAATGAGAAT	FARKNEN	+	-
4792	15743	TACATGGTACGCACCGGCGGC	YMVRTGG	++	+
4793	15744	TTTGCCAAGTTTAACCAAAAC	FAKFNQN	++	-
4794	15745	GGCTACAAGGGCACCATGCCC	GYKGTMP	++	+
4795	15746	TTTGTAGGCGGCCCCATGACC	FVGGPMT	+	-
4796	15747	CAATCACTGAAGGGCGCCGGC	QSLKGAG	+	-
4797	15748	CTGCTGCGCGAAGGCGACTGG	LLREGDW	+	-
4798	15749	TTCGCGAGGCCGAATTCCAAT	FARPNSN	++	-
4799	15750	TACAAGTCAGCCTCACCCAAC	YKSASPN	+	-
4800	15751	TTTTCAAAGCCCAACGCCAAC	FSKPNAN	+	-
4801	15752	GAACATGGCCGCGGCCATGAC	EHGRGHD	+	-
4802	15753	GGCCAAGTACGCACCCCCACC	GQVRTPT	+	-
4803	15754	TATATAGCGGGGCCGGTGAAA	YIAGPVK	++	-

4804	15755	TGGCATACCTCAATCCCCAAC	WHTSIPN	++	-
4805	15756	GATAAAGGGAAAGGGATGTAT	DKGKGMY	+	-
4806	15757	CATCGCTCATGGGGCGACGCC	HRSWGDA	+	-
4807	15758	TTCGCGAAAAATAATTTGAAT	FAKNNLN	+	-
4808	15759	TTCTCCAGGAAAGGGGATAAT	FSRKGDN	+++	-
4809	15760	TGGCGCAACGGCGAAGCCAAC	WRNGEAN	+	-
4810	15761	CACGGGCACGGGACGTATACG	HGHGTYT	+	-
4811	15762	AATTCCAAAGTGGGGAGGGAT	NSKVGRD	+	-
4812	15763	TTTGCCAAGCATAACGCCAAC	FAKHNAN	+	-
4813	15764	TTTGCCCGCCCCAACACCAAC	FARPNTN	+	-
4814	15765	CGCTCAACCGGCGGCGCCGGC	RSTGGAG	+	++
4815	15766	TATGGGTCCGGGACGCAGTAT	YGSGTQY	+	-
4816	15767	CAGGGGTCCACGAATTCCTAT	QGSTNSY	++	-
4817	15768	TACAACAACACCTCAATGCGC	YNNTSMR	++	-
4818	15769	AATAATTATGGGTCCCCGGGG	NNYGSPG	+	+
4819	15770	TTCGCGAAAAATAATGGGAAT	FAKNNGN	+	-
4820	15771	TACGTATCATACCAAGTAAAC	YVSYQVN	+	-
4821	15772	GAGATGAAACACGGGCACATG	EMKHGHM	+	-
4822	15773	GTGAGGGCGAATCACACGAAT	VRANHTN	+	-
4823	15774	TATAGGCCGGGGGCGCACGCG	YRPGAHA	+	-
4824	15775	TTCGCGAGGAATAATGATAAT	FARNNDN	++	-
4825	15776	TACCAACGCGACGTAATGCAA	YQRDVMQ	+	-
4826	15777	TGGCGCTCAGCCGCCGTACCC	WRSAAVP	++	-
4827	15778	TTTGCCAAGTACGGCGACAAC	FAKYGDN	+	-
4828	15779	TATGCGAGGGAGAATTTCAAT	YARENFN	++	-
4829	15780	TGTAAAAATGTGACGGCGGAG	CKNVTAE	+	-
4830	15781	CTGAAGTCACGCATCATCGAA	LKSRIIE	++	-
4831	15782	TTCTCCAAATTCAATGATAAT	FSKFNDN	+	-
4832	15783	ATGCAACCCTACGGCTCAGGC	MQPYGSG	+	-
4833	15784	TTCGCGAGGCCGAATTTGAAT	FARPNLN	+	-
4834	15785	TACTCACGCCCCGGCGACAAC	YSRPGDN	+++	-
4835	15786	TTCTCCAAACCGGGGAATAAT	FSKPGNN	+	-
4836	15787	TATAATAAAACGGGGGCGAAT	YNKTGAN	+	-
4837	15788	TTCGCGAAATATGGGGAGAAT	FAKYGEN	+	-
4838	15789	TTTGCCAAGCATAACTTTAAC	FAKHNFN	+++	++
4839	15790	TTTGCCCGCCCCGGCATCAAC	FARPGIN	+	-
4840	15791	TTCTCCAGGGGGGGGGAGAAT	FSRGGEN	++	-
4841	15792	CCGGATATAAATAAAAGGTCC	PDINKRS	+	-
4842	15793	AATGCGAAATATTCCGGGGAG	NAKYSGE	+	-
4843	15794	TTTTCACGCCCCAACGTAAAC	FSRPNVN	+	-
4844	15795	TATGCGAAAGTGAATTTGAAT	YAKVNLN	+	-
4845	15796	CGCGGCGACGTACAAGCCTGG	RGDVQAW	++	-
4846	15797	TTTGCCAAGATCAACAACAAC	FAKINNN	+	++
4847	15798	TTCGCGAAAAATGGGGAGAAT	FAKNGEN	+	-
4848	15799	TACTCAAAGACCAACGGCAAC	YSKTNGN	++	-

4849	15800	CTGAACATCAACTTTCATGGC	LNINFHG	+	-
4850	15801	TCCTATCACGATATGAGGGAT	SYHDMRD	+++	-
4851	15802	TTTTCAAAGCCCAACGTAAAC	FSKPNVN	+	-
4852	15803	TTTGCCAAGAACAACATGAAC	FAKNNMN	+	-
4853	15804	TTTGCCAAGTGGAACGAAAAC	FAKWNEN	++	-
4854	15805	AACGTAAAGGGCACCACCTAC	NVKGTTY	++	-
4855	15806	TTGACGTATGGGGATAGGTCC	LTYGDRS	+	-
4856	15807	AAATCCTCCTCCATGGGGGTG	KSSSMGV	+	-
4857	15808	TCAGTATACGGCGGCGCCGGC	SVYGGAG	+	-
4858	15809	TTCGCGAAAGTGAATCCGAAT	FAKVNPN	+	-
4859	15810	TTTTCACGCGACAACGCCAAC	FSRDNAN	++	-
4860	15811	TTCGCGAGGCCGGGGTATAAT	FARPGYN	+	-
4861	15812	TATGCGAGGGAGAATCCGAAT	YARENPN	++	-
4862	15813	AACATGAACAACTCATACTCA	NMNNSYS	+	-
4863	15814	ACCTCATACGGCCAAGGCTCA	TSYGQGS	+++	-
4864	15815	TTTGCCCGCCATGGCACCAAC	FARHGTN	+++	-
4865	15816	TTCTCCAAACCGAATTGGAAT	FSKPNWN	+	-
4866	15817	TCACGCGACAACCAACATTGG	SRDNQHW	++	-
4867	15818	TATTCCAATTTCTCCCACTCC	YSNFSHS	++	-
4868	15819	ACCAAGTCAGGCGACAAGGCC	TKSGDKA	+	-
4869	15820	CGCGACGGCCGCGACTCAGTA	RDGRDSV	+	-
4870	15821	CGCTCACATGCCGGCTCAGAC	RSHAGSD	+	-
4871	15822	TACCTGCTGAACTCACATTCA	YLLNSHS	++	-
4872	15823	AATGTGTTGGGGGTGCCGGTG	NVLGVPV	+	-
4873	15824	TTTGCCAAGATGAACCAAAAC	FAKMNQN	+	-
4874	15825	TACGCCAAGAACAACGACAAC	YAKNNDN	++	-
4875	15826	TTTGCCAAGCATAACACCAAC	FAKHNTN	+++	-
4876	15827	TTCTCCAGGTTCAATGGGAAT	FSRFNGN	++	-
4877	15828	TACGCCAAGATCAACCAAAAC	YAKINQN	+	-
4878	15829	TTTGCCAAGACCAACGACAAC	FAKTNDN	+	-
4879	15830	CATGGCAAGACCTCACGCGAA	HGKTSRE	+	-
4880	15831	TACTCAAAGCCCAACTCAAAC	YSKPNSN	+	-
4881	15832	ACCCCCATGTCAACCCATTTT	TPMSTHF	+	-
4882	15833	CTGTCACAAACCGTATCATAC	LSQTVSY	+	-
4883	15834	CGCCGCGCCGAACCCCAATCA	RRAEPQS	++	-
4884	15835	TACTCAAAGCCCGGCTGGAAC	YSKPGWN	+	+
4885	15836	TACGCCAAGTTTGGCAACAAC	YAKFGNN	+	-
4886	15837	TTCGCGAAACCGGGGTTGAAT	FAKPGLN	+	-
4887	15838	TCCAAAACGACGACGCAGTAT	SKTTTQY	+	-
4888	15839	ATGAAAAATGTGTCCAATTTC	MKNVSNF	+	-
4889	15840	TATCACAGGTCCCACGAGTTG	YHRSHEL	+	-
4890	15841	CGCATCACCGGCTCATCAACC	RITGSST	+	-
4891	15842	TTTTCACGCCCCGGCTCAAAC	FSRPGSN	++	+++
4892	15843	CTGGCCTCAAACGGCGTAAAC	LASNGVN	++	-
4893	15844	TTTGCCAAGATCAACCAAAAC	FAKINQN	+	-

4894	15845	TTCGCGAGGGAGGGGACGAAT	FAREGTN	++	-
4895	15846	GTGATGACGAGGAATGAGTGG	VMTRNEW	+	-
4896	15847	TTTGCCAAGGTAAACATCAAC	FAKVNIN	++	-
4897	15848	TTTGCCAAGAAGAACGACAAC	FAKKNDN	++	-
4898	15849	TTCTCCAGGATGGGGACGAAT	FSRMGTN	+	-
4899	15850	TACGCCAAGTTTGGCATCAAC	YAKFGIN	+	-
4900	15851	AACACCGACTACGGCTACGCC	NTDYGYA	+	-
4901	15852	AAGCATGCCAACATCATCGGC	KHANIIG	+	-
4902	15853	AACACCCGCATGACCGGCGCC	NTRMTGA	++	-
4903	15854	TTTGCCAAGAAGAACGAAAAC	FAKKNEN	+	-
4904	15855	CACTCCAGGAATTATACGGAT	HSRNYTD	+	-
4905	15856	TTCGCGAAACACGGGACGAAT	FAKHGTN	++	-
4906	15857	TTTGCCAAGATCAACGCCAAC	FAKINAN	+	-
4907	15858	TACGCCAAGGACGGCCTGAAC	YAKDGLN	+	-
4908	15859	TTTGCCAAGATCAACCCCAAC	FAKINPN	+	-
4909	15860	GGCCGCATGGAAAAGTCAACC	GRMEKST	+	-
4910	15861	TATGCGAAAGATGGGACGAAT	YAKDGTN	+	-
4911	15862	TTTGCCAAGCCCGGCGGCAAC	FAKPGGN	+	-
4912	15863	TGGACCAAGTCAAACACCGCC	WTKSNTA	+	-
4913	15864	ATAAGGAATATAACGGGGGAG	IRNITGE	+++	-
4914	15865	TGGACGAAAGCGAATGATCAC	WTKANDH	+	-
4915	15866	TATGCGAAAGATAATCCGAAT	YAKDNPN	+	-
4916	15867	TTTGCCCGCGACAACCATAAC	FARDNHN	+++	-
4917	15868	TCACCCACCGGCCGCGCCGCC	SPTGRAA	+	-
4918	15869	GGGGTGTCCAATATGATGGTG	GVSNMMV	++	-
4919	15870	GGCGACAACAAGCCCAACTGG	GDNKPNW	+	-
4920	15871	ATCATGGTACGCGACACCAAG	IMVRDTK	++	-
4921	15872	TTGGAGTCCTCCAGGGGGTAT	LESSRGY	++	-
4922	15873	TTCTCCAAACCGGGGCAGAAT	FSKPGQN	+	-
4923	15874	TCCAGGGGGTTGAATCCGTCC	SRGLNPS	++	-
4924	15875	ATCGCCGGCCTGAACAAGGCC	IAGLNKA	+++	-
4925	15876	AAGGTAAACGGCGGCTCAGGC	KVNGGSG	+	-
4926	15877	GTATCAAACAACATCCGCGGC	VSNNIRG	+	-
4927	15878	TCATCAAAGGGCACCAACGCC	SSKGTNA	+	+
4928	15879	TTTTCACGCGACGGCGTAAAC	FSRDGVN	+	-
4929	15880	TTTTCAAAGCCCAACATGAAC	FSKPNMN	+	-
4930	15881	TTCGCGAAAGATAATATAAAT	FAKDNIN	+	-
4931	15882	ACCAAGCATGGCGCCGACGTA	TKHGADV	+	-
4932	15883	GATCAGAATAAAAATACGTGG	DQNKNTW	+	-
4933	15884	TACTCAAAGGAAAACGTAAAC	YSKENVN	+	-
4934	15885	CATGGCCCCAACTCATACGGC	HGPNSYG	++	-
4935	15886	GGCAACTCAAACACCGCCCAT	GNSNTAH	+	-
4936	15887	CATTACGGCGACAAGTACCAA	HYGDKYQ	+	-
4937	15888	TATAGGTCCACGGTGGCGGAT	YRSTVAD	+	-
4938	15889	TTCTCCAGGAATAATCCGAAT	FSRNNPN	+	++

4939	15890	TACCGCCCCGGCTCAGGCGAC	YRPGSGD	+	-
4940	15891	AACAAGACCTGGGGCGACGCC	NKTWGDA	+	-
4941	15892	ACCGGCACCAACACCACCTAC	TGTNTTY	+++	-
4942	15893	GAAGCCCCCGCCAACCGCAAC	EAPANRN	++	-
4943	15894	TTCTCCAAAGAGGGGATGAAT	FSKEGMN	+	-
4944	15895	GGGGATGAGTCCAGGTATTAT	GDESRYY	+	-
4945	15896	TTTTCACGCCATAACATGAAC	FSRHNMN	+++	-
4946	15897	TACCTGAACAAGTCATACGAC	YLNKSYD	+	-
4947	15898	TTCTCCAAACCGGGGACGAAT	FSKPGTN	+	-
4948	15899	TTTGCCAAGTTTAACGAAAAC	FAKFNEN	++	-
4949	15900	TTTTCAAAGCCCAACAACAAC	FSKPNNN	+	-
4950	15901	GGCTTTCGCGGCGACGGCGCC	GFRGDGA	+	-
4951	15902	TTTGCCCGCCATAACATGAAC	FARHNMN	+++	-
4952	15903	TACTCAGGCTCATCATACGCC	YSGSSYA	+	-
4953	15904	TGGTTGAAACACGAGGCGTCC	WLKHEAS	+	-
4954	15905	TTTGCCAAGCCCGGCATGAAC	FAKPGMN	+	-
4955	15906	AAAACGGAGTCCGATAATAGG	KTESDNR	+	-
4956	15907	GTGAAAAGGTCCGAGCCGATA	VKRSEPI	+++	-
4957	15908	TTTTCACGCGACAACCAAAAC	FSRDNQN	+	-
4958	15909	TTTTCACGCCCCGGCCAAAAC	FSRPGQN	++	+++
4959	15910	TTTGCCCGCGACAACGCCAAC	FARDNAN	+	-
4960	15911	TATTATAAAAATGGGGCGGCG	YYKNGAA	+++	+
4961	15912	TTCGCGAGGGAGAATTGGAAT	FARENWN	+	-
4962	15913	TTCTCCAAACCGGGGTGGAAT	FSKPGWN	++	-
4963	15914	TTTGCCAAGGACAACGCCAAC	FAKDNAN	+++	-
4964	15915	AAGCCCAACGGCTACCCCGCC	KPNGYPA	+	-
4965	15916	TTCGCGAAATTGGGGGAGAAT	FAKLGEN	+	-
4966	15917	TTCGCGAAAGATGGGGAGAAT	FAKDGEN	+	-
4967	15918	TTCGCGAGGGAGAATGATAAT	FARENDN	+	-
4968	15919	CGCAAGTCAGAAACCGGCGGC	RKSETGG	+	-
4969	15920	CGCAACGAAGGCGCCGCCGGC	RNEGAAG	+	-
4970	15921	TTCGCGAAAGATGGGTCCAAT	FAKDGSN	+	-
4971	15922	TGGGAAAACAAGCAAGCCTGG	WENKQAW	+	-
4972	15923	TTCTCCAAAGATAATCAGAAT	FSKDNQN	+	-
4973	15924	GACGGCGGCCGCGGCCGCGAC	DGGRGRD	+++	-
4974	15925	TTTTCAAAGTACAACCCCAAC	FSKYNPN	++	-
4975	15926	TTTTCACGCCGCGGCGACAAC	FSRRGDN	+++	-
4976	15927	TTCTCCAAATTCGGGCACAAT	FSKFGHN	+++	-
4977	15928	TATTCCAGGTATGGGCCGAAT	YSRYGPN	+	-
4978	15929	TTCGCGAGGTTCAATAATAAT	FARFNNN	+++	-
4979	15930	TTTGCCCGCTTTAACGCCAAC	FARFNAN	+++	-
4980	15931	TATTCCAAATGGGGGCAGAAT	YSKWGQN	+	-
4981	15932	TATTCCAAATGGAATGGGAAT	YSKWNGN	+++	-
4982	15933	TTTTCACGCTACAACCAAAAC	FSRYNQN	++	-
4983	15934	TACGCCCGCCCCAACTACAAC	YARPNYN	++	-

4984	15935	TATTCCAGGAGGAATGAGAAT	YSRRNEN	+++	-
4985	15936	TTTTCAAAGGCCAACTGGAAC	FSKANWN	+	-
4986	15937	TTCGCGAGGGAGAATTATAAT	FARENYN	+	-
4987	15938	TACGCCCGCTTTGGCAACAAC	YARFGNN	+	-
4988	15939	TTTTCACGCCCCGGCTTTAAC	FSRPGFN	++	-

NT SEQ ID#	AA SEQ ID#	NT sequence	AA_sequence	Mixed BBB	hCME	mBMVEC_mSCMV_log2_Enr/v
5424	16375	TTTGCCCGCCGCGGCGAAAAC	FARRGEN	+++	-	-
5223	16174	TTTGCCAAGGGCAACTGGAAC	FAKGNWN	+++	-	-
5604	16555	TACGCCAAGGAAAACCTGAAC	YAKENLN	+++	-	-
5152	16103	TACGCCCGCGGCGGCCAAAAC	YARGGQN	+++	-	-
4999	15950	TATTCCAGGCACGGGGCGAAT	YSRHGAN	+++	-	-
5558	16509	TTTTCAAAGACCAACCAAAAC	FSKTNQN	+++	-	-
5489	16440	AATGCGAGGGATATAAGGTAT	NARDIRY	+++	-	-
5550	16501	TTTTCACGCGAAAACTCAAAC	FSRENSN	+++	-	-
5501	16452	TTTGCCAAGATCAACTACAAC	FAKINYN	+++	-	-
5555	16506	TATTCCAGGGATGGGGAGAAT	YSRDGEN	+++	-	-
5357	16308	CGCCGCGACGGCGTAAACGCC	RRDGVNA	+++	-	-
5310	16261	TTCTCCAGGATAAATCACAAT	FSRINHN	+++	-	-
5445	16396	TTCGCGAAATCCAATGCGAAT	FAKSNAN	+++	-	--
5292	16243	AGGGGGGATCACGCGGGGTTC	RGDHAGF	+++	-	-
5060	16011	CCGGCGTCCACGAATGGGGTG	PASTNGV	+++	-	-
5300	16251	TTCGCGAAACCGAATTGGAAT	FAKPNWN	+++	-	-
5520	16471	TTCTCCAGGGGGGGGGGAAT	FSRGGGN	+++	-	-
5319	16270	CTGTGGCGCAACGCCGAAAAC	LWRNAEN	+++	-	-
5243	16194	CGCGACTCACAAACCACCTGG	RDSQTTW	+++	-	-
5559	16510	TTCTCCAGGCCGAATGAGAAT	FSRPNEN	+++	-	-
5286	16237	CTGTCACGCAACAACGAAAAC	LSRNNEN	+++	-	-
5285	16236	TACTCACGCCCCGGCTCAAAC	YSRPGSN	+++	-	-
5070	16021	CAGGTGTCCACGAATGGGATA	QVSTNGI	+++	-	-
5504	16455	TTTTCAAAGGTAAACAACAAC	FSKVNNN	+++	-	-
5366	16317	TTCGCGAAATTGGGGCACAAT	FAKLGHN	+++	-	-
5054	16005	TATGCGAGGATAGGGTTGAAT	YARIGLN	+++	-	-
5071	16022	TACTCAAAGAACGGCATGAAC	YSKNGMN	+++	-	-
5443	16394	GACCAATCATCAACCACCTGG	DQSSTTW	+++	-	-
5386	16337	TATACGAGGGTGGATTCCAAT	YTRVDSN	+++	-	-
5232	16183	TTCGCGAGGGTGGGGTTCAAT	FARVGFN	+++	-	-
5416	16367	TACGCCCGCCATAACATCAAC	YARHNIN	+++	-	-
5474	16425	AAAGCGGATTCCTCCAGGTAT	KADSSRY	+++	-	-

5239	16190	TACTCAAAGGTAAACAACAAC	YSKVNNN	+++	-	-
5220	16171	TATGAGTCCGGGCCGATGAGG	YESGPMR	+++	-	-
5020	15971	TTTTCAAAGATCGGCTTTAAC	FSKIGFN	+++	-	--
5603	16554	GTACGCATCGACCAAGCCCAA	VRIDQAQ	+++	-	-
5317	16268	TTTGCCCGCCTGAACACCAAC	FARLNTN	+++	-	-
5136	16087	TACTCAAAGCTGGGCGGCAAC	YSKLGGN	+++	-	-
5283	16234	TCCTATTCCTCCAATGGGGTG	SYSSNGV	+++	-	-
5340	16291	GGCGACAAGGTAATCCGCTAC	GDKVIRY	+++	-	-
5234	16185	TTCTCCAGGATGGGGGTGAAT	FSRMGVN	+++	-	-
5263	16214	TCAATGACCGGCACCTCATAC	SMTGTSY	+++	-	-
5602	16553	TTTTCAAAGATCAACGACAAC	FSKINDN	+++	-	-
5401	16352	TTCTCCAAAACGAATCACAAT	FSKTNHN	+++	-	-
5027	15978	CACCAGTCCTCCAATGGGGTG	HQSSNGV	+++	-	-
5211	16162	TATGCGAAATATGGGTTCAAT	YAKYGFN	+++	-	-
5344	16295	AACTCACGCCTGAACGACAAC	NSRLNDN	+++	-	-
5077	16028	CTGGCCAAGGCCGGCGCCAAC	LAKAGAN	+++	-	-
5205	16156	TTTGCCAAGTCAGGCTCAAAC	FAKSGSN	+++	-	-
5466	16417	TATTCCAAAGATGGGAGGAAT	YSKDGRN	+++	-	-
5581	16532	GTAGTAGCCATGCATAAGCAA	VVAMHKQ	+++	-	-
5407	16358	TATATAAGGGGGAATACGAAT	YIRGNTN	+++	-	-
5331	16282	TTTTCAAAGTCAAACCATAAC	FSKSNHN	+++	-	-
5480	16431	TATTGGGGGGGGGAGAAACAG	YWGGEKQ	+++	-	-
5355	16306	TACTCACGCCCCGGCCAAAAC	YSRPGQN	+++	-	-
5295	16246	TACGCCAAGCTGAACGACAAC	YAKLNDN	+++	-	-
5248	16199	GTAGGCTCAATCAACGGCATC	VGSINGI	+++	-	-
5341	16292	TATGCGAAATATAATTTGAAT	YAKYNLN	+++	-	-
5320	16271	TTTGCCAAGACCGGCTCAAAC	FAKTGSN	+++	-	-
5122	16073	ACGAGGTCCGGGTTGAATGCG	TRSGLNA	+++	-	-
5052	16003	TACGCCAAGGCCAACTTTAAC	YAKANFN	+++	-	-
5368	16319	TTTGCCAAGCATGGCTCAAAC	FAKHGSN	+++	-	-
5433	16384	CAAGAATACGGCGGCTACCAA	QEYGGYQ	+++	-	-
5297	16248	TATTCCAGGCCGAATCCGAAT	YSRPNPN	+++	-	-
5088	16039	TTCGCGAAATCCGGGCAGAAT	FAKSGQN	+++	-	-

5349	16300	TATGCGTTGAAAGGGATGAAT	YALKGMN	++	-	-
5169	16120	TTCGCGAGGCAGGGGTTCAAT	FARQGFN	++	-	-
5199	16150	TACGCCAAGGCCAACGCCAAC	YAKANAN	++	-	--
5461	16412	TTCGCGAGGCAGAATGGGAAT	FARQNGN	++	-	-
5383	16334	TTTTCAAAGTCAAACAACAAC	FSKSNNN	++	-	-
5487	16438	TACGCCAAGCCCAACTCAAAC	YAKPNSN	++	-	-
5326	16277	TCACGCAACGGCGGCAACGCC	SRNGGNA	++	-	-
5468	16419	AGGGATCACATGGCGAGGGGG	RDHMARG	++	-	-
5015	15966	TACGCCAAGCAAGGCCATAAC	YAKQGHN	++	-	-
5542	16493	TTTGCCAAGATCGGCGGCAAC	FAKIGGN	++	-	-
5502	16453	ATCGGCTACTCAGGCGCCGAC	IGYSGAD	++	-	-
5512	16463	TTCTCCAAACCGAATTCCAAT	FSKPNSN	++	-	-
5019	15970	TTCTCCAGGGTGGGGTTCAAT	FSRVGFN	++	-	-
5365	16316	TTCGCGAGGATAAATATGAAT	FARINMN	++	-	-
5025	15976	TATTCCAAACAGGGGAATAAT	YSKQGNN	++	-	-
5556	16507	TACAACCAAAACACCTACAAG	YNQNTYK	++	-	-
5464	16415	TTCGCGAGGTTGAATGATAAT	FARLNDN	++	-	-
5049	16000	GCGATGTCCACGAATGGGAGG	AMSTNGR	++	-	-
5500	16451	ATAGTGAATTCCAGGAATTCC	IVNSRNS	++	-	-
5546	16497	TTCGCGAAATCCAATACGAAT	FAKSNTN	++	-	-
5577	16528	CGCCCCACCGGCCCCAACGGC	RPTGPNG	++	-	-
5062	16013	TATTCCAAAACGGGGCCGAAT	YSKTGPN	++	-	-
5607	16558	TACGCCAAGGACAACCAAAAC	YAKDNQN	++	-	-
5459	16410	TTCGCGAAAATGAATCCGAAT	FAKMNPN	++	-	-
5410	16361	TTCGCGAGGATAGGGGAGAAT	FARIGEN	++	-	-
5427	16378	TACTCAAAGGAAGGCTACAAC	YSKEGYN	++	-	-
5048	15999	TATGCGAGGCAGAATGCGAAT	YARQNAN	++	-	-
5104	16055	TACTCACGCCAAGGCGGCAAC	YSRQGGN	++	-	-
5571	16522	TTTTCACGCGACGGCCATAAC	FSRDGHN	++	-	-
5361	16312	TTCGCGAAACACAATATAAAT	FAKHNIN	++	-	-
5568	16519	TATATGAGGAATACGGTGCCG	YMRNTVP	++	-	-
5265	16216	TACTCACGCGAAGGCTACAAC	YSREGYN	++	-	-
5552	16503	TATGCGAAAATGAATGAGAAT	YAKMNEN	++	-	-

5467	16418	TTGTATGGGGGGACGAATCCG	LYGGTNP	++	-	-
5314	16265	TATAATGCGGTGATAATGAAA	YNAVIMK	++	-	-
4990	15941	TATTCCAAAATAAATATAAAT	YSKININ	++	-	-
5032	15983	TATGCGAGGTCCAATTCCAAT	YARSNSN	++	-	-
5083	16034	TTCTCCAGGATAGGGGAGAAT	FSRIGEN	++	-	-
5371	16322	GGCCCCGGCATCTCAAAGTAC	GPGISKY	++	-	-
5469	16420	AGGCCGTATGGGGGGTCCGAT	RPYGGSD	++	-	-
5600	16551	TACTCAAAGTTTGGCGTAAAC	YSKFGVN	++	-	-
5148	16099	TATGCGAAAAATGGGGATAAT	YAKNGDN	++	-	-
5126	16077	TATTCCAGGATGAATGAGAAT	YSRMNEN	++	-	-
5573	16524	TTCGCGAAACAGGGGGATAAT	FAKQGDN	++	-	-
5008	15959	TTCGCGAGGACGGGGCACAAT	FARTGHN	++	-	-
5579	16530	AACTCAGACCGCGGCAAGAAC	NSDRGKN	++	-	-
5138	16089	CTGGCCAAGCATGGCGTAAAC	LAKHGVN	++	-	-
5012	15963	TACGCCCGCCAAAACTTTAAC	YARQNFN	++	-	–
5034	15985	GGGTCCTCCACGTCCATATGG	GSSTSIW	++	-	-
5605	16556	TTTGCCCGCCCCAACCATAAC	FARPNHN	++	-	-
5176	16127	TCCGCGTCCACGAATGGGGTG	SASTNGV	++	-	-
5217	16168	TCAAACACCGGCCGCAACGCC	SNTGRNA	++	-	-
5491	16442	TACTCACGCGGCGACCATAAC	YSRGDHN	++	-	-
5548	16499	TTTGCCAAGGCCGGCGGCAAC	FAKAGGN	++	-	-
5463	16414	AGGTCCTCCGGGACGCCGGCG	RSSGTPA	++	-	-
5063	16014	TATTCCAAAATGAATGATAAT	YSKMNDN	++	-	-
5471	16422	GTAAACATGGGCAAGGCCTAC	VNMGKAY	++	-	-
5590	16541	TTCGCGAAAGAGAATTCCAAT	FAKENSN	++	-	-
5372	16323	AACACCGTAAACACCATGCGC	NTVNTMR	++	-	-
5016	15967	CTGCATAAGTCAGGCATGAAC	LHKSGMN	++	-	-
5091	16042	TATATGTCCACGAATGGGGTG	YMSTNGV	++	-	-
5388	16339	CACTCCAGGTTGACGGATAAT	HSRLTDN	++	-	-
5578	16529	TGGTCAGGCGGCTCAGGCGGC	WSGGSGG	++	-	-
5185	16136	TACTCAAAGTCAGGCGACAAC	YSKSGDN	++	-	-
5255	16206	TACTACTCATCAAACGGCGTA	YYSSNGV	++	-	-
5184	16135	GACTACACCGGCAAGTCAGCC	DYTGKSA	++	-	-

5010	15961	TTGTCCAAAGTGGGGCAGAAT	LSKVGQN	++	-	-
5453	16404	TTCGCGAAAATGAATTTCAAT	FAKMNFN	++	-	-
5045	15996	TACTCAAAGGTAGGCCAAAAC	YSKVGQN	++	-	-
5356	16307	TTTTCAAAGGGCAACACCAAC	FSKGNTN	++	-	-
5005	15956	TATTCCAAAGCGGGGTCCAAT	YSKAGSN	++	-	-
5137	16088	TTCTCCAGGGTGGGGGAGAAT	FSRVGEN	++	-	-
5039	15990	TTCGCGAGGTCCGGGTCCAAT	FARSGSN	++	-	-
5183	16134	GTACATTCAACCAACGGCATC	VHSTNGI	++	-	-
5390	16341	TTGCACGATTCCAGGACGTAT	LHDSRTY	++	-	-
5042	15993	TTCGCGAGGGAGAATAGGAAT	FARENRN	++	-	-
5253	16204	ATGTACGGCGGCGTAAACCCC	MYGGVNP	++	-	-
5099	16050	TTGTCCAAAGTGGCGGTGAAT	LSKVAVN	++	-	-
5315	16266	TACGCCCGCCCCAACGTAAAC	YARPNVN	++	-	-
5523	16474	TTCTCCAAAACGAATACGAAT	FSKTNTN	++	-	-
5442	16393	TACTCAAAGATCAACGGCAAC	YSKINGN	++	-	-
5259	16210	TACGCCCGCATGAACATGAAC	YARMNMN	++	-	-
4994	15945	TATGCGAAATCCGGGTATAAT	YAKSGYN	++	-	-
5261	16212	TATGCGAGGAATAATGATAAT	YARNNDN	++	-	-
5282	16233	CCGTTGTCCACGAATGGGGTG	PLSTNGV	++	-	-
5087	16038	TACGCCAAGAACGGCTTTAAC	YAKNGFN	++	-	-
5222	16173	TTCGCGAAAACGGGGGCGAAT	FAKTGAN	++	-	-
5569	16520	TATGAGAAATATACGAATTCC	YEKYTNS	++	-	-
5432	16383	TTTGCCAAGCTGGGCAACAAC	FAKLGNN	++	-	-
5363	16314	AACCGCTCAGGCATGGCCGCC	NRSGMAA	++	-	-
5531	16482	TTCGCGAAAATGAATACGAAT	FAKMNTN	++	-	-
5058	16009	TACGCCAAGGCCGGCCATAAC	YAKAGHN	++	-	-
5024	15975	TTGTCCAAAGCGAATGTGAAT	LSKANVN	++	-	-
5316	16267	CTGGCCCGCCCCGGCAACAAC	LARPGNN	++	-	-
5108	16059	GTGTATTCCACGAATGGGATA	VYSTNGI	++	-	-
5180	16131	TATGCGAGGTTGAATGAGAAT	YARLNEN	++	-	-
5103	16054	ATCATCTCAACCAACGGCGTA	IISTNGV	++	-	-
5532	16483	AAGGCCGACCGCAACCCCTAC	KADRNPY	++	-	-
5488	16439	TACGCCCGCTACAACCAAAAC	YARYNQN	++	-	-

5328	16279	TTTGCCAAGCAAGGCAACAAC	FAKQGNN	++	-	-
5515	16466	TTCGCGAGGATAAATGATAAT	FARINDN	++	-	-
5470	16421	TTCGCGAGGATAAATATAAAT	FARININ	++	-	-
5540	16491	TTCGCGAAACACAATGGGAAT	FAKHNGN	++	-	-
5473	16424	TTCGCGAAATTCGGGAATAAT	FAKFGNN	++	-	-
5323	16274	GGGCCGGTGCACGTGAATTAT	GPVHVNY	++	-	-
5377	16328	ACCCGCTCAGGCGGCTCACCC	TRSGGSP	++	-	-
5447	16398	TTCGCGAGGATGGGGGATAAT	FARMGDN	++	-	-
5096	16047	TACGCCAAGGGCGGCCTGAAC	YAKGGLN	++	-	-
5277	16228	TTCGCGAGGATAGGGTCCAAT	FARIGSN	++	-	---
5059	16010	TTCGCGAAAGGGGGGAATAAT	FAKGGNN	++	-	-
5507	16458	TTTTTTCAAGGCGGCCATCAT	FFQGGHH	++	-	-
5549	16500	GCCAACATGAACCGCACCGAA	ANMNRTE	++	-	-
5462	16413	TTGTCCTCCAATTTGAAATAT	LSSNLKY	++	-	-
5047	15998	TATGCGAGGGCGAATACGAAT	YARANTN	++	-	-
5197	16148	CTGTCAAAGACCGGCTCAAAC	LSKTGSN	++	-	-
5244	16195	CGCGTATCATCAAACGGCGTA	RVSSNGV	++	-	-
5572	16523	TTTTCAAAGCCCGGCATCAAC	FSKPGIN	++	-	-
5423	16374	TACAAGGGCGGCTACAACAAC	YKGGYNN	++	-	-
5306	16257	TATTCCAGGCCGGGGACGAAT	YSRPGTN	++	-	-
5149	16100	TACTCAAAGGTACAAACCAAC	YSKVQTN	++	-	-
5130	16081	TATTCCAAATTCAATGATAAT	YSKFNDN	++	-	-
5391	16342	TACGCCAAGTACAACGGCAAC	YAKYNGN	++	-	-
5478	16429	GACTCAGGCGTAGGCCGCTAC	DSGVGRY	++	-	-
5435	16386	GCGGAGTCCTCCAGGACGTAT	AESSRTY	++	-	-
5498	16449	TTCGCGAAATTGGGGGTGAAT	FAKLGVN	++	-	-
5102	16053	TTCTCCAAACAGAATCACAAT	FSKQNHN	++	-	-
5013	15964	TATGCGAGGCAGGGGGCGAAT	YARQGAN	++	-	-
5293	16244	TTTGCCAAGGAAAACCGCAAC	FAKENRN	++	-	-
5374	16325	TACTCAAAGACCAACCAAAAC	YSKTNQN	++	-	-
5172	16123	TATAAATCCTCCAATGGGGTG	YKSSNGV	++	-	-
5376	16327	CTGGCCAAGTCATCACCCATC	LAKSSPI	++	-	-
5431	16382	ATGACGGGGAATTCCGCGTAT	MTGNSAY	++	-	-

5195	16146	TTCGCGAAATTCAATATGAAT	FAKFNMN	++	-	-
5085	16036	TATGCGAAAATGGGGATGAAT	YAKMGMN	++	-	-
5601	16552	ATCGCCTCACTGGGCCGCGAC	IASLGRD	++	-	-
5582	16533	ATAGGGGGGAAACAGGGGTTG	IGGKQGL	++	-	-
5284	16235	CTGTCAAAGCAAGGCCTGAAC	LSKQGLN	++	-	-
5543	16494	TTCGCGAAACCGGGGTCCAAT	FAKPGSN	++	-	-
5385	16336	ATGAGGAATCAGCCGAATGCG	MRNQPNA	++	-	-
5338	16289	TACGCCAAGGACGGCTACAAC	YAKDGYN	++	-	-
5146	16097	TACTCAAAGATGAACCAAAAC	YSKMNQN	++	-	-
5441	16392	TGGACCTCAGGCTACTCAAAC	WTSGYSN	++	-	-
5346	16297	AGGGGGGAGCACAATGCGTGG	RGEHNAW	++	-	-
5420	16371	TTCGCGAAAGGGGGGGGGAAT	FAKGGGN	++	-	-
5541	16492	AGGAATATGGAGTCCATGTAT	RNMESMY	++	-	-
5304	16255	CTGTCACGCGTAAACATGAAC	LSRVNMN	++	-	-
5090	16041	TTGGCGAAAGCGGGGTTCAAT	LAKAGFN	++	-	--
5587	16538	TTTTCAAAGAACAACGAAAAC	FSKNNEN	++	-	-
5209	16160	TATTCCAGGCCGGGGGCGAAT	YSRPGAN	++	-	-
5486	16437	AAAGATAATGCGACGAGGTAT	KDNATRY	++	-	-
5337	16288	TTCGCGAGGGCGAATTTGAAT	FARANLN	++	-	-
5157	16108	TATGCGAAAAATGGGGCGAAT	YAKNGAN	++	-	-
5142	16093	TTGTCCAGGGCGAATGATAAT	LSRANDN	++	-	-
5415	16366	TACGCCCGCGACGGCATCAAC	YARDGIN	++	-	-
5567	16518	TTCGCGAGGTTCAATGAGAAT	FARFNEN	++	-	-
5191	16142	TATTCCAAAGGGGGGGCGAAT	YSKGGAN	++	-	-
5439	16390	TATAATCAGAGGGGGCAGAAT	YNQRGQN	++	-	-
5252	16203	TATTCCAAAAATGGGGGGAAT	YSKNGGN	++	-	-
5375	16326	TACGCCAAGTTTAACGCCAAC	YAKFNAN	++	-	-
5484	16435	TTCGCGAGGCCGGGGACGAAT	FARPGTN	++	-	-
5343	16294	TTCTCCAAAATGGGGTCCAAT	FSKMGSN	++	-	-
5119	16070	TTCAGGTCCACGAATGGGGTG	FRSTNGV	++	-	-
5353	16304	TCCTCCGGGTCCAATCACTGG	SSGSNHW	++	-	-
5404	16355	ATAACGAATGTGAATTATGGG	ITNVNYG	++	-	-
5529	16480	TTTGCCCGCATGAACGAAAAC	FARMNEN	++	-	-

5278	16229	AATCCGGGGAGGTCCTCCTAT	NPGRSSY	++	-	-
5535	16486	AATAATTTCGGGACGAGGGAT	NNFGTRD	++	-	-
5050	16001	CTGGCCAAGATGGGCGCCAAC	LAKMGAN	++	-	-
5395	16346	TTTGCCAAGGTAGGCAACAAC	FAKVGNN	++	-	-
5069	16020	CTGTCAAAGGCCAACATCAAC	LSKANIN	++	-	-
5140	16091	TTCGCGAAACAGGGGCCGAAT	FAKQGPN	++	-	-
5400	16351	TTTGCCAAGATGGGCGCCAAC	FAKMGAN	++	-	-
5551	16502	TTTTCAAAGGGCAACGAAAAC	FSKGNEN	++	-	-
5281	16232	GAGAGGAAACCGGGGAATATA	ERKPGNI	++	-	-
5200	16151	TATACGAAATCCAATACGCAC	YTKSNTH	++	-	-
5186	16137	TACTCACGCGTAAACGACAAC	YSRVNDN	++	-	-
5009	15960	GTGGCGATGAGGGGGATAGGG	VAMRGIG	++	-	-
5517	16468	GTATCAGGCTTTACCAAGCAA	VSGFTKQ	++	-	-
5007	15958	TATTCCAGGCCGGGGCCGAAT	YSRPGPN	++	-	--
5111	16062	TTGTCCAAACACAATTTCAAT	LSKHNFN	++	-	-
4991	15942	TATGCGAAATCCAATTATAAT	YAKSNYN	++	-	--
5273	16224	AGGGGGTCCCCGACGTTGTAT	RGSPTLY	++	-	-
5294	16245	TTCTCCAAAGGGAATGTGAAT	FSKGNVN	++	-	-
5408	16359	TTCTCCAGGCACAATGGGAAT	FSRHNGN	++	-	-
5117	16068	TATGCGAAAGGGAATGCGAAT	YAKGNAN	++	-	-
5553	16504	TACGCCAAGCCCAACATGAAC	YAKPNMN	++	-	-
5289	16240	GCGCACTCCTCCAATGGGGTG	AHSSNGV	++	-	-
5544	16495	TTCGCGAAAGCGGGGGATAAT	FAKAGDN	++	-	-
5143	16094	TTCGCGAGGGATAATAGGAAT	FARDNRN	++	-	--
5387	16338	TACTCACGCCCCGGCGGCAAC	YSRPGGN	++	-	-
5165	16116	TACTCAAAGTCAGGCGCCAAC	YSKSGAN	++	-	-
5409	16360	CGCGGCGGCAACACCATGCCC	RGGNTMP	++	-	-
5570	16521	CATGGCGGCACCAAGAACGGC	HGGTKNG	++	-	-
5076	16027	ACGGTGTCCACGAATGGGGTG	TVSTNGV	++	-	-
5247	16198	ATGCATGTAAAGTCACCCAAC	MHVKSPN	++	-	-
5290	16241	CGCGGCGACCAATCAACCTGG	RGDQSTW	++	-	-
5225	16176	TTCTCCAAATCCGGGATAAAT	FSKSGIN	++	-	-
5250	16201	ACGGGGTCCGCGGTGAAATGG	TGSAVKW	++	-	-

5367	16318	TTCGCGAAACAGAATAATAAT	FAKQNNN	++	-	-
5258	16209	CTGTCAAAGCATAACCAAAAC	LSKHNQN	++	-	-
5158	16109	TTTTCAAAGATGAACATCAAC	FSKMNIN	++	-	-
5036	15987	TTTTCACGCTCAGGCATGAAC	FSRSGMN	++	-	-
5084	16035	TACTCACGCGTAAACCTGAAC	YSRVNLN	++	-	-
5262	16213	ATCGAACGCGAACGCTACGCC	IERERYA	++	-	-
5537	16488	TATTTCCCGGGGACGATGCCG	YFPGTMP	++	-	-
5539	16490	TATGCGAGGGATGGGACGAAT	YARDGTN	++	-	-
5402	16353	AGGTTCTCCGGGGAGCCGTCC	RFSGEPS	++	-	-
5406	16357	TACCTGCCCGGCCATATGAAC	YLPGHMN	++	-	-
5477	16428	GACACCTACGGCACCAAGCAT	DTYGTKH	++	-	-
5412	16363	GGGGGGAATAAATCCAATTAT	GGNKSNY	++	-	-
5557	16508	TTTGCCAAGCTGAACGCCAAC	FAKLNAN	++	-	-
5035	15986	TATTCCAAACAGGGGCAGAAT	YSKQGQN	++	-	-
5056	16007	TACTCACGCGCCAACCAAAAC	YSRANQN	++	-	-
5434	16385	AACACCCGCGGCAACGGCTCA	NTRGNGS	++	-	-
5313	16264	TATGCGAGGATGAATCAGAAT	YARMNQN	++	-	---
5342	16293	TTCGCGAAAATGAATATAAAT	FAKMNIN	++	-	-
5238	16189	TATGCGAAACAGAATTGGAAT	YAKQNWN	++	-	-
5166	16117	TTTTCAAAGGCCAACATGAAC	FSKANMN	++	-	-
4996	15947	TATGCGAAAAATGGGAATAAT	YAKNGNN	++	-	-
5382	16333	TATGGGGCGATAGGGAGGAAT	YGAIGRN	++	-	-
5296	16247	AATAATAGGGGGACGCCGGCG	NNRGTPA	++	-	-
5514	16465	TTCTCCAAAGGGGGGGGGAAT	FSKGGGN	++	-	-
5521	16472	CAAAAGATCATGCGCGGCGAC	QKIMRGD	++	-	-
5566	16517	AACCTGTCACATGGCCATGGC	NLSHGHG	++	-	-
5002	15953	TTTGCCAAGGGCGGCCCCAAC	FAKGGPN	++	-	-
5414	16365	TTCGCGAGGCACGGGGATAAT	FARHGDN	++	-	-
5125	16076	TACTCAAAGCTGGCCCCCAAC	YSKLAPN	++	-	-
5006	15957	TATTCCAGGGCGAATTTGAAT	YSRANLN	++	-	-
5269	16220	TTCGCGAAATTGGGGTTCAAT	FAKLGFN	++	-	-
5351	16302	TTTGCCCGCTCAAACCAAAAC	FARSNQN	++	-	-
5472	16423	TTCGCGAAACCGGGGTGGAAT	FAKPGWN	++	-	-

5235	16186	CATCATTCAACCAACGGCGTA	HHSTNGV	++	-	-
5585	16536	TTTTCAAAGATCAACGGCAAC	FSKINGN	++	-	-
5584	16535	TACTACAAGACCGACTCATCA	YYKTDSS	++	-	-
5026	15977	TACTCAAAGGCCAACCTGAAC	YSKANLN	++	-	-
5518	16469	TTCTCCAGGTTCAATGAGAAT	FSRFNEN	++	-	-
5389	16340	GTAGGCTCAAACCATTCATGG	VGSNHSW	++	-	-
5362	16313	ACCCGCTCAGGCGGCGTAGCC	TRSGGVA	++	-	--
5224	16175	TATTCCAAAGTGAATCACAAT	YSKVNHN	++	-	-
5332	16283	TACGCCCGCGTAAACATCAAC	YARVNIN	++	-	-
5175	16126	TATGCGAAATATGGGTTGAAT	YAKYGLN	++	-	-
5394	16345	AAAGCGGAGTATGGGGCGGGG	KAEYGAG	++	-	-
5256	16207	TTCGCGAAACAGGGGCACAAT	FAKQGHN	++	-	-
5425	16376	TTTGCCCGCTACAACACCAAC	FARYNTN	++	-	-
5574	16525	TTTGCCAAGATCAACACCAAC	FAKINTN	++	-	-
5155	16106	TACTCAAAGCAAGGCTGGAAC	YSKQGWN	++	-	-
5339	16290	TATGCGAGGCCGGGGGATAAT	YARPGDN	++	-	-
5257	16208	AATGGGTCCACGAATGGGAGG	NGSTNGR	++	-	-
5178	16129	TTCTCCAGGTCCGGGGCGAAT	FSRSGAN	++	-	-
5037	15988	TACGCCAAGCTGGGCGCCAAC	YAKLGAN	++	-	-
4993	15944	TATGCGAAAACGAATATAAAT	YAKTNIN	++	-	-
5438	16389	TATGCGAAATTGAATGAGAAT	YAKLNEN	++	-	--
5561	16512	TTCGCGAGGGAGGGGGTGAAT	FAREGVN	++	-	-
5022	15973	TACGCCAAGATGGGCCCCAAC	YAKMGPN	++	-	-
5580	16531	GATAAAGGGAATAATGCGTAT	DKGNNAY	++	-	-
5213	16164	TACTCAAAGTCAAACCAAAAC	YSKSNQN	++	-	-
5534	16485	TCCAATGGGAAATGGTCCGGG	SNGKWSG	++	-	-
5301	16252	TTCTCCAGGAATGGGCAGAAT	FSRNGQN	++	-	-
5074	16025	TATTCCAAAGTGGGGTTGAAT	YSKVGLN	++	-	-
5221	16172	AAAGGGGAGGCGACGACGTGG	KGEATTW	++	-	-
5116	16067	CAGATATCCACGAATGGGAGG	QISTNGR	++	-	-
5327	16278	TGGGCGAAATTGTCCTTGAAT	WAKLSLN	++	-	--
5124	16075	TATTCCAAAGTGAATACGAAT	YSKVNTN	++	-	-
5381	16332	TTTTCAAAGGTAAACCCCAAC	FSKVNPN	++	-	-

5203	16154	TACGCCAAGTCAAACGTAAAC	YAKSNVN	++	-	-
5318	16269	AGGAATTCCCAGTCCGTGTTC	RNSQSVF	++	-	-
5270	16221	TTGTCCAAAACGAATTTCAAT	LSKTNFN	++	-	-
5547	16498	TATCACGGGCACACGTTGCAC	YHGHTLH	++	-	-
5231	16182	CAATTTTCAACCAACGGCATC	QFSTNGI	++	-	-
5018	15969	TATGCGAGGGAGAATAGGAAT	YARENRN	++	-	-
5429	16380	TTTGCCAAGTCAAACAACAAC	FAKSNNN	++	-	-
5156	16107	ACCTGGTCAACCAACGGCGTA	TWSTNGV	++	-	-
5299	16250	TACGCCCGCCCCAACCATAAC	YARPNHN	++	-	-
5589	16540	TACGCCAAGGACAACCTGAAC	YAKDNLN	++	-	-
5499	16450	TTCTCCAAAGAGGGGAAAAAT	FSKEGKN	++	-	-
5141	16092	CACTCCTCCTCCAATGGGGTG	HSSSNGV	++	-	-
5533	16484	TTTTCACGCGACGGCAAGAAC	FSRDGKN	++	-	-
5179	16130	TGGGTGAAATCCTCCCCGAAT	WVKSSPN	++	-	-
5350	16301	TTTGCCAAGTCAGGCGGCAAC	FAKSGGN	++	-	-
5168	16119	TTCTCCAAAGCGGGGATGAAT	FSKAGMN	++	-	-
5129	16080	TATGCGAAAACGGGGTCCAAT	YAKTGSN	++	-	-
5450	16401	TACCGCTCAAACGCCATCGTA	YRSNAIV	++	-	-
5055	16006	TATGCGAGGTTGGGGGAGAAT	YARLGEN	++	-	-
5522	16473	TACCAACGCGACGGCTACGGC	YQRDGYG	++	-	-
5398	16349	TATGCGAGGGGGTCCGATTTG	YARGSDL	++	-	-
5196	16147	TATTCCAAAGGGGGGCAGAAT	YSKGGQN	++	-	-
5609	16560	TTCGCGAAAAATAATTATAAT	FAKNNYN	++	-	-
5115	16066	CTGTCAAAGGCCAACCTGAAC	LSKANLN	++	-	-
5513	16464	TTTGCCAAGCTGAACTCAAAC	FAKLNSN	++	-	-
5066	16017	TATGCGAAAGGGGGGCCGAAT	YAKGGPN	++	-	-
5359	16310	TACTCAAAGCCCAACAACAAC	YSKPNNN	++	-	-
5336	16287	TACTCAAAGCCCGGCTTTAAC	YSKPGFN	++	-	-
5162	16113	ACGCACTCCACGAATGGGGTG	THSTNGV	++	-	-
5206	16157	TATTCCAGGATGGGGACGAAT	YSRMGTN	++	-	-
5364	16315	TATAGGCAGGGGTTGTCCAAT	YRQGLSN	++	-	-
5511	16462	TGGAAACCGGGGGTGCCGTCC	WKPGVPS	++	-	-
5021	15972	TTCTCCAGGATAGGGGCGAAT	FSRIGAN	++	-	-

5107	16058	TATGCGAAAACGGGGACGAAT	YAKTGTN	++	-	-
5072	16023	TATTCCAAAATGAATGCGAAT	YSKMNAN	++	-	-
5354	16305	ATGACGGGGACGTCCTCCTAT	MTGTSSY	++	-	-
5033	15984	CTGTCAAAGATCGGCTCAAAC	LSKIGSN	++	-	-
5554	16505	GGGAATCAGAATTCCAATTAT	GNQNSNY	++	-	-
5485	16436	CGCTCAGGCGGCGCCGGCGGC	RSGGAGG	++	-	-
5210	16161	TACGCCAAGATCGGCCAAAAC	YAKIGQN	++	-	-
5131	16082	TATTCCTCCACGAATGGGATA	YSSTNGI	++	-	-
5446	16397	TTCGCGAAACAGAATACGAAT	FAKQNTN	++	-	-
5242	16193	ATCTACTCATCAAACGGCGTA	IYSSNGV	++	-	-
5177	16128	TTGTCCAGGATGAATGAGAAT	LSRMNEN	++	-	-
5264	16215	TTTTCAAAGACCGGCATCAAC	FSKTGIN	++	-	-
5092	16043	CTGTCACGCACCGGCCAAAAC	LSRTGQN	++	-	-
5151	16102	TACGCCAAGCAAGGCATCAAC	YAKQGIN	++	-	-
5109	16060	TTTTCAAAGGTAGGCTCAAAC	FSKVGSN	++	-	-
5110	16061	TATATGTCCTCCAATGGGGTG	YMSSNGV	++	-	--
5345	16296	GTATCAAACAAGGGCGCCGGC	VSNKGAG	++	-	-
5456	16407	TTCTCCAGGGTGAATGGGAAT	FSRVNGN	++	-	-
5493	16444	TTCTCCAGGCCGGGGGCGAAT	FSRPGAN	++	-	-
5455	16406	AACGCCCGCGGCGCCAACGCC	NARGANA	++	-	-
5451	16402	TTCGCGAGGAATAATCAGAAT	FARNNQN	++	-	-
5481	16432	TTTGCCAAGTTTAACGCCAAC	FAKFNAN	++	-	-
5379	16330	TTTGCCAAGCAAGGCTCAAAC	FAKQGSN	++	-	--
5266	16217	TATACGAAATCCCAGACGGAT	YTKSQTD	++	-	-
5086	16037	TTTGCCAAGTCAGGCTACAAC	FAKSGYN	++	-	-
5182	16133	TTGGCGAAAAATGGGTTGAAT	LAKNGLN	++	-	-
5588	16539	TTCGCGAGGGATGGGGCGAAT	FARDGAN	++	-	-
4992	15943	TTGCACGCGAGGAATATAAAT	LHARNIN	++	-	--
4989	15940	TTCTCCAAAGCGAATTATAAT	FSKANYN	++	-	-
5159	16110	TACTCAAAGAACAACCTGAAC	YSKNNLN	++	-	-
5393	16344	TATTCCAGGGAGAATGCGAAT	YSRENAN	++	-	-
5181	16132	TATAGGTCCACGAATGGGATA	YRSTNGI	++	-	-
5043	15994	TATTCCAGGACGGGGGAGAAT	YSRTGEN	++	-	-

5207	16158	GTGATGTCCACGAATGGGGTG	VMSTNGV	++	-	-
5280	16231	TTGGCGAAAATGGGGACGAAT	LAKMGTN	++	-	-
5193	16144	TTCAAATCCTCCAATGGGGTG	FKSSNGV	++	-	-
5430	16381	TTTTCACGCGAAGGCCGCAAC	FSREGRN	++	-	-
5592	16543	TTCGCGAAATTGGGGGATAAT	FAKLGDN	++	-	--
5174	16125	TATGCGAAACAGGGGCAGAAT	YAKQGQN	++	-	-
5274	16225	TTCGCGAAAACGGGGACGAAT	FAKTGTN	++	-	-
5560	16511	TTTTCACGCCCCGGCGTAAAC	FSRPGVN	++	-	-
5073	16024	TTCTCCAAAATAGGGTTGAAT	FSKIGLN	++	-	-
5460	16411	TTCGTGAAATCCGCGAATGGG	FVKSANG	++	-	-
5068	16019	TATTCCAAACAGGGGGCGAAT	YSKQGAN	++	-	-
5324	16275	TATTCCGTGAGGCACCCGAAT	YSVRHPN	++	-	-
5465	16416	TACGCCAAGATGAACCAAAAC	YAKMNQN	++	-	-
5492	16443	TATAAAAATGGGATGTCCAAT	YKNGMSN	++	-	-
5127	16078	CTGTCAAAGTCAGGCATCAAC	LSKSGIN	++	-	-
5133	16084	TTTGCCCGCGGCAACACCAAC	FARGNTN	++	-	--
5279	16230	AATATGACGGGGAAATCCGCG	NMTGKSA	++	-	-
5405	16356	TATGTGCAGAATAGGCCGAAT	YVQNRPN	++	-	-
5251	16202	TACTACACCAAGGTACCCACC	YYTKVPT	++	-	-
5114	16065	TATGCGAAACAGAATTTCAAT	YAKQNFN	++	-	-
5101	16052	TTGTCCAGGGCGGGGCCGTTG	LSRAGPL	++	-	-
5530	16481	TATTCCAAACACAATGCGTCC	YSKHNAS	++	-	-
5029	15980	TTCTCCAAATTGAATTTCAAT	FSKLNFN	++	-	-
5098	16049	CATGTATCAACCAACGGCATC	HVSTNGI	++	-	---
5503	16454	TTCGCGAAATATAATGAGAAT	FAKYNEN	++	-	-
5229	16180	CGCGAATCATCAAACGGCGTA	RESSNGV	++	-	-
5311	16262	TACACCCGCTCACAAGAAATG	YTRSQEM	++	-	-
5565	16516	AACTCACAAGACACCAAGTGG	NSQDTKW	++	-	-
5144	16095	TTGTCCAGGACGAATGATAAT	LSRTNDN	++	-	-
5494	16445	TTTTCAAAGCCCGGCTACAAC	FSKPGYN	++	-	-
5097	16048	CTGTCAAAGTCAGGCGTAAAC	LSKSGVN	++	-	-
5276	16227	TTTTCAAAGATGAACATGAAC	FSKMNMN	++	-	-
5591	16542	GATTATAAAGGGTTCCCGTCC	DYKGFPS	++	-	-

5192	16143	TACGCCAAGCATGGCATGAAC	YAKHGMN	++	-	-
5419	16370	TCACTGGGCTCATCAAAGTAC	SLGSSKY	++	-	-
5212	16163	TTGTCCAAAGTGAATTTCAAT	LSKVNFN	++	-	-
5075	16026	TATGCGAAACAGGGGATGAAT	YAKQGMN	++	-	-
5302	16253	AAGTCAGGCGGCTACCCCTAC	KSGGYPY	++	-	-
5411	16362	CGCTCAAACGGCTCAGGCTCA	RSNGSGS	++	-	-
5245	16196	TTCGCGAAAGGGAATAATAAT	FAKGNNN	++	-	-
5563	16514	AATCACAAATCCACGGCGAAT	NHKSTAN	++	-	-
5201	16152	TTTTCAAAGACCGGCCATAAC	FSKTGHN	++	-	-
5519	16470	GTATCACTGGGCACCCGCAAC	VSLGTRN	++	-	-
5218	16169	TATGCGAGGATGAATGTGAAT	YARMNVN	++	-	-
5586	16537	CTGGGCGACGGCTGGGGCAAG	LGDGWGK	++	-	-
5358	16309	TATCACAAATATTCCACGGAT	YHKYSTD	++	-	-
5004	15955	TATGCGAAAGTGGGGAATAAT	YAKVGNN	++	-	-
5384	16335	TTCGCGAGGTTGAATCAGAAT	FARLNQN	++	-	-
5330	16281	TTTTCACGCCAAAACACCAAC	FSRQNTN	++	-	-
5329	16280	TACGCCAAGATCGGCGAAAAC	YAKIGEN	++	-	-
5325	16276	TTCGCGAAAGATAATAGGAAT	FAKDNRN	++	-	-
5516	16467	TTCGCGAAAACGAATTTGAAT	FAKTNLN	++	-	-
5370	16321	GATATGAGGAGGATGGGGGAG	DMRRMGE	+	-	-
5160	16111	TATTCCAAACACGGGATGAAT	YSKHGMN	+	-	-
5065	16016	TATTCCAGGTTGGGGGATAAT	YSRLGDN	+	-	-
5260	16211	CTGTCAAAGTCAAACCATAAC	LSKSNHN	+	-	-
5161	16112	GTACAATCAACCAACGGCCGC	VQSTNGR	+	-	–
5167	16118	TACTCAAAGCATGGCGTAAAC	YSKHGVN	+	-	-
5583	16534	AGGATAAAAGATACGCCGGAG	RIKDTPE	+	-	-
5418	16369	ACGAGGGATGTGGCGGGGAGG	TRDVAGR	+	-	-
5153	16104	TATGCGTCCACGAATGGGATA	YASTNGI	+	-	-
5495	16446	TTTTCACATGCCTCATCATAC	FSHASSY	+	-	-
5333	16284	TACGCCCGCATCAACATGAAC	YARINMN	+	-	-
4995	15946	TTCTCCAAAGTGGGGATAAAT	FSKVGIN	+	-	-
5606	16557	AATATACACGGGTATGTGACG	NIHGYVT	+	-	-
5064	16015	TATGCGAGGTCCAATGCGAAT	YARSNAN	+	-	-

5082	16033	TTTTCAAAGGTAGGCTTTAAC	FSKVGFN	+	-	-
5011	15962	ACCAACTACGGCCGCCCCTCA	TNYGRPS	+	-	--
5497	16448	TACTCACAAGGCAAGACCAAC	YSQGKTN	+	-	-
5246	16197	TTCTCCAGGATGGGGGATAAT	FSRMGDN	+	-	-
5226	16177	TATGCGAAAACGAATGCGAAT	YAKTNAN	+	-	-
5322	16273	TTGTCCAGGGCGCAGTCCATA	LSRAQSI	+	-	-
5106	16057	TATTCCAAATCCAATTTCAAT	YSKSNFN	+	-	-
5147	16098	TTTTCACGCAACGGCGTAAAC	FSRNGVN	+	-	-
4998	15949	TATGCGAAACCGGGGATAAAT	YAKPGIN	+	-	-
5598	16549	AATTCCTCCGGGATGAGGGAG	NSSGMRE	+	-	-
5041	15992	TACTCAAAGATGGGCATCAAC	YSKMGIN	+	-	-
5198	16149	TATTTCACGGGGATACACGGG	YFTGIHG	+	-	-
5421	16372	GGGAGGGATAGGGGGCCGGGG	GRDRGPG	+	-	-
5526	16477	ACCTCAGACTCACGCGGCTGG	TSDSRGW	+	-	-
5171	16122	CTGTCAAAGTCAGGCATGAAC	LSKSGMN	+	-	-
5510	16461	TATAGGTATGATGCGGTGGTG	YRYDAVV	+	-	-
5348	16299	ACGAAATCCGGGACGAATGCG	TKSGTNA	+	-	-
5597	16548	TACCCCGGCTCAGGCGGCCTG	YPGSGGL	+	-	-
5321	16272	AGGGGGACGTCCTCCAATTAT	RGTSSNY	+	-	-
5051	16002	CCCTACGCCAAGTCAGAACTG	PYAKSEL	+	-	-
5452	16403	TTCTCCAAAATGGGGGGGAAT	FSKMGGN	+	-	-
4997	15948	TATGCGAGGCCGGGGAATAAT	YARPGNN	+	-	--
5003	15954	TATTCCAAAACGGGGATAAAT	YSKTGIN	+	-	-
5095	16046	TACTCAAAGATCGGCGGCAAC	YSKIGGN	+	-	-
5017	15968	TCCACGTCCTCCTCCGGGAGG	STSSSGR	+	-	-
5030	15981	TATTCCAGGGGGAATACGAAT	YSRGNTN	+	-	-
5397	16348	TTTTCAAAGCATGGCTCAAAC	FSKHGSN	+	-	-
5440	16391	TTTGCCAAGACCAACCAAAAC	FAKTNQN	+	-	-
5194	16145	TATTCCAGGTTGAATGATGCG	YSRLNDA	+	-	-
5046	15997	TTGTCCAAAAATGGGCCGAAT	LSKNGPN	+	-	-
5403	16354	AAATCCGATGGGTCCACGTGG	KSDGSTW	+	-	-
5436	16387	AAGAACCATGGCGGCTCATAC	KNHGGSY	+	-	-
5449	16400	TATACGGATCACATGAGGAAT	YTDHMRN	+	-	-

5154	16105	TTCTCCAAATTGGGGGTGAAT	FSKLGVN	+	-	-
5454	16405	TTTGCCAAGCAAAACTCAAAC	FAKQNSN	+	-	-
5576	16527	TTTTCAAAGCCCAACCCCAAC	FSKPNPN	+	-	-
5545	16496	GATTTCGGGGTGTCCAGGCAC	DFGVSRH	+	-	-
5595	16546	TTCGCGAAAGCGAATGAGAAT	FAKANEN	+	-	-
5525	16476	CACGATAGGACGTCCACGTAT	HDRTSTY	+	-	-
5428	16379	TTCGCGAAAATGGGGCAGAAT	FAKMGQN	+	-	–
5271	16222	TACGCCAAGAACAACTACAAC	YAKNNYN	+	-	-
5335	16286	AATGTGAGGAATCAGATGGCG	NVRNQMA	+	-	-
5000	15951	TATGCGAAAATGGGGAATAAT	YAKMGNN	+	-	-
5219	16170	AAACAGTCCACGAATGGGGTG	KQSTNGV	+	-	-
5112	16063	TTCTCCAAATTGGGGATGAAT	FSKLGMN	+	-	-
5078	16029	TATTCCAAACAGGGGCACAAT	YSKQGHN	+	-	-
5347	16298	TATGAGAGGTTCATACCGAAT	YERFIPN	+	-	-
5135	16086	CTGTCACGCATGAACATGAAC	LSRMNMN	+	-	-
5476	16427	GGGGGGGTGGCGTCCTCCTAT	GGVASSY	+	-	-
5562	16513	TTTTCAAAGGACGGCCGCAAC	FSKDGRN	+	-	–
5312	16263	CTGTCAAAGCTGAACGGCAAC	LSKLNGN	+	-	-
5093	16044	ATGCGCAACGGCACCATGTCA	MRNGTMS	+	-	-
5593	16544	TTTGCCAAGGACGGCTACAAC	FAKDGYN	+	-	-
5132	16083	TATTCCAGGAATGGGGGGAAT	YSRNGGN	+	-	-
5564	16515	TTCGCGAGGCCGGGGCAGAAT	FARPGQN	+	-	-
5527	16478	TGGAGGACGGATGGGATGGGG	WRTDGMG	+	-	-
5298	16249	TTTGCCAAGCATGGCATGAAC	FAKHGMN	+	-	–
5458	16409	TACGCCAAGCCCAACAACAAC	YAKPNNN	+	-	-
5413	16364	TACTCACGCTCAGCCAAGGAC	YSRSAKD	+	-	-
5233	16184	TTCGCGAAAAATGGGCACAAT	FAKNGHN	+	-	-
5031	15982	TTCGCGAAAGGGGGGTTCAAT	FAKGGFN	+	-	-
5608	16559	TTTTCAAAGGAAAACCAAAAC	FSKENQN	+	-	--
5163	16114	TTCGCGAAACAGAATTATAAT	FAKQNYN	+	-	-
5164	16115	ATGTTGTCCACGAATGGGAGG	MLSTNGR	+	-	-
5023	15974	TACTCAAAGCTGGGCCAAAAC	YSKLGQN	+	-	-
5216	16167	GGGGGGTCCGGGATGAAATAT	GGSGMKY	+	-	-

5134	16085	TACGCCAAGCATGGCAACAAC	YAKHGNN	+	-	-
5475	16426	CGCGGCAACGGCACCGGCTCA	RGNGTGS	+	-	-
5360	16311	TTCGCGAAAATGGGGATAAAT	FAKMGIN	+	-	-
5187	16138	TACTCAAAGCAAAACTCAAAC	YSKQNSN	+	-	-
5308	16259	TACGCCAAGAAGGGCGAAAAC	YAKKGEN	+	-	-
5228	16179	TTTTCAAAGATGAACCTGAAC	FSKMNLN	+	-	-
5139	16090	TTGTCCAAATTGAATGAGAAT	LSKLNEN	+	-	-
5190	16141	GACAAGTACAACGACTACAAG	DKYNDYK	+	-	-
5528	16479	GGGGTGAAATCCGCGTATCAG	GVKSAYQ	+	-	-
5001	15952	TTCGCGAGGAATGGGAATAAT	FARNGNN	+	-	-
5369	16320	TTCTCCAAACAGGGGCAGAAT	FSKQGQN	+	-	-
5150	16101	CTGGCCCGCCAAGGCTCAAAC	LARQGSN	+	-	-
5378	16329	TACGCCAAGGGCAACGGCAAC	YAKGNGN	+	-	-
5392	16343	ACGTATTCCAAACCGAATTCC	TYSKPNS	+	-	-
5275	16226	TTTTCAAAGCATAACCTGAAC	FSKHNLN	+	-	-
5038	15989	TACGCCCGCATGAACCTGAAC	YARMNLN	+	-	-
5399	16350	TTCTCCAGGCCGAATATAAAT	FSRPNIN	+	-	-
5113	16064	TTTTCACGCCTGAACGAAAAC	FSRLNEN	+	-	-
5173	16124	CAATGGTCAACCAACGGCGTA	QWSTNGV	+	-	-
5426	16377	TACTCACGCCCCAACTCAAAC	YSRPNSN	+	-	-
5128	16079	ACGTTCTCCACGAATGGGATA	TFSTNGI	+	-	-
5437	16388	TATAAAGCGGATACGAGGAAT	YKADTRN	+	-	-
5287	16238	TTTTCAAAGATGAACCAAAAC	FSKMNQN	+	-	-
5575	16526	TACTCACGCGACGGCTCAAAC	YSRDGSN	+	-	-
5309	16260	TATGCGAAAGTGGGGACGAAT	YAKVGTN	+	-	--
5236	16187	CTGTCAAAGAACGGCTTTAAC	LSKNGFN	+	-	-
5508	16459	TTCGCGAAAATGAATGTGAAT	FAKMNVN	+	-	-
5291	16242	TTCTCCAAAATGGGGATGAAT	FSKMGMN	+	-	-
5145	16096	ATGCAGTCCACGAATGGGATA	MQSTNGI	+	-	-
5417	16368	TATGCGAGGGAGGGGGTGAAT	YAREGVN	+	-	-
5599	16550	TTTTCAAAGCCCAACCTGAAC	FSKPNLN	+	-	-
5053	16004	ACCCAATCAACCAACGGCATC	TQSTNGI	+	-	-
5067	16018	TATTCCAAAAATGGGCCGAAT	YSKNGPN	+	-	-

5079	16030	TATGCGAAATCCGGGGATAAT	YAKSGDN	+	-	-
5040	15991	TATGCGAAATATGGGAATAAT	YAKYGNN	+	-	-
5288	16239	ACGCCGGGGAGGTCCGGGTTC	TPGRSGF	+	-	–
5267	16218	TTGAATAGGTTGGGGCCGACG	LNRLGPT	+	-	-
5170	16121	TATTCCAAATTGGGGGAGAAT	YSKLGEN	+	-	-
5524	16475	CACTCCCACGGGGGGAGGGAT	HSHGGRD	+	-	-
5237	16188	TATTCCAGGCCGAATGCGAAT	YSRPNAN	+	-	–
5214	16165	TATATATCCTCCAATGGGGTG	YISSNGV	+	-	--
5089	16040	CTGTCAAAGCTGAACACCAAC	LSKLNTN	+	-	--
5272	16223	TCAGACGGCAACTCATCATAC	SDGNSSY	+	-	-
5506	16457	TACCATTCATCATCAGGCAAC	YHSSSGN	+	-	-
5123	16074	TACTCAAAGCTGGGCCTGAAC	YSKLGLN	+	-	-
5241	16192	ACCACCGACTTTAACGGCTTT	TTDFNGF	+	-	-
5061	16012	GTACTGTCATCAAACGGCGTA	VLSSNGV	+	-	-
5444	16395	TACGCCAAGCATAACGGCAAC	YAKHNGN	+	-	-
5189	16140	TTCGCGAAAACGGGGTTGAAT	FAKTGLN	+	-	-
5380	16331	TTCTCCAAAAATAATTCCAAT	FSKNNSN	+	-	-
5482	16433	ACCATCTCATCATCAAACTGG	TISSSNW	+	-	-
5509	16460	TACGCCAAGGTAAACATGAAC	YAKVNMN	+	-	-
5081	16032	TCCAAATCCACGAATGGGGTG	SKSTNGV	+	-	–
5373	16324	TTCTCCAAAGTGAATCAGAAT	FSKVNQN	+	-	–
5227	16178	TACTCACGCAACAACGAAAAC	YSRNNEN	+	-	-
5215	16166	TTCGCGAAAGCGAATTATAAT	FAKANYN	+	-	-
5044	15995	TACTCAAAGGGCAACTACAAC	YSKGNYN	+	-	-
5230	16181	TTGTCCAAACACAATGAGAAT	LSKHNEN	+	-	-
5014	15965	TATGCGAGGATAAATTATAAT	YARINYN	+	-	--
5080	16031	CTGTCAAAGGCCGGCAACAAC	LSKAGNN	+	-	-
5422	16373	ATAAAAGGGGGGTCCTCCGGG	IKGGSSG	+	-	-
5490	16441	ATAGGGCACATGGGGTCCGAT	IGHMGSD	+	-	-
5120	16071	TATTCCAGGGCGGGGGAGAAT	YSRAGEN	+	-	-
5396	16347	GGGACGTCCTCCGCGGCGTGG	GTSSAAW	+	-	-
5121	16072	CTGTCAAAGACCGGCACCAAC	LSKTGTN	+	-	-
5303	16254	TACGCCCGCTCATCAGACTCA	YARSSDS	+	-	-

5610	16561	TTTTCAAAGTTTGGCATCAAC	FSKFGIN	+	-	-
5204	16155	TTCTCCAGGCAGGGGGTGAAT	FSRQGVN	+	-	-
5505	16456	CATACCAACGTAACCGCCTGG	HTNVTAW	+	-	-
5496	16447	AAGGGCGACAAGATCACCTGG	KGDKITW	+	-	-
5334	16285	TTTTCAAAGTCAGGCTCAAAC	FSKSGSN	+	-	-
5208	16159	AATAATTCCACGAATGGGATA	NNSTNGI	+	-	-
5057	16008	TATGCGAAACCGGGGCCGAAT	YAKPGPN	+	-	-
5118	16069	CTGGCCAAGGTAGGCTTTAAC	LAKVGFN	+	-	-
5094	16045	TACGCCAAGTCAGGCTTTAAC	YAKSGFN	+	-	--
5305	16256	AAATCCGGGAATTCCTCCTAT	KSGNSSY	+	-	-
5594	16545	TTCGCGAAAGATGGGATGAAT	FAKDGMN	+	-	-
5538	16489	TATGCGCAGCAGGGGTTGAAT	YAQQGLN	+	-	-
5028	15979	TTCGCGAAAGGGAATTTCAAT	FAKGNFN	+	-	-
5240	16191	TTGGCGAAAATAGGGCACAAT	LAKIGHN	+	-	-
5249	16200	TACTCAAAGGTAAACCTGAAC	YSKVNLN	+	-	-
5202	16153	TTCGCGAGGATAGGGATGAAT	FARIGMN	+	-	-
5254	16205	CGCCCCAACACCGCCAACTTT	RPNTANF	+	-	-
5596	16547	TTCGCGAAAGAGGGGGGGAAT	FAKEGGN	+	-	-
5483	16434	ATAAAATATTCCTCCTCCGAT	IKYSSSD	+	-	-
5536	16487	TTCGCGAAAGTGAATGCGAAT	FAKVNAN	+	-	--
5448	16399	TTCTCCAAAGTGAATACGAAT	FSKVNTN	+	-	-
5352	16303	TTCGCGAAAATAGGGAATAAT	FAKIGNN	+	-	-
5457	16408	AATACGAGGGGGACGTCCGCG	NTRGTSA	+	-	-
5100	16051	TTGGCGAGGGTGGGGGCGAAT	LARVGAN	+	-	-
5268	16219	AGGTATTCCACGAATGGGGTG	RYSTNGV	+	-	--
5105	16056	ACGTTGTCCACGAATGGGGTG	TLSTNGV	+	-	-
5479	16430	TATTCCAGGGAGGGGGGGAAT	YSREGGN	+	-	-
5188	16139	TTGTCCAAAATGGGGATGAAT	LSKMGMN	+	-	-
5307	16258	ATGTCACGCCTGAACGCCACC	MSRLNAT	+	-	-

NT SEQ ID#	AA SEQ ID#	NT Sequence	AA sequence	hTFRC_log2enr	Fc-ctrl1_log2enr
5611	16562	TATTCCCGACTCTCCGCGATA	YSRLSAI	+++	-
5612	16563	TGGCCCCCGCCTGTTAATTCC	WPPPVNS	+++	n.d.
5613	16564	AGGACTGCACTCGTATTTCCA	RTALVFP	+++	n.d.
5614	16565	ATTCACCGTCTACTCCCTTCC	IHRLLPS	+++	-
5615	16562	TACTCACGTCTATCAGCTATC	YSRLSAI	+++	-
5616	13980	TATTCACGTATCAATGCAAAT	YSRINAN	+++	-
5617	16566	TATTTTACTGGCGTTGTGGCC	YFTGVVA	+++	n.d.
5618	16567	CGTAATGACATGGTTTTTCCC	RNDMVFP	++	-
5619	16568	TTGCATAGGCTCTTGAAAGAC	LHRLLKD	+++	-
5620	16569	TATCTTAAATCTCAGTCATAT	YLKSQSY	+++	-
5621	14328	TATTCTCGGATAAACACGAAC	YSRINTN	+++	-
5622	16563	TGGCCTCCACCGGTCAACAGC	WPPPVNS	+++	n.d.
5623	16570	TACACAAAGTCCGACGTGCGG	YTKSDVR	+++	-
5624	15970	TTCAGCCGCGTTGGCTTCAAT	FSRVGFN	+++	-
5625	16564	CGTACAGCCCTTGTGTTCCCG	RTALVFP	+++	n.d.
5626	16571	AAAACATATGATGCATTTGTG	KTYDAFV	+++	-
5627	16570	TATACTAAATCGGATGTACGA	YTKSDVR	+++	-
5628	13758	TATAGCAGATCTAACGCAAAT	YSRSNAN	+++	-
5629	15958	TATTCCCGGCCCGGCCCCAAT	YSRPGPN	+++	-
5630	16571	AAGACCTACGACGCGTTCGTC	KTYDAFV	+++	n.d.
5631	16572	TATCTTAAGTCTGAACGTAAT	YLKSERN	+++	-
5632	16573	AGATCCGAACATGTCTTTCCA	RSEHVFP	+++	-
5633	16574	TCATACGCGAAGTCCCTCTTG	SYAKSLL	+++	n.d.
5634	16575	TTATCTAAGCTAAGTGCAAAC	LSKLSAN	+++	-
5635	16576	TATTCGAGGTTATCTGGGAAT	YSRLSGN	+++	-
5636	14328	TACAGCCGTATCAATACCAAT	YSRINTN	+++	-
5637	16577	TATAGCAGACTAAACAAAGAC	YSRLNKD	+++	-
5638	16565	ATCCATAGACTTCTACCCTCA	IHRLLPS	+++	-
5639	16578	TACTCAGCCATTGGAATGAAC	YSAIGMN	++	-
5640	16569	TACCTGAAGAGCCAATCCTAC	YLKSQSY	+++	-
5641	16579	TATTTGAAGAGTCAGGGGAAC	YLKSQGN	+++	n.d.
5642	16005	TACGCGCGAATCGGGCTGAAC	YARIGLN	+++	-

5643	16567	CGGAACGATATGGTCTTCCCT	RNDMVFP	++	-
5644	16577	TACTCACGCCTTAATAAGGAT	YSRLNKD	+++	-
5645	16580	TATAGCAAACTTAATGATAAG	YSKLNDK	+++	-
5646	16038	TATGCCAAAAATGGCTTTAAC	YAKNGFN	++	-
5647	16100	TATTCGAAGGTCCAGACCAAT	YSKVQTN	++	-
5648	13758	TACTCTCGTTCCAATGCTAAC	YSRSNAN	+++	-
5649	14133	TACACTCGCTTAAACCAAAAT	YTRLNQN	+++	-
5650	16576	TACAGTAGATTGTCCGGAAAC	YSRLSGN	+++	-
5651	15967	CTACACAAGTCTGGAATGAAT	LHKSGMN	+++	-
5652	14483	CTTTCTAAGGTCGGAGCTAAT	LSKVGAN	++	-
5653	16581	TACTTAAAGTCGCAGGCTATG	YLKSQAM	+++	-
5654	16582	TACGTTAAATCCTCCAATAAT	YVKSSNN	++	-
5655	16583	TACGTCAAATCGGACCATCAC	YVKSDHH	+++	-
5656	14507	TATGCTCGGTTAGGAATGAAC	YARLGMN	+++	-
5657	14133	TATACCAGACTGAATCAGAAC	YTRLNQN	+++	-
5658	13761	TACGCGCGTGGAGGAATGAAT	YARGGMN	+++	-
5659	16584	CGAGGGATCGACTTCTACCCC	RGIDFYP	+++	-
5660	16585	TACGTAAGGTCGGATGTTCGG	YVRSDVR	+++	-
5661	16583	TATGTTAAGTCTGATCACCAT	YVKSDHH	+++	-
5662	16038	TACGCGAAGAACGGATTCAAT	YAKNGFN	++	-
5663	16572	TACCTGAAATCAGAGCGCAAC	YLKSERN	+++	-
5664	14301	TACTCACGGTTGAATATGAAC	YSRLNMN	+++	-
5665	16580	TACTCAAAGCTCAACGACAAA	YSKLNDK	+++	-
5666	13956	TATAGTCGGATGAATGCAAAT	YSRMNAN	+++	-
5667	16575	CTGAGCAAATTATCCGCCAAT	LSKLSAN	+++	-
5668	16586	TATCATAAGTTAGCGAATAAT	YHKLANN	+++	-
5669	13933	TATGCAAGAGGTGGAAACAAT	YARGGNN	+++	-
5670	16573	AGGTCGGAGCACGTATTCCCC	RSEHVFP	+++	-
5671	16022	TATAGCAAGAATGGGATGAAC	YSKNGMN	++	-
5672	16087	TATTCGAAACTCGGTGGGAAC	YSKLGGN	++	-
5673	13761	TATGCACGCGGTGGGATGAAC	YARGGMN	+++	-
5674	14249	TATTCGCGGATGAACACTAAC	YSRMNTN	+++	-
5675	14056	TATTCACGAATGAATAACAAT	YSRMNNN	+++	-

5676	16587	TATCACATTTTAGGGAAAAAT	YHILGKN	++	-
5677	16588	CTAAGTAGGGTGGGCATCGAT	LSRVGID	++	-
5678	14301	TATTCTCGCTTAAACATGAAT	YSRLNMN	+++	-
5679	16581	TATTTGAAAAGTCAAGCAATG	YLKSQAM	+++	-
5680	16566	TACTTCACAGGTGTCGTCGCA	YFTGVVA	+++	n.d.
5681	13803	TATTCTCGGATGAACTCTAAC	YSRMNSN	+++	-
5682	16589	ATGTCCCGTATTGGAGTGAAT	MSRIGVN	++	-
5683	16590	TTAAGCCGCTCTGGCAATAAC	LSRSGNN	++	-
5684	16116	TACTCTAAATCGGGAGCGAAT	YSKSGAN	++	-
5685	16591	TATAGCAAAGCTCAGCCGAAT	YSKAQPN	+++	-
5686	16592	TACCACAAGTCGCAAAGTAAT	YHKSQSN	+++	-
5687	16593	GATATGTCCTCGCGAATCTGG	DMSSRIW	+++	n.d.
5688	16594	CACTCGAGGTTGAACGTATCG	HSRLNVS	++	-
5689	16592	TATCATAAAAGCCAGTCGAAC	YHKSQSN	+++	-
5690	16014	TACTCCAAAATGAATGATAAC	YSKMNDN	+++	-
5691	16586	TACCACAAACTTGCCAACAAC	YHKLANN	+++	-
5692	16595	CGAACACCAACTGTGTATCCT	RTPTVYP	+++	-
5693	15967	TTGCATAAATCAGGCATGAAC	LHKSGMN	+++	-
5694	16596	TATACGCGACTCTCGATGAAT	YTRLSMN	+++	-
5695	16597	TATCTGAAATCGGACAAAAGC	YLKSDKS	+++	-
5696	16598	TATACACGTTCACAGACAGAA	YTRSQTE	++	n.d.
5697	11826	GTAACGTCCACCAATGGCATC	VTSTNGI	++	-
5698	13933	TACGCTCGGGGAGGGAATAAC	YARGGNN	+++	-
5699	16599	TTCGTTAAGTCCGATACTAAA	FVKSDTK	+++	-
5700	16596	TACACCCGTTTGAGTATGAAC	YTRLSMN	+++	-
5701	13803	TACAGTCGTATGAATTCCAAT	YSRMNSN	+++	-
5702	16600	AGGGCGCTTGAATGCTGCTAC	RALECCY	+++	-
5703	16601	CTGCACCGCGATGGAATTAAC	LHRDGIN	++	-
5704	16014	TATTCGAAGATGAACGACAAT	YSKMNDN	+++	n.d.
5705	16579	TACCTTAAATCACAAGGTAAT	YLKSQGN	+++	n.d.
5706	16602	GTACATCGCCTGCAAGATAAG	VHRLQDK	+++	-
5707	15958	TACTCTCGACCTGGGCCGAAC	YSRPGPN	+++	-
5708	16585	TATGTTCGGTCCGACGTGCGA	YVRSDVR	+++	-

5709	16603	TATGTGCGTTCAGATAGGAAC	YVRSDRN	+++	-
5710	16005	TATGCAAGAATAGGCCTAAAT	YARIGLN	+++	n.d.
5711	16597	TACCTTAAGTCAGATAAGTCG	YLKSDKS	+++	-
5712	14249	TACTCTCGAATGAATACCAAT	YSRMNTN	+++	-
5713	16604	TATTCGTCCACTCATGGCGTG	YSSTHGV	+++	-
5714	16604	TACTCTTCGACCCACGGTGTA	YSSTHGV	+++	-
5715	16598	TACACTCGCAGCCAAACGGAG	YTRSQTE	++	-
5716	14056	TACAGCCGCATGAACAATAAC	YSRMNNN	+++	-
5717	16100	TACTCCAAAGTGCAAACTAAC	YSKVQTN	++	-
5718	15970	TTTAGTCGAGTGGGGTTTAAC	FSRVGFN	+++	-
5719	16591	TACAGTAAGGCCCAACCTAAC	YSKAQPN	+++	-
5720	16605	TCAATGGAATCTCGACTGTGG	SMESRLW	+++	-
5721	14507	TACGCACGCCTTGGGATGAAT	YARLGMN	+++	-
5722	16606	CTCCACCGCCTAGCATCTTCG	LHRLASS	+++	-
5723	16607	GACCTTTCGAGTCATAACTGG	DLSSHNW	+++	n.d.
5724	16588	TTGTCAAGAGTAGGTATAGAC	LSRVGID	++	-
5725	16608	CTTCATGCATTAAGTCATAAC	LHALSHN	+++	n.d.
5726	11826	GTCACTAGCACGAACGGGATA	VTSTNGI	++	-
5727	13764	TATGCTAGAAGCGGTTTAAAC	YARSGLN	+++	-
5728	16022	TACTCAAAAAACGGCATGAAT	YSKNGMN	++	-
5729	16595	CGTACTCCTACCGTCTACCCC	RTPTVYP	+++	-
5730	15996	TACTCTAAGGTCGGGCAGAAT	YSKVGQN	+++	-
5731	13984	TACTCAAGAATGGGAATGAAT	YSRMGMN	+++	-
5732	16609	CTCCATGTCCGAAGCCTAAAC	LHVRSLN	+++	-
5733	16601	TTGCATCGGGACGGTATCAAT	LHRDGIN	++	-
5734	12385	TATAGTCGGCAGAACGAGAAT	YSRQNEN	+++	-
5735	16137	TACTCACGCGTTAATGATAAT	YSRVNDN	+++	-
5736	16593	GACATGAGTAGTAGAATATGG	DMSSRIW	+++	n.d.
5737	16610	TATGTGAAATATGAAGATAAA	YVKYEDK	+++	-
5738	16116	TATTCCAAGTCAGGTGCAAAC	YSKSGAN	++	-
5739	16611	TATAGTCGCTTGCAAGAAAAT	YSRLQEN	+++	n.d.
5740	16568	CTGCACAGACTGTTAAAGGAT	LHRLLKD	+++	-
5741	13764	TACGCGCGATCTGGCCTGAAT	YARSGLN	+++	-

5742	16612	CTTTCTAGAGTAGGTTTCAAT	LSRVGFN	+++	-
5743	16137	TATTCGCGTGTAAACGACAAC	YSRVNDN	+++	n.d.
5744	16613	TACGCTCGGGGAGGGCCCAAT	YARGGPN	+++	-
5745	16613	TATGCGCGTGGTGGACCTAAC	YARGGPN	+++	-
5746	16614	CACTGCGGAAAATGCCTAAAT	HCGKCLN	+++	n.d.
5747	16615	TTGCACAGATCAGGCGATAAT	LHRSGDN	+++	-
5748	16615	CTGCATCGTTCTGGGGACAAC	LHRSGDN	+++	-
5749	13984	TATTCCCGAATGGGTATGAAC	YSRMGMN	+++	-
5750	15996	TATTCCAAAGTAGGCCAAAAC	YSKVGQN	+++	-
5751	16616	AACTGTAAGCCTTGCTTCGAT	NCKPCFD	+++	-
5752	16612	CTGTCACGCGTGGGCTTTAAC	LSRVGFN	+++	-
5753	12385	TACTCACGCCAAAATGAAAAC	YSRQNEN	+++	-
5754	16610	TACGTAAAGTACGAGGACAAG	YVKYEDK	+++	-
5755	16611	TACTCACGATTACAGGAGAAC	YSRLQEN	+++	n.d.
5756	16584	AGAGGCATTGATTTTTATCCT	RGIDFYP	+++	n.d.
5757	16617	CATAGTCGCATGAATGAAAAT	HSRMNEN	++	-
5758	16603	TACGTCAGAAGTGACAGAAAT	YVRSDRN	+++	-
5759	16607	GATTTGTCATCGCACAATTGG	DLSSHNW	+++	-
5760	16618	TTGCATCGGCTATCCCCTTAT	LHRLSPY	+++	-
5761	16077	TACTCAAGGATGAACGAAAAT	YSRMNEN	+++	-
5762	16619	CTGCATAAAGCTGGATATAAT	LHKAGYN	+++	-
5763	16608	TTACACGCTTTGTCACACAAT	LHALSHN	+++	n.d.
5764	16077	TATAGCCGTATGAATGAGAAC	YSRMNEN	+++	-
5765	16620	TTGTCACGGATTTCTGTAAAC	LSRISVN	+++	-
5766	16609	CTACACGTACGTAGTCTGAAT	LHVRSLN	+++	-
5767	16621	TATTCGAGGATGAACGACAAC	YSRMNDN	+++	-
5768	16622	TTATGGAGGACAGGGATTAAC	LWRTGIN	+++	n.d.
5769	16623	TATTTTATGGGGCGGTCCGAC	YFMGRSD	+++	n.d.
5770	16621	TACTCCCGGATGAATGATAAT	YSRMNDN	+++	-
5771	16624	CTACACCGAGCTAGCAGCAAC	LHRASSN	+++	+
5772	16625	TACTCCCGTGTTGATGATCGC	YSRVDDR	++	-
5773	16624	CTGCATCGTGCGTCATCCAAT	LHRASSN	+++	+
5774	16626	TATTCGCGCAACAGCGACAAC	YSRNSDN	++	-

5775	16627	TATAGTGCTCGTGGGCCCAAT	YSARGPN	+++	-
5776	16600	AGAGCTCTGGAGTGTTGTTAT	RALECCY	+++	-
5777	16628	TTAACTAGGATCTCACACAAC	LTRISHN	+++	+
5778	16628	CTGACCCGAATTAGTCATAAT	LTRISHN	+++	+
5779	16629	CTTTGTCGTCCATGTTCAGAG	LCRPCSE	+++	-
5780	16630	TTAAGTCGCTTAAATCACAAT	LSRLNHN	+++	+
5781	16631	CTACACGTGCTTGGACCGAAT	LHVLGPN	+++	-
5782	16632	TACTTCACGGGCATCTGGGCT	YFTGIWA	+++	n.d.
5783	16633	TACATGAAATATGATACACAA	YMKYDTQ	++	-
5784	16634	ATGTCACGGCTGTCACAGAAC	MSRLSQN	+++	-
5785	16635	CTCCATCGCAGTAGTAATAAT	LHRSSNN	+++	+–
5786	13828	TACGCTCGGTCCGGGTATAAT	YARSGYN	+++	-
5787	16636	TACCATCGTTTGTCCAATAAC	YHRLSNN	+++	-
5788	16631	CTGCATGTCCTGGGGCCAAAC	LHVLGPN	+++	-
5789	13828	TATGCGCGCAGCGGATACAAC	YARSGYN	+++	-
5790	16635	TTGCACAGGTCTTCAAACAAC	LHRSSNN	+++	+–
5791	16636	TATCACCGGCTTTCTAACAAT	YHRLSNN	+++	-
5792	16637	TATCATGCTCGCGCTCCGAAT	YHARAPN	+++	-
5793	16629	CTATGCAGACCGTGCTCGGAA	LCRPCSE	+++	+
5794	16618	TTACACAGACTGAGCCCATAC	LHRLSPY	+++	-
5795	16637	TACCACGCACGGGCCCCAAAC	YHARAPN	+++	n.d.
5796	16638	AACGAAGACTGGGTGAAGTGG	NEDWVKW	+++	-
5797	16634	ATGTCCCGATTATCTCAAAAT	MSRLSQN	+++	-
5798	16639	ATTATGAGCAGTCGAAGCTGG	IMSSRSW	+++	-
5799	16638	AATGAGGATTGGGTAAAATGG	NEDWVKW	+++	n.d.
5800	16614	CATTGTGGTAAGTGTCTTAAC	HCGKCLN	+++	n.d.
5801	16640	TACGCTCGAACTTCGCATAAT	YARTSHN	+++	-
5802	16641	AATGGTCCTCACGGCTGGAAT	NGPHGWN	+++	-
5803	13556	TACTCCCGAGCTGGATATAAC	YSRAGYN	+++	-
5804	16642	TGGGTACGGTCGGACACAAAA	WVRSDTK	+++	-
5805	16643	TACCAACGCCAAGGATGGGAC	YQRQGWD	++	-
5806	16640	TATGCCCGGACCTCCCACAAC	YARTSHN	+++	-
5807	16644	CGACTCTATGACGCTTATCAG	RLYDAYQ	+++	-

5808	16645	GGGCCGGGGTATGTGAACTGG	GPGYVNW	+++	+–
5809	16642	TGGGTGAGGTCTGATACGAAG	WVRSDTK	+++	-
5810	16641	AACGGCCCGCATGGTTGGAAC	NGPHGWN	+++	-
5811	16646	CTTCATCGCAATACTCAAAAC	LHRNTQN	+++	+––
5812	16646	TTGCACAGGAACACCCAGAAT	LHRNTQN	+++	+–
5813	16647	ATGCCTAATGAGGGGTGGTTT	MPNEGWF	+++	n.d.
5814	16648	TATCTAGATCGTGTTGTTTAC	YLDRVVY	+++	n.d.
5815	16649	TCCTACGCCCGGTCTGTGAAC	SYARSVN	+++	-
5816	16644	AGGCTATACGATGCCTACCAA	RLYDAYQ	+++	n.d.
5817	16648	TACCTCGACCGCGTGGTATAT	YLDRVVY	+++	n.d.
5818	16647	ATGCCAAACGAAGGATGGTTC	MPNEGWF	+++	n.d.
5819	16650	CTGACAAGGCTTTCCCACAAT	LTRLSHN	+++	-
5820	16649	AGTTATGCACGCAGCGTAAAT	SYARSVN	+++	-
5821	13556	TATAGTCGGGCCGGCTACAAT	YSRAGYN	+++	-
5822	16651	TATCGAAGTCTAGTTGTCGGG	YRSLVVG	+++	n.d.
5823	16650	CTTACCAGATTAAGCCATAAC	LTRLSHN	+++	-
5824	16652	TATGTGAAGTCCGATCGATGC	YVKSDRC	+++	+–
5825	16622	CTTTGGCGCACGGGTATCAAT	LWRTGIN	+++	+–
5826	16632	TATTTTACAGGAATATGGGCA	YFTGIWA	+++	n.d.
5827	16653	TACCACAGGGCTCAAATGAAT	YHRAQMN	+++	-
5828	16654	GATGGGGGCCGATCTGCTTGG	DGGRSAW	+++	-
5829	16651	TACCGTTCACTGGTAGTGGGT	YRSLVVG	+++	-
5830	16654	GACGGAGGGAGATCAGCATGG	DGGRSAW	+++	n.d.
5831	16655	CTGAGCCGGTCATCATACAAT	LSRSSYN	+++	+
5832	16652	TACGTCAAATCGGACAGATGT	YVKSDRC	+++	+–
5833	16656	CGTGTATTAGCAAACTGGCCT	RVLANWP	+++	n.d.
5834	16657	CTAATGATAGACGCTTTTCCA	LMIDAFP	+++	n.d.
5835	16658	TACCATAGGACTGGGAATAAT	YHRTGNN	+++	+–
5836	16658	TATCACCGGACAGGCAACAAC	YHRTGNN	+++	+
5837	16657	TTAATGATTGATGCATTCCCT	LMIDAFP	+++	-
5838	16655	TTGAGTAGGTCTTCTTATAAC	LSRSSYN	+++	-
5839	16659	ATGACATACGACAGTTACGAC	MTYDSYD	++	n.d.
5840	16660	CGAAATCTATATGATACTCAA	RNLYDTQ	+++	n.d.

5841	16661	TTTAAGCAGTTAGTCAACTAC	FKQLVNY	+++	n.d.
5842	16662	CAGCCATATGAGCTACCATGG	QPYELPW	+++	n.d.
5843	16663	GAGATGGAGTCCTTTAATTGG	EMESFNW	++	n.d.
5844	16664	ATGCATCGGCTGGCAGTAAAT	MHRLAVN	+++	-
5845	16665	AGGGTCTCGGTGTTATGGCCC	RVSVLWP	+++	n.d.
5846	16666	TATAAAAATCTAATACAAGGC	YKNLIQG	+++	-
5847	16667	CTCCATAGGTTAGCAGCCAAT	LHRLAAN	+++	-
5848	16663	GAAATGGAATCATTCAACTGG	EMESFNW	++	n.d.
5849	16666	TACAAGAACCTTATCCAGGGG	YKNLIQG	+++	-
5850	16661	TTCAAACAACTGGTGAATTAT	FKQLVNY	+++	-
5851	16668	TATTTCAATGTTGTTAAGGGG	YFNVVKG	+++	n.d.
5852	16664	ATGCACAGACTTGCGGTTAAC	MHRLAVN	+++	-
5853	16669	CAGTATGTCCGATCATCAATA	QYVRSSI	+++	-
5854	16667	CTGCACCGGCTCGCTGCGAAC	LHRLAAN	+++	-
5855	16670	ATGTCAAGGTTCGACATTCAT	MSRFDIH	+++	n.d.
5856	16669	CAATACGTGCGTAGCTCGATC	QYVRSSI	+++	-
5857	16668	TACTTTAACGTAGTAAAAGGA	YFNVVKG	+++	-
5858	16671	CTTACGTACGACGCCTATGAA	LTYDAYE	+++	n.d.
5859	16672	TGGGGCTTATGGAGGCTGGAC	WGLWRLD	+++	n.d.
5860	16673	TACCGTGACATCATATCGGGT	YRDIISG	+++	-
5861	16673	TATCGAGATATAATTTCAGGA	YRDIISG	+++	-
5862	16671	TTGACATATGATGCATACGAG	LTYDAYE	+++	n.d.
5863	16674	TCCTATACCCGCCTCCAAACG	SYTRLQT	+++	n.d.
5864	16675	CAGTATACACGCAACGTGTCC	QYTRNVS	+++	-
5865	16674	TCATACACACGGCTACAGACT	SYTRLQT	+++	-
5866	16645	GGCCCTGGATACGTCAATTGG	GPGYVNW	+++	n.d.
5867	16676	TTACACGTCCGGCTCAACAAT	LHVRLNN	+++	-
5868	16677	AGAACCAGGGAAGTTTGGCCT	RTREVWP	+++	n.d.
5869	16678	AACGCCCCTCTATGGTTTTCC	NAPLWFS	+++	+--
5870	16679	CGTAACGCGTTTGACCATATG	RNAFDHM	+++	n.d.
5871	16675	CAATACACCCGAAATGTAAGT	QYTRNVS	+++	-
5872	16680	TTCTCGGGCAGGGTACTTTTT	FSGRVLF	+++	n.d.
5873	16681	AAGCATGGGACCATGTGGGGG	KHGTMWG	+++	n.d.

5874	16682	TCTCGCAAAACGGGATACCCT	SRKTGYP	+++	-
5875	16683	ATACAAAACAAACTATGGTCT	IQNKLWS	+++	n.d.
5876	16684	TCTTACACTAGGCTCACCTTG	SYTRLTL	+++	n.d.
5877	16678	AATGCGCCCCTCTGGTTCTCG	NAPLWFS	+++	n.d.
5878	16685	AACGATTTGGTCCACTGGCCT	NDLVHWP	+++	n.d.
5879	16682	AGCCGGAAGACTGGCTATCCA	SRKTGYP	+++	-
5880	16686	GCCTATAGCAGACTCATGTCT	AYSRLMS	+++	n.d.
5881	16687	TGGCCATCAATCACGACCTAT	WPSITTY	+++	n.d.
5882	16688	CAACTGTCCGGGCTATGGCCT	QLSGLWP	+++	n.d.
5883	16689	AATTCTCCCTTTGATACTTAC	NSPFDTY	+++	-
5884	16690	ATGTCACCGCTGGTGTGGACC	MSPLVWT	+++	n.d.
5885	16691	CGGCAAGGGACGTACTTTCCG	RQGTYFP	+++	n.d.
5886	16692	ACCAATACCATAAGATGGCCC	TNTIRWP	+++	+–
5887	16693	TACGCGATTTATTCAACCCAC	YAIYSTH	+++	n.d.
5888	16694	TCAGCACTGCACGGGTACCCT	SALHGYP	+++	n.d.
5889	16695	ATATATGTGAGATCGATTTCT	IYVRSIS	+++	n.d.
5890	16696	ACCCGGGGTATGGATTGGCCT	TRGMDWP	+++	n.d.
5891	16697	TACAAGCAATGGCATTTCGAT	YKQWHFD	+++	-
5892	16698	GTATACGTCCGATCGCAGTCC	VYVRSQS	+++	-
5893	16699	CTCATTAATGGCAGTTGGCCG	LINGSWP	+++	-
5894	16700	GTGCCCATATGGCATAATGGT	VPIWHNG	+++	-
5895	16701	GTAGTTCATGGGGTTTGGCCC	VVHGVWP	+++	n.d.
5896	16702	TCCTACGTCCGGAGTACCCAA	SYVRSTQ	+++	-
5897	16703	GGTAGCCCAATAAACTGGGCC	GSPINWA	+++	n.d.
5898	16694	AGTGCGCTACATGGTTATCCA	SALHGYP	+++	n.d.
5899	16704	ATATATAGTAAATTACAGCAT	IYSKLQH	+++	-
5900	16705	GAGGAATCTTTTTGGCGAGCA	EESFWRA	+++	n.d.
5901	16686	GCTTACAGTCGACTTATGTCA	AYSRLMS	+++	n.d.
5902	16706	GTTTGGGTTAAAAGCTCGATC	VWVKSSI	+++	n.d.
5903	16698	GTGTATGTAAGATCTCAAAGC	VYVRSQS	+++	-
5904	16707	ACTTACGTGCGATCTATTACT	TYVRSIT	+++	n.d.
5905	16708	AAGACAGGCGGAATTTGGCCA	KTGGIWP	+++	n.d.
5906	16690	ATGAGTCCCTTAGTCTGGACG	MSPLVWT	+++	n.d.

5907	16709	CCAGGCTCGCTGCGCTATGGC	PGSLRYG	+++	-
5908	16710	CTTGTGTCAAATGACTGGCCC	LVSNDWP	+++	n.d.
5909	16711	GGGAGAAGCGTAAGCACTTGG	GRSVSTW	+++	-
5910	16712	GGGAGCACCTACAGCCGGGCG	GSTYSRA	+++	-
5911	16709	CCGGGAAGTTTGAGATACGGT	PGSLRYG	+++	-
5912	16713	AAAATTAGTGGATCATGGCCA	KISGSWP	+++	n.d.
5913	16714	AAACTTGGAACAGCCTGGCCG	KLGTAWP	+++	n.d.
5914	16715	GTGTATAGTCGCATCGATATT	VYSRIDI	+++	-
5915	16716	ATTTACGTGCGAAGTGCTAGT	IYVRSAS	+++	-
5916	16689	AACAGTCCGTTCGACACGTAT	NSPFDTY	+++	n.d.
5917	16687	TGGCCCTCGATTACTACGTAC	WPSITTY	+++	n.d.
5918	16717	CGGAGCCTTTACGACACGTTG	RSLYDTL	+++	n.d.
5919	16718	TACTATGATCTTGTCGAATAC	YYDLVEY	+++	n.d.
5920	16719	ATGTTGGAATATTATAACAAT	MLEYYNN	+++	+
5921	16708	AAAACGGGTGGTATATGGCCT	KTGGIWP	+++	n.d.
5922	16685	AATGACCTGGTTCATTGGCCC	NDLVHWP	+++	n.d.
5923	16720	ACTAATATGTACGACACTTAT	TNMYDTY	+++	n.d.
5924	16721	AAGATCCTAACGGTGTGGCCA	KILTVWP	+++	n.d.
5925	16716	ATATATGTACGGTCGGCAAGC	IYVRSAS	+++	-
5926	16704	ATTTACTCGAAGCTGCAACAC	IYSKLQH	+++	-
5927	16715	GTTTACTCCCGGATAGACATA	VYSRIDI	+++	-
5928	16702	TCTTATGTACGCTCCACACAG	SYVRSTQ	+++	n.d.
5929	16722	TTGTATACTCGATTAGATATT	LYTRLDI	+++	-
5930	16723	AGAGATGAGGCCAACTGGCCT	RDEANWP	+++	n.d.
5931	16724	AAATCTCCTAACACGCCATGG	KSPNTPW	+++	-
5932	16725	GGGTTCATAACTGTCTACCCA	GFITVYP	+++	n.d.
5933	16726	ACCCGCAGCATGTGGAGCGAA	TRSMWSE	+++	n.d.
5934	16727	TATAAGACAAACAATTGGCCG	YKTNNWP	+++	n.d.
5935	16728	AAAAATGCAACCGTGTGGCCC	KNATVWP	+++	n.d.
5936	16729	GTTGTCAAAGATTACTGGCCT	VVKDYWP	+++	n.d.
5937	16730	GGGCTAGGCTGGATAAACGGC	GLGWING	+++	n.d.
5938	16731	CAATACGTGAGAACAGCAACA	QYVRTAT	+++	n.d.
5939	16731	CAGTATGTACGCACGGCGACT	QYVRTAT	+++	-

5940	16732	AGAAATACGTATGACTCATAT	RNTYDSY	+++	n.d.
5941	16733	GTTCCTACGATGTGGAGTGCG	VPTMWSA	+++	n.d.
5942	16734	ATCGTTGGGGAGGCGTGGCCT	IVGEAWP	+++	n.d.
5943	16707	ACCTATGTCCGGTCAATAACA	TYVRSIT	+++	-
5944	16735	ACTGTCACCGAAGTCTGGCCA	TVTEVWP	+++	n.d.
5945	16736	AAGCAACCGGTGTGGTTAGCA	KQPVWLA	+++	n.d.
5946	16723	AGGGACGAAGCTAATTGGCCC	RDEANWP	+++	n.d.
5947	16737	AAGTACACAAGGACCGAAATC	KYTRTEI	+++	-
5948	16738	CCCATGCCGAATATGGTGTGG	PMPNMVW	+++	n.d.
5949	16722	CTATACACCCGGCTTGACATC	LYTRLDI	+++	-
5950	16739	GCTCGTGGGCAGTTACCGTGG	ARGQLPW	+++	n.d.
5951	16740	CTGCAGGGGTCAAATTGGCCC	LQGSNWP	+++	+
5952	16741	ACGCAGGCACTCAACTGGCCC	TQALNWP	+++	n.d.
5953	16724	AAGTCACCGAATACTCCCTGG	KSPNTPW	+++	-
5954	16742	ATGTATGTTCGATCCGTGGAG	MYVRSVE	++	-
5955	16743	GCTTTGACGAGGCTCCAAATG	ALTRLQM	+++	-
5956	16697	TATAAACAGTGGCACTTTGAC	YKQWHFD	+++	n.d.
5957	16744	GATCCAAAAGGGTATTTTTTT	DPKGYFF	+++	n.d.
5958	16711	GGACGAAGTGTTTCCACCTGG	GRSVSTW	+++	-
5959	16677	CGTACTAGAGAGGTGTGGCCA	RTREVWP	+++	+-
5960	16745	TCTTATGTCCGAACGTTAAGT	SYVRTLS	+++	-
5961	16746	CGACAGAATAGTGTCTGGCCA	RQNSVWP	+++	-
5962	16747	GCTTTTGTTCGGAGCGTACCA	AFVRSVP	+++	-
5963	16748	AACAAGAACGGTAACTGGCCC	NKNGNWP	+++	-
5964	16699	CTGATAAACGGATCTTGGCCC	LINGSWP	+++	n.d.
5965	16749	CAGTACACTCGTCTGCAGCTT	QYTRLQL	+++	n.d.
5966	16750	GTAAAGCCTAATATAATGTGG	VKPNIMW	+++	-
5967	16751	AAGAGCGGGGACCACTGGCCA	KSGDHWP	+++	n.d.
5968	16752	ATCTATATAAAGTCAGCGGTG	IYIKSAV	+++	-
5969	16753	CGACTTAACGATACTTGGCCA	RLNDTWP	+++	-
5970	16717	AGGTCGCTATATGATACACTA	RSLYDTL	+++	n.d.
5971	16751	AAATCTGGCGATCATTGGCCC	KSGDHWP	+++	n.d.
5972	16754	ATGGTCAATAAAACCTGGCCG	MVNKTWP	+++	-

5973	16745	AGCTACGTGCGCACCTTGTCA	SYVRTLS	+++	-
5974	16755	GTCTATTCCCGACTAGATACA	VYSRLDT	+++	n.d.
5975	16713	AAGATATCCGGTTCTTGGCCT	KISGSWP	+++	-
5976	16756	TTAAAAGACCATAATTGGCCT	LKDHNWP	+++	-
5977	16757	AGTGCCCCGATCTATTTTAAT	SAPIYFN	+++	n.d.
5978	16737	AAATATACTCGGACTGAGATT	KYTRTEI	+++	-
5979	16758	TTGGTTCATGACGCTTGGCCG	LVHDAWP	+++	n.d.
5980	16759	AGGTGGGATCCACACGACCAA	RWDPHDQ	+++	n.d.
5981	16755	GTGTACAGCCGCCTTGACACC	VYSRLDT	+++	n.d.
5982	16760	CTCAATGTTTGGAAGCAACCA	LNVWKQP	+++	n.d.
5983	16761	AGGTTGACAGATACTTGGCCG	RLTDTWP	+++	n.d.
5984	16681	AAACACGGAACTATGTGGGGA	KHGTMWG	+++	+–
5985	16762	ATTTATGTTAAGAGTGTTAGT	IYVKSVS	+++	-
5986	16763	ATGAAAGGGAACAACTGGCCG	MKGNNWP	+++	-
5987	16764	AGAAACGTATATGATGGGTAC	RNVYDGY	+++	n.d.
5988	16765	ATATATATAAAGTCGAGCACC	IYIKSST	+++	-
5989	16766	ACTAAACACTATACATTTCCC	TKHYTFP	+++	n.d.
5990	16743	GCATTAACCCGGTTACAGATG	ALTRLQM	+++	-
5991	16750	GTTAAACCAAACATCATGTGG	VKPNIMW	+++	-
5992	16767	TGGAAAATGACTCAACTCGGC	WKMTQLG	+++	-
5993	16693	TATGCTATCTACTCGACACAT	YAIYSTH	+++	n.d.
5994	16768	CAGTATATTCGTTCTAGCAGT	QYIRSSS	+++	-
5995	16769	TCTATGATCCTTGACTGGAAG	SMILDWK	+++	n.d.
5996	16767	TGGAAGATGACGCAGCTTGGT	WKMTQLG	+++	-
5997	16770	CGCGAGTTCGAGCAGTGGCCA	REFEQWP	+++	-
5998	16771	TATACCGTCTATTCAACGTTC	YTVYSTF	+++	n.d.
5999	16761	AGACTAACGGACACATGGCCC	RLTDTWP	+++	-
6000	16770	AGGGAATTTGAACAATGGCCG	REFEQWP	+++	n.d.
6001	16747	GCCTTCGTAAGATCGGTTCCG	AFVRSVP	+++	-
6002	16766	ACGAAGCATTACACTTTCCCG	TKHYTFP	+++	-
6003	16772	AATAAGCCACTCGACTGGAAA	NKPLDWK	+++	-
6004	16728	AAGAACGCGACAGTCTGGCCG	KNATVWP	+++	-
6005	16762	ATCTACGTAAAATCTGTCTCG	IYVKSVS	+++	-

6006	16773	GCTACCTGGCCGTTGATGGGG	ATWPLMG	+++	n.d.
6007	16752	ATATACATTAAAAGTGCCGTA	IYIKSAV	+++	n.d.
6008	16774	GGTAACGAATTTTGGAGTCCA	GNEFWSP	+++	n.d.
6009	16695	ATCTACGTCCGCTCAATATCA	IYVRSIS	+++	n.d.
6010	16775	CTCATGAACAACGATTGGCCC	LMNNDWP	+++	n.d.
6011	16776	GTTACGGGGGCGGTTTGGCCG	VTGAVWP	+++	n.d.
6012	16696	ACGCGTGGCATGGACTGGCCG	TRGMDWP	+++	n.d.
6013	16777	TCGGGACCTATCTGGCTAGCA	SGPIWLA	+++	n.d.
6014	16778	CATAAAAACCCACTGTGGGGG	HKNPLWG	+++	-
6015	16779	TCCAACGGCAGGCTAAACTGG	SNGRLNW	+++	-
6016	16749	CAATATACCAGGTTGCAATTA	QYTRLQL	+++	n.d.
6017	16780	ATACGGGGTAATGAATGGCCA	IRGNEWP	+++	n.d.
6018	16781	AGGGGTCCAGTGTATCTTTCG	RGPVYLS	+++	-
6019	16782	AGGAACAAAGGAGACTGGCCT	RNKGDWP	+++	-
6020	16783	GTGTCGCTCTTTTCAAATCAC	VSLFSNH	+++	n.d.
6021	16763	ATGAAGGGCAATAATTGGCCT	MKGNNWP	+++	n.d.
6022	16782	CGCAATAAGGGGGATTGGCCG	RNKGDWP	+++	-
6023	16741	ACACAAGCTCTTAATTGGCCG	TQALNWP	+++	n.d.
6024	16736	AAACAGCCCGTTTGGCTTGCC	KQPVWLA	+++	n.d.
6025	16784	CAAGGCCTCTGGAGGGACGCC	QGLWRDA	+++	-
6026	16753	CGGCTCAATGACACCTGGCCT	RLNDTWP	+++	n.d.
6027	16684	TCCTATACGCGGTTAACACTC	SYTRLTL	+++	n.d.
6028	16785	TTTGTCGCATCCGAGTGGCCA	FVASEWP	+++	n.d.
6029	16786	GTCTATCATAAATTTCAGATC	VYHKFQI	+++	+
6030	16787	GGTCGTCCTAACCTACTATGG	GRPNLLW	+++	+
6031	16788	TGGCGCAGCACTAGTTTCGGG	WRSTSFG	+++	n.d.
6032	16780	ATTCGAGGCAACGAGTGGCCG	IRGNEWP	+++	n.d.
6033	16768	CAATACATAAGGTCCAGTTCG	QYIRSSS	+++	-
6034	16789	AATAACATATTTGCCACATAT	NNIFATY	+++	n.d.
6035	16790	TCACGATTAACGCTCTTCCCC	SRLTLFP	+++	-
6036	16791	CGGTATTTGAAAAGCCAAGAA	RYLKSQE	+++	-
6037	16778	CACAAGAATCCTTTGTGGGGT	HKNPLWG	+++	-
6038	16792	ACTTTTGTCAGGTCAGTTCTA	TFVRSVL	+++	n.d.

6039	16793	ACTCGTATGGCCATGTTCCCT	TRMAMFP	+++	-
6040	16794	CAATATACGCATAAAGTACTT	QYTHKVL	+++	-
6041	16795	ATGGCACAGGGTAATTGGCCT	MAQGNWP	+++	n.d.
6042	16796	GTCTACTCTAAATTGATGACC	VYSKLMT	+++	-
6043	16775	TTAATGAATAATGACTGGCCA	LMNNDWP	+++	-
6044	16706	GTGTGGGTGAAGTCGTCAATA	VWVKSSI	+++	n.d.
6045	16797	ATGATGTCGGACGCTTGGCCG	MMSDAWP	+++	n.d.
6046	16798	CGCAAAGAAAGCATGTGGCCC	RKESMWP	+++	n.d.
6047	16799	TCCGGCTGGCTGACCGAGGTT	SGWLTEV	+++	n.d.
6048	16740	TTGCAAGGCTCTAACTGGCCG	LQGSNWP	+++	-
6049	16800	GTGCTATCGGGCATGTGGCCC	VLSGMWP	+++	n.d.
6050	16733	GTGCCGACTATGTGGTCCGCA	VPTMWSA	+++	n.d.
6051	16801	TCTTATTCTAGGGTTCAGGTG	SYSRVQV	+++	-
6052	16802	GATGGGTTAGCCGGTTACTAT	DGLAGYY	+++	n.d.
6053	16803	GATCCAGTTAACGTGTGGGGC	DPVNVWG	+++	n.d.
6054	16804	GTGTACACGCGCATGGATATC	VYTRMDI	+++	-
6055	16791	AGATACCTGAAGAGTCAGGAG	RYLKSQE	+++	-
6056	16805	GTTGAACACAACAATTGGCCC	VEHNNWP	+++	n.d.
6057	16806	TCTTACGCACGCTCGGTCCCG	SYARSVP	+++	-
6058	16688	CAGTTGAGCGGCCTCTGGCCG	QLSGLWP	+++	n.d.
6059	16807	CAAAGAGCTACTTTATTTCCC	QRATLFP	+++	n.d.
6060	16765	ATTTACATCAAAAGCTCAACG	IYIKSST	+++	-
6061	16735	ACAGTTACTGAGGTGTGGCCC	TVTEVWP	+++	n.d.
6062	16781	AGAGGACCGGTTTACTTATCC	RGPVYLS	+++	n.d.
6063	16808	ACGTACAGTAGGCTGCAACTA	TYSRLQL	+++	-
6064	16809	ATGGATAAAGATGCTTGGCCG	MDKDAWP	+++	n.d.
6065	16810	GAAAAAGGGATGTGGACCCCC	EKGMWTP	+++	n.d.
6066	16811	CTATACGTAAAGTCAACAGTT	LYVKSTV	+++	-
6067	16804	GTCTATACCCGAATGGACATT	VYTRMDI	+++	n.d.
6068	16812	GCTATGGGGTCTCTTTGGCCG	AMGSLWP	+++	n.d.
6069	16813	ATGATGGGTCAGCAATGGCCC	MMGQQWP	+++	n.d.
6070	16754	ATGGTTAACAAGACATGGCCC	MVNKTWP	+++	-
6071	16814	AGTTATGTAAAGTCCTCCACT	SYVKSST	+++	-

6072	16815	CTAATTCTGGAAAATTGGCCC	LILENWP	+++	n.d.
6073	16816	CGCAATGGAGACAATTGGCCG	RNGDNWP	+++	-
6074	16718	TATTACGACCTCGTGGAGTAT	YYDLVEY	+++	+-
6075	16817	GTCTTCTCGAAGATACAGCAC	VFSKIQH	+++	-
6076	16818	GTAATGAAGGACCTTTGGCCG	VMKDLWP	+++	-
6077	16714	AAGCTAGGGACGGCATGGCCA	KLGTAWP	+++	+
6078	16726	ACTAGGTCTATGTGGTCAGAG	TRSMWSE	+++	n.d.
6079	16806	TCGTATGCCCGGTCTGTGCCT	SYARSVP	+++	n.d.
6080	16808	ACATATTCGCGTTTACAGTTA	TYSRLQL	+++	-
6081	16819	AAACGTCTCCAGGAATGGCCT	KRLQEWP	+++	-
6082	16812	GCGATGGGTTCGCTATGGCCC	AMGSLWP	+++	+-
6083	16820	CCTATGAACGGGAATTGGCCT	PMNGNWP	+++	n.d.
6084	16821	ATAAATCTGAAGGAGTGGCCG	INLKEWP	+++	n.d.
6085	16772	AACAAACCCTTAGATTGGAAG	NKPLDWK	+++	n.d.
6086	16822	CAATACGTCTTGTCGATGAAA	QYVLSMK	+++	-
6087	16734	ATAGTCGGAGAAGCTTGGCCG	IVGEAWP	+++	n.d.
6088	16823	AACTTGATGGGAACATGGCCC	NLMGTWP	+++	n.d.
6089	16824	GTGTTCTCGAAGAGCATGTAC	VFSKSMY	+++	-
6090	16825	CAGTATGTGAAATCCACCACT	QYVKSTT	+++	-
6091	16826	AAGCCCATGTATCTAGGTACG	KPMYLGT	+++	n.d.
6092	16727	TACAAAACTAATAACTGGCCA	YKTNNWP	+++	n.d.
6093	16811	TTGTATGTTAAAAGCACGGTG	LYVKSTV	+++	n.d.
6094	16827	CAGTACACCAAGAGCGTACCC	QYTKSVP	+++	-
6095	16828	CAGTTTGTGAAATCTATCTCT	QFVKSIS	+++	n.d.
6096	16829	GATGGTTTCACCAATCTCTGG	DGFTNLW	+++	n.d.
6097	16830	AAGAACGCCGAGGTGTGGCCT	KNAEVWP	+++	n.d.
6098	16831	TCACGTTCAAGCTTATTCCCT	SRSSLFP	+++	-
6099	16795	ATGGCTCAAGGGAACTGGCCC	MAQGNWP	+++	n.d.
6100	16832	GTATATCACAAACTTACCACA	VYHKLTT	+++	-
6101	16832	GTGTACCATAAGCTCACGACT	VYHKLTT	+++	-
6102	16833	GGTGGAATGTTCATGAGTCCC	GGMFMSP	+++	-
6103	16834	CAGTACGTACGCTCCGAACCG	QYVRSEP	+++	-
6104	16835	CGCAACAACTATGACAACTAT	RNNYDNY	+++	-

6105	16836	GTGTATGTCCGCAGTGCGGAG	VYVRSAE	+++	n.d.
6106	16837	CAGTATGTCATTAGTCAAAAG	QYVISQK	+++	-
6107	16756	CTCAAGGATCACAACTGGCCA	LKDHNWP	+++	-
6108	16838	AAAAATCCATTGCAGTTTCAT	KNPLQFH	+++	n.d.
6109	16839	CGTGGAACGTTTGACGTTTAC	RGTFDVY	+++	-
6110	16760	CTTAACGTCTGGAAACAGCCC	LNVWKQP	+++	-
6111	16840	CACCGCGGTGAACTCAACTGG	HRGELNW	+++	n.d.
6112	16841	ATGCGCGTAATCGACTGGTCT	MRVIDWS	+++	n.d.
6113	16842	ATTCATGATGGTGTTTGGCCT	IHDGVWP	+++	n.d.
6114	16843	GGCACTGCAAAGCACCCCTGG	GTAKHPW	+++	n.d.
6115	16843	GGAACAGCTAAACATCCATGG	GTAKHPW	+++	n.d.
6116	16825	CAATACGTTAAGTCAACTACA	QYVKSTT	+++	n.d.
6117	16844	TGGCGTGGCACCAGTATGCAA	WRGTSMQ	+++	-
6118	16784	CAGGGTCTATGGCGCGATGCG	QGLWRDA	+++	n.d.
6119	16845	TGGAAGGGAACCACATTTCAC	WKGTTFH	+++	-
6120	16813	ATGATGGGACAACAGTGGCCG	MMGQQWP	+++	n.d.
6121	16846	GTCTACACAAAGTCAACCTCT	VYTKSTS	+++	n.d.
6122	16785	TTCGTGGCTTCTGAATGGCCT	FVASEWP	+++	+
6123	16847	AACAATAAAGGAAACTGGCCG	NNKGNWP	+++	-
6124	16848	ACGGGTGTATGGATGCAAACG	TGVWMQT	+++	n.d.
6125	16849	GATCGGATTAACTACTTGGGG	DRINYLG	+++	-
6126	16850	ACCTACTCGAGGCTCGACTCG	TYSRLDS	+++	-
6127	16851	TCCTACATATATGATGGCGAC	SYIYDGD	+++	n.d.
6128	16852	GCCTATGTGAAATCTATAACC	AYVKSIT	+++	-
6129	16853	CAGTATACGAAGCACGTTTCA	QYTKHVS	+++	+-
6130	16854	CGCCAGCATGTGCTATTTCCC	RQHVLFP	+++	n.d.
6131	16739	GCGAGAGGACAATTGCCCTGG	ARGQLPW	+++	n.d.
6132	16855	GGAAAGAGCATAACGCATTGG	GKSITHW	+++	-
6133	16856	AGTTATGCGAAATCAGTAATA	SYAKSVI	+++	-
6134	16857	GGGCGAATTACGCTGTTTCCG	GRITLFP	+++	n.d.
6135	16858	ATTTACTCTGCTCTGCAAACG	IYSALQT	+++	n.d.
6136	16859	AAAGTACAGCAACAGTGGCCG	KVQQQWP	+++	-
6137	16860	GCATACGTGAAGTCCATGTCT	AYVKSMS	+++	-

6138	16861	AAACGTGATAGCATGTGGCCG	KRDSMWP	+++	n.d.
6139	16862	ATGTTAGCGGAGAACTGGCCG	MLAENWP	+++	n.d.
6140	16793	ACACGGATGGCGATGTTTCCA	TRMAMFP	+++	n.d.
6141	16826	AAACCTATGTACTTGGGGACA	KPMYLGT	+++	n.d.
6142	16831	AGTAGATCGAGTCTTTTTCCC	SRSSLFP	+++	-
6143	16759	CGTTGGGACCCCCATGATCAG	RWDPHDQ	+++	n.d.
6144	16863	CCAATGAGGGGCCACCTGTTC	PMRGHLF	+++	n.d.
6145	16845	TGGAAAGGTACTACGTTCCAT	WKGTTFH	+++	-
6146	16864	TACCAACGGGCTGATTGGCCG	YQRADWP	+++	-
6147	16865	GCGTACGTTAAGAGTTCAATC	AYVKSSI	+++	-
6148	16801	AGTTACAGCCGGGTACAAGTC	SYSRVQV	+++	-
6149	16866	TTCCTAAAGTATAGTGATTAC	FLKYSDY	+++	n.d.
6150	16867	CGCATTTCGAACGATTGGCCC	RISNDWP	+++	n.d.
6151	16827	CAATATACTAAAAGTGTGCCT	QYTKSVP	+++	-
6152	16868	AAATTTGAATCGAATTGGCCT	KFESNWP	+++	n.d.
6153	16869	GTAAAGGGAGAGGCTTGGCCG	VKGEAWP	++	-
6154	16870	CAATATGTAAAGCATCTATCT	QYVKHLS	+++	-
6155	16836	GTTTACGTACGGTCGGCTGAA	VYVRSAE	+++	-
6156	16810	GAGAAGGGAATGTGGACGCCG	EKGMWTP	+++	n.d.
6157	16871	AAAGTAGGGGCTCTGTGGCCC	KVGALWP	+++	n.d.
6158	16872	GTTTACACCCGTACAGAGAAG	VYTRTEK	+++	+--
6159	16873	GACACATGGAATATGGGAGGC	DTWNMGG	+++	n.d.
6160	16874	TACAACCATCCACTAAATTGG	YNHPLNW	+++	n.d.
6161	16872	GTGTATACACGAACCGAAAAA	VYTRTEK	+++	+--
6162	16764	CGAAATGTGTACGACGGTTAT	RNVYDGY	+++	n.d.
6163	16875	GTTCATCACAAAAGCATGACA	VHHKSMT	+++	+--
6164	16876	TGGCAGGGGGAGCATCCATGG	WQGEHPW	+++	n.d.
6165	16877	GACAGGAATAAACTTATCTGG	DRNKLIW	+++	-
6166	16796	GTGTATTCAAAGCTTATGACG	VYSKLMT	+++	-
6167	16878	TGGCAGCCCGACCCCTTTCCA	WQPDPFP	+++	n.d.
6168	16730	GGCTTGGGGTGGATTAATGGG	GLGWING	+++	n.d.
6169	16656	CGAGTTCTAGCGAATTGGCCG	RVLANWP	+++	-
6170	16879	TGGACAACTCATAATATCGTT	WTTHNIV	+++	-

6171	16807	CAGCGCGCAACCCTATTCCCT	QRATLFP	+++	n.d.
6172	16794	CAGTACACACACAAGGTTTTG	QYTHKVL	+++	-
6173	16732	CGTAACACATACGATAGCTAC	RNTYDSY	+++	n.d.
6174	16880	GACATGCCGAACTGGTCGTGG	DMPNWSW	+++	n.d.
6175	16881	ATATACGTAAAATTCGAATCG	IYVKFES	+++	n.d.
6176	16882	TACGTAGCTGACGATTGGCCA	YVADDWP	+++	n.d.
6177	16870	CAGTACGTCAAACACTTGTCC	QYVKHLS	+++	-
6178	16819	AAGCGGTTACAAGAGTGGCCA	KRLQEWP	+++	-
6179	16883	CGGGAAAGGAACGAGTGGCCT	RERNEWP	+++	n.d.
6180	16884	AAGATAGAGGGGAGCTGGCCA	KIEGSWP	+++	-
6181	16860	GCGTATGTTAAATCAATGAGT	AYVKSMS	+++	-
6182	16885	TCATATGTTAAGTCCCAAACT	SYVKSQT	+++	-
6183	16869	GTCAAAGGCGAAGCCTGGCCC	VKGEAWP	++	-
6184	16797	ATGATGAGCGATGCATGGCCC	MMSDAWP	+++	n.d.
6185	16886	TATTTGGATCTCGATTGGCCA	YLDLDWP	+++	-
6186	16852	GCTTACGTTAAGAGTATCACT	AYVKSIT	+++	-
6187	16814	AGCTACGTGAAATCATCGACA	SYVKSST	+++	-
6188	16886	TACCTTGACTTGGACTGGCCC	YLDLDWP	+++	n.d.
6189	16849	GACCGCATAAATTATCTTGGA	DRINYLG	+++	n.d.
6190	16887	AAGGTGGAGTACAACTGGCCG	KVEYNWP	+++	n.d.
6191	16888	TCAGAGCAAGAATTTAACTGG	SEQEFNW	+++	n.d.
6192	16850	ACTTATTCCCGACTGGATTCA	TYSRLDS	+++	-
6193	16889	GTATACACAAAGAATGAACGG	VYTKNER	+++	+–
6194	16890	ATCTACTCAAAACTGCAAACA	IYSKLQT	+++	-
6195	16855	GGCAAATCAATCACTCACTGG	GKSITHW	+++	n.d.
6196	16891	GGCATCTATGCTACCTTCCCG	GIYATFP	+++	n.d.
6197	16892	AACCATCCGCTTGCTTGGGAG	NHPLAWE	+++	n.d.
6198	16893	CGGCGCTCCGACAATTGGCCT	RRSDNWP	+++	-
6199	16828	CAATTCGTCAAGTCGATTAGT	QFVKSIS	+++	n.d.
6200	16805	GTCGAGCATAATAACTGGCCA	VEHNNWP	+++	-
6201	16894	CGACACACTACGGAGTGGCCT	RHTTEWP	+++	-
6202	16895	AATAAGCCTCTATATTTCTCC	NKPLYFS	+++	n.d.
6203	16896	GTGTATGTCAAGACTCAATCG	VYVKTQS	+++	-

6204	16887	AAAGTAGAATATAATTGGCCA	KVEYNWP	+++	-
6205	16897	GGCCAGCAGTATAGTTATTCG	GQQYSYS	+++	-
6206	16897	GGGCAACAATACTCATACAGC	GQQYSYS	+++	n.d.
6207	16848	ACAGGGGTTTGGATGCAGACT	TGVWMQT	+++	n.d.
6208	16866	TTTTTGAAATACTCTGACTAT	FLKYSDY	+++	n.d.
6209	16898	TCATACAGCCGCATTGCCCCA	SYSRIAP	+++	-
6210	16875	GTACACCATAAGTCTATGACT	VHHKSMT	+++	+--
6211	16792	ACATTCGTTCGATCCGTATTA	TFVRSVL	+++	n.d.
6212	16877	GATCGGAACAAGCTAATATGG	DRNKLIW	+++	-
6213	16899	TCTCGTGACGTTACGTGGCCC	SRDVTWP	++	-
6214	16900	CGAGACACTTTTTGGTCAGGC	RDTFWSG	+++	n.d.
6215	16885	AGTTACGTAAAATCTCAGACC	SYVKSQT	+++	n.d.
6216	16865	GCATATGTGAAAAGCAGTATA	AYVKSSI	+++	-
6217	16901	ACGTCGAGGCCGCTCAATTGG	TSRPLNW	+++	n.d.
6218	16902	CAATACCATAAGTCAGAGTCT	QYHKSES	+++	-
6219	16774	GGAAATGAGTTCTGGTCTCCC	GNEFWSP	+++	n.d.
6220	16903	AAAAACGAAGACATCTGGCCT	KNEDIWP	++	n.d.
6221	16904	TATAACGAAGGGTCCTGGCCG	YNEGSWP	+++	n.d.
6222	16905	TCGAGTATACACGATCGATAT	SSIHDRY	+++	-
6223	16820	CCGATGAATGGTAACTGGCCC	PMNGNWP	+++	n.d.
6224	16898	TCGTATTCTCGGATCGCTCCC	SYSRIAP	+++	-
6225	16906	CGCAATAACTATGACAGCATG	RNNYDSM	+++	n.d.
6226	16790	TCGCGTCTCACATTGTTTCCT	SRLTLFP	+++	n.d.
6227	16907	ATGCAAGACATCAAGTGGCCT	MQDIKWP	++	n.d.
6228	16908	AGAAATGTGTTCGATACCTCT	RNVFDTS	+++	n.d.
6229	16909	GAGGCAAATTTCAGTAATTGG	EANFSNW	++	n.d.
6230	16910	ACATATAGTCGCTTAGTCTTA	TYSRLVL	+++	-
6231	16911	ACATATGTGAGGTCGGAAGTC	TYVRSEV	+++	n.d.
6232	16912	CAATACACTAAATCAAGTATC	QYTKSSI	+++	-
6233	16851	TCATATATCTACGACGGTGAT	SYIYDGD	+++	n.d.
6234	16842	ATACACGACGGGGTCTGGCCG	IHDGVWP	+++	-
6235	16867	AGAATCAGTAATGACTGGCCA	RISNDWP	+++	-
6236	16913	TGGTCCACAAGGGAGATGATC	WSTREMI	+++	-

6237	16914	GGCTCTACGGATCCCTGGCCG	GSTDPWP	+++	n.d.
6238	16856	TCGTACGCTAAGTCCGTTATC	SYAKSVI	+++	-
6239	16868	AAGTTCGAGTCCAACTGGCCG	KFESNWP	+++	n.d.
6240	16915	TATTTCACCGACGAGTGGCCA	YFTDEWP	+++	n.d.
6241	16915	TACTTTACAGATGAATGGCCC	YFTDEWP	+++	n.d.
6242	16853	CAATACACAAAACATGTATCT	QYTKHVS	+++	+–
6243	16916	GTTATGTCGGAGGTCTGGCCA	VMSEVWP	++	n.d.
6244	16917	AGAGATCGGGCCGAATGGCCT	RDRAEWP	+++	n.d.
6245	16918	TCCTATAGCAGACTTATAGAG	SYSRLIE	++	-
6246	16919	GTAAATAGATTGGTAGACTGG	VNRLVDW	+++	n.d.
6247	16920	ACAGTAAAAATACAATGGCCC	TVKIQWP	+++	n.d.
6248	16902	CAGTATCACAAATCGGAAAGT	QYHKSES	+++	-
6249	16921	ACTTATACCAAGTCTCAAACG	TYTKSQT	+++	-
6250	16922	AGGAATCACTACGATACCCAA	RNHYDTQ	+++	n.d.
6251	16904	TACAATGAGGGATCATGGCCA	YNEGSWP	+++	n.d.
6252	16884	AAAATTGAAGGATCATGGCCG	KIEGSWP	+++	-
6253	16923	TTGAAAGTATTACAATGGGAC	LKVLQWD	+++	n.d.
6254	16924	TTCGTGTCTTCTGACTGGCCG	FVSSDWP	+++	n.d.
6255	16913	TGGTCAACCCGGGAAATGATT	WSTREMI	+++	-
6256	16925	GGGTTTGGCGAGAAGTGGCCT	GFGEKWP	+++	-
6257	16926	GCTTACGTGAAGAGCAATACG	AYVKSNT	+++	-
6258	16710	CTGGTTTCGAACGATTGGCCT	LVSNDWP	+++	n.d.
6259	16891	GGTATTTACGCAACGTTTCCA	GIYATFP	+++	n.d.
6260	16837	CAATACGTTATATCTCAGAAA	QYVISQK	+++	-
6261	16816	CGGAACGGCGATAACTGGCCT	RNGDNWP	+++	n.d.
6262	16799	TCGGGATGGTTGACAGAAGTC	SGWLTEV	+++	n.d.
6263	16894	CGCCATACAACAGAATGGCCC	RHTTEWP	+++	-
6264	16893	AGGAGATCAGATAACTGGCCA	RRSDNWP	+++	-
6265	16927	TCCAAATATCATGACGTCTTT	SKYHDVF	+++	-
6266	16928	GTATATACCAAGTCCGAGTGG	VYTKSEW	+++	n.d.
6267	16822	CAGTATGTACTTTCTATGAAG	QYVLSMK	+++	-
6268	16929	TATATGAGTCCTGATTGGCCA	YMSPDWP	+++	n.d.
6269	16912	CAGTATACGAAGAGCAGCATT	QYTKSSI	+++	-

6270	16930	AAAAAGAGCCTAGATTGGCCT	KKSLDWP	+++	-
6271	16931	AGCAGAAATGTACTGGGTTGG	SRNVLGW	+++	n.d.
6272	16926	GCGTATGTAAAATCCAACACT	AYVKSNT	+++	-
6273	16921	ACGTACACAAAATCCCAGACC	TYTKSQT	+++	-
6274	16834	CAATATGTCCGGTCGGAGCCA	QYVRSEP	+++	n.d.
6275	16932	GTTAAGGATGGCACATGGCCG	VKDGTWP	+++	-
6276	16917	CGTGACCGAGCAGAGTGGCCA	RDRAEWP	+++	-
6277	16873	GATACGTGGAACATGGGTGGT	DTWNMGG	+++	-
6278	16889	GTCTATACTAAAAACGAGCGA	VYTKNER	+++	+-
6279	16933	ATCACGGTAGATGGCTGGCCA	ITVDGWP	+++	n.d.
6280	16835	CGTAATAATTACGATAATTAC	RNNYDNY	+++	n.d.
6281	16934	TTCTCAGGCGATACGTGGCCG	FSGDTWP	+++	n.d.
6282	16935	GTTTACTCCAAATTAAACACG	VYSKLNT	+++	n.d.
6283	16936	ACGTCCAGGTTCGACACCTAC	TSRFDTY	+++	-
6284	16937	AAAGTAAATGATACATGGCCT	KVNDTWP	+++	-
6285	16927	AGTAAGTACCACGATGTTTTC	SKYHDVF	+++	n.d.
6286	16908	AGGAACGTCTTTGACACATCG	RNVFDTS	+++	n.d.
6287	16933	ATAACAGTCGACGGATGGCCT	ITVDGWP	+++	n.d.
6288	16938	TGGAAATTCCAGACAGAGATC	WKFQTEI	+++	n.d.
6289	16928	GTCTACACTAAATCGGAATGG	VYTKSEW	+++	n.d.
6290	16939	GGCACTTTTCAATTGTTTCCG	GTFQLFP	+++	n.d.
6291	16864	TATCAGCGCGCGGACTGGCCC	YQRADWP	+++	+
6292	16940	GTGTATGTACGGACGGAAATG	VYVRTEM	+++	-
6293	16941	CAGGTTGTGAAATACTTGCCT	QVVKYLP	+++	-
6294	16942	ACGTTCGTTAAGTCGCTAACG	TFVKSLT	+++	n.d.
6295	16943	AAGGTCGAATATGACTGGCCC	KVEYDWP	+++	n.d.
6296	16924	TTTGTCTCCTCCGATTGGCCC	FVSSDWP	++	n.d.
6297	16944	CAATGGACAAAGACAGTACCT	QWTKTVP	++	-
6298	16945	TCATTTGTGAGATCGGTTGAA	SFVRSVE	+++	-
6299	16919	GTTAACCGACTGGTTGATTGG	VNRLVDW	+++	n.d.
6300	16738	CCTATGCCTAACATGGTATGG	PMPNMVW	+++	n.d.
6301	16903	AAGAATGAGGATATTTGGCCC	KNEDIWP	+++	-
6302	16946	TTTAAGGAGGGGATCTGGCCT	FKEGIWP	+++	n.d.

6303	16947	GGGAAGAATGTATTATGGCCC	GKNVLWP	+++	+
6304	16945	AGCTTCGTACGATCTGTGGAG	SFVRSVE	+++	-
6305	16948	GTAGTTCGATTCTCAAATCAC	VVRFSNH	+++	n.d.
6306	16949	GTTCAGGCAGAGAGTTGGCCC	VQAESWP	+++	n.d.
6307	16950	GTACACGAGGAGCTATGGCCA	VHEELWP	+++	-
6308	16951	GCCTTCACTAGATTAGAAGTT	AFTRLEV	+++	-
6309	16824	GTATTTTCTAAAAGTATGTAT	VFSKSMY	+++	-
6310	16818	GTGATGAAAGATCTATGGCCC	VMKDLWP	+++	n.d.
6311	16952	CGCTATACCAAGCTTGAGGAG	RYTKLEE	+++	-
6312	16953	CGATATGAAGCGGATTGGCCC	RYEADWP	+++	-
6313	16906	AGGAACAATTACGATTCAATG	RNNYDSM	+++	n.d.
6314	16846	GTGTATACTAAATCCACAAGT	VYTKSTS	+++	n.d.
6315	16954	CTTTACGAAGATGTATGGCCA	LYEDVWP	+++	n.d.
6316	16787	GGCAGACCAAATCTTTTATGG	GRPNLLW	+++	n.d.
6317	16955	AAACAGGGCTCAGAGTGGCCA	KQGSEWP	+++	-
6318	16956	ATGCTTTTCAAATACGAGGCT	MLFKYEA	+++	n.d.
6319	16899	TCGAGAGATGTAACTTGGCCT	SRDVTWP	++	n.d.
6320	16882	TATGTGGCAGATGACTGGCCC	YVADDWP	+++	n.d.
6321	16896	GTCTACGTAAAAACGCAGAGT	VYVKTQS	+++	-
6322	16957	ATCCTATTTAAACGCGAGAGC	ILFKRES	+++	-
6323	16958	TACGACATGCCTGACTGGCCT	YDMPDWP	++	n.d.
6324	16959	ATTCTGGATCGGAACTGGCCT	ILDRNWP	+++	n.d.
6325	16960	ACACAAGTCGAACACTGGCCA	TQVEHWP	+++	n.d.
6326	16922	CGTAACCATTATGACACACAG	RNHYDTQ	+++	n.d.
6327	16961	CGACTGATTGAGAATTGGCCC	RLIENWP	+++	-
6328	16838	AAGAACCCTCTTCAATTCCAC	KNPLQFH	+++	n.d.
6329	16962	GCATACAGCCGGCTTGAGTCC	AYSRLES	+++	-
6330	16938	TGGAAGTTTCAAACGGAAATA	WKFQTEI	+++	n.d.
6331	16920	ACTGTTAAGATTCAGTGGCCA	TVKIQWP	+++	n.d.
6332	16942	ACCTTTGTCAAATCATTAACA	TFVKSLT	+++	n.d.
6333	16930	AAGAAATCGCTCGACTGGCCA	KKSLDWP	+++	-
6334	16955	AAGCAAGGTAGCGAATGGCCT	KQGSEWP	+++	-
6335	16857	GGTCGGATAACACTATTCCCA	GRITLFP	+++	n.d.

6336	16823	AATCTGATGGGGACTTGGCCG	NLMGTWP	+++	n.d.
6337	16963	TACGCTGAGGAAGACTGGCCA	YAEEDWP	++	n.d.
6338	16859	AAGGTCCAACAGCAATGGCCT	KVQQQWP	+++	-
6339	16957	ATTCTGTTCAAGAGAGAATCA	ILFKRES	+++	n.d.
6340	16964	CGCAATGCCTTCGACACACTA	RNAFDTL	+++	-
6341	16965	TGGAAAGATACACGATTTGAG	WKDTRFE	+++	-
6342	16966	AAAGAGTTTTATGTGGGAAGT	KEFYVGS	+++	-
6343	16967	AAGCCTCTATACGATGGTTCC	KPLYDGS	+++	-
6344	16925	GGTTTCGGTGAAAAATGGCCA	GFGEKWP	+++	n.d.
6345	16968	ACAGGTGTAGAGTTATGGCCC	TGVELWP	+++	n.d.
6346	16936	ACTAGCCGTTTTGATACTTAT	TSRFDTY	+++	-
6347	16969	CAGCTAACAAGGTTAGAGTCT	QLTRLES	+++	-
6348	16961	CGTCTTATAGAAAACTGGCCT	RLIENWP	+++	n.d.
6349	16960	ACGCAGGTGGAGCATTGGCCG	TQVEHWP	+++	n.d.
6350	16965	TGGAAGGACACTCGCTTCGAA	WKDTRFE	+++	n.d.
6351	16970	ATGAACGATAGGATCTGGCCT	MNDRIWP	+++	n.d.
6352	16971	GTTGTCAGTGAAATATGGCCG	VVSEIWP	+++	n.d.
6353	16932	GTCAAAGACGGTACCTGGCCT	VKDGTWP	+++	n.d.
6354	16972	ATCATTGATGCAGAATGGCCA	IIDAEWP	+++	n.d.
6355	16973	GTGTACACAAAGCATGAGTTT	VYTKHEF	+++	-
6356	16833	GGCGGTATGTTTATGTCCCCG	GGMFMSP	+++	n.d.
6357	16956	ATGCTCTTTAAGTATGAAGCG	MLFKYEA	+++	n.d.
6358	16974	GTGGACAACAACGAATGGCCC	VDNNEWP	+++	n.d.
6359	16881	ATTTATGTCAAGTTTGAGAGC	IYVKFES	+++	n.d.
6360	16975	GTGTATTCTAAGAGCCAAGAA	VYSKSQE	+++	-
6361	16954	TTATATGAGGACGTTTGGCCC	LYEDVWP	+++	n.d.
6362	16975	GTTTACAGCAAATCGCAGGAG	VYSKSQE	+++	-
6363	16937	AAGGTTAACGACACGTGGCCA	KVNDTWP	+++	n.d.
6364	16976	TGGCCTTCCGAGCTTGGGTGG	WPSELGW	+++	n.d.
6365	16977	GCCTACGTTAAGAGTGAAAGT	AYVKSES	+++	n.d.
6366	16725	GGTTTTATTACCGTATATCCG	GFITVYP	+++	+
6367	16978	CAACCAAGAGCCTTATTCCCC	QPRALFP	+++	n.d.
6368	16979	GTTTACGTCAAAAGTGAAAGT	VYVKSES	+++	-

6369	16980	CATGGGCCGAGTCTTTGGCCC	HGPSLWP	+++	n.d.
6370	16940	GTTTACGTTCGCACAGAGATG	VYVRTEM	+++	-
6371	16840	CATCGGGGGGAGCTAAATTGG	HRGELNW	+++	n.d.
6372	16981	GGTTGGATGAATCGAATCGCG	GWMNRIA	+++	-
6373	16935	GTGTATTCTAAGCTGAATACT	VYSKLNT	+++	n.d.
6374	16982	ATGACCGGACCAGTTTGGCCG	MTGPVWP	+++	n.d.
6375	16952	CGATACACTAAATTAGAAGAA	RYTKLEE	+++	n.d.
6376	16983	AAGGTTGAACAGGAATGGCCC	KVEQEWP	+++	n.d.
6377	16984	GGGTGGGTAAACCGCATTGAT	GWVNRID	+++	-
6378	16978	CAGCCGAGGGCTCTCTTTCCG	QPRALFP	+++	n.d.
6379	16985	CTCATGCAAGATGTCTGGCCT	LMQDVWP	+++	n.d.
6380	16959	ATCCTCGACCGTAATTGGCCC	ILDRNWP	+++	n.d.
6381	16863	CCTATGCGCGGACATCTATTT	PMRGHLF	+++	n.d.
6382	16971	GTGGTGTCCGAGATTTGGCCA	VVSEIWP	+++	n.d.
6383	16986	GTTGAAGAGATGAGTTGGCCT	VEEMSWP	++	n.d.
6384	16973	GTCTATACCAAACACGAATTC	VYTKHEF	+++	-
6385	16972	ATAATCGACGCTGAGTGGCCC	IIDAEWP	+++	n.d.
6386	16951	GCATTTACACGACTAGAGGTG	AFTRLEV	+++	-
6387	16987	ATTTGGATCAAGTCACAAACT	IWIKSQT	+++	-
6388	16943	AAAGTGGAGTACGATTGGCCG	KVEYDWP	+++	n.d.
6389	16977	GCTTATGTCAAATCCGAGTCG	AYVKSES	+++	n.d.
6390	16962	GCCTATTCCAGACTAGAAAGC	AYSRLES	+++	n.d.
6391	16958	TATGATATGCCGGATTGGCCC	YDMPDWP	+++	n.d.
6392	16979	GTCTATGTAAAGTCGGAGTCC	VYVKSES	+++	-
6393	16964	CGGAACGCTTTTGATACTCTC	RNAFDTL	+++	n.d.
6394	16888	AGCGAACAGGAGTTCAATTGG	SEQEFNW	+++	n.d.
6395	16953	CGTTACGAGGCTGACTGGCCT	RYEADWP	+++	n.d.
6396	16967	AAACCCCTTTATGACGGATCA	KPLYDGS	+++	n.d.
6397	16969	CAACTCACGCGGCTTGAATCG	QLTRLES	+++	n.d.
6398	16941	CAAGTAGTTAAGTATCTCCCG	QVVKYLP	+++	n.d.
6399	16895	AACAAACCCCTTTACTTTAGC	NKPLYFS	+++	n.d.
6400	16777	AGTGGGCCGATTTGGCTCGCG	SGPIWLA	+++	n.d.
6401	16988	TATTTTGACGATGAGTTCCCA	YFDDEFP	+++	n.d.

6402	16974	GTAGATAATAATGAGTGGCCG	VDNNEWP	+++	-
6403	16989	AGGAATCAATGGGACACAGCA	RNQWDTA	+++	n.d.
6404	16946	TTCAAAGAAGGCATATGGCCC	FKEGIWP	+++	n.d.
6405	16861	AAGCGGGACTCTATGTGGCCT	KRDSMWP	+++	-
6406	16950	GTGCATGAAGAACTCTGGCCG	VHEELWP	+++	-
6407	16990	TTTTACGACCCCGATTGGCCC	FYDPDWP	+++	n.d.
6408	16968	ACCGGGGTCGAATTGTGGCCT	TGVELWP	+++	+
6409	16991	AATGAAACAATGTGGTCGCCT	NETMWSP	+++	n.d.
6410	16798	AGGAAGGAGAGTATGTGGCCG	RKESMWP	+++	n.d.
6411	16923	CTCAAGGTGTTGCAGTGGGAT	LKVLQWD	+++	n.d.
6412	16988	TACTTCGATGACGAATTTCCG	YFDDEFP	+++	n.d.
6413	16966	AAGGAATTCTACGTCGGCAGC	KEFYVGS	+++	n.d.
6414	16876	TGGCAAGGAGAACACCCGTGG	WQGEHPW	+++	n.d.
6415	16992	CGAGACAGCATTGAGTGGCCT	RDSIEWP	+++	n.d.
6416	16883	CGCGAGAGAAATGAATGGCCG	RERNEWP	+++	n.d.
6417	16993	GTGCACGTCAAGTTCGAGTAC	VHVKFEY	++	n.d.
6418	16990	TTCTATGATCCAGACTGGCCT	FYDPDWP	++	n.d.
6419	16994	AAGCTTGAGTTGGAGTGGCCG	KLELEWP	+++	-
6420	16992	CGGGATTCGATAGAATGGCCA	RDSIEWP	+++	n.d.
6421	16991	AACGAGACCATGTGGAGCCCC	NETMWSP	+++	n.d.
6422	16949	GTCCAAGCGGAATCCTGGCCG	VQAESWP	+++	n.d.
6423	16892	AATCACCCTTTAGCATGGGAA	NHPLAWE	+++	n.d.
6424	16981	GGATGGATGAACCGTATTGCC	GWMNRIA	+++	n.d.
6425	16983	AAAGTAGAGCAAGAGTGGCCT	KVEQEWP	+++	-
6426	16858	ATATATTCGGCGCTCCAGACT	IYSALQT	+++	-
6427	16994	AAACTAGAACTTGAATGGCCT	KLELEWP	+++	-
6428	16986	GTCGAGGAAATGTCTTGGCCG	VEEMSWP	++	n.d.
6429	16916	GTCATGAGCGAAGTGTGGCCC	VMSEVWP	++	n.d.
6430	16721	AAAATTCTCACAGTTTGGCCT	KILTVWP	+++	n.d.
6431	16995	CTTTTCAACGGTAATTGGCCG	LFNGNWP	+++	n.d.
6432	16769	TCCATGATTCTCGATTGGAAA	SMILDWK	+++	n.d.
6433	16929	TACATGTCCCCCGACTGGCCG	YMSPDWP	+++	n.d.
6434	16996	ACGTATGTGCGGTTTGAACAA	TYVRFEQ	+++	n.d.

6435	16871	AAGGTGGGCGCATTGTGGCCA	KVGALWP	+++	n.d.
6436	16800	GTATTATCAGGAATGTGGCCG	VLSGMWP	+++	n.d.
6437	16997	CGGATGAATTTTGACTGGCCG	RMNFDWP	+++	n.d.
6438	16862	ATGCTCGCCGAAAATTGGCCC	MLAENWP	+++	n.d.
6439	16815	TTGATCCTAGAGAACTGGCCT	LILENWP	+++	n.d.
6440	16998	TACAAAGTGTTAGACTGGACA	YKVLDWT	+++	n.d.
6441	16982	ATGACTGGTCCGGTGTGGCCA	MTGPVWP	+++	n.d.
6442	16744	GACCCCAAGGGATACTTCTTC	DPKGYFF	+++	n.d.
6443	16985	CTAATGCAGGACGTATGGCCA	LMQDVWP	+++	n.d.
6444	16998	TATAAGGTCCTTGATTGGACT	YKVLDWT	+++	n.d.
6445	16997	CGAATGAACTTCGATTGGCCC	RMNFDWP	+++	n.d.
6446	16999	CACCGTCATGTTCTTTTCCCC	HRHVLFP	+++	n.d.
6447	16776	GTCACTGGTGCAGTATGGCCT	VTGAVWP	+++	n.d.
6448	16910	ACTTACTCGAGGCTCGTTCTC	TYSRLVL	+++	n.d.
6449	16999	CATCGGCACGTGCTATTTCCT	HRHVLFP	+++	-
6450	16996	ACATACGTCCGATTCGAGCAG	TYVRFEQ	+++	n.d.
6451	17000	TACAAGATGATGGAATGGCCC	YKMMEWP	+++	n.d.
6452	17000	TATAAAATGATGGAGTGGCCT	YKMMEWP	+++	n.d.
6453	16803	GACCCGGTAAATGTTTGGGGG	DPVNVWG	+++	n.d.
6454	16786	GTTTACCACAAGTTCCAAATT	VYHKFQI	+++	-
6455	17001	TCTGAAACCTGGGTGTTCCCA	SETWVFP	+++	n.d.
6456	16939	GGTACGTTCCAGCTTTTCCCC	GTFQLFP	+++	n.d.
6457	16880	GATATGCCAAATTGGTCCTGG	DMPNWSW	+++	n.d.
6458	16746	AGGCAAAACTCAGTATGGCCC	RQNSVWP	+++	n.d.
6459	16729	GTGGTGAAGGACTATTGGCCG	VVKDYWP	+++	n.d.
6460	16789	AACAATATCTTCGCTACTTAC	NNIFATY	+++	n.d.
6461	16672	TGGGGGCTGTGGCGACTAGAT	WGLWRLD	+++	n.d.
6462	16947	GGCAAAAACGTTCTTTGGCCA	GKNVLWP	+++	+
6463	16874	TATAATCACCCCCTGAACTGG	YNHPLNW	+++	n.d.
6464	16934	TTTTCCGGTGACACCTGGCCA	FSGDTWP	+++	n.d.
6465	16839	AGAGGCACCTTCGATGTCTAT	RGTFDVY	+++	n.d.
6466	17002	TATCTTGGAGAGCTCTGGCCC	YLGELWP	+++	n.d.
6467	16989	CGTAACCAGTGGGATACGGCG	RNQWDTA	+++	n.d.

6468	16665	CGCGTGTCCGTCTTGTGGCCG	RVSVLWP	+++	n.d.
6469	16703	GGCTCTCCGATCAATTGGGCT	GSPINWA	+++	n.d.
6470	17003	GCTAACGTTCTAAATTGGGCA	ANVLNWA	+++	n.d.
6471	17003	GCCAATGTATTGAACTGGGCG	ANVLNWA	+++	n.d.
6472	16691	AGACAGGGCACCTATTTCCCT	RQGTYFP	+++	n.d.
6473	16976	TGGCCGAGTGAACTAGGATGG	WPSELGW	+++	n.d.
6474	17004	AGGATCTCTATTTCCCCTTGG	RISISPW	+++	n.d.
6475	17005	CATAACGGGTTTTGGACAGGG	HNGFWTG	+++	n.d.
6476	17006	CGACTTTTCAGGCTGGAAGCT	RLFRLEA	+++	n.d.
6477	16878	TGGCAACCGGATCCTTTCCCT	WQPDPFP	+++	n.d.
6478	16841	ATGCGGGTGATTGATTGGAGC	MRVIDWS	+++	n.d.
6479	17005	CACAATGGTTTCTGGACCGGT	HNGFWTG	+++	n.d.
6480	16914	GGATCAACAGACCCGTGGCCC	GSTDPWP	+++	n.d.
6481	16783	GTTAGTTTGTTCAGCAACCAT	VSLFSNH	+++	n.d.
6482	17007	AAGTACTTTACGTTTGAACCA	KYFTFEP	+++	n.d.
6483	17008	ACAAATGATTTTGATGTGTAC	TNDFDVY	+++	n.d.

T5

NT SEQ ID#	AA SEQ ID#	NT sequence	AA sequence	hTFRC	Untransfected	Lenti-control
5742	16612	CTTTCTAGAGTAGGTTTCAAT	LSRVGFN	+++	-	-
5762	16619	CTGCATAAAGCTGGATATAAT	LHKAGYN	+++	-	-
6486	16630	CTATCCCGTTTGAACCATAAC	LSRLNHN	+++	-	-
6487	17009	AAAGAGAAACCCGATAAAAGA	KEKPDKR	+++	++	-
6488	17010	GGGCTGTGTCCGTCTACCAAA	GLCPSTK	+++	++	++
5740	16568	CTGCACAGACTGTTAAAGGAT	LHRLLKD	+++	++	++
5780	16630	TTAAGTCGCTTAAATCACAAT	LSRLNHN	+++	-	-
6491	17011	AGTTGTGCGGTATCTCATCGT	SCAVSHR	+++	++	-
5752	16612	CTGTCACGCGTGGGCTTTAAC	LSRVGFN	+++	-	-
5737	16610	TATGTGAAATATGAAGATAAA	YVKYEDK	+++	-	-
5770	16621	TACTCCCGGATGAATGATAAT	YSRMNDN	+++	-	-
5644	16577	TACTCACGCCTTAATAAGGAT	YSRLNKD	+++	-	-
6496	17012	TCTTGTCCCAAAAATGACCTC	SCPKNDL	+++	-	-
5637	16577	TATAGCAGACTAAACAAAGAC	YSRLNKD	+++	-	-
6498	17013	CGCAATGAATACACCACTTAT	RNEYTTY	+++	-	-
6499	17014	TTTTATAGATCAGACAACTGT	FYRSDNC	+++	++	-
6500	16619	CTTCACAAGGCAGGGTACAAC	LHKAGYN	+++	-	-
5754	16610	TACGTAAAGTACGAGGACAAG	YVKYEDK	+++	-	-
5619	16568	TTGCATAGGCTCTTGAAAGAC	LHRLLKD	+++	++	++
6503	17015	TGCAATTATGATTCCTTCCCT	CNYDSFP	+++	++	-
5787	16636	TACCATCGTTTGTCCAATAAC	YHRLSNN	+++	+	-
5791	16636	TATCACCGGCTTTCTAACAAT	YHRLSNN	+++	-	-
6506	17016	TATGTAAAGAACGACGCGAGA	YVKNDAR	+++	+++	+++
6507	17016	TACGTTAAAAATGATGCACGC	YVKNDAR	+++	+++	+++
6508	17017	CGCAATGAGAACCGAAAAGGT	RNENRKG	+++	++	++
5725	16608	CTTCATGCATTAAGTCATAAC	LHALSHN	+++	-	-
5744	16613	TACGCTCGGGGAGGGCCCAAT	YARGGPN	+++	-	-
6511	17013	CGAAACGAGTATACGACGTAC	RNEYTTY	+++	-	-
5678	14301	TATTCTCGCTTAAACATGAAT	YSRLNMN	+++	-	-
5664	14301	TACTCACGGTTGAATATGAAC	YSRLNMN	+++	-	-
5761	16077	TACTCAAGGATGAACGAAAAT	YSRMNEN	+++	-	-
6515	17018	CATAGTCGGGTCGGCCATAAC	HSRVGHN	+++	+	-

6516	17019	AGGCAAGCAAAGCAAAAGAAC	RQAKQKN	+++	-	-
5741	13764	TACGCGCGATCTGGCCTGAAT	YARSGLN	+++	-	-
5847	16667	CTCCATAGGTTAGCAGCCAAT	LHRLAAN	+++	+	-
5745	16613	TATGCGCGTGGTGGACCTAAC	YARGGPN	+++	-	-
5692	16595	CGAACACCAACTGTGTATCCT	RTPTVYP	+++	-	-
5767	16621	TATTCGAGGATGAACGACAAC	YSRMNDN	+++	-	-
6522	17020	AAGATGAGTTCTAGCACGTGG	KMSSSTW	+++	-	+
6523	17021	TCCACAAATTGTTACAAGAGT	STNCYKS	+++	+	+
6524	17022	TTAGATTGTGAGAGGTACCAA	LDCERYQ	+++	++	-
6525	17023	GTCTCCTCGAGCAATGGCCGT	VSSSNGR	+++	-	-
5786	13828	TACGCTCGGTCCGGGTATAAT	YARSGYN	+++	+	-
6527	17018	CACTCGCGCGTGGGTCACAAT	HSRVGHN	+++	+	-
5763	16608	TTACACGCTTTGTCACACAAT	LHALSHN	+++	-	-
6529	17024	TGTGACTATATTAGTTACGCG	CDYISYA	+++	++	-
5729	16595	CGTACTCCTACCGTCTACCCC	RTPTVYP	+++	-	-
5764	16077	TATAGCCGTATGAATGAGAAC	YSRMNEN	+++	-	-
5727	13764	TATGCTAGAAGCGGTTTAAAC	YARSGLN	+++	-	-
6533	16620	CTGTCTCGTATCTCCGTGAAT	LSRISVN	+++	-	-
5799	16638	AATGAGGATTGGGTAAAATGG	NEDWVKW	+++	-	+
5746	16614	CACTGCGGAAAATGCCTAAAT	HCGKCLN	+++	+	-
6536	17020	AAAATGTCGAGTTCAACATGG	KMSSSTW	+++	-	+
6537	17025	GTCGAGAGTTCCAACGGGCGC	VESSNGR	+++	-	-
5796	16638	AACGAAGACTGGGTGAAGTGG	NEDWVKW	+++	-	-
6539	17023	GTGTCGAGCAGTAACGGTAGA	VSSSNGR	+++	-	-
6540	17025	GTTGAATCATCGAATGGTAGG	VESSNGR	+++	-	-
5803	13556	TACTCCCGAGCTGGATATAAC	YSRAGYN	+++	++	-
5821	13556	TATAGTCGGGCCGGCTACAAT	YSRAGYN	+++	+	-
5632	16573	AGATCCGAACATGTCTTTCCA	RSEHVFP	+++	-	-
6544	17026	CGAGTTAATACCAGGGCCAAC	RVNTRAN	+++	++	-
6545	17027	TGCGCTTTCACAGGCACCAGA	CAFTGTR	+++	++	-
6546	17028	CATTACTGCCCTAACAAATTA	HYCPNKL	+++	++	-
6547	17029	CCCCGCATGTGTGCCAATAAT	PRMCANN	+++	++	++
6548	17030	AGGAATAAAGATCGCAACTCA	RNKDRNS	+++	+	+

6549	17031	CATAGGCAGGACAGTCGTCGA	HRQDSRR	+++	++	-
5724	16588	TTGTCAAGAGTAGGTATAGAC	LSRVGID	+++	-	-
6551	17032	AAAATGGATAGTAGGCTGTGG	KMDSRLW	+++	++	++
6552	17033	AGAAACATGTCCGTGTATCCC	RNMSVYP	+++	-	-
6553	17033	CGCAATATGTCTGTTTACCCA	RNMSVYP	+++	-	-
6554	17034	AGCGCGGAGTGGGTTTCATAC	SAEWVSY	+++	-	-
5835	16658	TACCATAGGACTGGGAATAAT	YHRTGNN	+++	+	-
5730	15996	TACTCTAAGGTCGGGCAGAAT	YSKVGQN	+++	-	-
5720	16605	TCAATGGAATCTCGACTGTGG	SMESRLW	+++	+	+
5765	16620	TTGTCACGGATTTCTGTAAAC	LSRISVN	+++	-	-
6559	17034	TCGGCAGAATGGGTCTCTTAT	SAEWVSY	+++	-	-
5670	16573	AGGTCGGAGCACGTATTCCCC	RSEHVFP	+++	-	-
5775	16627	TATAGTGCTCGTGGGCCCAAT	YSARGPN	+++	+	-
5789	13828	TATGCGCGCAGCGGATACAAC	YARSGYN	+++	-	-
6563	17035	CTCCGCAGTGAATGTTGTGTA	LRSECCV	+++	-	-
5712	14249	TACTCTCGAATGAATACCAAT	YSRMNTN	+++	-	-
5723	16607	GACCTTTCGAGTCATAACTGG	DLSSHNW	+++	-	-
6566	17036	CAGCTTGAAGCGCGGACGTGG	QLEARTW	+++	-	-
5778	16628	CTGACCCGAATTAGTCATAAT	LTRISHN	+++	+	+
5677	16588	CTAAGTAGGGTGGGCATCGAT	LSRVGID	+++	-	-
5714	16604	TACTCTTCGACCCACGGTGTA	YSSTHGV	+++	-	-
6570	17037	GAGATGCAGTCTAGAGCCTGG	EMQSRAW	+++	-	+
5807	16644	CGACTCTATGACGCTTATCAG	RLYDAYQ	+++	+	-
5667	16575	CTGAGCAAATTATCCGCCAAT	LSKLSAN	+++	-	-
6573	17038	ACCATGAGTGACCGCACCTGG	TMSDRTW	+++	-	-
6574	17039	CGAGAAGACGGGCTACGTTGG	REDGLRW	+++	-	-
6575	17040	CATAGTCGTTTAAATCTCCAA	HSRLNLQ	+++	-	-
6576	17041	CTCTGTAGGTCATGTGCCAAA	LCRSCAK	+++	-	-
6577	17042	AGAGGTAACGGGGGGCATAAG	RGNGGHK	+++	+	-
6578	17043	TACACATTTCTCGGCCGCAAT	YTFLGRN	+++	-	++
6579	17044	CTTTGTCGATACTCGGGCGGC	LCRYSGG	+++	++	-
6580	17045	TCTTCTAATTGCCTCCACTAC	SSNCLHY	+++	++	-
6581	17035	TTGAGGTCTGAGTGCTGCGTC	LRSECCV	+++	-	-

6582	17046	CGGACATTTGATTCGTTCGAG	RTFDSFE	+++	-	-
6583	17037	GAAATGCAAAGCCGAGCTTGG	EMQSRAW	+++	-	++
5757	16617	CATAGTCGCATGAATGAAAAT	HSRMNEN	+++	-	-
5668	16586	TATCATAAGTTAGCGAATAAT	YHKLANN	+++	-	-
5785	16635	CTCCATCGCAGTAGTAATAAT	LHRSSNN	+++	-	-
6587	16627	TACTCGGCGAGAGGTCCGAAC	YSARGPN	+++	+	-
5801	16640	TACGCTCGAACTTCGCATAAT	YARTSHN	+++	-	-
6589	17036	CAATTGGAGGCTCGCACTTGG	QLEARTW	+++	-	-
6590	17039	AGGGAGGATGGACTCAGATGG	REDGLRW	+++	-	-
5618	16567	CGTAATGACATGGTTTTTCCC	RNDMVFP	+++	-	-
6592	17032	AAGATGGACAGCCGATTATGG	KMDSRLW	+++	+	++
5854	16667	CTGCACCGGCTCGCTGCGAAC	LHRLAAN	+++	+	+
6594	17047	GTCCCCGGTGACTGCTGTGTT	VPGDCCV	+++	-	-
5652	14483	CTTTCTAAGGTCGGAGCTAAT	LSKVGAN	+++	-	-
5666	13956	TATAGTCGGATGAATGCAAAT	YSRMNAN	+++	-	-
6597	17038	ACTATGTCCGATCGAACTTGG	TMSDRTW	+++	-	-
6598	16605	TCTATGGAGTCAAGACTTTGG	SMESRLW	+++	+	+
5773	16624	CTGCATCGTGCGTCATCCAAT	LHRASSN	+++	+	-
5750	15996	TATTCCAAAGTAGGCCAAAAC	YSKVGQN	+++	-	-
6601	17048	ACAGAGTCATCATCTGGTAGA	TESSSGR	+++	-	-
5800	16614	CATTGTGGTAAGTGTCTTAAC	HCGKCLN	+++	++	-
5836	16658	TATCACCGGACAGGCAACAAC	YHRTGNN	+++	+	-
6604	17040	CACTCCAGACTTAACCTGCAG	HSRLNLQ	+++	-	-
5818	16647	ATGCCAAACGAAGGATGGTTC	MPNEGWF	+++	-	-
6606	17049	AAGATGTCATCCGCTAACTGG	KMSSANW	+++	-	-
6607	11015	CTATCTAAACTAAACGATAAC	LSKLNDN	+++	-	-
5643	16567	CGGAACGATATGGTCTTCCCT	RNDMVFP	+++	-	-
5713	16604	TATTCGTCCACTCATGGCGTG	YSSTHGV	+++	-	-
6610	14483	CTATCCAAAGTTGGTGCAAAC	LSKVGAN	+++	-	-
5659	16584	CGAGGGATCGACTTCTACCCC	RGIDFYP	+++	-	-
5690	16014	TACTCCAAAATGAATGATAAC	YSKMNDN	+++	-	-
6613	17046	AGGACGTTCGACAGTTTTGAA	RTFDSFE	+++	-	-
6614	17049	AAAATGTCTTCTGCCAATTGG	KMSSANW	+++	-	-

5759	16607	GATTTGTCATCGCACAATTGG	DLSSHNW	+++	-	-
6616	13956	TACTCTCGTATGAACGCCAAC	YSRMNAN	+++	-	-
5758	16603	TACGTCAGAAGTGACAGAAAT	YVRSDRN	++	+	+
6618	16617	CACAGCCGTATGAACGAGAAC	HSRMNEN	++	-	-
5697	11826	GTAACGTCCACCAATGGCATC	VTSTNGI	++	-	-
5777	16628	TTAACTAGGATCTCACACAAC	LTRISHN	++	+	+
5771	16624	CTACACCGAGCTAGCAGCAAC	LHRASSN	++	+	-
6622	17048	ACGGAATCCAGCTCGGGCCGA	TESSSGR	++	-	-
5674	14249	TATTCGCGGATGAACACTAAC	YSRMNTN	++	-	-
5858	16671	CTTACGTACGACGCCTATGAA	LTYDAYE	++	-	-
5704	16014	TATTCGAAGATGAACGACAAT	YSKMNDN	++	-	-
5706	16602	GTACATCGCCTGCAAGATAAG	VHRLQDK	++	-	-
6627	17050	CGGGAAACTTACGTGTACCCA	RETYVYP	++	+	-
5634	16575	TTATCTAAGCTAAGTGCAAAC	LSKLSAN	++	-	-
6629	16088	TTTTCTCGTGTAGGCGAGAAT	FSRVGEN	++	-	-
5701	13803	TACAGTCGTATGAATTCCAAT	YSRMNSN	++	-	-
5797	16634	ATGTCCCGATTATCTCAAAAT	MSRLSQN	++	-	-
5842	16662	CAGCCATATGAGCTACCATGG	QPYELPW	++	++	++
6633	17028	CACTATTGTCCGAATAAGCTC	HYCPNKL	++	++	++
6634	17051	TACAATAGTACTCACGGGAGA	YNSTHGR	++	-	-
5691	16586	TACCACAAACTTGCCAACAAC	YHKLANN	++	-	-
5726	11826	GTCACTAGCACGAACGGGATA	VTSTNGI	++	-	-
5862	16671	TTGACATATGATGCATACGAG	LTYDAYE	++	-	-
6638	17052	GTCTATGTCAGAACTGACAGA	VYVRTDR	++	++	++
6639	17053	GACGATGGCAGATCGAGGTAT	DDGRSRY	++	-	-
6640	11015	TTAAGCAAGCTCAATGACAAT	LSKLNDN	++	-	-
5942	16734	ATCGTTGGGGAGGCGTGGCCT	IVGEAWP	++	++	-
6642	17054	TGTTCAGGGTTTGAGCGTCGT	CSGFERR	++	++	-
6643	17055	TTCTTTTACAATAAACCAACG	FFYNKPT	++	++	-
6644	17056	AAACCCTATATTTTACATAAA	KPYILHK	++	-	-
6645	17057	AAGCGACCCCCTGAGGCCCGT	KRPPEAR	++	++	-
5920	16719	ATGTTGGAATATTATAACAAT	MLEYYNN	++	-	+
5688	16594	CACTCGAGGTTGAACGTATCG	HSRLNVS	++	-	-

5735	16137	TACTCACGCGTTAATGATAAT	YSRVNDN	++	-	-
5813	16647	ATGCCTAATGAGGGGTGGTTT	MPNEGWF	++	-	-
5823	16650	CTTACCAGATTAAGCCATAAC	LTRLSHN	++	+	+
6651	16594	CATTCCCGGCTGAATGTTAGT	HSRLNVS	++	-	-
5756	16584	AGAGGCATTGATTTTTATCCT	RGIDFYP	++	-	-
5739	16611	TATAGTCGCTTGCAAGAAAAT	YSRLQEN	++	-	-
6654	17058	AAACGCGAACCCGAACGCCGT	KREPERR	++	++	++
6655	17053	GATGACGGGAGGTCCCGATAC	DDGRSRY	++	-	-
5816	16644	AGGCTATACGATGCCTACCAA	RLYDAYQ	++	-	-
5776	16600	AGAGCTCTGGAGTGTTGTTAT	RALECCY	++	+	-
6658	17059	CTAAGTCGTGTAGCGATGAAT	LSRVAMN	++	-	-
5716	14056	TACAGCCGCATGAACAATAAC	YSRMNNN	++	-	-
6660	17047	GTGCCAGGCGATTGTTGCGTC	VPGDCCV	++	-	-
5755	16611	TACTCACGATTACAGGAGAAC	YSRLQEN	++	-	-
6662	17060	CGTATGTCAGATCACAATTGG	RMSDHNW	++	-	-
6663	13632	TACTCTCGTATGGGTCATAAT	YSRMGHN	++	-	-
6664	17061	CGCGTTGACCAACCCAAGAAA	RVDQPKK	++	++	++
6665	17051	TATAACTCAACGCATGGTCGC	YNSTHGR	++	-	-
6666	16602	GTGCACAGGCTTCAGGACAAA	VHRLQDK	++	-	-
6667	16088	TTCTCACGCGTTGGGGAAAAC	FSRVGEN	++	-	-
5806	16640	TATGCCCGGACCTCCCACAAC	YARTSHN	++	-	-
6669	17060	AGGATGAGCGACCATAACTGG	RMSDHNW	++	-	-
6670	17050	AGAGAGACGTATGTATATCCC	RETYVYP	++	-	-
5790	16635	TTGCACAGGTCTTCAAACAAC	LHRSSNN	++	-	-
5781	16631	CTACACGTGCTTGGACCGAAT	LHVLGPN	++	-	-
5788	16631	CTGCATGTCCTGGGGCCAAAC	LHVLGPN	++	-	-
5675	14056	TATTCACGAATGAATAACAAT	YSRMNNN	++	-	-
5819	16650	CTGACAAGGCTTTCCCACAAT	LTRLSHN	++	++	+
5844	16664	ATGCATCGGCTGGCAGTAAAT	MHRLAVN	++	+	+
6677	17062	AATTATGCTTCTCACTCCTGG	NYASHSW	++	+	-
6678	17063	CATGGGAGCACTAATGGAAAA	HGSTNGK	++	-	-
5852	16664	ATGCACAGACTTGCGGTTAAC	MHRLAVN	++	+	+
5753	12385	TACTCACGCCAAAATGAAAAC	YSRQNEN	++	-	-

6681	17064	CGCAATGGTACTAGCTCGTGG	RNGTSSW	++	-	-
5651	15967	CTACACAAGTCTGGAATGAAT	LHKSGMN	++	-	-
6683	17063	CACGGATCCACGAACGGGAAG	HGSTNGK	++	-	-
6684	17065	AAGATGCCTTCTCGAGATTGG	KMPSRDW	++	-	-
5734	12385	TATAGTCGGCAGAACGAGAAT	YSRQNEN	++	-	-
6686	17066	GGTGGCGATGGTAATCATTAT	GGDGNHY	++	-	-
5784	16634	ATGTCACGGCTGTCACAGAAC	MSRLSQN	++	+	+
6688	17067	ATGTACAACGACTGTTGCGTT	MYNDCCV	++	+	-
5684	16116	TACTCTAAATCGGGAGCGAAT	YSKSGAN	++	-	-
6690	17065	AAAATGCCAAGCCGGGACTGG	KMPSRDW	++	-	+
6691	16135	GATTACACGGGAAAGAGTGCT	DYTGKSA	++	-	-
6692	17052	GTTTACGTAAGGACGGATCGC	VYVRTDR	++	++	++
5702	16600	AGGGCGCTTGAATGCTGCTAC	RALECCY	++	+	-
6694	17068	GTACGCGAGTACATGTCTTAC	VREYMSY	++	-	-
6695	17069	TCTCTATTGAAACCTGCTAAA	SLLKPAK	++	++	+
6696	17070	TTCGAAGGAAGAGGATGGAAC	FEGRGWN	++	-	-
5736	16593	GACATGAGTAGTAGAATATGG	DMSSRIW	++	-	+
5660	16585	TACGTAAGGTCGGATGTTCGG	YVRSDVR	++	+	+
5831	16655	CTGAGCCGGTCATCATACAAT	LSRSSYN	++	+	-
6700	16135	GACTATACTGGTAAATCCGCG	DYTGKSA	++	-	-
5825	16622	CTTTGGCGCACGGGTATCAAT	LWRTGIN	++	++	-
5743	16137	TATTCGCGTGTAAACGACAAC	YSRVNDN	++	-	-
5645	16580	TATAGCAAACTTAATGATAAG	YSKLNDK	++	-	-
5665	16580	TACTCAAAGCTCAACGACAAA	YSKLNDK	++	-	-
5687	16593	GATATGTCCTCGCGAATCTGG	DMSSRIW	++	-	-
5832	16652	TACGTCAAATCGGACAGATGT	YVKSDRC	++	++	+
6707	17071	AAGCTGGAGCCGCCTAAGAGG	KLEPPKR	++	+++	+++
6708	17067	ATGTATAATGATTGCTGTGTA	MYNDCCV	++	++	-
6709	17064	CGGAACGGAACCTCGAGCTGG	RNGTSSW	++	-	-
6710	17061	AGGGTCGATCAGCCTAAAAAG	RVDQPKK	++	++	++
6711	17070	TTTGAGGGCCGCGGGTGGAAT	FEGRGWN	++	-	-
6712	17072	CGCAACTACGATACGTACCCT	RNYDTYP	++	-	-
6713	17068	GTTAGGGAATATATGTCCTAT	VREYMSY	++	-	-

5924	16721	AAGATCCTAACGGTGTGGCCA	KILTVWP	++	++	++
5838	16655	TTGAGTAGGTCTTCTTATAAC	LSRSSYN	++	+	-
5620	16569	TATCTTAAATCTCAGTCATAT	YLKSQSY	++	-	-
5708	16585	TATGTTCGGTCCGACGTGCGA	YVRSDVR	++	+	+
6718	17072	AGAAATTATGACACTTATCCC	RNYDTYP	++	-	-
6719	16643	TATCAGCGGCAGGGTTGGGAT	YQRQGWD	++	-	-
5805	16643	TACCAACGCCAAGGATGGGAC	YQRQGWD	++	-	-
6721	17058	AAGCGGGAGCCAGAGCGTCGA	KREPERR	++	++	++
5811	16646	CTTCATCGCAATACTCAAAAC	LHRNTQN	++	+	-
6723	17073	CAGTCGGTATGTACGACGAAG	QSVCTTK	++	++	-
6724	17062	AACTACGCGTCCCATAGTTGG	NYASHSW	++	+	-
5718	15970	TTTAGTCGAGTGGGGTTTAAC	FSRVGFN	++	-	-
5693	15967	TTGCATAAATCAGGCATGAAC	LHKSGMN	++	-	-
5812	16646	TTGCACAGGAACACCCAGAAT	LHRNTQN	++	+	-
5738	16116	TATTCCAAGTCAGGTGCAAAC	YSKSGAN	++	-	-
5798	16639	ATTATGAGCAGTCGAAGCTGG	IMSSRSW	++	-	-
6730	17074	AGGAATCATGAAACTTTCCCT	RNHETFP	++	-	-
6731	13902	TTTTCCCGGACGGGGTTTAAT	FSRTGFN	++	-	-
5710	16005	TATGCAAGAATAGGCCTAAAT	YARIGLN	++	-	-
6733	17066	GGAGGTGACGGGAACCACTAC	GGDGNHY	++	-	-
5640	16569	TACCTGAAGAGCCAATCCTAC	YLKSQSY	++	-	-
6735	17075	GGACTTATCGGTGTTTGGCCC	GLIGVWP	++	-	-
6736	17076	GATAAAGGGCACTGCCACCCG	DKGHCHP	++	++	-
5661	16583	TATGTTAAGTCTGATCACCAT	YVKSDHH	++	-	-
6738	17077	GCTCAACGCGTGAGGAGCATA	AQRVRSI	++	++	+
5629	15958	TATTCCCGGCCCGGCCCCAAT	YSRPGPN	++	-	-
6740	17078	AAGACGATCAATCCTGGAAAG	KTINPGK	++	++	++
6741	17079	CATAGTTCTACGAATGGAGCC	HSSTNGA	++	-	-
5707	15958	TACTCTCGACCTGGGCCGAAC	YSRPGPN	++	-	-
5681	13803	TATTCTCGGATGAACTCTAAC	YSRMNSN	++	-	-
5624	15970	TTCAGCCGCGTTGGCTTCAAT	FSRVGFN	++	-	-
6745	17080	GAAAATCACCCCCTATGGGGT	ENHPLWG	++	++	++
5625	16564	CGTACAGCCCTTGTGTTCCCG	RTALVFP	++	-	-

6747	16639	ATAATGTCGAGCCGGTCATGG	IMSSRSW	++	+	+
5669	13933	TATGCAAGAGGTGGAAACAAT	YARGGNN	++	-	-
5638	16565	ATCCATAGACTTCTACCCTCA	IHRLLPS	++	++	++
5642	16005	TACGCGCGAATCGGGCTGAAC	YARIGLN	++	-	-
6751	17078	AAAACAATTAACCCCGGTAAA	KTINPGK	++	++	++
6752	17081	TTTCATAAATTGATGTCGAAT	FHKLMSN	++	-	-
6753	17074	CGGAACCACGAGACGTTTCCG	RNHETFP	++	-	-
6754	17082	CACGATTTTAATTTCCGAGGT	HDFNFRG	++	-	-
5747	16615	TTGCACAGATCAGGCGATAAT	LHRSGDN	++	-	-
6756	17079	CACTCAAGCACAAACGGGGCT	HSSTNGA	++	-	-
6757	17012	AGCTGCCCGAAGAACGATCTT	SCPKNDL	++	++	+
5824	16652	TATGTGAAGTCCGATCGATGC	YVKSDRC	++	++	-
5709	16603	TATGTGCGTTCAGATAGGAAC	YVRSDRN	++	-	-
5655	16583	TACGTCAAATCGGACCATCAC	YVKSDHH	++	-	-
6761	13632	TATTCCAGGATGGGACACAAC	YSRMGHN	++	+	-
6762	17083	GATTGCCAGACAAATCGGTCC	DCQTNRS	++	++	-
5614	16565	ATTCACCGTCTACTCCCTTCC	IHRLLPS	++	++	++
6764	17084	ATCCCCAACTGTTATAAGCAT	IPNCYKH	++	++	-
5731	13984	TACTCAAGAATGGGAATGAAT	YSRMGMN	++	-	-
6766	17069	TCACTGCTTAAGCCAGCCAAG	SLLKPAK	++	++	++
6767	17085	CGGACGGACTGCGTTTATCCT	RTDCVYP	++	++	-
6768	17086	TGCGATAAAGAGGCTTATCAA	CDKEAYQ	++	++	-
6769	17087	GATTGTAAATATTTTAAGGCA	DCKYFKA	++	+	-
6364	16976	TGGCCTTCCGAGCTTGGGTGG	WPSELGW	++	++	++
5698	13933	TACGCTCGGGGAGGGAATAAC	YARGGNN	++	-	-
6772	17088	TACCTCCTGAGAGGTTGCGCG	YLLRGCA	++	++	++
5639	16578	TACTCAGCCATTGGAATGAAC	YSAIGMN	++	-	-
6774	15960	GTTGCTATGCGCGGGATTGGA	VAMRGIG	++	-	-
6775	17059	TTGTCTCGAGTGGCTATGAAC	LSRVAMN	++	-	-
6776	17089	CAAAGAGGTGTGCCAAATTGG	QRGVPNW	++	+++	++
6777	17090	GCCAGTACGCACTGCACGCGG	ASTHCTR	++	++	++
6778	17091	CAGATGAATCCAATTAAGAAA	QMNPIKK	++	-	+
6779	17092	TGCGGGGTCGATAAGTCCCGC	CGVDKSR	++	++	-

6780	17009	AAGGAAAAGCCAGACAAGAGG	KEKPDKR	++	++	++
6781	17093	GGTCGGATGGCAGTGAGAGTC	GRMAVRV	++	+	-
6782	17094	TGCCACCGCGAACACTCACTT	CHREHSL	++	+	-
6783	17095	CTTTGGCGGAATTGCGATGCA	LWRNCDA	++	++	++
6784	17080	GAGAACCATCCGCTGTGGGGC	ENHPLWG	++	++	++
6785	17096	TTAGTTAGGTATGAGAACGTA	LVRYENV	++	-	-
6786	17097	CATGGCTCAGGGAATTTTGTA	HGSGNFV	++	-	-
6787	16034	TTTAGTCGAATTGGGGAGAAT	FSRIGEN	++	-	-
6788	17096	CTTGTCAGATACGAAAATGTG	LVRYENV	++	-	-
6789	17071	AAATTGGAACCACCCAAACGT	KLEPPKR	++	+++	+++
5662	16038	TACGCGAAGAACGGATTCAAT	YAKNGFN	++	-	-
6791	17098	ACGGAGACGAAATTCTGCAAC	TETKFCN	++	++	++
6792	17099	AAGGAGAATAATGCGAAGAAA	KENNAKK	++	++	-
5848	16663	GAAATGGAATCATTCAACTGG	EMESFNW	++	-	-
5748	16615	CTGCATCGTTCTGGGGACAAC	LHRSGDN	++	-	-
6795	17100	TACGCGGCAGGCAGTTGGAAT	YAAGSWN	++	-	-
6796	17101	GAGAGAAACTCCTGCATGCAC	ERNSCMH	++	++	-
6797	17102	GATGCATATGAGCTCTGTGCT	DAYELCA	++	++	-
6798	17103	CGAACCCCGGATTCGTATTGC	RTPDSYC	++	++	-
5658	13761	TACGCGCGTGGAGGAATGAAT	YARGGMN	++	-	-
6800	17089	CAGCGTGGCGTACCCAACTGG	QRGVPNW	++	+++	++
5732	16609	CTCCATGTCCGAAGCCTAAAC	LHVRSLN	++	+	-
6802	17104	CGCGGGAATGAATGTTGGAGT	RGNECWS	++	++	-
5766	16609	CTACACGTACGTAGTCTGAAT	LHVRSLN	++	-	-
6804	17105	TCCAACAACGCGTATTGGGGG	SNNAYWG	++	+	+
6805	15960	GTGGCAATGAGAGGTATCGGC	VAMRGIG	++	-	-
6806	17097	CACGGGTCCGGAAACTTCGTG	HGSGNFV	++	-	-
5809	16642	TGGGTGAGGTCTGATACGAAG	WVRSDTK	++	+	-
6808	17106	CGCGTAGATTGTGGCTCAAGG	RVDCGSR	++	++	-
6809	17107	GGGAATCAGAACTATAAGAAG	GNQNYKK	++	-	++
6810	17108	TGCGGGTATACTAACCATGTA	CGYTNHV	++	++	+
6811	17109	CATAAGTGCCAAATTTCGGGT	HKCQISG	++	++	-
6812	17091	CAAATGAACCCGATAAAAAAG	QMNPIKK	++	+	++

6813	16578	TATTCTGCGATAGGCATGAAT	YSAIGMN	++	-	-
6814	14641	TTTGCGAAAGAAGGACGAAAT	FAKEGRN	++	-	-
5699	16599	TTCGTTAAGTCCGATACTAAA	FVKSDTK	++	-	-
6816	17110	TGCGAATTCTTCCAACGTGAA	CEFFQRE	++	++	-
6817	17111	CGTAAAGATAATCCACCGCGC	RKDNPPR	++	++	-
6818	17112	GGCTACGCAGGTAAGAGGAAT	GYAGKRN	++	++	++
6819	13586	TTCTCCCGATTGGGTCATAAC	FSRLGHN	++	-	-
5648	13758	TACTCTCGTTCCAATGCTAAC	YSRSNAN	++	-	-
6821	14641	TTCGCCAAGGAGGGTAGGAAC	FAKEGRN	++	-	-
6822	13902	TTCAGCCGCACTGGCTTCAAC	FSRTGFN	++	-	-
5719	16591	TACAGTAAGGCCCAACCTAAC	YSKAQPN	++	-	-
6824	17113	GGAAAATATCCTCCCCAAGGC	GKYPPQG	++	-	-
5656	14507	TATGCTCGGTTAGGAATGAAC	YARLGMN	++	-	-
6826	17114	TACAGCAAAGCTGGGTATGAC	YSKAGYD	++	-	-
6827	17114	TATAGTAAGGCGGGCTACGAT	YSKAGYD	++	-	-
6828	17019	CGGCAGGCTAAACAGAAAAAT	RQAKQKN	++	-	++
6829	17115	TGTGGTCCCCATTGGAATGCT	CGPHWNA	++	++	-
6830	17081	TTCCACAAGCTCATGAGCAAC	FHKLMSN	++	-	-
6831	17116	AGAGTAACACATTGTACTGGT	RVTHCTG	++	++	-
6832	17117	TTCAAAGCCGGGACTTGGAAT	FKAGTWN	++	-	-
6833	17118	CATTGGACTGAGTACAACAGC	HWTEYNS	++	++	+
6834	17119	CTACATCGATTGATAGCAGAT	LHRLIAD	++	-	-
6835	17120	ATGAACTGCGCCGCAATGCGC	MNCAAMR	++	+	-
6836	17121	AGTGAAAAGAAATTAAAATTT	SEKKLKF	++	++	++
5749	13984	TATTCCCGAATGGGTATGAAC	YSRMGMN	++	-	-
6838	17122	GCTTGTGATCGCTCCCATACG	ACDRSHT	++	++	-
6839	17123	AATCCCCACACATGTAACAAT	NPHTCNN	++	++	-
5804	16642	TGGGTACGGTCGGACACAAAA	WVRSDTK	++	+	-
6841	16108	TATGCTAAGAATGGCGCAAAT	YAKNGAN	++	-	-
6842	13698	TATGCGAAATTCGGCCCCAAT	YAKFGPN	++	-	-
5721	14507	TACGCACGCCTTGGGATGAAT	YARLGMN	++	-	-
6844	16590	CTATCGCGGTCCGGTAACAAT	LSRSGNN	++	-	-
6845	13954	TATAGTCGAGTTAATGTAAAT	YSRVNVN	++	-	-

6846	15971	TTTTCTAAAATTGGTTTTAAC	FSKIGFN	++	-	-
5628	13758	TATAGCAGATCTAACGCAAAT	YSRSNAN	++	-	-
6848	17017	AGGAACGAAAATCGCAAGGGA	RNENRKG	++	++	++
5685	16591	TATAGCAAAGCTCAGCCGAAT	YSKAQPN	++	-	-
6850	17124	AGTAAAAATTCGATATGGACC	SKNSIWT	++	++	+
6851	17120	ATGAATTGTGCTGCCATGCGT	MNCAAMR	++	++	-
6852	16034	TTCAGCCGGATAGGCGAAAAC	FSRIGEN	++	-	-
6853	16108	TACGCAAAAAACGGTGCGAAC	YAKNGAN	++	-	-
5705	16579	TACCTTAAATCACAAGGTAAT	YLKSQGN	++	-	-
6855	13788	TTCAGCAAATTGAATTCCAAT	FSKLNSN	++	-	-
6856	17125	TACGGATGTCAGTCAGGGTTC	YGCQSGF	++	++	+
6857	17113	GGCAAGTACCCGCCACAGGGG	GKYPPQG	++	-	-
6858	17126	TCCTGTAGAATTAGCGAGAAA	SCRISEK	++	++	++
5646	16038	TATGCCAAAAATGGCTTTAAC	YAKNGFN	++	-	-
6860	17127	AAAATGAGCTCGTCTGTTTGG	KMSSSVW	++	-	-
5650	16576	TACAGTAGATTGTCCGGAAAC	YSRLSGN	++	-	-
6862	17128	CTTCATAAAGGCTGTACAAAC	LHKGCTN	++	++	-
6863	17115	TGCGGCCCTCACTGGAACGCC	CGPHWNA	++	++	-
6864	17129	TGGATCTTTCAATCACACACG	WIFQSHT	++	-	-
6865	17130	TGCCGTGGTACAGTGTTTCCC	CRGTVFP	++	+	-
6866	17131	CTGCCTGTTCGTGGTAAACAT	LPVRGKH	++	-	-
6867	11564	TATAGCAAAAAGAATGAAAAT	YSKKNEN	++	-	-
6868	16035	TACTCCCGAGTAAACCTCAAT	YSRVNLN	++	-	-
6869	13698	TACGCCAAGTTTGGTCCGAAC	YAKFGPN	++	-	-
6870	17132	ATCATGATGATAACGCGGGGA	IMMITRG	++	++	++
6871	17133	GGCCAATGTGGCCCGAAGTCT	GQCGPKS	++	++	++
6872	17134	ACCACAATTCATTCAAGGTGG	TTIHSRW	++	++	++
6873	17135	AAATCGATCTGGACAGACGAC	KSIWTDD	++	-	-
6874	17136	TGTACCGGCAATAGCTCCAAA	CTGNSSK	++	++	+
6875	17137	TGCGACCGATCCAATGGGGGG	CDRSNGG	++	++	-
6876	17138	TGCAACCCGTCGGTATACAGA	CNPSVYR	++	++	++
6877	17139	TGTAAAAGCTACGGTTCGTCC	CKSYGSS	++	++	-
6878	17100	TATGCAGCGGGATCCTGGAAC	YAAGSWN	++	-	-

6879	17140	AATATTGTTAACTACCGCCAA	NIVNYRQ	++	++	++
5686	16592	TACCACAAGTCGCAAAGTAAT	YHKSQSN	++	-	-
6881	17141	TGCACACGAATGGACTACGGG	CTRMDYG	++	++	-
5673	13761	TATGCACGCGGTGGGATGAAC	YARGGMN	++	-	-
6883	17142	ATCAGTGAATACAGCAAATGG	ISEYSKW	++	-	-
6884	16659	ATGACCTATGATAGCTATGAT	MTYDSYD	++	-	-
6885	17143	ACTAATTGGGAATCATACTTA	TNWESYL	++	++	-
5622	16563	TGGCCTCCACCGGTCAACAGC	WPPPVNS	++	-	-
6887	17027	TGTGCATTTACCGGGACGCGC	CAFTGTR	++	++	++
6888	17144	TGGACTTGTTCTAGGAAGCAG	WTCSRKQ	++	-	++
6889	17145	TTCCATCACCGTCAAAACCAT	FHHRQNH	++	+	-
6890	17146	TTTAAAGTTTGGGATGGAGGC	FKVWDGG	++	++	++
5680	16566	TACTTCACAGGTGTCGTCGCA	YFTGVVA	++	-	-
6892	17147	AAAATTCCTATTAATTGGTCC	KIPINWS	++	++	++
6893	17148	GGCTACAGATCTTTATACCCG	GYRSLYP	++	+	++
6894	17149	AGGCAGGAGAAGCACTTGAGG	RQEKHLR	++	++	-
6895	13586	TTTTCGAGGCTCGGGCACAAT	FSRLGHN	++	-	-
5617	16566	TATTTTACTGGCGTTGTGGCC	YFTGVVA	++	-	-
6897	17111	CGAAAGGACAACCCTCCTCGG	RKDNPPR	++	++	-
5689	16592	TATCATAAAAGCCAGTCGAAC	YHKSQSN	++	-	-
5654	16582	TACGTTAAATCCTCCAATAAT	YVKSSNN	++	-	-
6900	17150	TACGCGCGCGAAACATGGAAT	YARETWN	++	-	-
6901	17151	TGTTGGGACACTAGTAACGCG	CWDTSNA	++	++	++
6902	16009	TACGCCAAAGCCGGCCACAAT	YAKAGHN	++	-	-
5839	16659	ATGACATACGACAGTTACGAC	MTYDSYD	++	-	-
6904	17127	AAGATGTCGTCCTCGGTGTGG	KMSSSVW	++	-	-
6905	14575	TACGCCAGGATGGGAATAAAT	YARMGIN	++	-	-
6906	17152	GATTCTCCGTGGTCAAACTGG	DSPWSNW	++	++	-
6907	17153	AATTCGACTTCATGTACACCG	NSTSCTP	++	++	-
5613	16564	AGGACTGCACTCGTATTTCCA	RTALVFP	++	-	-
6909	16009	TATGCGAAGGCTGGTCATAAC	YAKAGHN	++	-	-
6910	17154	CACAAGTGTGGTGACACTCGC	HKCGDTR	++	++	-
6911	17155	CTAGCTAGGAACGCGAGTAAT	LARNASN	++	-	-

6912	17156	AGAATGAAAGACGTCTACCCT	RMKDVYP	++	-	-
6913	17157	CGTTGCGAGATCAACGCTACA	RCEINAT	++	++	++
6914	17158	TATTCTGAGTATGACACCTAC	YSEYDTY	++	-	-
6915	17156	CGAATGAAGGATGTGTATCCC	RMKDVYP	++	-	-
6916	16599	TTTGTCAAATCGGACACCAAG	FVKSDTK	++	-	-
6917	13954	TACTCACGTGTCAACGTCAAC	YSRVNVN	++	-	-
5795	16637	TACCACGCACGGGCCCCAAAC	YHARAPN	++	-	-
6919	17140	AACATAGTCAATTATCGACAG	NIVNYRQ	++	++	++
6920	17159	TACATTTGTAGTAACGCCAAG	YICSNAK	++	++	-
6921	17160	ACCTTGATGGGAAAATGTACG	TLMGKCT	++	++	-
6922	17161	AGTACTATGGAATGCTCATCC	STMECSS	++	++	-
6923	17162	AAATGGGTTCGATCCGCTGTG	KWVRSAV	++	++	-
6924	17030	CGAAACAAGGACAGAAATAGT	RNKDRNS	++	++	-
6925	17163	CGTTGGTCAGAGCGGGATTGT	RWSERDC	++	++	-
6926	17164	GACAAGATGTGCTTCGCTAAG	DKMCFAK	++	++	-
5683	16590	TTAAGCCGCTCTGGCAATAAC	LSRSGNN	++	-	-
6928	17165	GTCCACGACTCAAGCCACTGT	VHDSSHC	++	++	-
5635	16576	TATTCGAGGTTATCTGGGAAT	YSRLSGN	++	-	-
6930	17166	TGCGATTACGGTTCGCGCTCA	CDYGSRS	++	++	-
6931	17167	TCCTGCAAATCCGGGAACGCT	SCKSGNA	++	++	+
6932	17168	CTGGGACTGTGGACCGAATCT	LGLWTES	++	-	-
6933	17169	ACGTGTAGGACGCTGAAAACA	TCRTLKT	++	++	-
6934	17170	TGTACAGAAAATCGAGGAGTA	CTENRGV	++	++	+
6935	17171	GGTCCCGGTACATGCAAATCC	GPGTCKS	++	++	-
6936	17172	TGCCAGTACGTTAAATGGGAA	CQYVKWE	++	++	+
6937	17098	ACCGAAACAAAGTTTTGTAAT	TETKFCN	++	++	-
6938	17173	AACTCTTCTGCTTGCCGCACC	NSSACRT	++	++	-
6939	17174	AGTGGATGTAGCCGGACGGAT	SGCSRTD	++	++	-
6940	17175	ATGTGTTCGATGCGAAATGCA	MCSMRNA	++	++	+
6941	17176	AGGTCCTGTTTGGGCTCCAAT	RSCLGSN	++	++	-
6942	17057	AAACGTCCGCCGGAAGCACGG	KRPPEAR	++	++	++
6943	13788	TTTTCTAAGCTAAACTCAAAC	FSKLNSN	++	-	-
6944	17177	AAGAATAACTGCACGTTTGGA	KNNCTFG	++	++	-

6945	17178	TGTAACAATAGTGGATACTCT	CNNSGYS	++	++	-
6946	16589	ATGTCTCGAATCGGCGTTAAC	MSRIGVN	++	-	-
5792	16637	TATCATGCTCGCGCTCCGAAT	YHARAPN	++	-	-
6948	17179	TTGAAGCTGTGTGCCCACAAT	LKLCAHN	++	++	-
6949	17180	AGATGCGATAAAATATTAACG	RCDKILT	++	++	-
6950	17181	TCAAAAACGTATAGCTGTCCG	SKTYSCP	++	++	-
6951	17182	AAAATGTTACCTGGTAACCGT	KMLPGNR	++	++	-
6952	17183	TATCAACGGCAATGTGAGAGC	YQRQCES	++	++	++
6953	17184	AATACATACCGATGTGATGGG	NTYRCDG	++	++	-
6954	17185	TCTTGTGGCGGATTACACGGG	SCGGLHG	++	++	-
6955	17142	ATTAGCGAGTATTCGAAGTGG	ISEYSKW	++	-	-
6956	17117	TTTAAGGCTGGAACCTGGAAC	FKAGTWN	++	-	-
6957	17167	TCTTGTAAGAGCGGCAATGCC	SCKSGNA	++	++	+
6958	17186	CTATCCAAGTTATCCTGCAAT	LSKLSCN	++	++	-
6959	13980	TACAGCAGAATTAACGCCAAC	YSRINAN	++	-	-
6960	17168	CTCGGGTTGTGGACAGAGTCC	LGLWTES	++	-	-
6961	17182	AAGATGTTGCCGGGAAATCGG	KMLPGNR	++	+	-
6962	17187	TACTGGAGTCAGACGCCTTCG	YWSQTPS	++	++	+
6963	17188	ACGGTTTGGACATCGGATTGT	TVWTSDC	++	++	+
6964	17108	TGTGGTTACACCAATCACGTT	CGYTNHV	++	++	-
5853	16669	CAGTATGTCCGATCATCAATA	QYVRSSI	++	++	++
6966	17189	AGTTGTATGAATGTCGCTCCG	SCMNVAP	++	++	+
6967	17190	GCCTTTTGTACAAACAAAACG	AFCTNKT	++	++	-
6968	17191	ACGCAGTGCAAAGAGCACTAC	TQCKEHY	++	++	-
6969	17163	CGGTGGAGCGAAAGAGACTGC	RWSERDC	++	++	++
6970	17192	TGTACATACAAGTGGAGTGAA	CTYKWSE	++	++	++
6971	17193	ATTAGCGTGTGTAAACAACAG	ISVCKQQ	++	++	++
6972	17194	TCCCACTGGAGTGACTGCGAC	SHWSDCD	++	-	-
5682	16589	ATGTCCCGTATTGGAGTGAAT	MSRIGVN	++	-	-
6974	11471	TACGCACGAGGGAATGATAAT	YARGNDN	++	-	-
6975	17195	AGCTGTCGACTAGTAGACGTT	SCRLVDV	++	++	-
6976	17131	TTGCCAGTGAGAGGGAAGCAC	LPVRGKH	++	++	-
6977	17135	AAGAGTATTTGGACCGATGAT	KSIWTDD	++	-	-

6978	17196	TGTCAATCAGAAGGTAGAACC	CQSEGRT	++	++	-
6979	17197	CTTTGCAGGCCATGCCGGGAA	LCRPCRE	++	++	+
6980	17198	TCTTGGACATACGAGGAATGT	SWTYEEC	++	++	+
6981	17199	ACCTGTCAGCGTCTGTCCGGT	TCQRLSG	++	++	-
6982	17119	TTGCACCGGCTTATCGCTGAC	LHRLIAD	++	-	-
6983	17200	TGTGACGGGACGGGGCGACGT	CDGTGRR	++	++	++
6984	17082	CATGACTTCAACTTTAGGGGA	HDFNFRG	++	-	-
6985	17190	GCGTTCTGCACCAATAAGACT	AFCTNKT	++	++	-
6986	17201	AGAGAGGTATTAAAATGGAGT	REVLKWS	++	++	++
6987	17202	ACGTGTGGAATGAGGGGAGCT	TCGMRGA	++	++	-
6988	17203	TGCGGTCGAGGAGCTGGAATA	CGRGAGI	++	++	-
6989	17204	TATTTCGAGAAGATATGTGAA	YFEKICE	++	++	-
6990	17029	CCTCGTATGTGCGCGAACAAC	PRMCANN	++	+	-
6241	16915	TACTTTACAGATGAATGGCCC	YFTDEWP	++	+	-
6992	17205	GGGTGCTCAGGGTTTAAGACA	GCSGFKT	++	++	+
6993	17206	TGCAAATGGATACGGGAAGGC	CKWIREG	++	++	+
6994	17207	ATGAAAATCACAGGTCCCCGC	MKITGPR	++	++	-
6995	17172	TGTCAATATGTCAAGTGGGAG	CQYVKWE	++	++	-
6996	17208	CGAACATACGACACTTACATC	RTYDTYI	++	-	-
6997	17209	CGATACGAGGCAAGTAATTGG	RYEASNW	++	+	-
6998	16087	TACAGCAAGCTAGGAGGTAAT	YSKLGGN	++	-	-
6999	16035	TATTCTCGGGTGAATCTGAAC	YSRVNLN	++	-	-
7000	17210	TACTTCGCCCATTTTTCCCAT	YFAHFSH	++	++	++
7001	17211	GGGTGCAACCGTTCAACGGCT	GCNRSTA	++	++	+
7002	17212	AAGCTCTGTCCCAATCTTATC	KLCPNLI	++	++	-
7003	17213	TGGCCTACAGCCTTTTACGCT	WPTAFYA	++	+	++
5779	16629	CTTTGTCGTCCATGTTCAGAG	LCRPCSE	++	++	-
7005	11564	TACTCTAAGAAAAACGAGAAC	YSKKNEN	++	-	-
7006	17214	TGCCTGATACGTGACGTTAAA	CLIRDVK	++	++	-
7007	17215	CACGACTCGGCCTGGAGCTGG	HDSAWSW	++	-	-
7008	17216	AGGGCAAAAATCAATTGGCCA	RAKINWP	++	++	++
6124	16848	ACGGGTGTATGGATGCAAACG	TGVWMQT	++	-	-
7010	17158	TACAGCGAATACGATACATAT	YSEYDTY	++	-	-

7011	17217	TACAGCCGCACCGGAAGCGAT	YSRTGSD	++	-	-
5728	16022	TACTCAAAAAACGGCATGAAT	YSKNGMN	++	-	-
7013	17166	TGTGACTATGGAAGCAGATCC	CDYGSRS	++	++	-
7014	17054	TGCTCGGGTTTCGAACGGCGA	CSGFERR	++	+	-
7015	17218	TGCAATATAGGCGATAAACGG	CNIGDKR	++	++	-
7016	17217	TATAGTAGAACGGGGAGTGAC	YSRTGSD	++	-	-
7017	17219	GGAGAGTGGTGTGTGAAGAAT	GEWCVKN	++	++	+
7018	17220	TACCATAAACATAGTCTGAAC	YHKHSLN	++	-	-
7019	16109	TTTTCTAAAATGAACATCAAT	FSKMNIN	++	-	-
7020	17221	ATATGCCGCGGATATACATCT	ICRGYTS	++	++	-
7021	17222	CAGTACCATATCTATAGCGGA	QYHIYSG	++	-	+
7022	17223	TGCATCATCAAGAACCAGGTG	CIIKNQV	++	++	-
7023	15966	TACGCGAAACAAGGCCATAAT	YAKQGHN	++	-	-
7024	17224	GAGCTCGGCCGCTTCGGATGC	ELGRFGC	++	++	-
7025	17225	GAATATCAGACTAGACCGTGC	EYQTRPC	++	++	-
7026	17226	ACTTCCGGGATTTGGAACGTT	TSGIWNV	++	-	-
7027	17105	AGCAATAATGCCTACTGGGGA	SNNAYWG	++	-	-
7028	17227	TGCGCCGTACAGGGTGTCAAG	CAVQGVK	++	++	-
5641	16579	TATTTGAAGAGTCAGGGGAAC	YLKSQGN	++	-	-
7030	17228	GAATGGTGCAATACGGACAAA	EWCNTDK	++	++	++
7031	17220	TATCACAAGCACTCCTTGAAT	YHKHSLN	++	-	-
7032	17229	ATGCGAACTCCTGTTATACGG	MRTPVIR	++	++	+
7033	17230	AGCTGTAAATCTTCTTATACG	SCKSSYT	++	++	+
7034	17224	GAACTAGGGCGTTTTGGGTGT	ELGRFGC	++	++	-
7035	17231	ATGTTGTGTGTAGCTGGTGAC	MLCVAGD	++	++	++
7036	17150	TATGCTCGTGAGACCTGGAAC	YARETWN	++	-	-
7037	17183	TACCAGCGTCAGTGCGAATCA	YQRQCES	++	++	+
7038	17171	GGCCCAGGAACTTGTAAGTCT	GPGTCKS	++	++	+
7039	17232	AGTTACAGCAACCCTTGGATC	SYSNPWI	++	+	-
7040	17233	TACGGTGCTGGTACCTGGCAT	YGAGTWH	++	-	-
7041	17234	TCAACTTGCAACATGCAAGCT	STCNMQA	++	++	-
7042	17235	ACAAAGCGCCAGCAATGGCCA	TKRQQWP	++	-	-
7043	17179	CTGAAACTATGCGCTCATAAC	LKLCAHN	++	++	-

7044	16103	TACGCTAGAGGCGGTCAAAAT	YARGGQN	++	-	-
7045	17236	TGTACATCTGATAGCTTTCCC	CTSDSFP	++	++	++
7046	13521	TTTTCAAAGATGAACTATAAT	FSKMNYN	++	-	-
5782	16632	TACTTCACGGGCATCTGGGCT	YFTGIWA	++	+	-
7048	17189	AGCTGCATGAACGTAGCCCCC	SCMNVAP	++	++	-
7049	17151	TGCTGGGATACATCGAATGCT	CWDTSNA	++	++	++
7050	17110	TGTGAGTTTTTTCAGAGAGAG	CEFFQRE	++	++	-
7051	17237	TGTACTAATAACGGCAACCGT	CTNNGNR	++	++	++
7052	16097	TACAGTAAAATGAACCAAAAT	YSKMNQN	++	-	-
7053	17157	CGGTGTGAAATTAATGCAACT	RCEINAT	++	++	-
7054	17238	CGTCATCCCTCCTTAAATTTT	RHPSLNF	++	+	+
5965	16749	CAGTACACTCGTCTGCAGCTT	QYTRLQL	++	+	+
7056	17155	TTGGCCCGGAATGCCTCAAAC	LARNASN	++	-	-
7057	17239	TACTTTCCCAATTTCATTTCG	YFPNFIS	++	-	-
5901	16686	GCTTACAGTCGACTTATGTCA	AYSRLMS	++	+	-
7059	17240	TCCTCAAAGTATTCGCCCTGG	SSKYSPW	++	+	-
7060	17044	CTGTGCCGGTATAGCGGTGGA	LCRYSGG	++	++	-
7061	17241	ACTCCTTATTGCAACCTTCGC	TPYCNLR	++	+	+
7062	17242	GCCTACGTCTCCAGTACCTGT	AYVSSTC	++	++	-
7063	17243	TGCTATAGACACGTTACAGCA	CYRHVTA	++	-	-
7064	17244	GATCAGTGGTGCAAAAAGGTG	DQWCKKV	++	++	-
7065	17245	AACTGTAATTTTGTTGGAAAA	NCNFVGK	++	++	-
7066	17246	TGCGTAGATTGGGGGCTTGAC	CVDWGLD	++	++	-
7067	17247	CGTATGTCTGCCAGTAACTGG	RMSASNW	++	++	-
7068	17014	TTCTACAGGTCCGATAATTGC	FYRSDNC	++	++	+
7069	17248	TACTCCAGGTATAATATTAAT	YSRYNIN	++	-	-
7070	17249	TGCCATCAGGTTCTCTTGCCT	CHQVLLP	++	++	-
7071	17214	TGTCTCATCCGGGATGTCAAG	CLIRDVK	++	++	-
7072	17026	CGTGTAAACACACGAGCTAAT	RVNTRAN	++	+	-
7073	17203	TGTGGCAGAGGGGCGGGGATC	CGRGAGI	++	++	-
7074	13528	TATGCACGTCAAAATTATAAT	YARQNYN	++	+	-
5616	13980	TATTCACGTATCAATGCAAAT	YSRINAN	++	-	-
5694	16596	TATACGCGACTCTCGATGAAT	YTRLSMN	++	+	-

7077	17250	CCGTGTGGCCCTTGTACTTAT	PCGPCTY	++	++	-
7078	17251	TATTTTTCAGGGAAGACCCTA	YFSGKTL	++	-	-
6448	16910	ACTTACTCGAGGCTCGTTCTC	TYSRLVL	++	++	+
5751	16616	AACTGTAAGCCTTGCTTCGAT	NCKPCFD	++	+	-
7081	17252	AATCTCGGCTGGCTAAAACCC	NLGWLKP	++	++	+
7082	11337	TACAGCAAAACCGGCGATAAT	YSKTGDN	++	-	-
7083	17253	GATTGGTCGACCCGAGAGTGG	DWSTREW	++	++	+
6016	16749	CAATATACCAGGTTGCAATTA	QYTRLQL	++	+	+
7085	15971	TTCAGCAAGATAGGCTTCAAT	FSKIGFN	++	-	-
7086	17146	TTCAAGGTGTGGGACGGGGGA	FKVWDGG	++	++	++
7087	17254	AACTATGTTAAAAGCACATGT	NYVKSTC	++	++	+
7088	17255	ATGCACTGGGACGCACTCCAT	MHWDALH	++	+	-
5672	16087	TATTCGAAACTCGGTGGGAAC	YSKLGGN	++	-	-
7090	17256	CTTTTTAGGTCTGGCCCTAAT	LFRSGPN	++	+	-
7091	17257	AACAAAAATTGGGTAATAGGA	NKNWVIG	++	-	-
7092	17010	GGCCTCTGCCCATCGACTAAG	GLCPSTK	++	++	-
7093	17258	CTACCTATCTACTCGTTAACC	LPIYSLT	++	++	-
5843	16663	GAGATGGAGTCCTTTAATTGG	EMESFNW	++	-	+
7095	17216	CGTGCCAAGATAAACTGGCCT	RAKINWP	++	+	-
7096	17259	TCTTGTGAGATCAAGCATATC	SCEIKHI	++	++	-
5768	16622	TTATGGAGGACAGGGATTAAC	LWRTGIN	++	++	-
7098	17260	ATGTGTTCGAACTATGGTAGC	MCSNYGS	++	++	++
7099	16987	ATCTGGATAAAATCCCAGACC	IWIKSQT	++	++	-
5630	16571	AAGACCTACGACGCGTTCGTC	KTYDAFV	++	-	-
7101	16779	AGTAATGGAAGACTGAATTGG	SNGRLNW	++	-	-
7102	16582	TATGTGAAGTCGAGTAACAAC	YVKSSNN	++	-	-
7103	17261	AACACCATGTGGTTAAATCCG	NTMWLNP	++	+	+
7104	17184	AACACGTATAGGTGCGACGGC	NTYRCDG	++	+	-
7105	17234	TCTACGTGTAATATGCAGGCA	STCNMQA	++	++	++
7106	11471	TATGCTCGGGGCAACGACAAC	YARGNDN	++	-	-
7107	17222	CAATATCACATATACTCAGGT	QYHIYSG	++	+	++
7108	17247	CGAATGTCAGCGTCAAATTGG	RMSASNW	++	+	-
5611	16562	TATTCCCGACTCTCCGCGATA	YSRLSAI	++	-	-

7110	17125	TATGGGTGCCAATCCGGCTTT	YGCQSGF	++	++	++
7111	17262	TGGATGAATATCAACGACTGC	WMNINDC	++	+	+
7112	14575	TATGCTCGCATGGGTATTAAC	YARMGIN	++	-	-
7113	17263	TACTTTAGTGGACAGATTTGT	YFSGQIC	++	++	-
7114	17242	GCGTATGTGTCGTCAACATGC	AYVSSTC	++	++	-
7115	17264	TATCACAAGGGGAATAACAAT	YHKGNNN	++	-	-
7116	17205	GGATGTTCGGGCTTCAAAACT	GCSGFKT	++	++	-
7117	17265	GGTTGCCAGGCGGGGATGAAA	GCQAGMK	++	++	++
7118	17195	AGTTGCAGGCTCGTCGATGTG	SCRLVDV	++	++	++
7119	17024	TGCGATTACATAAGCTATGCT	CDYISYA	++	++	-
7120	16136	TACTCCAAGTCTGGCGATAAT	YSKSGDN	++	-	-
7121	17266	AATCATTGGGTGCGTGATCAT	NHWVRDH	++	++	-
7122	17267	GTAATGAGTAATTGGAACCGC	VMSNWNR	++	++	-
7123	17174	TCGGGCTGCTCTCGAACTGAC	SGCSRTD	++	++	++
7124	17268	TATCACGTTGCGGACCGTTGC	YHVADRC	++	++	-
7125	17269	CGGGACCACGATTGCTACGCA	RDHDCYA	++	++	-
7126	17270	TCCCCAAACGGCTGTAATGGT	SPNGCNG	++	++	-
5733	16601	TTGCATCGGGACGGTATCAAT	LHRDGIN	++	-	-
7128	17271	GCCTGTGAAAGGAAAATGACA	ACERKMT	++	++	+
7129	17272	ATCTACCTTAAGAAGCAAGTC	IYLKKQV	++	++	-
7130	17273	AAGCACAGAACAATCGTGAAC	KHRTIVN	++	++	-
7131	17274	AATAGCTGCAATATGACTAGG	NSCNMTR	++	++	-
7132	17086	TGTGACAAGGAAGCCTACCAG	CDKEAYQ	++	++	++
5671	16022	TATAGCAAGAATGGGATGAAC	YSKNGMN	++	-	-
7134	17275	CGGGACTGGATTCAGTTCGAG	RDWIQFE	++	+	-
7135	17276	CACGAGACGTGCGTGCGTGGA	HETCVRG	++	++	-
7136	17277	GATAAATATCTGAACACATGT	DKYLNTC	++	++	+
5631	16572	TATCTTAAGTCTGAACGTAAT	YLKSERN	++	-	-
7138	17228	GAGTGGTGTAACACCGATAAG	EWCNTDK	++	++	-
7139	17278	GTGTTCTCGCGTTCCATGTGC	VFSRSMC	++	++	-
7140	17279	ACGCAAGTGTATTCCAATTGG	TQVYSNW	++	+	-
7141	17280	AGAACTCAACCTCCCGCTCGT	RTQPPAR	++	++	++
7142	17281	TTGGCACGGTCAGCAGTCAAT	LARSAVN	++	-	-

5636	14328	TACAGCCGTATCAATACCAAT	YSRINTN	++	-	-
6131	16739	GCGAGAGGACAATTGCCCTGG	ARGQLPW	++	++	++
7145	17282	GAGGGATATCATGACTGGGCG	EGYHDWA	++	-	+
7146	17283	GACAATACATTTTCTAATTGG	DNTFSNW	++	-	-
7147	17253	GACTGGTCTACGAGGGAATGG	DWSTREW	++	+	+
7148	17132	ATAATGATGATTACCCGTGGT	IMMITRG	++	+	-
7149	17148	GGTTATCGAAGTCTTTATCCT	GYRSLYP	++	+	-
7150	17284	TGGCATCGTCTTAGTGTGAAT	WHRLSVN	++	-	-
7151	17212	AAACTATGCCCTAACTTAATA	KLCPNLI	++	++	-
7152	17209	CGTTATGAAGCCTCTAACTGG	RYEASNW	++	-	+
7153	17285	GTCATGTGCGATGCTTATCCC	VMCDAYP	++	++	-
7154	17286	TCCCGCCGATTTTATGAGGAA	SRRFYEE	++	++	-
5626	16571	AAAACATATGATGCATTTGTG	KTYDAFV	++	-	-
7156	17287	GAACGCGGATACCTCGATTAT	ERGYLDY	++	-	-
7157	13942	TACAGCAGAACTAATACCAAT	YSRTNTN	++	-	-
7158	17288	AGTGAGTACTCATCGTGGCCC	SEYSSWP	++	++	-
7159	17201	CGTGAAGTGCTCAAGTGGTCT	REVLKWS	++	++	++
7160	17271	GCTTGCGAGCGTAAGATGACT	ACERKMT	++	++	-
7161	17289	CTTTGTTATCCGTGCAACTCC	LCYPCNS	++	++	+
5856	16669	CAATACGTGCGTAGCTCGATC	QYVRSSI	++	++	++
7163	17290	ATCTCAAATAAGCACTGGTCA	ISNKHWS	++	++	-
5866	16645	GGCCCTGGATACGTCAATTGG	GPGYVNW	++	+	-
7165	15985	GGGTCCTCAACCTCCATTTGG	GSSTSIW	++	-	-
5793	16629	CTATGCAGACCGTGCTCGGAA	LCRPCSE	++	++	-
7167	17291	TGTTATGGGACGTCGATGTAT	CYGTSMY	++	++	-
5911	16709	CCGGGAAGTTTGAGATACGGT	PGSLRYG	++	++	+
5703	16601	CTGCACCGCGATGGAATTAAC	LHRDGIN	++	-	-
7170	17281	CTCGCGCGTAGCGCGGTTAAC	LARSAVN	++	-	-
7171	16103	TATGCACGCGGTGGGCAGAAC	YARGGQN	++	-	-
7172	17147	AAGATACCCATCAACTGGAGT	KIPINWS	++	++	++
7173	17292	CCAAGACCGAACGTCTATAGC	PRPNVYS	++	++	++
5615	16562	TACTCACGTCTATCAGCTATC	YSRLSAI	++	-	-
7175	17293	CATAGTCATTATACTAATTAT	HSHYTNY	++	++	+

7176	17118	CACTGGACCGAATATAATAGT	HWIEYNS	++	++	+
7177	17294	ATGACCACGTGCGAAAACGTG	MTTCENV	++	++	+
7178	17237	TGCACGAACAATGGGAATAGA	CTNNGNR	++	++	-
7179	17177	AAAAACAATTGTACATTCGGC	KNNCTFG	++	++	+
5612	16563	TGGCCCCCGCCTGTTAATTCC	WPPPVNS	++	+	+
7181	17295	ATGTACAGCCAACATGAGTGT	MYSQHEC	++	++	-
7182	17296	AATACGTGGGCGCGAGATTAT	NTWARDY	++	+	-
7183	17297	AGACTGTTTAATACTATCCAA	RLFNTIQ	++	-	-
7184	17193	ATCTCTGTTTGCAAGCAGCAA	ISVCKQQ	++	++	-
7185	17298	AGAGGTGGGTTCTCACCATTC	RGGFSPF	++	++	++
7186	17136	TGCACGGGTAACAGTTCGAAG	CTGNSSK	++	++	-
7187	17299	TCGCGACTAATGTTTGTCGGA	SRLMFVG	++	++	++
7188	17300	TACAGTAAATCAAATTGCAAT	YSKSNCN	++	++	-
7189	17180	CGGTGTGACAAGATTCTCACA	RCDKILT	++	++	-
7190	17301	AAGGACATGTTACGTTGGGAC	KDMLRWD	++	-	-
7191	17302	CTTTGGAAAACCGGTCACAAT	LWKTGHN	++	-	-
7192	17303	TCGCGATACACATACTCTGAG	SRYTYSE	++	-	-
7193	17138	TGTAATCCAAGTGTGTATAGG	CNPSVYR	++	++	-
7194	17304	TTTAATTATTCGACGCTACCG	FNYSTLP	++	-	-
7195	17056	AAGCCATACATCCTGCACAAG	KPYILHK	++	++	-
7196	17305	AAAGCTATGTGTGGATCGGGC	KAMCGSG	++	++	-
7197	17265	GGATGTCAAGCCGGAATGAAG	GCQAGMK	++	++	-
5950	16739	GCTCGTGGGCAGTTACCGTGG	ARGQLPW	++	++	++
7199	17022	CTAGACTGCGAACGGTATCAG	LDCERYQ	++	++	-
7200	17204	TACTTTGAAAAAATTTGCGAG	YFEKICE	++	++	-
7201	17306	AATAGGAAATCGCAGTCGGTC	NRKSQSV	++	++	++
7202	17307	AAGTATTTCAATACCTTCCCC	KYFNTFP	++	++	+
7203	17308	TACCATAAAATGCAATGCAAT	YHKMQCN	++	++	-
7204	17309	ATACATAGGTTCACGACAAAT	IHRFTTN	++	++	++
7205	17199	ACTTGCCAACGCCTAAGCGGA	TCQRLSG	++	++	-
7206	17299	AGTAGATTAATGTTCGTAGGC	SRLMFVG	++	++	++
7207	17085	CGTACCGATTGTGTCTACCCG	RTDCVYP	++	++	-
7208	15963	TATGCAAGGCAAAACTTCAAT	YARQNFN	++	-	-

7209	17310	AACTACATTAAAGCTAATTGC	NYIKANC	++	++	+
7210	17311	CGCAATCAGGAGTGTGAGAGT	RNQECES	++	++	+
7211	17312	CAAAACACGAAATGGGCGTGT	QNTKWAC	++	++	++
7212	17292	CCTCGTCCCAATGTATACTCG	PRPNVYS	++	++	++
7213	17313	TACTACACAGGTCGTACTAAT	YYTGRTN	++	+	-
7214	16616	AATTGCAAACCATGTTTTGAC	NCKPCFD	++	+	-
7215	16109	TTCTCAAAGATGAATATAAAC	FSKMNIN	++	-	-
7216	16097	TATTCAAAGATGAATCAGAAC	YSKMNQN	++	-	-
7217	15942	TACGCCAAAAGTAATTACAAT	YAKSNYN	++	-	-
7218	17276	CATGAAACATGTGTCAGAGGG	HETCVRG	++	++	++
7219	17314	GTTTACTGGGTTGGAGAAGTG	VYWVGEV	++	-	-
7220	17315	GTGAGTGCATACAGAGGAGCT	VSAYRGA	++	++	+
7221	16136	TATTCTAAATCAGGTGACAAC	YSKSGDN	++	-	-
7222	17316	ACAAATGAATTTTATGGCTGG	TNEFYGW	++	-	-
7223	17317	TGCTTGAGAACGGATATTGCC	CLRTDIA	++	++	-
7224	17250	CCTTGCGGACCGTGCACGTAC	PCGPCTY	++	++	+
7225	17093	GGGCGCATGGCGGTAAGGGTA	GRMAVRV	++	+	-
7226	17318	CGGGTTTCCGATTACTCGTGG	RVSDYSW	++	-	-
6479	17005	CACAATGGTTTCTGGACCGGT	HNGFWTG	++	+	+
7228	17319	ATGGAGATAGACCCCATTTTT	MEIDPIF	++	-	-
7229	17254	AATTACGTCAAGTCGACGTGC	NYVKSTC	++	++	+
7230	17251	TACTTCAGCGGAAAAACGCTG	YFSGKTL	++	-	-
7231	11337	TATAGTAAGACGGGAGACAAC	YSKTGDN	++	-	-
7232	17320	AAATACGACCACCTCGGATCC	KYDHLGS	++	++	++
7233	17321	GGTAATACGGGGATCTGCTAC	GNTGICY	++	++	-
7234	17277	GACAAGTACTTGAATACCTGC	DKYLNTC	++	++	++
7235	17197	TTGTGTCGCCCGTGTAGGGAG	LCRPCRE	++	++	+
7236	17284	TGGCACAGATTATCCGTAAAC	WHRLSVN	++	+	-
7237	17322	GCTGGAGTGGCAACATATAGC	AGVATYS	++	+	+
7238	17323	AGCAACATGTACGACTCGTAC	SNMYDSY	++	-	-
7239	17324	TTGGCGTATAATGTATCGACA	LAYNVST	++	++	-
7240	17325	TATAGCGGCCAAGGGTGCGTA	YSGQGCV	++	++	-
7241	17326	AAATCCCCGTATGCTACGTTT	KSPYATF	++	++	-

7242	17221	ATTTGTCGTGGCTACACCAGT	ICRGYTS	++	-	-
7243	17327	TGTAACGGCTTTTATTGTGAA	CNGFYCE	++	++	+
7244	17328	TGCAATGGCGAGGCGGCATCT	CNGEAAS	++	++	-
7245	17324	CTAGCATACAACGTTTCCACG	LAYNVST	++	++	-
7246	17274	AACAGTTGTAACATGACGCGT	NSCNMTR	++	+	-
7247	17073	CAAAGCGTTTGCACCACAAAA	QSVCTTK	++	++	-
7248	17322	GCAGGTGTAGCCACGTACTCA	AGVATYS	++	++	+
7249	17329	CAGACGGACTGTGTAAACCAA	QTDCVNQ	++	++	-
7250	17330	TGCGTCGCGACAAAAGATCGT	CVATKDR	++	++	-
7251	13521	TTCTCGAAAATGAATTACAAC	FSKMNYN	++	-	-
7252	17331	ACAATGGTAGAATCCTGTCGA	TMVESCR	++	++	-
7253	17332	ACACATCAGGACTGGTCGTCT	THQDWSS	++	-	-
7254	17178	TGCAATAACTCAGGGTATTCG	CNNSGYS	++	++	-
7255	17200	TGCGATGGAACAGGTAGGAGG	CDGTGRR	++	++	-
7256	17154	CATAAATGCGGAGATACCCGT	HKCGDTR	++	++	-
7257	17126	TCGTGCCGAATCTCGGAAAAG	SCRISEK	++	++	-
7258	17333	AGCGCCTGTAATGTGAAGCAT	SACNVKH	++	++	-
7259	17334	TCAGCCGCCCAAGTTTGGCCG	SAAQVWP	++	-	-
5827	16653	TACCACAGGGCTCAAATGAAT	YHRAQMN	++	++	-
7261	17335	TGGTGCCGAGAATGCATGAAC	WCRECMN	++	-	-
7262	17303	TCAAGATATACTTATTCAGAA	SRYTYSE	++	+	-
7263	17336	CATAATAAGTACTCGAATTAT	HNKYSNY	++	++	-
7264	17337	ACTTACGCTAGCAGCAACTGG	TYASSNW	++	-	+
7265	17338	TATGTCCGCTCAGGCGATTGT	YVRSGDC	++	++	-
7266	17191	ACACAATGTAAGGAACATTAT	TQCKEHY	++	++	-
7267	17339	TTGTATATAAAATCCGCACTT	LYIKSAL	++	+	+
7268	17337	ACATATGCAAGTTCTAATTGG	TYASSNW	++	+	-
7269	17173	AATTCATCCGCCTGTCGGACA	NSSACRT	++	++	+
7270	17340	GCTAAGTCGGTCTTCCAGTCT	AKSVFQS	++	+	-
7271	17261	AATACTATGTGGCTCAACCCT	NTMWLNP	++	++	+
7272	17301	AAAGATATGCTTAGGTGGGAT	KDMLRWD	++	-	-
7273	15966	TATGCCAAGCAGGGGCACAAC	YAKQGHN	++	-	-
7274	14419	TATGCCCGGGGTGGAGTAAAC	YARGGVN	++	-	-

7275	17264	TACCATAAAGGCAACAATAAC	YHKGNNN	++	-	-
7276	17116	CGTGTTACCCACTGCACGGGC	RVTHCTG	++	++	-
7277	17341	GGGGAAACAAACTGGCGCTTT	GETNWRF	++	-	-
7278	17320	AAGTATGATCATTTAGGTTCT	KYDHLGS	++	++	++
7279	17342	AATGGGTGGGGCTACGGTCCC	NGWGYGP	++	-	-
7280	16692	ACAAACACTATCCGTTGGCCT	TNTIRWP	++	++	++
7281	17343	GTGCGTGGAGCAACCTGCGAG	VRGATCE	++	++	+
7282	17344	ATCCACCGAATGATGGTTAAT	IHRMMVN	++	-	-
7283	17345	CTCGTACGGGGCCTTAACTGG	LVRGLNW	++	++	+
7284	14332	TTTGCTCGGTCCGGTATGAAT	FARSGMN	++	-	-
7285	17233	TATGGGGCCGGAACTTGGCAC	YGAGTWH	++	-	-
7286	17346	GGCATGCGTATACGTGAGAAA	GMRIREK	++	-	-
7287	15963	TACGCTCGACAGAATTTTAAC	YARQNFN	++	-	-
6047	16799	TCCGGCTGGCTGACCGAGGTT	SGWLTEV	++	-	-
7289	17344	ATACATCGGATGATGGTAAAC	IHRMMVN	++	-	-
6346	16936	ACTAGCCGTTTTGATACTTAT	TSRFDTY	++	-	-
7291	17347	AAAGTTTACGGTTACAATCCG	KVYGYNP	++	+	-
5621	14328	TATTCTCGGATAAACACGAAC	YSRINTN	++	-	-
7293	17348	CTTCGAATGTGGGACGAAGCG	LRMWDEA	++	++	-
7294	17092	TGTGGCGTAGACAAATCAAGA	CGVDKSR	++	++	+
7295	17349	ACGTGGAAGGGTCCTCCTTGC	TWKGPPC	++	++	-
7296	17232	TCATATTCGAATCCGTGGATT	SYSNPWI	++	-	-
7297	13528	TACGCTCGACAGAACTACAAC	YARQNYN	++	+	-
5676	16587	TATCACATTTTAGGGAAAAAT	YHILGKN	++	-	-
7299	13769	TTCTCCAGGATGGGACCAAAT	FSRMGPN	++	+	-
7300	17350	AAGGGAAATTGGTACTCCGAA	KGNWYSE	++	-	-
7301	17257	AATAAGAACTGGGTTATCGGT	NKNWVIG	++	-	-
7302	15942	TATGCGAAGTCAAACTATAAC	YAKSNYN	++	-	-
7303	17351	TTCGGTCTGTCCGATCGGTGG	FGLSDRW	++	-	+
7304	17352	GTTTGTTCGTCAAACCTAGTC	VCSSNLV	++	++	-
7305	17290	ATAAGCAACAAACATTGGTCG	ISNKHWS	++	++	+
7306	17348	CTCAGGATGTGGGATGAGGCC	LRMWDEA	++	++	+
7307	17238	CGGCACCCAAGTCTCAACTTC	RHPSLNF	++	+	+

7308	17196	TGCCAGAGTGAGGGGCGAACT	CQSEGRT	++	++	-
7309	17353	ATTTACTACAAAGGGAATCTT	IYYKGNL	++	++	-
5945	16736	AAGCAACCGGTGTGGTTAGCA	KQPVWLA	++	+	+
7311	17331	ACTATGGTGGAGTCTTGCCGG	TMVESCR	++	++	-
7312	17354	TACTTTACTCGGCAGGTTAAC	YFTRQVN	++	+	-
7313	17355	TGCAACAAAACTTCGGTAACT	CNKTSVT	++	++	-
7314	17356	TGTCGCTGGTCAGATTGTTCA	CRWSDCS	++	+	-
7315	17357	TACGCGCGATCAGATTGCTGT	YARSDCC	++	++	-
7316	16712	GGATCGACATATTCTCGTGCC	GSTYSRA	++	++	+
7317	17104	CGTGGCAACGAGTGCTGGTCT	RGNECWS	++	++	++
7318	17230	AGTTGCAAGTCATCATACACC	SCKSSYT	++	++	-
7319	17358	TTACACAAGAGTACATGCGAT	LHKSTCD	++	++	-
5914	16715	GTGTATAGTCGCATCGATATT	VYSRIDI	++	-	-
7321	17359	CGGATTAAATTCGATACCTAC	RIKFDTY	++	-	-
7322	17350	AAAGGGAACTGGTATAGTGAG	KGNWYSE	++	++	++
7323	17252	AACTTAGGATGGCTTAAGCCT	NLGWLKP	++	++	+
7324	17360	GTAAGGTATACGGATAGTAAA	VRYTDSK	++	++	+
7325	17361	CTGTGGAGAAACGATAACCAA	LWRNDNQ	++	+	-
7326	17362	AAGCATCACGATGTTAATTGC	KHHDVNC	++	++	-
6174	16880	GACATGCCGAACTGGTCGTGG	DMPNWSW	++	+	-
7328	17363	AATAAATCCTGTAGTTCTATG	NKSCSSM	++	++	-
7329	16670	ATGAGTCGGTTTGATATCCAC	MSRFDIH	++	-	-
7330	17346	GGTATGCGCATTCGAGAAAAG	GMRIREK	++	-	-
7331	17364	GGGATAGCACCGTGTGGCAGT	GIAPCGS	++	++	+
6162	16764	CGAAATGTGTACGACGGTTAT	RNVYDGY	++	-	-
7333	17365	AGCCGTTTTGTATCATGGGAC	SRFVSWD	++	++	+
7334	14419	TACGCTCGAGGCGGCGTCAAT	YARGGVN	++	-	-
7335	17366	AATCGAATCGACGCAAAATGC	NRIDAKC	++	++	-
7336	17367	ACCGGGTGCATGGCCGGCAAA	TGCMAGK	++	++	-
7337	16757	TCGGCACCAATTTACTTCAAC	SAPIYFN	++	-	-
7338	17368	GCCAGCTGCAATGGGCTACGG	ASCNGLR	++	++	-
7339	16068	TACGCGAAAGGAAACGCGAAC	YAKGNAN	++	-	-
7340	17369	GTTTCAACTAACAACCCTTGC	VSTNNPC	++	+	-

7341	17370	CGGGATATCTGGCGTGACGCT	RDIWRDA	++	-	-
7342	17371	TCCCCCTGTTCGACGGGTAAT	SPCSTGN	++	++	-
7343	17372	AATAATTGCGCGGACAATTTC	NNCADNF	++	++	-
7344	13769	TTTAGTCGTATGGGCCCCAAC	FSRMGPN	++	+	-
7345	17373	GGTGGATGGAATCACCTAGTT	GGWNHLV	++	-	-
7346	17374	AAAAATGTGGGCCGTAACAAC	KNVGRNN	++	+	-
7347	17375	AATCGTGCACGCAACGTATCA	NRARNVS	++	-	++
7348	17376	GCAAACTGTGACGTCGTAGAC	ANCDVVD	++	++	-
7349	17377	TCGTGCGATTCTGGTAAAGCA	SCDSGKA	++	++	-
7350	17378	AAGTGGAGGGGAGATGAGTCA	KWRGDES	++	-	-
7351	17379	ATTTATGGAAGAGTGATTAAC	IYGRVIN	++	+	+
7352	15999	TATGCTCGGCAGAATGCAAAT	YARQNAN	++	-	-
7353	16719	ATGTTAGAGTACTACAATAAC	MLEYYNN	++	-	-
7354	17380	TCTCAAAATGCGTACGCTATG	SQNAYAM	++	++	-
7355	17381	TCTCTGTGCCCGAGACTTTCG	SLCPRLS	++	++	-
7356	17382	TACCTTAATTGCATGAAACCC	YLNCMKP	++	++	+
7357	17383	GGCATGATAAAGCCAACCCGG	GMIKPTR	++	++	-
7358	17208	AGGACTTATGATACCTATATA	RTYDTYI	++	-	-
5772	16625	TACTCCCGTGTTGATGATCGC	YSRVDDR	++	-	-
7360	17384	GAGTGGATGAGACCCGGACAA	EWMRPGQ	++	-	-
7361	17385	AGCAACTGGCGAACAGACCTT	SNWRTDL	++	-	-
7362	17386	GAGCATATGTGGCACACTGAG	EHMWHTE	++	+	-
7363	17387	TGCGTGTATGCAATAGGCTCC	CVYAIGS	++	++	-
7364	17388	TCCATATGTGCCAACGGTGAA	SICANGE	++	++	-
7365	17123	AACCCTCATACTTGCAATAAC	NPHTCNN	++	++	-
7366	17389	GACAGGCCGATATATTACTCG	DRPIYYS	++	++	++
7367	17352	GTATGCTCATCGAATTTGGTG	VCSSNLV	++	++	-
7368	17390	AACACTCAATTTACGTGTGTC	NTQFTCV	++	++	-
7369	17101	GAACGGAATAGCTGTATGCAT	ERNSCMH	++	++	+
7370	17312	CAGAATACCAAGTGGGCTTGC	QNTKWAC	++	++	-
7371	17391	ACGTACACTCGGCTAGTAAAT	TYTRLVN	++	+	+
6087	16734	ATAGTCGGAGAAGCTTGGCCG	IVGEAWP	++	-	+
7373	17318	AGGGTGAGCGACTATTCCTGG	RVSDYSW	++	++	-

7374	17309	ATTCACCGATTTACCACTAAC	IHRFTTN	++	++	-
7375	17186	CTCTCAAAATTGTCTTGTAAC	LSKLSCN	++	++	-
7376	13942	TATTCGAGGACCAACACAAAC	YSRTNTN	++	-	-
7377	17392	TGCGTAAATCTGATTCGTAAT	CVNLIRN	++	+	-
7378	17129	TGGATATTCCAGTCCCATACC	WIFQSHT	++	-	-
7379	17393	AGAAAACCCGAGGCTACCCGG	RKPEATR	++	-	-
7380	17314	GTATATTGGGTCGGCGAGGTC	VYWVGEV	++	+	+
7381	17363	AACAAGTCATGCTCTTCGATG	NKSCSSM	++	++	-
7382	17394	TATAGGCCATGTAATGCTTCA	YRPCNAS	++	++	+
7383	17395	TTCGTGTGCGATCCTTCAAAG	FVCDPSK	++	++	+
7384	17396	CGCACCCCAAATTACAATTAT	RTPNYNY	++	++	-
7385	17310	AATTATATCAAGGCGAACTGT	NYIKANC	++	++	+
5700	16596	TACACCCGTTTGAGTATGAAC	YTRLSMN	++	-	-
7387	17397	GTCCCCACCAGACAATGGCCG	VPTRQWP	++	++	-
7388	17398	TTCTCTATCCGCCTTGGTACC	FSIRLGT	++	-	+
7389	17387	TGTGTTTACGCGATTGGTAGT	CVYAIGS	++	++	-
7390	17206	TGTAAGTGGATCCGTGAGGGA	CKWIREG	++	++	-
7391	17399	CTCTCTAGAATCCAGACCAAT	LSRIQTN	++	-	-
7392	17211	GGCTGTAATCGCTCTACCGCG	GCNRSTA	++	++	-
7393	17103	CGGACGCCCGACAGTTACTGT	RTPDSYC	++	++	+
7394	17175	ATGTGCTCTATGAGGAACGCG	MCSMRNA	++	++	-
6127	16851	TCCTACATATATGATGGCGAC	SYIYDGD	++	+	-
7396	16055	TACAGCCGGCAAGGCGGAAAC	YSRQGGN	++	-	-
7397	17400	ACTACGAGGTGGGCAGGCCCT	TTRWAGP	++	++	-
6068	16812	GCTATGGGGTCTCTTTGGCCG	AMGSLWP	++	-	+
7399	17198	AGCTGGACTTATGAAGAGTGC	SWTYEEC	++	++	-
5663	16572	TACCTGAAATCAGAGCGCAAC	YLKSERN	++	-	-
6366	16725	GGTTTTATTACCGTATATCCG	GFITVYP	++	-	-
7402	17240	TCATCTAAATACTCCCCGTGG	SSKYSPW	++	++	-
7403	17401	CAATATTATAATTCCGCATCA	QYYNSAS	++	-	-
6444	16998	TATAAGGTCCTTGATTGGACT	YKVLDWT	++	++	++
7405	17402	CGCTATGACTGGCCGCATAAC	RYDWPHN	++	-	-
7406	17403	AAAGTATGTTCAGCAACTGAC	KVCSATD	++	+++	+

7407	17328	TGTAACGGTGAAGCAGCCTCA	CNGEAAS	++	++	+
7408	17404	ATGGAATGGCAGGAGAGGTAT	MEWQERY	++	-	-
7409	17356	TGCCGTTGGTCCGACTGCAGC	CRWSDCS	++	-	-
7410	17099	AAAGAAAACAACGCTAAAAAG	KENNAKK	++	+	++
7411	17405	TACTTTTCCGGAGTACCCAGT	YFSGVPS	++	-	-
7412	17406	TGGATCCCGGGAATGGGGACG	WIPGMGT	++	+	-
7413	17407	GGCCCGATCAACTGTAAGAGC	GPINCKS	++	++	-
7414	17325	TACAGTGGACAGGGTTGTGTC	YSGQGCV	++	++	+
7415	17332	ACGCACCAAGATTGGTCCAGT	THQDWSS	++	-	-
7416	17408	AACCGATGGAATAATCACGGC	NRWNNHG	++	++	-
6424	16981	GGATGGATGAACCGTATTGCC	GWMNRIA	++	-	-
6236	16913	TGGTCCACAAGGGAGATGATC	WSTREMI	++	++	++
7419	17300	TATTCTAAGTCGAACTGTAAC	YSKSNCN	++	++	-
7420	17347	AAGGTATATGGCTATAACCCA	KVYGYNP	++	++	+
7421	17407	GGGCCTATTAATTGCAAATCG	GPINCKS	++	++	+
7422	17227	TGTGCGGTTCAAGGCGTGAAA	CAVQGVK	++	++	-

NT SEQ ID#	AA SEQ ID#	NT sequence	AA sequence	hTFRC	Untransfected	Lenti-control
5742	16612	CTTTCTAGAGTAGGTTTCAAT	LSRVGFN	+++	-	-
5762	16619	CTGCATAAAGCTGGATATAAT	LHKAGYN	+++	+	-
6486	16630	CTATCCCGTTTGAACCATAAC	LSRLNHN	+++	-	–
5740	16568	CTGCACAGACTGTTAAAGGAT	LHRLLKD	+++	+	–
5780	16630	TTAAGTCGCTTAAATCACAAT	LSRLNHN	+++	-	–+
5752	16612	CTGTCACGCGTGGGCTTTAAC	LSRVGFN	+++	-	-
5737	16610	TATGTGAAATATGAAGATAAA	YVKYEDK	+++	-	-
5770	16621	TACTCCCGGATGAATGATAAT	YSRMNDN	++	-	-
5644	16577	TACTCACGCCTTAATAAGGAT	YSRLNKD	+++	+	–+
5637	16577	TATAGCAGACTAAACAAAGAC	YSRLNKD	+++	+	–
6498	17013	CGCAATGAATACACCACTTAT	RNEYTTY	+++	-	-
6499	17014	TTTTATAGATCAGACAACTGT	FYRSDNC	+++	-	-
6500	16619	CTTCACAAGGCAGGGTACAAC	LHKAGYN	+++	+	–
5754	16610	TACGTAAAGTACGAGGACAAG	YVKYEDK	+++	-	-
5619	16568	TTGCATAGGCTCTTGAAAGAC	LHRLLKD	++	+	–
5787	16636	TACCATCGTTTGTCCAATAAC	YHRLSNN	+++	-	-
5791	16636	TATCACCGGCTTTCTAACAAT	YHRLSNN	+++	-	-
6508	17017	CGCAATGAGAACCGAAAAGGT	RNENRKG	+++	-	-
5725	16608	CTTCATGCATTAAGTCATAAC	LHALSHN	++	-	-
5744	16613	TACGCTCGGGGAGGGCCCAAT	YARGGPN	+++	+	–
6511	17013	CGAAACGAGTATACGACGTAC	RNEYTTY	++	-	–
5678	14301	TATTCTCGCTTAAACATGAAT	YSRLNMN	+++	++	–
5664	14301	TACTCACGGTTGAATATGAAC	YSRLNMN	+++	+	–
5761	16077	TACTCAAGGATGAACGAAAAT	YSRMNEN	++	-	-
5741	13764	TACGCGCGATCTGGCCTGAAT	YARSGLN	++	-	-
5847	16667	CTCCATAGGTTAGCAGCCAAT	LHRLAAN	+++	-	-
5745	16613	TATGCGCGTGGTGGACCTAAC	YARGGPN	+++	+	-
5692	16595	CGAACACCAACTGTGTATCCT	RTPTVYP	++	-	-
5767	16621	TATTCGAGGATGAACGACAAC	YSRMNDN	++	-	-
5786	13828	TACGCTCGGTCCGGGTATAAT	YARSGYN	+++	+	-
5763	16608	TTACACGCTTTGTCACACAAT	LHALSHN	++	-	-
5729	16595	CGTACTCCTACCGTCTACCCC	RTPTVYP	++	-	-

5764	16077	TATAGCCGTATGAATGAGAAC	YSRMNEN	++	-	-
5727	13764	TATGCTAGAAGCGGTTTAAAC	YARSGLN	++	-	-
6533	16620	CTGTCTCGTATCTCCGTGAAT	LSRISVN	+++	+	–
5796	16638	AACGAAGACTGGGTGAAGTGG	NEDWVKW	++	-	-
5803	13556	TACTCCCGAGCTGGATATAAC	YSRAGYN	+++	++	–+
5821	13556	TATAGTCGGGCCGGCTACAAT	YSRAGYN	+++	+	-
5632	16573	AGATCCGAACATGTCTTTCCA	RSEHVFP	++	-	-
5835	16658	TACCATAGGACTGGGAATAAT	YHRTGNN	++	-	-
5730	15996	TACTCTAAGGTCGGGCAGAAT	YSKVGQN	++	-	-
5765	16620	TTGTCACGGATTTCTGTAAAC	LSRISVN	++	+	–
5670	16573	AGGTCGGAGCACGTATTCCCC	RSEHVFP	++	-	-
5775	16627	TATAGTGCTCGTGGGCCCAAT	YSARGPN	++	+	–
5789	13828	TATGCGCGCAGCGGATACAAC	YARSGYN	+++	+	-
5712	14249	TACTCTCGAATGAATACCAAT	YSRMNTN	++	+	–
5778	16628	CTGACCCGAATTAGTCATAAT	LTRISHN	+++	+	–
5714	16604	TACTCTTCGACCCACGGTGTA	YSSTHGV	++	-	-
5667	16575	CTGAGCAAATTATCCGCCAAT	LSKLSAN	+++	+	–
5668	16586	TATCATAAGTTAGCGAATAAT	YHKLANN	++	+	–
5785	16635	CTCCATCGCAGTAGTAATAAT	LHRSSNN	++	-	–
6587	16627	TACTCGGCGAGAGGTCCGAAC	YSARGPN	++	++	-
5801	16640	TACGCTCGAACTTCGCATAAT	YARTSHN	++	-	-
5854	16667	CTGCACCGGCTCGCTGCGAAC	LHRLAAN	++	-	-
5652	14483	CTTTCTAAGGTCGGAGCTAAT	LSKVGAN	++	-	–
5666	13956	TATAGTCGGATGAATGCAAAT	YSRMNAN	++	++	–
5773	16624	CTGCATCGTGCGTCATCCAAT	LHRASSN	++	-	-
5750	15996	TATTCCAAAGTAGGCCAAAAC	YSKVGQN	++	-	-
5836	16658	TATCACCGGACAGGCAACAAC	YHRTGNN	++	-	-
6607	11015	CTATCTAAACTAAACGATAAC	LSKLNDN	++	-	-
5659	16584	CGAGGGATCGACTTCTACCCC	RGIDFYP	++	-	-
6616	13956	TACTCTCGTATGAACGCCAAC	YSRMNAN	++	++	–
5758	16603	TACGTCAGAAGTGACAGAAAT	YVRSDRN	++	+	-
5697	11826	GTAACGTCCACCAATGGCATC	VTSTNGI	++	-	-
5777	16628	TTAACTAGGATCTCACACAAC	LTRISHN	+++	++	–+

5771	16624	CTACACCGAGCTAGCAGCAAC	LHRASSN	++	++	-
5674	14249	TATTCGCGGATGAACACTAAC	YSRMNTN	++	+	-
5704	16014	TATTCGAAGATGAACGACAAT	YSKMNDN	++	.	.
5706	16602	GTACATCGCCTGCAAGATAAG	VHRLQDK	+++	.	.
5634	16575	TTATCTAAGCTAAGTGCAAAC	LSKLSAN	++	.	.
5701	13803	TACAGTCGTATGAATTCCAAT	YSRMNSN	++	+	-
5797	16634	ATGTCCCGATTATCTCAAAAT	MSRLSQN	++	+	.
5691	16586	TACCACAAACTTGCCAACAAC	YHKLANN	++	+	-
5726	11826	GTCACTAGCACGAACGGGATA	VTSTNGI	++	.	.
6640	11015	TTAAGCAAGCTCAATGACAAT	LSKLNDN	++	.	.
5920	16719	ATGTTGGAATATTATAACAAT	MLEYYNN	+++	.	.
5739	16611	TATAGTCGCTTGCAAGAAAAT	YSRLQEN	++	.	.
6654	17058	AAACGCGAACCCGAACGCCGT	KREPERR	++	.	-
6658	17059	CTAAGTCGTGTAGCGATGAAT	LSRVAMN	++	+	-
5716	14056	TACAGCCGCATGAACAATAAC	YSRMNNN	++	++	.
5755	16611	TACTCACGATTACAGGAGAAC	YSRLQEN	++	.	.
6663	13632	TACTCTCGTATGGGTCATAAT	YSRMGHN	++	.	.
6666	16602	GTGCACAGGCTTCAGGACAAA	VHRLQDK	+++	.	.
5806	16640	TATGCCCGGACCTCCCACAAC	YARTSHN	++	.	.
5790	16635	TTGCACAGGTCTTCAAACAAC	LHRSSNN	++	+	-
5781	16631	CTACACGTGCTTGGACCGAAT	LHVLGPN	++	.	.
5788	16631	CTGCATGTCCTGGGGCCAAAC	LHVLGPN	++	.	.
5675	14056	TATTCACGAATGAATAACAAT	YSRMNNN	++	+	.
5819	16650	CTGACAAGGCTTTCCCACAAT	LTRLSHN	+++	++	.
5852	16664	ATGCACAGACTTGCGGTTAAC	MHRLAVN	++	.	.
5651	15967	CTACACAAGTCTGGAATGAAT	LHKSGMN	++	.	.
5784	16634	ATGTCACGGCTGTCACAGAAC	MSRLSQN	++	+	-
5660	16585	TACGTAAGGTCGGATGTTCGG	YVRSDVR	++	.	.
5831	16655	CTGAGCCGGTCATCATACAAT	LSRSSYN	++	.	.
5825	16622	CTTTGGCGCACGGGTATCAAT	LWRTGIN	++	+	.
5645	16580	TATAGCAAACTTAATGATAAG	YSKLNDK	++	.	.
5665	16580	TACTCAAAGCTCAACGACAAA	YSKLNDK	++	.	.
5687	16593	GATATGTCCTCGCGAATCTGG	DMSSRIW	++	++	.

5838	16655	TTGAGTAGGTCTTCTTATAAC	LSRSSYN	++	++	-+
5620	16569	TATCTTAAATCTCAGTCATAT	YLKSQSY	++	.	.
5708	16585	TATGTTCGGTCCGACGTGCGA	YVRSDVR	++	.	.
5811	16646	CTTCATCGCAATACTCAAAAC	LHRNTQN	++	++	.
5718	15970	TTTAGTCGAGTGGGGTTTAAC	FSRVGFN	++	.	.
5693	15967	TTGCATAAATCAGGCATGAAC	LHKSGMN	++	.	.
5812	16646	TTGCACAGGAACACCCAGAAT	LHRNTQN	++	+	.
6731	13902	TTTTCCCGGACGGGGTTTAAT	FSRTGFN	++	+	.
5640	16569	TACCTGAAGAGCCAATCCTAC	YLKSQSY	++	+	.
6740	17078	AAGACGATCAATCCTGGAAAG	KTINPGK	++	.	-
5681	13803	TATTCTCGGATGAACTCTAAC	YSRMNSN	++	+	-
6745	17080	GAAAATCACCCCCTATGGGGT	ENHPLWG	++	++	.
5669	13933	TATGCAAGAGGTGGAAACAAT	YARGGNN	++	.	-
5638	16565	ATCCATAGACTTCTACCCTCA	IHRLLPS	++	+	-
6752	17081	TTTCATAAATTGATGTCGAAT	FHKLMSN	++	+	.
6754	17082	CACGATTTTAATTTCCGAGGT	HDFNFRG	++	.	.
5747	16615	TTGCACAGATCAGGCGATAAT	LHRSGDN	++	.	.
5709	16603	TATGTGCGTTCAGATAGGAAC	YVRSDRN	++	.	.
5614	16565	ATTCACCGTCTACTCCCTTCC	IHRLLPS	++	++	-+
5731	13984	TACTCAAGAATGGGAATGAAT	YSRMGMN	++	.	-
5732	16609	CTCCATGTCCGAAGCCTAAAC	LHVRSLN	++	.	.
5766	16609	CTACACGTACGTAGTCTGAAT	LHVRSLN	++	.	.
6830	17081	TTCCACAAGCTCATGAGCAAC	FHKLMSN	++	++	-
5749	13984	TATTCCCGAATGGGTATGAAC	YSRMGMN	++	+	-
5628	13758	TATAGCAGATCTAACGCAAAT	YSRSNAN	++	+	-
5650	16576	TACAGTAGATTGTCCGGAAAC	YSRLSGN	++	++	-+
5686	16592	TACCACAAGTCGCAAAGTAAT	YHKSQSN	++	.	.
6897	17111	CGAAAGGACAACCCTCCTCGG	RKDNPPR	++	++	.
5689	16592	TATCATAAAAGCCAGTCGAAC	YHKSQSN	++	.	-
5654	16582	TACGTTAAATCCTCCAATAAT	YVKSSNN	++	.	.
6911	17155	CTAGCTAGGAACGCGAGTAAT	LARNASN	++	.	-
5795	16637	TACCACGCACGGGCCCCAAAC	YHARAPN	++	++	.
5635	16576	TATTCGAGGTTATCTGGGAAT	YSRLSGN	++	++	-

6943	13788	TTTTCTAAGCTAAACTCAAAC	FSKLNSN	++	-	-
5792	16637	TATCATGCTCGCGCTCCGAAT	YHARAPN	++	+	-
6959	13980	TACAGCAGAATTAACGCCAAC	YSRINAN	++	+	–
6986	17201	AGAGAGGTATTAAAATGGAGT	REVLKWS	++	+	-

NT SEQ ID#	AA SEQ ID#	NT Sequence	AA sequence	HEK_hTFRC_lo	HEK_GFP_log2enr
5611	16562	TATTCCCGACTCTCCGCGATA	YSRLSAI	+++	-
6999	16035	TATTCTCGGGTGAATCTGAAC	YSRVNLN	+++	-
5612	16563	TGGCCCCCGCCTGTTAATTCC	WPPPVNS	+++	-
5613	16564	AGGACTGCACTCGTATTTCCA	RTALVFP	+++	-
5614	16565	ATTCACCGTCTACTCCCTTCC	IHRLLPS	+++	---
5615	16562	TACTCACGTCTATCAGCTATC	YSRLSAI	+++	-
5616	13980	TATTCACGTATCAATGCAAAT	YSRINAN	+++	-
5617	16566	TATTTTACTGGCGTTGTGGCC	YFTGVVA	+++	-
5618	16567	CGTAATGACATGGTTTTTCCC	RNDMVFP	+++	-
7424	17409	ACACACAGGTTGATTGTAGCC	THRLIVA	+++	-
6752	17081	TTTCATAAATTGATGTCGAAT	FHKLMSN	+++	-
6867	11564	TATAGCAAAAAGAATGAAAAT	YSKKNEN	+++	-
5619	16568	TTGCATAGGCTCTTGAAAGAC	LHRLLKD	+++	---
5620	16569	TATCTTAAATCTCAGTCATAT	YLKSQSY	+++	-
5621	14328	TATTCTCGGATAAACACGAAC	YSRINTN	+++	-
7427	17410	TACTTCGCCGGCCAATTCAGT	YFAGQFS	+++	-
5622	16563	TGGCCTCCACCGGTCAACAGC	WPPPVNS	+++	-
6846	15971	TTTTCTAAAATTGGTTTTAAC	FSKIGFN	+++	-
6855	13788	TTCAGCAAATTGAATTCCAAT	FSKLNSN	+++	-
7005	11564	TACTCTAAGAAAAACGAGAAC	YSKKNEN	+++	-
5623	16570	TACACAAAGTCCGACGTGCGG	YTKSDVR	+++	-
6786	17097	CATGGCTCAGGGAATTTTGTA	HGSGNFV	+++	-
6640	11015	TTAAGCAAGCTCAATGACAAT	LSKLNDN	+++	-
6830	17081	TTCCACAAGCTCATGAGCAAC	FHKLMSN	+++	-
7078	17251	TATTTTTCAGGGAAGACCCTA	YFSGKTL	+++	-
5624	15970	TTCAGCCGCGTTGGCTTCAAT	FSRVGFN	+++	-
5625	16564	CGTACAGCCCTTGTGTTCCCG	RTALVFP	+++	-
5626	16571	AAAACATATGATGCATTTGTG	KTYDAFV	+++	-
5627	16570	TATACTAAATCGGATGTACGA	YTKSDVR	+++	-
5628	13758	TATAGCAGATCTAACGCAAAT	YSRSNAN	+++	-
5629	15958	TATTCCCGGCCCGGCCCCAAT	YSRPGPN	+++	-
5630	16571	AAGACCTACGACGCGTTCGTC	KTYDAFV	+++	-

5631	16572	TATCTTAAGTCTGAACGTAAT	YLKSERN	+++	-
7085	15971	TTCAGCAAGATAGGCTTCAAT	FSKIGFN	+++	-
5632	16573	AGATCCGAACATGTCTTTCCA	RSEHVFP	+++	-
7436	16047	TATGCTAAAGGTGGCCTAAAC	YAKGGLN	+++	-
5633	16574	TCATACGCGAAGTCCCTCTTG	SYAKSLL	+++	-
6917	13954	TACTCACGTGTCAACGTCAAC	YSRVNVN	+++	-
6834	17119	CTACATCGATTGATAGCAGAT	LHRLIAD	+++	-
6845	13954	TATAGTCGAGTTAATGTAAAT	YSRVNVN	+++	-
5634	16575	TTATCTAAGCTAAGTGCAAAC	LSKLSAN	+++	-
6915	17156	CGAATGAAGGATGTGTATCCC	RMKDVYP	+++	-
7441	16047	TACGCCAAGGGCGGATTAAAT	YAKGGLN	+++	-
5635	16576	TATTCGAGGTTATCTGGGAAT	YSRLSGN	+++	-
5636	14328	TACAGCCGTATCAATACCAAT	YSRINTN	+++	-
5637	16577	TATAGCAGACTAAACAAAGAC	YSRLNKD	+++	--
6905	14575	TACGCCAGGATGGGAATAAAT	YARMGIN	+++	-
5638	16565	ATCCATAGACTTCTACCCTCA	IHRLLPS	+++	---
6868	16035	TACTCCCGAGTAAACCTCAAT	YSRVNLN	+++	-
6658	17059	CTAAGTCGTGTAGCGATGAAT	LSRVAMN	+++	--
7230	17251	TACTTCAGCGGAAAAACGCTG	YFSGKTL	+++	-
5639	16578	TACTCAGCCATTGGAATGAAC	YSAIGMN	+++	-
7446	17411	TATGTAAAATCCAACCACGGC	YVKSNHG	+++	-
5640	16569	TACCTGAAGAGCCAATCCTAC	YLKSQSY	+++	-
7052	16097	TACAGTAAAATGAACCAAAAT	YSKMNQN	+++	-
7448	17412	TATGTCAAAAGTGACAATGCG	YVKSDNA	+++	-
5641	16579	TATTTGAAGAGTCAGGGGAAC	YLKSQGN	+++	-
5642	16005	TACGCGCGAATCGGGCTGAAC	YARIGLN	+++	-
7112	14575	TATGCTCGCATGGGTATTAAC	YARMGIN	+++	-
7274	14419	TATGCCCGGGGTGGAGTAAAC	YARGGVN	+++	-
5643	16567	CGGAACGATATGGTCTTCCCT	RNDMVFP	+++	-
6775	17059	TTGTCTCGAGTGGCTATGAAC	LSRVAMN	+++	--
7102	16582	TATGTGAAGTCGAGTAACAAC	YVKSSNN	+++	-
7453	17413	TGGTTTACGGGGTACAATGCA	WFTGYNA	+++	-
5644	16577	TACTCACGCCTTAATAAGGAT	YSRLNKD	+++	--

5645	16580	TATAGCAAACTTAATGATAAG	YSKLNDK	+++	-
7454	16003	TACGCTAAAGCGAATTTCAAC	YAKANFN	+++	-
6607	11015	CTATCTAAACTAAACGATAAC	LSKLNDN	+++	-
6651	16594	CATTCCCGGCTGAATGTTAGT	HSRLNVS	+++	-
7019	16109	TTTTCTAAAATGAACATCAAT	FSKMNIN	+++	-
6943	13788	TTTTCTAAGCTAAACTCAAAC	FSKLNSN	+++	-
7459	14514	TATTCACGGGTGAACAATAAC	YSRVNNN	+++	-
5646	16038	TATGCCAAAAATGGCTTTAAC	YAKNGFN	+++	-
6946	16589	ATGTCTCGAATCGGCGTTAAC	MSRIGVN	+++	–
5647	16100	TATTCGAAGGTCCAGACCAAT	YSKVQTN	+++	-
5648	13758	TACTCTCGTTCCAATGCTAAC	YSRSNAN	+++	–
7215	16109	TTCTCAAAGATGAATATAAAC	FSKMNIN	+++	-
5649	14133	TACACTCGCTTAAACCAAAAT	YTRLNQN	+++	–
6959	13980	TACAGCAGAATTAACGCCAAC	YSRINAN	+++	-
7463	15999	TACGCCCGACAAAACGCGAAC	YARQNAN	+++	-
5650	16576	TACAGTAGATTGTCCGGAAAC	YSRLSGN	+++	-
7464	17414	TATTACACGGGAGTCAAGGGA	YYTGVKG	+++	–
7465	16003	TATGCAAAGGCAAACTTTAAT	YAKANFN	+++	-
5651	15967	CTACACAAGTCTGGAATGAAT	LHKSGMN	+++	-
5652	14483	CTTTCTAAGGTCGGAGCTAAT	LSKVGAN	+++	-
6869	13698	TACGCCAAGTTTGGTCCGAAC	YAKFGPN	+++	-
5653	16581	TACTTAAAGTCGCAGGCTATG	YLKSQAM	+++	-
5654	16582	TACGTTAAATCCTCCAATAAT	YVKSSNN	+++	-
6610	14483	CTATCCAAAGTTGGTGCAAAC	LSKVGAN	+++	-
7157	13942	TACAGCAGAACTAATACCAAT	YSRTNTN	+++	-
6842	13698	TATGCGAAATTCGGCCCCAAT	YAKFGPN	+++	–
5655	16583	TACGTCAAATCGGACCATCAC	YVKSDHH	+++	-
5656	14507	TATGCTCGGTTAGGAATGAAC	YARLGMN	+++	-
7470	16587	TACCATATACTTGGAAAGAAC	YHILGKN	+++	-
5657	14133	TATACCAGACTGAATCAGAAC	YTRLNQN	+++	–
5658	13761	TACGCGCGTGGAGGAATGAAT	YARGGMN	+++	-
7208	15963	TATGCAAGGCAAAACTTCAAT	YARQNFN	+++	-
5659	16584	CGAGGGATCGACTTCTACCCC	RGIDFYP	+++	-

6911	17155	CTAGCTAGGAACGCGAGTAAT	LARNASN	+++	--
5660	16585	TACGTAAGGTCGGATGTTCGG	YVRSDVR	+++	---
6592	17032	AAGATGGACAGCCGATTATGG	KMDSRLW	+++	---
6916	16599	TTTGTCAAATCGGACACCAAG	FVKSDTK	+++	-
5661	16583	TATGTTAAGTCTGATCACCAT	YVKSDHH	+++	-
5662	16038	TACGCGAAGAACGGATTCAAT	YAKNGFN	+++	-
7475	16574	AGTTATGCCAAATCACTACTG	SYAKSLL	+++	-
7476	17415	TATTATCACGGGATGCTAGCC	YYHGMLA	+++	-
5663	16572	TACCTGAAATCAGAGCGCAAC	YLKSERN	+++	-
5664	14301	TACTCACGGTTGAATATGAAC	YSRLNMN	+++	-
7477	17416	TATACAAAGAGTGACTCGAAA	YTKSDSK	+++	-
7217	15942	TACGCCAAAAGTAATTACAAT	YAKSNYN	+++	-
5665	16580	TACTCAAAGCTCAACGACAAA	YSKLNDK	+++	-
5666	13956	TATAGTCGGATGAATGCAAAT	YSRMNAN	+++	-
6753	17074	CGGAACCACGAGACGTTTCCG	RNHETFP	+++	-
5667	16575	CTGAGCAAATTATCCGCCAAT	LSKLSAN	+++	-
5668	16586	TATCATAAGTTAGCGAATAAT	YHKLANN	+++	-
6998	16087	TACAGCAAGCTAGGAGGTAAT	YSKLGGN	+++	-
5669	13933	TATGCAAGAGGTGGAAACAAT	YARGGNN	+++	-
5670	16573	AGGTCGGAGCACGTATTCCCC	RSEHVFP	+++	-
7142	17281	TTGGCACGGTCAGCAGTCAAT	LARSAVN	+++	-
6563	17035	CTCCGCAGTGAATGTTGTGTA	LRSECCV	+++	--
6774	15960	GTTGCTATGCGCGGGATTGGA	VAMRGIG	+++	-
6841	16108	TATGCTAAGAATGGCGCAAAT	YAKNGAN	+++	-
5671	16022	TATAGCAAGAATGGGATGAAC	YSKNGMN	+++	-
6909	16009	TATGCGAAGGCTGGTCATAAC	YAKAGHN	+++	-
7486	14386	TACGCAAAAGGTAACATGAAT	YAKGNMN	+++	-
5672	16087	TATTCGAAACTCGGTGGGAAC	YSKLGGN	+++	-
5673	13761	TATGCACGCGGTGGGATGAAC	YARGGMN	+++	-
6589	17036	CAATTGGAGGCTCGCACTTGG	QLEARTW	+++	---
5674	14249	TATTCGCGGATGAACACTAAC	YSRMNTN	+++	-
5675	14056	TATTCACGAATGAATAACAAT	YSRMNNN	+++	-
5676	16587	TATCACATTTTAGGGAAAAAT	YHILGKN	+++	-

6853	16108	TACGCAAAAAACGGTGCGAAC	YAKNGAN	+++	.
6787	16034	TTTAGTCGAATTGGGGAGAAT	FSRIGEN	+++	.
7273	15966	TATGCCAAGCAGGGGCACAAC	YAKQGHN	+++	.
5677	16588	CTAAGTAGGGTGGGCATCGAT	LSRVGID	+++	.
7352	15999	TATGCTCGGCAGAATGCAAAT	YARQNAN	+++	.
5678	14301	TATTCTCGCTTAAACATGAAT	YSRLNMN	+++	-
5679	16581	TATTTGAAAAGTCAAGCAATG	YLKSQAM	+++	.
6852	16034	TTCAGCCGGATAGGCGAAAAC	FSRIGEN	+++	.
7171	16103	TATGCACGCGGTGGGCAGAAC	YARGGQN	+++	.
5680	16566	TACTTCACAGGTGTCGTCGCA	YFTGVVA	+++	.
7494	16050	CTCTCAAAAGTAGCTGTCAAT	LSKVAVN	+++	.
7170	17281	CTCGCGCGTAGCGCGGTTAAC	LARSAVN	+++	-
6824	17113	GGAAAATATCCTCCCCAAGGC	GKYPPQG	+++	.
6522	17020	AAGATGAGTTCTAGCACGTGG	KMSSSTW	+++	---
5681	13803	TATTCTCGGATGAACTCTAAC	YSRMNSN	+++	.
5682	16589	ATGTCCCGTATTGGAGTGAAT	MSRIGVN	+++	-
5683	16590	TTAAGCCGCTCTGGCAATAAC	LSRSGNN	+++	---
7498	17416	TACACCAAAAGCGATTCTAAG	YTKSDSK	+++	.
5684	16116	TACTCTAAATCGGGAGCGAAT	YSKSGAN	+++	.
5685	16591	TATAGCAAAGCTCAGCCGAAT	YSKAQPN	+++	.
6813	16578	TATTCTGCGATAGGCATGAAT	YSAIGMN	+++	.
5686	16592	TACCACAAGTCGCAAAGTAAT	YHKSQSN	+++	.
5687	16593	GATATGTCCTCGCGAATCTGG	DMSSRIW	+++	---
5688	16594	CACTCGAGGTTGAACGTATCG	HSRLNVS	+++	.
5689	16592	TATCATAAAAGCCAGTCGAAC	YHKSQSN	+++	.
7302	15942	TATGCGAAGTCAAACTATAAC	YAKSNYN	+++	.
7023	15966	TACGCGAAACAAGGCCATAAT	YAKQGHN	+++	.
6616	13956	TACTCTCGTATGAACGCCAAC	YSRMNAN	+++	.
6575	17040	CATAGTCGTTTAAATCTCCAA	HSRLNLQ	+++	-
7504	14151	TATGCGAGAGTAGGGACTAAT	YARVGTN	+++	.
5690	16014	TACTCCAAAATGAATGATAAC	YSKMNDN	+++	.
5691	16586	TACCACAAACTTGCCAACAAC	YHKLANN	+++	.
5692	16595	CGAACACCAACTGTGTATCCT	RTPTVYP	+++	-

6551	17032	AAAATGGATAGTAGGCTGTGG	KMDSRLW	+++	---
5693	15967	TTGCATAAATCAGGCATGAAC	LHKSGMN	+++	-
5694	16596	TATACGCGACTCTCGATGAAT	YTRLSMN	+++	--
6982	17119	TTGCACCGGCTTATCGCTGAC	LHRLIAD	+++	-
7507	16036	TACGCTAAAATGGGGATGAAT	YAKMGMN	+++	-
6756	17079	CACTCAAGCACAAACGGGGCT	HSSTNGA	+++	-
7509	17414	TACTATACCGGGGTAAAAGGT	YYTGVKG	+++	-
5695	16597	TATCTGAAATCGGACAAAAGC	YLKSDKS	+++	-
7510	16091	TTCGCTAAACAAGGACCCAAC	FAKQGPN	+++	-
6667	16088	TTCTCACGCGTTGGGGAAAAC	FSRVGEN	+++	-
7512	14386	TATGCTAAGGGAAATATGAAC	YAKGNMN	+++	-
5696	16598	TATACACGTTCACAGACAGAA	YTRSQTE	+++	-
5697	11826	GTAACGTCCACCAATGGCATC	VTSTNGI	+++	-
6666	16602	GTGCACAGGCTTCAGGACAAA	VHRLQDK	+++	--
5698	13933	TACGCTCGGGGAGGGAATAAC	YARGGNN	+++	-
7514	14514	TACAGTCGTGTTAATAACAAT	YSRVNNN	+++	-
5699	16599	TTCGTTAAGTCCGATACTAAA	FVKSDTK	+++	-
5700	16596	TACACCCGTTTGAGTATGAAC	YTRLSMN	+++	--
5701	13803	TACAGTCGTATGAATTCCAAT	YSRMNSN	+++	-
5702	16600	AGGGCGCTTGAATGCTGCTAC	RALECCY	+++	-
6832	17117	TTCAAAGCCGGGACTTGGAAT	FKAGTWN	+++	-
5703	16601	CTGCACCGCGATGGAATTAAC	LHRDGIN	+++	-
5704	16014	TATTCGAAGATGAACGACAAT	YSKMNDN	+++	-
7516	16036	TATGCCAAGATGGGTATGAAC	YAKMGMN	+++	-
7231	11337	TATAGTAAGACGGGAGACAAC	YSKTGDN	+++	-
7518	17399	CTGTCCCGTATTCAAACTAAC	LSRIQTN	+++	---
5705	16579	TACCTTAAATCACAAGGTAAT	YLKSQGN	+++	-
7214	16616	AATTGCAAACCATGTTTTGAC	NCKPCFD	+++	-
7520	17381	AGCTTGTGTCCCCGACTATCT	SLCPRLS	+++	---
6857	17113	GGCAAGTACCCGCCACAGGGG	GKYPPQG	+++	-
7056	17155	TTGGCCCGGAATGCCTCAAAC	LARNASN	+++	--
6606	17049	AAGATGTCATCCGCTAACTGG	KMSSANW	+++	---
7339	16068	TACGCGAAAGGAAACGCGAAC	YAKGNAN	+++	-

6822	13902	TTCAGCCGCACTGGCTTCAAC	FSRTGFN	+++	-
5706	16602	GTACATCGCCTGCAAGATAAG	VHRLQDK	+++	--
5707	15958	TACTCTCGACCTGGGCCGAAC	YSRPGPN	+++	.
6536	17020	AAAATGTCGAGTTCAACATGG	KMSSSTW	+++	---
5708	16585	TATGTTCGGTCCGACGTGCGA	YVRSDVR	+++	---
7391	17399	CTCTCTAGAATCCAGACCAAT	LSRIQTN	+++	---
7528	15941	TATTCTAAAATCAATATCAAT	YSKININ	+++	.
7031	17220	TATCACAAGCACTCCTTGAAT	YHKHSLN	+++	.
5709	16603	TATGTGCGTTCAGATAGGAAC	YVRSDRN	+++	---
7530	15941	TACTCAAAGATTAACATAAAC	YSKININ	+++	.
7082	11337	TACAGCAAAACCGGCGATAAT	YSKTGDN	+++	.
5710	16005	TATGCAAGAATAGGCCTAAAT	YARIGLN	+++	.
5711	16597	TACCTTAAGTCAGATAAGTCG	YLKSDKS	+++	.
5712	14249	TACTCTCGAATGAATACCAAT	YSRMNTN	+++	.
7532	14151	TACGCCCGGGTTGGCACCAAC	YARVGTN	+++	.
7376	13942	TATTCGAGGACCAACACAAAC	YSRTNTN	+++	.
7216	16097	TATTCAAAGATGAATCAGAAC	YSKMNQN	+++	.
7535	17411	TACGTCAAGAGCAATCATGGA	YVKSNHG	+++	.
6860	17127	AAAATGAGCTCGTCTGTTTGG	KMSSSVW	+++	--
7537	16606	CTACATCGGTTGGCCAGCTCC	LHRLASS	+++	-
7538	16050	TTATCGAAGGTGGCCGTGAAC	LSKVAVN	+++	.
7539	17405	TATTTCAGCGGCGTGCCGTCC	YFSGVPS	+++	.
7540	13689	TACTCGCGCACAAACCCAAAC	YSRTNPN	+++	.
6912	17156	AGAATGAAAGACGTCTACCCT	RMKDVYP	+++	.
7334	14419	TACGCTCGAGGCGGCGTCAAT	YARGGVN	+++	.
6730	17074	AGGAATCATGAAACTTTCCCT	RNHETFP	+++	.
5713	16604	TATTCGTCCACTCATGGCGTG	YSSTHGV	+++	.
6731	13902	TTTTCCCGGACGGGGTTTAAT	FSRTGFN	+++	-
5714	16604	TACTCTTCGACCCACGGTGTA	YSSTHGV	+++	.
6629	16088	TTTTCTCGTGTAGGCGAGAAT	FSRVGEN	+++	.
5715	16598	TACACTCGCAGCCAAACGGAG	YTRSQTE	+++	.
6574	17039	CGAGAAGACGGGCTACGTTGG	REDGLRW	+++	-
5716	14056	TACAGCCGCATGAACAATAAC	YSRMNNN	+++	.

7547	16073	ACTAGAAGTGGGCTGAACGCG	TRSGLNA	+++	-
7548	16068	TATGCCAAGGGCAATGCAAAT	YAKGNAN	+++	-
5717	16100	TACTCCAAAGTGCAAACTAAC	YSKVQTN	+++	-
6506	17016	TATGTAAAGAACGACGCGAGA	YVKNDAR	+++	---
6883	17142	ATCAGTGAATACAGCAAATGG	ISEYSKW	+++	-
6805	15960	GTGGCAATGAGAGGTATCGGC	VAMRGIG	+++	-
7411	17405	TACTTTTCCGGAGTACCCAGT	YFSGVPS	+++	-
7553	17417	TATACAAAGAGCAACCACCTG	YTKSNHL	+++	-
5718	15970	TTTAGTCGAGTGGGGTTTAAC	FSRVGFN	+++	-
6539	17023	GTGTCGAGCAGTAACGGTAGA	VSSSNGR	+++	-
7287	15963	TACGCTCGACAGAATTTTAAC	YARQNFN	+++	-
6826	17114	TACAGCAAAGCTGGGTATGAC	YSKAGYD	+++	-
5719	16591	TACAGTAAGGCCCAACCTAAC	YSKAQPN	+++	-
5720	16605	TCAATGGAATCTCGACTGTGG	SMESRLW	+++	---
6785	17096	TTAGTTAGGTATGAGAACGTA	LVRYENV	+++	-
5721	14507	TACGCACGCCTTGGGATGAAT	YARLGMN	+++	-
7558	15272	TATGCGAGGTTGGGAGGCAAT	YARLGGN	+++	-
7559	17418	ATTCACCCCACTAGATATGGT	IHPTRYG	+++	-
5722	16606	CTCCACCGCCTAGCATCTTCG	LHRLASS	+++	-
7284	14332	TTTGCTCGGTCCGGTATGAAT	FARSGMN	+++	-
7561	13797	TTTTCCAAGTTAGGAAATAAC	FSKLGNN	+++	-
5723	16607	GACCTTTCGAGTCATAACTGG	DLSSHNW	+++	---
7562	14431	TATGCGCGGCAGAATATGAAT	YARQNMN	+++	-
5724	16588	TTGTCAAGAGTAGGTATAGAC	LSRVGID	+++	-
6590	17039	AGGGAGGATGGACTCAGATGG	REDGLRW	+++	-
6552	17033	AGAAACATGTCCGTGTATCCC	RNMSVYP	+++	-
5725	16608	CTTCATGCATTAAGTCATAAC	LHALSHN	+++	-
5726	11826	GTCACTAGCACGAACGGGATA	VTSTNGI	+++	-
6956	17117	TTTAAGGCTGGAACCTGGAAC	FKAGTWN	+++	-
5727	13764	TATGCTAGAAGCGGTTTAAAC	YARSGLN	+++	-
7044	16103	TACGCTAGAGGCGGTCAAAAT	YARGGQN	+++	-
5728	16022	TACTCAAAAAACGGCATGAAT	YSKNGMN	+++	-
5729	16595	CGTACTCCTACCGTCTACCCC	RTPTVYP	+++	-

3480	14431	TACGCCCGCCAAAACATGAAC	YARQNMN	+++	-
6614	17049	AAAATGTCTTCTGCCAATTGG	KMSSANW	+++	---
7106	11471	TATGCTCGGGGCAACGACAAC	YARGNDN	+++	-
6806	17097	CACGGGTCCGGAAACTTCGTG	HGSGNFV	+++	-
5730	15996	TACTCTAAGGTCGGGCAGAAT	YSKVGQN	+++	-
6598	16605	TCTATGGAGTCAAGACTTTGG	SMESRLW	+++	---
5731	13984	TACTCAAGAATGGGAATGAAT	YSRMGMN	+++	-
6525	17023	GTCTCCTCGAGCAATGGCCGT	VSSSNGR	+++	-
5732	16609	CTCCATGTCCGAAGCCTAAAC	LHVRSLN	+++	-
7572	14332	TTCGCGCGCTCTGGCATGAAC	FARSGMN	+++	-
6827	17114	TATAGTAAGGCGGGCTACGAT	YSKAGYD	+++	-
5733	16601	TTGCATCGGGACGGTATCAAT	LHRDGIN	+++	-
7574	17417	TACACTAAAAGTAATCATTTG	YTKSNHL	+++	-
5734	12385	TATAGTCGGCAGAACGAGAAT	YSRQNEN	+++	-
6700	16135	GACTATACTGGTAAATCCGCG	DYTGKSA	+++	-
7576	17419	TATTTCCACGCCACGAGAGAT	YFHATRD	+++	-
7577	16091	TTTGCCAAGCAGGGGCCTAAT	FAKQGPN	+++	-
7578	15272	TACGCACGGCTTGGTGGAAAC	YARLGGN	+++	-
5735	16137	TACTCACGCGTTAATGATAAT	YSRVNDN	+++	-
6597	17038	ACTATGTCCGATCGAACTTGG	TMSDRTW	+++	---
6566	17036	CAGCTTGAAGCGCGGACGTGG	QLEARTW	+++	---
6573	17038	ACCATGAGTGACCGCACCTGG	TMSDRTW	+++	---
6540	17025	GTTGAATCATCGAATGGTAGG	VESSNGR	+++	-
5736	16593	GACATGAGTAGTAGAATATGG	DMSSRIW	+++	--
6690	17065	AAAATGCCAAGCCGGGACTGG	KMPSRDW	+++	---
7584	16073	ACACGCTCTGGTTTAAATGCC	TRSGLNA	+++	-
6974	11471	TACGCACGAGGGAATGATAAT	YARGNDN	+++	-
6604	17040	CACTCCAGACTTAACCTGCAG	HSRLNLQ	+++	-
7120	16136	TACTCCAAGTCTGGCGATAAT	YSKSGDN	+++	-
6618	16617	CACAGCCGTATGAACGAGAAC	HSRMNEN	+++	-
6553	17033	CGCAATATGTCTGTTTACCCA	RNMSVYP	+++	-
5737	16610	TATGTGAAATATGAAGATAAA	YVKYEDK	+++	-
7590	16131	TATGCGCGTCTCAACGAGAAT	YARLNEN	+++	-

6709	17064	CGGAACGGAACCTCGAGCTGG	RNGTSSW	+++	-
5738	16116	TATTCCAAGTCAGGTGCAAAC	YSKSGAN	+++	.
5739	16611	TATAGTCGCTTGCAAGAAAAT	YSRLQEN	+++	.
5740	16568	CTGCACAGACTGTTAAAGGAT	LHRLLKD	+++	---
6684	17065	AAGATGCCTTCTCGAGATTGG	KMPSRDW	+++	---
5741	13764	TACGCGCGATCTGGCCTGAAT	YARSGLN	+++	-
5742	16612	CTTTCTAGAGTAGGTTTCAAT	LSRVGFN	+++	---
6622	17048	ACGGAATCCAGCTCGGGCCGA	TESSSGR	+++	.
6902	16009	TACGCCAAAGCCGGCCACAAT	YAKAGHN	+++	.
6601	17048	ACAGAGTCATCATCTGGTAGA	TESSSGR	+++	.
5743	16137	TATTCGCGTGTAAACGACAAC	YSRVNDN	+++	.
6741	17079	CATAGTTCTACGAATGGAGCC	HSSTNGA	+++	.
5744	16613	TACGCTCGGGGAGGGCCCAAT	YARGGPN	+++	--
7011	17217	TACAGCCGCACCGGAAGCGAT	YSRTGSD	+++	.
5745	16613	TATGCGCGTGGTGGACCTAAC	YARGGPN	+++	--
6537	17025	GTCGAGAGTTCCAACGGGCGC	VESSNGR	+++	.
5746	16614	CACTGCGGAAAATGCCTAAAT	HCGKCLN	+++	-
7599	16131	TACGCCAGGTTGAATGAAAAC	YARLNEN	+++	.
5747	16615	TTGCACAGATCAGGCGATAAT	LHRSGDN	+++	.
7150	17284	TGGCATCGTCTTAGTGTGAAT	WHRLSVN	+++	.
6634	17051	TACAATAGTACTCACGGGAGA	YNSTHGR	+++	.
7018	17220	TACCATAAACATAGTCTGAAC	YHKHSLN	+++	.
7603	16142	TACTCGAAAGGTGGAGCGAAT	YSKGGAN	+++	.
7221	16136	TATTCTAAATCAGGTGACAAC	YSKSGDN	+++	.
6691	16135	GATTACACGGGAAAGAGTGCT	DYTGKSA	+++	.
6844	16590	CTATCGCGGTCCGGTAACAAT	LSRSGNN	+++	---
7165	15985	GGGTCCTCAACCTCCATTTGG	GSSTSIW	+++	.
5748	16615	CTGCATCGTTCTGGGGACAAC	LHRSGDN	+++	.
5749	13984	TATTCCCGAATGGGTATGAAC	YSRMGMN	+++	.
7236	17284	TGGCACAGATTATCCGTAAAC	WHRLSVN	+++	.
7609	17420	AATTACGCAAAGTCATATGCC	NYAKSYA	+++	-
7610	17421	TACTTTTCCGGTACCGAGAAT	YFSGTEN	+++	.
5750	15996	TATTCCAAAGTAGGCCAAAAC	YSKVGQN	+++	.

5751	16616	AACTGTAAGCCTTGCTTCGAT	NCKPCFD	+++	.
5752	16612	CTGTCACGCGTGGGCTTTAAC	LSRVGFN	+++	--
7611	17422	ATGAGCAGGGCAGGGAATAAC	MSRAGNN	+++	--
6581	17035	TTGAGGTCTGAGTGCTGCGTC	LRSECCV	+++	--
5753	12385	TACTCACGCCAAAATGAAAAC	YSRQNEN	+++	.
7613	17423	TACTGGGAAGGAACTCGACAC	YWEGTRH	+++	.
7016	17217	TATAGTAGAACGGGGAGTGAC	YSRTGSD	+++	.
6533	16620	CTGTCTCGTATCTCCGTGAAT	LSRISVN	+++	---
7616	13797	TTCTCGAAACTGGGTAACAAT	FSKLGNN	+++	.
6955	17142	ATTAGCGAGTATTCGAAGTGG	ISEYSKW	+++	.
5754	16610	TACGTAAAGTACGAGGACAAG	YVKYEDK	+++	-
7618	17424	TACTGGCAAGGGGTAAATGAA	YWQGVNE	+++	.
7619	17412	TACGTTAAGAGCGATAACGCT	YVKSDNA	+++	.
7620	17425	CTTTACTCACGACTCGATAAG	LYSRLDK	+++	-
5755	16611	TACTCACGATTACAGGAGAAC	YSRLQEN	+++	.
7621	17423	TATTGGGAGGGCACAAGACAT	YWEGTRH	+++	.
5756	16584	AGAGGCATTGATTTTTATCCT	RGIDFYP	+++	.
7622	17426	CATACTGATGATAGTTACCCG	HTDDSYP	+++	.
6594	17047	GTCCCCGGTGACTGCTGTGTT	VPGDCCV	+++	.
6711	17070	TTTGAGGGCCGCGGGTGGAAT	FEGRGWN	+++	.
7625	17421	TATTTCAGCGGCACGGAAAAC	YFSGTEN	+++	.
7626	14068	TACGCAAGACAGAATCAGAAT	YARQNQN	+++	.
5757	16617	CATAGTCGCATGAATGAAAAT	HSRMNEN	+++	.
7627	17427	TACGTTCGCAATGATGACAAA	YVRNDDK	+++	.
7628	14456	TTCGCGAAGCAGGGGTTCAAC	FAKQGFN	+++	.
6660	17047	GTGCCAGGCGATTGTTGCGTC	VPGDCCV	+++	.
5758	16603	TACGTCAGAAGTGACAGAAAT	YVRSDRN	+++	---
6500	16619	CTTCACAAGGCAGGGTACAAC	LHKAGYN	+++	--
7631	17415	TACTACCATGGTATGTTAGCG	YYHGMLA	+++	.
7275	17264	TACCATAAAGGCAACAATAAC	YHKGNNN	+++	.
7633	17420	AACTATGCGAAATCGTACGCT	NYAKSYA	+++	-
6795	17100	TACGCGGCAGGCAGTTGGAAT	YAAGSWN	+++	.
5759	16607	GATTTGTCATCGCACAATTGG	DLSSHNW	+++	---

7635	17428	CAAAAACATGCCCCGAATGCC	QKHAPNA	+++	-
6507	17016	TACGTTAAAAATGATGCACGC	YVKNDAR	+++	---
5760	16618	TTGCATCGGCTATCCCCTTAT	LHRLSPY	+++	-
7637	17428	CAGAAGCACGCTCCAAACGCT	QKHAPNA	+++	-
7638	17429	ACATGGTCTGACAATGGGGTA	TWSDNGV	+++	-
6996	17208	CGAACATACGACACTTACATC	RTYDTYI	+++	-
7640	15985	GGAAGCTCTACAAGCATATGG	GSSTSIW	+++	-
5761	16077	TACTCAAGGATGAACGAAAAT	YSRMNEN	+++	-
5762	16619	CTGCATAAAGCTGGATATAAT	LHKAGYN	+++	--
5763	16608	TTACACGCTTTGTCACACAAT	LHALSHN	+++	-
6681	17064	CGCAATGGTACTAGCTCGTGG	RNGTSSW	+++	-
7642	14068	TATGCGCGGCAAAACCAAAAC	YARQNQN	+++	-
7643	16142	TATTCTAAGGGAGGGGCCAAC	YSKGGAN	+++	-
7644	14476	TATGCGCGTGTTGGAGGCAAC	YARVGGN	+++	-
7645	17422	ATGAGTCGTGCCGGCAACAAT	MSRAGNN	+++	--
5764	16077	TATAGCCGTATGAATGAGAAC	YSRMNEN	+++	-
7646	17427	TATGTGAGGAACGACGATAAG	YVRNDDK	+++	-
6788	17096	CTTGTCAGATACGAAAATGTG	LVRYENV	+++	-
7648	17313	TATTATACCGGCAGGACGAAC	YYTGRTN	+++	-
7649	14476	TACGCTAGAGTCGGCGGTAAT	YARVGGN	+++	-
6696	17070	TTCGAAGGAAGAGGATGGAAC	FEGRGWN	+++	-
7115	17264	TATCACAAGGGGAATAACAAT	YHKGNNN	+++	-
7652	17424	TATTGGCAGGGAGTGAACGAG	YWQGVNE	+++	-
5765	16620	TTGTCACGGATTTCTGTAAAC	LSRISVN	+++	---
7653	17430	CGAACGAACAACGAATATCCC	RTNNEYP	+++	-
7654	14693	TATGCCCGGATGGGTGAGAAC	YARMGEN	+++	-
7655	17431	TATATAAAATCGGACTATCAG	YIKSDYQ	+++	-
7656	17426	CACACGGACGACAGCTATCCC	HTDDSYP	+++	-
7657	17419	TACTTTCATGCAACAAGGGAC	YFHATRD	+++	-
7658	14283	TACAGTCGAAACAATTCCAAT	YSRNNSN	+++	-
7659	17432	TACGCGCGTCTGGGTCCTTCG	YARLGPS	+++	-
7660	17433	CGAAATGGAACGTCAGTGTGG	RNGTSVW	+++	--
7661	14456	TTTGCCAAACAAGGCTTTAAT	FAKQGFN	+++	-

7662	17434	TATTATACGGGTATGAATAAT	YYTGMNN	+++	.
5766	16609	CTACACGTACGTAGTCTGAAT	LHVRSLN	+++	-
5767	16621	TATTCGAGGATGAACGACAAC	YSRMNDN	+++	-
7663	17435	TACTACTCAGGAGAACGAAAC	YYSGERN	+++	.
7664	14693	TACGCACGTATGGGAGAAAAT	YARMGEN	+++	.
7665	14143	TATTCAAGAGGTGGTTTCAAC	YSRGGFN	+++	.
7666	17425	TTGTATAGTAGGCTTGACAAA	LYSRLDK	+++	-
7667	17429	ACGTGGTCGGATAACGGAGTT	TWSDNGV	+++	.
6683	17063	CACGGATCCACGAACGGGAAG	HGSTNGK	+++	.
7669	14525	ACTCATAAATTGTCCGTGAAT	THKLSVN	+++	.
7670	16120	TTTGCACGGCAGGGCTTCAAT	FARQGFN	+++	.
7671	17432	TATGCTCGATTAGGCCCCAGC	YARLGPS	+++	-
6900	17150	TACGCGCGCGAAACATGGAAT	YARETWN	+++	.
7673	17436	TATTGGGCGGATAAGCACGCA	YWADKHA	+++	.
7674	16625	TATTCAAGAGTAGACGACAGA	YSRVDDR	+++	.
7675	17437	GACTACGCGAAATCACTCTTG	DYAKSLL	+++	.
7676	17430	CGCACAAATAATGAGTACCCA	RTNNEYP	+++	.
6665	17051	TATAACTCAACGCATGGTCGC	YNSTHGR	+++	.
6904	17127	AAGATGTCGTCCTCGGTGTGG	KMSSSVW	+++	-
6587	16627	TACTCGGCGAGAGGTCCGAAC	YSARGPN	+++	--
5768	16622	TTATGGAGGACAGGGATTAAC	LWRTGIN	+++	-
7680	16120	TTCGCTCGACAAGGATTTAAC	FARQGFN	+++	.
7681	14251	TTTAGTAGAATGAACCAGAAC	FSRMNQN	+++	.
7046	13521	TTTTCAAAGATGAACTATAAT	FSKMNYN	+++	.
7683	17409	ACTCATCGACTTATCGTCGCA	THRLIVA	+++	.
7684	14143	TACTCGCGAGGCGGATTTAAT	YSRGGFN	+++	.
6686	17066	GGTGGCGATGGTAATCATTAT	GGDGNHY	+++	.
7686	14451	TATTCTAGGCATAATTTAAAT	YSRHNLN	+++	.
7687	17433	CGGAACGGGACTTCTGTTTGG	RNGTSVW	+++	--
7688	13689	TATAGCAGGACGAATCCGAAT	YSRTNPN	+++	.
7689	14283	TATTCGAGAAATAACAGTAAC	YSRNNSN	+++	.
7690	17438	CTTAGGCGCAAGCCAGACCTT	LRRKPDL	+++	---
6878	17100	TATGCAGCGGGATCCTGGAAC	YAAGSWN	+++	.

7692	14251	TTCAGCCGGATGAATCAAAAT	FSRMNQN	+++	-
7693	17435	TATTATTCGGGTGAGCGCAAT	YYSGERN	+++	-
6678	17063	CATGGGAGCACTAATGGAAAA	HGSTNGK	+++	-
7695	16623	TACTTCATGGGTCGCAGTGAT	YFMGRSD	+++	-
7251	13521	TTCTCGAAAATGAATTACAAC	FSKMNYN	+++	-
7036	17150	TATGCTCGTGAGACCTGGAAC	YARETWN	+++	-
6747	16639	ATAATGTCGAGCCGGTCATGG	IMSSRSW	+++	--
5769	16623	TATTTTATGGGGCGGTCCGAC	YFMGRSD	+++	-
5770	16621	TACTCCCGGATGAATGATAAT	YSRMNDN	+++	-
7699	13907	TTTTCGCGTATGAACAGTAAT	FSRMNSN	+++	-
7700	17436	TACTGGGCAGACAAACATGCC	YWADKHA	+++	-
7701	14311	TTTGCTCGACAAGGCATGAAC	FARQGMN	+++	-
7702	14525	ACCCACAAGCTATCTGTAAAC	THKLSVN	+++	-
7703	13907	TTCAGCCGCATGAATTCCAAC	FSRMNSN	+++	-
7704	17439	TTTGTAAAGTTTCAAGTCAAC	FVKFQVN	+++	-
7705	17418	ATCCATCCGACGAGGTACGGG	IHPTRYG	+++	-
7706	17440	CAAAGTAAGCTGAGCACATGG	QSKLSTW	+++	-
7707	14451	TACTCCCGGCACAACCTAAAC	YSRHNLN	+++	-
7708	14311	TTCGCACGCCAGGGAATGAAT	FARQGMN	+++	-
5771	16624	CTACACCGAGCTAGCAGCAAC	LHRASSN	+++	--
7709	16099	TATGCGAAAAATGGCGACAAC	YAKNGDN	+++	-
6582	17046	CGGACATTTGATTCGTTCGAG	RTFDSFE	+++	-
7711	15987	TTCTCCCGTAGTGGCATGAAC	FSRSGMN	+++	-
5772	16625	TACTCCCGTGTTGATGATCGC	YSRVDDR	+++	-
5773	16624	CTGCATCGTGCGTCATCCAAT	LHRASSN	+++	--
7358	17208	AGGACTTATGATACCTATATA	RTYDTYI	+++	-
7713	16039	TTCGCAAAATCCGGACAAAAC	FAKSGQN	+++	-
7074	13528	TATGCACGTCAAAATTATAAT	YARQNYN	+++	-
7715	17441	TATTGGGTAGATAAGGTAGCT	YWVDKVA	+++	-
6583	17037	GAAATGCAAAGCCGAGCTTGG	EMQSRAW	+++	---
6670	17050	AGAGAGACGTATGTATATCCC	RETYVYP	+++	-
5774	16626	TATTCGCGCAACAGCGACAAC	YSRNSDN	+++	-
7213	17313	TACTACACAGGTCGTACTAAT	YYTGRTN	+++	-

5775	16627	TATAGTGCTCGTGGGCCCAAT	YSARGPN	+++	--
7719	17439	TTCGTCAAATTCCAGGTTAAT	FVKFQVN	+++	-
7720	15987	TTTAGTCGCTCAGGAATGAAT	FSRSGMN	+++	-
7721	17442	TACGCAAAGATGGGGTGGAAC	YAKMGWN	+++	-
7722	17434	TACTACACTGGGATGAACAAC	YYTGMNN	+++	-
7723	16626	TACAGTCGGAATTCTGATAAT	YSRNSDN	+++	-
7069	17248	TACTCCAGGTATAATATTAAT	YSRYNIN	+++	-
7725	17443	CGCACAGATCAGTACTTTCCG	RTDQYFP	+++	-
5776	16600	AGAGCTCTGGAGTGTTGTTAT	RALECCY	+++	-
6516	17019	AGGCAAGCAAAGCAAAAGAAC	RQAKQKN	+++	--
5777	16628	TTAACTAGGATCTCACACAAC	LTRISHN	+++	---
7727	17442	TATGCGAAAATGGGCTGGAAT	YAKMGWN	+++	-
7728	17444	TACATAAAAGGGGATTTATTT	YIKGDLF	+++	-
7729	17445	TACCATAGATATGGCATTGAC	YHRYGID	+++	-
6570	17037	GAGATGCAGTCTAGAGCCTGG	EMQSRAW	+++	---
5778	16628	CTGACCCGAATTAGTCATAAT	LTRISHN	+++	---
6486	16630	CTATCCCGTTTGAACCATAAC	LSRLNHN	+++	--
5779	16629	CTTTGTCGTCCATGTTCAGAG	LCRPCSE	+++	-
7732	17440	CAGTCGAAATTGTCGACCTGG	QSKLSTW	+++	-
5780	16630	TTAAGTCGCTTAAATCACAAT	LSRLNHN	+++	--
7733	16081	TATAGTAAATTCAATGACAAC	YSKFNDN	+++	-
7734	14470	TATGCTAAGTTAAACCATAAC	YAKLNHN	+++	-
6613	17046	AGGACGTTCGACAGTTTTGAA	RTFDSFE	+++	-
7736	17410	TATTTTGCAGGACAGTTTTCT	YFAGQFS	+++	-
7737	16039	TTTGCGAAGTCGGGCCAGAAT	FAKSGQN	+++	-
7738	14118	TATTCTAAATGGAACCAGAAT	YSKWNQN	+++	-
7739	17446	TATCTCATAAGCGATACTAAA	YLISDTK	+++	-
7740	16099	TACGCAAAGAACGGAGATAAT	YAKNGDN	+++	-
7741	17437	GATTATGCTAAGTCGTTGCTA	DYAKSLL	+++	-
7742	14458	TACGCCCGACCAGGCCACAAT	YARPGHN	+++	-
6733	17066	GGAGGTGACGGGAACCACTAC	GGDGNHY	+++	-
7744	14829	TTTGCCCGACAAGGATACAAT	FARQGYN	+++	-
6814	14641	TTTGCGAAAGAAGGACGAAAT	FAKEGRN	+++	-

6639	17053	GACGATGGCAGATCGAGGTAT	DDGRSRY	+++	-
7747	14470	TACGCGAAACTAAATCACAAT	YAKLNHN	+++	.
7748	17447	GAACATGGCAAGTCACTGTGG	EHGKSLW	+++	.
7749	16081	TACTCGAAGTTTAACGATAAT	YSKFNDN	+++	.
7750	17441	TACTGGGTGGACAAAGTGGCC	YWVDKVA	+++	.
7751	17445	TATCACCGGTACGGGATCGAT	YHRYGID	+++	.
7752	17446	TACCTGATTAGTGACACCAAG	YLISDTK	+++	.
7299	13769	TTCTCCAGGATGGGACCAAAT	FSRMGPN	+++	--
7754	17448	TGGTTCAGTGGGGAGCATTCC	WFSGEHS	+++	.
6821	14641	TTCGCCAAGGAGGGTAGGAAC	FAKEGRN	+++	.
5781	16631	CTACACGTGCTTGGACCGAAT	LHVLGPN	+++	.
6655	17053	GATGACGGGAGGTCCCGATAC	DDGRSRY	+++	-
7757	17413	TGGTTCACCGGTTATAACGCC	WFTGYNA	+++	.
7758	16633	TATATGAAGTACGACACCCAG	YMKYDTQ	+++	.
7759	17449	TTTGTTCGAAGTCAAATTAGT	FVRSQIS	+++	-
7760	14458	TATGCACGCCCGGGACATAAC	YARPGHN	+++	.
7761	17443	AGAACGGACCAATATTTCCCC	RTDQYFP	+++	.
6627	17050	CGGGAAACTTACGTGTACCCA	RETYVYP	+++	.
7020	17221	ATATGCCGCGGATATACATCT	ICRGYTS	+++	-
7764	16055	TATAGTCGTCAGGGAGGCAAT	YSRQGGN	+++	-
7765	17450	TATAAAGATGGTACGTGGTAC	YKDGTWY	+++	.
5783	16633	TACATGAAATATGATACACAA	YMKYDTQ	+++	.
7766	17451	TGCAAAAAAGGCTGCTTTGAG	CKKGCFE	+++	.
6895	13586	TTTTCGAGGCTCGGGCACAAT	FSRLGHN	+++	.
7297	13528	TACGCTCGACAGAACTACAAC	YARQNYN	+++	.
7769	14522	TTTGCGCGGGCAGGATTAAAT	FARAGLN	+++	.
7770	13518	TTTGCTCGAGGGGGGTACAAC	FARGGYN	+++	.
5784	16634	ATGTCACGGCTGTCACAGAAC	MSRLSQN	+++	---
7771	14118	TACTCGAAGTGGAATCAAAAC	YSKWNQN	+++	.
7772	17451	TGTAAGAAGGGTTGTTTCGAA	CKKGCFE	+++	.
5785	16635	CTCCATCGCAGTAGTAATAAT	LHRSSNN	+++	---
7344	13769	TTTAGTCGTATGGGCCCCAAC	FSRMGPN	+++	--
6708	17067	ATGTATAATGATTGCTGTGTA	MYNDCCV	+++	.

7396	16055	TACAGCCGGCAAGGCGGAAAC	YSRQGGN	+++	-
5786	13828	TACGCTCGGTCCGGGTATAAT	YARSGYN	+++	.
7776	17452	AACTATGCGCGTTCCAACAAT	NYARSNN	+++	.
5787	16636	TACCATCGTTTGTCCAATAAC	YHRLSNN	+++	-
7777	17431	TACATTAAGAGTGATTACCAA	YIKSDYQ	+++	.
5788	16631	CTGCATGTCCTGGGGCCAAAC	LHVLGPN	+++	.
5789	13828	TATGCGCGCAGCGGATACAAC	YARSGYN	+++	.
7778	14522	TTCGCTAGGGCTGGTCTGAAC	FARAGLN	+++	.
7779	17448	TGGTTTTCGGGTGAACACTCT	WFSGEHS	+++	.
5790	16635	TTGCACAGGTCTTCAAACAAC	LHRSSNN	+++	---
5791	16636	TATCACCGGCTTTCTAACAAT	YHRLSNN	+++	-
7780	17444	TATATCAAGGGCGACCTTTTC	YIKGDLF	+++	.
7312	17354	TACTTTACTCGGCAGGTTAAC	YFTRQVN	+++	.
5792	16637	TATCATGCTCGCGCTCCGAAT	YHARAPN	+++	.
5793	16629	CTATGCAGACCGTGCTCGGAA	LCRPCSE	+++	.
5794	16618	TTACACAGACTGAGCCCATAC	LHRLSPY	+++	.
5795	16637	TACCACGCACGGGCCCCAAAC	YHARAPN	+++	.
7782	17453	ATTGAAAGAGTGTCGTATGGA	IERVSYG	+++	-
7783	17454	CACCATAAAGGGAACATGAAT	HHKGNMN	+++	.
7784	14829	TTCGCGCGCCAGGGCTATAAC	FARQGYN	+++	.
6662	17060	CGTATGTCAGATCACAATTGG	RMSDHNW	+++	--
6819	13586	TTCTCCCGATTGGGTCATAAC	FSRLGHN	+++	.
7787	17453	ATCGAGCGAGTCTCATACGGT	IERVSYG	+++	-
7108	17247	CGAATGTCAGCGTCAAATTGG	RMSASNW	+++	-
5796	16638	AACGAAGACTGGGTGAAGTGG	NEDWVKW	+++	-
7789	14891	TACGCGAGGAACAATATGAAT	YARNNMN	+++	.
5797	16634	ATGTCCCGATTATCTCAAAAT	MSRLSQN	+++	---
5798	16639	ATTATGAGCAGTCGAAGCTGG	IMSSRSW	+++	--
7790	17447	GAGCACGGTAAAAGCCTCTGG	EHGKSLW	+++	.
5799	16638	AATGAGGATTGGGTAAAATGG	NEDWVKW	+++	-
7791	13518	TTCGCGCGCGGCGGTTATAAT	FARGGYN	+++	.
7792	17449	TTCGTAAGGTCTCAGATCTCC	FVRSQIS	+++	-
7793	17455	TGCGGTGCCTACTGGACAGAG	CGAYWTE	+++	---

7794	16010	TTTGCGAAGGGAGGAAATAAC	FAKGGNN	+++	-
7282	17344	ATCCACCGAATGATGGTTAAT	IHRMMVN	+++	-
5800	16614	CATTGTGGTAAGTGTCTTAAC	HCGKCLN	+++	–
7796	14891	TATGCACGAAATAACATGAAC	YARNNMN	+++	-
7797	16010	TTCGCTAAAGGGGGGAACAAT	FAKGGNN	+++	-
7798	17454	CATCACAAGGGCAATATGAAC	HHKGNMN	+++	-
7799	17456	TACACCCACTCCAACTTGCAT	YTHSNLH	+++	-
7800	17457	TCAAATGCACACTCCTCATGG	SNAHSSW	+++	-
5801	16640	TACGCTCGAACTTCGCATAAT	YARTSHN	+++	–
5802	16641	AATGGTCCTCACGGCTGGAAT	NGPHGWN	+++	-
7801	17458	TTGCACAGGATGGGAACGAGT	LHRMGTS	+++	-
6669	17060	AGGATGAGCGACCATAACTGG	RMSDHNW	+++	--
7276	17116	CGTGTTACCCACTGCACGGGC	RVTHCTG	+++	–
7804	17456	TATACTCATAGCAATCTCCAC	YTHSNLH	+++	-
7805	17459	TACGCCCGTTATGGTCTAAAT	YARYGLN	+++	-
7806	17460	ATTTCAGAATTGAGTCGCTGG	ISELSRW	+++	-
6545	17027	TGCGCTTTCACAGGCACCAGA	CAFTGTR	+++	-
7808	17452	AATTACGCTCGCAGCAATAAC	NYARSNN	+++	-
7809	17460	ATAAGTGAGCTGAGCCGTTGG	ISELSRW	+++	–
7810	13921	TTCGCAAGGATGGGTCCGAAC	FARMGPN	+++	-
6719	16643	TATCAGCGGCAGGGTTGGGAT	YQRQGWD	+++	-
5803	13556	TACTCCCGAGCTGGATATAAC	YSRAGYN	+++	-
5804	16642	TGGGTACGGTCGGACACAAAA	WVRSDTK	+++	–
5805	16643	TACCAACGCCAAGGATGGGAC	YQRQGWD	+++	-
7812	17450	TACAAGGACGGCACCTGGTAT	YKDGTWY	+++	-
5806	16640	TATGCCCGGACCTCCCACAAC	YARTSHN	+++	-
7285	17233	TATGGGGCCGGAACTTGGCAC	YGAGTWH	+++	-
5807	16644	CGACTCTATGACGCTTATCAG	RLYDAYQ	+++	-
7814	17461	TATCACCGCCTTGACAATCCA	YHRLDNP	+++	-
5808	16645	GGGCCGGGGTATGTGAACTGG	GPGYVNW	+++	-
7815	17462	TACGCTAGTGGACACTGGAAT	YASGHWN	+++	-
6559	17034	TCGGCAGAATGGGTCTCTTAT	SAEWVSY	+++	-
7817	17458	CTGCATCGCATGGGCACTAGC	LHRMGTS	+++	-

6577	17042	AGAGGTAACGGGGGGCATAAG	RGNGGHK	+++	–
6688	17067	ATGTACAACGACTGTTGCGTT	MYNDCCV	+++	–
7256	17154	CATAAATGCGGAGATACCCGT	HKCGDTR	+++	–
7821	17463	AACCAAAAGCATCTTATGTAT	NQKHLMY	+++	-
6712	17072	CGCAACTACGATACGTACCCT	RNYDTYP	+++	-
5809	16642	TGGGTGAGGTCTGATACGAAG	WVRSDTK	+++	–
7823	17354	TATTTCACCCGACAAGTGAAT	YFTRQVN	+++	-
5810	16641	AACGGCCCGCATGGTTGGAAC	NGPHGWN	+++	-
7824	17464	TATTGGAAAAATACTCCCGAC	YWKNTPD	+++	-
6718	17072	AGAAATTATGACACTTATCCC	RNYDTYP	+++	-
5811	16646	CTTCATCGCAATACTCAAAAC	LHRNTQN	+++	--
7826	17248	TATAGCCGCTACAACATAAAC	YSRYNIN	+++	-
7827	17461	TACCATAGATTGGATAACCCC	YHRLDNP	+++	-
7828	17465	TACACAAGGACACAAGCGTAC	YTRTQAY	+++	-
7829	14551	ATGAGTGCGCATGTTAAGTAT	MSAHVKY	+++	-
5812	16646	TTGCACAGGAACACCCAGAAT	LHRNTQN	+++	--
7830	17326	AAGAGCCCCTACGCAACCTTC	KSPYATF	+++	-
7831	17457	TCGAACGCCCATTCATCCTGG	SNAHSSW	+++	-
7832	17462	TATGCGTCTGGGCATTGGAAC	YASGHWN	+++	-
5813	16647	ATGCCTAATGAGGGGTGGTTT	MPNEGWF	+++	-
7833	14551	ATGTCCGCACACGTGAAATAC	MSAHVKY	+++	-
7067	17247	CGTATGTCTGCCAGTAACTGG	RMSASNW	+++	-
7835	17464	TACTGGAAGAACACACCGGAT	YWKNTPD	+++	-
7836	13921	TTTGCTCGCATGGGACCAAAT	FARMGPN	+++	-
5814	16648	TATCTAGATCGTGTTGTTTAC	YLDRVVY	+++	-
7837	17466	TTGTGTGGGAGTTGTCGGAGT	LCGSCRS	+++	-
7838	17467	AATTCGCCATACCGTCCTTTT	NSPYRPF	+++	-
7839	17468	CTGTGGAGGTCCGGAGTGAAC	LWRSGVN	+++	-
7040	17233	TACGGTGCTGGTACCTGGCAT	YGAGTWH	+++	-
7841	17469	AGATGCGGAGACTGTGTGTTC	RCGDCVF	+++	-
7235	17197	TTGTGTCGCCCGTGTAGGGAG	LCRPCRE	+++	–
5815	16649	TCCTACGCCCGGTCTGTGAAC	SYARSVN	+++	-
7843	13765	TACGCAAGGCAAAATCACAAT	YARQNHN	+++	-

7844	17470	TATTGGAAGGGCGACAATGGT	YWKGDNG	+++	-
7845	17470	TACTGGAAAGGAGATAACGGC	YWKGDNG	+++	-
7846	17471	TATTCCAGAAATGCTGATAAC	YSRNADN	+++	-
7847	17472	CGCGGAGAATGGCAATTTGCG	RGEWQFA	+++	-
7848	17473	TATGTGTACAGTAATACCCAC	YVYSNTH	+++	-
6554	17034	AGCGCGGAGTGGGTTTCATAC	SAEWVSY	+++	-
5816	16644	AGGCTATACGATGCCTACCAA	RLYDAYQ	+++	-
5817	16648	TACCTCGACCGCGTGGTATAT	YLDRVVY	+++	-
5818	16647	ATGCCAAACGAAGGATGGTTC	MPNEGWF	+++	-
7289	17344	ATACATCGGATGATGGTAAAC	IHRMMVN	+++	-
7851	17473	TACGTTTATTCGAACACACAT	YVYSNTH	+++	-
5819	16650	CTGACAAGGCTTTCCCACAAT	LTRLSHN	+++	--
7852	17474	TCCAAGTATGCACCAAATAGT	SKYAPNS	+++	-
6858	17126	TCCTGTAGAATTAGCGAGAAA	SCRISEK	+++	--
7854	17474	TCAAAATACGCGCCGAACTCT	SKYAPNS	+++	-
7855	17459	TATGCTCGCTACGGATTAAAC	YARYGLN	+++	-
5820	16649	AGTTATGCACGCAGCGTAAAT	SYARSVN	+++	-
5821	13556	TATAGTCGGGCCGGCTACAAT	YSRAGYN	+++	-
7856	17463	AATCAGAAACACCTGATGTAC	NQKHLMY	+++	-
6761	13632	TATTCCAGGATGGGACACAAC	YSRMGHN	+++	-
7858	17465	TATACCCGAACTCAGGCCTAT	YTRTQAY	+++	-
7261	17335	TGGTGCCGAGAATGCATGAAC	WCRECMN	+++	-
7860	17467	AACTCCCCTTATAGGCCGTTC	NSPYRPF	+++	-
6713	17068	GTTAGGGAATATATGTCCTAT	VREYMSY	+++	-
7862	16653	TATCATCGTGCACAGATGAAC	YHRAQMN	+++	-
5822	16651	TATCGAAGTCTAGTTGTCGGG	YRSLVVG	+++	-
7863	17316	ACGAACGAGTTCTACGGTTGG	TNEFYGW	+++	-
7864	13765	TATGCCCGACAGAACCATAAC	YARQNHN	+++	-
7865	17471	TACTCTCGCAACGCAGACAAT	YSRNADN	+++	-
7866	17475	TACCACCGCCTTGGATCAACT	YHRLGST	+++	-
6511	17013	CGAAACGAGTATACGACGTAC	RNEYTTY	+++	-
5824	16652	TATGTGAAGTCCGATCGATGC	YVKSDRC	+++	-
5825	16622	CTTTGGCGCACGGGTATCAAT	LWRTGIN	+++	-

7868	17476	TACCACAGGTCAAGTAGCAAT	YHRSSSN	+++	-
7869	17475	TATCATCGATTAGGTAGCACG	YHRLGST	+++	-
6498	17013	CGCAATGAATACACCACTTAT	RNEYTTY	+++	–
6677	17062	AATTATGCTTCTCACTCCTGG	NYASHSW	+++	–
7872	17231	ATGCTCTGCGTCGCAGGCGAT	MLCVAGD	+++	–
7873	17469	CGTTGTGGCGATTGCGTATTT	RCGDCVF	+++	-
7874	13741	TATGCTAGGTTAAACCATAAC	YARLNHN	+++	-
6818	17112	GGCTACGCAGGTAAGAGGAAT	GYAGKRN	+++	--
6958	17186	CTATCCAAGTTATCCTGCAAT	LSKLSCN	+++	-
6663	13632	TACTCTCGTATGGGTCATAAT	YSRMGHN	+++	-
5827	16653	TACCACAGGGCTCAAATGAAT	YHRAQMN	+++	-
5828	16654	GATGGGGGCCGATCTGCTTGG	DGGRSAW	+++	-
7343	17372	AATAATTGCGCGGACAATTTC	NNCADNF	+++	--
7879	17477	TCTTCTCCCAACCTTAGCTGG	SSPNLSW	+++	-
6887	17027	TGTGCATTTACCGGGACGCGC	CAFTGTR	+++	–
7152	17209	CGTTATGAAGCCTCTAACTGG	RYEASNW	+++	–
7882	17478	CGCAACGACTTCCAAGTCTAT	RNDFQVY	+++	-
5829	16651	TACCGTTCACTGGTAGTGGGT	YRSLVVG	+++	-
7883	13741	TACGCCCGTCTAAATCACAAT	YARLNHN	+++	-
5830	16654	GACGGAGGGAGATCAGCATGG	DGGRSAW	+++	-
6694	17068	GTACGCGAGTACATGTCTTAC	VREYMSY	+++	-
7191	17302	CTTTGGAAAACCGGTCACAAT	LWKTGHN	+++	-
7264	17337	ACTTACGCTAGCAGCAACTGG	TYASSNW	+++	-
7017	17219	GGAGAGTGGTGTGTGAAGAAT	GEWCVKN	+++	–
7888	17476	TATCATCGTTCGTCTTCTAAC	YHRSSSN	+++	-
7889	17302	TTGTGGAAGACTGGGCATAAC	LWKTGHN	++	-
7890	17479	AAGAATATGTGGCAAAATTCA	KNMWQNS	++	-
7891	17480	CAGCACGGACACTCCCAGTGG	QHGHSQW	++	-
7892	17478	AGAAATGATTTTCAGGTTTAC	RNDFQVY	++	-
6937	17098	ACCGAAACAAAGTTTTGTAAT	TETKFCN	++	-
6997	17209	CGATACGAGGCAAGTAATTGG	RYEASNW	++	–
7895	17481	TATTGGAAAAGCCAGACAGAT	YWKSQTD	++	-
7896	17477	TCATCCCCGAATCTCTCGTGG	SSPNLSW	++	-

7045	17236	TGTACATCTGATAGCTTTCCC	CTSDSFP	++	-
5834	16657	CTAATGATAGACGCTTTTCCA	LMIDAFP	++	-
5835	16658	TACCATAGGACTGGGAATAAT	YHRTGNN	++	-
5836	16658	TATCACCGGACAGGCAACAAC	YHRTGNN	++	-
7898	17335	TGGTGTCGTGAGTGTATGAAT	WCRECMN	++	-
5837	16657	TTAATGATTGATGCATTCCCT	LMIDAFP	++	-
6515	17018	CATAGTCGGGTCGGCCATAAC	HSRVGHN	++	-
7900	17481	TACTGGAAGTCACAAACCGAC	YWKSQTD	++	-
5839	16659	ATGACATACGACAGTTACGAC	MTYDSYD	++	-
7901	13808	TACGCGAGGCACGGACAGAAT	YARHGQN	++	-
5840	16660	CGAAATCTATATGATACTCAA	RNLYDTQ	++	-
7902	17482	TCCTCACCATACTCTCAATTC	SSPYSQF	++	-
5842	16662	CAGCCATATGAGCTACCATGG	QPYELPW	++	-
5843	16663	GAGATGGAGTCCTTTAATTGG	EMESFNW	++	–
6527	17018	CACTCGCGCGTGGGTCACAAT	HSRVGHN	++	-
7904	17483	TACTATCATGGGATGGCTGTC	YYHGMAV	++	-
7905	17472	CGGGGTGAGTGGCAGTTCGCA	RGEWQFA	++	-
7088	17255	ATGCACTGGGACGCACTCCAT	MHWDALH	++	-
7907	13808	TATGCCCGCCATGGCCAAAAC	YARHGQN	++	-
7908	17483	TATTACCACGGTATGGCGGTT	YYHGMAV	++	-
5858	16671	CTTACGTACGACGCCTATGAA	LTYDAYE	++	-
5859	16672	TGGGGCTTATGGAGGCTGGAC	WGLWRLD	++	-
5860	16673	TACCGTGACATCATATCGGGT	YRDIISG	++	-
5861	16673	TATCGAGATATAATTTCAGGA	YRDIISG	++	-
5862	16671	TTGACATATGATGCATACGAG	LTYDAYE	++	-

T8

NT SEQ ID#	AA SEQ ID#	label	AA sequence	hTFRC	marTFRC	HEK_GFP_log2	HEK_hTFRC _log2enr
7020	17221	EXT2 FC-hu-marTFRC	ICRGYTS	-++	+++	-	+++
5768	16622	EXT2 FC-hu-marTFRC	LWRTGIN	-++	+++	-	+++
7520	17381	EXT2 FC-hu-marTFRC	SLCPRLS	-++	+++	---	+++
6577	17042	EXT2 FC-hu-marTFRC	RGNGGHK	-	+++	-	+++
5800	16614	EXT2 FC-hu-marTFRC	HCGKCLN	-++	+++	-	+++
7276	17116	EXT2 FC-hu-marTFRC	RVTHCTG	-++	+++	-	+++
7017	17219	EXT2 FC-hu-marTFRC	GEWCVKN	-+	+++	-	+++
7256	17154	EXT2 FC-hu-marTFRC	HKCGDTR	-++	+++	-	+++
5620	16569	EXT2 FC-hu-marTFRC	YLKSQSY	-++	+++	.	+++
5640	16569	EXT2 FC-hu-marTFRC	YLKSQSY	-++	+++	.	+++
7766	17451	EXT2 FC-hu-marTFRC	CKKGCFE	-+	+++	.	+++
7772	17451	EXT2 FC-hu-marTFRC	CKKGCFE	-+	+++	.	+++
7235	17197	EXT2 FC-hu-marTFRC	LCRPCRE	-++	+++	-	+++
7690	17438	EXT2 FC-hu-marTFRC	LRRKPDL	n.d.	+++	---	+++
5793	16629	EXT2 FC-hu-marTFRC	LCRPCSE	-++	+++	.	+++
6545	17027	EXT2 FC-hu-marTFRC	CAFTGTR	-++	+++	.	+++
7793	17455	EXT2 FC-hu-marTFRC	CGAYWTE	-	+++	---	+++
5824	16652	EXT2 FC-hu-marTFRC	YVKSDRC	-++	+++	.	+++
5746	16614	EXT2 FC-hu-marTFRC	HCGKCLN	-++	+++	-	+++
6858	17126	EXT2 FC-hu-marTFRC	SCRISEK	-+	+++	--	+++
6958	17186	EXT2 FC-hu-marTFRC	LSKLSCN	-++	+++	.	+++
5779	16629	EXT2 FC-hu-marTFRC	LCRPCSE	-++	+++	.	+++
6522	17020	EXT2 FC-hu-marTFRC	KMSSSTW	-++	+++	---	+++
7045	17236	EXT2 FC-hu-marTFRC	CTSDSFP	-++	+++	.	++
6551	17032	EXT2 FC-hu-marTFRC	KMDSRLW	-++	+++	---	+++
6592	17032	EXT2 FC-hu-marTFRC	KMDSRLW	-++	+++	---	+++
5798	16639	EXT2 FC-hu-marTFRC	IMSSRSW	-++	+++	--	+++
6536	17020	EXT2 FC-hu-marTFRC	KMSSSTW	-++	+++	---	+++
7823	17354	EXT2 FC-hu-marTFRC	YFTRQVN	-++	+++	.	+++
6937	17098	EXT2 FC-hu-marTFRC	TETKFCN	-	+++	.	++
6570	17037	EXT2 FC-hu-marTFRC	EMQSRAW	-++	+++	---	+++

7343	17372	EXT2 FC-hu-marTFRC	NNCADNF	-+	+++	--	+++
6747	16639	EXT2 FC-hu-marTFRC	IMSSRSW	-++	+++	--	+++
5720	16605	EXT2 FC-hu-marTFRC	SMESRLW	-++	+++	---	+++
7872	17231	EXT2 FC-hu-marTFRC	MLCVAGD	-+	+++	-	+++
6583	17037	EXT2 FC-hu-marTFRC	EMQSRAW	-++	+++	---	+++
6860	17127	EXT2 FC-hu-marTFRC	KMSSSVW	-+	+++	--	+++
7837	17466	EXT2 FC-hu-marTFRC	LCGSCRS	-++	+++	.	+++
6887	17027	EXT2 FC-hu-marTFRC	CAFTGTR	-+	+++	-	+++
5723	16607	EXT2 FC-hu-marTFRC	DLSSHNW	-++	+++	---	+++
5736	16593	EXT2 FC-hu-marTFRC	DMSSRIW	-++	+++	--	+++
5759	16607	EXT2 FC-hu-marTFRC	DLSSHNW	-++	+++	---	+++
6904	17127	EXT2 FC-hu-marTFRC	KMSSSVW	-+	+++	-	+++
6598	16605	EXT2 FC-hu-marTFRC	SMESRLW	-++	+++	---	+++
7841	17469	EXT2 FC-hu-marTFRC	RCGDCVF	-+	+++	.	+++
6690	17065	EXT2 FC-hu-marTFRC	KMPSRDW	-+	+++	---	+++
6684	17065	EXT2 FC-hu-marTFRC	KMPSRDW	-+	+++	---	+++
7214	16616	EXT2 FC-hu-marTFRC	NCKPCFD	-++	+++	.	+++
5687	16593	EXT2 FC-hu-marTFRC	DMSSRIW	-++	+++	---	+++
5751	16616	EXT2 FC-hu-marTFRC	NCKPCFD	-++	+++	.	+++
7873	17469	EXT2 FC-hu-marTFRC	RCGDCVF	-+	+++	.	+++
6566	17036	EXT2 FC-hu-marTFRC	QLEARTW	-+	+++	---	+++
7108	17247	EXT2 FC-hu-marTFRC	RMSASNW	-+	+++	-	+++
6589	17036	EXT2 FC-hu-marTFRC	QLEARTW	-+	+++	---	+++
7067	17247	EXT2 FC-hu-marTFRC	RMSASNW	-+	+++	.	+++
6606	17049	EXT2 FC-hu-marTFRC	KMSSANW	-	+++	---	+++
6614	17049	EXT2 FC-hu-marTFRC	KMSSANW	-	+++	---	+++
6597	17038	EXT2 FC-hu-marTFRC	TMSDRTW	-	+++	---	+++
6573	17038	EXT2 FC-hu-marTFRC	TMSDRTW	-	+++	---	+++
7261	17335	EXT2 FC-hu-marTFRC	WCRECMN	-++	+++	.	+++
6677	17062	EXT2 FC-hu-marTFRC	NYASHSW	-	+++	-	+++
7898	17335	EXT2 FC-hu-marTFRC	WCRECMN	-++	+++	.	++
7704	17439	EXT2 FC-hu-marTFRC	FVKFQVN	-+	+++	.	+++
7719	17439	EXT2 FC-hu-marTFRC	FVKFQVN	-+	+++	.	+++

T9

NT SEQ ID#	AA SEQ ID#	AA_sequence	hTFRC pH7.4	hTFRC pH7.4-5.	marTFRC pH7.4	marTFRC pH5.5
7909	17484	SPFMRRE	+++	+--	+++	+++
7910	17485	NALVGRD	+++	+-	-	-
7911	17486	YVVTHRN	+++	+--	+++	+++
7912	17487	GRFSEGR	+++	+--	+++	+++
7913	17488	TKWGAHV	+++	+--	+++	+++
7914	17489	LRYSRTE	+++	+--	-	+++
7915	17490	FRGNCGP	+++	+--	+++	+++
7916	17491	GPGAGCN	+++	+--	+++	+++
7917	17492	YFSKQIA	+++	+--	++	++
7918	17493	DLSDRRW	+++	+-	+++	-
7919	17494	RKLPGVA	+++	+--	+++	+++
7920	17495	GRVVSKP	+++	+--	-	+++
7921	17496	LRDGTPS	+++	+-	-	-
7922	17497	FDEKVRR	+++	+--	+++	+++
7923	17498	VQVGRAC	+++	+--	+++	+++
7924	17499	VMEARAW	+++	+-	+++	++
7925	17500	GVAGCVA	+++	+--	+++	+++
7926	17501	NSYSRAF	+++	+--	++	+++
7927	17502	MRLSRQD	+++	+--	-	+++
7928	17503	LLESSKW	+++	+-	+++	-
7929	17504	SSLCLRE	+++	+--	+++	+++
7930	17505	GGPGSIW	+++	+-	-	-
7931	17506	YYRGPSG	+++	+--	+++	+++
7932	17507	GLGSTCS	+++	+--	+++	+++
7933	17508	YVRSSMG	+++	+--	++	-
7934	17509	CGGLSRG	+++	+--	+++	+++
7935	17510	WALRRME	+++	+--	++	+++
7936	17511	CMSDKRA	+++	+--	+++	+++
7937	17512	CSMINKS	+++	+--	+++	+++
7938	17513	DPVARSW	+++	+-	+++	-
7939	17514	ESSSRTW	+++	+-	+++	++
7940	17515	LSRASVN	+++	+--	-	++

7941	17516 DPSWKRV	+++	+--	+++	+++
7942	17517 YGQGYGR	+++	+--	+++	+++
7943	17518 LDAKCMP	+++	+--	+++	+++
7944	17519 YFAGRID	+++	+--	++	++
7945	17520 YFSGRVA	+++	+--	-	-
7946	17521 YSRLLPM	+++	+--	++	++
7947	17522 YSRIMAN	+++	+--	-	++
7948	17523 VRHRSEL	+++	+--	+++	+++
7949	17524 DMESAVW	+++	+-	+++	-
7950	17525 WTTRISH	+++	+--	+++	+++
7951	17526 HRFLKGE	+++	+--	+++	+++
7952	17527 WVGGRSN	+++	+--	++	+++
7953	17528 LHRQLPL	+++	+-	-	-
7954	17529 CEKLSSR	+++	+--	+++	+++
7955	17530 LRHISHT	+++	+--	++	+++
7956	17531 AWERKLM	+++	+--	++	++
7957	17532 FVARVRD	+++	+--	++	+++
7958	17533 WGHPSRA	+++	+--	+++	+++
7959	17534 AERGCCG	+++	+--	+++	+++
7960	17535 RMESSVW	+++	+-	+++	-
7961	17536 CVSVGRA	+++	+--	+++	+++
7962	12030 VESSNGV	+++	+-	-	-
7963	17537 DSDFTSW	+++	+-	-	-
7964	17538 AHRLLPS	+++	+-	-	++
7965	17539 GQDSRRN	+++	+--	++	+++
7966	17540 DLNSRSW	+++	+-	+++	++
7967	17541 ASITTCR	+++	+--	+++	+++
7968	17542 AFTHRVQ	+++	+--	+++	+++
7969	17543 YLKSQTS	+++	+--	-	-
7970	17544 CGSWQRE	+++	+--	+++	+++
7971	17545 YSRLHVD	+++	+-	-	-
7972	17546 RVSCPPP	+++	+--	+++	+++
7973	17547 RSDFVTY	+++	+-	-	-

7974	17548 QYARSLE	+++	+--	-	-
7975	17549 GMEPVRW	+++	+-	-	-
7976	17550 DMRMGTW	+++	+-	++	++
7977	17551 QPPSCKA	+++	+--	+++	+++
7978	17552 AQGADSW	+++	+-	-	-
7979	17553 GGHYMLK	+++	+--	++	+++
7980	13514 FSRLGIN	+++	+--	-	++
7981	17554 YSVIGPN	+++	+--	++	-
7982	17555 RDVTVFP	+++	+--	-	-
7983	17556 RNRDVYP	+++	+--	++	-
7984	17557 GMADRAW	+++	+-	+++	-
7985	17558 TESTNGR	+++	+-	-	-
7986	17559 SVRQERY	+++	+--	++	+++
7987	17560 GVDQVRW	+++	+-	-	-
7988	17561 NLMGCTG	+++	+--	+++	+++
7989	17562 GAEGVRW	+++	+-	-	++
7990	17563 VMEDRIW	+++	+-	+++	++
7991	17564 LTSREGI	+++	+-	-	-
7992	17565 WSTHKAF	+++	+--	++	+++
7993	17566 REEVSIW	+++	+-	-	++
7994	17567 NMASAGW	+++	+-	+++	-
7995	17568 LISGDGP	+++	+-	-	-
7996	17569 SAYSAKY	+++	+--	+++	+++
7997	17570 YARAGPD	+++	+--	++	++
7998	17571 VESSRLW	+++	+-	+++	++
7999	17572 DMSSVAW	+++	+	+++	-
8000	17573 DSFRGYD	+++	+-	-	-
8001	17505 GGPGSIW	+++	+-	-	++
8002	17574 DLASPDW	+++	+-	++	++
8003	17575 VSTHCCA	+++	+--	+++	+++
8004	17576 VLSSNVW	+++	+-	+++	++
8005	17577 VMPDRVW	+++	+-	+++	-
8006	17578 KMEDRSW	+++	+-	+++	-

8007	17579 RSMVGCD	+++	+--	+++	+++
8008	17580 SLSDRGW	+++	+-	++	++
8009	17581 TFAHTNR	+++	+--	++	+++
8010	11543 LSKVGTN	+++	+--	-	-
8011	17582 SGNYTAR	+++	+--	+++	+++
8012	17583 YHRAAAL	+++	+--	+++	+++
8013	17584 NMSAGTW	+++	+	+++	-
8014	17585 AKGWVRD	+++	+--	++	++
8015	17586 VMASQGW	+++	+-	++	++
8016	17587 DLSSGNW	+++	+-	+++	-
8017	17588 KLDDYGW	+++	+--	++	-
8018	17589 YSRLDVL	+++	+--	-	-
8019	17590 ILSDRSW	+++	+-	+++	++
8020	17591 YSRVGSG	+++	+--	-	+
8021	17592 GFARLRD	+++	+--	+++	+++
8022	17593 LSRIGTN	+++	+--	-	+
8023	17594 GGESSIW	+++	+-	-	-
8024	17595 ISEFSGY	+++	+-	++	++
8025	17596 RLADAYP	+++	+--	-	-
8026	17597 WFSGQIA	+++	+--	-	-
8027	17598 CTSKTGH	+++	+--	+++	+++
8028	17599 RTNRVEW	+++	+--	+++	+++
8029	17600 VEASRSW	+++	+-	+++	++
8030	17601 VLSASSW	+++	-	+++	+++
8031	17602 VLSERSW	+++	+	+++	-
8032	17603 LSALSVN	+++	+--	-	-
8033	17604 RGGGLFV	+++	+-	+	+
8034	17605 TESTHGR	+++	+-	-	-
8035	17606 YVRSDTA	+++	+--	-	-
8036	17607 REAVSTW	+++	+-	++	-
8037	17608 YYSGVKL	+++	+--	++	-
8038	17609 YRMSLER	+++	+--	++	+++
8039	17610 LMEQRTW	+++	+-	++	-

8040	17611 GCRHGDI	+++	+--	+++	+++
8041	17612 WRGSQHV	+++	+--	++	+++
8042	17613 GSEFVSY	+++	+-	++	-
8043	17580 SLSDRGW	+++	+-	++	++
8044	17614 YWHGKPE	+++	+--	-	-
8045	17615 FFRGNMG	+++	+--	+++	+++
8046	17616 VESSSRW	+++	+-	++	-
8047	17617 CGKAHSS	+++	+--	+++	+++
8048	17618 DMSVGKW	+++	+-	++	+
8049	17619 LLSSHDW	+++	+-	+++	+
8050	17620 MRDGTSS	+++	-	-	-
8051	17621 YVKSDVG	+++	+--	-	-
8052	17622 WSRVGVN	+++	+--	++	++
8053	17623 WSYKSNG	+++	+--	++	++
8054	17624 YWGGVVS	+++	+--	-	-
8055	17625 KMEAMTW	+++	+-	++	+
8056	17626 LSRLGGG	+++	+--	-	+
8057	17627 LMEAATW	+++	+-	++	-
8058	17628 KLDYLGT	+++	+--	+++	+++
8059	17629 LSRASHD	+++	+--	-	++
8060	17630 YFSGVQP	+++	+--	+	-
8061	17631 LSRVSPD	+++	+--	-	-
8062	17632 WRAGKDY	+++	+--	++	+++
8063	17633 RLESVQW	+++	+-	++	-
8064	17634 YFSGRDE	+++	+--	-	-
8065	17635 ILKCTNN	+++	+--	+++	+++
8066	17636 YSRVAPD	+++	+--	-	-
8067	17637 RLESTHW	+++	+-	+++	++
8068	17638 YWSGTVT	+++	+--	+	-
8069	17639 YARLSIN	+++	+--	-	-
8070	17640 RGEYHYP	+++	+-	++	++
8071	17641 FAAKWSS	+++	+--	-	++
8072	17642 YVKSQTI	+++	+--	-	-

8073	17643 SLCKTTS	+++	+--	+++	+++
8074	17644 PLSSGVW	+++	+-	+++	++
8075	17645 LMGGGTW	+++	+-	-	-
8076	17646 GSPGVSW	+++	+-	-	-
8077	17647 QDDYLTW	+++	+-	-	-
8078	17648 YVKSQQS	+++	+--	+	+
8079	17649 QNEYVIY	+++	+-	-	-
8080	17650 VPGRSGF	+++	+-	++	-
8081	17651 FWSGKAA	+++	+--	-	-
8082	17652 STYDSFP	+++	+--	-	-
8083	17653 YFSGRHE	+++	+--	-	+
8084	17654 HSKSGGW	+++	+--	+++	+++
8085	17655 GGPGSNW	+++	-	-	-
8086	17656 GSPGSIW	+++	+-	-	-
8087	17657 VSEFASY	+++	+-	-	-
8088	17658 LHKLSNN	+++	+--	++	++
8089	17659 LCKPCLT	+++	+--	+++	+++
8090	17660 RSLDSYP	+++	+--	-	-
8091	17661 CAPRVSS	+++	+--	+++	+++
8092	17662 PYAKSPL	+++	+--	++	-
8093	17663 SLSSRDW	+++	+-	+++	++
8094	17664 WVDRTRG	+++	+--	++	+++
8095	17665 IMPDRSW	+++	+-	++	-
8096	17666 INSREGI	+++	-	-	-
8097	17667 LSDGTSP	+++	+-	-	-
8098	17668 YVRSQPL	+++	+--	-	-
8099	17669 YFSGVRE	+++	+--	-	-
8100	17670 YSAYRSV	+++	+--	++	++
8101	17671 GGEHSTW	+++	+-	-	-
8102	17672 VMLDRGW	+++	+-	+++	-
8103	17673 GGGVVKY	+++	+-	++	++
8104	17674 YWSEVRA	+++	+--	++	-
8105	17675 IMSDRLW	+++	+-	+++	+++

8106	17676 LHSKLPN	+++	+-	++	++
8107	17677 YWSHVKE	+++	+--	++	++
8108	17678 APADRGW	+++	+-	+++	-
8109	17679 YYSGQHA	+++	+--	-	-
8110	17680 DLRMATW	+++	+-	+++	-
8111	11408 VVSTNGV	+++	+-	-	-
8112	17681 LSRVGQN	+++	+--	-	-
8113	17682 YFTGREK	+++	+--	++	++
8114	17683 YWSQVRE	+++	+--	++	++
8115	17684 LSRLSPV	+++	+-	-	-
8116	17685 SMSSAMW	+++	+-	+++	++
8117	17686 IGESRLW	+++	+	++	-
8118	17687 VRSTNGV	+++	+-	-	-
8119	17688 CMGALPE	+++	+--	++	+++
8120	17689 VLSSVSW	+++	+-	++	++
8121	17690 ITSSNGI	+++	+-	-	-
8122	17691 LSRTSID	+++	+--	-	-
8123	17692 YWSQVVE	+++	+--	-	-
8124	16059 VYSTNGI	+++	+-	-	++
8125	17693 SEALTRR	+++	+--	++	+++
8126	17694 MRDGTNA	+++	+-	-	-
8127	17695 KLDVGNW	+++	+-	-	-
8128	17696 DNASSVW	+++	+-	++	++
8129	17697 ILSSSGW	+++	+-	+++	-
8130	17698 LYESRAW	+++	+-	+++	-
8131	17699 YYGRTSS	+++	+--	++	+++
8132	17700 FSRIGGG	+++	+--	-	-
8133	17701 VALKGWD	+++	+--	-	-
8134	17702 MSRASYN	+++	+--	++	++
8135	17703 CGVGRIA	+++	+--	+++	+++
8136	17704 KDDFSVY	+++	+-	-	-
8137	17705 FVSKNGV	+++	+-	-	-
8138	17706 TWTGNNA	+++	+-	-	-

8139	17707 RGDSPSW	+++	+–	-	-
8140	17708 DMVSRSW	+++	+–	+++	++
8141	17709 YFTGSQN	+++	+––	++	-
8142	17710 VTSTMGR	+++	+–	-	-
8143	17711 VMADRAW	+++	+–	+++	+
8144	17712 AYRTDSR	+++	+––	++	+++
8145	17713 YFAGRLA	+++	+––	-	-
8146	17714 QLESRSW	+++	+–	+++	-
8147	17715 KMDYSTR	+++	+––	+++	+++
8148	17716 GESSVRW	+++	+–	-	-
8149	17717 HSRLNVV	+++	+–	-	-
8150	17718 LPDGDGP	+++	+–	-	-
8151	17719 YFTGAWD	+++	+––	-	-
8152	17720 RESGVSW	+++	+–	-	-
8153	17721 YEPGCKE	+++	+––	+++	+++
8154	17722 LARGGPD	+++	+––	-	-
8155	17723 YARQSNN	+++	+––	++	++
8156	17724 WKAGGKV	+++	+––	++	++
8157	17725 EPERGWF	+++	+––	-	-
8158	17726 RGESHSW	+++	+–	++	++
8159	17727 YWNANLE	+++	+––	-	-
8160	17728 YWSGVTE	+++	+––	++	-
8161	17729 SRSTNGV	+++	+–	-	-
8162	17730 YFTGRLD	+++	+––	-	-
8163	17731 WWSGYVE	+++	+––	-	-
8164	17732 YFTGVSS	+++	+––	-	-
8165	17733 RPVCPTG	+++	+––	+++	+++
8166	17734 YWSSVRE	+++	+––	-	-
8167	17735 LHVAMPN	+++	+–	-	-
8168	17736 LHRLSVD	+++	+––	+	-
8169	17737 RTYDSFA	+++	+––	-	-
8170	17738 RSLEGSD	+++	+–	-	-
8171	17739 LHRLGDS	+++	+–	-	-

8172	17740 TRDSPMF	+++	+–	+	-
8173	17741 LRSGMGP	+++	+–	-	-
8174	17742 GSGEERW	+++	+–	-	-
8175	17743 WTPMCKA	+++	+––	+++	+++
8176	17744 FWHGVSD	+++	+––	-	+
8177	17745 LTKLSNN	+++	+––	-	+
8178	17746 VGYRNQV	+++	+––	++	+++
8179	17684 LSRLSPV	+++	+–	-	-
8180	17747 LRERYSN	+++	+––	+++	+++
8181	17748 SYAKSVL	+++	+––	++	++
8182	17749 NMASSGW	+++	+	++	-
8183	17750 RTYDAIA	+++	+––	-	+
8184	17751 LSRVSFD	+++	+––	-	-
8185	17752 RSEFVSF	+++	+–	-	-
8186	17753 GGSLLMS	+++	+––	-	++
8187	17754 DPSSHSW	+++	+–	+++	-
8188	17755 VLASVTW	+++	+–	++	-
8189	17756 APASATW	+++	+–	+++	-
8190	17757 EVRTYPK	+++	+––	+++	++
8191	17758 GWGSNNK	+++	+––	++	+++
8192	17759 RNSTVYP	+++	+––	-	-
8193	17760 YWSGLND	+++	+––	-	-
8194	17761 AQGLSAG	+++	+–	-	-
8195	17762 LGSWRNS	+++	+––	++	+++
8196	17763 RTSTMGV	+++	+–	-	-
8197	17764 YFTGTLT	+++	+––	-	-
8198	17765 CEGKLHP	+++	+––	+++	+++
8199	17766 AYAYSAA	+++	+––	-	-
8200	17767 SMASNTW	+++	+–	+++	-
8201	17768 GSSTSNW	+++	+	-	-
8202	17769 LARGGFD	+++	+––	-	-
8203	17770 YVRFDNN	+++	+––	-	++
8204	17771 WGVRERG	+++	+––	+++	+++

8205	17772 FGKQQML	+++	+--	++	+++
8206	17773 YVRSGPM	+++	+--	-	+
8207	17774 RGDSPLW	+++	+-	-	-
8208	17775 LHRLSSD	+++	+-	-	-
8209	17776 LSKASSN	+++	+--	-	-
8210	17777 VALEGAD	+++	+	-	-
8211	17778 YSRVGPV	+++	+--	++	++
8212	17779 QPQDRSW	+++	+-	+++	+
8213	17780 FSRLSPL	+++	+--	++	++
8214	17781 YSRIQLD	+++	+--	+	-
8215	17782 CEKGIRC	+++	+--	++	+++
8216	17783 RGNSPLT	+++	+--	++	++
8217	11244 IVSTNGR	+++	+-	-	-
8218	17784 VLQSSVW	+++	+-	+++	-
8219	17785 TWDGLVA	+++	+--	-	-
8220	17786 RMSDAYA	+++	+--	-	-
8221	17787 GSYGGSR	+++	+--	++	++
8222	17788 LVRGGTN	+++	+--	-	++
8223	17789 GGGAQMW	+++	+-	++	-
8224	17790 GSSGVAW	+++	+	-	-
8225	17791 KWERSPI	+++	+--	++	+++
8226	17792 YHALNLD	+++	+-	-	-
8227	17793 GDALSHW	+++	+-	-	++
8228	17794 DTLLHLR	+++	+-	+++	++
8229	17795 SDGVSKW	+++	+-	++	++
8230	17796 LSRVGPD	+++	+--	-	-
8231	17797 DLSSTSW	+++	-	+++	-
8232	17798 GADFVKW	+++	+-	-	-
8233	17799 HDSTHGR	+++	+-	-	-
8234	17800 PSRLENR	+++	+--	-	-
8235	17801 LSKVGHN	+++	+--	+	+
8236	17802 VGVKGWD	+++	+	++	++
8237	17803 YGTGTWS	+++	+-	+	-

8238	17804 SLSSSVW	+++	+-	+++	-
8239	17805 YFTARME	+++	+--	-	-
8240	17806 RVPSKWD	+++	+--	++	+++
8241	17807 EDEFTGF	+++	+-	-	-
8242	17808 GGEGSFW	+++	+-	-	-
8243	17809 LHANLPN	+++	+-	-	-
8244	17810 FGGGLFV	+++	+--	-	-
8245	17811 VMGARDW	+++	+-	++	-
8246	17812 WTSTHGV	+++	+-	-	-
8247	17813 YSRAGGS	+++	+--	++	++
8248	17814 YYTGKLD	+++	+--	-	-
8249	17815 RSDWKIS	+++	+--	++	+++
8250	17816 NMNSSTW	+++	+-	++	-
8251	17817 RGDLVYP	+++	+-	-	++
8252	17818 DLRAGNW	+++	+-	++	-
8253	17819 APGNISW	+++	+-	-	-
8254	17820 VKYNVHL	+++	+--	++	+++
8255	17821 RGDDRGW	+++	+-	-	-
8256	17822 YFSGIHS	+++	+--	+	-
8257	17823 TPSTIYF	+++	+-	-	-
8258	17824 EMESSVW	+++	+-	++	-
8259	17825 WTEGTRY	+++	+-	-	-
8260	17826 EGIARTW	+++	+	+++	-
8261	17827 MYAFSIE	+++	+--	-	-
8262	17828 YVYSDSR	+++	+--	-	-
8263	17829 DSVYQLR	+++	+-	++	++
8264	17830 RLLDVYP	+++	+--	+	-
8265	17831 GRSYIPS	+++	+--	++	++
8266	17832 YFQGKIA	+++	+--	++	-
8267	17833 YVRSDGM	+++	+--	-	-
8268	17834 IPPLFNV	+++	+-	-	-
8269	17835 QGVSREW	+++	+-	+++	-
8270	17836 RLEAANW	+++	+	-	-

8271	17837 WWSEIRS	+++	+--	-	-
8272	17838 YSRLSAD	+++	+--	-	-
8273	17839 APGDIRW	+++	+-	-	-
8274	17840 RSDQWRG	+++	+--	++	++
8275	17841 HYPLSAK	+++	+--	++	++
8276	17842 MDDFTVY	+++	+-	-	-
8277	17843 GGLGSQW	+++	+-	-	-
8278	17844 LSRTAYD	+++	+--	-	-
8279	17845 RYGDVMR	+++	+--	++	++
8280	17846 DLRGTSA	+++	+	-	-
8281	17847 SYRGARE	+++	+--	++	+++
8282	17848 MHRLLSD	+++	+-	++	-
8283	17849 DLQSSSW	+++	+-	++	++
8284	17850 NRYGVVS	+++	+--	++	++
8285	17851 VVMTRDR	+++	+--	++	++
8286	17852 YSRIGAG	+++	+--	+	++
8287	17853 CGEGSKA	+++	+--	+++	+++
8288	17854 GSEFLGW	+++	+-	-	-
8289	17855 RDSDNGI	+++	+--	-	-
8290	17856 WRRESSS	+++	+--	++	+++
8291	17857 LSRLSQD	+++	+--	-	-
8292	17858 YFAGIAQ	+++	+--	++	-
8293	17859 SSPRGSD	+++	+--	+++	+++
8294	17860 FGLIMKA	+++	+--	+++	+++
8295	17861 KSIASPG	+++	+--	+++	+++
8296	17862 VLHSSNW	+++	+-	-	-
8297	17863 VADHLRW	+++	+-	-	++
8298	17864 YPPMLIA	+++	+-	-	-
8299	17865 GCKGSCG	+++	+--	+++	+++
8300	17866 HYEKTGR	+++	+--	++	+++
8301	17867 LARTGWD	+++	+--	-	-
8302	17868 GGGYGRN	+++	+--	++	++
8303	17869 WRLHKGD	+++	+--	++	++

8304	17870 LSRIANN	+++	+--	+	++
8305	17871 ALGDRTW	+++	+-	++	-
8306	17872 DFRGARL	+++	+--	++	+++
8307	17873 LAKTAHN	+++	+--	+	-
8308	17874 PMASLQW	+++	+-	+++	-
8309	13620 YARLGNN	+++	+--	++	-
8310	17875 GSELSSW	+++	+-	-	-
8311	17876 YFHSTKT	+++	+--	++	++
8312	17877 RMSSDYR	+++	+--	++	++
8313	17878 VMADAFP	+++	+--	-	-
8314	17879 WKGRETT	+++	+--	++	+++
8315	17880 LGSRERF	+++	+--	++	++
8316	17881 MGKVCNS	+++	+--	+++	+++
8317	17882 DGSSRSW	+++	+-	++	-
8318	17883 LSRLNAD	+++	+--	-	++
8319	17884 LFSGVGP	+++	+-	-	-
8320	17885 VASVCKG	+++	+--	+++	+++
8321	17886 YYDLKRS	+++	+--	++	+++
8322	17887 WVASRSS	+++	+--	++	++
8323	17888 VMTARDW	+++	+-	-	-
8324	17889 LSKLSSN	+++	+--	++	++
8325	17890 RGLEGMD	+++	+-	-	-
8326	17891 WAMRRVE	+++	+--	++	+++
8327	17892 YRGASNH	+++	+--	++	+++
8328	17893 QGNGLYR	+++	+-	++	++
8329	17894 TRSFSHG	+++	+--	++	++
8330	17895 YWTGLHE	+++	+--	-	-
8331	17896 VLSDITW	+++	+-	-	-
8332	17897 LLDSAKW	+++	+-	+++	-
8333	11419 STSTNGI	+++	+-	-	-
8334	17898 VPDWVDR	+++	+-	-	-
8335	17899 SGYRGAV	+++	+--	++	++
8336	17900 LKDGTSA	+++	+-	+++	-

8337	17901 YSRAGDD	+++	+--	-	-
8338	17902 LSRSSMN	+++	+--	++	++
8339	17903 YSKLSDR	+++	+--	++	++
8340	17904 DGYSGRD	+++	+-	-	-
8341	17905 YSRLNVG	+++	+--	++	++
8342	17906 EAWTDRG	+++	+-	-	-
8343	17907 VSNKSTG	+++	+--	++	++
8344	17908 WSRGAAT	+++	+--	++	++
8345	17909 DTYETRW	+++	+--	-	-
8346	17910 VMSSAGW	+++	+	+++	++
8347	17911 YTRVQEN	+++	+--	-	++
8348	17912 ELESWSW	+++	+-	+++	-
8349	17913 RDGVSAW	+++	+-	-	-
8350	17914 SFGPPYG	+++	+-	-	-
8351	17915 TFYGQNA	+++	+-	-	-
8352	17916 RMEVGDW	+++	-	-	-
8353	17917 YSKAQGV	+++	+--	+	-
8354	17918 HSKLNPM	+++	+-	+	-
8355	17919 LFDATPS	+++	-	-	-
8356	17920 REGYRGY	+++	+--	++	++
8357	17921 LARSGGG	+++	+--	-	-
8358	17922 FWGGVVD	+++	+--	-	-
8359	17923 VSSDNGM	+++	+--	-	-
8360	17924 YVRSDSS	+++	+--	-	-
8361	17925 ISKTCRE	+++	+--	+++	+++
8362	17926 SMQDRSW	+++	+-	+++	+
8363	17927 WSNRARD	+++	+--	++	++
8364	17928 YVISDRN	+++	+--	-	-
8365	17929 LRLHGRD	+++	+--	++	++
8366	17930 NQRYGSS	+++	+--	++	+++
8367	11162 FVSTNGV	+++	+-	-	-
8368	17931 SGGGLFP	+++	+-	-	-
8369	17932 DIAHKRY	+++	+--	++	++

8370	17933 VALKGAG	+++	+-	-	++
8371	17934 CTNVCNA	+++	+--	+++	+++
8372	17935 MWNGTPS	+++	+-	-	++
8373	17936 LYGSRQT	+++	+--	++	+++
8374	17937 AGDGLWV	+++	+--	-	-
8375	17938 VLSHATW	+++	+-	+++	-
8376	17939 YHAKGDN	+++	+-	++	+
8377	17940 ETDGWRN	+++	+-	-	-
8378	17941 LLSSADW	+++	+-	+++	+
8379	17942 KDGFSTY	+++	+-	-	-
8380	17943 GSEVTRR	+++	+--	++	+++
8381	17944 AEPPVMW	+++	+-	-	-
8382	17945 FAHIHGK	+++	+--	+++	+++
8383	17946 IQSTNGR	+++	+-	-	-
8384	17947 GTKWSDR	+++	+--	++	++
8385	17948 VWPGRST	+++	+--	++	++
8386	17949 LARLGPD	+++	+--	-	-
8387	17950 HCPTIPM	+++	+--	+++	+++
8388	17951 YARGSLN	+++	+--	-	-
8389	17952 YVKSAGS	+++	+--	++	++
8390	17953 WDAIRRN	+++	+--	++	++
8391	17954 LGENLRW	+++	+-	-	-
8392	17955 WFSGVQL	+++	+--	-	++
8393	17956 WWTGMIA	+++	+--	-	-
8394	17957 DHRGTGW	+++	+-	-	++
8395	17958 FFSGTKV	+++	+--	++	++
8396	17959 NGADGRW	+++	+-	-	-
8397	17960 SYRLVDK	+++	+--	++	+++
8398	17961 WPYGNDA	+++	+-	-	-
8399	17962 RGGGLYV	+++	+-	-	-
8400	17963 YSYAGGG	+++	+--	-	-
8401	17964 VYVKAHN	+++	+--	++	+++
8402	17965 YWSGTQG	+++	+--	-	++

8403	17966 EMAAYDW	+++	+--	++	++
8404	17967 RSDTTYP	+++	+-	-	-
8405	17968 REDFSAW	+++	+-	-	-
8406	15963 YARQNFN	+++	+--	++	++
8407	17969 MSSEYER	+++	-	-	-
8408	17970 WRKTDGG	+++	+--	++	++
8409	17971 WDNGVTG	+++	+-	-	-
8410	17972 KWQSVSA	+++	+--	++	+++
8411	17973 VEYRGIG	+++	+-	++	++
8412	17974 SLNDHLL	+++	+--	+++	+++
8413	17975 YVRSDRV	+++	+--	-	-
8414	17976 CRPVCTP	+++	+--	+++	++
8415	17977 NFRSDLR	+++	+--	++	++
8416	17978 PMRETLW	+++	+-	+++	++
8417	17446 YLISDTK	+++	+--	-	++
8418	17979 LWNGVGP	+++	+-	-	-
8419	17980 LAETRRY	+++	+--	+++	+++
8420	17981 SQSSRCA	+++	+-	++	++
8421	11432 LAKSGTN	+++	+--	-	-
8422	17982 ISKTCGS	+++	+--	+++	+++
8423	17983 LAGRGWD	+++	+-	++	-
8424	17984 ARHHTSS	+++	+--	++	++
8425	17985 WLKIGKA	+++	+--	++	++
8426	17986 MLSSQTW	+++	+-	+++	-
8427	17987 WWTGYVD	+++	+--	-	-
8428	17988 EWSSLDD	+++	+--	-	-
8429	17989 LRDGTLR	+++	+-	-	+
8430	17990 FQRVYKD	+++	+--	++	++
8431	17991 GGATSNW	+++	+-	-	-
8432	17992 KFHSNSL	+++	+--	++	+++
8433	17993 LSALNRN	+++	+-	-	+
8434	17994 GGESSVW	+++	+-	-	-
8435	17995 RLDAHDW	+++	+-	++	-

8436	17996	GVDVVRW	+++	+-	-	-
8437	17997	AQGISAG	+++	+-	-	-
8438	17998	NGVNGLW	+++	+-	-	-
8439	17999	DLRSSDW	+++	+-	+++	-
8440	18000	GGESSLW	+++	+-	-	-
8441	18001	LARGGWD	+++	+--	+	+
8442	18002	GNSERRW	+++	+--	++	++
8443	18003	YFTRTMA	+++	+--	-	+
8444	18004	GGEGSAW	+++	+	-	-
8445	18005	SGKCAAT	+++	+--	+++	+++
8446	18006	DGPVFNR	+++	+	-	-
8447	18007	LPQSSNW	+++	+-	-	-
8448	18008	VDEFLSW	+++	+-	-	-
8449	18009	FHGNARV	+++	+--	+++	++
8450	18010	RAFDSYS	+++	+--	++	-
8451	18011	LHRLMPD	+++	+--	-	-
8452	18012	YVKSQPG	+++	+--	-	+
8453	18013	YSKLNTH	+++	+--	+	++
8454	18014	LARSGYD	+++	+--	-	-
8455	18015	LSRVGAD	+++	+--	-	-
8456	18016	ELVTKRY	+++	+--	++	++
8457	18017	NAFEGAD	+++	+	-	-
8458	18018	MFDGSSA	+++	+	-	-
8459	18019	WASRTRD	+++	+--	++	++
8460	18020	WGSRREG	+++	+--	++	++
8461	18021	FSRLHID	+++	+-	-	-
8462	18022	AYRRPDA	+++	+--	++	++
8463	18023	DGSTSTW	+++	+-	-	-
8464	18024	AQGNWKG	+++	+--	++	++
8465	18025	CCGGRGP	+++	+--	+++	+++
8466	18026	VSESLYW	+++	+	-	-
8467	18027	SYAVRRE	+++	+--	++	+++
8468	18028	GGDFEHW	+++	+-	-	-

8469	18029 TSYGANA	+++	+–	-	-
8470	18030 FGNGSSY	+++	+–	-	-
8471	18031 FFTGVVG	+++	+––	-	-
8472	18032 LGGTSRY	+++	+–	++	++
8473	18033 TYEGAVA	+++	+	-	-
8474	18034 ADLTVRR	+++	+––	++	++
8475	18035 LARSGPD	+++	+––	-	-
8476	18036 TDETVYR	+++	+––	-	-
8477	18037 DDGSSRY	+++	+–	++	-
8478	18038 DSPEWRD	+++	+––	-	+
8479	18039 KVALLST	+++	+––	+++	+++
8480	18040 LHKLGDD	+++	+–	-	+
8481	18041 YYTGMIS	+++	+––	-	-
8482	18042 FEAPNSW	+++	+–	-	-
8483	18043 DEGGYPW	+++	+–	-	++
8484	18044 WVREANR	+++	+––	++	++
8485	18045 RYNMSRE	+++	+––	++	++
8486	11586 VLSTNGV	+++	+–	++	-
8487	18046 YNFKRDG	+++	+––	++	++
8488	18047 WWTGTVS	+++	+––	-	-
8489	18048 YWAGIPD	+++	+––	-	++
8490	18049 LWGGIPS	+++	+–	++	+
8491	18050 VVDYMSH	+++	+–	-	-
8492	18051 FFSGIID	+++	+––	++	++
8493	18052 YVRFDSG	+++	+––	-	-
8494	18053 RVGHTAW	+++	+––	++	+++
8495	18054 WSHMGKG	+++	+––	++	++
8496	18055 YYTGFTN	+++	+––	-	-
8497	18056 VIEDAYP	+++	+––	-	-
8498	18057 GVINVAW	+++	+–	++	-
8499	11309 YMSTNGI	+++	+–	-	-
8500	18058 IESFNGR	+++	+–	-	-
8501	18059 GMGSERW	+++	+–	-	-

8502	18060	SAYRGGG	+++	+--	++	++
8503	18061	HWAKSLE	+++	+-	-	-
8504	18062	DLGSASW	+++	+	+++	-
8505	14418	YSKQNFN	+++	+--	++	++
8506	18063	GFRHPGS	+++	+--	++	++
8507	18064	RMSSGVW	+++	+-	++	++
8508	18065	AESSRLW	+++	+-	++	+
8509	18066	LWDGTGA	+++	+-	-	++
8510	18067	SSDYSSY	+++	+	-	-
8511	18068	ENGGGRW	+++	+-	-	-
8512	18069	YDRLSDN	+++	+--	+++	+++
8513	18070	RNEFTGF	+++	+-	+	+
8514	18071	SDSTNGM	+++	+-	-	-
8515	18072	ERMNCHS	+++	+--	+++	++
8516	18073	YSRLGGD	+++	+--	-	-
8517	18074	LLQSSTW	+++	+	+++	++
8518	18075	WARGSGL	+++	+--	++	++
8519	18076	GADAVRW	+++	+-	-	-
8520	18077	DFYGRPA	+++	+-	-	-
8521	18078	SGATSNW	+++	+-	-	-
8522	18079	RALEGRD	+++	+-	-	-
8523	18080	QWKVTDR	+++	+--	++	++
8524	18081	GGVPPKY	+++	+--	+++	+++
8525	18082	GRSGGVW	+++	+--	++	++
8526	18083	YSRLSVD	+++	+--	-	+
8527	18084	FFAGVKD	+++	+--	-	-
8528	18085	WCEGVMT	+++	+--	+++	++
8529	18086	WRVSDQK	+++	+--	++	+++
8530	18087	YVKSDSH	+++	+--	+	+
8531	18088	GMGSSVW	+++	+-	++	-
8532	18089	AGESRGW	+++	+-	++	-
8533	18090	WARSPGS	+++	+--	++	++
8534	18091	KSVKFLG	+++	+--	++	++

8535	18092 TLVRTTG	+++	+--	+++	+++
8536	18093 YYTGRLE	+++	+--	-	-
8537	18094 KWTSNSG	+++	+-	++	++
8538	15961 LSKVGQN	+++	+--	-	-
8539	18095 VRAYATG	+++	+-	++	++
8540	18096 HSRLNES	+++	+-	-	-
8541	18097 TRYTGQH	+++	+--	++	++
8542	18098 RFHAGTM	+++	+--	++	++
8543	18099 YRVRDIG	+++	+--	++	++
8544	18100 VDSTCHA	+++	+--	+++	+++
8545	18101 KYSSFSA	+++	+--	++	++
8546	18102 RDGNSAW	+++	+-	-	-
8547	18103 WFSGETD	+++	+--	-	-
8548	18104 RSAFEPF	+++	+-	-	-
8549	18105 HHFSGKQ	+++	+--	++	++
8550	18106 SRWGDAA	+++	+-	+	-
8551	18107 LWRSDNN	+++	+--	-	++
8552	18108 GSEFHTW	+++	+	-	++
8553	18109 GAGTSSW	+++	+-	-	-
8554	18110 YVRSQVD	+++	+--	-	-
8555	18111 PNRFTKD	+++	+--	++	++
8556	18112 ASSTNGR	+++	+-	-	-
8557	18113 RVEDAFP	+++	+--	++	-
8558	18114 LHRESPN	+++	+-	-	-
8559	18115 FFSTNGV	+++	-	-	-
8560	18116 LTRISSN	+++	+-	-	++
8561	18117 RVPYKGD	+++	+--	++	+++
8562	18118 VSSQWRG	+++	+--	++	++
8563	18119 RSADAFP	+++	+--	-	-
8564	18120 YVGGAYS	+++	+--	+++	+++
8565	18121 TSYDSGW	+++	+-	+++	++
8566	18122 GADHVTW	+++	+-	-	-
8567	18123 YVRSMNT	+++	+--	++	+

8568	18124 LSRVSAD	+++	+--	-	+
8569	18125 SCTPCKA	+++	+--	+++	+++
8570	18126 VATHGAG	+++	+-	-	-
8571	18127 FPGSCCA	+++	+--	+++	+++
8572	18128 VESSRAW	+++	+-	++	-
8573	18129 FYGHPYD	+++	+--	-	-
8574	18130 RLESTGW	+++	+-	++	-
8575	18131 VARTYRE	+++	+--	++	++
8576	18132 YSKIGRD	+++	+--	++	+
8577	18133 KDDYTTF	+++	+--	++	++
8578	18134 WYSGIIA	+++	+--	-	-
8579	18135 RDVGCCG	+++	+--	++	++
8580	18136 LFTGFGP	+++	+	++	-
8581	18137 YFAGTHT	+++	+--	-	-
8582	18138 RTNVVFP	+++	+-	+	-
8583	18139 LVYGKNV	+++	+--	++	++
8584	18140 LTRLHAV	+++	+-	++	-
8585	18141 LHVSLEN	+++	+	-	-
8586	18142 MVRNQPN	+++	+--	-	-
8587	18143 HFPRSTG	+++	+--	++	++
8588	18144 DFTDRKW	+++	+-	+++	++
8589	18145 LPRTGDW	+++	+-	-	-
8590	18146 NDGHIKG	+++	+--	-	-
8591	18147 WGGHRGV	+++	+--	++	++
8592	18148 ATDSGPR	+++	+-	++	-
8593	18149 SWSGGTK	+++	+--	++	+++
8594	18150 FMPGHRT	+++	+--	++	++
8595	18151 VAMSGAG	+++	+-	-	-
8596	18152 KLPNYGY	+++	+-	-	-
8597	18153 EMLSVSW	+++	-	-	-
8598	18154 FLKHNNY	+++	+--	++	++
8599	18155 RSEHAYP	+++	+-	+	+
8600	18156 IGVKGWD	+++	+-	++	-

8601	18157 EALNGWD	+++	+-	-	++
8602	18158 HWSQNGV	+++	+-	-	+
8603	18159 SFGPRTS	+++	+--	++	++
8604	18160 YFERKPD	+++	+--	-	-
8605	18161 GSPGVAW	+++	+-	-	-
8606	18162 TGGGMFV	+++	+	-	-
8607	18163 GELMGIE	+++	+--	+++	+++
8608	18164 LWSGIGP	+++	+-	-	-
8609	18165 KDDYNTY	+++	+-	-	-
8610	18166 QGEARIW	+++	-	++	-
8611	18167 IDASSIW	+++	+-	++	-
8612	18168 AFDGTSA	+++	+-	-	-
8613	18169 ARYGGRE	+++	+--	++	++
8614	18170 DNRGLIA	+++	+	-	-
8615	18171 RSEVSVW	+++	+-	-	-
8616	18172 REGTSAW	+++	+	-	-
8617	18173 DPASRAW	+++	+	+++	++
8618	18174 CCTALSP	+++	+-	+++	+++
8619	18175 VVGVCPA	+++	+-	+++	+++
8620	18176 SPGYPSF	+++	+-	+	-
8621	18177 FFSGKLD	+++	+--	-	-
8622	18178 YWTGRPD	+++	+--	-	-
8623	18179 FESDNGV	+++	+--	-	-
8624	18180 LSKLSLN	+++	+-	-	-
8625	18181 VGERGWD	+++	+	-	-
8626	18182 GSALSSW	+++	+-	-	-
8627	18183 VSDFLVY	+++	+-	-	-
8628	18184 CLGELAA	+++	+--	+++	+++
8629	18185 GCGTKCG	+++	+--	+++	+++
8630	18186 GCRHSPV	+++	+--	+++	+++
8631	18187 GGLTCCG	+++	+--	+++	+++
8632	18188 IESTNGA	+++	+-	-	-
8633	18189 KNRDMSW	+++	+--	++	++

8634	18190 READAYA	+++	+--	-	-
8635	18191 RLIDVYP	+++	+--	-	-
8636	18192 CGSVQVN	+++	+-	-	++
8637	18193 GYQHMKM	+++	+--	++	++
8638	18194 AAKYSDR	+++	+--	++	++
8639	18195 MRDGTVA	+++	+-	-	-
8640	18196 GTEWQPF	+++	+-	-	-
8641	18161 GSPGVAW	+++	+-	-	-
8642	18197 DAINGRN	+++	+-	-	-
8643	18198 LHRLNPS	+++	+-	++	++
8644	18199 WIGYVKN	+++	+--	++	++
8645	18200 VMMLPNS	+++	+--	+++	++
8646	18201 PGRAGYL	+++	+--	++	+++
8647	18202 VMSTHGV	+++	-	-	-
8648	18203 NVKGISL	+++	+-	+++	+++
8649	18204 EVIGRRA	+++	+--	++	++
8650	18205 GHEPGWA	+++	+	-	-
8651	18206 TRSDYLR	+++	+-	++	++
8652	18207 GTPRRDW	+++	+--	++	++
8653	18208 FFAGKVS	+++	+-	-	-
8654	18209 RSLEGYF	+++	+-	-	-
8655	18210 VNSTNGM	+++	+	-	-
8656	18211 YFSGAVD	+++	+--	-	-
8657	18212 GDEWEHF	+++	+-	-	-
8658	18213 DLSAVDW	+++	+-	-	-
8659	18214 SAQGKYS	+++	+--	++	++
8660	18215 GYRSASL	+++	+--	++	++
8661	18216 KYAFSSE	+++	+--	+	++
8662	18217 GIRNVMH	+++	+-	-	-
8663	18218 DGRVNFR	+++	+--	++	++
8664	18219 RENHPRA	+++	+--	++	++
8665	18220 VGSCARA	+++	+-	+++	++
8666	18221 RVGKGDW	+++	+--	++	++

8667	18222 NVSEWRN	+++	+--	-	+
8668	18223 NRGNCRG	+++	+--	+++	+++
8669	18224 YVKSSNI	+++	+--	++	-
8670	18225 DLASSAW	+++	+-	+++	++
8671	18226 NSWGKGS	+++	+--	++	+++
8672	18227 GFRLGHG	+++	+--	++	++
8673	18228 QDGRSSY	+++	+-	-	-
8674	18229 SWARSEL	+++	+-	-	-
8675	18230 DSVEFLR	+++	+	-	-
8676	18231 PLDSYKW	+++	-	+++	-
8677	18232 LSRASAN	+++	+--	++	-
8678	18233 GYRTGNT	+++	+--	++	++
8679	18234 VSRDSYR	+++	+--	++	++
8680	18235 GKYQDKY	+++	+--	++	+++
8681	18236 HNNKYRD	+++	+--	++	++
8682	18237 YFQGTYN	+++	+--	-	-
8683	18238 CGPRNPE	+++	+--	+++	+++
8684	18239 FTGVLCA	+++	+--	+++	+++
8685	18240 AGGGLYI	+++	+-	-	-
8686	18241 SLAAHDW	+++	+	++	-
8687	18242 FVSSHSR	+++	+--	++	++
8688	18243 DLSTYDW	+++	+-	-	-
8689	18244 LARNLPN	+++	+--	-	+
8690	18245 HTIDSFP	+++	+--	-	-
8691	18246 GSQGSSW	+++	+	-	-
8692	18247 THHPRLS	+++	+--	++	++
8693	18248 CEKRQAS	+++	+--	+++	+++
8694	18249 WGSLHRT	+++	+--	++	++
8695	18250 GGTTSTW	+++	+	-	-
8696	18251 LHRMQTD	+++	+-	-	-
8697	18252 DKLPAYK	+++	+--	++	++
8698	18253 DYAYSKE	+++	+--	-	-
8699	18254 NLLSAQW	+++	+-	+++	-

8700	18255 GPEGIRW	+++	+-	-	-
8701	18256 HKYGSNV	+++	+--	++	++
8702	18257 PHASGPV	+++	+-	-	-
8703	18258 RDQGVSW	+++	-	-	-
8704	18259 DTVARRL	+++	+--	++	+++
8705	18260 NATVCCG	+++	+--	++	+++
8706	18261 LSRLTVN	+++	+--	-	-
8707	18262 TSEYHVY	+++	+-	-	-
8708	18263 GGETSQW	+++	+-	-	-
8709	18264 DMRSPNW	+++	-	+++	-
8710	18265 REENVRW	+++	+-	-	-
8711	18266 LHDATGP	+++	+-	-	-
8712	18267 GHLRERT	+++	+--	++	++
8713	18268 FHSTSRT	+++	+--	++	++
8714	18269 WSGPVRS	+++	+--	++	++
8715	18270 VSDWAPF	+++	+-	-	-
8716	18271 APSGIMA	+++	+--	+++	+++
8717	18272 TWTGMNA	+++	+--	-	++
8718	18273 YYSGVTS	+++	+--	-	-
8719	18274 SFGSDHD	+++	+--	-	+++
8720	18275 SYLADRK	+++	+--	++	++
8721	18276 VYVKSTS	+++	+--	++	++
8722	18277 ISEFRSY	+++	+-	+	+
8723	18278 LWDGSAS	+++	+-	-	-
8724	18279 LARSSSN	+++	+-	-	-
8725	18280 RGDDRSW	+++	+	-	-
8726	18281 YFSGSLS	+++	+--	-	-
8727	18282 PYARDAG	+++	+--	-	++
8728	18283 YFSNVAA	+++	+--	-	-
8729	18284 DLRDRAW	+++	+-	+++	-
8730	16626 YSRNSDN	+++	+--	+++	+++
8731	18285 QSGMLRC	+++	+--	-	-
8732	18286 VLGQGNW	+++	+-	-	-

8733	18287 TQLHGSN	+++	+--	+++	+++
8734	18288 ERYPSQR	+++	+--	++	++
8735	18289 VYHNKSV	+++	+--	++	++
8736	18290 GSGLSSW	+++	+-	+	+
8737	18291 EALRGWD	+++	+--	-	-
8738	18292 GVVNVSW	+++	-	-	-
8739	18293 WPTSRGT	+++	+-	++	++
8740	18294 FTVPGMD	+++	+-	+++	++
8741	18295 LHRLSGD	+++	+-	-	-
8742	18296 DGDWTVF	+++	+	-	-
8743	18297 GHGTNSF	+++	+--	+++	+++
8744	18298 GGKFHSG	+++	+--	++	++
8745	18299 CDGTKVS	+++	+--	+++	++
8746	18300 VHGMGWD	+++	+-	-	-
8747	18301 IDDWNAW	+++	+-	-	-
8748	18302 GYSERVR	+++	+--	++	++
8749	18303 VAHAGAG	+++	-	-	-
8750	18304 RSEGYLK	+++	+--	++	++
8751	18305 YYSGQVL	+++	+--	-	-
8752	18306 KEYGGSR	+++	+--	++	+++
8753	18307 DWAKRSV	+++	+-	++	++
8754	18308 VSGGTAG	+++	+	-	-
8755	18309 RDLDAYP	+++	+--	-	-
8756	18310 NWKSGSG	+++	+--	++	++
8757	18311 SYGMPRS	+++	+-	++	++
8758	18312 NALGCAG	+++	+-	+++	+++
8759	18313 WRGKPES	+++	+--	++	++
8760	18314 DGAIYLR	+++	+-	++	-
8761	18315 CGSYRQA	+++	+-	+++	++
8762	18316 VARMESV	+++	+-	-	-
8763	18317 GVLAKVV	+++	+--	-	++
8764	18318 GGDRFRT	+++	+--	++	++
8765	18319 VRSHFSA	+++	+-	++	++

8766	18320 YFSGTNN	+++	+--	-	-
8767	18321 VSTGSPP	+++	+-	+++	+++
8768	18322 SGGRWVG	++	+--	++	++
8769	18323 SRFESVR	++	+--	++	++
8770	18324 RGSERIC	++	+-	++	++
8771	18325 REDGSYW	++	+-	-	-
8772	18326 WNPIRHA	++	+--	++	++
8773	18327 AHSRPFV	++	+--	++	++
8774	18328 WKGHSGH	++	+--	++	++
8775	11083 YARLGDN	++	+--	++	-
8776	18329 IRMDAYP	++	+-	-	-
8777	18330 ELRFSKN	++	+--	++	++
8778	18331 RDELTTY	++	-	-	-
8779	18332 VATLGWD	++	+	-	-
8780	18333 SSPRWKD	++	+--	++	++
8781	18334 GWSSKNS	++	+--	++	++
8782	18335 WFTGIRD	++	+-	++	++
8783	18336 MDGNSLW	++	+-	-	-
8784	18337 DLTLSSW	++	+	++	-
8785	18338 TGQGYRS	++	+--	++	++
8786	18339 WDKGAGR	++	+--	++	++
8787	18340 VVSGSSA	++	+--	+++	++
8788	18341 VGGGTWN	++	+-	-	-
8789	18342 YVRSSTG	++	+--	+	-
8790	18343 WGRQGIG	++	+--	++	++
8791	18344 YWSQVAQ	++	+-	++	-
8792	18345 RSEFSTY	++	+-	-	++
8793	18346 MYKTSSH	++	+--	++	+++
8794	18347 YPFPQVS	++	+-	-	++
8795	18348 WFSGQTE	++	+--	-	-
8796	18349 WDRGKQL	++	+--	++	++
8797	18350 GVNEVRW	++	+-	-	-
8798	18351 HGSACGM	++	+-	+++	++

8799	18352 WSSGRER	++	+--	++	++
8800	18353 CRPVKDG	++	+--	+++	+++
8801	18354 GDEYHSW	++	+-	-	-
8802	18355 YSRAGSS	++	+--	+	++
8803	18356 GYLKRPP	++	+--	++	++
8804	18357 TYNPRSS	++	+--	++	+++
8805	18358 LHKLTTD	++	+-	-	-
8806	18359 TKDGWLP	++	-	-	-
8807	18360 FFSGERS	++	+--	+	-
8808	18361 LAGTQTE	++	+--	+++	+++
8809	18362 FARSGGG	++	+--	-	+
8810	18363 GDVEVRW	++	+-	-	-
8811	18364 VWEKARM	++	+--	++	++
8812	18365 WFSGKVD	++	+--	-	-
8813	18366 RYEGALR	++	+--	++	++
8814	18367 AGFDRQW	++	+	+++	++
8815	18368 YVRSNDL	++	+--	++	-
8816	18369 FGRAYGA	++	+-	++	++
8817	18370 RFGDMTR	++	+--	++	++
8818	18371 GLYDYVA	++	+-	+++	+++
8819	18372 SMPSSQW	++	-	++	-
8820	18373 LRSGVGP	++	+-	-	-
8821	18374 GSGDSKW	++	+-	-	-
8822	18375 YWSGVSA	++	+--	-	-
8823	18376 WPGQSGF	++	+-	-	-
8824	18377 LYHKSSS	++	+--	++	++
8825	18378 RYPNQTN	++	+--	++	++
8826	18379 RIFNKGE	++	+--	++	++
8827	18380 LASRGWD	++	+-	-	-
8828	18381 GEGVARW	++	+	-	-
8829	18382 DLTSAEW	++	+	+++	-
8830	18383 QNDSVRW	++	+-	-	-
8831	18384 VLQSASW	++	-	+++	-

8832	18385	TREGDPA	++	-	-	-
8833	18386	WVARTKD	++	+--	++	++
8834	18387	SLPPSYG	++	+-	++	-
8835	18388	NVARAAV	++	+--	-	+++
8836	18389	HHKWPNA	++	+--	++	++
8837	18390	GWRVREG	++	+--	++	++
8838	18391	THGTSTC	++	+-	++	++
8839	18392	SFRSVHQ	++	+-	++	++
8840	18393	GCAKLCD	++	+-	-	-
8841	18394	FGRIGWD	++	+-	+	-
8842	18395	RKSDVYP	++	+-	-	++
8843	18396	VADGLRW	++	+-	-	-
8844	18397	FDGHSAW	++	+-	-	-
8845	18398	SYAHRSP	++	+--	++	++
8846	18399	GVETSRW	++	+-	++	-
8847	18400	FSGKYGH	++	+--	++	++
8848	18401	MLDGTSA	++	+	-	-
8849	18402	HAPTDRR	++	+-	++	++
8850	14000	FSRAGSN	++	+--	-	-
8851	18403	LRNGNAA	++	+-	-	-
8852	18404	DMGAGSW	++	+	-	-
8853	18405	QEKWGKG	++	+--	++	++
8854	18406	YFSGETR	++	+-	-	-
8855	18407	FIEARRN	++	+--	++	++
8856	18408	GSMSSTW	++	+-	-	-
8857	18409	SDGSSKW	++	+-	-	-
8858	18410	GARSADY	++	-	-	-
8859	18411	VFRTQGG	++	+--	++	++
8860	18412	VIYPSGA	++	+-	+++	+++
8861	18413	KLVESDG	++	+--	+++	+++
8862	18414	SFDRQRS	++	+--	++	++
8863	18415	RFAHKEN	++	+--	++	++
8864	18416	RYPDRAL	++	+-	++	++

8865	18417 YSALQRN	++	+--	-	-
8866	18418 NSEFMSY	++	-	-	-
8867	18419 GQGNSVW	++	+-	-	-
8868	18420 VDEWSTF	++	+-	-	-
8869	18421 YYAGQRE	++	+--	-	-
8870	18422 CQKVGMI	++	+--	+++	+++
8871	18423 RDGQSSY	++	+-	+	+
8872	18424 PLSTSNW	++	+-	-	-
8873	18425 GCVHGGA	++	+-	+++	+++
8874	18426 YECCKQT	++	+-	+++	+++
8875	18427 RSEKGYH	++	+--	++	++
8876	18428 WWHGVSA	++	+--	-	-
8877	18429 AVIPSRG	++	+-	+++	+++
8878	18430 TYTKSAV	++	+-	-	-
8879	18431 REQMVSW	++	+-	-	++
8880	18432 AYGSVRS	++	+--	++	++
8881	18433 RLSESTW	++	+	-	-
8882	18434 DEEGALS	++	+-	-	+++
8883	18435 KHDSSRY	++	+--	++	++
8884	18436 WRSGNMG	++	+-	++	++
8885	18437 KYDSSSW	++	+-	++	++
8886	18438 LWDGTFA	++	+-	-	-
8887	18439 RAPDTRW	++	+--	++	++
8888	18440 YRPDGYG	++	+-	-	+
8889	18441 VHSDRSW	++	+-	+++	++
8890	18442 YLGQPYF	++	+-	-	-
8891	18443 ILHDSSE	++	+--	+++	+++
8892	18444 TVERARF	++	+-	++	++
8893	18445 YFSGVAA	++	+--	-	-
8894	18446 FFTGIAD	++	+--	-	-
8895	18447 WQSANGV	++	+-	++	++
8896	18448 VDDFNSF	++	+-	-	-
8897	18449 KAFHAGA	++	+-	++	++

8898	18450 RGGSYGS	++	+--	++	++
8899	18451 TDAFCAP	++	+-	++	+++
8900	18452 WNAPHRA	++	+-	++	++
8901	18453 CLGMCSE	++	+-	+++	+++
8902	18454 TRPGSHV	++	+--	-	-
8903	18455 TDAMSSW	++	+-	-	-
8904	18456 HHPRMGL	++	+-	++	++
8905	18457 YGVGTWS	++	+-	-	-
8906	18458 WQKRPTE	++	+--	++	++
8907	18459 QRYASPQ	++	+-	++	++
8908	18460 LSRASDN	++	+--	-	-
8909	18461 ADGSVRW	++	+-	-	-
8910	18462 RVVNVMP	++	+--	++	++
8911	18463 YPSGSAG	++	+-	-	+
8912	18464 IKSSWHA	++	+--	++	++
8913	18465 YTRLDND	++	+--	-	-
8914	18466 YFAGVSD	++	+--	-	-
8915	18467 NANFERR	++	+--	++	++
8916	18468 WKPNSKS	++	+--	++	++
8917	18469 YTRLNFD	++	+--	-	+
8918	18470 VHKLSLN	++	+-	++	++
8919	18471 GSYRGLG	++	+-	++	++
8920	13996 VFSSNGV	++	+-	++	+
8921	18472 FRSDRYG	++	+-	++	++
8922	18473 GSWIPHG	++	+--	-	-
8923	18474 RGGGISA	++	+-	+++	+++
8924	18475 GQLRYDK	++	+-	++	++
8925	18476 RGGTYHS	++	+-	++	++
8926	18477 PFAVSIE	++	+--	-	-
8927	18478 ENDQLPP	++	+-	+++	+++
8928	18479 GLSDNRR	++	+-	++	++
8929	18480 ALGREYR	++	+-	++	++
8930	18481 VGGSRFS	++	+--	++	++

8931	18482 LFRMRDG	++	+-	++	++
8932	18483 FFVGHHD	++	+-	-	-
8933	11953 MESSNGV	++	-	-	-
8934	18484 TESTVYS	++	+	-	-
8935	18485 CVNRCVV	++	+-	+++	++
8936	18486 NYSHIKS	++	+-	++	++
8937	18487 WDRMSAK	++	+--	++	++
8938	18488 DRASSSW	++	+-	-	-
8939	18489 REDSSMW	++	+	-	-
8940	18490 VAWQGTG	++	+-	-	-
8941	18491 YGTHRFT	++	+--	++	++
8942	18492 TRCVGEI	++	+-	+++	+++
8943	18493 LEDHLRW	++	+-	-	-
8944	18494 VYGTSRS	++	+-	++	++
8945	18495 WQGGQRG	++	+-	++	++
8946	18496 VPPLFAV	++	-	-	-
8947	18497 TVTHHRL	++	+--	++	++
8948	18498 GGPGTWN	++	+-	-	+
8949	18499 DRWGSSA	++	+-	+	-
8950	18500 SGYRAQA	++	+-	++	++
8951	18501 DLSSLEW	++	-	++	-
8952	11908 YESTNGV	++	+-	-	-
8953	18502 RGDYQVF	++	-	-	-
8954	18503 FNPPAMY	++	-	-	-
8955	18504 VFDNRRS	++	+-	++	++
8956	18505 GWRGVSA	++	+-	++	++
8957	18506 WWQGITE	++	+--	-	-
8958	18507 RCCGHFY	++	+-	+++	+++
8959	18508 GARTPTW	++	+--	++	++
8960	18509 YFGARRE	++	+--	++	++
8961	18510 WSSNRSS	++	+--	++	++
8962	18511 WWTGEVE	++	+--	-	-
8963	18512 VGSSKCV	++	+-	++	++

8964	18513	TDDWSTW	++	+-	-	-
8965	18514	TWSGMNA	++	+-	-	-
8966	18515	VSTSKHW	++	+-	++	++
8967	18516	NRYGAAH	++	+-	++	++
8968	18517	WNASYKQ	++	+-	++	++
8969	18518	TDEWSPY	++	+--	-	-
8970	18519	GQVGRYN	++	+-	++	++
8971	18520	CKPCTAN	++	+--	+++	+++
8972	18521	GGRGYNM	++	+-	++	++
8973	18522	GVANTMW	++	+-	-	-
8974	18523	LLDSRDW	++	+-	-	-
8975	18524	HKEGCGL	++	+-	+++	++
8976	18525	DLQAHDW	++	-	++	-
8977	18526	SGITCCP	++	+--	+++	+++
8978	18527	RGVYRSE	++	+-	++	++
8979	18528	GGFGADK	++	+--	++	+++
8980	18529	YSRVDYN	++	+--	++	+
8981	18530	GTHTSAC	++	+-	-	++
8982	18531	GSPSSSW	++	+-	+	-
8983	18532	WWSGVSV	++	+--	-	-
8984	18533	SRFRVTD	++	+-	++	++
8985	18534	VNEYSRY	++	+-	-	-
8986	18535	YFTAQLD	++	+--	-	+
8987	18536	CESVCLY	++	+-	++	-
8988	18537	CVQVKSG	++	+--	+++	+++
8989	18538	WADARRT	++	+-	++	++
8990	18539	YHSRPFA	++	+-	++	++
8991	18540	SQCTSSP	++	+-	+++	++
8992	18541	ISEFLGW	++	+-	-	-
8993	18542	IDEWASY	++	+-	++	-
8994	18543	LIASVSA	++	+-	++	++
8995	18544	LLSDVKW	++	+-	-	++
8996	18545	SGSRFNS	++	+--	++	++

8997	18546	SGNRGVW	++	+-	++	++
8998	18547	DKVPARF	++	+--	++	++
8999	18548	IERRGWD	++	+	-	-
9000	18549	SWLKDDV	++	+--	+++	++
9001	18550	RGREFRE	++	+--	++	++
9002	18551	HGSDRRF	++	+--	++	++
9003	18552	TPGNTSS	++	+--	+++	++
9004	18553	CDGSCKA	++	+--	+++	+++
9005	18554	GTRPSEP	++	+-	++	+++
9006	18555	SKYHGSG	++	+-	++	++
9007	18556	ARYSTGA	++	+-	++	++
9008	18557	QGNGSFI	++	+-	+	-
9009	18558	GGEGSSW	++	+	-	-
9010	18559	CCKGQPM	++	+--	++	+++
9011	18560	VFRGHVG	++	+-	++	++
9012	18561	KRDGTSA	++	+-	-	-
9013	18562	FPGSICV	++	+-	++	++
9014	18563	NGDSGKW	++	+-	-	-
9015	18564	NFGPRAT	++	+-	++	++
9016	18565	CEDVCHG	++	+-	+++	++
9017	18566	TLSTNGR	++	+-	-	-
9018	18567	LSDFKIY	++	+	-	-
9019	18568	DVCCTRV	++	+-	-	+++
9020	18569	GSMTSSW	++	+-	-	+
9021	18570	GNGEIRW	++	+-	-	++
9022	18571	DSVVHLR	++	+-	++	++
9023	18572	EYKTYGK	++	+--	++	++
9024	18573	RALDGWD	++	+-	-	-
9025	18574	GSGDSLW	++	+-	-	-
9026	18575	QGQPSKW	++	+-	++	++
9027	18576	GGSSSTW	++	+-	-	-
9028	18577	GSYQNTR	++	+-	++	++
9029	18578	MWKDKSN	++	+--	++	++

9030	18579 GSPGSHW	++	+-	-	++
9031	18580 VHRLQLD	++	+-	-	-
9032	18581 ERPSSKY	++	+-	++	++
9033	18582 GGNGVSW	++	+-	-	-
9034	18583 YHGKYQL	++	+--	++	++
9035	18584 FMRGMGS	++	+-	++	++
9036	18585 REGSSSW	++	+-	-	-
9037	18586 PSWGDHL	++	+-	-	-
9038	18587 FSKEWRP	++	+--	++	++
9039	18588 VEFEMSY	++	+--	-	-
9040	18589 DDVVSRR	++	+-	+++	+++
9041	18590 VFRSVEK	++	+-	++	++
9042	18591 LTRLSPD	++	+--	-	-
9043	18592 NWARSIE	++	+--	-	-
9044	18593 DMGDHGW	++	+	-	-
9045	18594 RESAVSW	++	+-	-	-
9046	18595 NLESHVW	++	+-	+++	-
9047	18596 YIKYDTG	++	+--	++	-
9048	18597 WWSGVIE	++	+--	-	-
9049	18598 GMSIEAR	++	+-	+++	++
9050	18599 RDAEVFP	++	+--	-	-
9051	18600 EKKFVPA	++	+-	++	++
9052	18601 LVKSTNY	++	+--	++	-
9053	18602 DWAVSIE	++	+-	-	-
9054	18603 WVRERAS	++	+-	++	++
9055	18604 LRDGTYA	++	+	-	-
9056	18605 DWTGNAA	++	+-	-	-
9057	17555 RDVTVFP	++	+-	-	-
9058	18606 EVDGLRW	++	+	-	-
9059	18607 VWSANGI	++	+-	++	++
9060	18608 PLADRMW	++	-	+++	-
9061	18609 CGDIGSV	++	+-	+++	+++
9062	18610 LSRLGID	++	+-	-	-

9063	18611 RYRDGAA	++	+-	++	++
9064	18612 IESSSGR	++	+-	-	++
9065	18613 DVMRSRS	++	+-	++	++
9066	18614 HDGSSQW	++	+-	-	-
9067	18615 NGFKDRG	++	+-	++	++
9068	18616 YFTGMTV	++	+--	+	-
9069	18617 CATRLAH	++	+-	++	-
9070	18618 GLGHQQC	++	+-	-	+++
9071	18619 ERTSVAA	++	+-	+++	+++
9072	18620 CGSGCSI	++	+-	++	+++
9073	18621 CTISRCP	++	+--	+++	+++
9074	18622 RTSMHPG	++	+-	++	++
9075	18623 CLAKHVA	++	+-	+++	+++
9076	18624 YSRTGQG	++	+--	+	++
9077	18625 ETDSGYW	++	+	-	-
9078	18626 YSTNWKS	++	+-	++	++
9079	18627 WVRASAS	++	+-	++	++
9080	18628 RRDGSPA	++	+-	-	-
9081	18629 GDTVVRW	++	+-	-	-
9082	18630 VFRSTPA	++	+-	++	++
9083	18631 SFKRANE	++	+-	++	++
9084	18632 CDSVCAY	++	+-	++	++
9085	18633 GCSGNSC	++	+-	+++	+++
9086	18634 FPLRRVD	++	+-	++	++
9087	18635 NLGSSTW	++	+-	++	++
9088	18636 LARLAYD	++	+-	++	-
9089	18637 ACRHNPA	++	+-	+++	+++
9090	18638 SWKSTSA	++	+-	++	++
9091	18639 AGPDYGW	++	+	-	-
9092	18640 APPDVRW	++	+-	+	+
9093	18641 VLSSTTW	++	-	+++	-
9094	18642 RLYDTFA	++	+--	-	-
9095	18643 WAGAGRT	++	+-	++	++

9096	18644 QYARQNH	++	+-	++	++
9097	18645 TRYKPTD	++	+-	++	++
9098	18646 NVGKANC	++	+-	+++	+++
9099	18647 VGKYAVH	++	+-	++	++
9100	18648 VGTRAAW	++	+-	++	++
9101	18649 LGDAVCR	++	+-	-	+++
9102	18650 AHNRSTY	++	+--	++	++
9103	18651 YVAGCKE	++	+--	+++	++
9104	18652 VGINCKE	++	+--	+++	+++
9105	18653 KGVYAHG	++	+-	++	++
9106	18654 GGPGYSR	++	+-	++	++
9107	18655 NAGVFTG	++	+-	-	+++
9108	18656 TLGSPDR	++	+--	+++	++
9109	18657 YWQGLAS	++	+--	-	-
9110	18658 GATVYRG	++	+-	++	++
9111	18659 RGDNIFP	++	+--	-	-
9112	18660 YVRHDTL	++	+--	-	-
9113	18661 GSGMNAW	++	-	-	-
9114	18662 SRDEWRD	++	+--	-	-
9115	18663 LARTALN	++	+--	++	-
9116	18664 RLAGECN	++	+-	+++	+++
9117	18665 LLSANTW	++	+-	+++	-
9118	18666 DLASMVW	++	+	-	-
9119	18667 NYAKSQN	++	+-	-	++
9120	18668 WRGNATV	++	+-	++	++
9121	18669 AYNGPRA	++	+-	++	++
9122	18670 CTRVVVD	++	+--	+++	++
9123	18671 FDEHEPP	++	+-	++	+++
9124	18672 PHLHRGA	++	+-	++	++
9125	18673 YFTGVVG	++	+--	-	-
9126	18674 WSGTRMQ	++	+-	++	++
9127	18675 WSVKRET	++	+-	++	++
9128	18676 LSKAATN	++	+-	-	-

9129	18677 YFSGVSD	++	+--	-	-
9130	18678 DLESARW	++	-	+++	-
9131	18679 HFAGTWD	++	+-	-	-
9132	18680 VPVGCCG	++	+--	+++	+++
9133	18681 GLGASRY	++	+-	++	++
9134	18682 VTDTNGV	++	-	-	-
9135	18683 YTRSDHN	++	+--	-	++
9136	18684 VRSVNGV	++	+-	-	-
9137	18685 WRAVRAE	++	+-	++	++
9138	18686 GSGTNAW	++	+-	-	-
9139	18687 FSERRGL	++	+-	++	++
9140	18688 VLASVSW	++	-	-	-
9141	18689 WRGGGGS	++	+-	++	++
9142	18690 STYDAIV	++	+-	-	-
9143	18691 YHRTASL	++	+-	++	++
9144	18692 RDNGYPW	++	+-	+	+
9145	12577 YDSTNGV	++	+-	-	-
9146	18693 LSRLGPI	++	+--	-	-
9147	18694 DLRVQTW	++	+-	+++	-
9148	18695 TYRDGGR	++	+-	++	++
9149	18696 AGGSRDW	++	+-	-	++
9150	18697 YFSGAHS	++	+--	-	-
9151	18698 FMDGTAA	++	+	-	-
9152	18699 LVRFENV	++	+-	-	-
9153	18700 GSATSGW	++	-	-	-
9154	18701 RCGECGV	++	+-	+++	++
9155	18702 WGSSRAT	++	+-	++	++
9156	18703 GDGESRW	++	-	-	-
9157	18704 LSRAANN	++	+-	-	-
9158	18705 AMLSSTW	++	+-	+++	-
9159	18706 SAYRSGT	++	+-	++	++
9160	18707 SLGDRTW	++	+-	++	-
9161	18708 RDGSSSW	++	+-	-	-

9162	18709 FRLPRET	++	+-	++	++
9163	18710 RMDSAAW	++	+	++	-
9164	18711 WINGMVA	++	+-	+++	+++
9165	18712 SLSDRTW	++	-	++	-
9166	18713 VSEFEIF	++	+-	-	-
9167	18714 WPNGVNG	++	+-	-	-
9168	18715 GDGASRY	++	+-	-	-
9169	18716 RYVNKES	++	+-	++	++
9170	11671 VKSSNGV	++	+-	-	-
9171	18717 RDQFSTY	++	+-	-	-
9172	18718 GGMLVER	++	+--	+++	+++
9173	18719 IASEGAG	++	+	-	-
9174	18720 AITAIGC	++	+-	-	++
9175	18721 YYSGQLA	++	+--	-	-
9176	18722 GTCGVEK	++	+-	+++	+++
9177	18723 NHLHARS	++	+-	++	++
9178	18724 SASALSW	++	+-	+++	+++
9179	18725 RWLKNEP	++	+-	++	++
9180	18726 YVRSDST	++	+-	-	-
9181	18727 CVTGCRD	++	+--	+++	++
9182	18728 FFSGAIE	++	+-	-	+
9183	18729 TDDFLAW	++	+-	-	-
9184	18730 FGGVSAY	++	-	-	-
9185	18731 CCGSKNA	++	+-	+++	+++
9186	18732 WYSGVLS	++	+--	-	-
9187	18733 DRHPDRR	++	+-	++	++
9188	18734 YSRLNGS	++	+-	-	-
9189	18735 NEDFVAW	++	+-	-	-
9190	18736 SRSYGSG	++	+-	++	++
9191	18737 WFSGEVA	++	+-	-	-
9192	18738 RDHHPRV	++	+-	++	++
9193	18739 VEATNGV	++	+-	-	-
9194	18740 RAGARYD	++	+-	++	++

9195	18741 IEIYKAN	++	+-	++	++
9196	18742 HWMGNKE	++	+-	-	-
9197	18743 VYGSSGR	++	+-	++	++
9198	18744 GSGASAW	++	-	-	-
9199	18745 GSDHVMW	++	+-	-	++
9200	18746 GSYRSVG	++	+-	++	++
9201	18747 DADEVHG	++	+--	+++	+++
9202	18748 GIETSKW	++	+-	-	-
9203	18749 GSEGSTW	++	+	-	-
9204	18750 TTVPTGL	++	+-	-	++
9205	18751 FNSTVAY	++	-	-	-
9206	18752 CRHPVTA	++	+-	++	-
9207	18753 GDNAFGG	++	+-	-	++
9208	18754 YWRGTMD	++	+-	-	-
9209	18755 ATSALEN	++	+-	+++	+++
9210	18756 GGGASTW	++	+-	-	-
9211	18757 DENAFPY	++	+-	-	-
9212	18758 CLKNERG	++	+--	+++	+++
9213	18759 YMSDRTW	++	-	++	-
9214	18760 TNCAINA	++	+--	+++	++
9215	18761 NMSQGSW	++	+	++	++
9216	18762 YGAMCLE	++	+-	+++	+++
9217	18763 GSSTSHW	++	+-	-	-
9218	18764 VMNASDS	++	+--	+++	+++
9219	18765 VNDYLSY	++	-	-	-
9220	18766 LTRLSPV	++	+-	-	-
9221	18767 KDSYHVF	++	+-	++	++
9222	18768 WSLERTW	++	+-	-	++
9223	18769 LFDGTES	++	-	-	-
9224	18770 WTSSNVA	++	+-	+++	+++
9225	18771 REDTSTW	++	+	-	-
9226	18772 LRTDCCV	++	+-	-	+++
9227	18773 VHSFNGV	++	+-	-	-

9228	18774	AQGGQSF	++	-	-	-
9229	18775	GVERAKW	++	+-	++	++
9230	18776	FGKGEWA	++	+-	++	+
9231	18777	KMDAVSW	++	+-	-	++
9232	18778	WFTGTVA	++	+-	-	-
9233	18779	GGGSSLW	++	+-	-	-
9234	18780	YFTGAPD	++	+-	-	-
9235	18781	WTGTKDP	++	+-	++	+++
9236	18782	HTMRGGY	++	+-	++	++
9237	18783	VDDDVWG	++	+-	+++	+++
9238	18784	LARSSTN	++	+--	-	++
9239	18785	GVTTSGW	++	+-	-	-
9240	18786	PEYGKSV	++	+-	+++	+++
9241	18787	YFSGYTS	++	+--	-	-
9242	18788	DARVVRH	++	+-	++	++
9243	18789	SDEYSTY	++	+	-	-
9244	18790	LFSGEAA	++	+	-	-
9245	18791	WQSHTRN	++	+-	++	++
9246	18792	CVSACER	++	+-	+++	+++
9247	18793	YFTDIRE	++	+-	-	-
9248	18794	PVASRDW	++	+-	++	-
9249	18795	TYRGQGG	++	+-	++	++
9250	18796	WSRDAQK	++	+-	++	++
9251	18797	FGGLCCS	++	+--	+++	+++
9252	18798	AGSIDGS	++	+-	+++	+++
9253	18799	IPDTCCV	++	+-	-	-
9254	18800	TTDYVMY	++	-	-	-
9255	18801	YAIECSK	++	+-	+++	+++
9256	18802	ISWSQVD	++	+-	-	-
9257	18803	TDGTSMW	++	-	-	-
9258	18804	VMISASW	++	-	+++	-
9259	18805	KHDFTGS	++	+--	+++	++
9260	18806	TVGTTML	++	+-	+++	+++

9261	18807 SYGKVMV	++	+-	++	-
9262	18808 GQWRTSA	++	+-	++	++
9263	18809 GIVSVSW	++	+-	-	-
9264	18810 DAVLHLR	++	-	-	-
9265	18811 VGRDNLT	++	+-	+++	+++
9266	18812 IASKGAG	++	+	-	+
9267	18813 VASHGAG	++	+-	-	-
9268	18814 DKRQPGW	++	+-	++	++
9269	18815 APVAQDG	++	+--	++	++
9270	18816 KHDEGNG	++	+-	+++	+++
9271	18817 QYRASAA	++	+-	++	++
9272	18818 WSSKAEE	++	+-	++	++
9273	18819 YDVGTWS	++	+-	-	-
9274	18820 IGALGWD	++	+	-	-
9275	18821 CNKPMTA	++	+-	+++	+++
9276	18822 AGSFSRS	++	+-	++	++
9277	18823 LHARGVD	++	+-	-	-
9278	18824 IMSGHDW	++	+-	++	-
9279	18825 GASSRNW	++	+-	++	++
9280	18826 YFSARLD	++	+-	-	-
9281	18827 SAPGTHC	++	+-	++	++
9282	18828 KSSVNHD	++	+--	++	+++
9283	18829 RTADSFI	++	+-	-	-
9284	18830 LPERLGS	++	+-	++	++
9285	18831 VNSSNGR	++	-	-	-
9286	18832 YPNCPGV	++	+-	+++	+++
9287	18833 ISLKCSE	++	+--	-	++
9288	18834 VLDSVRW	++	+-	-	-
9289	16127 SASTNGV	++	+-	-	++
9290	18835 VLSSKTW	++	+-	++	-
9291	18836 NRELGSS	++	+--	+++	+++
9292	18837 DSLPVDK	++	+-	+++	+++
9293	18838 SYGNRTT	++	+-	++	++

9294	18839 FTKSGPN	++	+-	+	+
9295	18840 YSKLDSM	++	+--	-	-
9296	18841 RTEGTFP	++	+-	-	-
9297	18842 GERVDRR	++	+-	++	++
9298	18843 VNSRWHA	++	+-	++	++
9299	18844 GSIGALW	++	+-	-	-
9300	18845 CKAQSCG	++	+-	+++	+++
9301	18846 YWSGNAA	++	+-	-	-
9302	18847 LMNDAYV	++	+-	-	-
9303	18848 YVRHDVM	++	+-	-	-
9304	18849 YFSGTNM	++	+--	+++	-
9305	18850 EPGERSG	++	+-	+++	++
9306	18851 AMSASNW	++	+	++	-
9307	18852 VWDANGV	++	+	-	-
9308	18853 CGGLCSS	++	+--	+++	+++
9309	18854 WFSGHVE	++	+-	-	-
9310	18855 KFDYSSI	++	+--	+++	+++
9311	18856 VYAKSQV	++	+--	+	-
9312	18857 LLSSATW	++	-	++	-
9313	18858 ARVEAFP	++	+-	+++	++
9314	18859 VEVARVR	++	+-	++	++
9315	18860 VGTGPCG	++	+-	+++	++
9316	18861 YYSGTYV	++	+-	-	-
9317	18862 NERGCCG	++	+--	++	+++
9318	18863 YFMGERE	++	+-	-	-
9319	18864 NSPACKA	++	+-	++	+++
9320	18865 FFTGVLN	++	+-	-	-
9321	18866 GGNGSSW	++	+-	-	-
9322	18867 SAYRQGT	++	+-	++	++
9323	18868 AGLDSRP	++	+-	+++	+++
9324	18869 SDLRCCA	++	+-	++	+++
9325	18870 VVKQTAT	++	+--	+++	+++
9326	18871 ACTTALI	++	+-	-	++

9327	18872 LKYSETR	++	+–	++	++
9328	18873 LTRVGLN	++	+–	+	+
9329	18874 GGIASTW	++	+	++	-
9330	18875 GWSSAGK	++	+–	++	++
9331	18876 IDDGSWA	++	+––	+++	+++
9332	18877 CCKLETP	++	+–	+++	++
9333	18878 VVYDAFV	++	+––	-	-
9334	18879 CGACSPN	++	+––	-	++
9335	18880 GSATSTW	++	+	-	-
9336	18881 CRGPCTG	++	+–	+++	+++
9337	18882 EIPPIRR	++	+–	++	++
9338	18883 CKANRVE	++	+–	++	+++
9339	18884 IGTSREW	++	+	++	-
9340	18885 CNLSPTS	++	+–	++	+++
9341	18886 GRSTDNT	++	+––	+++	++
9342	18887 SEFYAAV	++	+–	+++	++
9343	18888 PGGTSGW	++	+–	-	-
9344	18889 CCAGRTA	++	+–	++	+++
9345	18890 VDSTHGV	++	+	-	-
9346	18891 TVGGCCL	++	+–	+++	+++
9347	18892 GSEGSLW	++	+	-	-
9348	18893 KYLHADF	++	+–	+++	++
9349	18894 VGGASTW	++	+	-	-
9350	18895 MEGCCAG	++	+–	+++	++
9351	18896 ERSAEAH	++	+––	+++	++
9352	18897 RSQDSFP	++	+–	-	-
9353	18898 RPNESDW	++	+–	-	-
9354	18899 RLESHGW	++	+–	+++	-
9355	18900 MVQQCCG	++	+–	++	++
9356	18901 ARADGWG	++	-	-	-
9357	18902 WARGSNG	++	+–	++	++
9358	18903 LARLGAN	++	+–	-	-
9359	18904 HVTTHCS	++	+–	++	++

9360	18905 WPFGESA	++	+–	-	-
9361	18906 GRPPLKP	++	+–	++	++
9362	18907 YSRLDSV	++	+–	-	-
9363	18908 LTGQAEL	++	+–	++	++
9364	18909 QGLGCCV	++	+––	+++	-
9365	18910 YSRVSEL	++	+–	-	-
9366	18911 ECGGCRP	++	+–	-	++
9367	18912 YVRSDGT	++	+–	-	++
9368	18913 CDAEMRE	++	+–	+++	+++
9369	18914 HRKVAYD	++	+–	++	++
9370	18915 GTSAYRG	++	+–	++	++
9371	18916 LWIEKPT	++	+––	+++	+++
9372	18917 SRYKEVL	++	+–	++	++
9373	18918 YSRLGVQ	++	+–	++	++
9374	18919 YFTGSTD	++	+––	-	-
9375	18920 NLSDVRW	++	+–	++	-
9376	18921 KGNSGNL	++	+–	-	+++
9377	18922 WEGMKRN	++	+–	++	++
9378	18923 GVGSYIV	++	+–	+++	+++
9379	18924 PLSASSW	++	+	+++	-
9380	18925 CEGVSRE	++	+–	++	+++
9381	18926 FPDGKRF	++	+–	++	++
9382	18927 GWRAGGA	++	+–	++	++
9383	18928 LCADPSR	++	+–	++	+++
9384	18929 RNFGRDG	++	+–	++	++
9385	18930 MTTVVTA	++	+–	+++	+++
9386	18931 FQTESSV	++	+–	+++	+++
9387	18932 LLASATW	++	+–	++	++
9388	18933 DLRTASW	++	-	+++	-
9389	18934 GKGLEHI	++	+	-	-
9390	18935 QAQTSGW	++	+	++	-
9391	18936 NGDAGSW	++	-	-	-
9392	18937 YVRSDSA	++	+––	-	-

9393	18938 CGGGCPS	++	+–	+++	++
9394	18939 WRTGLGG	++	+–	++	++
9395	18940 ASTWNDP	++	+–	-	++
9396	18941 EKLCCHG	++	+–	+++	+++
9397	18942 CQLNCSV	++	+––	+++	++
9398	18943 TSGPPHR	++	+–	++	++
9399	18944 SFDGTPS	++	+	-	-
9400	18945 AGAAKTW	++	+–	++	++
9401	18946 DRVVSTV	++	+–	+++	+++
9402	18947 RGGDSAW	++	+	-	-
9403	18948 GWGDWKD	++	+–	++	-
9404	14230 LAKTGLN	++	+–	-	+
9405	18949 TYSGDLP	++	+	-	-
9406	18950 VEYDWQD	++	+–	-	-
9407	18951 KCTYEQN	++	+–	+++	+++
9408	18952 PGGSGTW	++	+–	+	+
9409	18953 LAHGPYN	++	+–	++	+++
9410	11280 YAKPGFN	++	+–	-	-
9411	18954 RDPSSSW	++	+–	++	-
9412	18955 SGPERSW	++	+–	-	-
9413	18956 RSIDAYP	++	+––	-	-
9414	18957 LWRGSDL	++	+––	+	-
9415	18958 GSWCTVP	++	+–	-	++
9416	18959 EVVSRAG	++	+–	++	++
9417	18960 GGLCCPS	++	+––	++	+++
9418	18961 YMVDAFV	++	+––	-	-
9419	18962 WNHSPAA	++	+–	-	++
9420	18963 IVSDSRG	++	+––	++	+++
9421	18964 ASNTRFH	++	+–	++	++
9422	18965 VSLEGRN	++	+	-	-
9423	18966 AHEFGPV	++	+	-	-
9424	18967 QLERGNW	++	+	+	+
9425	18968 YDLCSKR	++	+–	++	+++

9426	18969 VLTSQIW	++	-	++	-
9427	18970 GGPGVGW	++	+	-	++
9428	18971 VEEGWSW	++	+-	-	-
9429	18972 VAGGSAG	++	-	-	-
9430	18973 CGALRIS	++	+-	-	++
9431	18974 GLYAATL	++	+-	++	-
9432	18975 EGASVLW	++	-	-	-
9433	18976 GGAERRY	++	+-	++	++
9434	18977 GMFGRRD	++	+-	++	++
9435	18978 DSEGMRY	++	-	-	++
9436	18979 GMADPTW	++	+-	++	-
9437	18980 FYNQHSC	++	+-	-	++
9438	18981 FVKYDPS	++	+-	++	-
9439	18982 YQRYGTA	++	+-	++	++
9440	18983 RGSDTYP	++	+-	-	-
9441	18984 LLDSYDW	++	+-	-	-
9442	18985 HSRAASF	++	+-	++	++
9443	18986 GGAGSLW	++	+-	-	-
9444	18987 TNVPSLN	++	+-	++	++
9445	18988 VDLYVSW	++	+-	-	-
9446	18989 SKGCCDS	++	+-	+++	+++
9447	18990 FSDVDTL	++	+-	+++	+++
9448	18991 YHKLSVV	++	+-	-	-
9449	18992 GVYSMKT	++	+-	-	++
9450	18993 LMSGEGP	++	+	+	+
9451	18994 GDAAGRR	++	+-	++	++
9452	18995 TVYAGEP	++	+--	+++	+++
9453	18996 LHRLGVS	++	+	-	-
9454	18997 CGTKCSL	++	+-	++	+++
9455	18998 WLADKGS	++	+-	++	++
9456	18999 GGAHSNF	++	+-	-	++
9457	19000 KFEMNAL	++	+-	++	++
9458	19001 ADQRMRV	++	+-	++	++

9459	19002 WWAGVVS	++	+-	++	++
9460	19003 KFVAVSD	++	+--	+++	+++
9461	19004 IYADRTW	++	+-	+++	-
9462	19005 QGEARSW	++	-	-	-
9463	19006 CGFACPS	++	+-	-	+++
9464	19007 YYSGVTH	++	+-	-	+
9465	19008 YPSGSIG	++	+-	-	-
9466	19009 VLSQSLW	++	+	-	-
9467	19010 QGGSGAW	++	-	-	-
9468	19011 FLASRDW	++	-	-	-
9469	19012 LMSPCCG	++	+--	+++	++
9470	19013 CSGACAA	++	+--	++	+++
9471	19014 ASESLRR	++	+-	++	++
9472	19015 VQDGLRW	++	+-	-	-
9473	19016 VWKPEPG	++	+-	-	++
9474	19017 TTDYTMF	++	+-	++	++
9475	19018 CNDSTKS	++	+-	+++	+++
9476	19019 WAELRRA	++	+-	++	++
9477	19020 CCSGVGI	++	+-	++	++
9478	19021 MVFEDRV	++	+-	+++	++
9479	19022 YSRLSNV	++	+-	-	-
9480	19023 SLVKDAP	++	+-	+++	+++
9481	19024 ERGAGEV	++	+--	+++	+++
9482	19025 GPERMSV	++	+-	++	+++
9483	19026 RGESSIW	++	+	-	-
9484	19027 CRSGAAL	++	+-	++	++
9485	19028 PTADSIG	++	+-	-	-
9486	19029 LSRLLPD	++	+-	-	-
9487	19030 CGPSSAA	++	+-	++	++
9488	19031 VVGAEST	++	+-	+++	+++
9489	19032 CKLPCGL	++	+-	++	+++
9490	19033 LLCKAQG	++	+-	++	-
9491	19034 TWSGDNP	++	+-	-	-

9492	19035 GGGSQSW	++	+-	-	-
9493	19036 LGGAAYK	++	+-	++	++
9494	19037 YDSSNGI	++	+	-	-
9495	19038 FHVRGPD	++	+-	-	-
9496	19039 GVPYTMP	++	+-	-	++
9497	19040 GKSALNG	++	+-	-	-
9498	19041 QDGSSTW	++	+	-	-
9499	19042 WAAGGAR	++	+-	++	++
9500	19043 RCPDCHL	++	+-	+++	++
9501	19044 TRSGENA	++	-	-	-
9502	19045 RLESVAW	++	-	-	-
9503	19046 YYTGHSL	++	+-	-	-
9504	19047 CQTVCAA	++	+-	+++	++
9505	19048 YWSATTA	++	+-	++	+
9506	19049 ELSVVIH	++	+--	+++	+++
9507	19050 SVGSSER	++	+-	-	+++
9508	19051 WLEGESV	++	+-	+++	++
9509	19052 YARTSTP	++	+-	-	-
9510	19053 GGMSSTW	++	+-	-	-
9511	19054 PNGEATW	++	+-	-	-
9512	19055 WDSDNGR	++	+-	-	-
9513	19056 RGVGPDS	++	+--	+++	++
9514	19057 CYLTKCD	++	+-	++	+++
9515	19058 LYVRWCG	++	+-	++	+++
9516	19059 VASACCG	++	+-	+++	++
9517	19060 TIGGACI	++	+-	+++	+++
9518	19061 YYAGVLS	++	+-	++	-
9519	19062 LEYGMSG	++	+-	+++	++
9520	19063 TYRGKPD	++	+-	++	++
9521	19064 GGRNGIE	++	+--	+++	+++
9522	19065 LLGENPD	++	+-	++	++
9523	19066 GGDFSSY	++	-	-	-
9524	19067 RDEGSTW	++	+	-	-

9525	19068	SGASHLW	++	+-	++	++
9526	19069	GSSTSVW	++	+-	++	-
9527	19070	YVQGNKY	++	+-	++	++
9528	19071	VDSTEGV	++	+-	-	-
9529	19072	SSDAVRW	++	+-	-	-
9530	19073	TEGKRFT	++	+-	++	++
9531	19074	VASMGIG	++	-	-	-
9532	19075	WYSGIQM	++	+-	-	++
9533	19076	CGLGSEA	++	+-	++	++
9534	19077	WGARAER	++	+-	++	++
9535	19078	SSEYLVY	++	+-	-	-
9536	19079	SYHLKMG	++	+-	++	++
9537	19080	IGFVCSE	++	+-	++	++
9538	19081	YSSLNIN	++	+-	-	-
9539	19082	YFAGMVQ	++	+--	-	-
9540	19083	VGWRGRS	++	+-	-	+++
9541	19084	SMSDVRW	++	+	-	-
9542	19085	RLSDVAW	++	-	-	-
9543	19086	SSGMSSW	++	+	-	-
9544	19087	TSENVYF	++	+--	-	-
9545	19088	GDEYVAF	++	+-	-	-
9546	19089	YWSGIKE	++	+-	++	-
9547	19090	SAFVHCV	++	+--	+++	+++
9548	19091	GEGQSSW	++	+	-	-
9549	19092	LVSGEDV	++	+-	+++	++
9550	19093	RADSKQS	++	+-	-	+++
9551	19094	NALDWRD	++	+-	-	-
9552	19095	GLASSAW	++	-	-	-
9553	19096	SLGKYGH	++	+-	++	++
9554	19097	TLVLCRE	++	+-	-	+++
9555	19098	SDGACCA	++	+-	-	++
9556	19099	LDDGRFQ	++	+-	+++	+++
9557	19100	AGMENKM	++	+-	++	+++

9558	19101 GSDNSRW	++	+-	++	-
9559	19102 RRLSMSL	++	+--	-	+++
9560	19103 KLDHMGM	++	+--	+++	+++
9561	19104 DMMGNPA	++	+	-	-
9562	19105 GDSSVRK	++	+-	++	++
9563	19106 GYMEGGG	++	+-	++	++
9564	19107 WGRQALG	++	+-	++	++
9565	19108 DNSGRLY	++	+-	+++	++
9566	19109 GFALPGG	++	+-	+++	+++
9567	19110 GSGSALW	++	+-	-	-
9568	19111 YWLDNVG	++	+-	+++	++
9569	19112 WGSQGRG	++	+-	++	++
9570	19113 RLDDRSW	++	+-	-	++
9571	19114 CCKVAMS	++	+--	++	+++
9572	19115 MNCGMQC	++	+-	++	+++
9573	19116 VGTDRGW	++	+-	-	-
9574	19117 STSSRYS	++	+-	++	++
9575	19118 SWGAKQS	++	+-	++	++
9576	19119 APSHIAW	++	+-	-	-
9577	19120 DPMSLGW	++	+	-	-
9578	19121 LNTRWQG	++	+-	++	++
9579	19122 CKRGWSE	++	+-	-	++
9580	19123 MTVRTSL	++	+-	+++	++
9581	19124 DLRAVSW	++	+	+++	++
9582	19125 LLESRSW	++	-	++	-
9583	19126 YYSGVSE	++	+-	-	-
9584	19127 SYRSAVL	++	+-	++	++
9585	19128 YYSGVRD	++	+-	-	-
9586	19129 MRLGGLT	++	+-	+++	+++
9587	19130 IAGAERA	++	+-	+++	++
9588	19131 NHKNTPP	++	-	-	-
9589	19132 FIEQLPQ	++	+-	+++	++
9590	19133 SVVSQKS	++	+-	+++	+++

9591	19134 CSLKDRC	++	+-	++	++
9592	19135 FCIRLWL	++	+-	++	+++
9593	19136 AMVARDW	++	-	-	-
9594	19137 ILAERTA	++	+-	-	-
9595	19138 YNEVSIA	++	+-	+++	++
9596	19139 GIGCTKL	++	+-	-	-
9597	19140 GSGVSNW	++	+	-	-
9598	19141 SVRLQSE	++	+-	++	++
9599	19142 VMKSVST	++	+--	-	+++
9600	19143 VPGRGAG	++	+	-	-
9601	19144 LWDGTRA	++	+	-	-
9602	19145 FSGYSSS	++	+-	++	++
9603	19146 DMESNRW	++	+-	++	-
9604	19147 LDDWSHF	++	+-	-	-
9605	19148 YARGALN	++	+-	-	-
9606	19149 YRSTSHL	++	+-	++	++
9607	19150 CRPEHGP	++	+-	+++	+++
9608	19151 MYKSRVD	++	+-	++	++
9609	19152 LSNAPVG	++	+--	+++	++
9610	19153 SAPERLL	++	+-	+++	+++
9611	19154 AGEGVKW	++	+	+	-
9612	19155 GTLPAYR	++	+-	++	++
9613	19156 WSRDTDN	++	+-	+++	+++
9614	19157 RGSGFHG	++	+-	++	++
9615	19158 CGTPCSA	++	+-	++	++
9616	19159 IGSAVLR	++	+-	++	+++
9617	19160 RMADSVW	++	+	++	++
9618	19161 DFFGHDA	++	+-	-	-
9619	19162 TGATVGC	++	+-	+++	+++
9620	19163 ERYGLCA	++	+-	+++	+++
9621	19164 RDERPGG	++	+-	-	++
9622	19165 ARFDAFP	++	+-	-	-
9623	19166 YDPRSNN	++	+-	+++	-

9624	19167 ELDSIQW	++	+	-	-
9625	19168 YVRAPLS	++	+-	++	++
9626	19169 YSRIGDH	++	+-	-	-
9627	19170 ITFRCGK	++	+-	++	++
9628	19171 VETVRYK	++	+-	++	++
9629	19172 DLMSLSW	++	+	-	-
9630	19173 ASDYQTF	++	+-	++	-
9631	19174 MSDGTGP	++	+	-	-
9632	19175 ASDEWRD	++	+-	-	-
9633	19176 YLGGDHW	++	+-	-	-
9634	19177 LPTGWGP	++	+-	-	-
9635	19178 GPETVKW	++	+	-	-
9636	19179 YSSVVAE	++	+-	+++	++
9637	19180 YFEGVKG	++	+-	-	-
9638	19181 GPNLHPS	++	+--	+++	+++
9639	19182 REDYVYP	++	+-	-	-
9640	19183 CSKPSAV	++	+-	-	-
9641	19184 YGCNGCS	++	+-	++	++
9642	19185 DMSSTKW	++	-	++	-
9643	19186 GAGNSLW	++	+-	-	-
9644	19187 MIADGGA	++	+-	+++	-
9645	19188 WYSGRTE	++	+-	-	-
9646	19189 CKYGAEA	++	+-	-	++
9647	19190 VVPLCDP	++	+-	+++	+++
9648	19191 TRSGSNA	++	+-	-	-
9649	19192 LASACLS	++	+-	++	++
9650	19193 AGACDAS	++	+-	+++	++
9651	19194 CNSGCSV	++	+-	++	+++
9652	19195 WSRGGSA	++	+-	++	++
9653	19196 EISKTQI	++	+-	+++	++
9654	19197 FDRKPQI	++	+-	++	++
9655	19198 YTSDNGL	++	+-	-	-
9656	19199 NGANGVW	++	+-	-	-

9657	19200 LEAVSRA	++	+-	-	++
9658	19201 EMLPYRG	++	+-	++	+++
9659	19202 SADTWRD	++	+-	-	-
9660	19203 LTVATVE	++	+-	++	++
9661	19204 LTEKLAS	++	+-	++	++
9662	19205 YFSGSSA	++	+-	-	-
9663	19206 MFGSTAG	++	+-	++	+++
9664	19207 YDYDAYP	++	+-	-	-
9665	19208 SNPAPHS	++	+-	-	-
9666	19209 YFVGERE	++	+-	-	-
9667	19210 WGKNMGL	++	+-	++	++
9668	19211 VAHVPLC	++	+-	++	+++
9669	19212 YARTGTS	++	+-	-	-
9670	19213 GGGTSSW	++	+-	-	-
9671	19214 GNLDNGG	++	+-	++	++
9672	19215 RTYDSMP	++	+-	-	-
9673	19216 GGESTSW	++	+	-	-
9674	19217 YRLRISD	++	+-	++	++
9675	19218 IAATCCN	++	+-	+++	++
9676	19219 GGEGLRW	++	+-	-	-
9677	19220 CAPDYRE	++	+-	++	++
9678	19221 ILSDRVW	++	-	++	++
9679	19222 AQGIGTW	++	+-	-	-
9680	19223 DESVRTW	++	-	++	+
9681	19224 WLKSQAG	++	+-	++	++
9682	19225 KSTTSEP	++	+-	+++	+++
9683	19226 GEMSVRW	++	+-	-	-
9684	19227 LSALSNN	++	+-	-	++
9685	19228 GGDYIGT	++	+-	-	-
9686	19229 DMGSADW	++	+	++	-
9687	13135 WLAGPSA	++	+	+	-
9688	19230 VADHVRW	++	+-	-	-
9689	19231 REGTVYW	++	+	-	-

9690	19232 SLSSQEW	++	+-	+++	-
9691	19233 DQGYSTW	++	-	-	-
9692	19234 LARLGYD	++	+-	+	-
9693	19235 TATGCCP	++	+-	+++	+++
9694	19236 TYSVDLG	++	+-	+++	++
9695	19237 LGAYSLH	++	+-	-	++
9696	19238 CKMGRDE	++	+-	++	+++
9697	19239 LRGDDCA	++	+-	++	++
9698	19240 LPSGDSP	++	-	++	-
9699	19241 CGKDLLH	++	+-	+++	++
9700	19242 EMGGREW	++	+-	++	+
9701	19243 YVKFESG	++	+-	-	-
9702	19244 GTGGDTG	++	+-	+++	+++
9703	19245 VTGACCS	++	+-	+++	+++
9704	19246 DYASIKW	++	+-	++	+
9705	19247 GDESSVW	++	+	-	-
9706	19248 QSSVFND	++	+--	+++	++
9707	19249 GDKETAA	++	+-	+++	++
9708	19250 SAYSPLS	++	+-	+++	-
9709	19251 NPLASNW	++	+-	-	-
9710	19252 REDVSLW	++	+	-	-
9711	19253 YFTGHLE	++	+--	-	-
9712	19254 GLNVVAW	++	+-	-	+
9713	19255 MMTSSQW	++	+-	++	++
9714	19256 PDFSTRY	++	+-	++	++
9715	19257 CIVTANC	++	+-	+++	++
9716	19258 VNDGVKW	++	-	-	-
9717	19259 LCKSCGS	++	+--	++	++
9718	19260 TVWGDAA	++	+	-	-
9719	19261 DLESSYW	++	-	-	-
9720	19262 VDSTNGL	++	+-	-	-
9721	19263 RLESAVW	++	+	++	++
9722	19264 PMSAVGW	++	+-	++	++

9723	19265	RDPSVFP	++	+-	-	-
9724	19266	TNAQILT	++	+--	+++	++
9725	19267	FSVRGNL	++	+-	++	++
9726	19268	CLAMSKP	++	+-	+++	++
9727	19269	TREGDAP	++	+-	-	-
9728	19270	VLSHTDL	++	+-	++	+++
9729	19271	YTRLDSS	++	+-	++	-
9730	19272	QDEWTYV	++	+--	-	-
9731	19273	VIGMGRD	++	+-	++	++
9732	19274	GDEYISY	++	+	-	-
9733	19275	SNSSLNC	++	+-	+++	++
9734	19276	TSLEFGA	++	+-	++	+++
9735	19277	GVTEVSW	++	+-	-	-
9736	19278	SFDADRW	++	+-	-	-
9737	19279	FFSGAVE	++	+-	-	-
9738	19280	MRFCKDS	++	+-	++	+++
9739	19281	YSDFAPF	++	+-	-	-
9740	19282	GSTVCKD	++	+-	-	++
9741	19283	GEPRSGN	++	+-	+++	++
9742	19284	FGYRQGS	++	+-	-	-
9743	19285	SMCKDDC	++	+-	+++	+++
9744	19286	GYSDFRN	++	+-	-	-
9745	19287	GLYVEAG	++	+-	++	+++
9746	19288	NIPGMMY	++	+-	-	-
9747	19289	LSVDICA	++	+-	++	++
9748	19290	VSMGSAG	++	-	-	-
9749	19291	TRQGDEA	++	-	-	-
9750	19292	GGINYDL	++	+-	+++	++
9751	19293	WNAGGAF	++	+-	-	-
9752	19294	RMDHTNF	++	+-	+++	+++
9753	19295	IMSDLAW	++	-	-	-
9754	19296	CGEAILM	++	+-	-	++
9755	19297	SSTQSSF	++	+-	-	+++

9756	19298 GLSSATW	++	-	+++	-
9757	19299 VSAGYQW	++	+-	-	-
9758	19300 YFAGIPA	++	+-	-	-
9759	19301 ELMAHSW	++	+	++	-
9760	19302 GGTPVNV	++	+--	+++	++
9761	19303 GVTAVAW	++	+	-	-
9762	19304 EPESRSW	++	-	+++	-
9763	19305 CDGVPRG	++	+-	+++	++
9764	19306 RDGGRIG	++	+-	+++	++
9765	19307 NGQGGHW	++	+-	-	-
9766	19308 VESSSLW	++	+-	++	-
9767	19309 TCTGTCS	++	+-	+++	+++
9768	19310 VDSDNGR	++	+--	-	-
9769	19311 IVSICAA	++	+-	+++	++
9770	19312 DHANPPD	++	+-	+++	+++
9771	19313 FSGMSPS	++	+--	+++	+++
9772	19314 CMTGLKC	++	+-	+++	-
9773	19315 NCNASCV	++	+-	-	++
9774	19316 KVGDLRA	++	+-	++	+++
9775	17025 VESSNGR	++	+-	-	-
9776	19317 EFDARTW	++	+-	-	-
9777	19318 ICSRVNG	++	+--	+++	+++
9778	19319 HVKCCPP	++	+-	++	++
9779	19320 SSMVSCA	++	+-	++	+++
9780	19321 LSAGELW	++	+-	+++	+++
9781	19322 VMNSSGA	++	+-	-	++
9782	19323 LDGCCSA	++	+-	++	++
9783	19324 FRDGTAA	++	+	-	-
9784	19325 CDTACTR	++	+-	+++	+++
9785	19326 GELTVRW	++	+	-	-
9786	19327 LEGREEG	++	+-	+++	++
9787	19328 CLKICTP	++	+-	++	++
9788	19329 MERNSSS	++	+-	+++	++

9789	19330	GGERSTW	++	+-	-	-
9790	19331	WHSTNGL	++	+-	-	-
9791	19332	GGSDRIW	++	+	+++	-
9792	19333	CAVVCSS	++	+-	+++	-
9793	19334	VFSRLDT	++	+--	-	-
9794	19335	GHCGATV	++	+-	++	-
9795	19336	GVAGASF	++	+-	++	+++
9796	19337	AGEWVTY	++	+	-	-
9797	19338	LEHRLVN	++	+-	++	++
9798	19339	DSASRAW	++	+-	++	-
9799	19340	GCCTNEV	++	+-	++	++
9800	19341	YSRASDD	++	+-	-	-
9801	19342	MWNGINP	++	+-	-	-
9802	19343	GGMGVSW	++	-	-	-
9803	19344	CCDPSNV	++	+-	++	++
9804	19345	GIPNCRE	++	+-	+++	++
9805	19346	LCKLAQP	++	+-	++	++
9806	19347	PRSTHGV	++	+-	-	-
9807	19348	EMHADVI	++	+-	+++	+++
9808	19349	LITKPGY	++	+-	+++	++
9809	19350	TIADAYP	++	+-	-	-
9810	19351	TMRDAFP	++	+-	-	-
9811	19352	ATNWRLA	++	+-	-	-
9812	19353	SAQSWTD	++	+-	-	-
9813	19354	LHASQMN	++	+-	-	-
9814	19355	MHRLSMD	++	+-	-	-
9815	19356	VAQAGAG	++	-	-	-
9816	19357	GAPDSIR	++	+-	+++	++
9817	19358	REDFSTF	++	+-	++	-
9818	19359	HEDSCSA	++	+-	+++	+++
9819	19360	YYSGRSE	++	+-	-	-
9820	19361	FFNTAHS	++	+--	+++	+++
9821	19362	YVKSQGV	++	+-	++	-

9822	19363 CTKNVNA	++	+-	+++	++
9823	19364 MVSCGGC	++	+-	++	++
9824	16056 TLSTNGV	++	+	-	-
9825	19365 SASTAKS	++	+-	+++	+++
9826	19366 VMSEASW	++	-	-	-
9827	19367 LGAATCQ	++	+-	-	++
9828	19368 CCGNVKI	++	+-	++	++
9829	19369 SGEYTPF	++	+-	-	-
9830	19370 CKVSANL	++	+-	+++	++
9831	19371 GSDTSRW	++	+-	-	-
9832	19372 RCPFVET	++	+-	-	+++
9833	19373 MLSLCCA	++	+-	++	++
9834	19374 QNCVDRC	++	+--	-	++
9835	19375 FEVPGDK	++	+--	-	++
9836	19376 PGASSVW	++	+	+++	++
9837	19377 GFGDFQN	++	+-	-	-
9838	19378 STAGTSC	++	+-	+++	++
9839	19379 GMVPRDM	++	+-	-	-
9840	11976 AWSTNGV	++	+-	-	-
9841	19380 CSNKCTV	++	+-	+++	+++
9842	19381 WWSGTPD	++	+-	-	-
9843	19382 ECLASCR	++	+-	-	++
9844	19383 FDASTLS	++	+-	++	++
9845	19384 ITERVNT	++	+-	-	+++
9846	19385 YSKAAPL	++	+-	++	-
9847	19386 GLSSSSW	++	+-	++	-
9848	19387 RLENPHT	++	+-	+++	+++
9849	19388 KLDEVYP	++	+-	-	++
9850	19389 PSAKNLG	++	+--	+++	+++
9851	19390 EGPPPRN	++	-	-	-
9852	19391 VGQQVVL	++	+-	+++	++
9853	19392 VSDFDIF	++	+-	-	-
9854	19393 GSFRQGG	++	+-	++	++

9855	19394 HEPSRTW	++	+–	++	-
9856	19395 TGVHVTP	++	+–	+++	+++
9857	19396 CMQLKSH	++	+–	++	++
9858	19397 HDAFSSW	++	+–	++	-
9859	19398 TWHGDGP	++	+	-	+
9860	19399 WGSQGGT	++	+–	+++	+++
9861	19400 IEGLRAS	++	+–	-	++
9862	19401 LSRISMD	++	+–	-	-
9863	19402 CERNECP	++	+–	++	-
9864	19403 DYESACV	++	+–	-	++
9865	19404 AWDNEAM	++	+–	++	++
9866	19405 KNGSSSW	++	+–	-	-
9867	19406 TDSEWRD	++	+––	-	-
9868	19407 CCGPGKS	++	+–	++	++
9869	19408 VSDTNGI	++	+	++	-
9870	19409 MGLGLHI	++	+––	+++	++
9871	19410 CVIVKQV	++	+–	++	++
9872	19411 SEICSSP	++	+–	++	++
9873	19412 CAAGTSP	++	+–	++	+++
9874	19413 ICGAPCV	++	+–	+++	++
9875	19414 DSMATER	++	+–	++	+++
9876	19415 FCLGNSG	++	+–	++	++
9877	19416 NDGRSGW	++	+–	+	-
9878	19417 GPTSVLW	++	+–	-	++
9879	19418 DRIFLSA	++	+––	+++	+++
9880	19419 MDNAAQR	++	+–	++	++
9881	19420 ADGGTVY	++	+–	+++	++
9882	19421 YWSRVSE	++	+––	-	-
9883	19422 WSERLRS	++	+–	++	++
9884	19423 YWEGVTS	++	+–	-	-
9885	19424 VKGIAVS	++	+–	+++	+++
9886	19425 CVASYTC	++	+–	++	-
9887	19426 KEFLSDR	++	+–	++	+++

9888	19427 WEFKHLG	++	+-	+++	++
9889	19428 PMHATSW	++	+-	++	-
9890	19429 DKKSDLV	++	+-	+++	++
9891	19430 RVELSPL	++	+-	++	+++
9892	19431 SACKTTE	++	+-	+++	++
9893	19432 IPNRCEA	++	+-	-	++
9894	19433 CNPSSEK	++	+-	+++	++
9895	19434 LSHCCDS	++	+-	-	-
9896	19435 GINVPTG	++	+-	++	++
9897	19436 CGVKCQL	++	+-	++	++
9898	19437 SGTFSGE	++	+-	+++	+++
9899	19438 LVICRGH	++	+-	++	++
9900	19439 LSVNSSG	++	+-	+++	++
9901	19440 LHKLSVT	++	+-	-	-
9902	19441 YFSGQAE	++	+-	-	-
9903	19442 YVLSDSR	++	+-	++	-
9904	19443 ELIGGGS	++	+-	++	++
9905	19444 MTVDCSR	++	+-	++	++
9906	19445 LEYHKVP	++	+-	++	-
9907	19446 VGTFREG	++	+--	++	++
9908	19447 VPDAVRW	++	-	-	-
9909	19448 IGGSSGW	++	+-	-	+
9910	19449 EMFLNGV	++	+-	+++	++
9911	19450 SGKGWSA	++	+-	++	++
9912	19451 GASAGTF	++	+-	+++	+++
9913	19452 RGVYSNV	++	+-	++	++
9914	19453 GGGDQRW	++	+	-	-
9915	19454 DLDHEGV	++	+-	++	++
9916	19455 PGNSHAW	++	+-	+++	++
9917	19456 CSLGSDR	++	+-	+++	++
9918	19457 VTASGCA	++	+-	++	++
9919	19458 LGLKGWD	++	-	-	-
9920	19459 VEGVTGH	++	+-	++	+++

9921	19460	IGHVSDW	++	-	-	++
9922	19461	GRNFGTP	++	+-	+++	++
9923	19462	YFSAVTA	++	+-	-	-
9924	19463	SGGTSLW	++	+	-	-
9925	19464	GLMHEHL	++	+-	++	++
9926	19465	SQDCCGP	++	+-	++	++
9927	19466	LWTGAGP	++	-	-	-
9928	19467	VTGDRIV	++	+-	-	++
9929	19468	RSMDIFP	++	+-	-	-
9930	19469	FFSGTLE	++	+-	-	-
9931	19470	CEFQKCP	++	+-	++	+++
9932	19471	VEMGRTG	++	+-	++	+++
9933	19472	TSLVRVS	++	+-	-	+++
9934	19473	SMLKYPS	++	+-	++	+++
9935	19474	YFSLERD	++	+-	++	++
9936	19475	GGDLRQQ	++	+-	+++	+++
9937	19476	IRGGGAG	++	+-	-	-
9938	19477	AWTEANR	++	+-	++	+++
9939	19478	GGNGSSY	++	-	-	-
9940	19479	GVTEIKC	++	+-	-	++
9941	19480	LVTHGSL	++	+-	+++	+++
9942	19481	GMRDSVT	++	+--	-	++
9943	19482	GDLFLAV	++	+-	-	-
9944	19483	ELTSDPG	++	+-	++	+++
9945	19484	ALGMPLQ	++	+-	+++	++
9946	19485	FSRLNDD	++	+-	-	-
9947	19486	FSVGICS	++	+-	++	+++
9948	19487	SRVTYRE	++	+-	++	++
9949	19488	LCLGACT	++	+-	+++	++
9950	19489	GGAGSAW	++	+	+	-
9951	19490	DSSPSCP	++	+-	-	++
9952	19491	GLSSPLW	++	-	++	-
9953	19492	CITREHV	++	+-	+++	++

9954	19493 NAPVGAG	++	-	-	-
9955	19494 VPSSVTW	++	+-	++	-
9956	19495 YSRVQGD	++	+--	++	-
9957	19496 LSKIGYN	++	+-	-	++
9958	19497 RGEGRLY	++	+-	++	++
9959	19498 KVGEQTR	++	+-	+++	++
9960	19499 SLSTENL	++	+-	-	+++
9961	19500 ACSTIHL	++	+-	-	++
9962	19501 DQAVRVS	++	+-	++	+++
9963	19502 DSTSQLS	++	+-	++	+++
9964	19503 GAGTSGW	++	+	-	-
9965	19504 DPSTQLW	++	+-	-	-
9966	19505 QGASSSW	++	+	-	-
9967	19506 LVKCVVG	++	+-	-	++
9968	19507 WSSTKTH	++	+-	++	++
9969	19508 VPYETPV	++	-	-	-
9970	19509 VGADRQW	++	+	-	-
9971	19510 WRAEVSR	++	+--	+++	++
9972	19511 IVAGYSF	++	+-	++	+++
9973	19512 TRTGENA	++	-	-	-
9974	19513 VCSGAEG	++	+-	++	++
9975	19514 DFKALGT	++	+-	+++	+++
9976	19515 DSFGNAA	++	-	++	-
9977	19516 DPFAPSW	++	+-	+++	-
9978	19517 LWDAQGK	++	+-	++	+++
9979	19518 FNSSVGF	++	+-	-	-
9980	19519 IGNGTWN	++	+-	-	-
9981	19520 KSGTVGE	++	+-	++	++
9982	19521 VAMSSCC	++	+-	++	++
9983	19522 VDTIVCE	++	+-	-	++
9984	19523 FGGHSSY	++	+-	-	-
9985	19524 FGRCDIT	++	+-	++	++
9986	19525 YYTAVVG	++	+-	++	-

9987	19526 YVFSGPV	++	+-	-	+
9988	19527 PGQIMTA	++	+-	+++	++
9989	19528 IDYAPGE	++	+-	++	++
9990	19529 ESATLVL	++	+-	-	-
9991	19530 SDPKIVA	++	+-	+++	++
9992	19531 LQKFDRS	++	+-	++	++
9993	19532 CCKSVTA	++	+-	-	++
9994	19533 GLSSAVW	++	+	+++	++
9995	19534 NGVWTNP	++	+-	-	-
9996	19535 VTTRGPN	++	+-	-	-
9997	19536 STEWIPY	++	+	-	-
9998	19537 DVSSRTW	++	+	++	++
9999	19538 SDGVSVR	++	+-	-	-
10000	19539 FESNEPW	++	+-	+++	++
10001	19540 GSVGNAW	++	+-	++	-
10002	19541 VPGIPVN	++	+-	+++	++
10003	19542 VCNGNIC	++	+-	+++	++
10004	19543 VATEGRD	++	+-	-	-
10005	19544 REGIESW	++	+--	+++	+++
10006	19545 AVEGCCG	++	+-	++	-
10007	19546 ISGISMY	++	+-	++	++
10008	19547 DWSRCSK	++	+-	+++	-
10009	19548 YWAGVES	++	+-	-	-
10010	19549 FYSGVLS	++	+-	++	-
10011	19550 RVADCAP	++	+-	++	++
10012	19551 YIAGCGN	++	+-	+++	++
10013	19552 GSGQSIW	++	-	-	-
10014	19553 SLSSTTW	++	-	+++	-
10015	19554 SLGGSTW	++	+-	-	-
10016	19555 PIRVSDV	++	+-	+++	+++
10017	19556 SCSTGYP	++	-	++	++
10018	19557 VGVSSSG	++	+-	+++	-
10019	19558 GLVSSAM	++	+-	+++	++

10020	19559 VGCAHLP	++	+-	++	++
10021	19560 LHALSTD	++	+-	++	++
10022	19561 ELDSRDW	++	+-	-	-
10023	19562 DVRTDSN	++	+-	+++	+++
10024	19563 VAGQITI	++	+-	-	-
10025	19564 GVDRHMP	++	+-	+++	-
10026	19565 GCIIPGV	++	+-	++	++
10027	19566 RLDDVLW	++	-	-	-
10028	19567 GGSTSVW	++	+-	-	-
10029	19568 YFSGRES	++	+-	+	-
10030	19569 GSSSSAW	++	+-	++	-
10031	19570 RDRNSYV	++	+-	++	++
10032	19571 LGGVLTV	++	+-	+++	++
10033	19572 MVACGCG	++	+-	++	++
10034	19573 CDGVGVA	++	+-	++	++
10035	19574 SGSTSGW	++	+-	-	-
10036	19575 ELSSREW	++	+	-	-
10037	19576 GVKMNCS	++	+-	+++	++
10038	19577 WLKQTLL	++	+-	+++	++
10039	19578 RDIDCLS	++	+-	+++	++
10040	19579 RIYDAVP	++	+-	-	-
10041	19580 GRAYAHP	++	+-	-	++
10042	19581 VAGRCCR	++	+-	-	++
10043	19582 GSAGVSW	++	+	-	-
10044	19583 MEVRESG	++	+-	++	+++
10045	19584 REGVSAW	++	+	-	-
10046	19585 TWEGSPA	++	-	-	-
10047	19586 GSHGVSW	++	+-	++	++
10048	19587 GVRNVMP	++	+-	-	-
10049	19588 DDSFYPS	++	+-	-	-
10050	19589 LDICCKV	++	+-	++	++
10051	19590 VGVSPLW	++	+-	-	-
10052	19591 ALLAARS	++	+-	++	++

10053	19592 DAYSGRD	++	-	-	-
10054	19593 GQDGNAW	++	+	-	-
10055	19594 SSGTSLW	++	+-	-	+
10056	19595 SGASPLW	++	-	-	-
10057	19596 LLGVCDA	++	+-	+++	+++
10058	19597 FVDPRCT	++	+-	+++	+++
10059	19598 LASRDAA	++	+-	+++	++
10060	19599 TVHSLSD	++	+-	-	++
10061	19600 GLKVGAI	++	+-	++	+++
10062	19601 QSSPLVR	++	+-	-	-
10063	19602 VDDWSMY	++	+-	-	-
10064	19603 DALEWRD	++	+-	-	-
10065	19604 LSRAGFD	++	+-	-	-
10066	17603 LSALSVN	++	+-	-	-
10067	19605 IFAGPGP	++	+	-	-
10068	19606 AMESTQW	++	+	-	-
10069	19607 HNIGRDV	++	+-	++	++
10070	19608 RSETVYV	++	+-	-	-
10071	19609 DEGNFRS	++	+-	++	+++
10072	19610 SRCEKVV	++	+-	+++	++
10073	19611 RTGSFCI	++	+-	+++	++
10074	19612 CGRSGTH	++	+-	+++	++
10075	19613 GELTVKW	++	+-	+	++
10076	19614 YARNAPS	++	+-	-	+
10077	19615 VDDWSLY	++	+-	-	-
10078	19616 VTDYVTY	++	-	-	-
10079	19617 CTSGNEA	++	+-	++	-
10080	19618 NESTSSW	++	+-	-	-
10081	19619 CDSPCTA	++	+-	++	++
10082	19620 RMMSGDW	++	+	-	-
10083	19621 LHGGCCA	++	+-	+++	++
10084	19622 VVNPGHD	++	+-	+++	++
10085	19623 SHDSCQN	++	+-	+++	-

10086	19624 VPPELHA	++	+	-	-
10087	19625 LLHTGNW	++	+-	-	-
10088	19626 YNASGGN	++	+-	+++	+++
10089	19627 DMTSSVW	++	-	++	-
10090	19628 ISGQSGW	++	+	-	-
10091	19629 VCCGPRG	++	+-	++	+++
10092	19630 LYEFDHT	++	+-	++	-
10093	19631 LVNSVAR	++	+-	+++	++
10094	19632 LAASCCV	++	+-	-	++
10095	19633 QLPGNCG	++	+-	++	++
10096	19634 WHHGTNV	++	+-	++	++
10097	19635 LSKLSYD	++	+-	-	-
10098	19636 VHREDGV	++	+-	++	++
10099	19637 GMDSNSV	++	+-	+++	-
10100	19638 ELGSHTW	++	+-	+++	-
10101	19639 SHALAPG	++	+-	-	+++
10102	19640 RGESVSW	++	+-	++	-
10103	19641 RAIDSPM	++	+-	+++	++
10104	19642 GGSASTW	++	+-	-	-
10105	19643 RMDDSYA	++	+-	-	-
10106	19644 SFWGDLP	++	+-	-	-
10107	19645 DEWTLSP	++	+-	++	+++
10108	19646 SWTGQAA	++	+	-	-
10109	19647 VANAGWD	++	+	-	+
10110	19648 DLSSNSW	++	+	+++	-
10111	19649 VGYVGIG	++	+-	-	-
10112	19650 VPQSVHW	++	+-	++	-
10113	19651 MESQVRW	++	+-	-	-
10114	19652 DGSARLW	++	+	++	+
10115	19653 RALSGAG	++	+	-	-
10116	19654 KFDFNAV	++	+-	+++	+++
10117	19655 ANDYMSY	++	+-	-	-
10118	19656 PARGETW	++	+-	++	++

10119	19657 WLAASDK	++	+-	++	-
10120	19658 GSREVAW	++	+-	++	++
10121	19659 MLLESCG	++	+-	-	++
10122	19660 VAHEGIG	++	+	-	-
10123	19661 MERGGST	++	+-	++	++
10124	19662 YPNGNAG	++	+-	-	-
10125	19663 YLKNDPL	++	+-	-	-
10126	19664 DQSAHSW	++	+-	++	-
10127	19665 VSTRPYS	++	+-	++	++
10128	19666 REHTSNW	++	+-	-	-
10129	19667 GRGQTGE	++	+-	+++	++
10130	19668 SVRPSHE	++	+-	+++	++
10131	19669 FASSMCC	++	+-	-	-
10132	19670 PYSSIME	++	+-	++	++
10133	19671 GSEVSSW	++	+-	-	++
10134	19672 SEAGNTF	++	+-	++	++
10135	19673 GQSTSSW	++	-	-	-
10136	19674 CVVDVRC	++	+-	++	++
10137	19675 EPNGRGV	++	+-	++	-
10138	19676 YFMGVRE	++	+-	-	-
10139	19677 EGAETTP	++	+-	+++	+++
10140	19678 CGCVMSP	++	+-	+++	++
10141	19679 ITGFSTD	++	+-	++	++
10142	19680 ADGSQGA	++	+-	+++	++
10143	19681 YSANGPN	++	+-	-	-
10144	19682 VDQASRA	++	+-	++	++
10145	19683 SKFQRMD	++	+-	++	++
10146	19684 ISCGTCD	++	+-	+++	++
10147	19685 ITSTNGA	++	+-	-	-
10148	19686 TLGGNGC	++	+-	++	+++
10149	19687 DGSSSKW	++	+-	++	+
10150	19688 REGYSHW	++	+-	-	-
10151	19689 DRLPASH	++	+-	++	++

10152	19690 GLPDRTW	++	-	++	-
10153	19691 SGFSESN	++	+-	-	++
10154	19692 TVGVEWT	++	+-	+++	++
10155	19693 GGSTSGW	++	+-	+	-
10156	19694 GELCCVG	++	+-	++	++
10157	19695 PLASGSW	++	+	-	-
10158	19696 CKPSGVM	++	+-	++	+++
10159	13805 YARAGVN	++	+-	++	++
10160	19697 YVRSSDQ	++	+-	-	-
10161	19698 VMSVSSW	++	+-	-	-
10162	19699 SSDLASG	++	+-	+++	+++
10163	19700 GCCDKPM	++	+-	+++	++
10164	19701 ELEGFQY	++	-	-	-
10165	19702 LDYLPPE	++	+-	++	++
10166	19703 CQGLRLC	++	+-	++	++
10167	19704 RFDGTPP	++	+	-	-
10168	19705 GESSHNL	++	+-	+++	++
10169	19706 RSEFTEY	++	+-	-	-
10170	19707 APVSREW	++	+	++	-
10171	19708 GLPCCSA	++	+-	++	++
10172	19709 YGPSTCN	++	+-	++	++
10173	19710 IESREGI	++	+-	-	-
10174	19711 GHCGRDC	++	+-	+++	-
10175	19712 IGSPTGV	++	+-	++	+++
10176	19713 WWSAMPN	++	+-	-	-
10177	19714 HGDPMRW	++	+-	+++	-
10178	19715 CERRCVD	++	+-	++	-
10179	19716 FVLLGDG	++	+-	++	++
10180	19717 KCQGGCA	++	+-	+++	+++
10181	19718 ITSFNGV	++	-	-	-
10182	19719 ISGGGAG	++	+	-	-
10183	19720 VNNSCLT	++	+-	++	++
10184	19721 LDDYSMY	++	+	-	-

10185	19722 AGGTSLW	++	+-	-	++
10186	19723 LETCCTA	++	+-	++	+++
10187	19724 WYSNIKD	++	+-	-	+
10188	19725 SPSRTRP	++	+	-	-
10189	19726 WFSNIQA	++	+-	-	-
10190	19727 SGAYMRA	++	+-	++	++
10191	19728 RVTWVVG	++	+-	-	-
10192	19729 SADAVRW	++	+	-	-
10193	19730 SWARSVE	++	+-	+	+
10194	19731 GYAVSEC	++	+-	-	-
10195	19732 QDVKGKW	++	+-	++	++
10196	19733 CNQGGTV	++	+-	++	++
10197	19734 ACRHGGP	++	+-	++	++
10198	19735 NGRGGEW	++	+-	-	-
10199	17821 RGDDRGW	++	+	-	-
10200	19736 REGGHLN	++	+-	+++	++
10201	19737 QSSLTQD	++	+-	+++	++
10202	19738 IQSSSGI	++	+-	-	-
10203	19739 PYAVSPL	++	+-	-	-
10204	19740 SKDCCIG	++	+-	++	++
10205	19741 DHSAGSG	++	+-	-	++
10206	19742 CINLWVQ	++	+-	+++	++
10207	19743 GTVPPGS	++	+	-	-
10208	19744 KVQDAYP	++	+-	-	-
10209	19745 QFAYSRE	++	+-	++	++
10210	19746 SDGFRIS	++	+-	-	++
10211	19747 GSRAMYP	++	+-	++	++
10212	19748 YSLVSTK	++	+-	++	++
10213	19749 CAPSMEK	++	+-	+++	+++
10214	19750 GSGPCCA	++	+-	++	++
10215	19751 CLERSTL	++	+-	-	-
10216	19752 NGFDGSW	++	+-	-	-
10217	19753 PIDETCS	++	+-	++	-

10218	19754	WDVGTWN	++	+-	-	++
10219	19755	IMESATW	++	-	++	-
10220	19756	RDVVNGT	++	+-	+++	++
10221	19757	FGGNGLQ	++	+-	++	++
10222	19758	GGDGSAY	++	+	-	-
10223	19759	GGGFVAY	++	+	-	-
10224	19760	FAKCSVV	++	+-	+++	++
10225	19761	STDYVSW	++	+-	-	-
10226	19762	CGGACAS	++	+-	++	++
10227	19763	CQTSDRP	++	+-	+++	++
10228	19764	LCAPAKC	++	+-	++	+++
10229	19765	AYRPLSG	++	+-	++	-
10230	19766	WLKGLTD	++	+-	++	++
10231	19767	ELLSSHW	++	+	-	-
10232	19768	TMGQGVP	++	+-	+++	++
10233	19769	CAPAFRE	++	+-	++	++
10234	19770	DWHGLIA	++	+-	-	-
10235	19771	LMGSCCP	++	+-	+++	++
10236	19772	NGMTERW	++	+-	+++	-
10237	19773	SMCWLLV	++	+-	-	++
10238	19774	SIGVHRA	++	+-	-	-
10239	19775	DSSRAYP	++	+	-	++
10240	19776	LSRAAHD	++	+-	-	-
10241	19777	TGLATSC	++	+-	+++	-
10242	19778	NSDFKVF	++	+-	-	-
10243	19779	GWLKELH	++	+-	++	++
10244	19780	TSDYKTY	++	+-	-	++
10245	19781	TYDNVFR	++	+-	-	-
10246	19782	CIPCVPR	++	+-	+++	+++
10247	19783	HWDGSAA	++	-	-	-
10248	19784	TDGKCCM	++	+-	+++	-
10249	19785	CIDSCVR	++	+-	++	++
10250	19786	VPGYGAG	++	+-	+	-

10251	19787 PNTTHGG	++	+-	-	-
10252	19788 ASGQSAW	++	+	-	-
10253	19789 GRIAPHS	++	+-	++	-
10254	19790 CLPGNAC	++	+-	+++	++
10255	19791 DSLSGRN	++	+	-	-
10256	19792 CAGECRA	++	+-	+++	++
10257	19793 RDGAVSW	++	+-	++	+
10258	19794 YFAGQAE	++	+-	-	-
10259	19795 WEGGLSG	++	+-	++	++
10260	19796 VDASCSA	++	+-	++	++
10261	19797 HETKVPA	++	+-	++	++
10262	19798 KRDRLYG	++	+-	-	-
10263	19799 RETGVEW	++	+-	++	-
10264	19800 VPMRGAD	++	+-	++	++
10265	19801 LVSKVSC	++	+-	-	-
10266	19802 REPDVRY	++	+	-	-
10267	19803 LHRTSVD	++	+-	-	-
10268	19804 YWSDKMA	++	+-	-	-
10269	19805 MSRVSNN	++	+-	-	-
10270	19806 KENHVTW	++	+-	+	+
10271	19807 NLGSAHW	++	+-	++	-
10272	19808 GLTGCCG	++	+-	++	++
10273	19809 VPCGLVR	++	+-	++	+++
10274	19810 YFQGVAL	++	+-	-	-
10275	19811 SSSSSTW	++	+-	-	-
10276	19812 SVAKMTG	++	+-	++	++
10277	19813 YVRSALN	++	+-	-	-
10278	19814 HKWLDTD	++	+-	+++	++
10279	19815 TAGMPGA	++	+-	++	++
10280	19816 AYYLKDS	++	+-	+++	++
10281	19817 GGELRTW	++	-	-	-
10282	19818 LGHGTWD	++	+-	++	++
10283	19819 FPISGCG	++	+-	++	++

10284	19820 FSHVDNG	++	+-	++	++
10285	19821 ESSTHGV	++	+-	-	-
10286	19822 FVCVMLV	++	+-	++	++
10287	19823 YFEGKQS	++	+-	-	-
10288	19824 EWARSLM	++	+-	-	++
10289	19825 NDSTSKW	++	+	-	-
10290	19826 AADFVRY	++	-	-	-
10291	19827 LSGSCCA	++	+-	++	+++
10292	19828 LFSGEAP	++	-	-	-
10293	19829 RTADSFA	++	+-	-	-
10294	19830 YTKLNDN	++	+-	-	-
10295	19831 CELPCCE	++	+-	++	++
10296	19832 YIKSDVG	++	+-	-	-
10297	19833 NLLSLAH	++	+-	++	++
10298	19834 GSHDSHW	++	+-	++	++
10299	19835 GSAESCA	++	+-	+++	++
10300	19836 TINVAMA	++	+-	+++	+++
10301	12088 IGSTNGV	++	-	-	++
10302	19837 FWNGNSP	++	+-	-	-
10303	19838 AEISRSW	++	-	-	-
10304	19839 VTDGVRW	++	+-	-	-
10305	19840 YFSAVAA	++	+-	-	-
10306	19841 GEGTSHW	++	+-	-	-
10307	19842 VIDRSLS	++	+-	++	+++
10308	19843 INESSKD	++	+-	++	++
10309	19844 EMKAVHA	++	+-	-	-
10310	19845 SGGGSSW	++	+	+	-
10311	19846 RDEINHW	++	-	-	-
10312	19847 YVRTDMY	++	+-	-	+
10313	19848 CMSSPCS	++	+-	+++	++
10314	19849 WGSVCCA	++	+-	-	++
10315	19850 RDVEVFP	++	+-	-	-
10316	19851 VTFGNPL	++	+-	-	++

10317	19852 LCRNYLT	++	+-	+++	+++
10318	19853 PMGTALW	++	+	-	-
10319	19854 FFTHKMD	++	+-	++	++
10320	19855 VRVMSSE	++	+-	+++	++
10321	19856 GSHVSSW	++	+-	-	-
10322	19857 GASDSRW	++	+	++	++
10323	19858 GDGSSLW	++	+	-	-
10324	19859 FTRLHAD	++	+-	-	-
10325	19860 RDGNSAY	++	-	-	-
10326	19861 RLSTNGI	++	+-	-	-
10327	19862 SRSGSVV	++	+-	++	++
10328	19863 LHRLSEG	++	+-	+	-
10329	19864 TLADRGW	++	-	-	-
10330	19865 VGIASEA	++	+-	+++	+++
10331	19866 TAGMILG	++	+-	++	+++
10332	19867 PLYDGPR	++	+-	-	-
10333	19868 NDGSSSY	++	-	-	-
10334	19869 FTGTSGT	++	+-	++	++
10335	19870 DLSKAMW	++	+	++	+
10336	19871 LSVVCCA	++	+-	++	++
10337	19872 FDGNSAY	++	-	-	-
10338	19873 TMSSSAW	++	-	++	-
10339	19874 WPSGGQG	++	-	-	-
10340	19875 YSRGGPD	++	+-	-	-
10341	19876 PSRAEAD	++	+-	+++	+++
10342	19877 FEGQYKV	++	+-	+++	++
10343	19878 CLEVKIA	++	+-	++	++
10344	19879 ASSLIIL	++	+-	+++	++
10345	19880 CGGSCAA	++	+-	+++	++
10346	19881 WTKDAAW	++	+-	++	++
10347	19882 DRGFLQS	++	+-	++	++
10348	19883 ALTSQSW	++	-	++	-
10349	19884 HGSGMMI	++	+	+	-

10350	19885 WARSSSG	++	+-	++	++
10351	19886 VPTKGIG	++	-	-	-
10352	19887 TLLNSPN	++	+-	+++	++
10353	19888 LASRVTA	++	+-	+++	++
10354	19889 YARLGYD	++	+-	-	++
10355	19890 CGHSCVS	++	+-	++	++
10356	19891 VNKVCAD	++	+-	++	++
10357	19892 DGLSGSD	++	-	++	++
10358	19893 YFSGSVF	++	+-	-	-
10359	19894 MWSENHG	++	+-	++	++
10360	19895 VNVVPTL	++	+-	++	++
10361	19896 RTLTQGT	++	+-	++	-
10362	19897 VLGSSNW	++	+	-	+
10363	19898 SVVGYGS	++	+-	++	++
10364	19899 DLRGQAA	++	-	-	-
10365	19900 GDGSVRY	++	+-	-	-
10366	19901 AFQTSMM	++	+-	+++	++
10367	19902 DYGGRLL	++	+-	++	++
10368	19903 HPPLLVV	++	-	-	-
10369	19904 YFSNIPT	++	+-	-	-
10370	19905 RDPMTSY	++	+	-	-
10371	19906 VSEFTTY	++	-	-	-
10372	19907 WRNPDIV	++	+	-	++
10373	19908 MVMLQSA	++	+-	++	++
10374	19909 FGELREG	++	+-	++	++
10375	19910 DYESRVW	++	-	-	-
10376	19911 APNTVSW	++	-	-	-
10377	19912 REVAVSW	++	+	-	-
10378	19913 TVNNVYH	++	+-	+	-
10379	19914 VESVNGI	++	-	-	-
10380	19915 IATLGIG	++	+	-	-
10381	19916 GDVAGFS	++	+-	++	++
10382	19917 YSKLDPL	++	+-	-	-

10383	19918	STPSSPT	++	+-	++	-
10384	19919	GCCPMEA	++	+-	++	++
10385	19920	GSNLLPV	++	+-	+++	++
10386	19921	PGEVREW	++	-	-	-
10387	19922	FYTGVSA	++	+-	++	-
10388	19923	SDPLSRP	++	+-	++	++
10389	19924	LHRLQDD	++	-	-	-
10390	19925	GVDSVKW	++	-	-	+
10391	19926	SGSTSTW	++	+	-	-
10392	19927	KFDNSGS	++	+-	+++	++
10393	19928	YPSGGAG	++	+	-	-
10394	19929	CRCFRGI	++	+-	+++	++
10395	19930	DAGLAEV	++	+-	++	++
10396	19931	KFDNTGS	++	+-	++	++
10397	19932	CAPYLHE	++	+-	+++	+++
10398	19933	FAAYVST	++	+-	++	++
10399	19934	DVGLRPW	++	+-	+++	++
10400	19935	YYQGTVD	++	+-	-	-
10401	19936	GNRDAVE	++	+-	-	+++
10402	19937	CGGPCQS	++	+-	++	++
10403	19938	ASVAGVR	++	+-	+++	++
10404	19939	NVSHERG	++	+-	++	++
10405	19940	IKMTGRD	++	+-	++	+++
10406	19941	GGTDRTW	++	-	++	++
10407	19942	CSPMRDC	++	+-	++	++
10408	19943	DVYGGFA	++	+-	++	++
10409	19944	NMGDRVW	++	-	++	-
10410	19945	EGPSRGW	++	+-	++	++
10411	19946	GYGSPHS	++	+-	-	-
10412	19947	DCRAACK	++	+-	++	+++
10413	19948	LPPLYQV	++	+	-	-
10414	19949	ATAVPKT	++	+-	++	++
10415	19950	TPVKGAM	++	+-	-	++

10416	19951 SDGSSNW	++	+	-	-
10417	19952 GQVADGW	++	+-	++	++
10418	19953 GSGSSPW	++	+	-	-
10419	19954 LGHDYFP	++	+	+	-
10420	19955 LVGLKQL	++	+-	++	++
10421	19956 SKDWSGS	++	+-	+++	++
10422	19957 YVRYDTG	++	+-	-	-
10423	19958 EAHNPVY	++	+-	-	++
10424	19959 ISDERCC	++	+-	-	++
10425	19960 GVDYNTG	++	+-	+++	++
10426	19961 RDDSSSW	++	+	-	-
10427	19962 VHESVHW	++	+	-	-
10428	19963 VWADHSW	++	+-	-	+++
10429	19964 WKMGCAD	++	+-	++	++
10430	19965 TPQSPMF	++	-	-	-
10431	19966 PLSSNLW	++	+	++	-
10432	19967 NGDDQSM	++	+-	++	+++
10433	19968 GPPESMI	++	+-	-	-
10434	19969 VDREATA	++	+-	++	++
10435	19970 CCSPQKV	++	+-	++	++
10436	19971 TSSACCS	++	+-	+++	++
10437	19972 GWNSTLG	++	+	-	-
10438	19973 TNYGVGA	++	+	-	-
10439	19974 CGKQTCI	++	+-	++	++
10440	19975 GNEGSSL	++	+-	++	++
10441	19976 FDGTVPF	++	-	-	-
10442	19977 CGSSSNC	++	+-	+++	++
10443	19978 WLKDSTI	++	+-	++	++
10444	19979 GGGSSGW	++	-	-	-
10445	19980 RLEVGSW	++	+	-	-
10446	19981 APGHVGW	++	-	-	-
10447	19982 LHRAGID	++	+	-	-
10448	19983 QLYDAGV	++	+-	-	-

10449	19984 PMGANTW	++	-	++	-
10450	19985 LDAFSGW	++	-	++	-
10451	19986 YVRFEDP	++	+--	-	-
10452	19987 SVTCTLP	++	+-	++	++
10453	19988 KDSFTSW	++	+-	-	-
10454	19989 GGPATTG	++	+-	++	++
10455	11420 VYSSNGV	++	+-	-	-
10456	19990 TSGPSRL	++	+-	++	++
10457	19991 NRMDGDP	++	+-	+++	++
10458	19992 SNSTSGW	++	+-	-	-
10459	19993 NVHSEPC	++	+-	++	++
10460	19994 YAGEMIV	++	+-	+++	++
10461	19995 YWSGQGA	++	+-	-	-
10462	19996 PANGVVG	++	+-	++	++
10463	19997 LSAHTTP	++	+-	++	++
10464	19998 VSDYASY	++	-	-	-
10465	19999 DWTGVMA	++	+-	-	-
10466	20000 AYAPEVS	++	+-	++	++
10467	20001 YDPTLTN	++	+-	+++	++
10468	20002 LLTPACD	++	+-	++	-
10469	20003 IAHLGSG	++	+	-	+
10470	20004 SLDTVRW	++	+	-	+
10471	20005 WLIAEAD	++	+-	++	++
10472	20006 GMSNSSW	++	+-	++	++
10473	20007 GEDQVRW	++	+-	-	-
10474	20008 RPGGSAG	++	+-	-	-
10475	20009 ACSDCMV	++	+-	++	++
10476	20010 CGIGSCH	++	+-	++	++
10477	20011 VGSITQW	++	+-	++	++
10478	20012 GAHTSTW	++	+-	+	-
10479	20013 TVKGAAL	++	+-	++	++
10480	20014 QPESRSW	++	-	++	+
10481	20015 GASSSSW	++	+-	-	+

10482	20016 CGGCVGV	++	+-	++	+++
10483	20017 VVRCDGC	++	+-	++	++
10484	20018 MEGRCCS	++	+-	++	+++
10485	20019 LVGLKSL	++	+-	++	++
10486	20020 GDGVSLW	++	-	-	-
10487	20021 SVAPLCA	++	+-	+++	++
10488	20022 YSKLDAT	++	+-	-	-
10489	20023 VWDAMGV	++	+-	++	++
10490	20024 MPALDLG	++	+-	++	++
10491	20025 LWDGQSA	++	-	-	-
10492	20026 TAWLKQD	++	+-	++	++
10493	20027 HLASANW	++	-	++	++
10494	20028 YVRSSNE	++	+-	-	-
10495	20029 LSSSNGR	++	+-	-	-
10496	20030 AMADTTW	++	-	-	-
10497	20031 CGVMEKC	++	+-	++	+++
10498	20032 VSSTCTA	++	+-	++	++
10499	20033 ICASRLS	++	+-	++	++
10500	20034 SSQFVSY	++	+	-	-
10501	20035 SVSHEGG	++	+-	++	++
10502	20036 LWNGVSS	++	+-	++	-
10503	20037 FDSSNGR	++	-	-	-
10504	20038 TESSQGR	++	-	-	-
10505	20039 YFHGLPD	++	+-	-	-
10506	20040 VGSSSSW	++	+-	++	++
10507	20041 VVGCSPD	++	+-	+++	++
10508	20042 ASGNSSW	++	-	-	-
10509	20043 LKNGTPA	++	+-	++	-
10510	20044 MEGKGWD	++	-	-	-
10511	20045 HPPDYSA	++	-	-	-
10512	20046 ETRLGAG	++	+-	+++	+++
10513	20047 LTYDAGI	++	+-	-	-
10514	20048 LPSAYPF	++	+	-	-

10515	20049	GGPTSQW	++	+	-	-
10516	20050	ITGVSGN	++	+-	++	++
10517	20051	NCSIKPC	++	+-	+++	++
10518	20052	DRAPASA	++	+-	++	+++
10519	20053	VDRGSTI	++	+-	++	++
10520	20054	YVRTDKG	++	+-	++	+
10521	20055	GVDAGVR	++	+-	++	++
10522	20056	DQSPVKW	++	+-	-	-
10523	20057	PYAQSPM	++	+-	-	-
10524	20058	CQDGSGA	++	+-	-	++
10525	20059	KTDHVFP	++	-	-	-
10526	20060	GGDYSSF	++	+	-	-
10527	20061	VCRQSCE	++	+-	++	++
10528	20062	WSAITDN	++	+-	++	++
10529	20063	GGGSASW	++	+-	-	-
10530	20064	REDSRSW	++	+-	-	-
10531	20065	LATGDGP	++	-	-	-
10532	20066	VSHGSAG	++	+-	-	-
10533	20067	ASETSTW	++	-	-	-
10534	20068	IMLPGHG	++	+-	++	++
10535	20069	LSVAGRM	++	+-	+++	++
10536	20070	KWDSQGT	++	+-	++	++
10537	20071	GLDSRAA	++	+-	++	++
10538	20072	IMNSGVW	++	+-	++	-
10539	20073	FSAPNAF	++	+	-	-
10540	20074	GSGQHGA	++	+-	++	++
10541	20075	CNECPHP	++	+-	-	++
10542	20076	SFNPKCE	++	+-	++	++
10543	20077	SGVTDAR	++	+-	++	++
10544	20078	EVERRAP	++	+-	++	++
10545	20079	RGDSVHW	++	+-	-	-
10546	20080	YQPLLTV	++	+-	-	-
10547	20081	RPACTVC	++	+-	+++	++

10548	11360	GGSNSSW	++	+	-	-
10549	20082	GIHQEPH	++	+-	++	++
10550	20083	VADPSAA	++	+-	+++	++
10551	20084	GPSSSLW	++	+-	-	-
10552	20085	VAERGAG	++	+	-	-
10553	20086	TNESVYV	++	+-	-	-
10554	20087	TSPVAVN	++	+-	+++	++
10555	20088	VERCCVA	++	+-	++	++
10556	20089	CLDACNR	++	+-	++	++
10557	20090	NGARLPG	++	+-	-	-
10558	20091	DMSKSCV	++	+-	++	++
10559	20092	AMTGAST	++	+-	++	++
10560	20093	CLSCPKS	++	+-	++	++
10561	20094	GSNTSGW	++	+-	+	-
10562	20095	EPGSVRW	++	+	++	-
10563	20096	FYTGRSE	++	+-	+	-
10564	20097	GSDRSGS	++	+-	++	+++
10565	20098	GRGDSGW	++	+	-	-
10566	20099	WNSNADN	++	+-	++	++
10567	20100	SPSEVNS	++	+-	+++	++
10568	20101	LMDNVSH	++	+-	++	++
10569	20102	LSDGWRD	++	-	-	-
10570	20103	GLEGSKW	++	+-	-	-
10571	20104	DGAAIMS	++	+-	++	++
10572	20105	WTKSQEW	++	+-	++	++
10573	20106	RPESSQW	++	-	++	-
10574	20107	VEGRMWS	++	+-	-	++
10575	20108	IDGTSMW	++	-	-	-
10576	20109	VPHDREW	++	-	+++	-
10577	20110	GGSSSVW	++	+	++	-
10578	20111	RLPESTD	++	+-	++	++
10579	20112	LGDSNMV	++	+-	++	++
10580	20113	REEVGVW	++	+	-	-

10581	20114 DLDSYLD	++	+-	++	++
10582	20115 LAKGGYD	++	+-	-	-
10583	20116 LDGVSLY	++	-	-	-
10584	20117 REAQSGW	++	+-	-	-
10585	20118 GLSSASW	++	+-	+++	+
10586	20119 YFEGMFD	++	+-	-	-
10587	20120 GAPGDAK	++	+-	+++	++
10588	20121 CCGLKSG	++	+-	++	++
10589	20122 GGHVSSW	++	+-	-	-
10590	20123 NASTSSW	++	+	+	-
10591	20124 WSMTTDN	++	+-	+++	++
10592	20125 TQIAPDR	++	+-	+++	++
10593	20126 YLVMSSS	++	+-	++	++
10594	20127 REEAERG	++	+-	++	++
10595	20128 VGGTSLY	++	+	-	-
10596	20129 GVIQGCC	++	+-	++	++
10597	20130 YWSAMAE	++	+-	++	-
10598	20131 GSPSSGW	++	-	++	-
10599	20132 WSRLNSD	++	+-	-	-
10600	20133 YFHAMQS	++	+-	++	++
10601	20134 RSDTSSW	++	+	-	-
10602	20135 MSPMSQN	++	+-	++	++
10603	20136 ELLAATW	++	-	-	-
10604	20137 YSKSSPL	++	+-	++	-
10605	20138 EDRGLEG	++	+-	+++	++
10606	20139 RTPSEYP	++	+-	-	-
10607	20140 GRVDMYD	++	+-	++	++
10608	20141 CGRDYCP	++	+-	++	++
10609	20142 SGGSHTW	++	+-	++	-
10610	20143 DRCVQPC	++	+-	+++	++
10611	20144 CLSSPCS	++	+-	++	++
10612	20145 VPDTVRY	++	-	+	-
10613	20146 CKGSCEQ	++	+-	++	++

10614	20147 EWSAICK	++	+-	++	++
10615	20148 REMSVHW	++	+-	-	-
10616	20149 FLNGCCS	++	+-	++	++
10617	20150 SPWGDPS	++	+-	-	-
10618	20151 SEEAFPY	++	-	-	-
10619	20152 CFLSDCL	++	+-	++	++
10620	20153 GSLDSRW	++	+	-	-
10621	20154 YFSREIS	++	+-	-	-
10622	20155 VEPCCRM	++	+-	++	++
10623	20156 VGPVLCS	++	+-	++	++
10624	20157 AQSVGTW	++	+	+	+
10625	20158 LHKLSVG	++	+-	++	+
10626	20159 ARADLGS	++	+-	++	++
10627	20160 GSPSASW	++	-	-	-
10628	20161 VPGFGAG	++	-	-	-
10629	20162 GGAIREW	++	+	++	-
10630	20163 TAQSYTF	++	+	+	-
10631	20164 WLLKSDV	++	+-	++	++
10632	20165 GPPHVAW	++	+-	++	-
10633	20166 CSQVACP	++	+-	++	++
10634	20167 VRSGSAG	++	+-	-	-
10635	20168 CAITGCR	++	+-	++	++
10636	20169 VMTSAGW	++	+	++	-
10637	20170 INSSSVW	++	+-	++	+
10638	20171 CGSSCAA	++	+-	++	++
10639	20172 GLESREW	++	-	-	-
10640	20173 TWTGDGA	++	-	-	-
10641	20174 DWLEKGI	++	+-	++	++
10642	20175 PLMSGPI	++	+	-	-
10643	20176 WARGHDN	++	+-	++	++
10644	20177 CGSSTCS	++	+-	++	++
10645	20178 YANVAHN	++	+-	++	++
10646	20179 VASMYGI	++	+	+	++

10647	20180 GSAASAW	++	+	-	-
10648	20181 SDGESSW	++	+-	-	-
10649	20182 YWSGSIA	++	+-	-	-
10650	20183 IAGRGAG	++	+	-	-
10651	20184 RGTEVYP	++	+	-	-
10652	20185 SSGSSTW	++	+	-	-
10653	20186 DDGDSRW	++	-	-	-
10654	20187 DMNVGAW	++	+	-	+
10655	20188 REGGGSW	++	+	-	-
10656	20189 VSGGALA	++	+-	+++	++
10657	20190 VGVSGNG	++	+-	+++	++
10658	20191 GELCCET	++	+-	-	++
10659	20192 GGSGVSW	++	-	++	-
10660	20193 RSSVNGV	++	+	-	-
10661	20194 GVESSPQ	++	+-	++	++
10662	20195 RDSGSAW	++	+	-	-
10663	20196 SSGSSMW	++	+	-	-
10664	20197 RTVDLFP	++	+-	-	-
10665	20198 ASSGNLM	++	+-	++	++
10666	20199 YSSSNGL	++	+-	-	-
10667	20200 RENTPGW	++	-	-	-
10668	20201 ILSERAW	++	+	-	-
10669	20202 NERGGVV	++	+-	++	++
10670	20203 TDEWQSY	++	-	-	-
10671	20204 VAASSTW	++	+	-	-
10672	20205 IHRALHD	++	+-	+	+
10673	20206 CGVRCQD	++	+-	++	++
10674	20207 GVPGTMP	++	-	-	-
10675	20208 LYGGSIG	++	+-	++	++
10676	20209 DYSGRSA	++	+	-	-
10677	20210 SGLAYAM	++	+-	++	++
10678	20211 GHSCCTL	++	+-	++	++
10679	20212 CMPNCLV	++	+-	++	++

10680	20213 AGGGYIL	++	+-	++	++
10681	20214 NLRGSGA	++	+-	-	-
10682	20215 GYSACSH	++	+-	-	++
10683	20216 VLVDAYV	++	+-	-	-
10684	20217 FEADAYP	++	+-	-	-
10685	20218 NQLGDRL	++	+-	++	++
10686	20219 GEVMSLT	++	+-	++	++
10687	20220 WMAKVVE	++	+-	++	++
10688	20221 NKWGDPS	++	+-	++	-
10689	20222 GLIAPHS	++	-	-	-
10690	20223 RGIDEFP	++	+-	-	-
10691	20224 IGLTGDW	++	-	-	-
10692	20225 GGGQTSW	++	+-	++	++
10693	20226 PSSLMAS	++	+-	++	+
10694	20227 MTGLSIV	++	+-	++	++
10695	20228 GMSEVLW	++	+	-	-

T10

NT SEQ ID#	AA SEQ ID#	NT sequence	AA_sequence	hTFRC pH7.4	hTFRC_pH7.4 -	bead only control
10696	20229	ACGCAGGTTTCGTCTTATAAG	TQVSSYK	+--	+++	++
10697	20230	TGGAAGAGTGGGGGTGCGCTG	WKSGGAL	+--	+++	-
10698	20231	CAGAAGGGTCTGGGGATTGCG	QKGLGIA	+--	+++	-
10699	20232	TGGGCTTTGGCGACGATTCAT	WALATIH	+--	+++	-
10700	20233	TCTTTGATTGAGAAGCTTAGG	SLIEKLR	+--	+++	-
10701	20234	CTTACTTTGACGAATATTAAG	LTLTNIK	+--	+++	-
10702	20235	TATAAGCTGGGTCTTCTTGGG	YKLGLLG	+--	+++	-
10703	20236	TATAAGTCTTTGTCGGCTGCT	YKSLSAA	+--	+++	+
10704	20237	AGTGGGCTGAGTACGACTAAG	SGLSTTK	+--	+++	-
10705	20238	GCTAGTTTGACGTCTCAGCAT	ASLTSQH	+--	+++	-
10706	20239	AATTCTTTGGCGACGTTTAAG	NSLATFK	+--	+++	-
10707	20240	GGGAAGATGGGGGCTTTGTCG	GKMGALS	+--	+++	-
10708	20241	ACGCTGATGACGAAGGTGGGT	TLMTKVG	+--	+++	-
10709	20242	TCTACGATTGCTAGTCCTCAT	STIASPH	+--	+++	-
10710	20243	GCTAGTTTGTCTAGTCGTAGT	ASLSSRS	+--	+++	-
10711	20244	TCGAAGGGGTTGGGTGCGGTG	SKGLGAV	+--	+++	-
10712	20245	ACGAATGTTTCGAATGGTAAG	TNVSNGK	+--	+++	-
10713	20246	ATGATGACTATTTCGACTAAG	MMTISTK	+--	+++	-
10714	20247	CATTCTTTGTCTAGTTCTGGT	HSLSSSG	+--	+++	-
10715	20248	ACGACTACGTCTAGTCATGCT	TTTSSHA	+--	+++	-
10716	20249	CAGGCTATTAAGCTTATGCCG	QAIKLMP	+--	+++	-
10717	20250	GTGATTACGATTGGTTCGAAG	VITIGSK	+--	+++	-
10718	20251	GATGGGATGTCGATGAATAGG	DGMSMNR	+--	+++	-
10719	20252	AGTAAGCTTTCTCTGTCTGGT	SKLSLSG	+--	+++	-
10720	20253	ACGGTGCCGACGCAGACTAAG	TVPTQTK	+--	+++	-
10721	20254	AGTATTGGGCTTGTGAAGCCG	SIGLVKP	+--	+++	-
10722	20255	TGGTCGCTTGCGTCGACGGGT	WSLASTG	+--	+++	-
10723	20256	TTGAAGGGGTCGCATGCTGAT	LKGSHAD	+--	+++	-
10724	20257	TCTAAGGTTCCGCTGATGCCG	SKVPLMP	+--	+++	-
10725	20258	CTTTCGAAGATGCCGTTTGGG	LSKMPFG	+--	+++	-
10726	20259	CAGTGGTCTTCGAAGTTGTTT	QWSSKLF	+--	++	-

10727	20260	ATGTCGCTTAAGGGGGTTAAT	MSLKGVN	+--	++	-
10728	20261	ACGCTGGTGTCTAATACTAAG	TLVSNTK	+--	++	-
10729	20262	GTGGGGTGGAGTCGGCTGGATCTTACTACT	VGWSRLDLTT	+--	+++	+++
10730	20263	GGGGGTTTGGGTAATCTTCGTCATTGTGTG	GGLGNLRHCV	+--	+++	-
10731	20264	CTTGGGTATGTTAGTATTGGGGCTGCTTGT	LGYVSIGAAC	+--	+++	++
10732	20265	CGGGAGGCTGGTCGTATTGTGAGTCAGGAG	REAGRIVSQE	+--	+++	-
10733	20266	CTTCGGTATAGTAAGACTCAGGGGGAGTCT	LRYSKTQGES	+--	+++	++
10734	20267	AAGCCTTATGCGCTTAATGGTAGGGAGGTG	KPYALNGREV	+--	+++	+
10735	20268	TATTCTCTGACGGGTGGGTCTATTTGTCTT	YSLTGGSICL	+--	+++	-
10736	20269	CTGGGTCCGCCTCCTGCTATTGGGAAGTGT	LGPPPAIGKC	+--	+++	-
10737	20270	CTTGGTTTTACTAAGTCGTCTGGTTCGGAT	LGFTKSSGSD	+--	+++	+
10738	20271	TCGCCGTATGCTAGGAGTTCTGCGGGGGTG	SPYARSSAGV	+--	+++	+
10739	20272	TTGGGTTGGGCTTCGAATTCGGTGGCTTCT	LGWASNSVAS	+--	+++	+
10740	20273	TCGTCGATTAATGGTCCGCCGAAGTGGTCG	SSINGPPKWS	+--	+++	+
10741	20274	TTGGGGTTTGCTCGTACTGGTGCTGCGGAT	LGFARTGAAD	+--	+++	+
10742	20275	AAGACGATGAATGGGATGTCTAGGGCTATT	KTMNGMSRAI	+--	+++	+
10743	20276	AAGCCTCTTCATGCGTTGGGGTCTGTGTTG	KPLHALGSVL	+--	+++	+
10744	20277	TTTTGGCCTAATAGTAGTCTGCCTATTCGG	FWPNSSLPIR	+--	+++	-
10745	20278	CAGCGTTTTTCGGCTGCTTCTGTTTCGCCG	QRFSAASVSP	+--	+++	-
10746	20279	GGTAATATGCTGGCGAGGCAGAGTGCGTTT	GNMLARQSAF	+--	+++	-
10747	20280	CTGCGTTATTCGGTTGCGGGTTCTTCGGTT	LRYSVAGSSV	+--	+++	-
10748	20281	ATTGGGATGGTTCCTGCGACTGGGTTTTGT	IGMVPATGFC	+--	++	-
10749	20282	TCTGCTCTTTTGGGGGTTCCGAAGTGTACG	SALLGVPKCT	+--	+++	+
10750	20283	GATCCTCATAGGGTTCATCTGGGTTTGGGT	DPHRVHLGLG	+--	+++	-
10751	20284	GGGGTGTTGAAGAGTTTGACTTGGACGGGG	GVLKSLTWTG	+--	+++	-
10752	20285	ATTCCTTTTTCGCGGGTTAATCCGGATACG	IPFSRVNPDT	+--	+++	-
10753	20286	AATCTGATTGTGGGGTTTGATCCGATGGCG	NLIVGFDPMA	+--	+++	-
10754	20287	CTGCTTCCGAATTTGGTGGGTTCTAGGGCG	LLPNLVGSRA	+--	+++	-
10755	20288	GCTGGTGGGCATCCGGAGGGGTATGTTAAT	AGGHPEGYVN	+--	+++	-

T11

NT SEQ ID#	AA SEQ ID#	AA_sequence	hTFRC pH7.4	hTFRC_pH7.4 - bead only control	hTFRC-mApical	hTFRC-mApical - bead only control
10756	20289	YWTQRYA	++	--	+++	---	++
10757	20290	YWGQRAV	++	--	+++	---	++
10758	20291	YYSQQSR	++	--	+++	---	+
10759	20292	FWTQKGS	++	--	+++	---	++
10760	20293	YWSQRAF	++	--	+++	---	++
10761	20294	YFGQSCR	+++	---	+++	---	++
10762	20295	FMYQKGC	++	---	+++	---	++
10763	20296	ATRDLHR	++	--	+++	---	++
10764	20297	FMRQSSC	+++	--	+++	---	++
10765	20298	YWGQGRC	+++	---	+++	---	++
10766	20299	FWGQRTG	++	--	+++	---	++
10767	20300	FSHQRSL	++	--	+++	---	++
10768	20301	FTLQRCL	++	--	+++	---	++
10769	20302	YFAQHGF	++	--	+++	---	+
10770	20303	YFGQGRS	++	--	+++	---	++
10771	20304	RLFVKEA	+++	---	+++	---	++
10772	20305	FRSQQRT	++	---	+++	---	++
10773	20306	FLSQRCA	++	--	+++	---	+
10774	20307	FFKQVGK	++	--	+++	---	++
10775	20308	FGFQKSQ	+++	---	+++	---	+
10776	20309	FIAQQRR	++	--	+++	---	+
10777	20310	FSLQKRW	++	---	+++	---	+
10778	20311	FVGQRGC	++	--	+++	---	+
10779	20312	FRSQQFC	++	--	+++	---	+
10780	20313	FIHQRNQ	++	-	+++	---	+
10781	20314	FSAQRCA	++	--	+++	---	+
10782	20315	FLSQKCH	++	--	+++	---	+
10783	20316	FHSQGRS	+	-	+++	---	++
10784	20317	WYSQMKG	++	---	+++	---	+
10785	20318	CDGGVRM	++	--	+++	---	+
10786	20319	VGYKGVG	++	--	+++	---	-

10787	20320 FFKQVHC	++	-	+++	---	-
10788	20321 FAYQRAS	++	--	+++	---	+
10789	20322 FGAQKVY	++	-	+++	---	++
10790	20323 ACNDSAR	++	--	+++	---	+
10791	20324 YFLQKPC	+	-	+++	---	-
10792	20325 NCAHVSG	++	--	+++	---	-
10793	20326 ATKPALS	+	-	+++	--	-
10794	20327 QDPIKAR	++	--	++	--	-
10795	20328 LSNTKCV	+	-	++	--	-
10796	20329 GLKSLTP	+	-	++	--	-
10797	20330 RLVTNKLVQL	+++	---	+++	---	+++
10798	20331 RLAYMTDTLL	+++	---	+++	---	++
10799	20332 YRRMDMDRVV	+++	--	+++	---	++
10800	20333 LTGGQPRNRL	++	--	+++	---	++
10801	20334 WWMGSDNSGI	++	--	+++	---	++
10802	20335 VMGYLTEGCT	+++	---	+++	---	-
10803	20336 CPGDSQGSVG	+++	---	+++	---	++
10804	20337 SKTAREAFPF	++	--	+++	---	++
10805	20338 VREGFEGYGL	+++	---	+++	---	++
10806	20339 ENFDRTRPRS	++	-	+++	---	++
10807	20340 SYADAFCDRC	++	-	+++	---	-
10808	20341 TYSGDGDVAC	+++	--	+++	---	++
10809	20342 RLRVDMGSWA	+	-	+++	---	+
10810	20343 NYDSRSCSRC	++	--	+++	---	+
10811	20344 AFPNLVSSRF	++	--	+++	---	-
10812	20345 SYVSSSSTCI	+	-	+++	---	+
10813	20346 QYLSGRVGQC	++	--	+++	---	+
10814	20347 GISLNTRNHL	++	--	+++	---	+
10815	20348 LSNDSNWVNC	++	-	+++	---	-
10816	20349 REAWKRESGL	++	--	+++	---	++
10817	20350 STVSVDRPRV	++	--	+++	---	-
10818	20351 LMKTSYLESD	+	-	+++	---	+
10819	20352 SRSTASMVCC	+	--	+++	---	+

10820	20353 CPERSHSSVD	++	--	+++	---	++
10821	20354 FFPNHNKSAQ	+++	--	+++	---	+
10822	20355 MDRLDRFTAC	++	-	+++	---	-
10823	20356 ELFSQSRSGY	+	-	+++	---	+
10824	20357 MYHLNVPKGV	+	-	+++	---	+
10825	20358 LLPNGRGLVT	++	--	+++	---	-
10826	20359 YFPNKLVEVA	++	---	+++	---	-
10742	20275 KTMNGMSRAI	+++	---	+++	--	+

T12

NT SEQ ID#	AA SEQ ID#	AA sequence	hTFRC pH7.4	hTFRC pH5.5	Fc control pH7.4	Fc control pH5.5	bead only pH7.4	bead only pH5.5
10827	20360	YHKAMQN	+++	---	+	+	+	+
10828	20361	YPSGMRL	+++	---	-	-	-	-
10829	20362	YHKNMPN	+++	---	+	+	+	+
10830	20363	YPFPTEA	+++	---	-	-	-	-
10831	20364	VLGRPSY	+++	---	-	-	+	-
10832	20365	NAREGRN	+++	--	-	-	-	-
10833	20366	CRANCVP	+++	---	+	-	+	+
10834	20367	LHRSGID	+++	-	-	-	-	-
10835	20368	YFSGIQS	+++	---	-	-	-	-
10836	20369	MIRDAYP	+++	---	-	-	-	-
10837	20370	DHKGNIA	+++	-	-	-	-	-
10838	20371	HHKLQTL	+++	---	++	+-	++	++
10839	20372	KPASTSW	+++	-	-	-	-	-
10840	18126	VATHGAG	+++	-	-	-	-	-
10841	20373	YWSGIPE	+++	---	-	-	-	-
10842	20374	RSKADDH	+++	---	-	-	-	-
10843	11535	YAKGGSN	+++	---	-	-	-	-
10844	20375	FPYGQKM	+++	---	-	-	+	-
10845	20376	TDLTVYR	+++	--	-	-	-	-
10846	20377	DMSTRTW	+++	-	-	-	-	-
10847	20378	CKQGCMT	+++	---	-	-	-	+
10848	20379	LHKFAEN	+++	--	-	-	-	-
10849	20380	YVKSQVI	+++	---	-	-	-	-
10850	20381	CNQKCAA	+++	---	-	-	-	-
10851	20382	CNKLCTP	+++	---	+	-	-	-
10852	20383	SYDGTAA	+++	-	-	-	-	-
10853	20384	TFKHNPF	+++	---	-	+-	++	++
10854	11671	VKSSNGV	+++	-	+	-	-	-
10855	20385	RESPYKL	+++	---	-	+	+	+
10856	20386	CPRLGCA	+++	---	+	-	-	-
10857	20387	PHVRQTI	+++	---	++	+-	+	++

10858	20388	CKQTCMM	+++	---	+	-	-	-
10859	20389	RVNGDWP	+++	---	-	-	-	-
10860	20390	CDKKCTT	+++	---	+	-	+	+
10861	20391	CGQACKP	+++	---	-	-	-	-
10862	20392	YHASGPK	+++	---	+	+-	++	++
10863	20393	KEGPVWP	+++	--	-	-	-	-
10864	20394	HTRLSNG	+++	---	-	-	-	-
10865	20395	LLASSEW	+++	-	-	-	-	-
10866	20396	CTKTRDC	+++	---	-	-	-	-
10867	20397	CEGRHTC	+++	---	-	-	-	-
10868	20398	CNQRCAP	+++	---	-	-	+	-
10869	20399	CNVTRNC	+++	---	-	+	-	+
10870	20400	LRNGTNP	+++	-	-	-	-	-
10871	20401	CSGSQKC	+++	---	-	-	+	-
10872	20402	PCKTGGE	+++	---	-	+	+	-
10873	20403	EPVARSW	+++	-	-	-	-	-
10874	20404	VAYDAIV	+++	---	+	-	-	-
10875	20405	CRADCHP	+++	---	-	-	-	-
10876	20406	CALKNCP	+++	---	-	-	-	-
10877	20407	QDVRQTK	+++	--	+	+	+	-
10878	20408	CRGVTGC	+++	---	+	-	-	+
10879	20409	CEKVLKP	+++	---	-	-	-	+
10880	20410	YWHAKVE	+++	---	-	-	-	-
10881	20411	QFVRSEP	+++	---	-	-	-	-
10882	20412	DPVSPKW	+++	-	-	-	-	-
10883	20413	CRTTCHE	+++	---	-	-	-	-
10884	20414	CKSACHE	+++	---	-	-	-	-
10885	20415	NLRGQAA	++	-	-	-	-	-
10886	20416	CARNSTC	+++	---	-	-	-	-
10887	20417	VYHRTQE	+++	--	-	-	-	-
10888	20418	CKDGPML	+++	---	-	-	++	-
10889	20419	WYDGTGP	+++	-	-	-	-	-
10890	20420	IMSSSAW	+++	-	-	-	-	-

10891	20421	CKGQTMD	+++	---	-	-	+	+
10892	20422	YSKSGPG	+++	---	-	-	-	-
10893	20423	NMESRDW	+++	-	-	-	-	-
10894	20424	CRIGVCP	+++	---	-	-	-	-
10895	20425	RNDYNYP	+++	--	-	-	-	-
10896	20426	PCKNGMA	+++	---	-	+	+	-
10897	20427	CHKLNCA	++	--	-	-	-	-
10898	20428	CALQKCA	+++	--	-	-	-	-
10899	20429	AGDDCKK	+++	---	-	-	-	+
10900	20430	YNGGPMQ	++	-	-	-	-	-
10901	20431	PEDFHQL	+++	-	-	-	-	-
10902	20432	CANHTKP	+++	---	-	+	++	+
10903	20433	YKSDCCV	+++	---	-	-	+	-
10904	20434	FTKTNCN	+++	---	-	-	++	-
10905	20435	YTRTSPI	++	---	-	-	-	-
10906	20436	CIKNTAC	+++	---	-	-	-	+
10907	20437	MYMSGKG	++	--	-	-	-	-
10908	20438	PDHDKCK	+++	---	-	+-	-	++
10909	20439	RAEDYFP	+++	--	-	-	-	-
10910	20440	TKGGTYG	++	--	-	-	-	-
10911	20441	CMSTRCE	++	--	-	-	-	-
10912	20442	PGDTYPA	+++	-	-	-	-	+
10913	20443	CGKLCSH	+++	---	-	+	-	-
10914	20444	YHKASIG	++	---	+	+	+	+
10915	20445	TRNGMNA	+++	-	-	-	-	-
10916	20446	CRANSGC	+++	---	-	-	-	-
10917	20447	YKQGVMN	++	-	-	-	-	-
10918	20448	MKGGSAG	++	-	-	-	-	-
10919	20449	RDGMRGF	++	---	-	-	-	-
10920	20450	RMDTGKW	+++	---	-	+	-	+
10921	20451	HHRAQDN	++	---	-	-	-	-
10922	20452	CNAMKCA	+++	---	-	-	-	-
10923	20453	QLQSQQW	++	-	-	-	-	-

10924	20454	VLEDRSW	+++	-	-	-	-	-
10925	20455	YARGSAL	++	--	-	-	-	-
10926	20456	CTQKGCS	++	--	-	-	-	-
10927	20457	NEAASTW	++	-	-	-	-	-
10928	20458	WLVKTSG	++	--	-	-	-	-
10929	20459	CGSKVCN	++	--	-	-	-	-
10930	20460	CSKSCMV	+++	---	-	-	-	-
10931	20461	CSSVKCM	++	--	-	-	-	-
10932	20462	LWRTEPD	+++	---	-	-	-	-
10933	20463	CGQKCSH	+++	---	+++	+-	++	++
10934	20464	CADRCNS	+++	---	-	-	-	-
10935	20465	YSKSMPN	++	--	+	-	-	-
10936	20466	IMAHNNW	+++	-	-	-	-	-
10937	20467	CPKQLCI	++	--	-	-	-	-
10938	20468	CRLGECH	++	--	-	-	-	-
10939	20469	DLRASQW	++	-	-	-	-	-
10940	20470	CRDQCMQ	++	--	-	-	-	-
10941	20471	YAKSSPS	++	--	-	-	-	-
10942	20472	QSDYKYF	++	-	-	-	-	-
10943	20473	LSRSGRD	++	---	+	-	-	+
10944	20474	YHRLDAM	++	-	-	-	-	-
10945	20475	MRSGSGP	++	-	-	-	-	-
10946	20476	HPLASGW	++	-	-	-	-	-
10947	20477	GGTRGNT	++	-	++	+-	+	++
10948	20478	YAKSAQN	++	--	-	-	-	-
10949	20479	TVGSRTA	++	--	-	-	-	-
10950	20480	YQKNMMN	++	--	-	-	-	-
10951	20481	WKDWMPN	+	-	-	-	-	-

T13

AA SEQ ID#	x1	x2	cluster	AA SEQ ID#	x1	x2	cluster
18871	-1.5040674	9.260608	1	18345	-1.9674224	8.230603	14
19901	-1.4652944	9.280726	1	19706	-2.043258	8.165468	14
18945	-1.0071123	10.182563	1	17752	-2.2033098	8.248658	14
12369	-1.335853	10.1144	1	16717	-2.1945646	7.640453	14
19722	-1.4436473	9.478717	1	17034	-2.1386893	8.40278	14
19222	-0.9039905	10.208962	1	20151	-2.0440476	8.362124	14
16739	-1.5983717	9.883782	1	17323	-2.2128246	7.655347	14
20067	-1.2004334	9.486561	1	11488	-1.9604807	7.852649	14
12790	-1.5330182	9.392017	1	18067	-2.0311844	7.9712787	14
20042	-1.5298594	9.319116	1	19078	-1.9867796	7.946589	14
19788	-1.5172187	9.379949	1	17045	-1.9446357	7.935358	14
11046	-1.4889811	9.475804	1	17482	-1.9802485	8.005367	14
13123	-1.5108646	9.460582	1	20034	-2.2074726	8.29521	14
19404	-1.3429834	8.829806	1	19297	-1.9953605	8.017404	14
20397	-1.1248773	9.747052	1	19536	-2.050925	8.410452	14
19751	-1.0997044	9.594815	1	18729	-2.0125883	8.720517	14
17355	-0.7273681	9.381634	1	18513	-1.8921807	8.768615	14
19433	-0.88836503	9.77696	1	20203	-2.0543363	8.451597	14
16654	-0.7943721	9.1902275	1	18518	-1.9993392	8.469306	14
12806	-1.1740961	10.627397	1	15652	-1.7987221	8.484052	14
10953	-1.1414341	9.242888	1	17008	-1.8708593	7.766153	14
13306	-0.95933396	9.801519	1	17316	-2.1288328	8.568176	14
18404	-1.0036013	10.236528	1	13292	-2.120339	8.566795	14
16880	-0.5276279	9.794522	1	16720	-2.1867135	7.67281	14
19233	-1.531694	9.787312	1	12325	-2.027897	7.9185486	14
17152	-0.8985322	9.697006	1	19780	-1.913825	7.8919134	14
16909	-1.1356233	9.84225	1	11052	-2.053801	7.929951	14
11055	-0.95065534	9.855503	1	18262	-2.0126383	7.94015	14
17447	-1.6421102	9.684746	1	16936	-1.9481686	7.851837	14
17386	-1.2118869	10.320459	1	19017	-1.643909	7.6869206	14
19638	-1.3409088	10.365101	1	18800	-1.6690024	7.734354	14
13178	-0.53030807	9.462896	1	19615	-1.7942538	8.539319	14

18397	-1.072561	8.911764	1	19602	-1.8235279	8.469812	14
19877	-1.3811791	9.306022	1	18008	-2.1141362	8.639873	14
11694	-0.7112349	9.215611	1	11614	-2.031798	8.431084	14
19186	-1.441593	9.592261	1	18420	-1.940929	8.488102	14
19503	-1.197435	9.651763	1	18588	-2.1276908	8.150146	14
18109	-1.2211418	9.636052	1	18765	-2.0987258	7.9942822	14
20012	-1.0685692	9.636347	1	17068	-2.098228	8.134709	14
12652	-1.1853237	9.642609	1	19392	-1.9075357	7.7176695	14
18508	-0.99039465	9.68726	1	18183	-1.8450211	7.7751884	14
19857	-0.80388075	9.174371	1	18270	-1.905325	7.705995	14
17211	-1.0338644	9.36191	1	19998	-2.08269	8.007879	14
17793	-1.0041766	9.628414	1	17657	-2.151188	8.225833	14
19247	-1.0829904	10.200003	1	18713	-2.1280854	8.224339	14
18354	-0.9757796	9.307833	1	19906	-2.0397062	8.148809	14
18703	-1.468889	9.725087	1	18026	-2.0844834	8.67731	14
19858	-1.5799067	9.789055	1	16468	-1.9768444	8.127	14
20020	-1.5880264	9.639354	1	16783	-2.0881813	8.350878	14
15870	-1.5009108	9.745789	1	18234	-1.9492162	8.789645	14
13201	-1.0281043	9.296199	1	19616	-1.6989866	7.7822695	14
12966	-1.0999678	9.292825	1	18050	-2.0929506	8.015531	14
19091	-1.3435975	9.67857	1	15458	-2.057283	8.473807	14
19841	-1.2674099	9.60175	1	19281	-1.8965087	7.7209697	14
11936	-1.3902406	9.816471	1	17158	-2.0076475	7.956822	14
19283	-1.0789915	9.139485	1	19014	1.734231	8.765608	15
20219	-1.248792	9.748192	1	19769	2.3024044	9.198804	15
19377	-0.818587	9.053035	1	13587	2.5052943	9.2396755	15
14683	-0.7315908	10.024561	1	19220	2.1271138	9.243859	15
17991	-0.7970092	9.622279	1	19749	2.3218088	9.222478	15
17671	-0.9271305	9.689604	1	19932	2.2738638	9.234676	15
19330	-0.9828658	9.443612	1	17227	2.5644307	9.243738	15
17594	-1.0861806	10.200731	1	19134	1.8555272	8.688712	15
18000	-1.105294	10.187686	1	17246	1.5187037	8.646497	15
17994	-1.095255	10.266747	1	15459	2.3984098	9.166327	15

19216	-1.1103468	10.243352	1	17083	2.229248	9.190393	15
18263	-0.7870467	9.375147	1	17872	1.6790346	9.0888195	15
17789	-1.4316287	10.1243105	1	18296	1.4838048	8.838473	15
18756	-1.3554463	9.986389	1	18978	1.9780729	8.76785	15
19453	-1.4642035	10.13844	1	13081	2.1918402	8.739106	15
20225	-1.2453173	10.178403	1	15525	2.3032985	9.173844	15
20063	-1.2968583	10.316689	1	13277	2.0355096	8.796229	15
19035	-1.4070174	10.181066	1	12830	1.9512136	8.739381	15
19979	-1.4334301	10.030337	1	13388	1.9571353	8.883712	15
18779	-1.4623932	9.954353	1	17909	2.3746295	8.9484415	15
11877	-1.3467448	9.745167	1	19958	2.0310082	9.308786	15
19213	-1.3083149	9.651585	1	13184	2.08462	9.023709	15
20122	-0.6797438	9.358391	1	15893	2.2879493	9.112733	15
18874	-1.0555747	10.0563755	1	12979	2.024685	9.225463	15
19053	-1.1541159	10.225372	1	13241	2.3046641	8.732862	15
19989	-0.92024356	10.224399	1	17906	2.171116	9.079272	15
20049	-0.61033165	9.25136	1	12989	2.0723746	9.252208	15
19642	-0.9917689	10.180342	1	13325	2.2288232	8.742942	15
12608	-0.8642088	10.196906	1	13249	2.2927618	8.643935	15
11360	-0.5479326	9.719574	1	19390	2.1755722	8.818337	15
19693	-0.75861096	9.656664	1	19348	1.9910423	9.34338	15
19567	-0.6905144	9.688696	1	19201	1.8303405	9.06804	15
18250	-0.992472	9.713796	1	14876	2.0363724	8.522484	15
18297	-1.3062059	9.624273	1	13474	1.9698807	9.124747	15
18748	-0.7556008	9.337972	1	14769	1.9835116	9.304692	15
19139	-0.96796286	8.918296	1	17101	1.989401	9.270936	15
13094	-1.4394412	9.615202	1	17940	2.1810422	8.8556795	15
15599	-0.98624396	9.179483	1	17945	2.4050999	9.372853	15
13278	-0.6330919	9.422036	1	11069	2.4715984	9.168531	15
16855	-0.743827	10.09929	1	19757	1.4081563	8.77466	15
17010	-1.2865216	9.976846	1	17772	1.680887	8.783354	15
20103	-0.65712744	9.212941	1	18407	2.3497186	8.91059	15
18618	-1.4330053	10.209608	1	19132	1.7205753	8.768107	15

17507	-1.3542047	10.324128	1	17117	2.4358354	8.45338	15
13078	-1.3826063	10.368233	1	18926	2.0451622	8.872824	15
16730	-1.4021919	10.306361	1	14546	2.287205	8.709444	15
19464	-1.4015007	10.202563	1	18842	1.7359056	8.88028	15
18059	-0.92009735	9.01043	1	17592	1.8023292	8.803364	15
18088	-1.4197323	9.963897	1	18318	1.4696462	8.544106	15
15429	-0.90911174	8.8617	1	18498	2.4116635	8.470209	15
11138	-1.31692	9.898731	1	19064	1.4780998	8.472884	15
13097	-0.84103686	9.35232	1	11299	2.193094	8.423412	15
18570	-1.4464046	10.018371	1	15483	2.0086353	8.296512	15
13168	-0.79752177	9.841495	1	17943	1.9577551	8.794232	15
15340	-0.76634943	9.374282	1	17112	2.2709963	8.682858	15
15013	-0.71400905	9.544544	1	19130	2.371998	9.078937	15
19025	-1.0038197	9.301082	1	19519	2.390279	8.456704	15
16645	-1.4476148	9.749507	1	15732	1.50481	8.601558	15
19968	-0.6447756	9.151421	1	17132	1.8197805	9.055893	15
12719	-1.1205372	10.385045	1	17925	1.9282631	8.463268	15
12155	-1.5085055	9.639644	1	18833	1.9120533	8.497885	15
18419	-1.4641643	9.666325	1	18963	1.8362485	9.037024	15
12638	-1.4662535	9.955935	1	18928	1.7734423	8.201725	15
16897	-1.4062605	9.600162	1	19764	1.811155	8.273282	15
19673	-0.6358378	9.895993	1	17659	1.8153406	8.26118	15
20098	-1.3595966	9.400612	1	17197	1.8406558	8.300882	15
16787	-0.6061316	9.618956	1	16629	1.8496933	8.263032	15
16711	-1.0123583	10.139913	1	17289	1.8139895	8.251944	15
20180	-1.0241854	9.6464615	1	17404	2.0262134	8.537834	15
19835	-1.0054444	9.46256	1	11076	2.3349483	9.233987	15
18182	-0.9932115	9.465926	1	18467	2.4704866	9.154662	15
13189	-0.6502984	9.742302	1	13057	2.4735286	9.162426	15
18700	-1.054299	9.47341	1	16616	1.8257968	8.253043	15
18880	-1.0498148	9.544278	1	12953	1.8474162	9.385885	15
19101	-0.984851	9.289439	1	15402	2.3561666	9.214623	15
20097	-1.0064024	9.130419	1	19288	1.9815257	8.802681	15

19371	-0.8753917	9.301174	1	20218	2.3387125	8.863569	15
18108	-1.1700451	9.31496	1	17173	2.1114376	8.872643	15
18892	-0.809664	9.221372	1	15226	2.1321988	8.851612	15
18749	-0.8949308	9.344297	1	16549	2.1531348	8.882259	15
17875	-0.8940409	9.439191	1	13215	2.1748912	9.258037	15
11767	-0.8997314	9.34655	1	18222	1.9813298	9.243784	15
19671	-0.8697484	9.360092	1	19939	1.9402695	9.1116905	15
19393	-0.85127836	9.150213	1	18285	1.6727314	8.738277	15
18744	-1.4503586	9.633175	1	17259	1.9546418	8.241668	15
18374	-1.2661644	9.383732	1	17126	1.9511383	8.2711315	15
18574	-1.3843403	9.428971	1	17693	1.9984484	8.771316	15
17742	-1.4865893	9.858822	1	15537	2.2876089	8.400138	15
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18290	-1.1406727	9.516527	1	17069	1.5581607	8.596115	15
18661	-1.347417	9.725381	1	17484	1.8505805	8.710791	15
20074	-1.5052408	9.359559	1	17286	2.0091078	8.295755	15
19552	-1.5078936	9.4636135	1	13339	1.9986376	8.762054	15
19110	-1.4049752	9.85228	1	16905	1.8589201	8.689873	15
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18686	-1.2628797	9.707592	1	13049	2.2331767	8.285898	15
19140	-1.4445289	9.63944	1	19141	2.0331197	8.302317	15
19834	-1.3016715	9.40162	1	19668	2.0107381	8.291707	15
19856	-0.8030316	9.385617	1	17559	2.0601242	8.516593	15
18844	-0.9306651	9.323988	1	20035	1.8746089	9.113204	15
20153	-1.1020089	9.315059	1	18275	1.5478103	8.692791	15
18408	-1.146081	10.20642	1	18338	1.9135762	9.2813	15
18569	-0.7311319	9.713192	1	19097	1.840643	8.439528	15
13475	-1.0387044	9.269871	1	15547	2.293458	8.7267	15
20094	-1.0088438	9.527039	1	15696	2.3189976	8.68702	15
18579	-0.6963212	9.241797	1	20061	1.8807724	8.268958	15
17656	-0.67420864	9.196511	1	11881	2.158574	8.662158	15
20160	-0.8344375	9.750755	1	18341	2.3885934	8.449223	15
20131	-0.89305186	9.673025	1	13051	2.206123	9.2573395	15

18531	-0.7968913	9.720495	1	16470	2.3004787	8.744662	15
18246	-0.78155434	9.367262	1	15877	2.6520193	8.648748	15
13172	-0.5113147	9.676768	1	18118	2.6752868	8.705704	15
18763	-0.7099723	9.736685	1	12804	1.9366416	8.871159	15
15985	-0.72448164	9.600382	1	19851	1.6304734	8.972695	15
17768	-0.73901725	9.767471	1	17335	1.9012936	8.242167	15
19069	-0.72959375	9.696407	1	17953	2.4162922	8.780088	15
16712	-0.96898305	9.3128805	1	19754	2.3929992	8.446468	15
18746	-0.91008353	9.171163	1	18922	1.6498578	8.730952	15
18196	-1.4616271	10.098661	1	18791	2.3191197	8.757659	15
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12068	-1.446458	10.143505	1	17825	2.0758116	8.827597	15
18530	-0.9338669	9.444691	1	15392	1.7039299	8.724252	15
18775	-0.96042424	9.352186	1	16400	2.1205585	8.874077	15
20194	-1.1011361	10.178893	1	18194	4.136164	7.086744	16
18399	-0.84327227	9.355605	1	17271	3.3064766	5.929166	16
18785	-0.9808733	9.538026	1	20009	3.3826046	5.822897	16
18992	-0.9688011	10.204227	1	19001	3.6512442	5.841743	16
18948	-1.0208119	9.099187	1	17542	3.3905165	5.194128	16
17758	-1.4271301	10.2358055	1	16951	3.5642443	5.9050083	16
19972	-0.913191	10.230489	1	18327	3.5249872	5.8081255	16
19286	-0.8287065	9.050574	1	17340	3.4372945	5.9443665	16
12711	-0.9811341	9.827695	1	16743	3.5575354	5.951605	16
19397	-1.369748	9.477226	1	15637	3.1047633	5.255052	16
18614	-1.7262467	9.68692	1	18755	3.5637732	6.0042276	16
11062	-1.1555072	9.532689	1	17531	3.4042468	6.011397	16
18143	-1.0183033	9.315758	1	20000	4.1434093	6.107776	16
12506	-0.9557481	9.765692	1	18669	4.1154733	5.930002	16
16840	-1.6492968	9.920186	1	19765	3.4344952	6.144236	16
18167	-1.7686411	9.669232	1	18022	3.5309162	6.040004	16
14161	-1.7150705	9.558692	1	16962	3.5486894	5.965439	16
20108	-1.4393089	9.303649	1	16686	3.508035	5.9666495	16
19448	-1.410852	10.040446	1	16852	3.6435227	6.748875	16

19460	-1.3485538	10.083181	1	16865	3.5324268	6.799692	16
19843	-1.009048	10.0977745	1	19816	3.5474892	6.0334115	16
19959	-1.039817	9.005514	1	18617	3.5545511	5.969778	16
17460	-1.1133968	9.676013	1	19782	3.0033278	4.9886093	16
11968	-1.1649939	9.72887	1	19492	3.5135515	5.9073443	16
17142	-1.1111706	9.762532	1	19183	4.391472	7.2426353	16
19628	-1.4645063	9.407286	1	13105	3.9013338	7.05706	16
11726	-1.6096536	9.470341	1	17228	3.9584768	6.9228563	16
12021	-1.569194	9.415508	1	19135	3.5750604	5.974138	16
12208	-1.6757042	9.509544	1	18208	4.27692	5.8645163	16
12820	-1.5804596	9.8989105	1	18865	3.2587328	5.358147	16
12404	-1.2974898	9.387073	1	18031	3.2179449	5.4824915	16
19405	-1.2191144	9.584288	1	16866	4.04417	7.1142945	16
16354	-0.8517059	9.297984	1	15753	3.3757179	6.5067673	16
16724	-0.5964289	9.667214	1	18808	3.2046545	6.4029126	16
19498	-1.5490184	9.841381	1	11039	3.9494374	7.094804	16
17791	-1.062659	9.71732	1	15030	3.8111093	7.153827	16
13403	-0.79686624	9.960718	1	19903	4.1369176	7.388715	16
19985	-1.2745973	9.498573	1	19318	3.39745	5.493094	16
13467	-1.388979	9.309333	1	17834	4.0920253	7.3633685	16
19571	-1.1293919	10.297757	1	17290	3.3479002	6.47383	16
17645	-0.94206595	10.271487	1	17193	3.661883	6.8417625	16
14523	-1.1195652	9.648	1	16704	3.820519	6.3557363	16
18336	-1.6092077	9.552169	1	16890	3.812877	6.3964496	16
12303	-1.4777895	9.989484	1	19426	4.2037487	7.1678195	16
12275	-1.0390475	9.245772	1	16737	3.533148	6.259235	16
11427	-1.1678699	9.555123	1	19121	3.5597064	5.977785	16
11387	-1.1834544	9.650065	1	19948	4.1107354	7.361942	16
12948	-1.1662233	9.520729	1	17425	3.566471	6.0311184	16
12467	-1.0751485	9.780305	1	16722	3.5623946	6.0253215	16
18655	-1.3826503	10.292325	1	19659	3.9770198	7.735111	16
11029	-1.5325016	9.302261	1	19280	3.729803	7.1064353	16
12738	-1.298126	9.046022	1	19123	3.2409077	6.488755	16

19416	-1.4427654	9.118909	1	19572	3.9166887	7.6707706	16
19825	-0.63533115	10.020404	1	17295	3.5388157	6.064029	16
13295	-1.1700546	10.4006405	1	15793	4.220113	7.0782685	16
10988	-1.17875	10.43699	1	16991	3.4118686	6.033279	16
19807	-1.2908835	10.561429	1	17257	3.105671	5.7861667	16
12598	-1.3820565	10.376104	1	20221	3.0856564	4.926487	16
18635	-1.3838806	10.348259	1	15813	4.003331	7.5290337	16
11700	-1.3433837	9.311557	1	17375	4.2211018	6.775743	16
13272	-1.553153	9.951594	1	19996	3.0641804	5.73288	16
13313	-1.2753453	10.443003	1	18586	3.061264	5.0579076	16
11994	-0.7392768	9.954733	1	16969	3.552564	5.9527626	16
12271	-1.3174514	8.992697	1	18080	3.975642	6.9220085	16
19656	-0.90072215	9.712777	1	16794	3.4505277	6.1106014	16
18952	-1.0154691	10.309762	1	16853	3.3925264	6.2458925	16
18888	-1.286045	9.67096	1	16827	3.3968647	6.219494	16
19984	-1.3880767	10.129288	1	16749	3.5403328	5.955948	16
19853	-1.3590882	10.172766	1	16675	3.4728804	6.084666	16
19428	-1.0934932	10.3254595	1	16870	3.398402	6.4486337	16
16738	-0.5295076	9.875446	1	18738	4.0136666	5.9523797	16
17978	-1.0707413	10.283505	1	16419	4.088929	6.0542636	16
19054	-1.4215456	10.066782	1	18219	4.0572805	5.9489527	16
18935	-1.193514	9.640049	1	18415	3.5678294	5.439691	16
19041	-1.7679342	9.674271	1	18664	3.573821	5.374885	16
15621	-1.8156787	9.360327	1	17006	3.545507	5.933924	16
11444	-1.7704743	9.488913	1	15378	3.7326677	7.0323815	16
17480	-1.5798624	9.618698	1	17019	3.591262	5.453381	16
11582	-1.3734884	9.5975685	1	20076	3.6121423	6.4557414	16
12615	-1.2188401	10.362678	1	17385	3.2701507	6.513987	16
17089	-1.5681074	9.741631	1	20100	3.0397687	5.036663	16
17440	-1.1873462	9.495579	1	20150	3.0363905	4.9825463	16
18102	-1.0245376	8.951454	1	19812	4.1874967	6.7003274	16
17913	-0.92049986	8.951754	1	17232	3.5475926	6.072033	16
20195	-0.95805407	8.931549	1	16898	3.6429532	6.1044726	16

18947	-0.7194354	9.11903	1	16918	3.5582502	5.997398	16
17064	-1.2341754	9.586021	1	16801	3.5719922	5.9747615	16
17433	-0.9382009	9.3620615	1	16674	3.569062	5.9758677	16
15432	-0.701493	9.192388	1	16684	3.5732148	6.0066595	16
16269	-0.8206889	9.276505	1	16814	3.6487741	6.7466736	16
12314	-0.70805866	9.118023	1	17098	3.6998749	6.384316	16
19430	-1.0759175	10.055936	1	16942	3.651021	6.7560315	16
18053	-0.5996093	9.147675	1	19887	4.121654	7.6915646	16
18706	-1.3893363	9.062121	1	17331	3.6752925	6.736765	16
20181	-1.6471276	9.49496	1	18987	3.763315	6.9516697	16
18409	-1.7610689	9.674792	1	15468	4.0942154	7.369771	16
11897	-1.7198005	9.695752	1	18357	3.254595	5.9103394	16
19951	-1.6794969	9.8420315	1	16343	3.0675442	5.972406	16
17795	-1.7866249	9.674915	1	16850	3.5449252	6.0113487	16
19538	-1.7770827	9.632797	1	16808	3.5743015	5.9739494	16
16888	-1.6343515	9.938336	1	16910	3.5694315	5.9798245	16
11297	-1.7147747	9.490153	1	17391	3.5692246	6.0288625	16
18274	-1.6551131	9.726205	1	19522	3.1471267	5.417726	16
18078	-0.9428958	9.851952	1	16817	3.8477356	6.3494687	16
19845	-0.6726084	9.457465	1	16824	3.831895	6.304422	16
20142	-1.1807923	10.323196	1	19334	3.6148777	6.1198196	16
19463	-1.4163026	9.539759	1	17278	3.6072235	6.201313	16
18546	-0.6433871	9.532856	1	16875	3.7964568	6.3184023	16
19574	-0.9543352	9.794194	1	19855	3.5351908	6.884494	16
19926	-0.7575761	9.953775	1	16532	3.5132198	5.183154	16
19437	-1.4745635	9.021818	1	16706	3.5360534	6.8587885	16
12835	-1.5144469	9.863802	1	15142	3.556441	6.409785	16
19554	-1.5595798	9.844	1	16832	3.751045	6.2852283	16
17457	-1.110359	9.8439045	1	16796	3.7933962	6.2857637	16
12263	-1.2088625	10.06559	1	16935	3.7530048	6.2669625	16
12856	-0.8616122	9.951337	1	16975	3.8176155	6.379231	16
11754	-1.1570221	10.164856	1	16715	3.580914	6.138145	16
13266	-0.7860983	9.798684	1	16755	3.5974588	6.111431	16

16779	-1.6283436	9.886175	1	16804	3.5628607	6.1501307	16
19992	-0.7950235	9.934976	1	16872	3.600128	6.3954144	16
13245	-1.6183572	9.86081	1	17052	3.560267	6.4668097	16
15817	-0.95789796	9.379237	1	16940	3.5757184	6.4919076	16
12760	-1.5118119	9.772163	1	19042	3.3182256	5.2724457	16
19086	-1.5624291	9.597774	1	17510	3.0751815	5.208843	16
16304	-1.5699136	9.755579	1	17891	3.0654173	5.2160816	16
20196	-1.6033407	9.667506	1	18085	3.1013768	5.869165	16
12140	-1.5621543	9.681684	1	17724	3.3267171	5.255379	16
20185	-1.5879256	9.805768	1	16965	2.9678137	5.189437	16
19594	-1.515991	9.543219	1	20481	4.0162883	7.473255	16
17240	-1.5630257	9.61743	1	18468	3.9819677	7.561052	16
17477	-0.5956823	9.674165	1	20005	3.305377	5.1327076	16
12927	-1.6110305	9.906056	1	20164	3.7061548	7.2065835	16
10954	-1.7544221	9.711572	1	20458	3.5172174	7.0926876	16
19918	-0.83475304	9.810368	1	19293	3.3134165	5.260534	16
19050	-1.7198492	9.735072	1	16563	3.0248291	5.036127	16
18455	-1.3986667	9.382194	1	12456	3.5922153	5.320398	16
11824	-1.4636593	9.215431	1	17632	3.3087456	5.217192	16
18803	-1.4657056	9.203512	1	15760	3.3920252	5.217033	16
12851	-1.3938932	9.343265	1	13382	3.364459	5.1587796	16
12212	-1.3773289	9.586456	1	16913	3.3797889	6.08239	16
13107	-1.3967501	9.663159	1	15740	3.9015965	7.5142975	16
18391	-1.0900999	9.717404	1	19713	4.1289988	7.5018625	16
13790	-1.1001948	9.743641	1	19180	3.2177896	5.6307006	16
17279	-1.1187274	10.211206	1	16668	3.1659074	5.732517	16
17226	-1.4696372	9.68563	1	16566	3.2623086	5.301496	16
11839	-1.5131519	9.671156	1	18673	3.2405248	5.5445647	16
13023	-0.5778663	9.671448	1	16666	3.141878	5.7810698	16
16901	-1.5098139	9.735354	1	20126	4.1979356	7.629175	16
18121	-1.3553042	9.345275	1	20080	4.201936	7.426801	16
17134	-1.3801923	9.619538	1	15101	3.186607	5.673	16
17337	-1.1048297	10.227515	1	16651	3.3077445	5.538301	16

18894	-1.4157085	9.772716	1	17506	3.3825552	6.086685	16
18412	-1.481836	8.928646	1	19525	3.2516618	5.579892	16
16750	-0.55938524	9.694772	1	17414	3.257294	5.6169953	16
15190	-0.6355166	9.827175	1	16202	3.228436	5.609283	16
13412	-0.8775203	9.781523	1	18367	0.853367	10.5383415	17
18515	-0.9055538	9.856007	1	19100	0.27353504	10.8992	17
18517	-1.0765835	9.768564	1	17871	0.7567495	10.700797	17
16876	-1.5411074	9.931356	1	19136	0.806426	11.142295	17
16844	-1.476514	9.235174	1	17678	0.7502015	10.543492	17
15546	-0.8650082	8.844919	1	17756	0.273491	10.665464	17
15903	-1.5867041	9.656951	1	19707	0.5673511	10.735154	17
18815	3.5109165	7.957101	2	17206	1.3400576	10.489095	17
18901	2.8700128	7.300516	2	11007	0.4012439	10.819756	17
13324	3.2404957	8.822179	2	19223	0.18277657	10.797715	17
15578	3.1972194	8.786076	2	18144	0.88684076	10.7368355	17
18362	3.0530138	7.699257	2	19652	0.29354104	10.726946	17
17070	3.7943757	8.100199	2	17882	0.24643265	10.828633	17
17146	2.7044544	7.759195	2	18284	0.8076557	10.759564	17
15608	3.8153386	8.058479	2	17493	0.8098187	10.742456	17
19819	2.881994	7.693784	2	18593	0.94490045	10.946223	17
18709	2.690416	7.3136363	2	16593	0.19517526	10.822995	17
18472	2.9171717	7.342686	2	20377	0.16675094	10.7656355	17
18163	3.5904248	8.378881	2	17708	0.28667632	10.881749	17
16372	3.0493667	7.3157325	2	18173	0.35105148	10.795156	17
19106	3.28865	7.9487457	2	19516	0.1437299	11.031145	17
17109	2.760434	7.061765	2	15741	0.43212745	10.817141	17
15500	3.4911265	8.593955	2	17513	0.2424643	10.98675	17
15757	3.241632	8.189662	2	20412	0.22819144	10.916482	17
15699	3.6212277	8.89044	2	17244	0.72287816	10.445196	17
20183	3.0135527	7.710608	2	19339	0.35859868	10.678736	17
20003	3.0990489	7.7208533	2	19537	0.17535451	10.768499	17
14561	3.0432997	7.743529	2	19246	0.21951312	10.839967	17
18719	3.0564477	7.781393	2	19910	0.19978037	10.955484	17

18812	3.064132	7.736986	2	19317	0.19986798	11.139427	17
19915	3.123416	7.8247657	2	19945	0.6331593	10.50207	17
12493	2.951575	8.334931	2	17912	0.20925002	11.184233	17
16434	3.0591946	8.384935	2	17966	0.7967564	11.156168	17
13100	3.1172638	8.364981	2	19242	0.5136303	10.947512	17
20068	3.2005422	8.568393	2	17037	0.55779755	10.907791	17
17379	3.8371663	8.002781	2	19304	0.22523375	11.123493	17
16483	3.3464518	7.431485	2	20403	0.18426666	11.018692	17
16345	3.0331142	7.7014875	2	17514	0.22058275	10.784041	17
17305	3.09091	7.7140126	2	18959	0.5206035	10.855087	17
19654	3.4856522	7.440604	2	19909	1.2576897	10.516006	17
19000	3.5590587	7.471023	2	11112	0.899626	10.684105	17
15675	2.7981648	7.7458763	2	20162	0.96507543	10.745947	17
18653	3.0296326	7.5289497	2	19475	1.1741276	10.546681	17
15852	3.7518914	8.437004	2	19817	0.93651617	10.699848	17
18816	3.4566731	8.204534	2	19332	0.93258154	10.724782	17
16681	3.4601765	8.231906	2	19941	0.8958647	10.760511	17
18413	3.3079846	7.3809624	2	12791	0.9050813	10.757798	17
17182	3.2232678	8.5873995	2	20172	0.27449027	11.166719	17
19798	3.0293496	7.308481	2	19690	0.7670169	10.76296	17
15615	3.317601	8.722823	2	18979	0.8649355	10.815546	17
17861	3.795775	8.00799	2	17557	0.9159865	10.855511	17
18091	3.4411616	7.267849	2	19481	1.4467729	10.28814	17
18893	2.9341297	7.279738	2	17346	1.338884	10.487143	17
17131	3.5213695	8.028946	2	18002	0.8456669	10.708999	17
15386	2.902353	7.386777	2	18475	0.8383497	10.706055	17
15557	2.9347956	7.6455765	2	18207	0.79689866	10.828416	17
19058	3.5796895	7.906491	2	18390	1.362546	10.480643	17
15415	3.0752459	8.3207855	2	18302	0.7648684	10.581854	17
15508	2.7110553	7.2488184	2	18551	0.879044	10.694914	17
15783	2.729367	7.203237	2	11081	0.113734275	10.97339	17
13132	2.9185534	7.334301	2	17686	0.68275446	10.495787	17
20437	3.5189073	7.7892823	2	18884	0.7849659	10.601261	17

18312	2.93761	7.624773	2	17418	0.7378695	10.873596	17
19493	3.011387	7.689528	2	19137	0.7779359	10.645534	17
12937	3.4009166	8.889589	2	17590	0.7018831	10.896066	17
15891	3.2091956	8.247289	2	19221	0.7604894	10.861291	17
16517	2.9666374	7.8991423	2	20201	0.7201338	10.947664	17
19991	2.880434	7.3458624	2	17665	0.61357605	10.899482	17
17184	2.9109342	7.7070093	2	17675	0.36184388	10.871676	17
15436	3.0160902	7.7267165	2	16639	0.24788962	10.839131	17
19389	3.5139902	7.265929	2	19004	0.8052956	10.783789	17
19732	3.3072395	8.030287	2	17578	0.7010493	10.889034	17
18405	3.574792	7.8332825	2	12230	0.24223475	10.951123	17
16384	3.5975158	8.472979	2	17980	0.3743727	11.067934	17
14803	3.646258	8.446741	2	16341	0.3578946	10.865502	17
16472	2.7529297	8.250376	2	18872	0.38520452	10.997685	17
13158	3.5117936	8.570699	2	19125	0.25676858	11.148605	17
15391	3.290207	7.936504	2	17610	0.19526553	10.888611	17
15747	3.1906464	7.7047625	2	17489	0.4133875	10.9805565	17
19653	3.0701838	7.758746	2	17698	0.38775826	11.051076	17
14893	3.002053	7.7011685	2	15007	0.64833456	10.530599	17
15426	2.8445761	7.5341787	2	19944	0.9486038	10.976538	17
17494	3.1949954	8.608114	2	17501	0.43854055	10.809817	17
15713	3.224679	8.367806	2	17296	0.80085623	11.141136	17
15427	3.1182032	7.352346	2	19921	0.7669628	10.674679	17
18611	3.2019784	8.646352	2	18608	0.80344695	10.665194	17
18060	3.0403426	7.7750125	2	18794	0.5431139	10.594284	17
17377	2.8865204	7.469265	2	18166	0.4409102	10.899894	17
19556	2.6963358	7.4534135	2	19005	0.3475313	11.009709	17
16799	3.3490396	7.145575	2	14189	0.4337617	10.939537	17
13478	2.8114393	7.395298	2	16784	0.7017293	10.482613	17
18555	2.7732563	7.263153	2	17835	0.7179293	10.651888	17
15209	2.8451521	7.4072604	2	17036	0.2631117	11.065272	17
16682	2.8148553	7.45379	2	17714	0.21993217	11.196787	17
18736	2.7041144	7.1486974	2	20014	0.22288579	11.12821	17

17303	3.2368097	8.369048	2	17779	0.6722109	10.9271345	17
19699	2.632827	7.08962	2	19980	0.23553067	11.1516285	17
16851	2.7661176	8.239531	2	19153	0.5343459	10.835697	17
17847	3.6159866	8.706469	2	17174	0.67338544	10.495934	17
19950	3.24287	7.9360566	2	18955	0.49829778	10.844134	17
18097	3.2629492	8.382385	2	18707	0.76447487	10.772801	17
20085	3.0875626	7.746418	2	17580	0.8199455	10.79484	17
18303	3.0656226	7.7343717	2	18712	0.7046649	10.80579	17
11009	3.1313908	7.768381	2	17926	0.59931296	10.896602	17
19660	3.120621	7.7672057	2	19864	0.8147813	10.675982	17
19211	3.0694957	7.7551694	2	17038	0.29465556	10.927206	17
17933	3.0773067	7.743144	2	13442	0.20254855	11.055	17
15960	3.1256855	7.7619753	2	16477	0.5749885	10.549665	17
18151	3.075663	7.7434072	2	19509	0.93778276	10.847992	17
19356	3.062736	7.732749	2	19116	0.8978604	10.782734	17
19059	3.0836797	7.802518	2	19446	1.2671027	10.508478	17
18813	3.0572445	7.7646556	2	18441	0.75965476	10.973583	17
19074	3.1334033	7.775926	2	20454	0.62355286	11.013644	17
12676	3.0689154	7.7543745	2	17602	0.63356924	10.944417	17
17885	3.0805655	7.7891593	2	17711	0.92721325	10.963796	17
18126	3.046888	7.738168	2	17499	0.83758706	11.100423	17
18490	3.1259818	7.7147036	2	17563	0.8998787	10.986288	17
12531	3.21609	8.365805	2	17811	0.79885465	11.138789	17
11744	3.0444193	8.389043	2	17672	0.9270894	10.946281	17
18950	3.0899282	8.383232	2	18764	0.7647077	11.140644	17
17973	3.1010602	7.787195	2	17577	0.9090781	10.9482975	17
20190	3.0322144	7.7173495	2	17888	0.76085085	11.166044	17
19557	3.1948197	7.4425235	2	15284	0.83549404	11.08562	17
19649	3.0967932	7.7914643	2	20109	0.9128346	10.933904	17
16993	3.4722433	7.241609	2	19467	0.9062405	10.987329	17
11283	3.094739	8.3632145	2	16672	0.7183356	10.469388	17
15171	3.2484856	8.372525	2	18998	0.825824	10.626467	17
15385	3.8168266	8.067024	2	18293	0.6756492	10.552846	17

20161	3.0114324	7.8714604	2	18768	0.5340606	10.774708	17
19541	3.4237297	8.088604	2	17144	0.5899567	10.6209	17
19143	3.052806	7.904683	2	19881	0.84749734	10.885047	17
19786	2.9933262	7.865482	2	18759	0.30480808	10.892802	17
12545	3.0809135	7.7204537	2	17077	4.772606	8.562502	18
16700	2.982878	7.777511	2	18169	3.7032518	8.643736	18
19800	3.1352327	7.9840636	2	13494	4.2710443	8.535101	18
12926	3.1866155	7.922522	2	19938	4.2304964	8.600948	18
18496	2.961157	7.8491592	2	18218	4.806931	8.824729	18
12870	2.9382794	7.778632	2	19312	4.16698	8.672099	18
12709	3.1642983	7.9507594	2	18837	4.8330474	8.792261	18
19886	3.0903218	7.7820587	2	12569	4.1016335	8.621165	18
13016	3.1744814	7.9625845	2	14643	4.006759	8.753618	18
11645	3.2298706	8.377761	2	19375	4.0134735	8.503044	18
11510	3.2315657	8.368097	2	17145	4.194007	8.615824	18
17360	3.2369628	8.369424	2	19038	4.087523	8.600926	18
16296	3.1809247	7.6585355	2	18634	4.0665183	8.521227	18
13208	3.2450404	7.3774676	2	19820	4.1955256	8.705584	18
17907	3.3019693	7.3122396	2	18587	4.0326576	8.953316	18
19190	2.8605006	7.892137	2	12177	4.1005926	8.87207	18
17314	3.3072703	7.3277225	2	15607	4.25199	8.783044	18
18538	2.9583893	7.050908	2	17700	4.1430664	8.970776	18
19885	3.4757888	7.723187	2	19267	4.125125	8.649849	18
14767	3.4659698	7.4123607	2	18294	4.035525	8.616329	18
13047	2.9164298	7.3916793	2	19716	4.017008	8.251407	18
16478	2.9025772	7.3438005	2	19936	3.657332	8.786011	18
18675	3.4445975	7.1671925	2	19282	4.500019	8.991771	18
17623	3.3668158	7.366215	2	18215	3.674509	8.831258	18
17664	2.9699173	7.0782466	2	13112	4.2537456	8.49709	18
12718	3.1814816	7.8254404	2	16475	3.7738335	9.018097	18
12775	2.94266	7.6213098	2	14129	4.9233713	8.85726	18
13421	3.0521233	7.721642	2	17018	4.7639523	9.076691	18
16673	2.739749	7.048502	2	15659	4.6217713	8.915515	18

18440	2.9738045	7.3468575	2	19684	3.7674289	8.878279	18
12008	3.1095846	7.35909	2	15366	4.346362	8.597586	18
19165	-0.4049162	3.991329	3	17135	4.410384	8.99054	18
18858	-0.19100031	4.5214376	3	18828	4.248335	9.0455065	18
17130	-0.09637871	4.735996	3	19338	4.299979	8.721565	18
20166	-0.046853602	4.3481517	3	14060	4.38868	8.697613	18
17236	-0.85882616	3.9910722	3	17809	4.295847	8.661948	18
19775	-0.6396283	4.1906853	3	11257	3.8156853	8.714681	18
18478	-0.36925104	4.355137	3	18823	4.069226	8.722241	18
20078	-0.37857667	3.9829245	3	15943	4.5574646	8.777482	18
20217	-0.58010435	3.9650705	3	19354	4.6943445	8.924829	18
16725	-0.23723711	4.5842834	3	12196	4.8567863	9.007518	18
18371	-0.67415404	3.773291	3	13020	4.802337	8.937076	18
19580	-0.10037385	4.712948	3	13330	4.6221485	8.898055	18
16857	-0.015094253	4.725392	3	12265	4.375109	8.701465	18
20140	-0.64752114	3.9954631	3	17676	4.300897	8.656076	18
16939	-0.21213384	4.4572544	3	17735	4.2982516	8.553009	18
16999	-0.044917442	4.6549625	3	16631	4.3128953	8.548321	18
17426	-0.86513513	4.0063353	3	11656	4.2443314	8.579618	18
18245	-0.769767	3.9945457	3	16676	4.210755	8.609148	18
15887	-0.86420596	4.1006465	3	16609	4.24837	8.557707	18
13187	-0.3874832	4.6197505	3	18141	4.2258477	8.618892	18
18329	-0.60521245	3.9563806	3	15572	4.511683	9.0533085	18
13400	-0.48284778	4.2649965	3	19661	4.5296474	8.833795	18
19388	-0.5098894	4.403872	3	16198	4.272299	8.590959	18
20059	-0.36692873	4.405287	3	17231	4.490429	9.00981	18
16571	-0.7417607	3.7140458	3	19151	4.050916	8.510434	18
19744	-0.49475667	3.8693337	3	17266	4.7582483	8.57022	18
17307	-0.25246352	4.3809056	3	17930	4.6974	8.525611	18
17518	-0.17673147	4.72196	3	18836	4.431223	8.437354	18
19954	-0.42014265	4.1006494	3	15762	4.2154307	8.997523	18
16657	-0.35513353	3.8877017	3	15409	4.218325	8.489251	18
18847	-0.70527565	3.7379038	3	20387	4.257838	8.57673	18

20047	-0.7480608	3.7135942	3	19867	4.2413054	8.465571	18
16671	-0.735516	3.7919083	3	18111	4.378001	8.998618	18
16758	-0.25697574	3.871625	3	19876	4.7617335	9.081197	18
16809	-0.25418133	3.8138378	3	19737	4.258553	9.031773	18
17319	-0.40950486	3.8809927	3	19248	4.240593	9.027587	18
17255	-0.2989986	3.8028612	3	17238	4.187433	8.638969	18
20369	-0.4656439	3.8485281	3	17579	4.290681	9.120038	18
16797	-0.24359645	3.8222818	3	19127	3.6485229	8.783928	18
16659	-0.8986288	3.9579308	3	18811	4.910393	8.893501	18
17366	-0.5988448	3.8446565	3	12198	4.3421125	8.663243	18
15851	-0.6601868	4.523528	3	20176	4.6491	8.80953	18
17261	-0.1962707	4.4633656	3	18075	4.7627344	8.701199	18
17029	-0.54757065	3.9872346	3	18902	4.700626	8.78085	18
19028	-0.92142326	4.0246387	3	18349	4.669489	8.733324	18
19983	-0.7306796	3.7319348	3	20099	4.5132165	9.024689	18
16978	-0.051730067	4.658242	3	20062	4.5591817	8.988707	18
16807	-0.08788022	4.7368565	3	18054	4.1569896	8.992761	18
11731	-0.69537574	3.820257	3	20124	4.5522795	9.028956	18
17329	-0.44625846	4.6238604	3	18796	4.6275315	9.116208	18
14813	-0.34740433	4.38002	3	19156	4.5829396	9.041043	18
20439	-0.38889852	4.1841335	3	17622	4.682132	9.111817	18
18010	-0.8275888	4.0628753	3	11229	4.395061	8.90563	18
19641	-0.8396755	4.150018	3	17570	4.435662	8.885173	18
11475	-0.5242599	4.2726035	3	20455	4.9269342	8.557642	18
13358	-0.6104159	3.9762259	3	16349	4.940628	8.635476	18
18599	-0.3050107	4.4088097	3	17432	4.8185287	8.638589	18
15702	-0.35859108	4.374465	3	13605	4.5312247	8.851909	18
17269	-0.7511845	4.1731896	3	17475	4.528961	8.8237095	18
18309	-0.6000488	3.9935381	3	11705	4.5601473	8.846484	18
19265	-0.2376572	4.3114986	3	17445	4.5250635	8.855258	18
12180	-0.4271777	4.4617853	3	15568	4.4925766	8.75847	18
19850	-0.22129728	4.42327	3	12942	4.391986	9.034571	18
17555	-0.22972253	4.5328164	3	16473	4.3778443	8.845491	18

17275	-0.9320137	4.0221424	3	15776	4.5037804	8.80577	18
18190	-0.6506721	4.0300336	3	16643	4.55535	8.854983	18
19182	-0.50132364	4.42596	3	18982	4.492359	8.7557955	18
17050	-0.5016748	4.3817267	3	17114	4.4691906	8.849355	18
12451	-0.28453135	4.5090995	3	18132	4.2532773	8.952224	18
17817	-0.49110395	4.402649	3	12779	4.4640436	8.939012	18
18659	-0.30733234	4.3998384	3	17901	4.667426	8.810344	18
12758	-0.27692333	4.405128	3	14607	4.738857	8.674448	18
17472	-0.43882176	4.313716	3	17813	4.8769555	8.639563	18
17640	-0.5090011	4.3924193	3	18355	4.780466	8.673768	18
16360	-0.26656926	4.4445605	3	19341	4.933091	8.728246	18
20223	-0.4189826	4.186078	3	19875	4.533891	8.860564	18
16584	-0.5045597	4.2485776	3	17852	4.561161	8.653868	18
12611	-0.5071808	4.438948	3	19169	4.7452736	8.625929	18
14710	-0.43118426	4.4565086	3	17781	4.73632	8.902178	18
18983	-0.4687789	4.223675	3	18073	4.8916593	8.811981	18
11476	-0.4711976	4.2829666	3	13863	4.862976	8.866296	18
15338	-0.39293522	4.431745	3	18624	4.6623693	8.668226	18
15407	-0.31792304	4.462762	3	17217	4.7702765	8.746423	18
20184	-0.46569	4.3909655	3	17636	4.578793	9.013154	18
11616	-0.4840431	4.4092436	3	16625	4.93895	8.5969095	18
16534	-0.4986874	4.1458697	3	14098	4.7653146	8.786906	18
19579	-0.62030154	3.8726192	3	17778	4.6323156	8.805244	18
18395	-0.60779625	4.2698607	3	17591	4.629476	8.69749	18
17596	-0.5820705	4.0060625	3	19495	4.649267	8.900929	18
18191	-0.5875756	4.216203	3	14545	4.9599032	8.68603	18
17830	-0.5942777	4.238138	3	17963	4.714061	8.658476	18
12426	-0.6407656	4.022388	3	15470	4.4571247	8.81589	18
14495	-0.67813873	3.8376353	3	19838	0.42043194	10.095168	19
16644	-0.68384784	3.8686686	3	17944	0.7074231	9.7325	19
18642	-0.7189789	3.8629491	3	18065	0.27524802	10.410962	19
19643	-0.7821927	4.1435857	3	16386	0.3443083	10.5754	19
17156	-0.5723464	4.255584	3	19154	0.04860265	9.026578	19

17786	-0.69954926	4.006689	3	18089	0.6206179	10.464395	19
12526	-0.31450817	4.3575377	3	18696	0.613362	10.440363	19
16567	-0.35300282	4.3765826	3	14962	0.5864544	10.489067	19
20425	-0.52479094	4.4037514	3	18639	0.80175424	10.370415	19
17074	-0.22752503	4.3986464	3	12879	-0.16798367	8.909073	19
17033	-0.412293	4.473089	3	13239	-0.009894954	10.390523	19
17556	-0.53834414	4.27637	3	13469	0.007370186	9.54128	19
17759	-0.4461605	4.482501	3	20030	0.05196088	10.521657	19
17072	-0.47894603	4.1562934	3	19606	0.008810562	10.40366	19
20081	-0.49882182	4.2293477	3	17376	0.8436879	9.907051	19
13276	-0.5167623	4.106956	3	13473	0.7900817	9.957023	19
16691	-0.27373502	4.7248077	3	17839	0.6274996	9.818865	19
16854	-0.2817501	4.3558674	3	19981	0.6689048	9.797092	19
15290	-0.59413016	4.276929	3	17819	0.59785056	9.806769	19
13079	-0.876188	4.002901	3	19911	0.62291086	9.729746	19
13428	-0.58759063	4.2795696	3	18640	0.7735136	9.757869	19
15330	-0.90577143	4.032017	3	19119	0.5009516	9.902523	19
12468	-0.8254641	4.070554	3	19352	0.68784726	10.4518	19
18119	-0.48169845	4.043706	3	12762	-0.4377757	9.030623	19
17967	-0.46737173	4.6692915	3	11373	1.1107858	10.079821	19
11794	-0.5284346	4.670205	3	17516	1.0935211	10.128152	19
18155	-0.6169154	4.3730216	3	13415	0.6028385	9.3692045	19
16573	-0.52688193	4.43882	3	18975	-0.19299853	9.694105	19
15587	-0.36866266	4.641918	3	12449	0.880811	9.880938	19
15270	-0.1420877	4.436632	3	19049	0.8659759	9.899088	19
18956	-0.664685	4.123433	3	18042	0.30507308	9.692326	19
17660	-0.7031371	4.137672	3	19539	-0.17651673	9.6800785	19
19468	-0.52553827	4.095174	3	17395	0.3414701	9.889374	19
12430	-0.23776774	4.390289	3	19597	0.283976	9.656322	19
15012	-0.6160787	4.2451224	3	17562	0.17042118	9.097184	19
11241	-0.33026442	4.3117795	3	19357	-0.5945984	9.077911	19
18897	-0.5155393	4.0886855	3	15090	-0.6055563	9.057938	19
19829	-0.9073303	4.014351	3	18633	-0.03863294	8.875721	19

18829	-0.91341925	4.035875	3	19489	-0.41061252	9.1464405	19
16564	-0.36336696	4.3742156	3	18986	-0.2613546	9.201133	19
17085	-0.49013045	4.4423165	3	12874	-0.20790726	9.386289	19
17443	-0.31767806	4.362324	3	18999	-0.5097353	9.162194	19
18841	-0.33826047	4.3297987	3	20060	-0.4992829	8.673077	19
17046	-0.92805976	4.006271	3	19219	-0.05261388	9.073305	19
17430	-0.45663518	4.576536	3	18004	-0.3315662	9.130573	19
18138	-0.3385639	4.4146943	3	17808	-0.33423987	9.029214	19
17103	-0.8902803	4.0144086	3	18558	-0.30198124	9.136834	19
20139	-0.47730228	4.6028633	3	18528	-0.21181197	8.6559	19
16595	-0.43938535	4.5552864	3	19292	-0.49579155	9.454919	19
20197	-0.35007045	4.26676	3	18298	-0.3433304	8.633946	19
17750	-0.8434229	3.8087292	3	17843	-0.39957595	9.0753	19
17737	-0.8984416	3.956675	3	16833	-0.19348657	8.710504	19
19215	-0.90658206	3.9739566	3	19343	0.022023609	8.931146	19
17208	-0.7543512	3.9808338	3	18718	0.16192831	8.851959	19
19550	-0.460474	4.090835	3	18866	-0.38471606	8.987798	19
18113	-0.41068375	4.004428	3	18582	-0.029557465	8.946305	19
17546	-0.43416396	4.2546296	3	17505	-0.5194924	9.135579	19
18462	-0.19728306	4.491549	3	17655	-0.56535083	9.103878	19
13138	-0.81509167	4.1178694	3	18970	-0.003616761	8.999783	19
17334	-0.04782248	4.354838	3	18654	-0.15711655	8.938104	19
17333	-0.062096372	4.4295855	3	20192	-0.001335462	8.966783	19
17189	-0.14304751	4.4748144	3	12320	-0.31310105	9.379853	19
17001	-0.23434752	4.49439	3	20006	-0.49317804	9.766625	19
18526	-0.18640193	4.674394	3	16774	-0.267969	8.711243	19
18690	-0.7467009	3.7303162	3	19975	-0.2299568	8.889757	19
17652	-0.8564681	3.9908822	3	12123	-0.08127016	8.756413	19
19350	-0.54570246	3.9011865	3	17107	-0.6015446	8.695584	19
16766	-0.19002098	4.363626	3	15886	0.24532843	8.954504	19
19351	-0.33660567	3.8708892	3	18255	0.10522506	9.048285	19
16793	-0.06475627	4.6134086	3	19582	0.12010349	9.05689	19
19781	-0.33905727	4.4698224	3	19586	0.14853553	9.05348	19

20404	-0.7055705	3.7361858	3	18161	0.26503715	8.9324	19
18056	-0.5272792	3.8624146	3	17646	0.12928519	9.052202	19
20216	-0.67523015	3.7906125	3	17790	0.1692266	9.065598	19
17878	-0.37567756	3.8819454	3	19540	-0.12157527	8.858041	19
17285	-0.5050553	3.8373284	3	17787	0.122931994	9.128328	19
18878	-0.7307844	3.7118356	3	18471	0.009575922	9.106177	19
16878	-0.46403572	4.1609116	3	16843	-0.045352403	9.858651	19
19207	-0.5259403	3.8921604	3	18722	0.15710512	8.983268	19
18961	-0.7220791	3.7274349	3	13000	-0.34089443	9.468838	19
16461	-0.7171567	3.731204	3	19394	0.32993335	10.54981	19
19500	3.097497	4.269476	4	13344	0.48892695	10.394061	19
18271	3.1479068	4.319186	4	17654	0.6268119	10.455978	19
19879	3.2010708	4.322654	4	16456	-0.31361455	9.690786	19
19588	3.575952	4.3526196	4	19159	0.28974533	10.590323	19
18434	3.1715963	4.6367025	4	13134	0.016004158	9.040741	19
19902	3.192548	4.636367	4	14465	-0.2622665	9.908881	19
16542	3.1922991	4.660498	4	12872	0.20755138	9.76737	19
18084	3.7083077	4.9360237	4	12063	0.18834746	10.327148	19
19361	3.6302083	4.5108733	4	12054	0.18386362	10.57011	19
16458	3.7689416	4.8024335	4	12036	0.52836	10.121426	19
18728	3.6101294	4.684165	4	16447	0.437328	10.149453	19
19279	3.6108825	4.6484814	4	17350	-0.31929642	8.644313	19
18360	3.530573	4.535786	4	17032	0.35371673	10.395017	19
12922	3.6899185	4.583632	4	17065	0.33614418	10.564323	19
18051	3.644712	4.709578	4	12348	0.24224404	9.413959	19
18177	3.7167206	4.6974573	4	12837	0.2986784	10.299516	19
17958	3.6305492	4.759757	4	12499	0.2716397	10.306529	19
19469	3.6289349	4.6850233	4	18189	0.6186565	10.440838	19
18446	3.7150404	4.80075	4	20372	0.29405484	10.271302	19
19854	3.7221677	4.734258	4	18437	-0.28172886	9.486949	19
18483	3.7229927	4.8034854	4	15872	0.33000237	10.572801	19
18150	3.0779731	4.8360825	4	17954	-0.022507418	9.358288	19
20375	3.6523476	4.8676944	4	18544	0.87661487	9.879149	19

19486	3.2021782	4.5589457	4	19321	-0.21303885	9.30792	19
17532	3.6047416	5.0546837	4	19329	-0.4957538	9.737253	19
15746	3.1623085	4.889687	4	20457	-0.05174849	9.5338745	19
17922	3.443107	4.6729045	4	13489	0.79907966	9.81633	19
17744	3.1611485	4.8263183	4	18735	0.20477965	9.362576	19
11233	3.4128647	4.5732703	4	11613	0.30398422	9.284023	19
17651	3.3807902	4.167663	4	13136	-0.4756949	9.129755	19
19549	3.3959358	4.488882	4	12039	0.1953541	10.187341	19
12525	3.7949939	4.7620134	4	18595	0.073380284	10.151486	19
17950	3.0482144	4.2375793	4	18920	0.9756837	9.771721	19
18742	3.4467561	4.7749557	4	20423	0.1960723	10.494135	19
17028	3.4289947	4.9327645	4	13262	0.96497273	9.788409	19
17221	3.6909487	4.344956	4	16516	-0.12746228	9.735564	19
13459	3.247558	4.795472	4	13705	1.036623	10.236855	19
17850	3.3703904	4.6472983	4	17062	0.25256136	10.057561	19
18486	3.2929766	4.431592	4	20431	0.09085902	9.4074545	19
16353	3.5135145	4.4571104	4	19695	0.77043694	9.999541	19
18149	3.4802852	4.2020197	4	12997	0.12500481	9.062671	19
19063	3.4665053	4.6278996	4	18575	-0.50491047	8.979149	19
17448	3.5771694	4.463673	4	17091	-0.47917628	8.696419	19
18103	3.7214675	4.6200366	4	13128	0.11916911	10.374384	19
18737	3.4319348	4.474384	4	19093	0.2992607	9.951058	19
18854	3.4844663	4.619127	4	11605	0.012046651	9.944111	19
18365	3.681606	4.6305327	4	17180	0.27122068	9.674571	19
17597	3.3560097	4.3257976	4	17157	-0.022040326	9.842791	19
18348	3.4587438	4.651194	4	19961	-0.13777071	9.456163	19
17955	3.4068172	4.3191967	4	19067	-0.04243743	9.783996	19
19726	3.3105638	4.3474474	4	19846	-0.02847148	9.851098	19
18335	3.7580173	4.8023543	4	11289	-0.01336921	9.854523	19
18778	3.1832347	4.8733244	4	19793	0.014638472	9.330762	19
16462	3.1734016	4.8566575	4	18708	-0.41442412	9.348044	19
19978	3.3196256	5.0046134	4	18692	0.24043462	9.332112	19
19766	3.3291256	4.9656744	4	13433	0.35631934	9.084657	19

20220	3.4953558	5.0460453	4	18954	-0.24297537	9.40548	19
15706	3.142229	4.440124	4	18258	0.22284262	9.343238	19
16687	3.8001719	4.7406473	4	16194	-0.18906833	9.989965	19
15658	3.464121	5.0034595	4	12432	-0.19070514	9.894579	19
18458	3.3040667	4.914652	4	16900	-0.024992712	9.152058	19
15623	3.0879538	4.7039785	4	20117	-0.08600705	9.426353	19
18352	3.085525	4.6886396	4	17607	-0.08495294	9.4649105	19
18818	3.258272	4.725046	4	17968	-0.07519557	9.496298	19
18386	3.5736356	5.049378	4	19358	-0.054716226	9.469285	19
19002	3.4229481	4.830253	4	18325	-0.051185902	9.482985	19
18506	3.4238725	4.668305	4	20064	0.39248443	9.915671	19
17837	3.5904384	4.199564	4	18489	-0.10273619	9.500703	19
19381	3.769785	4.6423864	4	18771	-0.1182062	9.508688	19
18597	3.3880022	4.5786095	4	19252	-0.06327187	9.567575	19
18532	3.1175392	4.631635	4	20113	-0.052489687	9.849233	19
17731	3.4232233	4.689257	4	17566	-0.07166481	9.6905985	19
18511	3.4082732	4.782064	4	12234	-0.017708274	9.2964525	19
18047	3.431465	4.8263116	4	20188	0.029466482	9.324715	19
17987	3.3951135	4.774693	4	19736	0.20098032	9.265127	19
18134	3.3072517	4.34795	4	19544	-0.13251527	9.25658	19
19075	3.3365602	4.36986	4	18585	-0.20931923	9.390727	19
19188	3.330466	4.71279	4	18172	-0.546516	9.171744	19
18732	3.382299	4.511647	4	19231	-0.23762703	9.083354	19
19724	3.2737107	4.3746157	4	19584	-0.49199626	9.2687235	19
20133	3.8472326	4.446914	4	19688	-0.52450293	9.2448845	19
19810	3.6371348	4.343651	4	19666	-0.21082027	9.377802	19
19840	3.6340425	4.010825	4	20148	0.5574146	9.589723	19
19462	3.6382794	4.0083237	4	13228	0.118593186	9.263558	19
18697	3.7675056	4.5127687	4	20200	-0.22362858	9.34267	19
18406	3.794446	4.5998034	4	18431	0.21901381	9.402897	19
17822	3.7688608	4.391912	4	18594	0.1701433	9.489063	19
20368	3.8164995	4.4007144	4	11546	0.42558995	9.532523	19
17251	3.7789059	4.580394	4	14348	0.257647	9.3457	19

19441	3.8248348	4.130283	4	17720	0.25939068	9.413864	19
17263	3.4466639	4.2464566	4	20385	0.39673895	9.508913	19
17634	3.8414197	4.1881266	4	19912	0.22618909	9.418875	19
19568	3.8182063	4.388242	4	14840	0.35227543	9.843191	19
17653	3.8832643	4.1643753	4	11739	0.49609366	9.853978	19
17520	3.7053115	4.3970995	4	17821	0.6381599	10.217747	19
18281	3.6913404	4.3588934	4	18280	0.5034523	10.014513	19
12850	3.6871119	4.404773	4	16243	0.46732426	10.018875	19
19205	3.6469088	4.2813406	4	16241	-0.114008844	9.656793	19
19893	3.6959088	4.3773174	4	17774	0.27296013	9.967045	19
18445	3.6252623	4.1720414	4	17707	0.257571	9.924041	19
17405	3.6934369	4.290664	4	20079	0.32873452	9.871921	19
17630	3.7880793	4.233226	4	15796	0.051221445	9.763504	19
17669	3.821099	4.174996	4	16297	-0.004180155	9.830171	19
18787	3.7917411	4.4113393	4	12245	0.035481572	9.866325	19
11966	3.7641242	4.104558	4	17726	0.029412113	9.950037	19
17492	3.4851563	4.2753925	4	19026	-0.12536384	9.924205	19
19474	3.755523	4.583154	4	19640	0.07346446	9.8735895	19
18283	3.6346242	4.0270267	4	15389	-0.106237784	9.662792	19
14746	3.8668396	4.1721807	4	14402	0.481911	9.89918	19
20154	3.6834471	4.585499	4	17783	0.19453886	9.999502	19
14369	3.777344	4.41268	4	15535	0.7011717	10.358137	19
18539	3.5678284	4.5039186	4	18527	0.45050567	9.879541	19
15888	3.6397169	4.0238175	4	15841	0.007328564	9.014039	19
19179	3.680357	4.0159287	4	17995	0.14752133	10.002755	19
19548	3.5222023	4.4978237	4	19113	0.45419648	10.073934	19
19423	3.610093	4.448797	4	19566	0.75694066	9.929254	19
16431	3.6012647	4.3365545	4	12235	0.17276418	10.051921	19
17624	3.4807467	4.5196614	4	17836	0.06156179	10.13542	19
20410	3.8037934	3.9915547	4	19387	0.20560245	9.965272	19
17614	3.9390123	4.12928	4	19263	0.088485844	10.142676	19
17727	3.771524	3.9793916	4	18899	0.148336	10.0824	19
18657	3.513901	4.3976593	4	18130	0.14386186	10.069317	19

17424	3.5387223	4.390507	4	17637	0.11051174	10.076731	19
20130	3.7575958	4.010782	4	19045	0.32401443	9.834499	19
19048	3.6048036	4.0368586	4	17633	0.18667886	10.015621	19
19804	3.5757012	4.069243	4	11809	0.15820599	10.025762	19
17674	3.6274815	4.0620017	4	19085	0.7926655	9.906797	19
19089	3.855489	4.1794996	4	14790	0.69784147	10.1354885	19
20373	3.9088376	4.095847	4	18710	0.122185566	10.124691	19
18846	3.5363996	4.2057395	4	20450	0.22213	9.982754	19
19995	3.6344645	4.23845	4	17916	0.09922704	10.034999	19
20182	3.520802	4.215524	4	19620	0.119297184	10.122147	19
18375	3.598365	4.181301	4	13329	0.21724205	10.039928	19
17728	3.6940546	4.1347523	4	12306	0.18260035	9.375033	19
17677	3.7171566	4.034446	4	11181	-0.0480305	9.42836	19
17187	3.6959713	4.2015896	4	12057	0.43736246	9.430887	19
18344	3.69446	4.015855	4	14879	-0.1212178	9.589689	19
17683	3.6882768	4.0202208	4	11636	0.7754878	9.922601	19
17692	3.6894798	4.037271	4	14947	0.09474413	10.03213	19
19421	3.707804	4.109857	4	12770	0.4821314	9.699204	19
17734	3.6796649	4.0271583	4	20106	-0.11975847	10.104134	19
17441	3.6497092	4.0175595	4	18898	-0.24309854	10.1722765	19
19061	3.5507133	4.5222597	4	16205	-0.16898532	9.374504	19
15450	3.522773	4.6318297	4	16528	0.15934783	8.945515	19
16718	3.7989001	4.321324	4	16420	0.2612285	9.233201	19
17679	3.8219028	4.561616	4	19102	-0.20640929	9.421256	19
17608	3.8434393	4.301836	4	11591	-0.1705244	9.590532	19
19128	3.8298523	4.299884	4	20134	-0.38771528	9.628738	19
19126	3.8171592	4.225383	4	18171	-0.08280213	9.853039	19
19007	3.7829425	4.267496	4	13371	0.1151213	9.614249	19
18273	3.7779047	4.3411465	4	17106	0.27077657	9.281208	19
17190	-1.8959723	5.6982546	5	17061	0.28411472	9.928329	19
12018	-1.8496608	5.7115545	5	18221	-0.06414269	9.329942	19
17541	-1.802642	5.6500034	5	17026	-0.41868794	9.156101	19
20198	-1.869056	5.6096168	5	17318	0.332695	9.830469	19

18112	-1.7905867	5.7088666	5	16759	0.19493356	9.832956	19
17108	-1.9146495	5.788045	5	17402	0.35410872	9.864943	19
13366	-1.9206977	6.308437	5	19672	0.17737357	9.513979	19
16873	-1.1467756	6.149509	5	18392	0.67501056	9.563454	19
19449	-2.019678	5.883903	5	19068	-0.01668025	10.179547	19
12130	-1.7368706	5.8751435	5	19595	0.026812062	10.023305	19
13423	-1.7679409	5.9147267	5	19691	0.26347825	9.968716	19
19821	-1.5211357	5.527048	5	13025	0.13431004	10.217168	19
17384	-1.1403409	5.8804774	5	16605	0.22570777	10.427633	19
20037	-1.9300386	6.289798	5	19084	0.94098735	9.722532	19
18179	-2.0047028	5.818734	5	17371	0.20923197	10.036989	19
18115	-1.9858825	5.7440968	5	17960	0.70726085	9.507526	19
13497	-1.9797025	6.2820997	5	19162	-0.25477365	9.493424	19
19518	-1.9152522	6.4209747	5	13321	-0.26182875	9.151236	19
13308	-1.9287542	5.694157	5	17600	0.48214382	9.984267	19
19822	-2.023867	5.7619076	5	18971	0.11959611	9.418828	19
17705	-1.9850115	5.749181	5	18128	0.21037585	10.330606	19
18242	-1.851019	6.4936337	5	17571	0.24534293	10.33325	19
13254	-1.7421633	5.9060516	5	19308	0.09983584	10.335887	19
18479	-1.7213823	5.9554014	5	17616	0.08194643	10.295587	19
19637	-1.4534154	6.537957	5	18590	0.6850013	9.544764	19
17487	-1.8399054	6.423429	5	18481	0.7014	10.347953	19
17799	-1.5728533	5.608761	5	19590	0.21335907	10.02961	19
18351	-1.6099015	5.8869905	5	19962	0.6279828	9.563145	19
17063	-1.7528042	5.750676	5	17820	0.58794063	9.641245	19
11184	-1.8163837	5.7228794	5	18688	0.66084814	9.74761	19
11691	-1.8257602	5.657662	5	12541	0.5808894	9.44499	19
12328	-1.551695	5.5262957	5	19891	0.3199142	10.070168	19
17079	-1.8380581	5.7310925	5	19720	0.23178446	10.244946	19
13420	-2.0852947	6.0634274	5	16919	0.6790099	9.480872	19
18158	-2.0152977	5.9194245	5	19895	0.31484592	10.048606	19
15875	-1.1644267	6.084088	5	19650	0.6263677	9.588772	19
13429	-1.7669467	6.0163164	5	19299	-0.451263	9.585079	19

12792	-1.8816707	6.1952205	5	19963	0.3673786	10.0186205	19
18058	-1.6990533	6.1211615	5	15922	-0.3585079	9.443492	19
19710	-1.1716801	5.8228183	5	19176	-0.47119528	8.869704	19
18612	-1.7070978	6.398607	5	19138	0.055431765	9.664153	19
18188	-1.6460832	5.929754	5	18461	0.93148553	8.22476	20
13170	-1.6195211	6.0636535	5	18868	0.6105112	8.184591	20
11462	-1.7320364	5.950277	5	18822	0.67619383	8.240141	20
17666	-1.1447225	5.8458514	5	15614	0.5473514	8.205865	20
11298	-1.1247456	6.1090927	5	17585	1.038057	7.987273	20
19738	-1.708712	6.374024	5	19591	0.9648259	7.963039	20
17946	-1.7553676	5.9604106	5	18429	0.42735967	7.990819	20
13481	-1.2203349	6.202524	5	17243	0.8587655	8.116629	20
13881	-1.9529134	5.8068438	5	14787	0.80250674	8.703368	20
14016	-1.7991462	5.7047806	5	18757	0.44538915	8.603088	20
11985	-2.0112987	6.183472	5	15756	1.0780581	8.301284	20
19170	-1.3534684	5.9994493	5	19108	0.6199589	7.9166136	20
16355	-1.2909638	5.8203187	5	12400	0.47484222	8.565506	20
13294	-1.2886534	5.822302	5	13460	1.069586	8.233757	20
12654	-1.6316888	6.062149	5	11551	0.991507	8.211235	20
19718	-1.5568795	6.0144153	5	16705	0.72378755	8.4751	20
17690	-1.6355898	6.131228	5	13046	1.0945948	8.203913	20
19685	-1.4770067	5.9650946	5	15375	1.2121094	8.254767	20
18767	-1.5364387	5.5959682	5	19701	0.9873468	8.236614	20
15807	-1.9932061	6.0619674	5	18068	1.1271257	8.230244	20
12217	-1.1417031	5.8797674	5	12998	1.1676781	8.231964	20
20112	-1.4530041	6.538329	5	20095	0.9501837	8.466527	20
11405	-1.747877	5.885897	5	13159	1.10398	8.24121	20
20029	-2.013288	6.1874175	5	19933	0.9682952	8.737382	20
12396	-2.100657	6.063667	5	16661	0.6087886	8.678184	20
17564	-1.1515888	5.8468685	5	14792	0.015022245	8.116544	20
13155	-1.5359544	5.5998945	5	20120	0.28614914	8.742985	20
19517	-1.8832855	6.0324807	5	18393	1.1460878	8.545188	20
13229	-1.5636117	6.5081	5	17205	-0.059716903	8.31132	20

20051	-1.3939991	5.7361903	5	19900	0.23896903	8.24632	20
15445	-1.6131759	5.9661646	5	16291	0.46410543	8.6790495	20
13053	-1.4822894	6.022088	5	19105	0.2474784	8.246226	20
14517	-1.5489727	6.0847845	5	12595	0.32419118	8.498596	20
12090	-1.7473377	5.910981	5	18976	0.44597638	8.4892645	20
19787	-1.5234523	5.538998	5	11584	-0.2245847	8.446048	20
19347	-1.5486841	5.568035	5	17066	-0.20474614	8.389615	20
12669	-1.7242218	6.1518955	5	19228	1.203528	8.4858885	20
15767	-1.8260186	5.740006	5	19759	0.32962388	8.449706	20
12647	-1.1291671	5.8461113	5	14801	0.34765032	8.446117	20
11597	-1.9152769	5.7202773	5	17673	0.28678167	8.492446	20
12524	-1.1432766	5.8612533	5	17868	0.9184051	8.201929	20
17855	-1.8691537	6.116132	5	17553	0.8017198	8.614971	20
12098	-1.8704731	5.901386	5	13086	0.53831863	8.468951	20
19756	-1.9309454	6.1181455	5	16167	-0.051483877	8.253642	20
12066	-1.2628337	6.263993	5	19302	0.84188133	8.570649	20
13083	-1.9075568	6.150861	5	20477	1.394891	8.583701	20
15919	-1.189746	6.193016	5	18081	0.3097033	8.498356	20
19861	-1.7617016	5.9000325	5	17373	1.0015789	8.636549	20
12640	-1.4857811	6.431106	5	18267	1.3920033	8.51438	20
13139	-1.2899779	6.2618203	5	13413	0.26982927	8.751967	20
12991	-1.2599084	6.243702	5	18235	0.34069827	8.505549	20
20193	-2.0067327	5.928688	5	20222	0.92220503	7.787898	20
19896	-1.3795817	6.039339	5	17383	0.87258714	7.76192	20
12398	-1.4458963	5.970092	5	12200	1.1113524	8.583785	20
17280	-1.5649586	6.333257	5	17491	1.1607239	8.126706	20
18622	-1.1595176	6.1678104	5	13068	-0.0604257	8.64103	20
12048	-1.2456698	6.2234664	5	12983	0.47558087	8.580802	20
13099	-1.1705935	6.196741	5	16274	0.42072344	8.541599	20
14954	-1.1565366	6.1867647	5	17133	-0.06664592	8.281546	20
17763	-1.261852	6.1031847	5	19593	-0.046695016	8.664	20
12636	-1.8504257	6.2717557	5	13088	-0.15589148	8.328125	20
11410	-1.887056	6.264513	5	18886	1.4120147	8.530686	20

18071	-1.8848991	5.801917	5	13075	0.39625624	8.401973	20
15089	-1.5897411	5.6263785	5	13416	0.4605486	8.621335	20
12223	-1.7797269	6.433775	5	12905	0.40595523	8.529683	20
13290	-1.8505372	6.18442	5	19779	1.2461121	8.540519	20
20077	-1.5087464	6.2246118	5	18233	1.413312	8.562233	20
17388	-1.8187828	6.077945	5	18782	1.0239698	8.310142	20
11491	-1.1407354	5.832358	5	19080	0.65122646	7.893462	20
12748	-1.8167567	5.7672033	5	13209	1.144715	8.261654	20
11507	-1.876364	5.73199	5	15240	0.45779455	8.560245	20
17729	-1.9118433	5.7331934	5	16425	-0.01152537	8.455903	20
19487	-1.7917804	5.733731	5	17099	0.38489208	8.611821	20
12955	-2.0062933	6.186408	5	18435	-0.038670894	8.439191	20
12086	-1.8453623	5.732828	5	17071	0.38306713	8.619314	20
12423	-1.7013726	5.7171226	5	17972	0.9942296	8.595716	20
13384	-1.8648305	6.0554867	5	17324	1.1352592	8.616275	20
11606	-1.6857269	6.2417197	5	13246	0.1996438	8.205197	20
15968	-1.7183101	6.3839526	5	18543	1.0869552	8.445105	20
12896	-1.581624	6.219369	5	20101	1.1460537	8.621311	20
12414	-1.6711509	5.7760806	5	19419	0.37927485	8.594825	20
12511	-1.7588459	6.3987103	5	19187	1.0705748	8.393692	20
20038	-1.7528813	6.4018435	5	17120	0.37737042	8.552629	20
17048	-1.7470146	6.3916836	5	14551	0.50996107	8.616392	20
17605	-1.5812894	5.651528	5	19256	0.15815338	8.108605	20
17558	-1.6934023	5.9576607	5	15792	0.468676	7.8057847	20
11544	-1.7227626	5.996058	5	18370	0.47330227	8.323792	20
12242	-2.0556715	5.9389753	5	19497	0.49034196	7.966154	20
11278	-1.6990275	6.0204916	5	17393	0.5650626	8.270188	20
12665	-2.0819376	5.9614673	5	18304	0.48013216	7.956906	20
18566	-1.6950603	5.9139347	5	18366	0.51909417	7.9166927	20
11402	-1.528699	5.593418	5	17845	0.47181618	8.386518	20
17823	-1.638021	5.7806144	5	18416	0.5679693	8.466417	20
17241	-1.6985624	6.020818	5	18378	0.57320297	8.257543	20
12019	-1.6977518	5.9993806	5	15321	-0.33075646	8.514226	20

11649	-1.7327737	6.385955	5	19623	0.09126153	8.581489	20
12985	-1.5096418	5.599598	5	19774	0.40368727	7.7699075	20
15609	-1.6312854	6.5016255	5	15286	0.041227307	8.256654	20
11469	-1.8580539	5.7673297	5	15639	1.1424044	8.213671	20
16369	-1.8186501	5.759752	5	20125	0.8951026	7.770209	20
13437	-2.1059723	5.9594655	5	19990	0.37745073	7.8262467	20
13487	-1.8268093	5.7554016	5	19796	0.8930278	7.7566657	20
11996	-1.9392427	5.789943	5	19391	0.59859955	8.473612	20
12994	-1.71172	5.7998734	5	18220	0.656429	8.155925	20
16192	-1.8382854	6.7385817	5	17165	-0.00759859	8.46851	20
11434	-1.666653	6.1155334	5	15686	0.24004154	8.057605	20
17429	-2.0176842	5.912102	5	15773	0.65955824	7.9184294	20
13320	-1.7382306	6.0325284	5	19457	0.87188494	7.860779	20
20179	-1.9640133	6.1232204	5	15506	0.7349636	8.07247	20
14739	-1.9178523	5.794198	5	17533	0.55465627	8.020895	20
17352	-2.1033487	6.093558	5	18269	0.9552046	8.002402	20
19310	-1.8574435	6.1613555	5	12999	0.71799916	7.9893827	20
12247	-1.5739748	5.7420373	5	18762	0.7222892	7.9296107	20
18100	-1.4955446	5.695774	5	19734	1.3434122	7.91295	21
19071	-1.609566	5.688416	5	18432	1.1328387	7.9011626	21
18890	-1.5335553	5.597096	5	17200	1.0982903	7.5619745	21
19262	-1.8664749	5.801423	5	19305	1.1750914	7.596764	21
13401	-1.6325603	5.7957263	5	17137	1.4314635	7.5816903	21
18739	-1.9912491	5.832121	5	14240	1.1017445	7.5449953	21
17025	-1.8362519	6.3625016	5	17509	1.1785558	7.6592712	21
19914	-1.884708	6.145608	5	17196	1.6182777	7.979961	21
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16199	-1.8969641	6.130489	5	17536	1.5572448	8.034328	21
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17746	-2.0631115	5.944904	5	18314	1.6139767	7.568859	21
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15662	-1.402436	5.6856546	5	19882	1.8445626	7.33858	21
19636	-2.1630936	5.6435356	5	16849	1.8895713	7.370586	21

18773	-2.0249474	5.875847	5	17389	1.8194294	7.3180356	21
11155	-2.0444946	5.9472017	5	19502	1.6399958	7.516139	21
11671	-2.0650923	6.046849	5	18911	1.3632226	8.113431	21
17267	-1.8539546	6.321598	5	19024	1.3047109	8.028341	21
18202	-1.5251646	5.573247	5	18896	1.2694787	7.6171327	21
12433	-1.9913169	5.804997	5	19383	1.8610477	7.5776377	21
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18831	-1.9129258	6.291913	5	19919	1.1522037	7.886904	21
18210	-1.9150801	5.81197	5	19340	1.1255097	7.9268475	21
16112	-1.7344136	5.9168234	5	19565	1.0489082	7.7532654	21
13284	-1.4278722	6.4508862	5	17265	1.3255808	7.9905467	21
12452	-1.9022129	5.752924	5	17611	1.3649772	7.9109426	21
11566	-1.8890244	5.7382627	5	18186	1.3748634	7.912187	21
17687	-1.9502068	5.7728686	5	18425	1.2942364	7.8676376	21
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14591	-1.3899063	6.3825583	5	19916	1.3747414	7.971386	21
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13194	-1.4197006	5.5751514	5	18063	1.1183585	7.626445	21
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12014	-2.02854	5.915727	5	19435	2.3057892	7.860548	21
17023	-1.947415	6.273816	5	17113	2.407598	7.7719536	21
20032	-1.8056768	5.670721	5	19287	2.3309085	7.833312	21
12699	-1.8730339	6.710277	5	13458	1.3908378	8.018514	21
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11408	-1.9719044	5.76746	5	17831	1.9337603	7.340215	21
20023	-1.8636436	6.0266576	5	18473	0.98734003	7.716917	21
18852	-1.8724138	6.0239286	5	19743	1.0942369	7.6524544	21
18607	-1.9179678	6.1227665	5	19336	2.1618729	7.5042143	21

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19055	-1.7648581	6.101564	5	18927	1.332614	7.9628415	21
15576	-1.7316935	6.0592504	5	19946	1.2457117	7.696083	21
19331	-1.7649606	5.9691534	5	18193	1.2902519	7.843649	21
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18447	-1.6702273	6.0837827	5	17082	1.7790784	7.817817	21
11539	-1.6656291	6.177597	5	17276	1.748357	7.8012915	21
13500	-1.5155363	6.079365	5	20033	1.7991399	7.5437875	21
13035	-1.3038816	5.5130157	5	19528	1.5417595	7.503671	21
19507	-1.3540734	5.513136	5	16957	2.279875	7.2675276	21
12585	-1.5227325	6.0086517	5	17084	2.198892	8.112682	21
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17812	-1.5019573	5.5913944	5	17177	2.1413717	7.5912776	21
16879	-1.5256475	6.042797	5	17466	1.4791809	8.088519	21
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12199	-1.7323047	6.125929	5	19531	1.3446965	8.113449	21
13127	-1.6227208	5.656121	5	19152	2.3323038	7.842344	21
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16604	-1.51545	5.539822	5	18615	1.8106345	7.816761	21
13499	-1.4612355	5.982444	5	16895	1.7636719	7.2097697	21
19198	-1.8438075	6.068259	5	18223	1.8213588	7.740735	21
17538	5.2107744	9.92012	6	17408	2.1220028	7.209689	21
19612	4.432037	9.524753	6	18388	2.2975981	7.6102333	21
19947	4.9596868	9.550642	6	15823	2.1801448	7.707962	21
19382	4.9537225	9.562246	6	16709	1.7962466	7.7688355	21
20046	4.270333	9.408594	6	18672	1.2974566	7.8265176	21

17990	4.826073	9.246985	6	17733	2.2789192	7.938962	21
18410	4.404516	9.5605135	6	15556	1.989203	8.153211	21
18227	4.2652907	9.317796	6	19431	2.3301125	7.4441104	21
19181	5.1767955	9.882144	6	18867	2.2800462	7.9309015	21
19920	5.1608343	9.803249	6	17569	2.2014875	7.927466	21
19747	4.950687	9.446972	6	19250	2.1326232	7.858133	21
18554	5.2565274	9.56832	6	17230	2.329786	7.713993	21
18914	4.5126452	9.146176	6	19746	1.6833701	7.2796435	21
18985	4.9640155	9.538932	6	18887	2.2548177	7.685179	21
20394	5.2814593	9.563544	6	17914	2.2971592	7.5564556	21
20205	4.891609	9.791305	6	18159	1.7535787	7.328209	21
17309	5.3124814	9.766296	6	19727	2.194299	7.778904	21
16565	5.2179317	9.911227	6	19369	2.2014484	7.654675	21
17344	5.4422703	9.776735	6	18322	2.0179613	7.6736345	21
17273	5.4918547	9.757292	6	18005	2.2055306	7.655372	21
18361	4.5195203	9.425015	6	20210	2.1391494	7.6253295	21
13226	4.355327	9.601529	6	17582	2.1623046	7.6556277	21
11034	4.364363	9.487794	6	17899	2.2921796	7.6331367	21
12971	4.7634096	9.312732	6	18989	1.644438	7.302497	21
18903	4.316985	9.603424	6	17474	1.6455575	7.45167	21
17949	4.226555	9.535333	6	17643	2.1946156	7.409811	21
17155	4.412865	9.563547	6	17381	2.0188646	7.4348025	21
18244	4.4995785	9.568457	6	18387	2.3613994	7.689265	21
17281	4.4141297	9.570349	6	17105	2.1376565	7.592411	21
11104	4.417925	9.595568	6	19208	1.5725571	7.4506154	21
18279	4.490974	9.550851	6	17380	2.0919523	7.5984197	21
18784	4.516596	9.506097	6	15874	1.8148518	7.4092817	21
18663	4.4459863	9.534639	6	17161	2.0654898	7.532515	21
15843	4.3927364	9.580514	6	17021	2.0789342	7.5816703	21
19852	4.5928135	9.58759	6	19117	2.0805218	7.569323	21
17041	4.6942983	9.55844	6	19898	2.0116904	7.520391	21
17044	5.1967287	9.953303	6	19118	1.5653331	7.3714848	21
19702	5.1110053	9.772239	6	18311	1.2106229	7.7203965	21

18482	4.565262	9.747355	6	15346	2.5169327	7.3639307	21
17256	4.4586563	9.601805	6	18364	1.3891834	7.396918	21
19560	5.2518897	9.941234	6	18643	1.800932	8.068382	21
18040	5.098632	9.886246	6	19077	1.855231	7.7724533	21
12946	4.5787935	9.293785	6	19107	1.8560892	7.8777804	21
13702	5.2237306	9.715121	6	18343	1.8421156	7.9225044	21
19982	4.720687	9.819331	6	18249	1.6712611	7.888216	21
14489	4.851119	9.925296	6	19399	1.7499226	7.874188	21
16624	5.233785	9.6075535	6	19112	1.8095397	7.8445096	21
11161	4.779784	9.755763	6	18020	1.8078866	7.8071704	21
16601	4.716854	9.82076	6	18702	1.4777848	7.8840322	21
18114	5.2337112	9.644569	6	17771	1.853877	7.77707	21
16667	5.3390517	9.795205	6	18199	2.406885	7.298566	21
16606	5.266851	9.871032	6	15600	2.5476427	7.288018	21
17739	5.1348114	9.9489155	6	15442	2.465288	7.223315	21
18996	5.242411	9.914732	6	18313	2.0015266	7.3176103	21
17119	5.190153	9.957182	6	18668	2.1813037	7.4299736	21
16568	5.152076	9.974645	6	15475	2.2806861	7.425114	21
18011	5.1442513	9.94511	6	17869	2.5016363	7.359714	21
18198	5.20999	9.91407	6	16392	2.4542086	7.1862407	21
19924	5.1490564	9.99335	6	17527	2.4378135	7.1715555	21
19863	5.2356286	9.909739	6	19680	-0.282848	6.2863445	22
18295	5.223318	9.941833	6	18034	-0.4089595	5.238581	22
16618	5.207044	9.885956	6	17937	-0.2691385	6.6478972	22
17775	5.2121687	9.947928	6	18240	-0.26275983	6.665528	22
17736	5.2338743	9.923684	6	18798	-0.08877509	6.4433827	22
17458	5.105133	9.980521	6	18556	-0.05811039	6.251186	22
18251	5.087615	10.005123	6	18964	-0.8494435	5.5962543	22
13841	5.2427745	9.733952	6	20432	0.33690283	4.754941	22
15611	5.084371	9.985326	6	18025	-0.18568572	6.135061	22
16646	5.2409577	9.72767	6	19020	-0.019282838	6.0834723	22
17528	4.998432	9.763676	6	20409	0.10883271	4.8706756	22
10956	4.7536836	9.877051	6	20016	-0.2965266	6.3090835	22

16615	4.5945797	9.656583	6	17203	-0.17293878	6.8545675	22
20367	4.6754875	9.80739	6	18620	-0.08585816	6.869952	22
16635	4.7082	9.351547	6	17249	0.08214968	4.712635	22
19803	5.2092137	9.882265	6	19929	-0.09910464	6.032315	22
15275	4.6729236	9.573581	6	20408	0.044165388	5.8603334	22
16923	5.070237	9.977441	6	17170	-1.0791029	6.1117516	22
13377	4.7730103	9.317863	6	17598	-0.14840858	5.899706	22
16218	4.5880823	9.565569	6	19454	0.26895386	5.6363792	22
13240	4.4945893	9.663925	6	16803	-1.037869	6.174485	22
15258	4.5829053	9.546256	6	15883	0.46958578	4.9196434	22
18145	4.4943786	9.720045	6	16877	0.4282819	4.9755454	22
20048	4.515945	9.67216	6	15539	0.2896157	5.0508437	22
17530	5.236219	9.538825	6	18946	0.2741243	5.01227	22
17438	4.5125275	9.683061	6	19414	-0.004140766	7.3013854	22
15376	5.0573363	9.623194	6	18568	0.2844547	4.330054	22
19776	4.9653907	9.625155	6	19677	0.2934576	4.806392	22
18704	5.0127873	9.498579	6	19675	-0.17580403	6.1311536	22
19604	4.5396175	9.320517	6	17497	-0.41961995	5.246672	22
16052	4.5557404	9.382357	6	12635	-0.29155496	7.16506	22
16273	5.063178	9.602686	6	17810	-0.28631768	6.6490464	22
18232	5.0891633	9.479103	6	19284	-0.17030327	6.3331075	22
18460	5.093687	9.409403	6	18503	-0.29073125	7.338543	22
17629	4.9783096	9.595841	6	18751	-0.31459317	7.2478704	22
14583	5.0630617	9.559861	6	17304	0.18023665	4.235383	22
17515	5.1000133	9.4763365	6	18687	-0.413882	6.2578573	22
17870	4.908038	9.483433	6	16934	0.07570873	3.8877792	22
17593	4.813427	9.428743	6	18400	-0.32347557	6.087015	22
17399	4.832461	9.453132	6	16680	-0.390781	5.5369873	22
19401	4.88289	9.520973	6	17398	-0.7543557	6.2934093	22
16620	5.017958	9.546921	6	13464	-0.382631	5.4458237	22
17626	4.2787027	9.264471	6	19869	-0.93240076	6.511009	22
18610	4.493852	9.391134	6	18185	-0.05528485	5.15192	22
18693	4.6264353	9.4665165	6	13335	0.41594088	4.6620355	22

19029	5.065713	9.735932	6	16891	0.36065248	4.4850435	22
17684	5.124789	9.709726	6	13183	0.4039182	4.5824537	22
17857	5.068105	9.604031	6	16947	0.30902562	4.764719	22
14102	4.7163134	9.46318	6	17075	0.07115438	4.3974075	22
16590	4.5869045	9.528512	6	13149	0.5524109	3.9835565	22
20473	4.387959	9.351643	6	19667	0.3566449	5.675605	22
15411	4.5106015	9.44746	6	19461	0.029145712	4.7097955	22
14008	4.588068	9.533126	6	18906	0.020924356	4.720372	22
11038	4.874263	9.649969	6	17495	0.01932258	4.7218804	22
17902	4.8259296	9.480359	6	16703	0.5058934	6.2137203	22
12812	4.914631	9.61011	6	16914	0.012254433	3.8222005	22
16655	4.828103	9.562819	6	18958	0.8323609	4.4479704	22
17844	4.8993425	9.712864	6	18522	0.6095553	4.852871	22
16043	4.7621765	9.212689	6	12421	0.7412993	4.880446	22
17691	4.9227786	9.5981045	6	12811	0.6183223	4.8257437	22
14860	4.8302665	9.474873	6	20207	0.54722893	4.766605	22
17059	4.8868213	9.348281	6	19039	0.5587215	4.7642455	22
18015	4.5918236	9.248525	6	19587	0.54287404	4.851765	22
14453	4.617757	9.289031	6	15869	0.6048497	4.846293	22
16612	4.7366886	9.224307	6	16521	-0.118832774	5.1126614	22
16588	4.5255866	9.303996	6	19884	-0.17281988	6.8190694	22
17796	4.55744	9.1772585	6	17097	-0.32907024	6.6579695	22
17681	4.7758555	9.257247	6	18456	-0.4251213	6.296462	22
18124	4.803995	9.342787	6	16778	0.42551795	4.875886	22
17751	4.806221	9.306172	6	17526	0.41168916	5.634256	22
17631	4.7877035	9.33629	6	13231	-1.0807602	6.0981636	22
20069	4.393027	9.351004	6	13273	-1.2050803	6.507481	22
15368	4.327465	9.317413	6	16533	-0.31496108	6.2944627	22
18116	5.227084	9.553063	6	19712	-1.29015	6.570066	22
18140	5.1148777	9.741888	6	18464	0.47091278	6.1119967	22
18591	5.078995	9.727448	6	15359	-1.0085989	6.1082315	22
18766	5.122955	9.744791	6	16683	0.40743718	4.872709	22
12628	4.7575827	9.657409	6	15864	0.35381663	5.6082897	22

18873	4.7412276	9.302235	6	13345	-0.9364409	5.7137003	22
17788	4.811658	9.43237	6	12194	-0.053553108	5.923365	22
18957	4.5327015	9.633406	6	20050	-1.0236129	6.6190286	22
16270	4.580868	9.598939	6	16933	-0.07418677	3.955443	22
17095	4.5732236	9.660187	6	16966	0.35770264	5.50358	22
17361	4.59775	9.584667	6	19927	0.37632304	5.5164123	22
18107	4.6114674	9.538198	6	19931	0.45086464	5.4614463	22
17468	4.552764	9.571894	6	18805	0.42457208	5.4772553	22
20462	5.0787816	9.816603	6	17362	0.30051064	5.5067024	22
16622	4.73891	9.511024	6	17147	0.43619588	6.078274	22
16664	5.451737	9.7793665	6	17212	0.117612444	5.961796	22
17848	5.161832	9.977259	6	17588	0.05119812	5.8783607	22
19355	5.2087255	9.942902	6	19103	0.27756572	5.6260767	22
15839	5.0286884	9.391534	6	17628	0.32127696	5.6015477	22
16719	5.031224	9.507063	6	11193	0.00611877	5.9078836	22
17422	4.9508257	9.401568	6	12412	0.00509663	5.9266686	22
17702	5.0492167	9.447015	6	18152	0.01655594	5.909879	22
16589	4.996704	9.448455	6	16838	-0.19211972	7.2144556	22
19805	5.082845	9.431865	6	16967	0.37466642	5.521798	22
11050	5.0594177	9.451026	6	16826	0.37321687	5.5573645	22
19315	4.879069	9.589945	6	15685	-0.2784883	5.9846063	22
16892	5.3151035	9.808676	6	17057	0.31367698	5.9736214	22
12967	5.3260493	9.808117	6	19520	-0.7689347	5.647781	22
18201	4.2678614	9.315363	6	13361	0.018117558	5.8799005	22
17012	4.482545	9.679982	6	17078	-1.0687402	6.0746975	22
19639	5.2722607	9.733495	6	16937	0.026078839	3.9768584	22
17194	4.152873	9.197037	6	20070	0.33785313	5.6237173	22
17409	5.5084386	9.728184	6	17320	0.38329145	5.511209	22
16602	5.1196847	10.019958	6	19192	0.70130444	5.9173594	22
18580	5.1409483	10.0347395	6	19598	0.70281	5.8950353	22
17284	5.4583535	9.735445	6	19888	0.7145498	5.79599	22
17521	5.1435204	9.72088	6	16985	-0.067273304	3.9198203	22
18168	1.7670395	4.8341565	7	13265	-0.29902792	7.263666	22

20213	1.127619	5.8028765	7	18830	0.5495407	5.242152	22
20092	2.2159135	5.4093037	7	19997	0.2730139	4.8095827	22
17984	1.7006866	4.804104	7	19204	0.516758	5.198303	22
19412	2.1091805	5.625185	7	19801	0.73933566	5.6678743	22
20436	1.3725299	4.8534966	7	16954	0.06547246	3.8816853	22
15780	1.3604835	5.014413	7	17260	0.3035714	5.4705076	22
19122	1.8801562	5.54117	7	19409	-0.24891992	6.764151	22
19790	1.9040695	5.8072505	7	17969	-0.089986	7.2637963	22
17317	1.8193456	5.3087077	7	16754	0.29894656	4.281103	22
20058	1.6022644	5.250096	7	17245	-0.36875084	5.252575	22
20468	1.323992	6.2386246	7	15083	0.52519304	4.775503	22
19645	1.6874632	5.189952	7	16323	0.83382094	5.1603746	22
17957	1.820474	5.1604285	7	12237	-0.31326884	5.3130164	22
11041	1.4052551	4.7091026	7	17292	-0.22239618	5.314604	22
18252	1.2246113	4.75834	7	12633	-0.41590118	5.197354	22
17164	1.202915	4.730026	7	17893	-0.32741284	6.812239	22
14716	1.2531316	4.69449	7	12249	-0.26943192	6.757939	22
17277	1.2050955	4.717903	7	19601	-1.065049	7.2893777	22
16141	1.2272675	4.68887	7	16941	0.5701753	4.2578654	22
19899	2.0058973	5.240269	7	16944	0.83375734	4.393031	22
13061	1.7787069	5.2055902	7	13269	-0.6231826	6.580584	22
17846	2.0824063	5.0910234	7	18507	-0.1933125	6.711767	22
16321	1.5246938	5.4363523	7	17469	-0.8278476	6.8255324	22
18170	2.1272268	5.2073965	7	18701	-0.24728604	6.6119037	22
11782	2.1334727	5.178792	7	20449	-0.62984776	6.5949306	22
12725	2.076219	5.2539616	7	13300	-0.8701465	6.5467944	22
13341	1.7925843	5.2446904	7	17920	-0.84377635	6.5407934	22
20052	1.9541055	5.1088324	7	17201	0.29044905	3.9598675	22
19418	1.936518	5.067645	7	13598	-0.23082832	6.662717	22
19689	1.2872746	4.825774	7	18502	-0.9275491	6.900669	22
18499	1.8985276	5.001535	7	17604	-0.28633022	6.640283	22
16428	1.4619851	5.421473	7	17962	-0.26734808	6.666525	22
13334	1.4881397	4.225295	7	18450	-0.41099486	6.2437506	22

13114	1.5050673	4.3036675	7	12708	-0.7670318	6.5638437	22
16135	2.2452073	5.3505793	7	16224	-1.3783596	6.9069867	22
18776	1.7870938	4.875731	7	14475	-1.3411672	6.960805	22
18369	1.3007159	5.6423764	7	18379	-1.0516154	6.2271423	22
20149	1.7615839	4.6354456	7	17297	-0.011944802	4.1814213	22
18698	1.6054693	4.6937833	7	16753	0.034034796	3.9757113	22
18584	1.5670286	5.413938	7	16761	0.02283867	3.9144711	22
19324	1.6278645	4.6671963	7	15264	-0.96360093	6.564861	22
19249	1.6241388	4.6554604	7	15034	-0.43613496	5.0487227	22
15901	1.9837806	4.81231	7	16746	0.049440112	3.9901109	22
18521	1.2999452	5.6209884	7	13389	-0.5633492	4.9864306	22
12768	1.2334971	5.4593563	7	11064	-0.5255753	4.971676	22
19155	1.1945647	4.8055058	7	18427	-0.56360674	4.906961	22
12755	1.650283	5.0548368	7	11357	-0.5190746	4.931272	22
15745	1.4370089	4.2804003	7	19608	-0.5041361	4.975225	22
13482	1.4754512	5.586788	7	20374	-0.561136	4.8721976	22
19359	1.75625	4.9599066	7	18209	-0.65065265	5.1126947	22
15617	1.2344165	5.6849656	7	15520	-0.9890481	6.78365	22
18256	1.6721222	5.2417684	7	19611	-0.78150904	6.0339885	22
19783	1.7532619	5.058471	7	17806	-0.90297186	6.306351	22
17866	0.85851806	5.4584403	7	18117	-0.9374593	6.3242955	22
18876	1.6849114	5.0934896	7	19530	0.15291649	6.974436	22
15492	1.6638751	5.858449	7	17931	-0.26755485	6.6596074	22
12093	1.8129115	4.611541	7	13082	-1.448805	6.845069	22
17479	1.5309335	6.1219826	7	12402	-1.4534317	6.8320475	22
18561	1.7886845	4.682931	7	13457	-1.4330137	6.873456	22
17378	1.6944014	5.1819487	7	13581	-1.4131314	6.8973436	22
17919	1.3456829	4.9210005	7	19956	0.37655503	5.558085	22
18769	1.4344149	4.947252	7	17124	0.2967104	4.6396065	22
19367	1.11576	4.9043927	7	19096	-0.028637132	5.951907	22
18649	1.0931051	4.870238	7	17974	0.032078277	4.0396914	22
17168	1.633877	5.915994	7	19023	0.64471054	4.048827	22
17762	1.5812073	6.078768	7	10987	-0.4577564	5.077434	22

18266	1.3465552	4.3316107	7	16899	0.6302928	4.552726	22
12071	1.4779797	4.949918	7	18533	0.8358836	5.369366	22
17900	1.7626606	4.5654855	7	17365	0.7393811	5.1919565	22
12885	1.6680669	5.9574385	7	16790	0.014704883	4.760487	22
12491	1.5376929	4.7509966	7	16931	0.30382773	4.8886504	22
17989	1.4898612	4.79128	7	16831	0.08264724	4.806849	22
17496	1.5338502	4.934993	7	17234	-0.9801079	6.154816	22
18604	1.6601285	4.5987787	7	19987	0.27667758	4.2916317	22
20400	1.6860553	4.3189154	7	19866	-0.4647691	6.6532593	22
17667	1.3837287	4.342445	7	20163	-1.276746	7.064195	22
19203	1.1777675	4.944221	7	17202	-0.47990143	6.5887523	22
15806	1.7850984	4.826811	7	17169	-0.20233531	5.0906963	22
19631	1.5325589	4.3861837	7	18036	-0.41940397	5.2031903	22
20025	1.7747533	4.5083385	7	11587	-0.40452293	5.2138643	22
18278	1.6745232	4.9878526	7	20376	-0.41779366	5.2021637	22
18438	1.7580552	4.4935207	7	10975	-0.39026803	5.2220736	22
18066	1.676488	4.5506563	7	19073	-0.479848	6.567279	22
19144	1.7315956	4.5333223	7	15433	-0.3837142	5.2375083	22
18049	1.6824993	4.974733	7	18484	-0.34215248	5.2251353	22
13161	1.4071836	4.4342265	7	17367	-0.73512363	7.3960576	22
16418	1.5144819	4.200739	7	18162	-0.29340884	6.623361	22
18018	1.7707069	4.9462337	7	19395	-0.19883214	6.4826584	22
14278	1.8285381	4.5321198	7	16848	-0.23980509	6.575385	22
12549	1.5998856	4.8486032	7	18656	-1.1730946	7.041985	22
13418	1.711413	4.792113	7	13296	0.013505486	5.4643717	22
15414	1.8501434	4.717991	7	19266	-0.4660787	6.554304	22
18401	1.732584	4.7543774	7	20086	-0.41932186	5.232306	22
19115	1.8104936	5.331842	7	10991	-0.4157816	5.227092	22
17694	1.7224882	4.6748137	7	17143	-0.49310905	7.357488	22
17620	1.632618	4.728519	7	13340	-1.074615	6.178085	22
18195	1.759566	4.6392465	7	15832	-1.293547	7.046439	22
16044	1.6967697	4.6874986	7	19965	-1.2884274	7.0531135	22
19174	1.3398682	4.339475	7	17740	-1.2998531	7.0633287	22

14376	1.437116	4.364024	7	19087	-0.38868967	5.274264	22
17935	1.7084274	4.720258	7	15065	-0.34288427	5.311101	22
12375	1.6171138	4.9083767	7	19971	0.5560154	5.971412	22
16204	1.4789457	4.107333	7	13391	-1.455407	6.984448	22
16406	2.0691488	5.1125927	7	17400	0.80675733	4.2263756	22
14926	1.5666373	5.4871197	7	18750	-0.98627996	6.731263	22
13368	1.6753354	5.383719	7	20479	-0.52809584	6.632071	22
13322	1.3683484	5.540004	7	18806	-0.53550535	7.2195454	22
12780	1.2846545	5.4254217	7	19913	-0.33212906	5.3081403	22
13056	1.3191048	5.5551834	7	17188	-0.517327	7.361536	22
13492	1.9684986	5.302238	7	19236	-0.3604435	6.622139	22
19534	1.2398702	5.458306	7	18448	-1.880515	7.058852	22
17342	1.2949438	5.578629	7	19459	-0.80860656	6.4405985	22
13488	1.4601234	5.402758	7	18504	0.46424544	5.5167375	22
13015	2.1295247	5.3127866	7	19809	-0.9619206	7.2662854	22
16557	1.3117168	5.5691104	7	18095	-0.19655935	5.0113263	22
13327	1.4029614	5.382846	7	17343	0.5165016	5.665996	22
13250	1.7416055	5.337276	7	15660	-0.8978979	5.629903	22
14815	1.501799	4.263497	7	17315	-0.88372904	5.6235433	22
12157	1.5321069	5.3593516	7	18147	-0.32372248	6.354376	22
12319	1.3818011	5.369004	7	19210	-0.29785654	6.321632	22
15210	1.6320829	5.557509	7	17213	-1.0449584	6.110991	22
20415	1.7769684	5.2968926	7	19907	0.4635345	4.987719	22
20214	1.5173664	5.3842416	7	18674	-0.9248128	5.6340766	22
15610	1.5250895	5.4352436	7	18781	-0.24545258	4.9162545	22
15401	1.5208031	5.365409	7	16548	-0.29522747	6.2655787	22
13402	1.7124248	5.3170424	7	14960	0.81730956	5.4075217	22
13198	1.3636513	5.5068445	7	17712	5.5447783	7.4905367	23
16230	2.1643853	5.373775	7	18559	5.2906623	6.875861	23
13491	1.5304891	5.3808923	7	19114	5.3199677	6.9369884	23
13350	1.6389436	5.395266	7	18248	5.3346977	7.104531	23
16486	1.893985	5.4248967	7	18758	5.448992	7.1297	23
12895	1.9692729	5.5082397	7	18422	5.1971445	7.002635	23

16247	1.8967837	5.4035034	7	17141	5.847437	7.796817	23
15591	1.9270602	5.408232	7	15051	5.9524236	7.5838223	23
15499	1.9235204	5.42642	7	19429	5.7329435	7.2376704	23
15769	1.6077684	5.4053965	7	15398	6.1660347	7.436519	23
13323	1.7129076	5.379486	7	19562	5.900845	7.704344	23
12933	1.4004118	5.3420916	7	16232	5.303934	7.120638	23
13052	1.2810814	5.5575986	7	19524	5.9276967	7.469495	23
17463	1.1829613	5.4504128	7	18154	5.5970826	7.132876	23
14936	1.6093866	5.369392	7	15672	5.5939875	7.1330214	23
13453	1.5399741	5.368425	7	17439	5.7674575	7.9001856	23
14357	1.3391544	5.546255	7	16411	5.6389227	7.1909795	23
14898	1.5022913	5.3685837	7	16599	5.8203106	7.284038	23
15023	1.2759836	5.430278	7	14733	5.6064353	7.2104135	23
12413	1.3961693	5.3695803	7	18981	5.328093	7.547236	23
13150	1.4115762	5.3732686	7	11152	5.925005	7.4267354	23
18226	1.3868729	5.488169	7	13145	5.9518247	7.5628996	23
16385	1.4446603	5.4662976	7	17449	5.8312216	7.458826	23
16408	2.0041156	5.3436985	7	17014	5.9212694	7.567205	23
15853	1.2637801	5.386668	7	20082	5.356879	7.527417	23
13463	1.3774451	5.3877883	7	19600	5.179655	7.027668	23
15805	1.1095054	5.2947135	7	15312	5.324262	7.5590277	23
16286	0.88534516	5.0855103	7	19576	5.505265	7.427834	23
15175	1.4990873	5.4489384	7	19319	5.30643	7.2191696	23
12193	2.0371246	5.214299	7	18904	6.0203757	7.6150928	23
20442	1.7297332	5.351267	7	15871	5.827294	7.187435	23
19753	1.303378	4.987235	7	17009	5.7802925	7.273252	23
19633	1.9334079	5.8051257	7	17992	5.6559415	7.337146	23
18459	1.6036338	5.381855	7	17403	5.784956	7.600067	23
12074	1.6233745	5.020144	7	18094	5.574717	7.2557664	23
18817	1.506616	5.5910873	7	19438	6.2173104	7.401192	23
15296	1.2098466	5.764681	7	18601	5.695092	7.253298	23
19704	1.7006875	4.960531	7	18699	6.128807	7.347718	23
17104	1.0981233	5.9054327	7	17345	6.1635904	7.2908316	23

12671	1.1014581	5.8525953	7	12917	6.0083923	7.3921623	23
17042	1.1530969	5.785575	7	17096	6.131925	7.295649	23
16426	1.1787821	5.751948	7	18139	6.1497445	7.266146	23
19056	1.1773638	5.7794824	7	19021	5.9913363	7.506533	23
11575	1.5405875	4.9372315	7	19908	4.726932	6.695148	23
17111	1.773452	5.149891	7	19364	6.2171206	7.393746	23
17311	1.0839343	6.0097528	7	18346	5.438356	7.607096	23
12181	1.644304	5.001772	7	17977	5.90186	7.456403	23
18628	1.6972861	5.0447783	7	19833	5.229039	7.120993	23
11713	1.5157135	4.90474	7	17306	5.477046	7.201834	23
16308	1.638627	4.85229	7	18646	5.61481	7.164396	23
15512	1.2175897	5.748085	7	19993	5.4210353	7.5564423	23
16362	1.2031327	5.7411175	7	18310	5.4373918	7.3016887	23
12116	1.7025428	5.041598	7	15722	5.44782	7.220028	23
18827	2.0012264	5.70095	7	19374	5.9821634	7.5134177	23
15457	1.8722365	5.84254	7	19133	5.519039	7.19481	23
13495	1.5328903	5.3328037	7	19599	5.8262215	7.49847	23
17121	1.9341749	5.9061565	7	15907	5.4367228	7.650533	23
18944	1.5424939	4.959317	7	20017	6.2068443	7.4014487	23
19450	1.914469	4.7420726	7	16948	6.002575	7.5607204	23
16927	1.2299434	4.635437	7	15755	5.029492	7.30566	23
15669	1.6731132	6.0493174	7	15904	5.2687473	7.082116	23
16214	2.1587942	5.4983163	7	17985	5.1586604	7.047759	23
19465	1.3214462	4.318263	7	19577	5.251312	7.210676	23
15878	1.8172239	4.778366	7	19224	5.342406	7.1136227	23
19378	2.0810785	5.610861	7	15010	5.350697	7.118652	23
12996	2.0864005	5.5724936	7	15400	5.2068973	7.209052	23
18638	1.8361251	4.74584	7	17612	5.405783	7.227405	23
20383	1.6284801	4.685221	7	17856	5.6890206	7.750274	23
18247	2.0648153	5.0311913	7	18086	5.8600116	7.207698	23
19686	1.6655277	5.653587	7	20105	5.327109	7.111482	23
15694	2.095764	5.061121	7	14640	5.3254223	7.1673293	23
11931	2.0996118	5.082391	7	16130	5.2584896	7.2277403	23

15962	2.0546975	4.990965	7	18627	5.730181	7.7292104	23
18645	1.0189285	5.472466	7	18044	5.937735	7.6885543	23
19472	2.0994341	5.020995	7	18603	5.6941	7.7010684	23
18695	0.98039377	5.41905	7	16642	5.8856907	7.2995644	23
18630	2.0441992	4.9196434	7	18801	5.5168204	7.550365	23
18200	1.6384339	5.9935703	7	15586	5.523491	7.366525	23
18870	0.92922115	5.0000734	7	17357	5.917554	7.6519604	23
19019	2.411869	5.660802	7	14817	5.67650 56	7.712319	23
19634	1.9249438	4.695395	7	16520	5.4947805	6.99089	23
18326	2.1028018	5.6484456	7	17268	5.988122	7.5208154	23
20419	1.3746684	4.346088	7	17159	5.5818744	7.440665	23
12939	1.27678	5.572263	7	15655	5.45283	7.063644	23
17517	1.3187718	5.550372	7	13651	5.746535	7.243387	23
13304	1.3396518	5.0132747	7	19832	5.764607	7.2800145	23
17886	1.6853943	5.2922225	7	17431	5.7485604	7.2893486	23
19826	0.66868025	9.144319	8	18596	5.799213	7.491061	23
20429	1.4662616	9.507046	8	13394	5.819882	7.91191	23
18609	1.3789321	9.352329	8	17446	5.7269244	7.2212296	23
19296	1.5060067	9.700496	8	15661	5.69834	7.2360415	23
17511	1.0413823	9.642777	8	16597	5.677815	7.165871	23
19674	0.9885435	9.445764	8	16572	5.4396653	7.3347645	23
18747	1.0406446	9.127286	8	16581	5.434972	7.173119	23
13129	1.4219943	9.462257	8	16579	5.471068	7.262337	23
16802	1.6365551	9.56143	8	16569	5.4660945	7.205151	23
18547	1.5072771	9.190353	8	17543	5.5060573	7.1440396	23
13360	0.5704203	9.271911	8	12667	5.489267	7.1533337	23
18259	1.3564532	9.273563	8	11073	5.533166	7.413403	23
14244	1.0064183	9.213838	8	16633	5.7900295	7.5278587	23
19844	0.9953698	9.198044	8	17609	5.8401947	7.3589745	23
18153	0.95620865	9.201018	8	17416	5.7435427	7.3462877	23
18606	1.0866717	9.358351	8	16570	5.787958	7.343375	23
18076	0.93237877	9.137712	8	17417	5.5820956	7.2840757	23
17798	0.8780327	9.172111	8	16151	5.5715227	7.309992	23

18122	0.91805786	9.114545	8	16217	5.4935846	7.1469154	23
18658	0.97576475	8.874639	8	18683	5.827871	7.8123493	23
12581	0.5705213	8.736747	8	12226	5.910778	7.7212095	23
18629	0.76612943	8.945161	8	16598	5.7099752	7.8632417	23
18363	0.94112825	9.101175	8	13195	5.6649175	7.441917	23
20007	0.9783291	9.114019	8	11788	5.664163	7.357461	23
11127	0.986435	9.013988	8	17928	5.9795914	7.5442295	23
18381	1.2115899	8.995666	8	19243	5.8608127	7.4183345	23
19613	0.9522285	9.137101	8	17016	5.6961436	7.5018506	23
19326	0.9807238	9.061652	8	17952	5.507925	7.099665	23
19226	0.9332538	9.047585	8	15250	5.5304055	7.1003904	23
13441	0.7045449	8.791623	8	16583	5.7120514	7.2897935	23
19705	0.81087804	8.896737	8	17412	5.736785	7.296943	23
17716	0.940318	9.012602	8	11008	5.6926045	7.246246	23
17341	1.1555635	8.938251	8	16652	5.9171133	7.450741	23
11329	0.9767419	9.032002	8	18087	5.769383	7.377349	23
17219	0.9362048	9.112497	8	17621	5.7217817	7.263506	23
18028	0.6573138	9.256362	8	17411	5.6231027	7.2834163	23
19345	1.2818373	8.908455	8	14111	5.6348047	7.4049244	23
18217	1.1724145	8.911074	8	19362	5.5164323	7.1677737	23
18809	0.8227254	8.937848	8	18012	5.5143957	7.183187	23
15116	1.0862293	9.045322	8	17648	5.5302043	7.1867037	23
19254	0.75846106	8.999061	8	17642	5.4935813	7.1726713	23
17549	0.9623018	9.20671	8	20380	5.5283866	7.1903276	23
11697	1.1174321	8.931682	8	18224	5.6230507	7.313053	23
20228	0.58177817	9.115487	8	16582	5.636707	7.430816	23
14907	0.49783504	9.110325	8	16610	5.7815657	7.873939	23
12907	0.593047	8.991425	8	19442	5.8631153	7.4684367	23
19178	0.85400474	9.2177305	8	13404	5.948387	7.5128846	23
20165	0.36789852	9.045046	8	19168	5.8637295	7.6733475	23
19417	0.56742555	9.121913	8	17770	5.9472475	7.6634197	23
17093	0.89972097	9.032531	8	18052	5.9401016	7.6302094	23
15860	0.32760924	8.897072	8	19986	5.79902	7.842151	23

18745	0.90530765	9.125888	8	18660	5.9419656	7.635907	23
19658	0.449897	9.045213	8	18848	5.946818	7.4872947	23
17560	0.929726	9.098082	8	17427	5.875595	7.7499223	23
19925	0.900605	9.179867	8	13143	5.8170824	7.703712	23
17996	0.9454566	9.101149	8	15260	5.7215805	7.7511435	23
18057	0.7830534	8.9578285	8	15220	5.756122	7.6483364	23
20129	0.9907581	8.821693	8	19813	5.771713	7.6944895	23
18350	0.858145	9.0337715	8	17833	6.0279584	7.495149	23
19303	0.74913716	8.97257	8	18912	6.053821	7.4847236	23
19479	0.7731396	8.917361	8	16603	5.9422092	7.568239	23
19277	0.7314677	8.955652	8	17975	5.9855533	7.525492	23
18292	0.8307099	8.931403	8	18937	5.956887	7.6003594	23
19714	1.0751796	9.22637	8	17924	5.9082026	7.621645	23
19384	1.4275557	9.883933	8	18726	5.9453053	7.5563436	23
19806	0.8966032	9.056082	8	17606	5.932261	7.5922446	23
18921	1.4674395	9.705606	8	16585	5.8820777	7.4850454	23
18777	1.0032367	9.311173	8	17338	5.7628965	7.7859116	23
15906	1.452301	9.871504	8	14186	5.715033	7.7259026	23
18493	1.0502886	9.382101	8	17773	5.6500254	7.7183137	23
14329	0.7224331	9.313951	8	18123	5.935008	7.58618	23
13202	0.8665085	9.018381	8	18368	5.773672	7.8199425	23
12891	0.8507876	9.056951	8	14285	5.7266617	7.5316854	23
19651	0.89658314	9.058361	8	13746	5.8380938	7.594971	23
13216	0.8898062	9.074043	8	17668	5.738271	7.6706457	23
16638	0.55497813	9.254376	8	18110	5.712844	7.558298	23
17959	1.3936305	9.50836	8	19697	5.781444	7.7793946	23
19199	1.3985039	9.48348	8	17508	5.7845235	7.682408	23
18936	1.3904796	9.493219	8	20028	5.838254	7.603847	23
19967	1.3554717	9.464987	8	14248	5.765955	7.67328	23
15718	1.3315251	9.353424	8	18342	5.8229733	7.6522636	23
18563	1.4725705	9.566751	8	20054	5.970287	7.694972	23
13466	1.5638508	9.530834	8	19847	5.9160523	7.758907	23
19752	1.3914372	9.477716	8	12969	5.948225	7.6848674	23

19772	1.5917169	9.474063	8	19957	5.9054775	7.6619115	23
19307	1.4027036	9.473429	8	17486	5.990717	7.6216145	23
19735	1.4017128	9.475257	8	17828	5.8821173	7.47591	23
17998	1.43177	9.342009	8	17473	5.6521864	7.4063296	23
17140	1.2329738	9.02796	8	17470	5.680323	7.1871815	23
11372	1.3903052	9.5591	8	17481	5.4943366	7.134384	23
15656	1.0380617	9.075629	8	16535	5.5601416	7.590045	23
16530	1.5780126	9.539153	8	17122	3.6252928	6.728493	24
13425	0.70782876	9.103529	8	16747	3.658031	6.670171	24
11847	0.8913719	9.231814	8	17766	4.405942	6.3608627	24
13378	1.7329737	9.397164	8	16977	3.4882045	6.648537	24
18383	0.8710969	9.373932	8	16860	3.552759	6.632563	24
18439	0.8277571	9.390096	8	16926	3.6379576	6.729526	24
19043	0.55944955	8.895976	8	17242	3.6791081	6.7062545	24
19372	0.49037543	9.015451	8	19501	4.642094	6.427287	24
17039	1.0145668	9.405232	8	18307	4.7004123	6.4839544	24
18265	0.57517093	9.07327	8	18602	4.445346	6.3796086	24
12163	0.40457052	9.118791	8	17437	4.3481812	6.392815	24
19802	0.56282675	9.075635	8	18253	4.4051323	6.3718333	24
11364	0.5055216	9.071328	8	19196	3.7912636	6.433606	24
19799	0.37685657	9.056188	8	19824	4.3679447	6.4054356	24
12825	0.4727779	9.087022	8	17641	4.709335	6.4857354	24
17599	0.40001303	9.067179	8	19197	3.7893708	6.442896	24
17396	0.4167494	8.978663	8	19731	4.4104314	6.331019	24
19729	1.0015796	9.244865	8	18061	4.360866	6.402866	24
17195	0.7666273	9.4777	8	17841	3.831452	6.5823894	24
19278	1.0733703	9.172302	8	18741	3.8750873	6.603334	24
20004	0.9672228	9.255748	8	16987	3.843196	6.559767	24
19072	1.0208684	9.270165	8	16752	3.890401	6.526777	24
19761	0.98029053	9.224363	8	16765	3.8739228	6.5618615	24
11982	0.892667	9.076866	8	17272	3.8484921	6.419843	24
13333	1.5763952	9.640698	8	16881	3.500534	6.621703	24
12659	0.83453304	9.339892	8	16762	3.5499904	6.604532	24

13438	0.52609456	9.185725	8	16716	3.6457171	6.5965676	24
11808	0.7891116	9.4671135	8	16695	3.600653	6.684717	24
12077	0.9733201	9.306777	8	17353	3.9509597	6.4806437	24
13658	0.8589542	9.231047	8	18039	4.75616	6.635744	24
18444	1.5186177	9.200589	8	17162	3.6734354	6.5987306	24
18396	1.0269406	9.343176	8	18216	4.4583335	6.4467936	24
17863	1.0296462	9.327685	8	17007	3.5103328	6.6215324	24
19230	0.99364287	9.3184805	8	19200	4.4066534	6.36819	24
18783	1.032761	9.351063	8	19237	4.2648582	6.6338	24
18988	0.8091046	9.173075	8	17936	3.471329	6.655991	24
13447	1.5757556	9.608067	8	18377	3.4786131	6.5808244	24
18834	0.89384204	9.412352	8	17339	3.9307177	6.5248365	24
19142	0.940521	9.290319	8	16811	3.6023157	6.685928	24
19258	0.7778432	9.39493	8	19444	3.1615756	6.632359	24
13303	0.5345962	9.21546	8	17827	4.4100537	6.3733196	24
19447	0.96921784	9.337749	8	16742	3.6923647	6.5869255	24
20145	0.80179995	9.33803	8	15619	3.602863	6.736369	24
17898	0.7850325	9.353676	8	18592	4.406979	6.3871355	24
19015	1.087384	9.349976	8	18667	4.1686153	6.4336505	24
19839	1.0460827	9.337313	8	17420	4.294343	6.4206367	24
13452	-0.6850692	10.770346	9	17452	4.2421083	6.5059037	24
19883	-0.3749136	11.173935	9	17310	3.9020572	6.532186	24
18705	-0.5358237	10.515651	9	17254	3.638709	6.6558685	24
18851	-0.5248123	10.500367	9	18477	4.4312387	6.350515	24
12781	-0.39260563	10.338163	9	11997	4.3900604	6.3125668	24
14859	-0.7844047	10.490261	9	16002	4.362911	6.353107	24
17552	-0.9740134	10.39089	9	17662	4.352843	6.3481407	24
18774	-0.7550196	10.253933	9	14423	4.3044877	6.359416	24
20157	-0.3109309	10.551211	9	20057	4.3884296	6.314676	24
19930	-1.0686249	10.755272	9	18282	4.1109967	6.4223366	24
16829	-0.50683284	10.215245	9	11259	4.4033256	6.327997	24
10985	-0.08608132	10.693734	9	19739	4.399685	6.3364744	24
19687	-0.26894653	10.4894905	9	19745	4.4066696	6.341736	24

18023	-0.48105323	10.153133	9	16828	3.6242542	6.7110786	24
19741	-0.8171965	11.086882	9	20411	3.6248274	6.656653	24
18814	-0.3716835	11.166688	9	17073	3.479272	6.7939687	24
18666	-0.5783535	10.943948	9	18644	4.2274942	6.4576383	24
17574	-0.5618479	10.987927	9	17548	4.315973	6.4107256	24
18225	-0.6632392	10.913638	9	14246	3.446899	6.7111564	24
12221	-0.15966661	11.105165	9	17222	3.172716	6.778563	24
20114	-0.42818964	11.174474	9	16902	3.4759345	6.574294	24
18678	-0.33518577	10.833147	9	16768	3.488273	6.591797	24
19261	-0.6079162	11.008029	9	16912	3.4675753	6.6976275	24
18062	-0.94412386	10.852755	9	16837	3.5752082	6.6460395	24
19172	-0.40788084	11.150326	9	16825	3.5808718	6.7422934	24
17540	-0.23482399	11.113145	9	16822	3.5666752	6.6520658	24
18525	-0.40652195	10.91203	9	16834	3.589327	6.639455	24
17849	-0.5654804	11.067175	9	16669	3.5035267	6.6858025	24
17818	-0.10982589	11.208733	9	16731	3.5952194	6.6017	24
20469	-0.4565523	11.080573	9	17401	3.514353	6.625144	24
19124	-0.3422884	11.044006	9	15545	4.315753	6.3347864	24
17680	-0.22962458	11.161888	9	16791	3.7762623	6.48865	24
17999	-0.54382044	11.056004	9	18045	4.3528	6.2452674	24
18933	-0.36072513	11.090521	9	16952	3.6042335	6.570018	24
18694	-0.2999221	11.127434	9	18716	3.4308786	6.6677136	24
18213	-0.26492774	10.905201	9	17011	4.3950334	6.33071	24
11126	-0.300158	11.07405	9	18414	3.0076342	6.793564	24
19870	-0.2852865	11.104248	9	16945	3.6719983	6.602196	24
17587	-0.2507447	11.198536	9	19285	3.2171428	6.8488955	24
16607	-0.30706215	11.151532	9	19773	3.2329972	6.835181	24
18501	-0.3475439	11.2097645	9	19725	3.184243	6.615251	24
19648	-0.33857766	11.135676	9	19610	4.120265	6.5137544	24
17797	-0.25675252	11.043393	9	18323	4.152479	6.547444	24
18243	-0.21174529	10.939484	9	17299	4.1528907	6.4655676	24
18337	-0.57400686	11.076018	9	18917	4.1900473	6.4568815	24
18382	-0.44138286	11.226227	9	18229	4.308122	6.4157596	24

17524	-0.22196874	10.684841	9	19730	4.301264	6.4155483	24
19146	-0.23040335	10.699339	9	18549	3.2559211	6.856541	24
19229	-1.0443175	10.766707	9	18398	4.577769	6.392152	24
13144	-0.16416074	10.690121	9	16574	4.265695	6.4391894	24
20187	-0.18546559	10.549344	9	16856	4.2576876	6.4224973	24
17550	-0.28150785	11.063395	9	17748	4.2801485	6.416276	24
18264	-0.301253	11.140565	9	16649	4.237047	6.4759254	24
20091	-0.2863831	10.768876	9	16806	4.215551	6.4290004	24
19185	-0.14114687	10.793085	9	18027	4.5398993	6.3963127	24
17572	-0.18631239	10.686092	9	15423	4.4277115	6.335156	24
17618	-0.20843734	10.725133	9	18807	3.3022292	6.7366157	24
19627	-0.5895763	10.4411125	9	18838	3.3128872	6.732076	24
17696	-0.9077376	10.434528	9	15801	4.421376	6.3434014	24
10983	-0.029837016	10.832624	9	19079	3.0489137	6.8551626	24
17283	-0.9485023	10.407753	9	16885	3.674536	6.6855726	24
19120	-0.19298606	11.083417	9	16702	3.6445327	6.6224337	24
17754	-0.23312864	11.050787	9	16745	3.5513735	6.538613	24
19504	-0.20451209	10.5761175	9	16792	3.6606052	6.666495	24
19664	-0.68431693	10.91118	9	18092	4.863631	6.27535	24
20056	-0.16120268	10.800864	9	18430	3.8313267	6.487082	24
16394	-0.13229209	10.957953	9	16921	3.7486265	6.443562	24
18488	-0.67504704	10.812229	9	16996	3.621783	6.6304655	24
17537	-0.27593473	10.284179	9	16911	3.6521661	6.64704	24
12627	-0.28062347	10.657563	9	16707	3.625348	6.6976204	24
19934	-1.0158118	10.748191	9	18859	3.480772	6.5431457	24
19547	-0.7838241	11.100531	9	19842	3.5731351	6.6851015	24
17253	-0.044688683	10.679031	9	17523	3.9146256	6.5287614	24
19403	-0.17601736	10.889114	9	18856	3.9034584	6.3991375	24
17826	-0.023234626	11.058174	9	18494	3.465997	6.7210364	24
13242	-0.24998367	10.479919	9	16786	3.8089955	6.422126	24
15627	-0.150282	10.406872	9	18289	3.0398664	6.805365	24
19167	-0.1758172	11.408933	9	20417	3.644996	6.4973125	24
19561	-0.054644547	11.419141	9	16973	3.5970511	6.5658994	24

20136	-0.12356132	11.196196	9	16889	3.5690303	6.5719004	24
19767	-0.27886763	11.294113	9	16928	3.6034377	6.569974	24
19301	-0.5861429	10.895825	9	16846	3.566753	6.6181054	24
19575	-0.070225105	11.329016	9	17964	3.5610986	6.555716	24
19483	-0.24076444	11.292967	9	16979	3.5374212	6.621413	24
12573	-0.7065291	10.440829	9	18276	3.601039	6.6547465	24
16663	-0.123518355	10.497344	9	16896	3.615527	6.5484915	24
17824	-0.43061474	10.490277	9	16836	3.707018	6.5618052	24
11122	-0.62630516	10.122606	9	16698	3.6154356	6.5911827	24
18625	-0.04739014	11.436564	9	18685	4.525155	6.401645	24
20147	-0.7100351	11.19357	9	17887	4.8082786	6.592816	24
17988	-0.52402043	11.202415	9	15467	4.9897776	6.3403325	24
17351	-0.12256893	10.608692	9	15743	4.895534	6.260335	24
19011	-0.014798863	11.384146	9	18099	4.945376	6.291812	24
19451	-0.82420444	11.100628	9	19111	4.5451684	6.3084006	24
18825	-0.5342754	10.503739	9	17322	4.1502953	5.280559	25
20015	-0.6120335	10.260392	9	18720	4.237308	4.434202	25
18576	-0.83569384	10.274071	9	18980	3.9650283	4.3795857	25
20110	-0.83408654	10.3319	9	20096	3.9441893	4.3531003	25
12797	-0.8647837	10.292473	9	18679	4.324329	4.723813	25
19040	-0.8675069	11.060614	9	15761	4.28033	5.1473675	25
19095	-0.643717	10.826704	9	13186	4.270608	5.1434298	25
20071	-0.012256295	11.421524	9	18951	4.146907	5.1096916	25
13477	-0.64933574	10.767053	9	19003	4.138201	4.306998	25
20118	-0.67928284	11.217476	9	19818	4.28249	5.1987305	25
19298	-0.5776667	11.275033	9	19309	4.1339254	4.9913473	25
19533	-0.65436834	11.19446	9	17581	4.258241	4.60401	25
19491	-0.6280664	11.107103	9	18652	4.480813	4.44401	25
19386	-0.67331034	10.815546	9	14772	3.8588746	4.7404833	25
19558	-0.756417	10.713339	9	13238	3.8619483	4.703704	25
18974	-0.40205562	11.258412	9	17100	4.5369067	4.7910867	25
18598	-0.21808541	10.706839	9	17462	4.312394	4.9307413	25
13362	-0.6834451	11.201301	9	18819	4.232461	5.1582503	25

20084	-0.7848516	10.494306	9	18426	4.0690136	4.672726	25
17539	0.029936194	11.453079	9	17721	4.43538	4.4659047	25
19952	-0.95565534	10.3443985	9	13363	4.233464	4.6996484	25
19569	-0.57771	10.655323	9	16171	3.98644	4.8089776	25
18915	-0.8401735	11.066394	9	17858	4.196097	4.420283	25
16347	-0.6991198	11.191272	9	19300	4.0364795	4.4252644	25
11810	-0.74600524	11.15871	9	11036	4.3149114	4.5159373	25
18875	-0.7027571	11.201361	9	19082	4.2342362	4.4262605	25
18334	-0.62686497	10.73871	9	19794	4.173813	4.220696	25
20215	-0.8179814	11.076132	9	17410	4.203845	4.3650527	25
17215	-0.5587845	10.832603	9	17519	4.310022	4.487748	25
20027	-0.34430188	11.342987	9	17713	4.046189	4.5191345	25
20476	-0.30701655	10.657949	9	18137	4.2574086	4.629791	25
20224	-0.0733814	10.476137	9	12845	3.9008758	4.4784093	25
18443	-0.6665023	10.8622265	9	18466	4.1399703	4.360314	25
17697	-0.968602	10.623704	9	17210	4.1990266	4.231252	25
20466	-0.69992256	10.435409	9	14881	4.1507273	4.224302	25
19755	-0.169605	10.680958	9	13087	4.223729	4.2416196	25
20072	-0.2615699	10.551687	9	12721	3.8608255	4.9535127	25
13483	-0.000695295	10.65765	9	19823	3.9401057	4.603699	25
19295	0.09620874	10.764729	9	20119	4.295021	4.520807	25
18824	0.099408	10.824874	9	17204	4.087993	4.234147	25
20420	-0.24352884	10.720137	9	13185	4.2502756	4.4748597	25
15570	-0.5245689	10.001517	9	18160	3.9485304	4.442633	25
20170	-0.80305797	10.362522	9	18509	4.1915107	4.2448063	25
16858	0.03557804	10.727327	9	15008	4.1132474	4.697665	25
14415	-0.6949176	10.448416	9	17419	4.241263	4.287481	25
19988	-0.23658636	10.314076	9	20039	4.2575707	4.5642557	25
12538	-0.60165095	10.070566	9	17876	4.257951	4.668092	25
16172	-0.20074895	10.683005	9	18863	4.0929303	4.184902	25
14488	0.13289396	11.263463	9	16623	4.1222243	4.4045367	25
17695	0.09697035	11.252063	9	19676	4.0424027	4.1286316	25
17625	-0.18331072	10.702557	9	16488	4.182164	4.771586	25

17049	-0.5929914	10.688301	9	17832	4.1257086	4.696957	25
17020	-0.5753063	10.624752	9	18237	4.2403064	4.8079343	25
17127	-0.4823943	10.650352	9	12590	4.170888	4.795634	25
18932	-0.26775995	11.357617	9	18826	4.2182865	4.3185377	25
20395	-0.6251452	10.981943	9	13080	3.9989402	4.8081784	25
19033	-0.18690817	11.381314	9	18211	3.871916	4.539008	25
17897	-0.10142417	11.351313	9	17421	4.181403	4.808438	25
18523	-0.037843592	11.37781	9	18849	4.161231	4.734787	25
18984	-0.06799253	11.40021	9	18320	4.2090096	4.838937	25
17503	-0.66857374	10.957082	9	11741	3.981692	4.6072893	25
19625	-0.039227545	11.194996	9	18677	3.9592445	4.3200994	25
18074	-0.71532196	11.005309	9	19904	3.896383	4.3872743	25
15748	-0.05244748	11.361607	9	18535	4.246278	4.2907133	25
18665	-0.27256918	11.403292	9	17805	4.209947	4.3134885	25
13315	-0.29176706	11.413462	9	18793	4.1795764	4.303935	25
17941	-0.14328165	11.397167	9	18780	4.2333846	4.516312	25
18857	-0.26057276	11.396742	9	17719	4.252962	4.474837	25
17619	-0.09531373	11.328452	9	19253	4.102475	4.3322415	25
20002	-0.13265474	11.408646	9	16149	4.0892997	4.412175	25
17627	-0.066903085	10.835336	9	16632	4.1644344	4.4920273	25
18007	-1.0934103	10.544582	9	18616	4.1392345	4.565355	25
13397	-0.06843204	10.383886	9	17682	4.1627727	4.4143004	25
17986	-0.29746458	11.348377	9	17730	4.166243	4.4546638	25
19255	-0.5706919	10.443921	9	14295	4.1340513	4.475139	25
14841	-0.76569074	10.15552	9	17709	4.2123656	4.7103095	25
20123	-0.60887104	10.074599	9	18919	4.1897907	4.549168	25
19618	-0.60247934	10.052214	9	17764	4.213908	4.5447493	25
17363	-0.6223573	10.119533	9	12300	4.2261744	4.7534046	25
15039	-0.5968559	10.217598	9	11638	4.1998467	4.7165747	25
18254	-0.38497868	11.33212	9	17732	4.087889	4.421039	25
13398	-0.621866	10.880486	9	12042	4.2062635	4.27565	25
17567	-0.7084923	10.5838785	9	13234	4.228288	4.330526	25
17749	-0.7336325	10.50994	9	17354	4.220778	4.2822556	25

17816	-0.70912665	10.530755	9	18003	4.1820984	4.64986	25
17584	-0.31124866	10.531962	9	19209	4.0330486	4.130828	25
18761	-0.46027452	10.187564	9	17233	4.24338	5.1488986	25
17372	-0.45172366	10.407031	9	17803	4.2326984	5.148153	25
19251	-0.3841757	10.386462	9	18491	4.1597357	4.388924	25
12843	-0.35471728	10.697755	9	18457	4.2233777	5.173065	25
13356	-0.09044069	10.8765135	9	13210	3.9509025	5.0594697	25
12560	-0.14539118	10.911826	9	19551	4.4419975	4.545879	25
19376	-0.89215577	10.344807	9	15754	4.2619734	4.4517307	25
19455	-0.08350559	10.383176	9	17444	4.0907807	4.5178986	25
18231	-0.10622049	11.3495245	9	16374	4.231187	4.8874135	25
18924	-0.68329173	10.785973	9	15695	3.831406	4.732581	25
17644	-0.50699806	11.008221	9	16443	4.1802936	4.8678994	25
19966	-0.52699655	11.08642	9	20447	4.188086	4.92021	25
18424	-0.4849106	10.13812	9	16697	4.281195	4.7627363	25
17874	-0.7299342	10.523358	9	16357	4.2328606	4.9359555	25
19264	-0.010719743	10.46438	9	13365	3.9658852	5.039207	25
19670	-0.543587	10.959441	9	15654	4.1906023	5.122286	25
19505	-0.4766367	10.395362	9	16265	4.2186804	4.449899	25
19010	-0.12615694	10.356114	9	20430	3.9385421	4.9969583	25
18967	0.14706668	11.212057	9	16874	4.256941	4.6085725	25
20453	-0.3630502	11.302782	9	15650	4.150293	4.399783	25
18098	-0.3180325	10.528673	9	16507	4.2564926	4.615749	25
17004	-0.29974508	10.180293	9	18347	4.055568	4.7810435	25
11856	-0.30945152	10.225475	9	20363	3.9954345	4.819137	25
18433	-0.26151505	10.212271	9	20361	3.8666277	4.55069	25
19160	-0.37067604	10.372257	9	13379	4.1142807	4.9311576	25
17535	-0.22434314	10.292736	9	19217	4.0052185	4.3590174	25
17247	-0.33447528	10.246145	9	15678	3.9926636	4.155691	25
17060	-0.25571254	10.327829	9	16315	4.1786757	4.8529744	25
17877	-0.17422897	10.701797	9	15419	4.30952	4.7878213	25
18064	-0.2562779	10.57982	9	16448	4.216168	4.826406	25
17209	-0.3025731	10.274781	9	13370	4.5776567	4.9123883	25

18724	-0.66788316	10.844301	9	12567	4.3911037	4.887373	25
15224	-0.24327217	10.487995	9	14331	4.6430144	5.005703	25
18241	-0.0594718	11.374155	9	17456	4.5944786	4.9818172	25
19232	-0.3165751	11.297474	9	14863	4.5712214	4.946209	25
17663	-0.13140121	11.341915	9	15461	4.4203773	4.9768176	25
17804	-0.5525109	10.961579	9	15109	4.013066	4.3458066	25
19553	-0.23785949	11.229802	9	18651	4.4376144	4.447966	25
19499	-0.4800607	10.102948	9	18120	3.9295876	5.049733	25
17767	-0.73414695	10.50878	9	13237	4.137539	4.853401	25
18372	-0.5642124	10.35317	9	15771	4.090747	4.819812	25
17685	-0.5974098	10.796857	9	17436	4.0092993	4.5612397	25
12618	-0.6733545	10.195167	9	18048	4.1033177	4.4072766	25
17981	-0.09912747	11.174555	9	17423	4.0149083	4.901136	25
13028	-0.47370535	10.834047	9	17464	4.10866	4.5973115	25
19811	-0.8039595	10.435038	9	18754	4.0821686	4.699708	25
19777	-0.3115613	10.403625	9	17760	3.9573455	4.5168176	25
13038	-0.341925	10.383733	9	17965	4.046363	4.884016	25
16201	-0.05863038	10.533298	9	17638	4.0455728	4.773286	25
13069	-0.09869059	10.478986	9	17895	3.9629326	4.2955894	25
12578	-0.2917242	10.402807	9	18178	4.1440616	4.4817324	25
13282	-0.34634858	10.409091	9	18421	4.256521	4.26671	25
16433	-0.6252735	10.697523	9	17699	3.9797754	4.9132595	25
19873	-0.36503166	10.709384	9	17483	4.080698	4.7686915	25
20204	-0.6846285	10.555828	9	17415	3.9682817	4.700011	25
19521	-0.7159799	10.55697	9	14819	4.0034547	4.7994905	25
11022	-0.09088172	10.355838	9	19935	4.118765	4.7142577	25
11102	-0.48980698	10.46977	9	14927	4.157814	4.73822	25
20011	-0.46500164	10.400148	9	17435	3.8919272	4.458406	25
16340	-0.48696196	10.375109	9	12890	3.9700418	4.6833653	25
20040	-0.46946135	10.39857	9	12023	3.9351165	4.46782	25
18648	-0.5929626	10.679988	9	18721	3.899889	4.622986	25
17755	-0.34817863	10.937807	9	18305	3.9176192	4.5978518	25
18286	-0.1172392	11.226717	9	19360	3.90715	4.311383	25

19897	-0.8644461	10.827063	9	18861	4.0696855	4.781663	25
17862	-0.7300643	10.937729	9	18055	4.1286736	4.800276	25
18384	-0.5503374	11.080002	9	19046	3.9563844	4.37992	25
17784	-0.6089673	10.978486	9	12288	4.0061	4.673557	25
17601	-0.6170701	10.724436	9	17814	4.0222964	4.476601	25
17896	-0.074027605	11.180879	9	13212	4.096307	4.8535786	25
17938	-0.24195905	11.338316	9	18041	4.133437	4.7117825	25
19270	-0.2464773	11.272714	9	17434	4.144617	4.8162384	25
19009	-0.1774548	10.418126	9	18093	4.0464344	4.3967495	25
18835	-0.30964965	11.175624	9	17313	4.136213	4.79914	25
17576	-0.42993438	11.084733	9	12330	4.1335115	4.793169	25
18641	-0.25596634	11.170382	9	18637	5.6787	9.009913	26
17689	-0.27447113	11.001564	9	17003	5.71003	9.022181	26
18969	-0.3798902	11.205267	9	18940	5.7259855	8.728911	26
17586	-0.7085472	10.574491	9	20427	5.743401	9.010419	26
18804	-0.6096945	10.715896	9	20386	4.9922714	9.10446	26
19322	-0.68826056	10.595672	9	19942	5.2420506	8.507287	26
19366	-0.56920207	10.595949	9	18670	5.1882987	8.745462	26
17910	-0.63632137	10.65826	9	18600	5.8369346	8.915333	26
19698	-0.5282731	10.491877	9	18330	5.346469	9.531161	26
15846	-0.5793661	10.735428	9	15772	5.008908	9.138177	26
20169	-0.6016502	10.659702	9	19760	5.7550125	9.274312	26
13018	-0.54184526	10.417839	9	11086	5.468126	8.747036	26
11068	-0.4226393	11.031291	9	17055	5.790028	8.684971	26
19494	-0.27466166	11.056966	9	13886	5.569383	8.969815	26
19657	-0.10230118	11.316853	9	17081	5.6999497	9.067173	26
16976	-0.19628012	11.065491	9	15733	5.680447	9.247514	26
18966	4.8216457	7.811144	10	18021	5.22677	8.986008	26
17368	4.7662754	8.272594	10	19485	5.2790236	8.938617	26
18148	4.7569685	7.867936	10	11014	5.257396	9.076473	26
17094	5.87059	8.146034	10	17780	5.3149786	9.183422	26
18520	4.3865595	7.956285	10	12941	5.270284	8.784529	26
20460	4.5312624	7.289997	10	19859	5.264201	8.952705	26

19514	4.8034472	7.6030726	10	15612	4.993159	8.556727	26
17757	5.7305293	7.9678364	10	13410	5.835665	8.804062	26
13711	5.788537	8.054643	10	17454	5.7199616	8.7051	26
20073	5.267982	8.300187	10	20371	5.664484	9.02396	26
18839	4.8777666	7.835515	10	18389	5.72389	8.835808	26
20434	5.410259	7.8371315	10	20451	5.0218163	9.248237	26
15292	5.8075805	7.952099	10	19814	5.266229	8.960397	26
18923	5.1232886	7.5250897	10	17918	5.5500975	8.639736	26
16479	5.0664897	7.4657087	10	13393	5.6936035	8.723448	26
18105	4.6947246	7.72149	10	10957	5.6402593	8.742821	26
19218	5.581345	8.437963	10	12599	5.289187	8.863456	26
18802	5.465981	7.755167	10	18096	5.3183103	8.671103	26
18142	5.0108895	8.055683	10	17040	5.3584404	8.735311	26
19131	5.0870233	8.024737	10	11618	5.367577	8.739822	26
13248	5.3356767	7.607866	10	16594	5.377898	8.675856	26
17123	5.644272	8.213161	10	17717	5.3562455	8.737102	26
18257	4.776594	7.7894983	10	16339	5.1836104	9.107721	26
20175	4.601783	7.855367	10	16617	5.3192067	8.643121	26
16863	5.5697703	8.373325	10	15855	4.9167776	9.219764	26
15239	4.306131	8.017286	10	17635	5.339143	9.325238	26
13369	4.5478454	8.060507	10	19225	5.736016	8.74058	26
16757	4.539518	8.04404	10	16327	5.6118054	9.304663	26
19535	4.606755	7.8841195	10	17873	5.3268404	9.131721	26
15865	5.395806	7.7853003	10	19346	5.625999	9.453105	26
17525	4.833322	7.3757935	10	19445	5.5714984	9.479167	26
15677	5.5217557	8.41912	10	16608	5.4231462	9.3585825	26
13692	4.7375937	8.030654	10	16619	5.034214	9.074899	26
19994	5.116564	7.7797236	10	11169	5.6242785	9.431322	26
14199	4.5005674	7.9864235	10	20379	5.2294493	9.275902	26
16693	5.848359	8.5240555	10	17128	5.238782	9.288544	26
17442	4.871161	7.984414	10	13614	5.761731	9.362062	26
16222	4.9887824	7.9835105	10	17658	5.63368	9.285436	26
20478	5.4106574	7.998638	10	11018	5.6948833	9.304548	26

12001	5.3449726	7.8793287	10	20158	5.744996	9.3952875	26
20471	5.311508	7.636172	10	19440	5.7180223	9.412578	26
15485	5.4104548	8.156001	10	18358	5.2686086	9.288954	26
16300	4.7217064	8.027114	10	11136	5.679797	9.43827	26
11820	4.636397	8.002957	10	12034	5.302909	9.269976	26
20178	5.626933	8.309676	10	15967	4.971859	9.062028	26
16489	5.430934	8.256568	10	17358	5.0653744	9.322563	26
11134	5.58344	8.342322	10	14057	5.2325015	9.272101	26
17150	5.577702	8.313752	10	17179	5.342733	9.263293	26
19148	5.5653896	8.325781	10	16760	5.5831113	9.491728	26
13661	5.5869336	8.316311	10	17258	5.5921535	9.514779	26
16613	5.553644	8.309606	10	17747	5.3061333	9.560503	26
17951	5.606607	8.384806	10	17993	5.3939285	9.213555	26
13644	5.6603837	8.242982	10	19227	5.5103893	9.30002	26
19614	4.7039747	7.9850893	10	17603	5.509774	9.270692	26
15362	4.986241	8.407542	10	11646	5.145701	9.19427	26
17723	5.519887	8.373842	10	18676	5.485807	9.29905	26
13930	5.5699534	8.338818	10	13031	5.6119704	9.326711	26
11016	4.8967576	8.508285	10	17776	5.578078	9.337339	26
19212	5.2368646	8.49007	10	19496	5.0050006	9.069218	26
14276	5.6085625	8.391144	10	16575	5.63521	9.252435	26
16640	5.6333146	8.401535	10	17186	5.657155	9.311332	26
11901	5.771976	8.460315	10	18180	5.6957006	9.32568	26
19052	5.66394	8.434928	10	17889	5.6360435	9.274599	26
17459	5.5674276	8.317596	10	19635	5.618079	9.331095	26
11365	4.7355227	8.042431	10	14631	5.0341353	8.986025	26
20001	4.565876	8.011217	10	12397	4.9687195	9.061084	26
16298	5.2651052	8.037063	10	13176	5.5440836	9.379355	26
17239	4.2674174	7.593369	10	11236	5.5511928	9.341209	26
16333	4.688424	8.0745945	10	16050	5.340102	9.257551	26
19184	4.178034	7.79248	10	17801	4.954131	9.125936	26
19709	5.19612	7.638864	10	17883	5.122995	9.253016	26
14750	4.960064	8.429247	10	14327	5.328607	9.075863	26

17939	4.7962112	8.235377	10	16630	5.2937946	9.187977	26
16637	4.7902846	7.9311852	10	11005	5.148167	9.237396	26
20392	4.8508263	7.7955384	10	11970	5.1201506	9.1176405	26
11030	4.994528	7.993117	10	11538	5.1681347	9.120411	26
12846	4.8789334	7.9298735	10	18261	5.259008	9.247201	26
13288	4.7713494	8.259413	10	10995	5.0659485	9.296004	26
18583	5.816688	8.112395	10	19439	5.6200747	9.355574	26
16587	4.8511677	8.3270445	10	18908	5.387984	9.567808	26
20360	5.2934613	8.041057	10	17745	5.6182947	9.350543	26
17264	5.692273	8.31441	10	16628	5.2801	9.543917	26
17308	5.2937503	7.967022	10	16650	5.3041096	9.547486	26
11512	5.05666	8.064699	10	19955	5.484868	9.497373	26
20362	5.0682826	7.974897	10	20019	5.3994102	9.523884	26
12500	5.4139314	7.8295736	10	19506	5.7848034	9.3828335	26
16592	5.377895	7.672535	10	19480	5.328067	9.314169	26
11284	5.643574	8.385108	10	18916	5.5734725	9.508056	26
17583	5.8302	8.134653	10	17302	4.940503	9.212654	26
16653	5.4463077	8.12267	10	19630	5.2266026	9.437311	26
13211	5.766003	7.9442573	10	15185	5.7636876	9.165108	26
15840	5.8175893	8.033905	10	11192	5.6351533	8.977222	26
17476	5.303088	7.9486637	10	16690	5.1448283	9.153666	26
18691	5.8227296	8.13822	10	20135	5.126311	9.325485	26
16658	5.600249	8.278575	10	16258	5.40775	9.036122	26
16457	5.162454	7.9735155	10	16634	5.1292295	9.22917	26
12003	4.745601	8.302675	10	14708	5.115188	9.391573	26
16358	5.5486207	8.274342	10	18578	5.6627474	8.990733	26
14613	5.5575643	8.150381	10	16514	5.0436463	9.047414	26
16388	4.559356	8.017062	10	16295	5.310564	9.008	26
15277	4.475382	8.006198	10	19555	5.0224175	8.631099	26
15750	5.0018463	7.716037	10	17800	5.098061	9.17864	26
15408	5.8294034	8.048443	10	20226	5.380805	8.621089	26
19663	5.323742	7.603272	10	11075	5.7585115	9.033867	26
15822	4.201496	7.71517	10	17176	5.3287687	8.879867	26

17088	4.1862664	7.974531	10	20384	5.694552	8.769029	26
15437	5.087658	7.7988906	10	14525	5.724169	9.320614	26
15431	5.0137453	7.8158817	10	18287	5.198022	8.799238	26
15231	5.591268	8.384047	10	20087	5.145152	9.152395	26
16519	5.6482935	7.953904	10	18470	5.7286744	9.231754	26
19626	4.934554	7.899872	10	18321	5.756505	8.71833	26
15787	5.002758	8.336069	10	17369	5.7566113	8.721997	26
15768	5.6480756	8.427613	10	16278	5.724912	9.27293	26
16390	4.7633386	8.052067	10	14651	5.6532316	8.994304	26
15729	4.940177	7.959984	10	15318	5.630983	8.893815	26
20480	4.9955406	7.9434743	10	13171	5.0041876	9.173182	26
15579	4.6007237	7.75384	10	20132	5.1645503	8.944501	26
17394	5.0196	8.21652	10	17639	5.489221	8.532946	26
12736	5.255527	8.288085	10	18968	5.435345	8.555006	26
16578	4.779163	8.061763	10	19166	5.4524956	8.520754	26
18417	5.3991427	8.205618	10	18069	5.435596	8.576916	26
19681	4.77756	8.080225	10	17792	5.761951	9.050319	26
16627	4.793959	8.03692	10	16498	5.9380584	8.923074	26
11067	5.2421427	8.422975	10	20444	5.9137907	8.838093	26
12011	4.8904095	7.9251895	10	17220	5.923098	8.865483	26
17670	5.23243	8.338432	10	16586	5.543099	8.668778	26
13396	4.7760167	8.08868	10	14868	5.8077846	9.015207	26
17325	4.81727	8.168531	10	11019	5.818128	9.103392	26
19385	5.2194705	7.9001145	10	14572	5.76475	9.022488	26
17917	5.1541386	7.932649	10	14714	5.7373843	8.935912	26
16591	5.151731	7.9091077	10	18991	5.796741	9.245359	26
16142	4.9752326	8.408659	10	14689	5.9304276	8.864251	26
16481	5.429768	8.290891	10	16309	5.911643	8.816795	26
16076	5.2137885	8.040193	10	20474	5.3660192	8.743009	26
15163	5.273797	8.338267	10	17461	5.475863	8.526214	26
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19917	5.27805	7.937186	10	17382	5.226032	8.700474	26
18840	5.3446965	8.052671	10	15897	5.0981326	8.76728	26

16580	5.3961916	8.314954	10	13121	5.3814096	8.636231	26
18013	5.422671	8.364347	10	17183	4.989443	8.572901	26
12220	5.2932253	8.176125	10	19748	4.9914045	8.707646	26
17903	5.262176	8.27969	10	13427	5.240734	8.724315	26
11910	4.9987082	8.489843	10	11072	4.9806795	8.668348	26
20422	5.028415	7.8107777	10	13196	5.255557	8.712088	26
20465	5.0823574	7.8264475	10	11020	5.196385	8.798534	26
17300	5.3602962	7.757113	10	18907	5.2172894	8.643864	26
20137	5.1857777	7.777898	10	17589	5.26581	8.750022	26
11667	4.947719	8.476573	10	18918	5.127888	8.798145	26
11760	5.006514	8.455724	10	17545	5.188885	8.779887	26
16100	5.2202067	8.190596	10	16145	5.411634	8.87836	26
15818	4.21022	7.7046633	10	18734	5.1456738	8.607816	26
13267	4.7843213	8.093214	10	16577	5.195066	8.828717	26
16442	5.2051635	8.302146	10	17905	5.225519	8.777919	26
17522	5.243455	8.387435	10	17838	5.1526036	8.8125925	26
16611	5.3657265	8.298349	10	16562	5.1933274	8.685006	26
16621	5.2154098	8.493203	10	16576	5.232073	8.6696825	26
11071	4.8687377	8.479048	10	19022	5.2446647	8.726436	26
16083	4.8263865	8.410903	10	18083	5.181501	8.766541	26
14846	5.222727	8.395568	10	17471	5.1195226	8.540543	26
14206	4.9528503	8.498291	10	16626	5.045601	8.622176	26
14002	5.16374	8.441274	10	16364	5.0501328	8.822715	26
15373	5.2504034	8.407992	10	13319	5.0981426	8.854356	26
13599	4.921598	8.516965	10	18910	4.981866	8.676252	26
18529	4.9818683	8.512405	10	15234	4.982615	8.681243	26
17248	5.247	8.411317	10	11170	5.344724	8.499016	26
19081	5.309918	8.48476	10	18465	5.2896457	8.776927	26
18626	4.2303205	7.7149963	10	18469	5.265004	8.770091	26
17554	4.82462	8.079002	10	16596	5.348803	8.623398	26
12650	5.177692	8.307749	10	19420	-0.772139	7.6646414	27
16275	4.818527	8.025509	10	12338	-1.2932247	8.146333	27
17043	5.2643943	8.122325	10	19337	-1.608831	8.293603	27

14428	5.578226	8.03976	10	12509	-1.108793	8.011885	27
19830	5.3191023	8.107602	10	18650	-1.0897866	8.073744	27
15514	5.2681303	8.105272	10	11349	-0.8962579	7.979551	27
12624	5.196659	7.8324385	10	11998	-0.8984267	8.388122	27
15671	5.3433185	7.6527796	10	17997	-1.2442156	8.7979145	27
19271	5.6146026	7.9674754	10	17761	-1.2314287	8.786344	27
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16262	5.6703763	7.9505315	10	20416	-1.3654766	8.076726	27
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20435	5.716687	8.152613	10	17024	-1.619644	8.648863	27
16337	5.508138	8.060362	10	18925	0.027638165	8.021758	27
17911	5.5502143	8.047997	10	20421	-0.58069867	7.738217	27
14302	4.8786993	7.5691533	10	11234	0.22343136	7.591935	27
16771	5.9003134	8.473733	10	17136	-1.1539729	8.435573	27
19526	5.2333355	7.633598	10	17291	-0.6488378	7.941418	27
16356	4.9464135	8.013004	10	18810	0.07199783	7.3923016	27
14275	5.58817	8.170971	10	20186	-0.079138115	8.042772	27
12910	4.4850693	7.742567	10	17053	-0.16009782	8.027184	27
15911	5.0336766	8.204114	10	18037	-0.088782705	8.037625	27
19193	0.8190327	6.668253	11	18589	-0.021281717	7.899107	27
19484	0.30680618	7.49928	11	19609	-0.010250478	7.9890428	27
18480	0.30807263	7.507838	11	16496	-0.051639147	7.9807963	27
16500	1.1621244	6.788642	11	12584	-0.65250605	7.9371943	27
20159	0.99348384	7.450062	11	11716	-0.565858	7.915063	27
12512	0.74139774	6.305805	11	11440	-0.28137338	7.936335	27
20464	0.5278667	6.8476634	11	18006	0.040844843	7.600349	27
17027	0.7484835	6.41055	11	13117	-0.17579348	8.051298	27
19792	0.9639401	7.2019925	11	17932	-0.094441615	7.996134	27
20168	0.7818584	6.351902	11	16531	-1.1900419	8.448506	27
20428	0.96419525	6.5290217	11	12522	-0.85932976	8.364488	27
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19333	0.7159036	6.975174	11	12924	-0.37948284	8.25188	27

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20121	0.7033041	7.06405	11	18230	0.032601696	7.382541	27
19368	0.8069135	6.8618197	11	18571	0.074293196	7.389692	27
19407	0.9010113	7.1482577	11	17829	0.05640054	7.394299	27
18731	0.721188	7.208137	11	12527	-0.16206522	8.007409	27
18877	0.62226677	6.89648	11	17794	0.08228568	7.3832045	27
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19970	0.8601759	6.8409243	11	13343	-0.8724654	7.8358984	27
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18553	0.8754825	7.2049775	11	18850	-0.99833	7.8245707	27
18299	0.8932688	7.515303	11	17287	-1.1727005	8.329169	27
19573	0.99683756	7.387609	11	18581	-0.95542544	8.355713	27
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19158	0.89092463	7.0022235	11	11301	-0.64502656	7.9117913	27
17092	0.7576763	7.0564895	11	12424	-0.81003237	7.8739705	27
17703	1.231355	6.2773685	11	15830	-0.19587111	8.015434	27
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19785	1.1131501	7.059841	11	17005	-1.153522	8.434061	27
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19257	0.65792036	6.980992	11	12980	-1.3510269	8.520817	27

18883	1.0256462	6.7166486	11	14884	-1.0928441	8.259057	27
18845	1.0238853	6.4749646	11	12279	-1.209253	8.238623	27
20146	0.8697287	7.217115	11	13116	-1.0503627	7.96388	27
19032	0.9017405	6.2799864	11	11380	-0.63805425	7.9114575	27
19696	0.65825456	6.406052	11	13217	-0.9150152	8.237055	27
20414	0.37580925	7.0403585	11	19546	-1.0456525	8.163462	27
17139	0.80366987	6.643968	11	19679	-1.2167116	7.9683027	27
19370	0.8208656	6.3401513	11	14039	-1.0713226	8.161722	27
18623	1.12784	6.3060718	11	13218	-1.6330969	7.829579	27
19268	0.9746242	6.4794054	11	17942	-1.4152985	8.140295	27
20089	0.46391067	6.9383316	11	16437	-0.054263335	8.082172	27
19878	0.8754193	6.94144	11	12440	-1.2663795	7.9994655	27
18184	0.9772201	7.130349	11	15356	-1.0590725	8.190937	27
18453	0.45184213	7.1840973	11	16256	-1.0667046	8.175048	27
19328	0.6306492	6.7899055	11	15383	-0.24448785	8.0614605	27
20093	0.6532652	6.3627305	11	13422	-1.2333497	8.57152	27
20144	0.64211714	6.446037	11	13032	-1.2769551	8.372348	27
17688	0.44885984	7.1118355	11	20116	-1.2922094	8.529421	27
20212	0.51670045	6.888913	11	19036	-0.3456389	7.8946533	27
19396	0.7027736	7.091179	11	12416	-0.5002524	8.007504	27
19848	0.73333585	6.4317307	11	18032	-0.27939495	7.9353833	27
20441	0.48325628	7.0894547	11	19065	-0.20212075	8.268333	27
19314	1.1336675	6.2384596	11	14889	-0.85551125	8.352692	27
20452	1.0046833	6.455766	11	11780	-0.21247864	8.047757	27
19018	0.6144278	6.436064	11	16413	-0.85946107	7.4841886	27
20075	0.63830435	6.667778	11	15633	-0.7217853	8.258217	27
17328	0.8492508	7.1618967	11	15199	-1.054096	8.024879	27
17327	0.49541405	7.059749	11	13050	-0.42503408	7.9603634	27
17218	0.97014076	6.333405	11	15112	-1.0928696	8.320021	27
20382	0.671178	6.760644	11	20227	-1.0731312	8.32386	27
18821	0.4599498	7.270159	11	16382	-1.1685611	8.436861	27
18885	0.65909547	6.452651	11	16305	-0.98118037	8.210957	27
17178	0.64804125	6.4330606	11	18146	-1.1536984	8.696889	27

17138	0.59980077	6.430885	11	11789	-0.8891041	8.054607	27
19733	0.8155732	6.738704	11	19868	-0.99311674	8.206419	27
20381	0.80157334	6.948868	11	13395	-0.8133142	7.9403386	27
20398	0.7047937	6.7493353	11	13164	-0.98837	8.230985	27
19194	0.41697884	6.882985	11	15513	-0.86039275	7.976732	27
20399	0.6672202	6.9546094	11	16229	-0.9300253	7.9905124	27
17015	0.7086592	6.626291	11	15629	-0.95048094	8.107595	27
20467	0.867499	6.522804	11	13207	-1.0444113	8.155196	27
19703	0.75773054	7.0045404	11	11429	-0.97538984	8.255419	27
18942	0.42682382	6.8881173	11	12583	-0.9774204	8.139566	27
19047	0.8717805	7.002937	11	13156	-0.9821621	8.155104	27
17172	0.8947471	6.904181	11	15311	-0.9842485	8.250637	27
20405	0.6488306	6.757547	11	15727	-1.072114	8.154748	27
20366	0.6655704	6.7406225	11	14987	-1.1758599	8.796431	27
20446	0.6977895	6.7286563	11	17250	-1.0921382	7.93419	27
20470	0.5633593	6.7984085	11	12753	-0.97768235	7.980802	27
20424	0.9768245	6.2765765	11	11186	-1.181957	8.305882	27
19150	0.60732466	6.711344	11	18228	-0.98247993	8.148043	27
17976	0.6207065	6.7626185	11	20407	-1.2889448	8.175616	27
20413	0.49167132	6.915538	11	13233	-0.63270956	8.253579	27
17356	0.75723654	6.422476	11	13434	-0.6388109	7.9206004	27
19013	0.93874633	7.1811266	11	18557	-0.44823283	8.370452	27
17054	0.27537858	7.542504	11	17649	-1.6822796	8.228845	27
20401	0.7791127	7.005435	11	13264	-0.5328534	8.260787	27
17512	0.560536	6.270923	11	17312	-0.91420233	8.556805	27
19380	1.111826	6.904683	11	12786	-0.85224175	7.944775	27
20461	0.8999238	6.9335136	11	13261	-0.6702231	7.9085956	27
18621	0.8159495	6.332528	11	15153	-0.71050483	8.502407	27
19363	0.46313605	7.2297645	11	13795	-1.5711757	8.088221	27
20396	0.48906258	7.0345626	11	13419	-1.3274411	8.456797	27
17237	0.70363265	6.3929195	11	11404	-1.5585405	8.176653	27
17934	0.7385698	7.0702853	11	18331	-1.5671047	8.217133	27
20456	0.75998336	6.4132423	11	19164	-1.6279793	8.209325	27

17192	0.8981482	6.483135	11	12425	-1.598673	8.209762	27
19425	0.8304483	6.7536817	11	12352	-1.2120736	8.303383	27
17330	0.22903325	7.0042567	11	19860	-1.2395192	8.396954	27
18792	0.26701784	7.0519295	11	12139	-1.3214201	8.311422	27
17151	0.5613489	7.120848	11	18423	-1.2047347	8.26319	27
19057	1.042521	6.488369	11	15820	-0.95007235	8.289862	27
20104	1.0258589	6.791345	11	13204	-1.4268739	8.356601	27
19490	0.9294365	6.944783	11	19905	-1.5483521	8.188016	27
17224	0.24847224	7.5010304	11	18717	-1.4860877	8.309742	27
18072	0.8457451	6.669013	11	19570	-1.3057622	8.462246	27
18619	1.0845813	7.2877336	11	15197	-1.3831917	8.4038925	27
17225	0.6174337	6.994944	11	14703	-1.29092	8.49279	27
19669	0.5919932	6.575386	11	11414	-0.6627956	7.905187	27
17860	0.26259267	6.946631	11	13385	-1.414112	8.359479	27
17490	0.611107	6.478302	11	17298	-0.80897945	7.967072	27
17753	1.0394979	6.9615736	11	14534	-0.86273015	7.9826555	27
17947	0.40885708	7.078657	11	14255	-0.82330376	7.9246144	27
19400	0.9242525	7.128895	11	16272	-0.9295595	8.019268	27
19311	0.55983984	6.2559633	11	19452	-0.888954	8.023211	27
15663	0.98374295	6.1790123	11	20111	-1.0648812	8.626178	27
16736	1.0464475	6.9449143	11	19294	-1.5923492	7.998408	27
15703	0.915725	6.1446295	11	13299	-1.0913985	8.547977	27
16253	0.9897098	6.1327696	11	16492	-1.087157	8.545456	27
19316	1.0398779	7.2581325	11	15325	-1.23839	8.460361	27
17881	0.86994886	7.058945	11	12270	-1.5330673	7.842281	27
17207	0.7709951	6.3238726	11	17149	0.111779325	7.366026	27
19527	0.28556067	6.9466696	11	13811	-1.081219	8.203082	27
18476	0.5319231	7.455666	11	15583	-1.0993537	8.367125	27
16781	0.6842482	7.365321	11	13289	-1.242765	8.061215	27
18324	1.1770159	6.587125	11	13332	-1.033977	8.091479	27
18125	1.1619524	6.619085	11	18789	-1.7380372	8.40754	27
16777	0.23077509	6.9824376	11	13102	-1.1809567	8.188667	27
19275	0.38858524	6.6547494	11	16223	-1.1695318	8.204997	27

19815	1.0710437	7.37458	11	19923	-1.6080444	8.649734	27
18451	0.6125623	6.772059	11	19411	-1.6981434	8.578672	27
18943	0.42628384	7.668931	11	17288	-1.658669	8.693412	27
18647	0.7899806	7.281056	11	12462	-0.45390278	8.346864	27
20156	0.8862015	7.0795484	11	13268	-0.47380194	8.085326	27
17498	1.202167	6.4964666	11	13285	-0.4194742	8.536257	27
18175	0.79545283	7.263077	11	15017	-0.67425895	7.804814	27
19849	0.9061697	6.956817	11	15838	-0.61645395	7.7197914	27
18452	0.73569506	7.418708	11	17181	-1.6327579	8.71248	27
18962	0.79784924	7.2443624	11	16370	-1.0192587	8.45954	27
15712	0.9374097	7.2835226	11	13043	-0.95452005	8.082212	27
17090	1.5771947	6.6811147	12	16485	-1.044528	8.159635	27
19949	1.888878	7.1019893	12	12723	-1.038138	8.1341095	27
19545	2.164289	6.39011	12	12963	-0.5183067	7.796324	27
17782	2.049497	5.926374	12	13426	-0.53090996	8.2945385	27
19715	1.2374023	7.011933	12	18176	-0.91633534	7.7781715	27
19742	1.2711248	7.0330663	12	18540	-1.6237296	8.380436	27
17214	1.2417042	7.0165844	12	13432	-0.84994966	8.360555	27
18881	1.2689067	7.280488	12	13311	-1.0389985	8.154749	27
18353	1.4920651	7.2510805	12	12121	-1.386992	8.044516	27
17392	1.3824966	7.039157	12	12818	-1.3814387	8.558448	27
18485	1.2373015	7.0135636	12	12875	-0.6359666	7.896323	27
18537	1.6220261	7.2144675	12	14890	-0.6267859	7.783817	27
18727	2.0419002	5.991071	12	15892	-1.3403801	7.9389277	27
17102	1.4596205	6.8028517	12	15244	-1.0591404	8.122624	27
18572	2.1204457	6.167336	12	13359	-0.64490694	7.8072753	27
18797	1.1961184	7.1358733	12	15076	-1.0120078	8.051564	27
18127	1.4928048	6.935486	12	18552	-0.67026967	8.0599	27
18562	1.3993437	7.110695	12	16239	-0.95543665	7.6760316	27
18239	1.3730156	6.9605517	12	17191	-1.0479888	7.8098903	27
18187	1.9914225	6.9215884	12	15172	-1.3483803	7.8876467	27
19711	1.5202318	6.4143033	12	13227	-1.2369211	8.045234	27
18205	1.5455437	6.593006	12	12609	-1.4190223	8.150518	27

19708	1.7505951	6.902709	12	19563	-1.1901723	7.8816695	27
19808	2.1669421	6.376413	12	14913	-0.98097163	8.069456	27
18977	1.4646173	6.4055715	12	15377	-1.6225499	8.624885	27
19379	1.4536606	6.43892	12	19682	-1.6052418	8.623689	27
17407	1.5009217	7.055485	12	19969	-1.6762128	8.601213	27
15554	1.831297	6.938123	12	20053	-1.6748805	8.580132	27
18519	1.432182	6.3819137	12	19559	-0.5562187	8.151687	27
19750	1.4958012	6.8140974	12	13279	-0.91765994	7.8379965	27
16981	1.4354602	6.367249	12	13205	-1.1213834	7.9445367	27
16984	1.4567604	6.3834314	12	20128	-0.5870197	8.010641	27
19607	1.5868717	6.2902684	12	19865	-0.858983	8.699612	27
20045	1.8145239	6.937981	12	13280	-0.54333204	8.29479	27
19413	1.2711027	7.124988	12	20364	0.001286441	7.5951247	27
18799	1.7357608	6.9109097	12	18534	-1.4517989	8.39296	27
17982	1.9316161	6.6389923	12	13133	-0.80020964	8.288019	27
17374	1.4863855	6.253055	12	16422	-0.19096513	7.92528	27
17056	1.805556	6.8849897	12	17650	-0.91799736	7.6896224	27
19632	1.8053035	6.673353	12	14916	-0.832432	7.9190702	27
19259	1.9193951	6.6917944	12	13941	-0.94323975	7.960546	27
19488	1.965913	6.0980873	12	13274	-0.97304296	7.940833	27
19323	1.5705324	6.827732	12	19031	-0.18808864	7.7937593	27
19589	1.5848051	6.8011518	12	20041	-0.20085464	7.741964	27
19723	1.594375	6.873014	12	19016	-1.3385377	8.801375	27
19621	1.6177983	6.765966	12	18487	-1.3717266	8.467342	27
19596	1.5835503	6.837748	12	13152	-0.70503503	8.257462	27
19771	1.5058371	6.9240384	12	16938	-0.5895611	7.681715	27
19012	2.0409882	6.5786705	12	18328	-0.2656288	7.774267	27
19239	1.7668707	6.7387524	12	16845	-0.6045747	7.705676	27
15061	2.0089447	6.0768056	12	13331	-0.30091435	8.184912	27
17035	1.7966642	6.6602244	12	18376	-0.88191605	7.661831	27
18772	1.8099763	6.698458	12	17125	-0.8511443	7.574088	27
19827	1.5766417	6.790557	12	13108	-0.6352154	7.8517966	27
19434	1.628076	6.8145084	12	15766	-0.6461992	7.6249003	27

19289	1.6799021	6.767642	12	17450	-0.5266691	7.5783577	27
19871	1.6027647	6.7565784	12	15155	-0.8837577	8.396493	27
20018	1.2753471	7.167513	12	13192	-0.5538979	7.6349583	27
19373	1.6422846	6.710294	12	16648	-0.5355774	7.620259	27
19129	1.9827003	6.076236	12	18442	0.20564172	7.5213947	27
17067	1.8473364	6.70346	12	12103	-0.53384197	8.270671	27
18260	2.1707828	6.426375	12	15025	-0.95667	7.7978597	27
18864	1.6988714	6.948389	12	14606	-1.1557142	8.683955	27
17153	1.5315886	6.6737204	12	17892	-0.18511075	7.966179	27
20402	2.2797854	6.0528526	12	13297	-0.81831616	7.936988	27
20438	1.8749948	6.673272	12	13286	-0.6053134	7.5122604	27
18909	1.8916267	6.663387	12	19070	-0.25004238	8.208012	27
17551	1.7659637	6.9378343	12	15370	-0.5671102	7.497818	27
15555	1.5242211	7.1940923	12	17534	2.2449312	6.368071	28
16662	1.796909	6.8826933	12	16773	2.2977853	6.402076	28
19306	1.8668854	6.487031	12	15159	2.6004057	6.088997	28
19578	1.4545872	6.391772	12	20138	2.413746	6.3294015	28
17370	1.4939967	6.40771	12	18941	2.128721	7.090915	28
18135	2.0468585	6.4271317	12	19443	2.2760494	6.836574	28
15634	1.7350919	6.5705767	12	17080	2.2833982	6.4327564	28
18550	1.3191612	6.7052646	12	19415	2.5993323	6.19846	28
19157	1.7121754	6.4818783	12	17615	2.585512	6.1280313	28
11051	2.026254	6.4601226	12	15238	2.5259743	6.789763	28
15920	1.6208264	6.4180884	12	17865	2.4578032	6.5570974	28
17017	1.5859011	6.3618526	12	20191	2.121165	7.049956	28
18929	1.5749499	6.359478	12	19694	2.0536988	7.0526075	28
17030	1.496336	6.304471	12	18960	2.0739565	7.0761943	28
13293	1.7731314	7.1619787	12	20211	2.081212	7.0579085	28
15834	1.6987866	7.197285	12	19244	2.303485	6.2521567	28
17116	2.0450373	6.427711	12	16373	2.3045528	6.7162576	28
17163	1.4580417	6.430105	12	15188	2.7390425	6.614999	28
19090	1.5906534	6.622151	12	19476	2.4750395	6.8203964	28
19098	1.4423851	6.8658075	12	12815	2.6071181	6.500881	28

18869	1.4392073	6.8651834	12	13372	2.3664455	6.8662286	28
19320	1.5948714	6.6950045	12	19719	2.4315403	6.859146	28
20021	1.4419085	6.8841944	12	15364	2.3889225	6.9415913	28
19235	2.0638628	6.2399087	12	18306	2.7860618	6.2019005	28
19784	1.4359885	6.8326235	12	16387	2.7765567	6.132084	28
19060	1.9616303	6.1377196	12	15876	2.7963223	6.0903387	28
17160	2.0260005	6.1099358	12	19327	2.7484207	6.844333	28
18891	1.973835	6.2896943	12	19062	2.4395716	6.770189	28
18497	1.9707464	6.287521	12	17880	2.6258671	6.9791327	28
19581	1.247912	7.1536355	12	15781	2.9486356	6.4140267	28
20107	1.3574458	7.272398	12	15248	2.6494255	6.4811325	28
20155	1.5473135	7.296499	12	20208	2.3260887	6.680909	28
20088	1.6542585	7.0324774	12	18895	2.2006664	6.9808593	28
18860	2.2097743	6.388533	12	19583	2.7371361	6.8066106	28
19424	1.34967	7.28014	12	19206	2.3438728	6.925764	28
17047	1.3232479	7.1285653	12	20448	2.343964	6.7379184	28
19624	1.8227489	6.9318533	12	13191	2.6666222	6.420514	28
16733	1.6530024	6.732926	12	13417	2.3733292	6.939512	28
18680	2.1894817	6.3902607	12	18900	2.2311194	6.784566	28
19508	1.8400376	6.9096828	12	19894	2.597831	6.584262	28
17575	1.5948678	6.730921	12	18862	2.2413833	6.40368	28
19665	2.068136	6.5076766	12	20202	2.2744093	6.332294	28
19245	1.2313656	7.1438317	12	17561	2.2653165	6.3707542	28
18090	1.8121104	6.1503797	12	20426	2.4879591	5.787518	28
17743	1.7622906	6.914498	12	18786	2.6005473	6.314362	28
20433	1.8536603	6.698171	12	15690	2.684674	6.7153835	28
18046	1.6280905	6.3359714	12	15721	2.3605206	6.788072	28
17864	1.8109865	6.9289894	12	15194	2.2776072	6.7539816	28
19477	2.3228462	5.2213306	13	20008	2.3628144	6.658225	28
20418	2.6293154	5.2993445	13	16436	2.2229981	6.677798	28
14770	2.7497408	5.258051	13	14385	2.3995526	6.935524	28
17451	2.8101122	5.263943	13	15765	2.4659798	6.9000354	28
19238	2.8835661	5.223822	13	19365	2.9958358	6.0811934	28

20378	2.8055453	5.3005743	13	17185	2.4571915	6.7108493	28
20388	2.7777772	5.2933364	13	17167	2.542397	5.855767	28
19189	2.2213593	4.5410914	13	18631	2.906086	6.0210743	28
18752	1.6971134	3.9547956	13	18545	3.0068147	6.088663	28
19027	2.2942333	4.121009	13	19740	2.2175758	7.079206	28
19617	2.0363662	4.4837303	13	19473	2.062035	6.9961123	28
17087	2.4497776	5.3980947	13	17270	2.8731277	6.06396	28
18043	2.9569554	4.736751	13	15808	2.5328734	6.8874145	28
19161	2.1688902	4.916698	13	17199	2.635396	6.692948	28
12703	2.1057134	4.921047	13	20440	2.348343	6.727431	28
18077	2.173422	4.8871045	13	15455	2.5302227	6.782261	28
20370	2.3785634	5.109955	13	17894	2.5814943	6.4923997	28
12680	2.3735611	5.1234407	13	18795	2.491716	6.1063848	28
13485	2.3528135	5.0407524	13	20083	2.5225093	6.57137	28
19104	2.1471565	4.922771	13	18972	2.4696548	6.6907015	28
16744	2.382293	4.977128	13	19629	2.3762434	6.481255	28
20143	2.5564358	5.0542073	13	19513	2.5186462	6.525784	28
18733	1.5648229	3.8570845	13	19471	2.3502557	6.457264	28
12604	2.5157938	4.7276053	13	18560	2.6620984	6.087224	28
19515	2.1298053	4.930944	13	18411	2.700238	6.2482767	28
10992	2.0063844	4.5690517	13	16554	2.6893303	6.675913	28
19943	2.171361	4.891223	13	15174	2.722926	6.743157	28
19770	2.3546429	5.051411	13	20167	2.5907226	6.5449414	28
18605	2.29602	4.8949766	13	14446	2.594695	6.479305	28
19999	2.3848538	5.0023174	13	18308	2.4258623	6.7107663	28
20209	2.712816	4.485964	13	20066	2.5918345	6.735876	28
11505	2.377997	4.9990582	13	19290	2.5366762	6.703815	28
17282	2.3154285	4.576876	13	17971	2.945036	5.8903866	28
18882	1.5595118	3.8602526	13	19427	2.7983224	6.442482	28
19163	2.4047077	4.5929236	13	19795	2.4597745	6.8949065	28
18288	1.5470656	3.8566134	13	16767	2.7284317	6.407632	28
18204	2.2237625	4.5691214	13	18714	2.959691	5.8838925	28
15337	1.8273873	4.45977	13	19874	2.660966	6.284346	28

19837	1.7436751	4.338758	13	18495	2.3751204	6.6375365	28
19922	2.490611	5.330368	13	18689	2.35322	6.7200923	28
19335	2.0693936	4.7202463	13	17970	2.2802012	6.2081265	28
12600	2.0119467	4.397067	13	18436	2.5905857	6.4719377	28
13125	2.035652	4.4418044	13	16788	2.6095102	6.4926486	28
17500	2.255281	4.4328127	13	18939	2.3941128	6.412565	28
18505	2.6319335	4.830161	13	16529	2.274765	6.676953	28
18402	1.551502	3.8665633	13	17565	2.5112295	6.9728527	28
19797	2.761097	5.5534234	13	13203	2.7153857	6.4007835	28
17154	2.2515776	4.627401	13	19662	2.7072055	6.3754106	28
18524	2.6411948	5.2468357	13	19928	2.7056787	6.4228106	28
17031	1.5005627	3.864061	13	18463	2.6851995	6.4144716	28
15725	2.5216913	4.0709386	13	19008	2.6895943	6.397865	28
17118	2.7299292	4.7470546	13	16812	0.66194177	3.5047839	29
19605	2.048576	3.6574562	13	20406	0.4401744	3.5352433	29
15273	2.4249194	4.178957	13	17765	0.6532987	3.5193896	29
19432	2.057992	4.5059543	13	19402	0.22754678	3.6783748	29
19511	2.635593	4.4098687	13	19763	0.7327629	3.4797907	29
15673	1.9846848	4.499381	13	17076	0.7516311	3.6205723	29
19717	2.4460063	4.612584	13	16810	0.78287214	3.6236331	29
15915	2.0721269	4.52683	13	16946	0.5358823	3.7847917	29
12877	2.5834877	4.3097053	13	16785	0.25712216	3.669048	29
18101	2.6148357	4.384688	13	16924	0.24518487	3.4466224	29
20065	1.9372557	3.614591	13	16990	0.17142858	3.4245462	29
19099	1.8542286	4.477898	13	16925	0.69869596	3.5252879	29
18790	2.7313414	3.8897774	13	18934	0.83257437	3.6860042	29
19828	2.2891593	3.747362	13	19564	0.14919817	3.7435956	29
17884	2.0475361	3.6543307	13	18356	0.4316716	3.4859855	29
18136	1.9649037	3.605727	13	16980	0.606786	3.5807078	29
16537	1.9060688	3.6065176	13	16842	0.647146	3.7012992	29
13430	2.1821172	3.845149	13	16972	0.4717641	3.4627616	29
17568	2.009477	3.607444	13	16959	0.340961	3.6470597	29
19349	1.9631956	3.6193025	13	16821	0.42284012	3.475955	29

13450	1.9389106	4.524782	13	16780	0.53975284	3.4836888	29
11443	1.913722	4.525742	13	16734	0.7069059	3.5359402	29
20043	1.8996041	4.480821	13	20393	0.7156165	3.5192397	29
18993	2.0463815	3.6231472	13	16868	0.34883967	3.5602834	29
17718	1.8981731	3.6446903	13	16884	0.5100559	3.6906817	29
19240	1.9930273	3.6406202	13	16721	0.50415695	3.7017055	29
19177	1.9351516	3.6221783	13	16713	0.48146105	3.6536539	29
17348	2.3874896	4.2836676	13	16930	0.2206902	3.4276237	29
15381	1.7542008	4.3382707	13	16994	0.34355944	3.5427277	29
18403	1.953179	4.386135	13	16714	0.69801104	3.547411	29
11709	1.951493	4.4257855	13	16830	0.3897271	3.8869636	29
12857	2.0037382	4.3158903	13	16728	0.38197932	3.888753	29
12453	2.2017558	3.8191617	13	16903	0.38417155	3.7977226	29
17741	2.0095134	3.6491318	13	16955	0.6227177	3.5088246	29
18373	2.0153599	3.6681504	13	16861	0.38491505	3.586527	29
19092	2.482378	3.7349963	13	17058	0.35859573	3.535048	29
13232	1.8797024	4.441995	13	16819	0.40780345	3.5204089	29
17979	2.0094793	3.6886172	13	16751	0.20855357	3.8113008	29
20036	1.8810014	4.5141516	13	16708	0.6900693	3.535861	29
18164	2.023682	3.6417727	13	16983	0.34586173	3.5390096	29
19466	1.972243	3.645374	13	16943	0.24333647	3.5189667	29
17175	2.6955738	4.5149994	13	16887	0.3049665	3.569457	29
15666	1.480421	3.832594	13	16871	0.6677993	3.526996	29
16336	2.1019437	4.285379	13	16859	0.5579075	3.5166762	29
20475	2.0214696	3.7253895	13	17347	0.5586631	3.663623	29
12315	1.9137703	3.76437	13	16995	0.57358134	3.6400058	29
17229	1.6027478	3.8663378	13	16815	0.5232239	3.694142	29
17294	2.3860977	4.559304	13	16699	0.5139374	3.7097282	29
18930	2.7115622	5.5603437	13	16756	0.53758574	3.5970078	29
19342	1.8326012	4.4565253	13	16775	0.17497832	3.4739175	29
13163	2.749498	4.3055325	13	16740	0.627265	3.5298667	29
12267	2.667474	4.5073347	13	16710	0.21819325	3.4745033	29
12961	2.2631567	4.608326	13	16795	0.5286784	3.6107635	29

16314	2.2928193	4.299363	13	16763	0.5828743	3.5331693	29
15528	2.5342886	4.493504	13	16862	0.5712566	3.6300564	29
18516	2.2918909	4.07918	13	16813	0.64304274	3.5303578	29
12932	2.7254713	4.572048	13	16970	0.17819144	3.722885	29
18203	2.6225548	4.419682	13	16907	0.20365301	3.6867557	29
12272	2.512104	4.2381587	13	16982	0.7254779	3.5788777	29
17428	2.5158448	4.224067	13	16685	0.3065377	3.5262275	29
12335	2.0483923	4.477988	13	16748	0.53826797	3.6552773	29
14636	2.0576968	4.464501	13	16772	0.2240588	3.4109943	29
18474	1.9932978	4.638787	13	17252	0.6321132	3.5255017	29
11923	2.0124695	4.4930396	13	16823	0.40754858	3.834107	29
16414	2.1184447	4.777214	13	16847	0.46617872	3.6472025	29
15079	2.0862792	4.8637147	13	16820	0.5685621	3.6249852	29
19644	2.409107	4.1627793	13	16688	0.49625942	3.5493593	29
18500	2.1891947	4.676354	13	17216	0.38792226	3.643637	29
16168	2.4274917	4.8277745	13	16723	0.25371277	3.5753155	29
15868	2.3752549	4.8499155	13	16917	0.23602512	3.5295033	29
12461	2.3025749	4.5936723	13	16992	0.25803387	3.5358248	29
16277	2.1495502	4.35422	13	20127	0.25674328	3.5279484	29
19862	2.6043632	4.3665986	13	16770	0.37547895	3.7711642	29
15130	2.4633932	4.7614946	13	16883	0.27184695	3.635643	29
15360	2.4240649	4.8114243	13	16894	0.24529184	3.5811055	29
18106	2.2776685	4.385016	13	16867	0.20471118	3.4884908	29
15038	2.2544184	4.5178437	13	16798	0.22300844	3.6526406	29
15561	2.3428462	4.9418883	13	16961	0.43023324	3.7629957	29
19646	2.3632486	4.917852	13	16997	0.18802296	3.615705	29
17198	2.4364662	4.875071	13	16816	0.3317522	3.690624	29
14439	2.2908425	4.7021093	13	16782	0.31652942	3.6522892	29
15291	2.4211142	4.7111487	13	16893	0.18379153	3.6706624	29
13505	2.2641232	4.3929434	13	16677	0.45791224	3.769788	29
12475	2.316416	4.3907294	13	16656	0.4440371	3.6682124	29
12546	2.8905466	4.293509	13	20389	0.2877843	3.6317995	29
17915	2.3607974	4.3813615	13	16665	0.2920758	3.5068066	29

15465	2.1564069	4.3231697	13	12537	0.41693267	3.8345208	29
17332	2.6388915	4.6327085	13	19728	0.426736	3.9103615	29
12367	2.0139608	3.6430435	13	18725	0.41146025	3.5652094	29
11195	2.5944571	4.489472	13	16953	0.20419805	3.522947	29
19836	2.2565012	4.2776165	13	16769	0.22349948	3.4317837	29
18359	2.0423853	4.0728416	13	16968	0.59377575	3.639321	29
14989	2.2574627	4.5819817	13	17235	0.56971276	3.5591743	29
15882	2.1767607	4.1814675	13	19768	0.663801	3.5390062	29
11248	2.4519174	4.2754374	13	16692	0.7104889	3.7920876	29
12766	2.0220618	4.4664497	13	16741	0.64712036	3.589544	29
15819	2.505627	4.2424555	13	16960	0.6143736	3.626535	29
12660	2.4384005	4.1682677	13	19692	0.61743975	3.6964066	29
11642	2.4687972	4.2518034	13	16920	0.56647605	3.638531	29
16299	2.5160768	4.231917	13	16735	0.59976774	3.7353468	29
17488	2.2509677	4.353316	13	18995	0.6215998	3.6482255	29
15268	2.2607822	4.462208	13	16974	0.26144624	3.5589018	29
15503	2.4313498	4.6931663	13	16986	0.5367712	3.661616	29
13326	2.19684	4.296653	13	16805	0.4045785	3.5526574	29
18760	2.4345279	4.2601957	13	16950	0.54457134	3.616157	29
14793	2.4485571	4.2168007	13	16932	0.63670295	3.8598557	29
19973	2.2652826	4.4394274	13	16869	0.68871415	3.5511665	29
13111	2.3365147	4.4318533	13	16800	0.5607093	3.708237	29
15472	2.2927873	4.776653	13	16818	0.3893514	3.6793983	29
15042	2.3300047	4.441715	13	16916	0.49644238	3.6959636	29
13271	2.2369761	4.2705383	13	17397	0.49138004	3.561965	29
18492	2.5800154	4.9159365	13	16949	0.58628714	3.6401484	29
15636	2.1470332	4.515453	13	16776	0.68791544	3.6077385	29
19269	2.3358448	4.120467	13	16701	0.6149724	3.6998982	29
18385	2.4167018	4.2235284	13	16729	0.44078702	3.6667945	29
12943	2.3490813	4.1035786	13	16971	0.5433583	3.6555688	29
16696	2.2643788	4.0628505	13	17879	0.83097357	3.7048974	29
15196	2.538034	4.781989	13	16963	0.24611384	3.43338	29
11151	2.306637	4.284244	13	16958	0.22913612	3.4519858	29

11912	2.2227914	4.3160253	13	16988	-0.08371653	3.6924543	29
20445	2.2109694	4.325738	13	13503	-0.001655988	3.6262064	29
11148	2.066871	4.363029	13	16915	0.09711443	3.6181831	29
12657	2.1425989	4.3536825	13	17000	0.2317044	3.532026	29
18454	2.5927968	4.374157	13	16727	0.39048192	3.5626092	29
19291	2.4287207	4.3242774	13	16998	0.23483317	3.4083765	29
13142	2.4076757	4.560451	13	16886	0.24838436	3.4539614	29
13101	2.5357616	4.676598	13	17002	0.63941425	3.5426621	29
18206	2.5293095	4.5087905	13	16929	0.24308605	3.4550917	29
15221	2.6341019	4.5870137	13	16904	0.47870857	3.7965658	29
11463	2.559706	4.342962	13	16864	0.23379281	3.4435394	29
19044	2.4773142	4.3532515	13	16882	0.20363702	3.4716728	29
16328	2.557787	4.689906	13	19175	2.8541236	8.920278	30
16313	2.5828288	4.3913355	13	17086	3.9491806	9.655622	30
16073	2.5316708	4.3552666	13	18197	2.689916	9.212965	30
19191	2.513796	4.3679137	13	19603	2.8098722	8.957435	30
11392	2.5820618	4.4408464	13	11834	2.7074528	9.178453	30
16726	2.6388235	4.6338825	13	12954	2.6607249	9.230739	30
13381	2.2850149	4.352129	13	18788	2.6579635	9.250073	30
19512	2.3967946	4.504421	13	13024	3.2259674	9.14917	30
15566	2.34265	4.4833374	13	19592	2.959974	9.2701235	30
15160	2.2823079	4.3708134	13	15924	3.1235888	9.268023	30
14663	2.3221867	4.504745	13	19892	3.1519701	9.360738	30
15589	2.651575	4.5327535	13	17904	3.0339937	9.3280525	30
19276	2.2348845	4.357376	13	17573	3.328587	9.080183	30
15252	2.3337138	4.6868153	13	19791	2.686014	9.11449	30
18029	2.300882	4.3838024	13	18038	2.8417835	8.930524	30
15814	2.309203	4.4962115	13	12386	2.8516119	8.917348	30
20013	2.3909454	4.298911	13	12663	3.065333	9.290386	30
19260	2.3469033	4.324794	13	20174	2.8795152	8.712255	30
17785	2.2101414	4.41812	13	18157	3.221105	9.260986	30
19585	2.4746487	4.2721343	13	18291	3.3109684	9.195388	30
19398	2.021681	3.826624	13	11031	2.5909245	9.220038	30

17349	2.4656913	4.2083054	13	13414	3.1529133	9.325305	30
12949	2.268593	4.4143033	13	13090	3.1830716	9.279987	30
19034	2.4593227	4.147849	13	15752	3.3729956	8.981193	30
18514	2.456989	4.252801	13	15374	4.028827	9.396638	30
20173	2.1610208	4.225903	13	13336	3.2374744	9.327946	30
18272	2.349065	4.573472	13	17725	3.2741168	9.195855	30
17706	2.3306177	4.5475135	13	18394	3.3553834	9.348321	30
12834	1.9620959	3.7650936	13	18129	3.3562012	8.958842	30
18033	2.3741765	4.239724	13	14742	2.8426373	8.934645	30
15626	2.3962271	4.230434	13	17148	3.9882877	9.376684	30
18949	2.428897	4.1544747	13	15203	3.3773468	9.185335	30
12580	2.5415115	4.2427197	13	18236	3.0567899	8.936639	30
12751	2.5273712	4.276521	13	12427	3.9447188	9.418056	30
11240	2.4713044	4.2538533	13	16552	3.0215673	9.244578	30
19542	2.023087	4.328301	13	13451	3.3249884	9.051657	30
18319	2.6041126	4.4617205	13	16213	3.939117	9.681591	30
20189	2.2748501	4.4460626	13	18548	3.4207947	9.339602	30
18340	2.664526	4.413952	13	17453	3.9974802	9.645033	30
17948	2.8513699	4.7861133	13	18820	3.2056162	9.32205	30
17413	2.5799868	4.7677417	13	16441	3.2020638	9.35768	30
17129	2.7768788	4.8444085	13	12883	3.1005375	9.378355	30
18711	2.8322556	4.788543	13	18156	3.2868195	9.31468	30
17406	2.8102663	4.829493	13	16453	3.0973837	9.371158	30
19964	2.7716646	5.22428	13	19940	2.9927783	9.275188	30
13135	2.3723426	5.0783925	13	17301	3.182979	9.318884	30
19051	2.387059	5.028495	13	17983	3.382881	9.17094	30
17262	2.0475557	4.3512883	13	18953	3.7968602	9.329525	30
18905	2.2891772	4.7410183	13	20115	3.8596601	9.372725	30
17961	2.1599076	4.627751	13	14961	3.7455845	9.294689	30
19510	2.4197419	5.2687597	13	12864	3.3270054	9.160676	30
15777	2.225624	3.8130045	13	13342	3.636256	9.439117	30
17908	2.4754581	4.620781	13	17769	3.8847992	9.43979	30
19195	2.449963	4.921188	13	17722	4.005232	9.4290905	30

18510	2.907868	4.588184	13	14882	3.8534524	9.434908	30
18428	2.6602254	4.920417	13	18001	3.685885	9.422012	30
17956	2.598396	4.859783	13	18636	3.9139924	9.491636	30
15774	2.3105025	3.9861515	13	19234	3.9428415	9.452697	30
15890	2.2067034	3.8670733	13	17921	4.1152177	9.593442	30
16401	2.2686868	3.8391557	13	18035	4.113001	9.537718	30
13252	-1.8052382	8.125879	14	18014	3.982988	9.5157795	30
19655	-2.0995235	7.957111	14	17867	3.6479557	9.416327	30
19173	-2.033319	7.93634	14	15254	4.0666237	9.543997	30
11094	-2.1436663	8.220713	14	18380	3.320858	9.211669	30
12304	-1.7685531	7.8028464	14	17022	3.9477322	9.689962	30
19456	-1.9627606	8.643051	14	19458	3.2334366	9.328843	30
17807	-1.9581283	8.362029	14	12878	3.3808901	8.957474	30
18990	-2.1572254	7.656649	14	14745	2.8203816	8.867716	30
12588	-1.8291373	8.005477	14	11722	3.9832757	9.637462	30
15895	-2.024998	8.492733	14	14462	3.3295238	8.933911	30
18212	-1.9894181	8.464486	14	17929	2.9547791	9.145118	30
19274	-2.114331	8.376391	14	20102	2.81411	8.895503	30
19088	-1.9967582	8.498781	14	20044	3.3123684	9.280587	30
19482	-2.0949936	8.687892	14	16647	3.168789	9.374773	30
10969	-2.099487	7.959479	14	14937	4.073208	9.587381	30
13367	-1.7696986	8.1446705	14	18017	3.0631819	9.107601	30
17854	-2.1189187	8.661385	14	19094	2.6953256	9.017922	30
17613	-2.2073348	8.274354	14	17485	2.7753158	9.144424	30
18577	-1.6842602	7.8477936	14	16678	2.8130019	8.92336	30
19960	-1.781012	8.133168	14	16440	2.608148	9.228256	30
17293	-1.9377811	7.902789	14	20365	2.6424265	9.21978	30
15622	-2.2183921	8.29664	14	12992	4.0039024	9.35061	30
18301	-1.949263	8.755185	14	12368	3.0981266	9.224165	30
18542	-2.0921764	8.427851	14	13175	3.3557186	8.949028	30
10964	-1.9818184	8.495189	14	16641	2.8970625	9.261481	30
18541	-2.1253278	8.624513	14	18723	2.6205926	9.097505	30
18277	-2.20252	8.281053	14	12351	2.7336502	8.836919	30

17595	-2.1197793	8.363371	14	13140	3.3577662	9.063567	30
17704	-1.7547036	7.8704467	14	18740	3.7574947	9.401317	30
18165	-1.8396215	8.122096	14	18573	3.2633626	9.077664	30
18133	-1.8630552	8.057732	14	16600	3.1218555	9.056565	30
18855	-1.9966011	7.9936132	14	11707	3.187258	8.96385	30
17715	-1.8714694	8.137994	14	18079	3.0900257	9.089546	30
13214	-2.185075	8.263	14	17890	3.1176224	9.058011	30
17326	-1.9187528	7.972625	14	17840	2.724762	8.781887	30
19147	-1.8990874	8.542522	14	15821	3.6858542	9.096884	30
19721	-1.7902603	8.426813	14	17738	3.1926591	9.071096	30
18567	-1.9142236	7.780741	14	19202	2.8063493	8.9382715	30
15833	-2.2008488	8.290583	14	16694	2.8642516	9.16321	30
17842	-1.7387441	7.896297	14	18214	3.69823	9.26746	30
16670	-1.9402784	7.7514186	14	19353	2.7200553	8.960358	30
16789	-2.1060169	7.6772656	14	13008	3.2475348	9.329123	30
12720	-1.6539721	7.810307	14	18662	2.823693	8.897775	30
17274	-1.8333789	8.000295	14	17859	3.3371942	9.075354	30
19778	-1.8745607	7.7455163	14	18333	3.3107588	9.03603	30
18418	-2.1672707	8.204654	14	20026	3.9139738	9.449117	30
16689	-1.981641	7.935227	14	19406	2.8392518	8.930061	30
17467	-2.005645	7.8679996	14	12321	3.3412368	9.0025625	30
17390	-2.0521226	8.477826	14	17777	3.137085	9.127295	30
17647	-1.9848524	8.71028	14	17701	3.2179134	9.289629	30
19272	-2.0272768	8.503638	14	19647	3.1592712	9.325806	30
20472	-1.9683422	7.881295	14	15698	3.0346975	9.211405	30
16839	-1.9955817	7.6934633	14	18316	3.4944353	9.379221	30
17359	-1.9754456	7.8325696	14	18131	2.7197282	9.231468	30
16679	-2.2388363	7.6279516	14	19543	3.0937421	9.243123	30
16964	-2.2316284	7.6253	14	18332	3.2055678	9.298358	30
17478	-1.8966446	7.723114	14	12568	3.3737633	9.352876	30
18070	-2.084792	8.436592	14	19171	3.9358351	9.680255	30
17013	-1.7608224	8.15398	14	18181	3.2369916	9.240737	30
16922	-2.2422147	7.626293	14	15151	3.3205414	9.340534	30

16660	-2.2315829	7.6258855	14	13383	3.1667528	9.2670145	30
16835	-2.2450402	7.623734	14	17802	3.2826905	9.294557	30
16906	-2.2428787	7.624965	14	19083	3.0138795	9.213681	30
16989	-2.2435296	7.6214604	14	18300	3.234839	9.183222	30
16732	-2.2352808	7.6328406	14	19273	3.1986735	9.209034	30
16908	-2.235533	7.62945	14	18965	2.660013	8.979759	30
16764	-2.2528968	7.6149387	14	19622	3.1290305	9.29399	30
18104	-1.8861806	7.716773	14	18019	3.03272	9.192224	30
17547	-1.851799	7.8512316	14	17927	2.760823	8.735382	30
17815	-1.9568278	7.7695746	14	19889	4.069274	9.309575	30

T14

AA SEQ ID#	Fc-human-TFR1 pH7	Fc-hTFR1 60+pH5.5 wash	Fc-macaque TFR1 pH7	Fc-macaque TFR1 60+pH5.5 wash	Fc-marmoset TFR1 pH7	Fc-marmoset TFR1 60+pH5.5 wash	Fc-mouse TFR1 pH7	Fc-mouse TFR1 60+pH5.5 wash	Fc-control pH7	Fc-hTFR1 60+pH5.5 wash
36241	+++	-	---+	+++	-	-	-	-	-	-
36242	+++	-	---+	+++	+++	+++	-	-	-	-
36243	+++	++	–	+	+	+	-	-	-	-
36244	+++	+	---+	+++	+++	+++	-	-	-	-
36245	+++	+++	---+	+++	+++	+++	-	-	-	-
17241	+++	-	---+	+++	+++	+++	-	-	-	-
36246	+++	+++	–	+	+	+	-	-	-	-
36247	+++	+++	–	+	+	+	-	–	-	-
36248	+++	+++	-	-	-	-	-	-	-	-
36247	+++	+++	–	+	+	+	+	–	-	-
36246	+++	+++	–	+	+	+	-	-	+	-
36249	+++	+++	-	+	-	+	-	-	-	-
36248	+++	+++	-	-	-	-	-	–	-	-
36250	+++	+++	–	+	+	+	+	-	-	-
36251	+++	-	-	-	-	-	-	-	-	-
36251	+++	+	–	+	-	+	-	-	-	-
36252	+++	+++	–	+	+	+	-	-	-	-
36250	+++	+++	–	+	+	+	-	-	-	-
36248	+++	+++	-	-	-	-	-	-	-	-
36253	+++	+++	–	+	+	+	-	-	-	-
36243	+++	++	–	+	+	+	-	-	-	-
36254	+++	++	–	++	-	-	-	-	-	-
36255	+++	+	-	-	-	-	-	-	-	-
36256	+++	+++	-	-	-	-	-	–	-	-
36257	+++	+	-	-	-	-	-	-	-	-
18857	+++	-	---+	+	+++	-	-	–	-	-
36258	+++	+++	-	-	-	-	-	-	-	-
36259	+++	+	-	-	-	-	-	-	-	-
36252	+++	+++	–	+	+	+	-	–	-	-

36260	+++	+++	–	+	+	+	-	-	-	-
36261	+++	+++	–	+	+	+	-	-	++	-
36262	+++	++	–	+	+	+	-	-	-	-
36263	+++	+++	-	-	+	+	-	-	-	-
36259	+++	+	-	-	-	-	-	-	-	-
36264	+++	+++	-	-	-	-	-	-	-	-
36265	+++	+	-	+	+	-	-	–	-	-
36255	+++	+	-	-	-	-	-	-	-	-
12165	+++	+++	-	-	-	-	-	-	-	-
36243	+++	++	–	+	+	+	-	-	-	-
36266	+++	+	–	+	+	+	-	–	-	-
36249	+++	+++	-	+	+	-	+	-	-	-
11947	+++	+++	-	-	-	+	+	-	-	-
36265	+++	+	–	+	-	+	-	-	-	-
36255	+++	+	-	-	-	-	-	-	-	-
36267	+++	+++	-	-	-	-	-	-	-	-
36268	+++	+++	–	+	+	+	-	-	-	-
36269	+++	+++	-	-	-	+	-	-	-	-
36248	+++	+++	-	-	-	-	-	-	-	-
36261	+++	+++	–	+	+	+	-	–	-	-
36257	+++	+	-	+	-	+	-	-	-	-
36270	+++	+++	-	-	-	-	-	-	-	-
36271	+++	+	–+	+	-	-	+	–	-	-
36272	+++	-	–+	++	+++	+	+	–	+++	-
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36253	+++	+++	–	+	+	+	-	-	-	-
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36274	+++	+++	-	-	-	-	-	-	-	-
36275	+++	+	-	-	-	-	-	-	-	-
36276	+++	-	–+	++	+++	-	+	-	-	-
36277	+++	+	–	+	+	+	+	–	-	-
36243	+++	++	–	+	+	+	-	-	-	-
36278	+++	+++	–	+	+	+	+	-	-	-

36268	+++	+++	–	+	+	+	-	-	-	-
36279	+++	-	–	+	-	-	-	-	-	-
36280	+++	-	-	+	-	-	-	-	-	-
36281	+++	+++	–	+	+	+	-	-	-	-
36268	+++	+++	–	+	+	+	-	-	-	-
36258	+++	+++	-	-	-	-	-	-	-	-
36282	+++	-	–+	+	+++	+	+	-	-	-
36278	+++	+++	–	+	+	+	-	–	-	-
36283	+++	-	–+	+++	+++	+++	-	-	-	-
36284	+++	-	–+	+++	+++	+++	-	-	-	-
36285	+++	-	-	+	-	-	-	-	-	-
36262	+++	++	–	+	+	+	-	-	-	-
36250	+++	+++	–	+	+	+	-	-	-	-
36286	+++	+	–	+	-	+	-	-	-	-
36280	+++	-	-	+	-	-	-	-	-	-
13734	+++	+++	–	-	+	-	-	-	-	-
36287	+++	+++	-	-	-	-	-	-	-	-
36268	+++	+++	–	+	+	+	-	-	-	-
36288	+++	+++	-	-	-	+	-	-	-	-
36289	+++	+++	-	-	-	-	-	–	-	-
36290	+++	+	-	-	-	-	-	-	-	-
14198	+++	+++	-	-	-	+	-	-	-	-
36281	+++	+++	–	+	+	+	-	–	-	-
36291	+++	+++	-	-	-	-	-	-	-	-
17830	+++	+++	-	-	-	-	+	–	-	-
36259	+++	+	-	-	-	-	-	-	-	-
36257	+++	+	-	-	-	+	-	-	-	-
36292	+++	+++	-	-	-	-	-	-	-	-
36257	+++	+	-	-	-	-	-	-	-	-
36250	+++	++	–	+	+	+	+	–	-	-
36293	+++	-	-	+	-	-	-	-	-	-
36294	+++	+	-	+	-	+	-	-	-	-
12220	+++	+++	-	-	-	-	-	-	-	-

36260	+++	+++	–	+	+	+	-	-	-	-
36266	+++	+	–	+	+	+	+	–	-	-
36280	+++	+	-	-	-	-	-	-	-	-
36259	+++	+	-	-	-	-	-	-	-	-
36295	+++	+	–	+	+	+	+	–	-	-
36296	+++	+++	-	-	-	-	-	-	-	-
36297	+++	+++	-	-	-	+	-	-	-	-
36298	+++	++	––+	+++	+++	+++	-	-	-	-
36251	+++	+	-	+	-	+	-	-	-	-
36299	+++	+	–	+	+	+	-	-	-	-
36300	+++	+++	-	-	-	-	-	-	-	-
36301	+++	-	-	+	-	-	-	-	-	-
36302	+++	+	-	-	-	-	-	-	-	-
36303	+++	++	–	+	+	+	-	-	-	-
12165	+++	+++	-	+	-	+	-	-	-	-
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36304	+++	+++	-	-	-	+	-	-	-	-
36305	+++	++	–	+	+	+	-	-	-	-
36306	+++	-	––+	+++	+	-	+++	–––	-	-
36307	+++	-	––+	++	+++	+	+++	–	-	-
11154	+++	+++	-	-	-	+	-	-	-	-
36308	+++	++	-	-	-	-	-	-	-	-
36309	+++	+++	-	+	-	+	-	-	-	-
36310	+++	+++	-	-	-	-	+	-	-	-
36255	+++	+	-	-	-	-	-	-	-	-
36279	+++	-	-	-	-	-	-	-	-	-
36270	+++	+++	-	-	-	-	-	-	-	-
16090	+++	+++	-	-	-	-	-	-	-	-
36295	+++	+	–	+	+	+	-	-	-	-
36311	+++	+++	-	-	-	-	-	-	-	-
36312	+++	+	–	+	+	+	-	-	-	-
36301	+++	-	-	+	-	-	-	-	-	-
36313	+++	+++	-	-	-	-	+	–	-	-

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36314	+++	+++	-	+	-	+	-	-	-	-
36251	+++	+	-	+	-	-	-	-	-	-
36277	+++	+	–	+	+	+	-	-	-	-
36315	+++	-	-	+	-	-	-	-	-	-
36316	+++	+++	-	-	-	-	-	-	-	+
36280	+++	-	-	-	-	-	-	-	-	-
36317	+++	++	-	-	-	-	-	-	-	-
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16631	+++	+	-	-	-	-	-	-	-	-
36320	+++	+++	-	-	-	-	-	-	-	-
36321	+++	+++	-	-	-	-	-	-	-	-
36277	+++	+	–	+	+	+	+	-	-	-
11326	+++	+++	-	-	-	-	-	-	-	-
36293	+++	-	-	-	-	-	-	-	-	-
36316	+++	+++	-	-	-	+	-	-	-	-
36322	+++	-	–+	+	+++	+	+	-	-	-
36275	+++	+	-	-	-	-	-	-	-	-
36292	+++	+++	-	-	-	+	+	-	-	-
36323	+++	+	-	-	-	-	-	-	-	-
36324	+++	+	–	+	+	+	+++	---	+	-
36325	+++	+++	-	-	-	-	-	-	-	-
36300	+++	+++	-	+	-	+	-	-	-	-
36326	+++	-	-	-	-	-	-	-	-	-
16575	+++	+++	-	-	-	-	-	-	-	-
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36328	+++	++	-	-	-	-	-	-	-	-
12312	+++	+	-	-	-	-	-	-	-	-

36312	+++	+	–	+	+	+	+	-	-	-
36329	+++	-	––+	+	++	-	+	–	-	-
36330	+++	+++	-	+	-	+	-	-	-	-
36318	+++	+++	-	-	-	-	-	-	-	-
19559	+++	++	––+	+++	+++	+++	-	-	-	-
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36331	+++	+++	-	-	-	+	+	–	-	-
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12165	+++	+++	-	-	-	+	-	-	-	-
11239	+++	+++	-	-	-	-	-	-	-	-
36289	+++	+++	-	-	-	-	-	-	-	-
36334	+++	-	––+	+	+++	+	-	-	-	-
36335	+++	+++	-	-	-	-	-	-	-	-
36287	+++	+++	-	-	-	-	-	-	-	-
36336	+++	+	-	-	-	-	-	-	-	-
36264	+++	+++	-	-	-	-	-	-	-	-
36337	+++	-	-	-	-	-	-	-	-	-
11078	+++	+++	-	-	-	-	-	-	-	-
36263	+++	+++	-	-	-	+	-	-	-	-
36338	+++	++	-	-	-	-	-	-	-	-
36339	+++	+	-	-	-	-	-	-	-	-
36340	+++	+++	-	+	+	+	-	-	-	-
11609	+++	+++	-	-	-	-	-	-	-	-
12206	+++	+	-	-	-	-	-	-	-	-
11531	+++	-	-	-	-	-	-	-	-	-
36341	+++	+++	-	-	-	-	-	-	-	-
36342	+++	-	––+	+	+++	+	-	-	-	-
36343	+++	+++	–	+	+	+	-	-	-	-
36344	+++	+++	–	+	+	+	-	-	-	-
36309	+++	+++	-	+	-	+	-	-	-	-

36345	+++	+++	-	-	-	-	+	-	-	-
11239	+++	+++	-	-	-	+	-	-	-	-
36346	+++	++	--+	+++	+++	+++	-	-	-	-
13882	+++	+++	-	-	-	-	-	-	-	-
36319	+++	+++	-	-	-	-	-	-	-	-
36290	+++	+	-	-	-	-	-	-	-	-
36347	+++	+++	-	-	-	+	-	-	-	-
36331	+++	+++	-	-	-	-	+	-	-	-
36348	+++	+++	-	-	-	-	+	-	-	-
16657	+++	+++	-	-	-	-	-	-	-	-
36349	+++	+++	-	-	-	-	-	-	-	-
36347	+++	+++	-	-	-	+	-	-	-	-
17701	+++	++	-	-	-	-	-	-	-	-
36350	+++	-	-	+	-	-	-	-	-	-
36320	+++	+++	-	-	-	-	-	-	-	-
36351	+++	-	--+	++	+++	+	+	-	-	-
36345	+++	+++	-	-	-	-	-	–	-	-
36352	+++	+++	-	-	-	+	+	-	-	-
36353	+++	+	-	-	-	-	-	-	-	-
36286	+++	+	–	+	+	+	-	-	-	-
36354	+++	+	–	+	+	+	-	-	-	-
36355	+++	-	--+	+	+	-	-	-	-	-
36356	+++	+++	-	-	-	-	-	–	-	-
36357	+++	+++	-	-	-	-	-	-	-	-
36274	+++	+++	-	-	-	-	-	-	-	-
16631	+++	+	-	-	-	-	-	-	-	-
36325	+++	+++	-	-	-	+	-	-	-	-
36358	+++	+++	-	-	-	+	-	-	-	-
36341	+++	+++	-	-	-	-	+	–	-	-
36315	+++	-	-	-	-	-	-	-	-	-
36308	+++	++	-	-	-	-	-	-	-	-
36274	+++	+++	-	+	-	+	-	-	-	-
36299	+++	+	–	+	+	+	-	-	-	-

36288	+++	+++	-	-	-	-	-	-	-	-
36359	+++	+++	-	-	-	+	-	–	-	-
36360	+++	+	–	+	+	+	-	-	-	-
36348	+++	+++	-	-	-	-	-	-	-	-
36361	+++	++	-	-	-	-	-	-	-	-
36286	+++	+	–	+	+	+	-	-	-	-
36299	+++	+	–	+	+	+	+++	---	++	-
11609	+++	+++	-	-	-	-	-	-	-	-
36305	+++	++	–	+	+	+	-	-	-	-
19635	+++	+++	-	-	-	-	-	-	-	-
11553	+++	+++	-	-	-	-	-	-	-	-
36310	+++	+++	-	-	-	-	-	-	-	-
36272	+++	-	--+	++	+++	+	+	–	-	-
36277	+++	+	–	+	+	+	-	–	-	-
36343	+++	+++	–	+	+	+	-	-	-	-
36362	+++	-	-	-	-	-	-	-	-	-
36304	+++	+++	-	-	-	-	-	-	-	-
36363	+++	-	--+	+	+++	+	+	–	-	-
36364	+++	+++	--+	+++	+++	+++	-	–	-	-
36365	+++	-	--+	+	+++	+	-	-	-	-
36366	+++	+	-	-	-	-	-	-	-	-
36367	+++	+++	-	-	-	-	-	-	-	-
36368	+++	-	--+	+	++	-	-	-	-	-
36369	+++	+++	-	-	-	-	-	-	-	-
36258	+++	+++	-	-	-	-	-	-	-	-
13938	+++	+++	–	+	+	+	-	-	-	-
36354	+++	+	–	+	+	+	-	-	-	-
36370	+++	-	--+	+	+++	-	+	–	-	-
36321	+++	+++	-	-	-	-	-	-	-	-
36371	+++	-	-	-	-	-	-	-	-	-
36372	+++	+++	-	-	-	+	+	-	-	-
14441	+++	+++	-	-	-	-	-	-	-	-
36373	+++	+++	-	-	-	-	-	-	-	-

36374 +++	-	-	-	-	-	-	-	-	-
36373 +++	+++	-	-	-	+	-	-	-	-
36375 +++	+++	-	+	-	+	-	-	-	-
36376 +++	+	-	-	-	-	-	–	-	-
11271 +++	+++	-	-	-	-	-	-	-	-
36377 +++	+++	-	-	-	+	-	-	-	-
36328 +++	++	-	-	-	-	-	-	-	-
36378 +++	+++	-	-	-	-	-	–	-	-
36353 +++	+	-	-	-	-	-	-	-	-
36379 +++	+++	-	-	-	-	-	-	-	-
36302 +++	+	-	-	-	-	-	-	-	-
13777 +++	+++	-	-	-	-	-	-	-	-
11326 +++	+++	-	-	-	-	-	-	-	-
36264 +++	+++	-	-	-	-	-	-	-	-
36344 +++	+++	–	+	+	+	-	-	-	-
11553 +++	+++	-	-	-	-	-	-	-	-
36380 +++	+++	-	+	+	+	-	-	-	-
36381 +++	-	–+	+	++	-	+	-	+++	-
36374 +++	-	-	+	-	+	-	-	-	-
36323 +++	+	-	-	-	-	-	-	-	-
36382 +++	+++	–+	+++	+++	+++	+	–	+++	+++
11011 +++	+++	-	-	-	-	-	-	-	-
11154 +++	+++	-	-	-	-	-	-	-	-
36309 +++	+++	-	-	-	+	-	-	-	-
36383 +++	+++	-	+	+	+	-	-	-	-
14581 +++	+++	-	-	-	-	-	-	-	-
36299 +++	+	–	+	+	+	-	–	-	-
36309 +++	+++	-	+	-	+	-	-	-	-
36384 +++	++	-	-	-	-	-	-	-	-
36314 +++	+++	-	+	-	-	-	-	-	-
36385 +++	++	-	+	-	+	-	-	-	-
14176 +++	+++	–	+	+	+	-	-	-	-
36386 +++	-	-	-	-	-	-	-	-	-

11927	+++	+++	-	-	-	-	-	-	-	-
36360	+++	+	–	+	+	+	-	-	-	-
18012	+++	+++	-	+	+	+	-	-	-	-
36387	+++	++	–	+	+	+	-	-	-	-
36388	+++	+	-	-	-	-	-	-	-	-
14018	+++	+++	-	-	-	-	-	-	-	-
36389	+++	+++	-	-	-	-	-	-	-	-
14005	+++	+++	-	+	-	+	-	-	-	-
36390	+++	+	-	-	-	-	-	-	-	-
36269	+++	+++	-	-	-	-	-	-	-	-
36391	+++	+	–	+	+	+	+	-	-	-
36392	+++	-	–+	+	++	-	+	–	+++	-
36393	+++	+++	-	-	-	-	-	-	-	-
36394	+++	+++	-	-	-	+	-	-	-	-
36390	+++	+	-	-	-	-	-	-	-	-
14018	+++	+++	-	-	-	+	-	-	-	-
36361	+++	++	-	-	-	-	-	-	-	-
36395	+++	+	-	-	-	-	-	-	-	-
36351	+++	-	–+	++	+++	+	-	–	-	-
36396	+++	-	-	-	-	-	-	-	-	-
14018	+++	+++	-	-	-	+	-	-	-	-
36397	+++	-	-	-	-	-	+	-	-	-
17889	+++	+++	-	-	-	-	-	-	-	-
11947	+++	+++	-	-	-	-	-	-	-	-
13981	+++	+++	-	-	-	-	+	-	-	-
36398	+++	+++	-	-	-	-	-	-	-	-
36384	+++	++	-	-	-	-	-	-	-	-
18191	+++	+++	-	-	-	-	-	-	-	-
16586	+++	+++	–	+	+	-	-	-	-	-
36399	+++	-	–+	++	+++	++	-	-	+++	-
36400	+++	+++	-	-	-	-	-	-	-	-
36386	+++	-	-	-	-	-	-	-	-	-
36401	+++	+++	-	-	+	+	-	-	-	-

17658	+++	++	–	+	+	+	-	-	-	-
36328	+++	++	-	-	-	-	-	-	-	-
36402	+++	++	-	-	-	-	-	-	-	-
36403	+++	++	-	+	-	-	-	–	-	-
11887	+++	+++	-	-	-	-	-	-	-	-
36404	+++	++	–+	+++	+++	+++	-	-	-	-
36356	+++	+++	-	-	-	-	-	-	-	-
36405	+++	+++	-	-	-	+	-	-	-	-
36406	+++	++	-	-	-	-	-	-	-	-
36407	+++	+++	-	-	-	-	-	-	-	-
12030	+++	+	-	-	-	-	-	-	-	-
11522	+++	++	-	-	-	-	-	-	-	-
14274	+++	+++	-	-	-	+	-	-	-	-
36313	+++	+++	-	-	-	-	+	-	-	-
36408	+++	+	-	-	-	-	-	-	-	-
36409	+++	+++	-	-	-	-	-	-	-	-
11609	+++	+++	-	-	-	+	+	-	-	-
11947	+++	+++	-	-	-	-	-	-	-	-
36410	+++	-	-	-	-	-	-	-	-	-
36411	+++	+	-	-	-	-	-	-	-	-
36412	+++	+	–+	+++	+++	++	+++	---	+++	-
36413	+++	+++	-	-	-	+	-	-	-	-
11887	+++	+++	-	-	-	+	-	-	-	-
12148	+++	+++	-	-	-	-	-	-	-	-
36414	+++	+++	-	-	-	-	-	-	-	-
36366	+++	+	-	-	-	-	-	-	-	-
17659	+++	+++	–+	+++	+++	+++	+	-	-	-
14521	+++	+++	-	-	-	+	-	-	-	-
11368	+++	+++	-	-	-	-	-	-	-	-
36410	+++	-	-	-	-	-	-	-	-	-
36415	+++	+++	-	-	-	-	-	-	-	-
14483	+++	+++	-	-	-	-	-	-	-	-
36416	+++	+++	-	-	-	-	-	-	-	-

36417	+++	+	−+	+++	+++	+++	+	−	-	-
36349	+++	+++	-	-	-	-	-	-	-	-
36416	+++	+++	-	-	-	-	-	-	-	-
36418	+++	+	−−	+	++	++	+++	−−−	-	-
36419	+++	-	−	+	+	+	-	-	-	-
36420	+++	+++	-	-	-	-	-	-	-	-
36421	+++	+++	-	-	-	-	-	-	-	-
36385	+++	++	-	+	-	-	-	-	-	-
36422	+++	+++	-	-	-	-	-	-	-	-
36333	+++	+++	-	-	-	+	-	-	-	-
36423	+++	++	-	-	-	-	-	-	-	-
36340	+++	+++	-	+	+	+	-	-	-	-
36424	+++	+++	-	-	-	-	-	-	-	-
36425	+++	+	-	-	-	-	-	-	-	-
13938	+++	+++	−	+	+	+	-	-	-	-
36413	+++	+++	-	-	-	+	-	-	-	-
13614	+++	-	-	-	-	-	-	-	-	-
16040	+++	+++	-	-	-	-	-	-	-	-
36426	+++	+++	−	+	++	+++	-	-	-	-
11276	+++	+++	-	-	-	+	-	-	-	-
36427	+++	++	-	-	-	-	-	-	-	-
36428	+++	+	-	-	-	-	-	-	-	-
13777	+++	+++	-	-	-	-	-	-	-	-
18180	+++	+++	-	-	-	+	-	-	-	-
36429	+++	-	-	-	-	-	-	-	-	-
36430	+++	-	−+	+++	+++	+++	-	-	-	-
36285	+++	-	-	-	-	-	-	-	-	-
36429	+++	-	-	-	-	-	-	-	-	-
36297	+++	+++	-	-	-	-	-	-	-	-
36387	+++	++	−	+	+	+	-	-	-	-
36357	+++	+++	-	-	-	+	-	-	-	-
36431	+++	++	-	-	-	-	-	-	-	-
12206	+++	+	-	-	-	-	-	-	-	-

36390 +++	+	-	-	-	-	-	-	-	-
12037 +++	+	-	-	-	-	-	-	-	-
14673 +++	+++	-	-	-	-	-	-	-	-
36334 +++	-	–+	+	+++	+	+	–	-	-
36432 +++	-	-	-	-	-	-	-	-	-
36433 +++	+++	–	+	+	-	-	-	-	-
36347 +++	+++	-	-	-	-	-	-	-	-
11531 +++	-	-	-	-	-	-	-	-	-
36369 +++	+++	-	-	-	-	-	-	-	-
14018 +++	+++	-	-	-	+	-	-	-	-
36418 +++	+	–	+	+	+	+++	–––	+++	-
36434 +++	+++	–+	+++	+++	+++	-	-	-	-
36435 +++	+++	–+	+++	+++	+++	+	-	-	+++
36408 +++	+	-	-	-	-	-	-	-	-
36406 +++	++	-	-	-	-	-	-	-	-
36436 +++	+++	-	-	-	-	-	-	-	-
36437 +++	+++	–+	+++	+++	+++	-	-	++	++
14060 +++	++	-	-	-	-	-	-	-	-
16158 +++	-	-	-	-	-	-	-	-	-
36368 +++	-	–+	+	++	-	-	-	-	-
36329 +++	-	–+	+	++	+	+	–	-	-
36438 +++	+++	–+	+++	+++	+++	-	-	+++	-
36282 +++	-	––	+	+++	+	+	–	-	-
36439 +++	+++	–	-	-	+	-	-	-	-
11714 +++	-	-	-	-	-	-	-	-	-
36440 +++	-	–+	+	+++	-	+	-	-	-
36441 +++	+++	–+	+++	+++	+++	+	–	-	+++
36439 +++	+++	-	-	-	+	-	-	-	-
36442 +++	+++	-	-	-	+	-	-	-	-
36443 +++	+++	-	-	-	-	-	-	-	-
36444 +++	-	–+	+	+++	-	-	-	-	-
36445 +++	+++	-	-	-	-	-	-	-	-
36446 +++	-	–+	+	+	-	-	–	+++	-

36336 +++	+	-	-	-	-	-	-	-	-
36389 +++	+++	-	-	-	-	-	-	-	-
36447 +++	-	--+	+	+++	+	-	-	+++	-
36448 +++	+	--+	+++	+++	+++	-	-	-	-
36449 +++	+	-	-	+	+	+	-	-	-
36450 +++	-	--+	+	+++	+	-	-	-	-
36451 +++	-	-	-	-	-	-	-	-	-
16566 +++	+++	-	-	-	-	-	-	-	-
36442 +++	+++	-	-	-	+	-	-	-	-
36407 +++	+++	-	-	-	-	-	-	-	-
36402 +++	+	-	-	-	-	-	-	-	-
36391 +++	+	–	+	+	+	-	-	-	-
36332 +++	+	-	-	+	-	+	–	-	-
36452 +++	+	-	-	-	-	-	-	-	-
36453 +++	+++	-	-	-	-	-	-	-	-
36454 +++	-	--+	++	+++	+	+	–	+++	-
36454 +++	-	--+	++	+++	++	+	-	+++	-
36378 +++	+++	-	-	-	-	-	-	-	-
36455 +++	-	--+	++	+++	+	+	-	+++	-
36456 +++	+++	–	+	++	++	-	-	-	-
17658 +++	++	–	+	+	+	-	-	-	-
36457 +++	+++	–	+	++	+++	-	-	-	-
16619 +++	+	–	+	+	+	-	-	-	-
36458 +++	+++	–	+	++	+++	-	-	-	+
36459 +++	+++	-	-	-	-	-	-	-	-
11522 +++	++	-	-	-	-	-	-	-	-
11826 +++	+	-	-	-	-	-	-	-	-
36365 +++	-	--+	+	+++	+	-	-	+++	-
36460 +++	+++	-	-	+	+	-	-	-	-
36461 +++	+	-	-	-	-	-	-	-	-
36380 +++	+++	-	+	+	+	-	-	-	-
36462 +++	-	--+	+	+++	+	-	-	-	-
11826 +++	+	-	-	-	-	-	-	-	-

36433	+++	+++	-	-	-	-	-	-	-	-
11927	+++	+++	-	-	-	-	-	-	-	-
36463	+++	+++	-	-	-	-	-	-	-	-
36336	+++	+	-	-	-	-	-	-	-	-
12038	+++	+	-	-	-	-	-	-	-	-
18857	+++	-	--+	+	+++	+	+	-	-	-
36464	+++	+	-	-	-	-	-	-	-	-
36416	+++	+++	-	-	-	-	-	-	-	-
12737	+++	+	-	-	-	-	-	-	-	-
36465	+++	+++	-	-	+	+	-	-	-	-
36466	+++	-	-	+++	+++	+++	-	-	-	-
36467	+++	+++	-	+	+	+	+	-	-	-
36456	+++	+++	-	+	++	++	-	-	-	-
36468	+++	+++	-	+	-	+	-	-	-	-
36367	+++	+++	-	-	-	-	-	-	-	-
16591	+++	+++	-	-	-	+	-	-	-	-
13978	+++	+++	-	-	-	-	-	-	-	-
36469	+++	+	-	-	-	-	-	-	-	-
36372	+++	+++	-	-	-	-	-	-	-	-
36470	+++	+++	-	-	-	-	-	-	-	-
36416	+++	+++	-	-	-	-	-	-	-	-
13991	+++	+++	-	-	-	-	-	-	-	-
36471	+++	+++	-	-	+	-	+	-	-	-
12737	+++	+	-	-	-	-	-	-	-	-
36472	+++	-	--+	+	+++	+	-	-	+++	-
36473	+++	+	-	+	+	+	-	-	-	-
36474	+++	-	--+	+	+++	+	-	-	+++	-
36363	+++	-	--+	+	+++	+	-	-	-	-
36475	+++	++	-	-	-	+	-	-	-	-
19087	+++	+++	-	-	-	-	-	-	-	-
36476	+++	+++	-	-	-	-	-	-	-	-
36443	+++	+++	-	-	-	-	-	-	-	-
36477	+++	+++	-	-	-	-	-	-	-	-

16158 +++	+	-	-	-	-	-	-	-	-
18180 +++	+++	-	-	-	+	-	-	-	-
36478 +++	+++	-	+	-	+	-	-	-	-
36441 +++	+++	--+	+++	+++	+++	-	-	+++	-
36414 +++	+++	-	-	-	-	-	-	-	-
36405 +++	+++	-	-	-	+	-	-	-	-
36469 +++	+	-	-	-	-	-	-	-	-
36326 +++	-	-	-	-	-	-	-	-	-
36422 +++	+++	-	-	-	-	-	-	-	-
36390 +++	+	-	-	-	-	-	-	-	-
36479 +++	+++	-	-	-	-	-	-	-	-
36480 +++	+++	-	-	-	-	-	-	-	-
14441 +++	+++	-	-	-	+	-	-	-	-
36481 +++	-	-	-	-	-	-	-	-	-
36429 +++	-	-	-	-	-	-	-	-	-
36482 +++	+++	-	+	+	+	-	-	-	-
36483 +++	+++	-	-	-	-	-	-	-	-
36484 +++	++	-	-	-	-	-	-	-	-
36355 +++	-	--+	+	+	-	-	-	-	-
12707 +++	-	-	-	-	-	-	-	-	-
36485 +++	+++	-	+	+	+	+	-	-	-
14483 +++	+++	-	-	-	-	-	-	-	-
36486 +++	+++	-	-	-	-	-	-	-	-
36487 +++	+++	-	-	-	-	-	-	-	-
11352 +++	+++	-	-	-	-	-	-	-	-
36488 +++	+++	-	++	+++	+++	+++	---	+++	+++
36330 +++	+++	-	+	-	-	-	-	-	-
11015 +++	+++	-	-	-	-	-	-	-	-
36256 +++	+++	-	-	-	-	+	-	-	-
36489 +++	+++	-	+	++	++	-	-	-	-
36490 +++	+	-	+	+	+	-	-	-	-
16599 +++	+++	-	+	+	+	-	-	-	-
36471 +++	+++	-	-	-	-	+	-	-	-

36420	+++	+++	-	-	-	-	-	-	-	-
36491	+++	+++	-	-	-	-	-	-	-	-
36405	+++	+++	-	-	-	+	-	-	-	-
36492	+++	++	--+	+++	+++	+++	-	-	-	-
36493	+++	+++	--+	+++	+++	+++	+	–	+++	+++
36431	+++	++	-	-	-	-	-	-	-	-
13952	+++	+++	-	-	-	-	-	-	-	-
36409	+++	+++	-	-	-	-	-	-	-	-
36494	+++	++	-	-	-	-	-	–	-	-
36495	+++	+++	-	-	-	-	-	-	-	-
11239	+++	+++	-	-	-	-	-	-	-	-
36496	+++	+++	--	++	+++	+++	-	-	++	++
12037	+++	+	-	-	-	-	-	-	-	-
36497	+++	+++	-	-	+	+	-	-	-	-
36498	+++	+++	-	-	-	-	-	-	-	-
36459	+++	+++	-	-	-	-	-	-	-	-
36499	+++	+++	-	-	-	-	-	-	-	-
36381	+++	-	--+	+	++	-	-	–	-	-
36500	+++	-	--+	+	+	-	-	-	+++	-
36307	+++	-	--+	++	+++	-	+++	--	-	-
13734	+++	+++	-	-	-	+	-	-	-	-
14054	+++	+++	-	-	-	-	-	-	-	-
36501	+++	-	--+	+	+++	+	-	-	-	-
36502	+++	-	-	-	-	-	-	-	-	-
11008	+++	+++	-	-	-	-	-	-	-	-
36394	+++	+++	-	+	-	+	-	-	-	-
36503	+++	+++	-	-	-	-	+	–	-	-
14040	+++	+++	-	+	-	+	-	-	-	-
36379	+++	+++	-	-	-	-	-	-	-	-
11531	+++	-	-	-	-	-	-	-	-	-
36504	+++	+	-	-	-	-	-	-	-	-
36505	+++	-	--+	+	+++	+	-	-	+++	-
11477	+++	+++	-	-	-	-	-	-	-	-

36506	+++	+++	-	-	-	-	-	-	-	-
36473	+++	+	–	+	+	+	-	-	-	-
36507	+++	-	––+	+	+++	+	-	-	-	-
36359	+++	+++	-	-	-	-	-	-	-	-
36508	+++	+++	–	+	+	+	-	-	-	-
36388	+++	+	-	-	-	-	-	-	-	-
16158	+++	+	-	-	-	-	-	-	-	-
36319	+++	+++	-	-	-	-	-	-	-	-
36509	+++	+++	-	-	-	-	-	-	-	-
36510	+++	+	-	+	-	-	-	-	-	-
36510	+++	+	-	+	-	-	-	-	-	-
14054	+++	+++	-	-	-	-	-	-	-	-
36511	+++	-	-	-	-	-	-	-	-	-
36437	+++	+++	––+	+++	+++	+++	-	-	-	+++
36512	+++	+++	-	-	-	-	-	-	-	-
36358	+++	+++	-	-	-	+	-	-	-	-
36513	+++	-	––+	+++	+++	+++	-	-	-	-
16568	+++	++	-	-	+	+	-	-	-	-
36421	+++	+++	-	-	-	-	-	-	-	-
36514	+++	+++	-	-	-	-	-	–	-	-
36515	+++	+++	-	-	-	-	-	-	-	-
14549	+++	++	-	-	-	-	-	-	-	-
36516	+++	-	––+	+++	+++	+++	-	-	-	-
36517	+++	+++	––+	+++	+++	++	-	-	-	-
36518	+++	+++	-	-	-	-	+	–	-	-
16074	+++	+++	-	-	-	-	-	-	-	-
19496	+++	+++	-	+	-	+	-	-	-	-
36459	+++	+++	-	-	-	-	-	-	-	-
36358	+++	+++	-	-	-	+	-	-	-	-
36519	+++	++	–	-	-	+	+	–	-	-
36450	+++	-	––+	+	+++	+	-	-	+++	-
36520	+++	+	–	+	+	+	+	–	-	-
36484	+++	++	-	-	-	-	-	-	-	-

11472	+++	+	-	-	-	-	-	-	-	-
36521	+++	+++	–	+	+	+	+	–	-	-
36423	+++	++	-	-	-	-	-	-	-	-
36522	+++	-	-	-	-	-	-	-	-	-
36523	+++	++	-	+	-	+	-	-	-	-
36524	+++	+	–	+	+	+	+++	---	+++	+++
16619	+++	+	–	+	+	+	-	-	-	-
14441	+++	+++	-	-	-	-	-	-	-	-
36484	+++	++	-	-	-	-	-	-	-	-
16575	+++	+++	-	-	-	-	-	-	-	-
16158	+++	-	-	-	-	-	-	-	-	-
14176	+++	+++	-	+	+	+	-	-	-	-
36525	+++	-	-	-	-	-	-	-	-	-
36526	+++	+++	-	+	+	+	-	-	-	-
36527	+++	-	--+	+++	+++	+++	-	-	-	-
36528	+++	+++	-	-	-	-	-	-	-	-
36395	+++	-	-	-	-	-	-	-	-	-
36529	+++	-	--+	+++	+++	+++	-	-	-	-
16657	+++	+++	-	-	-	-	-	-	-	-
12265	+++	-	-	-	-	-	-	-	-	-
36477	+++	+++	-	-	-	-	-	-	-	-
14499	+++	-	-	-	-	-	-	-	-	-
36452	+++	-	-	-	-	-	-	-	-	-
16599	+++	+++	–	+	+	+	-	-	-	-
11077	+++	+++	-	-	-	-	-	-	-	-
36383	+++	+++	–	+	-	+	-	-	-	-
16650	+++	+++	-	+	+	+	+	–	-	-
36530	+++	+++	-	-	-	-	-	-	-	-
36480	+++	+++	-	-	-	-	-	-	-	-
36531	+++	+++	-	-	-	-	+	-	-	-
36532	+++	+	--+	+	-	-	-	-	-	-
36533	+++	+	--+	++	+++	++	-	–	-	-
36534	+++	++	-	-	-	-	-	-	-	-

36535	+++	++	--+	+++	+++	+++	-	-	-	-
36536	+++	-	-	+	-	+	-	-	-	-
36537	+++	+++	-	-	-	-	-	-	-	-
36424	+++	+++	-	-	-	-	-	-	-	-
36451	+++	-	-	-	-	-	-	-	-	-
36493	+++	+++	--+	+++	+++	+++	+	-	+++	+++
11522	+++	++	-	-	-	-	-	-	-	-
36538	+++	+++	-	-	-	+	-	-	-	-
36339	+++	+	-	-	-	-	-	-	-	-
36506	+++	+++	-	-	-	-	-	-	-	-
36539	+++	++	-	-	-	-	-	-	-	-
36540	+++	+	-	+	+	+	-	-	-	-
36541	+++	+++	-	-	-	-	-	-	-	-
36491	+++	+++	-	+	-	+	-	-	-	-
36458	+++	+++	-	+	++	+++	-	-	-	-
36542	+++	++	-	-	-	-	-	-	-	-
36543	+++	-	--+	+	+++	++	-	-	-	-
14060	+++	++	-	-	-	-	-	-	-	-
36544	+++	-	--+	++	+++	-	+	-	+++	-
36545	+++	-	--+	+	+++	+	-	-	-	-
36546	+++	++	-	-	-	-	-	-	-	-
36453	+++	+++	-	-	-	-	-	-	-	-
15980	+++	+++	-	+	-	-	-	-	-	-
14040	+++	+++	-	+	-	-	-	-	-	-
11160	+++	+	-	-	-	-	-	-	-	-
14343	+++	+++	-	-	-	-	-	-	-	-
36538	+++	+++	-	-	-	+	-	-	-	-
36547	+++	-	-	-	-	-	-	-	-	-
11221	+++	+++	-	-	-	+	-	-	-	-
36431	+++	+++	-	-	-	-	-	-	-	-
11482	+++	+++	-	-	-	-	-	-	-	-
36459	+++	+++	-	-	-	-	-	-	-	-
36548	+++	+++	-	++	++	++	+	-	-	-

36467	+++	+++	-	+	-	+	-	-	-	-
36549	+++	-	--+	+++	+++	-	+++	-	-	-
36550	+++	+++	-	-	-	-	+	-	-	-
36551	+++	+++	-	-	-	-	-	-	-	-
36364	+++	+++	--+	+++	+++	+++	+	-	+++	+++
36328	+++	++	-	-	-	-	-	-	-	-
11586	+++	-	-	-	-	-	-	-	-	-
36393	+++	+++	-	-	-	-	-	-	-	-
13780	+++	++	-	-	-	-	-	-	-	-
17796	+++	+++	-	-	-	-	-	-	-	-
11077	+++	+++	-	-	-	-	-	-	-	-
36487	+++	+++	-	-	-	-	-	-	-	-
36322	+++	-	--+	+	+++	+	-	-	-	-
11547	+++	+++	-	-	-	-	-	-	-	-
36445	+++	++	-	-	-	-	-	-	-	-
36552	+++	+++	-	-	-	-	-	-	-	-
36553	+++	+++	--+	+++	+++	+++	+	-	++	+++
36411	+++	+	-	-	-	-	-	-	-	-
11522	+++	++	-	-	-	-	-	-	-	-
36554	+++	+++	-	-	-	-	-	-	-	-
36555	+++	++	-	-	-	-	-	-	-	-
36556	+++	+++	-	-	-	-	-	-	-	-
36557	+++	-	-	-	-	-	-	-	-	-
14222	+++	+++	-	-	-	-	-	-	-	-
11757	+++	-	-	-	-	-	-	-	-	-
36463	+++	+++	-	-	-	-	-	-	-	-
36558	+++	-	--+	+	+++	+	-	-	-	-
12190	+++	++	-	-	-	-	-	-	-	-
14005	+++	+++	-	+	-	+	-	-	-	-
12265	+++	-	-	-	-	-	-	-	-	-
36371	+++	+	-	-	-	-	-	-	-	-
36548	+++	+++	-	++	++	++	+	-	-	+++
36508	+++	+++	-	+	+	+	-	-	-	-

36559	+++	+++	-	-	-	-	-	-	-	-
19496	+++	+++	-	-	-	-	-	-	-	-
36560	+++	+	-	-	-	-	-	-	-	-
36561	+++	+++	-	-	-	-	-	-	-	-
14499	+++	-	-	-	-	-	-	-	-	-
36486	+++	+++	-	-	-	-	-	-	-	-
36562	+++	++	-	-	-	-	-	-	-	-
36563	+++	+++	-	+	-	+	-	-	-	-
36560	+++	+	-	-	-	-	-	-	-	-
36564	+++	+++	-	-	-	-	-	-	-	-
36434	+++	+++	--+	+++	+++	+++	+	-	-	-
11846	+++	+	-	-	-	-	-	-	-	-
36565	+++	-	-	-	-	-	-	-	-	-
18641	+++	-	--+	+	+++	+	-	-	-	-
36566	+++	+++	-	-	-	-	-	-	-	-
36567	+++	++	-	-	-	-	-	-	-	-
16608	+++	+	-	-	-	-	-	-	-	-
36568	+++	+++	-	-	-	-	-	-	-	-
12312	+++	-	-	-	-	-	-	-	-	-
36569	+++	+++	-	-	-	-	-	-	-	-
36570	+++	+++	-	-	-	-	+	-	-	-
36490	+++	+	-	+	+	+	-	-	-	-
36504	+++	+	-	-	-	-	-	-	-	-
36338	+++	++	-	-	-	-	-	-	-	-
36460	+++	+++	-	+	+	+	-	-	-	-
16100	+++	+++	-	+	-	-	-	-	-	-
36571	+++	+++	-	-	-	+	-	-	-	-
36572	+++	+	-	-	-	-	-	-	-	-
14521	+++	+++	-	-	-	-	-	-	-	-
36566	+++	+++	-	-	-	-	-	-	-	-
36573	+++	+	--+	++	+++	+	+	-	-	-
36515	+++	+++	-	-	-	-	-	-	-	-
14094	+++	+++	-	-	-	-	-	-	-	-

36574	+++	+++	-	-	-	-	-	-	-	-
36497	+++	+++	-	-	+	+	-	-	-	-
17067	+++	++	–	+	-	++	-	-	-	-
36575	+++	+++	-	-	+	+	-	-	-	-
36438	+++	+++	–-+	+++	+++	+++	+	–	-	-
36478	+++	+++	-	-	-	+	-	-	-	-
36576	+++	+++	-	-	-	-	-	-	-	-
36577	+++	++	-	-	-	-	-	-	-	-
36502	+++	-	-	-	-	-	-	-	-	-
36578	+++	++	-	-	-	-	-	-	-	-
14807	+++	+++	-	-	-	+	-	-	-	-
16018	+++	+++	-	-	-	-	-	-	-	-
36579	+++	+++	-	-	-	-	-	-	-	-
11846	+++	+	-	-	-	-	-	-	-	-
36576	+++	+++	-	-	-	-	+	-	-	-
36580	+++	-	–-+	+	+++	+	+	-	-	-
36496	+++	+++	––	++	+++	+++	-	-	++	-
36581	+++	+++	-	-	+	+	-	-	-	-
36551	+++	+++	-	-	-	-	-	-	-	-
36464	+++	+	-	-	-	-	-	-	-	-
36574	+++	+++	-	-	-	-	-	-	-	-
14379	+++	+++	-	-	-	+	-	-	-	-
36486	+++	+++	-	-	-	-	-	-	-	-
36582	+++	+++	-	-	-	-	-	-	-	-
16013	+++	+++	-	-	-	-	-	-	-	-
36411	+++	+	-	+	-	-	-	-	-	-
17047	+++	+	–	++	+	+++	-	-	-	-
36583	+++	+++	-	-	-	-	-	-	-	-
36584	+++	+	–	+	+	+	-	-	-	-
36585	+++	+++	-	-	-	-	-	-	-	-
17889	+++	+++	-	-	-	-	-	-	-	-
36586	+++	-	–-+	+	+++	+	-	–	+++	-
36587	+++	+	-	-	-	-	-	-	-	-

11397 +++	++	-	+	-	-	-	-	-	-
11160 +++	+	-	-	-	-	-	-	-	-
14370 +++	+++	-	-	-	+	-	-	-	-
36588 +++	+	--+	++	+++	++	+	-	-	+++
36461 +++	+	-	-	-	-	+	-	-	-
36589 +++	-	--+	+	+++	+	-	-	+++	-
36590 +++	-	--+	+++	+++	+++	-	-	-	-
36591 +++	+++	-	-	-	-	-	-	-	-
36447 +++	-	--+	+	+++	+	-	-	+++	-
36476 +++	+++	-	-	-	-	-	-	-	-
36496 +++	+++	--	++	+++	+++	-	-	++	++
36592 +++	+++	-	-	-	-	-	-	-	-
36425 +++	+	-	-	-	-	-	-	-	-
36593 +++	+++	-	-	-	-	-	-	-	-
36594 +++	++	-	-	-	-	-	-	-	-
36595 +++	+++	-	+	-	+	-	-	-	-
36596 +++	+++	-	+	+	+	+	-	-	-
36569 +++	+++	-	-	-	-	+	-	-	-
11663 +++	+	-	-	-	-	-	-	-	-
36296 +++	+++	-	-	-	-	-	-	-	-
36496 +++	+++	--	++	+++	+++	-	-	++	++
36597 +++	-	-	-	-	-	-	-	-	-
36598 +++	++	-	+	+	+	+	-	-	-
36599 +++	-	--+	+	+++	-	-	-	-	-
36600 +++	-	-	+	-	-	-	-	-	-
36486 +++	+++	-	-	-	-	-	-	-	-
36601 +++	+	-	+	+	+	-	-	-	-
36602 +++	-	--+	+	+++	+	-	-	+++	-
36603 +++	+++	-	-	-	-	-	-	-	-
36604 +++	+++	-	-	-	-	-	-	-	-
36605 +++	+++	-	-	-	-	-	-	-	-
13978 +++	+++	-	-	-	-	-	-	-	-
36411 +++	+	-	-	-	-	-	-	-	-

11865	+++	+++	-	-	-	-	-	-	-	-
11826	+++	+	-	-	-	-	-	-	-	-
36512	+++	+++	-	-	-	-	-	-	-	-
36606	+++	+	-	-	-	-	-	-	-	-
36426	+++	+++	–	+	++	++	-	-	-	-
36607	+++	+++	–	+	+	+	-	-	-	-
36608	+++	-	-	-	-	-	-	-	-	-
36540	+++	+	–	+	+	+	-	-	-	-
11113	+++	+++	-	-	-	-	-	-	-	-
36609	+++	+++	-	-	-	-	-	-	-	-
36610	+++	-	-	-	-	-	-	-	-	-
36592	+++	+++	-	-	-	-	-	-	-	-
17701	+++	++	-	-	-	-	-	-	-	-
36358	+++	+++	-	-	-	+	-	-	-	-
36397	+++	+	-	-	-	-	+	-	-	-
11663	+++	+	-	-	-	-	-	-	-	-
11355	+++	++	-	-	-	-	-	-	-	-
36611	+++	+	–	+	+	+	+	–	-	-
36428	+++	+	-	-	-	-	-	-	-	-
36595	+++	+++	-	-	-	+	-	-	-	-
36612	+++	+	-	-	-	-	-	-	-	-
36571	+++	+++	-	-	-	-	+	–	-	-
36613	+++	+++	-	-	-	-	-	-	-	-
36614	+++	+++	-	-	-	-	-	-	-	-
36615	+++	++	-	-	-	-	-	-	-	-
36525	+++	-	-	-	-	-	-	-	-	-
36596	+++	+++	–	+	+	+	+	–	-	-
36616	+++	+++	-	-	-	+	-	-	-	-
16612	+++	+++	-	-	-	-	-	–	-	-
36617	+++	-	-	-	-	-	-	-	-	-
36398	+++	+++	-	-	-	-	-	-	-	-
36618	+++	-	-	-	-	-	-	-	-	-
17810	+++	++	-	-	-	-	-	-	-	-

36435	+++	+++	--+	+++	+++	+++	+	-	.	.
36488	+++	+++	-	++	+++	+++	+++	---	+++	+++
36561	+++	+++	.	.	.	.	.	.	.	.
36619	+++	+++	.	.	.	.	.	.	.	.
36620	+++	+++	.	.	.	.	.	.	.	.
36621	+++	+++	.	.	.	.	.	.	.	.
11477	+++	+++	.	.	.	.	.	.	.	.
36622	+++	+++	.	.	.	.	+	.	.	.
15980	+++	+++	.	+	.	+	.	.	.	.
36486	+++	+++	.	.	.	.	.	.	.	.
14379	+++	+++	.	+	+	+	.	.	.	.
11829	+++	+++	.	.	.	.	.	.	.	.
36623	+++	.	-	+	.	.	+	-	.	.
36604	+++	+++	.	.	.	.	.	.	.	.
36624	+++	.	--+	++	+++	+++	.	.	.	.
36625	+++	.	.	.	.	.	.	.	.	.
36626	+++	+++	.	.	.	.	.	-	.	.
36627	+++	++	.	.	.	.	.	.	.	.
36628	+++	.	.	.	.	.	.	.	.	.
36556	+++	+++	.	.	.	.	.	.	.	.
36429	+++	.	.	.	.	.	.	.	.	.
36629	+++	+++	--+	+++	+++	+++	.	.	.	.
36630	+++	++	.	.	.	.	.	.	.	.
36631	+++	+	.	.	.	.	.	.	.	.
36632	+++	.	.	.	.	.	.	.	.	.
36633	+++	+++	.	.	.	.	.	-	.	.
36335	+++	+++	.	.	.	.	.	.	.	.
14581	+++	+++	.	.	.	.	.	.	.	.
36634	+++	++	.	.	.	.	.	.	.	.
36635	+++	+++	-	+	++	+++	.	.	.	.
36636	+++	+++	.	.	.	.	.	.	.	.
36539	+++	++	.	.	.	.	.	.	.	.
36637	+++	.	.	+	.	.	.	.	.	.

36638	+++	+	-	-	-	-	-	-	-	-
36639	+++	+++	--+	+++	+++	+++	+	-	+++	-
11015	+++	+++	-	-	-	-	-	-	-	-
36640	+++	+++	-	-	-	+	-	-	-	-
36521	+++	+++	-	+	+	+	+	-	-	-
36641	+++	+	-	-	-	-	-	-	-	-
36563	+++	+++	-	-	-	+	-	-	-	-
36393	+++	+++	-	-	-	-	-	-	-	-
11011	+++	+++	-	-	-	-	-	-	-	-
36642	+++	+	--+	++	+++	+	+	-	-	-
11927	+++	+++	-	-	-	-	-	-	-	-
36551	+++	+++	-	-	-	-	-	-	-	-
11348	+++	+++	-	-	-	+	-	-	-	-
11276	+++	+++	-	-	-	+	-	-	-	-
36626	+++	+++	-	-	-	-	-	-	-	-
11865	+++	+++	-	-	-	+	-	-	-	-
36643	+++	-	--+	+	+++	+	-	-	-	-
36644	+++	+++	-	-	-	-	-	-	-	-
36398	+++	+++	-	-	-	-	-	-	-	-
36645	+++	-	-	-	-	-	-	-	-	-
14274	+++	+++	-	-	-	-	-	-	-	-
36603	+++	+++	-	-	-	-	-	-	-	-
14159	+++	+++	-	-	-	-	-	-	-	-
36594	+++	++	-	-	-	-	-	-	-	-
36553	+++	+++	--+	+++	+++	+++	-	-	-	-
36597	+++	-	-	-	-	-	-	-	-	-
36646	+++	+++	-	-	-	+	-	-	-	-
36647	+++	++	-	-	-	+	-	-	-	-
36336	+++	+	-	-	-	-	-	-	-	-
18659	+++	+++	-	-	-	-	-	-	-	-
16058	+++	+++	-	-	-	-	-	-	-	-
36648	+++	+	--+	+++	+++	+++	-	-	-	-
11262	+++	+	-	-	-	-	-	-	-	-

36361	+++	++	-	-	-	-	-	-	-	-
36649	+++	+++	-	-	-	+	+	-	-	-
11188	+++	+++	-	-	-	-	-	-	-	-
36650	+++	+++	-	+	-	+	-	-	-	-
17878	+++	+++	-	-	-	-	-	-	-	-
14229	+++	+++	-	-	-	-	-	-	-	-
11596	+++	+	-	-	-	-	-	-	-	-
36651	+++	-	-	-	-	-	-	–	-	-
36652	+++	+++	-	-	-	-	-	-	-	-
36653	+++	-	–+	+	+++	-	-	-	-	-
36654	+++	+++	–	+	+	+	-	-	-	-
17047	+++	+	–	++	++	+++	-	-	-	-
11766	+++	+++	-	-	-	-	-	-	-	-
36655	+++	-	-	-	-	-	-	-	-	-
36656	+++	+++	-	-	-	-	-	-	-	-
36657	+++	+++	–	-	-	+	+	-	-	-
36658	+++	+++	-	-	-	-	-	-	-	-
36659	+++	+++	–+	+++	+++	+++	+	-	-	-
36660	+++	-	–+	+	+++	+	-	-	+++	-
36661	+++	+++	-	-	-	-	-	-	-	-
14289	+++	+++	-	-	-	-	-	-	-	-
36505	+++	-	–+	+	+++	+	-	-	-	++
36662	+++	+++	–	++	++	++	-	-	-	-
36663	+++	++	–	+	+	+	+	–	-	-
36377	+++	+++	-	-	-	+	-	-	-	-
36583	+++	+++	-	-	-	-	-	-	-	-
36347	+++	+++	-	-	-	-	-	-	-	-
18591	+++	+++	-	-	-	-	-	-	-	-
13938	+++	+++	–	+	-	+	-	-	-	-
36509	+++	+++	-	-	-	-	-	-	-	-
36664	+++	+++	–	-	+	+	-	–	-	-
36396	+++	-	-	-	-	-	-	-	-	-
12229	+++	-	-	-	-	-	-	-	-	-

36665	+++	+++	-	-	-	-	-	-	-	-
36458	+++	+++	–	+	++	+++	-	-	-	-
12517	+++	++	-	-	-	-	-	-	-	-
36603	+++	+++	-	-	-	-	-	-	-	-
36666	+++	-	-	-	-	-	-	-	-	-
36667	+++	+	-	-	-	-	+	–	-	-
36668	+++	-	–+	+	+++	+	-	-	-	-
36669	+++	-	–+	+	+	-	-	-	-	-
36375	+++	+++	-	+	-	+	-	-	-	-
36670	+++	+++	-	-	-	-	-	-	-	-
36584	+++	+	–	+	-	-	-	-	-	-
36671	+++	+++	-	-	-	-	-	-	-	-
36393	+++	+++	-	-	-	-	-	-	-	-
36672	+++	++	–	+	+	+	++	––	+++	-
36673	+++	++	-	-	-	-	-	-	-	-
36514	+++	+++	-	-	-	-	-	–	-	-
14018	+++	+++	-	-	-	-	-	-	-	-
36674	+++	-	–+	+	+++	+	-	-	+++	-
36636	+++	+++	-	-	-	-	-	-	-	-
12037	+++	+	-	-	-	-	-	-	-	-
16030	+++	+++	-	-	-	-	-	-	-	-
12707	+++	-	-	-	-	-	-	-	-	-
36666	+++	-	-	-	-	-	-	-	-	-
36532	+++	-	–+	+	-	-	+	–	-	-
36432	+++	-	-	-	-	-	-	-	-	-
36675	+++	+++	-	-	-	-	-	-	-	-
36638	+++	+	-	-	-	-	-	-	-	-
36676	+++	-	–+	+++	+++	+++	-	-	-	-
13657	+++	+++	-	-	-	-	-	-	-	-
11579	+++	+++	-	-	-	-	-	-	-	-
36677	+++	+++	-	-	-	-	-	-	-	-
36483	+++	+++	-	-	-	-	-	-	-	-
36565	+++	-	-	-	-	-	-	-	-	-

11547	+++	+++	-	-	-	-	-	-	-	-
36431	+++	++	-	-	-	-	-	-	-	-
36585	+++	+++	-	-	-	-	-	-	-	-
36399	+++	-	--+	++	+++	++	-	-	-	-
36678	+++	+	-	-	-	-	-	-	-	-
11865	+++	+++	-	-	-	-	-	-	-	-
36679	+++	+++	-	+	+	+	-	-	-	-
36680	+++	-	--+	+	+++	+	-	-	-	-
14416	+++	+++	-	-	-	-	-	-	-	-
36537	+++	+++	-	-	-	-	-	-	-	-
36681	+++	++	--+	+++	+++	+++	-	-	-	-
14416	+++	+++	-	+	+	+	-	-	-	-
36444	+++	-	--+	+	+++	-	-	-	+++	-
17986	+++	-	--+	+	+++	++	-	-	+++	-
11720	+++	-	-	-	-	-	-	-	-	-
36627	+++	++	-	-	-	-	+	-	-	-
36484	+++	++	-	-	-	-	-	-	-	-
19635	+++	+++	-	-	-	-	-	-	-	-
36682	+++	+++	--+	+++	+++	+++	-	-	+++	+++
36683	+++	+++	-	-	-	-	-	-	-	-
36582	+++	+++	-	-	-	-	-	-	-	-
11238	+++	+++	-	-	-	-	-	-	-	-
36684	+++	-	--+	++	+++	+	-	-	+++	+++
11559	+++	+++	-	-	-	-	-	-	-	-
36591	+++	+++	-	-	-	-	-	-	-	-
36685	+++	+++	-	+	+	+	-	-	-	-
36686	+++	+++	-	-	-	-	-	-	-	-
36440	+++	-	--+	+	+++	-	-	-	+++	-
36687	+++	++	-	-	-	-	-	-	-	-
36688	+++	+++	--+	+++	+++	+++	+	-	-	+++
36689	+++	+	-	+	+	+	-	-	-	-
36341	+++	+++	-	-	-	-	+	-	-	-
36690	+++	-	--+	+	+++	+	-	-	+++	-

36691	+++	+++	-	-	-	-	-	–	-	-
36692	+++	+++	-	-	-	-	-	-	-	-
14602	+++	+++	-	-	-	-	-	-	-	-
36672	+++	++	–	+	+	++	+	–	+++	+++
13814	+++	+++	-	-	-	-	-	-	-	-
17613	+++	-	-	-	-	-	-	-	-	-
36693	+++	+	-	-	-	-	-	-	-	-
11203	+++	+++	-	-	-	-	-	-	-	-
36358	+++	+++	-	-	-	-	-	-	-	-
36694	+++	+++	-	-	-	-	+	–	-	-
14290	+++	+++	-	-	-	-	-	-	-	-
36481	+++	-	-	-	-	-	-	-	-	-
36695	+++	+++	-	-	-	-	-	-	-	-
16566	+++	+++	-	-	-	-	+	-	-	-
36587	+++	-	-	-	-	-	-	-	-	-
36696	+++	-	–+	+	+++	+	-	-	-	-
11757	+++	-	-	-	-	-	-	-	-	-
36486	+++	+++	-	-	-	-	-	-	-	-
16013	+++	+++	-	-	-	-	-	-	-	-
36697	+++	+	–	+	+	+	-	-	-	-
36698	+++	-	–+	+	+++	-	+	-	-	-
11967	+++	+++	-	-	-	-	-	-	-	-
36699	+++	-	–+	+	+++	+	+	-	+++	-
36640	+++	+++	-	-	-	-	-	-	-	-
11974	+++	+	-	-	-	-	-	-	-	-
36700	+++	-	–+	+	+++	+	-	-	+++	-
36530	+++	+++	-	-	-	-	-	-	-	-
36701	+++	++	–	+	+	-	-	-	-	-
36609	+++	+++	-	-	-	-	-	-	-	-
36702	+++	+++	–+	+++	+++	+++	-	-	-	-
11391	+++	+++	-	+	-	+	-	-	-	-
36697	+++	+	–	+	+	+	-	-	-	-
11065	+++	+++	-	-	-	-	-	-	-	-

14075	+++	+++	-	-	-	-	-	-	-	-
36684	+++	-	--+	++	+++	+	-	-	-	-
11338	+++	-	-	-	-	-	-	-	-	-
36528	+++	+++	-	-	-	-	-	-	-	-
16014	+++	++	-	-	-	-	-	-	-	-
36703	+++	-	--	+	+	-	-	-	-	-
36704	+++	+++	-	-	-	+	-	-	-	-
36705	+++	-	-	+	-	+	-	-	-	-
36706	+++	+++	-	-	-	-	-	-	-	-
36707	+++	-	-	-	-	-	-	-	-	-
36708	+++	-	-	-	-	-	-	-	-	-
36709	+++	+++	-	-	-	-	-	-	-	-
36361	+++	++	-	-	-	-	-	-	-	-
11845	+++	+++	-	-	-	-	-	-	-	-
17036	+++	-	--+	+	+++	+	-	-	-	+++
36496	+++	+++	--	++	+++	+++	-	-	+	+
11528	+++	+++	-	-	-	-	-	-	-	-
36710	+++	+++	-	-	-	-	-	-	-	-
36545	+++	-	--+	+	+++	+	+	-	+++	-
12043	+++	+++	-	-	-	-	-	-	-	-
36711	+++	+	-	+	+	+	++	--	-	-
36523	+++	++	-	+	-	-	-	-	-	-
16076	+++	+++	-	-	-	-	-	-	-	-
36712	+++	+	--+	+	+++	+	-	-	+++	-
36327	+++	-	--+	+	+++	-	-	-	-	-
36695	+++	+++	-	-	-	-	-	-	-	-
36713	+++	+++	-	-	-	-	-	-	-	-
36714	+++	+++	-	-	-	-	-	-	-	-
16158	+++	+	-	-	-	-	-	-	-	-
36715	+++	-	-	-	-	-	-	-	-	-
11579	+++	+++	-	-	-	-	-	-	-	-
16017	+++	+++	-	-	-	-	-	-	-	-
11574	+++	++	-	-	-	-	-	-	-	-

16652	+++	+++	--+	+++	+++	+++	-	-	-	-
36675	+++	+++	-	-	-	-	-	-	-	-
11829	+++	+++	-	-	-	-	-	-	-	-
14036	+++	+++	-	-	-	-	-	-	-	-
36405	+++	+++	-	+	+	+	-	-	-	-
36716	+++	-	--+	+	+++	+	+	-	-	-
36717	+++	-	-	-	-	-	-	-	-	-
36563	+++	+++	-	-	-	+	-	-	-	-
36694	+++	++	-	-	-	-	-	–	-	-
36529	+++	+	--+	+++	+++	+++	+	-	-	-
36392	+++	-	--+	++	++	-	+	–	+++	-
36341	+++	+++	-	-	-	-	+	–	-	-
36622	+++	+++	-	-	-	-	-	–	-	-
36460	+++	+++	-	+	+	+	-	-	-	-
36718	+++	+++	-	-	-	-	-	-	-	-
17554	+++	+++	-	-	-	-	-	-	-	-
18291	+++	+++	-	-	-	-	-	-	-	-
36719	+++	+++	-	-	-	-	-	-	-	-
36382	+++	+++	--+	+++	+++	+++	+	–	-	-
36720	+++	+	--+	++	+++	++	+	–	-	-
12006	+++	+++	-	-	-	-	-	-	-	-
14075	+++	+++	-	-	-	-	-	-	-	-
36721	+++	+++	-	-	-	-	-	-	-	-
18085	+++	-	--+	+++	+++	+++	-	-	-	-
36536	+++	-	-	+	-	-	-	-	-	-
11397	+++	++	-	-	-	-	-	-	-	-
16090	+++	+++	-	-	-	-	-	-	-	-
36722	+++	-	–	+	++	-	-	–	-	-
11609	+++	+++	-	-	-	-	-	-	-	-
36723	+++	+++	-	-	-	-	-	-	-	-
16616	+++	+++	--+	+++	+++	+++	+	-	-	-
36724	+++	+++	-	-	-	-	+	-	-	-
11762	+++	+++	-	-	-	-	-	-	-	-

36652	+++	+++	-	-	-	-	-	-	-	-
16040	+++	+++	-	-	-	-	-	-	-	-
36568	+++	+++	-	-	-	-	-	-	-	-
36725	+++	-	--+	+	+++	-	+	-	-	-
11078	+++	+++	-	-	-	-	-	-	-	-
17796	+++	+++	-	-	-	-	-	-	-	-
36559	+++	+++	-	-	-	-	-	-	-	-
36705	+++	+	-	+	-	+	-	-	-	-
36718	+++	+++	-	-	-	-	-	-	-	-
36663	+++	+	-	+	+	+	+	-	-	-
11451	+++	-	-	-	-	-	-	-	-	-
36622	+++	+++	-	-	-	-	-	-	-	-
11008	+++	+++	-	-	-	-	-	-	-	-
36537	+++	+++	-	-	-	-	-	-	-	-
36455	+++	-	--+	++	+++	+	-	-	-	-
11559	+++	+++	-	-	-	+	-	-	-	-
36496	+++	+++	--	++	+++	+++	-	-	-	-
11690	+++	-	-	-	-	-	-	-	-	-
36726	+++	+++	-	-	-	+	-	-	-	-
36518	+++	+++	-	-	-	-	+	-	-	-
18035	+++	+++	-	-	-	-	-	-	-	-
36462	+++	-	--+	+	+++	+	-	-	-	-
14018	+++	+++	-	-	-	+	-	-	-	-
17127	+++	-	--+	++	+++	++	+	-	+++	-
36727	+++	+++	--+	+++	+++	+++	+	-	+++	-
11707	+++	+	-	-	-	-	-	-	-	-
36720	+++	+	--+	++	+++	++	+	-	-	-
36728	+++	+++	-	-	-	-	-	-	-	-
36603	+++	+++	-	-	-	-	-	-	-	-
36607	+++	+++	-	+	+	+	+	-	-	-
36576	+++	+++	-	-	-	-	-	-	-	-
36729	+++	+	-	+	+	-	+	-	-	-
14036	+++	+++	-	-	-	-	-	-	-	-

36730	+++	++	-	-	-	-	-	-	-	-
19710	+++	-	-	-	-	-	-	-	-	-
36649	+++	+++	-	-	-	-	-	-	-	-
36731	+++	+	-	-	-	-	-	-	-	-
36732	+++	-	-	-	-	-	-	-	-	-
36733	+++	+	-	-	+	+	+	–	-	-
36579	+++	+++	-	-	-	-	-	-	-	-
36615	+++	++	-	-	-	-	-	-	-	-
36613	+++	+++	-	-	-	-	-	-	-	-
36494	+++	++	-	-	-	-	-	-	-	-
36734	+++	+	–+	+++	+++	++	+	-	+++	-
14207	+++	+++	-	-	-	-	-	-	-	-
36735	+++	+++	–	+	+	+	-	-	-	-
11865	+++	+++	-	-	-	+	-	-	-	-
36736	+++	+++	-	+	+	+	-	-	-	-
36726	+++	+++	-	-	+	+	-	-	-	-
14222	+++	+++	-	-	-	-	-	-	-	-
36724	+++	++	-	-	-	-	-	–	-	-
14226	+++	+++	-	-	-	-	-	-	-	-
11979	+++	-	-	-	-	-	-	-	-	-
36737	+++	++	–+	+++	+++	+++	-	-	-	-
36539	+++	++	-	-	-	-	-	-	-	-
11927	+++	+++	-	-	-	-	-	-	-	-
36572	+++	+	-	-	-	-	-	-	-	-
36711	+++	+	-	-	+	+	++	––	-	-
11074	+++	++	-	-	-	-	-	-	-	-
11865	+++	+++	-	-	-	-	-	-	-	-
17621	+++	+++	-	-	-	-	-	-	-	-
16017	+++	+++	-	-	-	-	-	-	-	-
17676	+++	+	-	-	-	-	-	-	-	-
36738	+++	+++	-	-	-	-	-	-	-	-
12220	+++	+++	-	-	-	-	-	-	-	-
36534	+++	++	-	+	-	-	-	-	-	-

36608	+++	-	-	-	-	-	-	-	-	-
36739	+++	+	-	+	-	-	-	-	-	-
36685	+++	+++	-	+	+	+	-	-	-	-
36664	+++	+++	-	+	+	+	-	-	-	-
36670	+++	+++	-	-	-	-	-	-	-	-
36654	+++	+++	-	-	-	-	-	-	-	-
36740	+++	+++	-	-	-	-	-	-	-	-
17801	+++	+++	-	-	-	-	-	-	-	-
36718	+++	+++	-	-	-	-	-	-	-	-
11296	+++	+++	-	-	-	-	-	-	-	-
14290	+++	+++	-	+	-	-	-	-	-	-
36741	+++	++	-	-	-	-	-	-	-	-
16608	+++	+	-	-	-	-	-	-	-	-
36742	+++	+++	-	-	-	-	-	-	-	-
36723	+++	+++	-	-	-	-	-	-	-	-
36743	+++	-	--+	+	-	-	+	-	-	-
16582	+++	+++	-	+	-	+	-	-	-	-
36457	+++	+++	-	+	++	+++	-	-	-	-
36744	+++	+++	-	-	-	-	-	-	-	-
14234	+++	+++	-	-	-	-	-	-	-	-
36745	+++	+	-	-	-	-	-	-	-	-
18035	+++	+++	-	-	-	-	-	-	-	-
36661	+++	+++	-	-	-	-	-	-	-	-
36619	++	+++	-	-	-	-	-	-	-	-
36472	++	-	--+	+	+++	+	-	-	+++	+++
36458	++	+++	-	+	++	+++	-	-	-	-
12148	++	+++	-	-	-	-	-	-	-	-
36746	++	++	-	-	-	-	-	-	-	-
18641	++	-	--+	-	+++	+	-	-	-	-
14111	++	+++	-	+	+	+	-	-	-	-
36588	++	+	--+	++	+++	++	+	-	-	-
11746	++	++	-	-	-	-	-	-	-	-
36747	++	+++	-	-	-	+	-	-	-	-

36520 ++	+	-	+	+	+	-	-	-	-
17566 ++	-	-	-	-	-	-	-	-	-
36748 ++	++	--+	+++	+++	+++	+	-	-	+
36602 ++	-	--+	+	+++	+	-	-	-	-
36350 ++	-	-	+	-	-	-	-	-	-
36749 ++	++	--+	+++	+++	+++	-	-	-	-
36741 ++	++	-	-	-	-	-	-	-	-
36750 ++	+	-	-	-	+	-	–	-	-
36751 ++	++	--	++	+	++	+++	---	-	-
36576 ++	+++	-	-	-	-	-	-	-	-
36342 ++	-	--	+	+++	+	+	-	-	-
36752 ++	+++	-	-	-	-	-	-	-	-
36620 ++	+++	-	-	-	-	-	-	-	-
36753 ++	++	–	+	+	+	-	-	-	-
36550 ++	+++	-	-	-	-	+	-	-	-
11765 ++	-	-	-	-	-	-	-	-	-
16595 ++	+++	-	-	-	-	-	–	-	-
12206 ++	+	-	-	-	-	-	-	-	-
36754 ++	+++	-	-	-	-	-	-	-	-
36755 ++	-	-	-	-	-	-	-	-	-
16628 ++	+++	-	+	+	+	+	–	-	-
17809 ++	-	-	-	-	-	-	-	-	-
36622 ++	++	-	-	-	-	-	-	-	-
36756 ++	-	--+	+	-	-	-	-	-	-
36755 ++	-	-	-	-	-	-	-	-	-
36757 ++	+	-	-	-	-	-	–	-	-
11292 ++	+	-	-	-	-	-	-	-	-
36601 ++	+	–	+	+	+	-	-	-	-
11967 ++	+++	-	-	-	-	-	-	-	-
36651 ++	-	-	-	-	-	-	-	-	-
36758 ++	+++	-	-	-	-	-	-	-	-
36728 ++	+++	-	-	-	-	-	-	-	-
12055 ++	++	-	-	-	-	-	-	-	-

36759 ++	-	--+	+++	+++	+++	-	-	-	-
36540 ++	+	-	+	+	+	-	-	-	+
36760 ++	++	-	-	-	-	-	-	-	-
36526 ++	+++	-	+	+	+	-	-	-	-
36761 ++	-	--+	+	++	-	-	-	-	-
36762 ++	-	--+	+	++	-	-	-	+++	-
36419 ++	+	-	+	+	+	+	-	-	-
13557 ++	+++	-	-	-	-	-	-	-	-
16076 ++	+++	-	-	-	-	-	-	-	-
11352 ++	+++	-	-	-	-	-	-	-	-
11796 ++	+++	-	-	-	-	-	-	-	-
11766 ++	+++	-	-	-	-	-	-	-	-
16025 ++	+++	-	-	-	-	-	-	-	-
36763 ++	+	-	-	-	-	-	-	-	-
14281 ++	+++	-	-	-	-	-	-	-	-
36764 ++	+++	-	-	-	-	-	-	-	-
11482 ++	+++	-	-	-	-	-	-	-	-
14807 ++	+++	-	-	-	-	-	-	-	-
36735 ++	+++	-	+	+	+	-	-	-	-
36765 ++	+++	-	-	-	-	-	-	-	-
36766 ++	++	-	-	-	-	-	-	-	-
11848 ++	-	-	-	-	-	-	-	-	-
36767 ++	-	--+	+	+++	-	+	-	-	-
36499 ++	+++	-	-	-	-	-	-	-	-
36723 ++	+++	-	-	-	-	-	-	-	-
14094 ++	+++	-	-	-	-	-	-	-	-
36768 ++	+++	-	-	-	-	-	-	-	-
18012 ++	+++	-	-	+	+	-	-	-	-
16588 ++	+++	-	-	-	-	-	-	-	-
16158 ++	-	-	-	-	-	-	-	-	-
36769 ++	+++	-	-	-	-	-	-	-	-
36770 ++	-	--+	+	+++	+	-	-	+++	-
36515 ++	+++	-	-	-	-	-	-	-	-

15961 ++	++	-	-	-	-	-	-	-	-
17621 ++	+++	-	-	-	-	-	-	-	-
36695 ++	+++	-	-	-	-	-	-	-	-
36771 ++	-	--+	+	+++	+	-	-	-	-
10981 ++	+++	--+	+++	+++	+++	+	-	-	-
36712 ++	+	--+	+	+++	+	+	-	-	-
14238 ++	+++	-	-	-	-	-	-	-	-
36678 ++	+	-	-	-	-	-	-	-	-
14388 ++	+++	-	-	-	-	-	-	-	-
36772 ++	+++	-	-	-	-	-	-	-	-
36773 ++	-	-	-	-	-	-	-	-	-
11996 ++	+	-	-	-	-	-	-	-	-
36511 ++	-	-	-	-	-	-	-	-	-
36663 ++	+	–	+	+	+	-	-	-	-
36534 ++	++	-	-	-	-	-	-	-	-
36337 ++	-	-	-	-	-	-	-	-	-
13938 ++	+++	–	+	+	+	-	-	-	-
36704 ++	+++	-	-	-	-	-	-	-	-
36674 ++	-	--+	+	+++	+	-	-	-	-
36774 ++	-	--+	+	+	-	+	–	-	-
18015 ++	+++	-	-	-	-	-	-	-	-
17659 ++	+++	--+	+++	+++	+++	+	–	-	+++
16018 ++	+++	-	-	-	+	-	-	-	-
36621 ++	+++	-	-	-	-	-	-	-	-
36775 ++	-	--	+	+++	+	-	-	-	-
36776 ++	++	-	-	-	-	-	-	-	-
36777 ++	+++	-	-	-	-	-	-	-	-
36778 ++	+++	–	+	+	+	-	-	-	-
36540 ++	+	–	+	+	+	-	-	-	-
16568 ++	++	-	+	+	-	-	-	-	-
12034 ++	-	-	-	-	-	-	-	-	-
17250 ++	+	--+	+++	+++	+++	-	-	-	-
14050 ++	+++	-	-	-	-	-	-	-	-

36779 ++	+	--+	+++	+++	+++	-	-	-	-
36412 ++	+	--+	+++	+++	++	+++	---	-	+++
36692 ++	+++	-	-	-	-	-	-	-	-
36780 ++	+++	-	-	-	-	-	-	-	-
11865 ++	+++	-	-	-	-	-	-	-	-
11043 ++	++	-	-	-	-	-	-	-	-
16579 ++	+++	-	-	-	+	-	-	-	-
16583 ++	+++	–	+	+	+	-	-	-	-
14416 ++	+++	-	+	-	-	-	-	-	-
36358 ++	+++	-	-	-	+	-	-	-	-
12165 ++	+++	-	-	-	-	-	-	-	-
36781 ++	-	--	-	+++	-	-	-	-	-
16650 ++	+++	-	-	-	-	-	–	-	-
36782 ++	+	--+	++	+++	++	+++	–	+++	+++
36415 ++	+++	-	-	-	-	-	-	-	-
36783 ++	+	-	-	-	-	-	-	-	-
36669 ++	-	--+	+	+	-	-	-	-	-
36640 ++	+++	-	-	-	-	-	-	-	-
36784 ++	+	--+	+++	+++	+++	+++	---	+++	+++
14461 ++	+++	-	+	+	+	-	-	-	-
13752 ++	++	-	-	-	-	-	-	-	-
36534 ++	++	-	-	-	-	-	-	-	-
36785 ++	-	-	-	-	-	-	-	-	-
36708 ++	-	-	-	-	-	-	-	-	-
13537 ++	+++	-	-	-	-	-	-	-	-
36614 ++	+++	-	-	-	-	-	-	-	-
36479 ++	+++	-	-	-	-	-	-	-	-
36701 ++	++	–	+	-	-	-	-	-	-
13762 ++	+++	-	+	+	+	-	–	-	-
11458 ++	+++	-	-	-	-	-	-	-	-
36786 ++	-	-	-	-	-	+	–	-	-
11418 ++	++	-	-	-	-	-	-	-	-
36723 ++	+++	-	-	-	-	-	-	-	-

36787 ++	-	-	-	-	-	-	-	-	-
16074 ++	+++	-	-	-	-	-	-	-	-
36788 ++	+	-	-	-	-	-	-	-	-
36789 ++	+++	-	-	-	-	-	-	-	-
36790 ++	++	–	+	+	+	+	–	-	-
36550 ++	+++	-	-	-	-	+	–	-	-
36791 ++	++	-	-	-	-	-	-	-	-
11227 ++	++	-	-	-	-	-	-	-	-
36792 ++	-	-	-	-	-	-	-	-	-
36793 ++	+++	-	-	-	-	-	-	-	-
11338 ++	-	-	-	-	-	-	-	-	-
36794 ++	+++	-	-	-	-	-	-	-	-
36795 ++	+++	-	-	-	-	-	-	-	-
36796 ++	+++	-	-	-	-	-	-	-	-
36797 ++	-	–+	-	+	-	-	-	-	-
36798 ++	-	–+	+	+	-	-	-	-	-
36636 ++	+++	-	-	-	-	-	-	-	-
36799 ++	+	-	-	-	-	-	-	-	-
36680 ++	-	–+	++	+++	+	-	-	-	-
36563 ++	+++	-	-	-	-	-	-	-	-
36449 ++	+	-	+	+	+	+	–	-	-
36800 ++	-	–+	+	++	+	-	-	+++	-
36474 ++	-	–+	+	+++	+	+	–	-	-
36801 ++	++	-	-	-	-	-	-	-	-
36802 ++	-	-	-	-	-	-	-	-	-
36514 ++	+++	-	-	-	-	-	–	-	-
36803 ++	-	-	-	-	-	-	-	-	-
12333 ++	++	-	-	-	-	-	-	-	-
36804 ++	-	–	++	++	-	+++	---	-	-
36805 ++	+++	-	-	-	-	-	-	-	-
11817 ++	+++	-	-	-	-	-	-	-	-
19087 ++	+++	-	-	-	-	-	-	-	-
36806 ++	+++	-	-	-	-	-	-	-	-

36807 ++	+++	–	-	+	+	-	-	-	-
36808 ++	-	–-+	+	+	-	-	-	-	-
36809 ++	+++	-	-	-	-	-	-	-	-
36613 ++	+++	-	-	-	-	-	-	-	-
11734 ++	+++	-	-	-	-	-	-	-	-
11996 ++	+	-	-	-	-	-	-	-	-
14159 ++	+++	-	-	-	-	-	-	-	-
36500 ++	-	–-+	+	++	-	-	-	-	-
36810 ++	+++	-	-	-	-	-	-	-	-
36714 ++	+++	-	-	-	-	-	-	-	-
14198 ++	+++	-	-	-	-	-	-	-	-
36811 ++	-	-	-	-	-	-	-	-	-
36812 ++	-	-	-	+++	+	-	-	-	-
36479 ++	+++	-	-	-	-	-	-	-	-
36778 ++	+++	–	+	+	+	-	-	+	-
11817 ++	+++	-	-	-	-	-	-	-	-
11230 ++	+++	-	-	-	-	-	-	-	-
36813 ++	-	-	-	-	-	-	-	-	-
36814 ++	-	-	-	-	-	-	-	-	-
36760 ++	++	-	-	-	-	-	-	-	-
36691 ++	+++	-	-	-	-	-	-	-	-
19263 ++	-	–-+	+	+	-	-	–	-	-
36625 ++	-	-	-	-	-	-	-	-	-
36465 ++	+++	-	-	-	+	-	-	-	-
11878 ++	-	-	-	-	-	-	-	-	-
36815 ++	+++	-	-	-	-	-	-	-	-
36555 ++	++	-	-	-	-	-	-	-	-
18673 ++	++	-	-	-	-	-	-	-	-
36816 ++	++	-	-	-	-	-	-	-	-
11720 ++	-	-	-	-	-	-	-	-	-
36817 ++	+	–	++	+	++	+++	---	+++	+++
36818 ++	+++	-	-	-	-	-	-	-	-
36819 ++	-	-	-	+++	-	-	-	-	-

11920 ++	-	-	-	-	-	-	-	-	-
36820 ++	+++	--+	+++	+++	+++	-	-	-	+++
36687 ++	+	-	-	-	-	-	-	-	-
12707 ++	-	-	-	-	-	-	-	-	-
36821 ++	+	-	-	-	-	-	-	-	-
36822 ++	++	-	-	+	-	+	–	-	-
36823 ++	++	-	-	-	-	-	-	-	-
36489 ++	+++	–	+	++	++	-	-	-	-
36498 ++	+++	-	-	-	-	-	-	-	-
15973 ++	+++	-	-	-	-	-	-	-	-
11106 ++	-	-	-	-	-	-	-	-	-
36370 ++	-	--+	+	+++	+	-	-	-	-
36567 ++	++	-	-	-	-	-	-	-	-
36824 ++	+++	-	-	-	-	-	-	-	-
36764 ++	+++	-	-	-	-	-	-	-	-
36825 ++	+++	-	-	-	-	+	–	-	-
36826 ++	+++	-	-	-	-	-	-	-	-
36693 ++	-	-	-	-	-	-	-	-	-
36827 ++	-	--	+	+++	+	-	–	-	-
18087 ++	+++	-	+	+	+	-	-	-	-
36609 ++	+++	-	-	-	-	-	-	-	-
36828 ++	+	-	-	-	-	-	-	-	-
15956 ++	+++	-	-	-	+	-	-	-	-
36719 ++	+++	-	-	-	-	+	-	-	-
36829 ++	+++	-	-	-	-	-	-	-	-
36830 ++	-	--+	-	++	-	-	-	-	-
36831 ++	+++	-	-	-	-	+	-	-	-
11817 ++	+++	-	-	-	-	-	-	-	-
16588 ++	+++	-	-	-	-	-	-	-	-
36832 ++	-	--+	+	-	-	-	-	-	-
36833 ++	+++	–	+	-	-	-	-	-	-
36834 ++	+++	–	+	+	+	+	–	-	-
19288 ++	+	-	-	-	-	-	-	-	-

36835 ++	-	--+	+	+	-	-	-	-	-
36730 ++	+	-	-	-	-	-	-	-	-
36557 ++	+	-	-	-	-	-	-	-	-
36836 ++	+++	-	-	-	-	-	-	-	-
36837 ++	-	--	+	+++	+	-	-	-	-
36688 ++	+++	--+	+++	+++	+++	+	-	+++	+++
17968 ++	++	-	-	-	-	-	-	-	-
13886 ++	-	-	+	+	+	-	-	-	-
36777 ++	+++	-	-	-	-	-	-	-	-
36838 ++	+	-	-	-	-	-	-	-	-
18133 ++	+++	-	-	-	-	-	-	-	-
14673 ++	+++	-	-	-	-	-	-	-	-
36756 ++	-	--+	+	+	-	-	-	-	-
36780 ++	+++	-	-	-	-	-	-	-	-
36564 ++	+++	-	-	-	-	-	-	-	-
13651 ++	+++	-	+	+	+	-	-	-	-
36436 ++	+++	-	-	-	-	+	-	-	-
36839 ++	++	-	-	-	-	-	-	-	-
36537 ++	+++	-	-	-	-	-	-	-	-
12043 ++	+++	-	-	-	-	-	-	-	-
36633 ++	+++	-	-	-	-	-	-	-	-
36840 ++	+++	-	+	+	+	-	-	-	+
36841 ++	+++	-	-	-	-	-	-	-	-
14181 ++	+++	-	-	-	-	-	-	-	-
36677 ++	+++	-	-	-	-	-	-	-	-
36715 ++	-	-	-	-	-	-	-	-	-
36783 ++	+	-	-	-	-	-	-	-	-
13806 ++	+++	-	-	-	-	-	-	-	-
36842 ++	-	-	-	-	-	-	-	-	-
36819 ++	-	-	-	+++	-	-	-	-	-
36843 ++	-	-	-	-	-	-	-	-	-
36844 ++	+++	-	+	+	+	+	-	-	-
36845 ++	-	-	-	-	-	-	-	-	-

36846 ++	+++	-	-	-	-	-	-	-	-
36686 ++	+++	-	-	-	-	-	-	-	-
36671 ++	++	-	-	-	-	-	-	-	-
36847 ++	-	--+	+++	+++	+++	-	-	-	-
36848 ++	+++	-	-	-	-	-	-	-	-
36849 ++	+	-	-	-	-	-	-	-	-
36850 ++	-	-	-	-	-	-	-	-	-
36851 ++	+++	--+	+++	+++	+++	+	–	-	-
36852 ++	-	-	-	-	-	-	-	-	-
14226 ++	+++	-	-	-	-	-	-	-	-
36853 ++	-	--+	+	+	-	-	-	-	-
36401 ++	+++	-	-	-	-	+	-	-	-
36600 ++	-	-	-	-	-	-	-	-	-
36854 ++	+++	-	-	-	-	-	-	-	-
36855 ++	+++	-	+	-	-	-	-	-	-
36778 ++	++	–	+	+	+	-	-	-	-
36856 ++	+++	-	-	-	-	-	-	-	-
36857 ++	-	--+	+	++	-	-	-	-	-
36858 ++	-	--+	+++	+++	+++	-	–	-	-
36859 ++	+++	–	-	-	+	+	–	-	-
36829 ++	+++	-	-	-	-	-	-	-	-
36581 ++	+++	-	-	-	+	-	-	-	-
17543 ++	+++	-	+	+	+	-	-	-	-
36468 ++	++	-	+	-	-	-	-	-	-
36829 ++	+++	-	-	-	-	-	-	-	-
36428 ++	+	-	-	-	-	-	-	-	-
36860 ++	+++	-	-	-	-	-	-	-	-
14388 ++	+++	-	-	-	-	-	-	-	-
36861 ++	+++	–	+	+	+	+	–	-	-
36857 ++	-	--+	+	++	-	-	-	-	-
36764 ++	+++	-	-	-	-	-	-	-	-
19755 ++	-	--+	+	-	-	-	-	-	-
36820 ++	+++	--+	+++	+++	+++	-	–	-	-

36362 ++	-	-	-	-	-	-	-	-	-
17588 ++	++	–	-	-	-	-	-	-	-
16591 ++	+++	-	-	-	-	-	-	-	-
36846 ++	++	-	-	-	-	-	-	-	-
36862 ++	-	–+	+	+++	-	+	–	-	-
36863 ++	++	-	-	-	-	-	-	-	-
36650 ++	+++	-	-	-	+	-	-	-	-
11366 ++	-	-	-	-	-	-	-	-	-
36864 ++	+++	-	-	-	-	-	-	-	-
16676 ++	+	-	+	-	+	+	–	-	-
11826 ++	+	-	-	-	-	-	-	-	-
36865 ++	-	-	-	-	-	-	-	-	-
36866 ++	+	-	-	-	-	-	-	-	-
36546 ++	++	-	-	-	-	-	-	-	-
36867 ++	+++	-	-	-	-	-	-	-	-
36868 ++	-	-	-	-	-	-	-	-	-
36869 ++	+	–+	++	+++	++	++	–	+++	-
36856 ++	+++	-	-	-	-	-	-	-	-
36870 ++	-	–	+	+	+	+	–	-	-
36871 ++	++	–+	+++	+++	+++	+	–	-	-
36872 ++	+++	-	-	-	-	-	-	-	-
36514 ++	+++	-	-	-	-	-	-	-	-
36873 ++	+++	-	-	-	-	-	-	-	-
36874 ++	-	-	-	-	-	-	-	-	-
36813 ++	-	-	-	-	-	-	-	-	-
36875 ++	+++	-	-	-	-	-	-	-	-
11945 ++	+++	-	-	-	-	-	-	-	-
36876 ++	-	–	+	+	+	+	-	-	-
36807 ++	+++	-	-	+	+	-	-	-	-
13795 ++	+	-	-	-	-	-	-	-	-
12737 ++	+	-	-	-	-	-	-	-	-
36877 ++	+	–+	++	+++	++	+	–	-	-
36878 ++	+	–+	+++	+++	+++	+++	---	+++	+++

36558 ++	-	--+	+	+++	+	+	-	-	-
12190 ++	++	-	-	-	-	-	-	-	-
36855 ++	+++	-	+	-	+	-	-	-	-
36879 ++	+++	-	-	-	-	-	-	-	-
17605 ++	-	-	-	-	-	-	-	-	-
36880 ++	+++	-	-	-	+	-	-	-	-
36881 ++	-	-	-	-	-	-	-	-	-
36882 ++	-	-	-	-	-	-	-	-	-
36883 ++	-	-	-	-	-	-	-	-	-
36884 ++	+++	-	-	+	+	-	-	-	-
17020 ++	+	--+	+++	+++	+++	+	–	+++	+++
13837 ++	+++	-	-	-	-	-	-	-	-
13904 ++	+++	-	-	-	-	-	-	-	-
11115 ++	+++	-	-	-	-	-	-	-	-
14600 ++	-	-	-	-	-	-	-	-	-
36519 ++	++	–	-	-	-	-	–	-	-
11366 ++	-	-	-	-	-	-	-	-	-
36885 ++	+	-	-	-	-	-	-	-	-
36886 ++	+++	-	-	-	+	-	-	-	-
11644 ++	-	-	-	-	-	-	-	-	-
14342 ++	+++	-	-	-	+	-	-	-	-
11350 ++	+++	-	-	-	-	-	-	-	-
36886 ++	+++	-	-	-	+	-	-	-	-
36772 ++	+++	-	-	-	-	-	-	-	-
11492 ++	+++	-	-	-	-	-	-	-	-
36810 ++	+++	-	-	-	-	-	-	-	-
36630 ++	+++	-	-	-	-	-	-	-	-
36887 ++	+	-	-	-	-	-	-	-	-
36888 ++	+	-	-	-	-	-	-	-	-
36753 ++	++	–	+	+	+	-	-	-	-
36889 ++	+	-	+	-	-	-	-	-	-
11077 ++	+++	-	-	-	-	-	-	-	-
36605 ++	+++	-	-	-	-	-	-	-	-

36738 ++	+++	-	-	-	-	-	-	-	-
36745 ++	+	-	-	-	-	-	-	-	-
36682 ++	+++	--+	+++	+++	+++	+	-	-	-
36890 ++	-	--+	+	+++	+	+	-	-	-
17412 ++	+++	-	-	-	+	-	-	-	-
36891 ++	+	-	+	+	+	+	-	-	-
11043 ++	++	-	-	-	-	-	-	-	-
19906 ++	-	-	-	-	-	-	-	-	-
36892 ++	-	-	-	-	-	-	-	-	-
36893 ++	-	--+	++	+++	+	+	-	+++	-
36894 ++	-	-	-	-	-	-	-	-	-
13882 ++	+++	-	-	-	-	-	-	-	-
36895 ++	+++	-	-	-	-	-	-	-	-
36896 ++	+	-	-	-	-	-	-	-	-
11276 ++	+++	-	-	-	-	-	-	-	-
36897 ++	-	-	-	-	-	-	-	-	-
36898 ++	+++	-	-	-	-	-	-	-	-
36899 ++	-	-	-	+	-	-	-	-	-
36609 ++	+++	-	-	-	-	-	-	-	-
36900 ++	+++	-	-	-	-	-	-	-	-
11720 ++	-	-	-	-	-	-	-	-	-
36855 ++	+++	-	-	-	+	-	-	-	-
12379 ++	+++	-	-	-	-	-	-	-	-
13886 ++	+	-	+	+	+	-	-	-	-
36598 ++	++	-	+	+	+	+	-	-	-
36758 ++	+++	-	-	-	-	-	-	-	-
36842 ++	-	-	-	-	-	-	-	-	-
36639 ++	+++	--+	+++	+++	+++	+	-	+++	-
11017 ++	+++	-	-	-	-	-	-	-	-
16586 ++	++	-	+	-	+	-	-	-	-
11384 ++	+++	-	-	-	-	-	-	-	-
12069 ++	-	-	-	-	-	-	-	-	-
36495 ++	+++	-	-	-	-	-	-	-	-

36901 ++	+++	-	-	-	-	-	-	-	-
36902 ++	+	---+	+	+++	+	-	-	+++	+++
36903 ++	+++	-	+	+	+	-	-	-	-
17676 ++	+	-	-	-	-	-	-	-	-
36904 ++	+++	-	-	-	-	-	-	-	-
36905 ++	++	-	-	-	-	-	-	-	-
11295 ++	+++	-	-	-	-	-	-	-	-
36906 ++	+	---+	++	+++	++	++	--	+++	+++
36660 ++	-	---+	++	+++	+	-	-	+++	-
36907 ++	+++	-	-	-	-	-	-	-	-
18573 ++	++	-	-	-	-	-	-	-	-
36501 ++	-	---+	-	+++	+	-	-	-	-
14035 ++	+++	-	-	-	-	-	-	-	-
16108 ++	+++	-	-	-	-	-	-	-	-
36856 ++	+++	-	+	-	-	-	-	-	-
12737 ++	+	-	-	-	-	-	-	-	-
17554 ++	+++	-	-	-	-	-	-	-	-
16583 ++	++	-	+	+	+	-	-	-	-
36908 ++	+	-	-	-	-	-	-	-	-
14327 ++	+++	-	-	-	-	-	-	-	-
12144 ++	-	-	-	-	-	-	-	-	-
14291 ++	+++	-	-	-	-	-	-	-	-
11106 ++	-	-	-	-	-	-	-	-	-
36828 ++	++	-	-	-	-	-	-	-	-
11070 ++	+++	-	-	-	-	-	-	-	-
36909 ++	+++	-	-	-	-	-	-	-	-
36910 ++	+++	-	-	-	-	-	-	-	-
36911 ++	+	-	-	-	-	-	-	-	-
36912 ++	-	-	-	+	+	-	-	-	-
36913 ++	-	---+	++	+++	+++	+	-	-	-
36914 ++	-	---+	+	+++	+	+	-	-	-
14111 ++	+++	-	+	+	+	-	-	-	-
11816 ++	+++	-	-	-	-	-	-	-	-

36829 ++	+++	-	-	-	-	-	-	-	-
36673 ++	++	-	-	-	-	-	-	-	-
36846 ++	+++	-	-	-	-	-	-	-	-
36790 ++	++	–	+	+	+	+	–	-	-
36695 ++	+++	-	-	-	-	-	-	-	-
36915 ++	+++	-	-	-	-	-	-	-	-
36706 ++	+++	-	-	-	-	-	-	-	-
36814 ++	-	-	-	-	-	-	-	-	-
36916 ++	-	–+	+++	+++	+++	-	-	-	-
36917 ++	-	–+	+	+++	+	-	-	-	-
36918 ++	-	–+	+	++	+	-	-	-	-
36841 ++	+++	-	-	-	-	-	-	-	-
36479 ++	+++	-	-	-	-	-	-	-	-
36655 ++	-	-	-	-	-	-	-	-	-
36919 ++	+++	-	-	-	-	-	-	-	-
12069 ++	-	-	-	-	-	-	-	-	-
14207 ++	+++	-	-	-	-	-	-	-	-
36747 ++	+++	-	-	-	+	-	-	-	-
36550 ++	++	-	-	-	-	+	–	-	-
36920 ++	-	––	+	+++	+	-	–	-	-
36683 ++	+++	-	-	-	-	-	-	-	-
11891 ++	+++	-	-	-	-	-	-	-	-
36921 ++	++	-	-	-	-	-	-	-	-
36718 ++	+++	-	-	-	-	-	-	-	-
36922 ++	+	-	-	-	-	-	-	-	-
36923 ++	++	-	-	-	-	-	-	-	-
36924 ++	++	–	+	+++	+++	-	-	-	-
17801 ++	+++	-	-	-	-	-	-	-	-
36907 ++	+++	-	-	-	-	-	-	-	-
36925 ++	+	-	-	-	-	-	-	-	-
36852 ++	+	-	-	-	-	-	-	-	-
12177 ++	+++	-	-	-	-	-	-	-	-
36746 ++	++	-	-	-	-	-	-	-	-

36707 ++	-	-	-	-	-	-	-	-	-
36721 ++	+++	-	-	-	-	-	-	-	-
36894 ++	+	-	-	-	-	-	-	-	-
36640 ++	+++	-	-	-	-	-	-	-	-
36926 ++	+++	-	-	-	-	-	-	-	-
36764 ++	+++	-	-	-	-	-	-	-	-
16607 ++	-	--+	+	+++	+	-	-	-	-
36764 ++	+++	-	-	-	+	-	-	-	-
36927 ++	++	-	-	-	-	-	-	-	-
12434 ++	-	-	-	-	-	-	-	-	-
11564 ++	+++	-	+	-	-	-	-	-	-
17566 ++	-	-	-	-	-	-	-	-	-
19543 ++	+	-	-	-	-	-	-	-	-
36637 ++	-	-	-	-	-	-	-	-	-
36928 ++	+	-	-	-	-	-	-	-	-
17681 ++	+++	-	-	-	-	-	-	-	-
11740 ++	+++	-	-	-	-	-	-	-	-
36929 ++	++	-	-	-	-	-	-	-	-
11271 ++	+++	-	-	-	-	-	-	-	-
11026 ++	++	-	-	-	-	-	-	-	-
36910 ++	+++	-	-	-	-	-	-	-	-
36930 ++	+	--+	++	+++	+	+	-	+++	-
12441 ++	-	-	-	-	-	-	-	-	-
36931 ++	-	-	-	-	-	-	-	-	-
17857 ++	+++	-	-	-	-	-	-	-	-
36932 ++	+++	-	+	+	+	++	--	-	++
36888 ++	+	-	-	-	-	-	-	-	-
36933 ++	+++	--+	+++	+++	+++	+	-	-	-
36744 ++	+++	-	-	-	-	-	-	-	-
16100 ++	+++	-	-	-	+	-	-	-	-
14602 ++	+++	-	-	-	-	-	-	-	-
36934 ++	+	-	-	-	-	-	-	-	-
14503 ++	+++	-	-	-	-	-	-	-	-

36935 ++	+++	-	-	-	-	-	-	-	-
36936 ++	+++	--+	+++	+++	+++	+	–	-	-
11338 ++	-	-	-	-	-	-	-	-	-
36788 ++	+	-	-	-	-	-	-	-	-
17895 ++	++	-	-	-	-	-	-	-	-
11113 ++	+++	-	-	-	-	-	-	-	-
36872 ++	+++	-	-	-	-	-	-	-	-
12177 ++	+++	-	-	-	-	-	-	-	-
36791 ++	+++	-	-	-	-	-	-	-	-
36937 ++	-	--+	+	+++	-	-	-	+++	-
18558 ++	-	-	-	-	-	-	-	-	-
36938 ++	-	--+	+	+++	+	-	-	-	-
11690 ++	-	-	-	-	-	-	-	-	-
36939 ++	++	-	-	-	-	-	-	-	-
36834 ++	+++	–	+	+	+	+	–	-	-
36940 ++	+++	-	-	-	-	-	-	-	-
36815 ++	+++	-	-	-	+	-	-	-	-
36647 ++	++	-	-	-	-	+	–	-	-
17986 ++	-	--+	+	+++	+	-	-	-	-
36941 ++	-	-	-	-	-	-	-	-	-
36699 ++	-	--+	+	+++	+	+	-	-	-
36942 ++	+++	-	-	-	-	-	-	-	-
36943 ++	+	-	+	-	-	-	-	-	-
11974 ++	+	-	-	-	-	-	-	-	-
36944 ++	-	--+	+	+++	-	-	-	-	-
17138 ++	-	--+	+++	+++	+++	-	-	-	-
16584 ++	++	-	-	-	-	-	-	-	-
36765 ++	+++	-	-	-	-	-	-	-	-
36533 ++	+	--+	+	+++	++	-	–	+++	-
19710 ++	-	-	-	-	-	-	-	-	-
14079 ++	+++	-	-	-	-	-	-	-	-
36945 ++	-	-	-	-	-	-	-	-	-
36946 ++	+++	--+	+++	+++	+++	-	–	-	-

16080 ++	+++	-	-	-	-	-	-	-	-
14304 ++	+++	-	-	-	-	-	-	-	-
16134 ++	+	-	-	-	-	-	-	-	-
36829 ++	+++	-	-	-	-	-	-	-	-
18074 ++	-	–	+	-	+	-	–	-	-
11561 ++	+++	-	-	-	-	-	-	-	-
36947 ++	++	-	+	-	+	-	-	-	-
36948 ++	-	-	-	-	-	-	-	-	-
16600 ++	+++	–+	+++	++	+++	-	-	-	-
36920 ++	-	–	-	+++	+	+	–	-	-
36624 ++	-	–+	+	+++	++	+	-	-	-
36911 ++	+	-	-	-	-	-	-	-	-
36795 ++	+++	-	-	-	-	-	-	-	-
36597 ++	-	-	-	-	-	-	-	-	-
36949 ++	+++	-	-	-	-	-	-	-	-
36950 ++	+++	-	-	-	-	-	-	-	-
36951 ++	+++	-	-	-	-	-	-	-	-
36952 ++	++	-	-	-	-	-	-	-	-
36953 ++	-	-	-	-	-	-	-	-	-
14342 ++	+++	-	-	-	+	-	-	-	-
36954 ++	+++	-	-	-	-	-	-	-	-
36768 ++	+++	-	-	-	-	-	-	-	-
36955 ++	+++	-	-	-	+	-	-	-	-
36271 ++	+	–+	+	-	-	-	-	-	-
36956 ++	+	-	-	-	-	-	-	-	-
36957 ++	++	-	-	-	-	-	-	-	-
11207 ++	+++	-	-	-	-	-	-	-	-
14081 ++	++	-	-	-	-	-	-	-	-
36926 ++	+++	-	-	-	-	-	-	-	-
36958 ++	-	–+	+++	+++	+++	+++	---	-	-
36552 ++	+++	-	-	-	-	-	-	-	-
36959 ++	-	–+	+++	+++	+++	-	-	-	-
11557 ++	+++	-	-	-	-	-	-	-	-

17025 ++	-	-	-	-	-	-	-	-	-
36960 ++	+	--+	+++	+++	+++	+++	---	+++	+++
36830 ++	-	--+	+	++	-	-	-	-	-
36635 ++	+++	-	+	++	++	-	-	-	-
36961 ++	+++	-	-	-	-	+	-	-	-
36503 ++	+++	-	+	-	+	-	-	-	-
11493 ++	-	-	-	-	-	-	-	-	-
11492 ++	+++	-	-	-	-	-	-	-	-
36756 ++	-	--+	+	-	-	-	-	+++	-
36962 ++	++	-	+	+	-	+	-	-	-
36963 ++	-	--+	+	+++	+	+	-	+++	-
36964 ++	+++	-	-	-	-	-	-	-	-
18766 ++	++	-	-	-	-	-	-	-	-
15974 ++	+++	-	-	-	-	-	-	-	-
36829 ++	+++	-	-	-	-	-	-	-	-
13913 ++	+++	-	-	-	-	-	-	-	-
17412 ++	+++	-	-	-	-	-	-	-	-
36597 ++	-	-	-	-	-	-	-	-	-
36965 ++	+++	-	-	-	-	-	-	-	-
11476 ++	++	-	-	-	-	-	-	-	-
11026 ++	++	-	-	-	-	-	-	-	-
36593 ++	+++	-	-	-	-	-	-	-	-
14370 ++	+++	-	+	+	+	-	-	-	-
11734 ++	++	-	-	-	-	-	-	-	-
36966 ++	++	-	-	-	-	-	-	-	-
36539 ++	++	-	-	-	-	-	-	-	-
36764 ++	+++	-	-	-	-	-	-	-	-
36967 ++	-	-	-	-	-	-	-	-	-
36923 ++	+++	-	-	-	-	-	-	-	-
36968 ++	+++	-	-	-	-	-	-	-	-
36969 ++	++	-	-	-	-	-	-	-	-
36874 ++	-	-	-	-	-	-	-	-	-
36699 ++	-	--+	++	+++	+	-	-	+++	-

14441 ++	+++	-	-	-	-	-	-	-	-
16571 ++	++	-	-	-	-	-	-	-	-
13593 ++	+++	-	-	-	+	-	-	-	-
36970 ++	-	--+	-	-	-	-	-	-	-
36971 ++	++	-	+	-	-	-	-	-	-
36930 ++	+	--+	++	+++	+	+	-	+++	-
36968 ++	+++	-	-	-	-	-	-	-	-
36825 ++	+++	-	-	-	-	+	-	-	-
36742 ++	+++	-	-	-	-	-	-	-	-
36972 ++	++	-	-	+	+	-	-	-	-
36973 ++	+++	-	-	-	-	-	-	-	-
36915 ++	+++	-	-	-	-	-	-	-	-
36656 ++	+++	-	-	-	-	-	-	-	-
36940 ++	+++	-	-	-	-	-	-	-	-
36974 ++	+	-	-	-	-	-	-	-	-
36975 ++	+++	-	+	+	+	+	-	-	-
36798 ++	-	--+	+	+	-	-	-	+++	-
36976 ++	+++	-	-	-	-	-	-	-	-
13537 ++	+++	-	-	-	-	-	-	-	-
16580 ++	+++	-	+	-	-	-	-	-	-
36977 ++	+	-	-	-	-	-	-	-	-
36978 ++	+	-	-	-	-	-	-	-	-
36838 ++	+	-	-	-	-	-	-	-	-
36805 ++	+++	-	-	-	-	-	-	-	-
36575 ++	+++	-	-	-	+	-	-	-	-
36979 ++	+++	-	-	-	+	-	-	-	-
36551 ++	+++	-	-	-	-	-	-	-	-
36980 ++	+	-	-	-	-	-	-	-	-
36681 ++	+++	--+	+++	+++	+++	-	-	-	-
36893 ++	-	--+	++	+++	+	+	-	-	-
11288 ++	-	-	-	-	-	-	-	-	-
36781 ++	-	-	-	+++	-	-	-	-	-
36919 ++	+++	-	-	-	-	-	-	-	-

36967 ++	-	-	-	-	-	-	-	-	-
36974 ++	+	-	-	-	-	-	-	-	-
11407 ++	+++	-	-	-	-	-	-	-	-
11547 ++	+++	-	-	-	-	-	-	-	-
36934 ++	+	-	-	-	-	-	-	-	-
14102 ++	+++	-	-	-	-	-	-	-	-
36981 ++	-	-	-	-	-	-	-	-	-
11418 ++	++	-	-	-	-	-	-	-	-
36617 ++	-	-	-	-	-	-	-	-	-
36848 ++	+++	-	-	-	-	-	-	-	-
36725 ++	-	--+	+	+++	+	+	-	-	-
36889 ++	-	-	+	-	-	-	-	-	-
11762 ++	+++	-	-	-	-	-	-	-	-
36554 ++	++	-	-	-	-	-	-	-	-
36982 ++	++	-	-	-	-	-	-	-	-
36879 ++	+++	-	-	-	-	-	-	-	-
36845 ++	-	-	-	-	-	-	-	-	-
36983 ++	+	-	-	-	+	+	-	-	-
36740 ++	+++	-	-	-	-	-	-	-	-
36984 ++	-	-	-	-	-	-	-	-	-
14289 ++	+++	-	-	-	-	-	-	-	-
36985 ++	++	-	+	+	+	+	-	-	-
36986 ++	+++	-	-	-	-	-	-	-	-
36987 ++	++	-	-	-	-	-	-	-	-
36988 ++	+++	-	-	-	-	-	-	-	-
36731 ++	+	-	-	-	-	-	-	-	-
36710 ++	+++	-	-	-	-	-	-	-	-
36989 ++	++	-	-	-	-	-	-	-	-
36990 ++	+++	-	-	+	+	-	-	-	-
14619 ++	+++	-	-	-	-	-	-	-	-
36991 ++	+++	-	-	-	-	-	-	-	-
14619 ++	+++	-	-	-	-	-	-	-	-
11295 ++	+++	-	-	-	-	-	-	-	-

36872 ++	+++	-	-	-	-	-	-	-	-
36610 ++	-	-	-	-	-	-	–	-	-
36992 ++	++	-	-	-	-	-	-	-	-
36580 ++	-	–+	+	+++	+	-	-	-	-
36993 ++	++	-	-	-	-	-	-	-	-
14238 ++	+++	-	-	-	-	-	-	-	-
11338 ++	+	-	-	-	-	-	-	-	-
15945 ++	+++	-	-	-	-	-	-	-	-
36994 ++	+++	-	-	-	+	-	-	-	-
36995 ++	+++	-	-	-	-	-	-	-	-
36996 ++	+	-	-	-	-	-	-	-	-
36997 ++	-	-	-	-	-	-	-	-	-
36998 ++	-	–+	+	+	-	-	-	-	-
36849 ++	+	-	-	-	-	-	-	-	-
36999 ++	+++	-	-	-	-	-	-	-	-
17020 ++	+	–+	++	+++	++	+	–	+++	+++
37000 ++	-	–	-	-	-	+	-	-	-
36895 ++	+++	-	-	-	-	-	-	-	-
36495 ++	+++	-	-	+	-	-	-	-	-
11924 ++	-	-	-	-	-	-	-	-	-
37001 ++	-	–+	+	+	+	+	–	-	-
37002 ++	+	–+	+	+	+	+	–	-	-
37003 ++	+	–	+	+	+	-	-	-	-
37004 ++	-	–+	+	-	-	-	-	-	-
37005 ++	+++	-	-	-	-	-	-	-	-
37006 ++	+++	-	-	-	-	-	-	-	-
36531 ++	+++	-	-	-	-	-	-	-	-
37007 ++	++	-	-	-	-	-	-	-	-
37008 ++	++	-	-	-	-	-	-	-	-
37009 ++	++	-	-	-	-	-	-	-	-
16573 ++	+	-	-	-	-	-	-	-	-
37010 ++	-	–+	+	-	-	-	-	+++	-
37011 ++	-	-	-	-	-	-	-	-	-

18839 ++	++	–	+	+	+	+	–	-	-
37012 ++	+++	-	-	-	-	-	-	-	-
37013 ++	-	-	-	-	-	-	-	-	-
37014 ++	-	–+	+	++	-	+	–	-	-
36810 ++	+++	-	-	-	-	-	-	-	-
36821 ++	+	-	-	-	-	-	-	-	-
37015 ++	+	-	-	-	-	-	-	-	-
37016 ++	+++	–+	+++	+++	+++	-	–	-	-
11003 ++	++	-	-	-	-	-	-	-	-
36460 ++	+++	-	-	+	+	-	-	-	-
36495 ++	+++	-	-	-	-	-	-	-	-
36898 ++	+++	-	-	-	-	-	-	-	-
36636 ++	+++	-	-	-	-	-	-	-	-
36972 ++	++	-	-	+	+	-	-	-	-
11239 ++	+++	-	-	-	+	-	-	-	-
36642 ++	-	–+	+	+++	+	-	-	+++	-
11383 ++	++	-	-	-	-	-	-	-	-
11418 ++	++	-	-	-	-	-	-	-	-
37017 ++	++	-	-	-	-	-	-	-	-
14085 ++	+++	-	+	-	-	-	-	-	-
36947 ++	++	-	-	-	-	-	-	-	-
37018 ++	-	–+	++	+++	+	+	–	+++	-
37019 ++	+	-	-	-	-	-	-	-	-
14234 ++	+++	-	-	-	-	-	-	-	-
18878 ++	++	-	-	-	-	-	-	-	-
36841 ++	+++	-	-	-	-	-	-	-	-
37020 ++	+	-	-	-	-	-	-	-	-
36903 ++	+++	–	+	+	+	-	-	-	-
37021 ++	++	-	-	-	-	-	-	-	-
37022 ++	-	–+	+	+++	+	+	–	-	-
37023 ++	++	-	-	-	-	-	-	-	-
37024 ++	+	-	-	+	-	+	–	-	-
37025 ++	++	-	-	-	-	-	-	-	-

37026 ++	++	-	-	-	-	-	-	-	-
37027 ++	++	-	-	-	-	-	-	-	-
37028 ++	+++	-	-	-	-	-	-	-	-
36589 ++	-	--+	+	+++	+	-	-	+++	-
11384 ++	+++	-	-	-	-	-	-	-	-
11865 ++	++	-	-	-	+	-	-	-	-
36770 ++	-	--+	+	+++	-	-	-	-	-
36932 ++	+++	–	+	+	+	++	--	-	-
36866 ++	+	-	-	-	-	-	-	-	-
37029 ++	+	-	-	-	-	-	-	-	-
36971 ++	++	-	+	-	-	-	-	-	-
36837 ++	-	--	+	+++	+	-	–	-	-
36841 ++	+++	-	-	-	-	-	-	-	-
36659 ++	+++	--+	+++	+++	+++	-	–	-	-
11265 ++	++	-	-	-	+	-	-	-	-
37030 ++	+	-	-	-	-	-	-	-	-
36866 ++	+	-	-	-	-	-	-	-	-
11262 ++	-	-	-	-	-	-	-	-	-
11230 ++	++	-	-	-	-	-	-	-	-
36860 ++	+++	-	-	-	-	-	-	-	-
36793 ++	+++	-	-	-	-	-	-	-	-
18996 ++	-	-	-	-	+	-	–	-	-
37031 ++	++	-	-	-	-	-	-	-	-
37032 ++	++	--+	+++	+++	+++	-	–	-	-
36997 ++	-	-	-	-	-	-	-	-	-
17081 ++	+	–	+	+	+	+	–	-	-
37033 ++	+++	-	-	-	-	-	-	-	-
13991 ++	+++	-	-	-	-	-	-	-	-
37034 ++	+++	-	-	-	-	-	-	-	-
37035 ++	+++	-	-	-	-	-	-	-	-
37036 ++	-	--+	+	+++	+	-	-	-	-
37019 ++	+	-	-	-	-	-	-	-	-
17036 ++	-	--+	+	+++	+	-	-	-	-

36757 ++	-	-	-	-	-	-	-	-	-
36941 ++	-	-	-	-	-	-	-	-	-
37037 ++	-	–	+	+++	-	+	-	-	-
19288 ++	+	-	-	-	-	-	-	-	-
37038 ++	-	–+	++	+++	+	+	-	-	-
37039 ++	-	-	-	-	-	-	-	-	-
13557 ++	+++	-	-	-	-	-	-	-	-
16597 ++	+++	-	+	-	+	-	-	-	-
14259 ++	+++	-	-	-	-	-	-	-	-
17714 ++	-	–+	+	+++	-	-	-	+++	-
14229 ++	+++	-	+	-	-	-	-	-	-
36709 ++	+++	-	-	-	-	-	-	-	-
36878 ++	+	–+	+++	+++	+++	+++	–	+++	+++
37040 ++	++	-	-	-	-	-	-	-	-
36833 ++	+++	–	+	-	-	-	-	-	-
36862 ++	-	–+	+	+++	+	-	-	-	-
14066 ++	+++	-	-	-	+	-	-	-	-
11408 ++	-	-	-	-	-	-	-	-	-
37041 ++	-	-	-	-	-	-	-	-	-
37042 ++	++	-	-	-	-	-	-	-	-
36740 ++	+++	-	-	-	-	-	-	-	-
37043 ++	+++	-	-	-	-	-	-	-	-
37044 ++	+	-	-	-	-	-	-	-	-
37018 ++	-	–+	++	+++	+	+	–	+++	-
37045 ++	+	-	-	-	-	-	-	-	-
37046 ++	+++	-	-	+	+	-	-	-	-
37047 ++	+	–+	++	+++	++	++	-	+++	-
37048 ++	-	–	+	++	+	-	-	-	-
37049 ++	-	–+	+	+++	+	-	-	-	-
37010 ++	-	–+	+	-	-	-	-	-	-
37050 ++	+	-	-	+	-	+	–	-	-
36746 ++	++	-	-	-	-	-	-	-	-
13983 ++	++	-	-	-	-	-	-	-	-

37037	++	-	–	-	+++	+	-	–	-	-
37051	++	+	-	+	-	-	+	–	-	-
17725	++	++	-	-	-	-	-	-	-	-
37052	++	++	-	-	-	-	-	-	-	-
37053	++	-	-	-	-	-	-	-	-	-
36485	++	+++	-	+	-	+	+	–	-	-
36825	++	+++	-	-	-	+	+	–	-	-
10995	++	++	-	-	-	-	-	-	-	-
37054	++	+	–	+	++	++	+++	–––	+++	+++
11720	++	-	-	-	-	-	-	-	-	-
36825	++	+++	-	-	-	-	+	–	-	-
13806	++	+++	-	-	-	-	-	-	-	-
36887	++	+	-	-	-	-	-	-	-	-
37055	++	++	-	+	-	-	+	–	-	-
12333	++	+	-	-	-	-	-	-	-	-
12030	++	-	-	-	-	-	-	-	-	-
18191	++	+++	-	-	-	-	-	-	-	-
16113	++	-	-	-	-	-	-	-	-	-
36791	++	+++	-	-	-	-	-	-	-	-
36899	++	-	-	-	-	-	-	-	-	-
17890	++	+	-	-	-	-	-	-	-	-
37056	++	+++	-	-	-	-	-	-	-	-
17637	++	+	––	+	-	-	-	-	-	-
16045	++	+++	-	-	-	-	-	-	-	-
37057	++	-	-	-	-	-	-	-	-	-
36713	++	+++	-	-	-	-	-	-	-	-
18358	++	-	-	-	-	-	-	-	-	-
36826	++	+++	-	-	-	-	-	-	-	-
36872	++	+++	-	-	-	-	-	-	-	-
36991	++	+++	-	-	-	-	-	-	-	-
37058	++	++	-	-	-	-	-	-	-	-
12379	++	+++	-	-	-	-	-	-	-	-
11542	++	+++	-	-	-	-	-	-	-	-

36957 ++	++	-	-	-	-	-	-	-	-
37059 ++	++	-	-	-	-	-	-	-	-
36562 ++	++	-	-	-	-	-	–	-	-
37060 ++	++	-	+	-	+	-	-	-	-
13780 ++	+++	-	-	-	-	-	-	-	-
36792 ++	-	-	-	-	-	-	-	-	-
36376 ++	+	-	-	-	-	-	-	-	-
11915 ++	-	-	-	-	-	-	-	-	-
36398 ++	+++	-	-	-	-	-	–	-	-
37061 ++	++	-	-	-	-	-	-	-	-
12038 ++	+	-	-	-	-	-	-	-	-
36796 ++	+++	-	-	-	-	-	-	-	-
37062 ++	++	–	+	+	+	+	–	-	-
37063 ++	+++	-	+	+	+	+	-	-	-
36947 ++	++	-	-	-	-	-	-	-	-
11995 ++	+++	-	-	-	-	-	-	-	-
16121 ++	+++	-	-	-	-	-	-	-	-
37064 ++	+++	-	-	-	-	-	-	-	-
14224 ++	++	-	-	-	+	-	-	-	-
12037 ++	+	-	-	-	-	-	-	-	-
37065 ++	-	––	-	-	-	-	-	-	-
36324 ++	+	–	+	+	+	+++	–––	-	-
37066 ++	+++	-	-	+	+	+	–	-	-
37067 ++	-	-	-	-	-	-	-	-	-
37068 ++	+++	-	-	-	-	-	-	-	-
37069 ++	++	-	+	+	+	+	-	-	-
36901 ++	+++	-	-	-	-	-	-	-	-
37070 ++	+	-	-	-	-	-	-	-	-
16582 ++	+++	-	-	-	-	-	-	-	-
18079 ++	++	-	-	-	-	-	-	-	-
37071 ++	-	––+	+++	+++	+++	-	––	-	-
36822 ++	+	-	-	-	-	+	–	-	-
17873 ++	++	-	-	-	-	-	-	-	-

37072 ++	-	--	+	+++	+	-	-	-	-
37073 ++	+	--+	+++	+++	++	++	--	-	-
37074 ++	-	-	-	+	+	-	-	-	-
37075 ++	+++	-	-	-	-	-	-	-	-
36810 ++	+++	-	-	-	-	-	-	-	-
18663 ++	+++	-	-	-	-	-	-	-	-
11227 ++	++	-	-	-	-	-	-	-	-
37076 ++	+	-	-	-	-	-	-	-	-
37044 ++	+	-	-	-	-	-	-	-	-
37077 ++	+++	-	-	-	-	-	-	-	-
17593 ++	++	-	-	-	-	-	-	-	-
11865 ++	+++	-	-	-	-	-	-	-	-
37078 ++	++	-	+	-	-	-	-	-	-
37079 ++	++	-	-	-	-	-	-	-	-
15996 ++	+++	-	-	-	-	-	-	-	-
37080 ++	++	-	-	-	-	-	-	-	-
36885 ++	+	-	-	-	-	-	-	-	-
11557 ++	+++	-	-	-	-	-	-	-	-
36864 ++	+++	-	-	-	-	-	-	-	-
37081 ++	++	-	-	-	+	+	-	-	-
11486 ++	++	-	-	-	-	-	-	-	-
36850 ++	-	-	-	-	-	-	-	-	-
37082 ++	+++	-	-	+	+	-	-	-	-
36586 ++	-	--+	+	+++	+	-	-	+++	-
37038 ++	-	--+	+	+++	+	+	–	-	-
11717 ++	-	-	-	-	-	-	-	-	-
12482 ++	++	-	-	-	-	-	-	-	-
37083 ++	+++	-	-	-	-	-	-	-	-
37084 ++	-	--	-	-	-	-	-	-	-
16014 ++	+++	-	-	-	-	-	-	-	-
36789 ++	+++	-	-	-	-	-	-	-	-
37085 ++	++	-	-	-	-	+	-	-	-
37075 ++	+++	-	-	-	-	-	-	-	-

37086 ++	-	-	-	-	-	-	-	-	-
37087 ++	-	--+	+	+++	+	+	-	-	-
36811 ++	-	-	-	-	-	-	-	-	-
36319 ++	+++	-	-	-	-	-	-	-	-
14452 ++	+++	-	-	-	-	-	-	-	-
36774 ++	-	--+	-	+	-	+	-	-	-
37088 ++	++	-	-	-	-	-	-	-	-
37089 ++	++	-	-	-	-	-	-	-	-
36840 ++	+++	–	+	+	+	-	-	++	-
11203 ++	+++	-	-	-	-	-	-	-	-
11668 ++	++	-	-	-	-	+	–	-	-
37090 ++	++	-	-	-	-	-	-	-	-
37091 ++	+++	-	+	+	+	-	-	-	-
37092 ++	++	-	-	-	-	-	-	-	-
37093 ++	+++	-	-	-	-	-	-	-	-
37094 ++	-	-	-	-	-	-	-	-	-
37095 ++	+	-	-	-	-	-	-	-	-
13788 ++	+++	-	-	-	-	-	-	-	-
11315 ++	++	-	-	-	-	-	-	-	-
36812 ++	-	-	-	+++	+	-	-	-	-
15977 ++	+++	-	-	-	-	-	-	-	-
37096 ++	++	-	-	-	-	-	-	-	-
36689 ++	+	–	+	+	+	-	–	-	-
36954 ++	+++	-	-	-	-	-	-	-	-
37097 ++	-	–	-	-	-	-	-	-	-
15973 ++	+++	-	-	-	+	-	-	-	-
37098 ++	+++	-	-	-	-	-	-	-	-
36775 ++	-	--	-	++	+	+	-	-	-
37031 ++	++	-	-	-	-	-	-	-	-
36823 ++	+++	-	-	-	-	-	-	-	-
36839 ++	++	-	-	-	-	-	-	-	-
37099 ++	-	--+	+++	+++	+++	-	-	-	-
37078 ++	++	-	+	-	-	-	-	-	-

11542 ++	+++	-	-	-	-	-	-	-	-
37100 ++	+++	-	-	-	-	-	-	-	-
37101 ++	+++	-	-	-	-	-	-	-	-
37102 ++	++	-	-	-	+	-	-	-	-
37103 ++	++	--+	+++	+++	+++	+	-	-	-
13981 ++	+++	-	-	-	-	-	-	-	-
37104 ++	++	-	-	-	-	+	-	-	-
36988 ++	+++	-	-	-	-	-	-	-	-
36632 ++	-	-	-	-	-	-	-	-	-
37097 ++	-	-	-	-	-	-	-	-	-
36906 ++	+	--+	++	+++	++	++	--	+++	-
37105 ++	+++	-	+	+	-	+	-	-	-
37106 ++	+	-	-	-	-	-	-	-	-
37107 ++	-	-	+	-	-	+	-	-	-
37108 ++	-	--+	+	+++	+	-	-	+++	-
36971 ++	++	-	-	-	-	-	-	-	-
11667 ++	++	-	-	-	-	-	-	-	-
17065 ++	+	--+	+++	+++	++	++	--	+++	-
17558 ++	++	-	-	-	-	-	-	-	-
37109 ++	-	-	-	-	-	-	-	-	-
36570 ++	+++	-	-	-	-	-	-	-	-
37110 ++	+	-	+	+	+	+	-	-	-
37111 ++	+++	-	-	-	-	-	-	-	-
37112 ++	++	-	+	-	-	-	-	-	-
37113 ++	-	--+	+	-	-	-	-	+++	-
11348 ++	+++	-	-	-	-	-	-	-	-
37114 ++	+	--+	+	+	-	+	-	-	-
37115 ++	+++	-	-	-	-	-	-	-	-
37041 ++	-	-	-	-	-	-	-	-	-
36907 ++	+++	-	-	-	-	-	-	-	-
13576 ++	++	-	-	-	+	-	-	-	-
15480 ++	++	-	+	+	-	++	--	-	-
36679 ++	+++	-	+	+	-	+	-	-	-

37116 ++	+	-	-	-	-	-	-	-	-
11945 ++	++	-	-	-	-	-	-	-	-
36901 ++	+++	-	-	-	-	-	-	-	-
37117 ++	++	-	-	-	-	-	-	-	-
36428 ++	+	-	-	-	-	-	-	-	-
18591 ++	+++	-	-	-	+	-	-	-	-
37118 ++	+	-	-	-	-	-	-	-	-
36740 ++	+++	-	-	-	-	-	-	-	-
37119 ++	+	-	-	-	-	-	-	-	-
19485 ++	+++	-	-	-	-	-	-	-	-
37120 ++	-	--+	++	+++	+++	+++	---	-	-
37029 ++	+	-	-	-	-	-	-	-	-
11315 ++	+++	-	-	-	-	-	-	-	-
11451 ++	-	-	-	-	-	-	-	-	-
14094 ++	+++	-	-	-	-	-	-	-	-
11924 ++	-	-	-	-	-	-	-	-	-
36872 ++	+++	-	-	-	-	-	-	-	-
18074 ++	-	-	-	-	-	+	-	-	-
37121 ++	++	-	-	-	-	-	-	-	-
37122 ++	++	-	-	-	-	-	-	-	-
13651 ++	+++	-	+	+	+	-	-	-	-
36769 ++	+++	-	-	-	-	-	-	-	-
37123 ++	++	--+	+++	+++	+++	-	-	-	-
11408 ++	-	-	-	-	-	-	-	-	-
36446 ++	-	--+	+	+	-	+	-	-	-
36935 ++	+++	-	-	-	-	-	-	-	-
36988 ++	+++	-	-	-	-	-	-	-	-
37124 ++	+++	-	-	-	-	-	-	-	-
12426 ++	++	-	-	-	-	-	-	-	-
11418 ++	++	-	-	-	-	-	-	-	-
37125 ++	-	--+	+	++	-	-	-	-	-
37126 ++	++	-	-	-	-	-	-	-	-
36977 ++	+	-	-	-	-	-	-	-	-

37066 ++	+++	-	-	+	-	-	-	-	-
37105 ++	++	-	+	-	-	-	–	-	-
36778 ++	++	–	+	+	+	-	-	-	-
37127 ++	+	-	-	-	-	-	–	-	-
12206 ++	+	-	-	-	-	-	-	-	-
14304 ++	+++	-	-	-	-	-	-	-	-
37128 ++	++	-	-	-	-	-	–	-	-
37129 ++	++	-	-	-	-	-	-	-	-
16087 ++	++	-	-	-	-	-	-	-	-
36968 ++	+++	-	-	-	-	-	-	-	-
36989 ++	++	-	-	-	-	-	-	-	-
37017 ++	++	-	-	-	-	-	-	-	-
37011 ++	+	-	-	-	-	-	-	-	-
37130 ++	-	-	-	-	-	-	-	-	-
37005 ++	++	-	-	-	-	-	-	-	-
37079 ++	++	-	-	-	-	-	-	-	-
37131 ++	-	–	+	-	+	-	-	-	-
37132 ++	+++	–	+	+	+	-	-	-	-
37133 ++	++	-	-	-	-	-	-	-	-
11543 ++	++	-	-	-	-	-	-	-	-
37134 ++	+++	–+	+++	+++	+++	-	-	-	-
37135 ++	+++	-	-	-	-	-	-	-	-
37136 ++	+	-	-	-	-	-	-	-	-
37137 ++	-	–+	-	-	-	-	-	-	-
12294 ++	-	-	-	-	-	-	-	-	-
13904 ++	+++	-	-	-	-	-	-	-	-
37138 ++	-	-	-	-	-	-	-	-	-
36995 ++	+++	-	-	-	-	-	-	-	-
37139 ++	-	–+	+	++	-	+	-	-	-
36846 ++	+++	-	-	-	-	-	-	-	-
37140 ++	+++	-	-	-	-	-	-	-	-
37003 ++	+	-	+	+	+	-	-	-	-
37141 ++	-	–+	+	+++	+	-	-	+++	++

37142 ++	+	-	-	-	-	-	-	-	-
37143 ++	-	--+	+	+	-	-	-	-	-
11878 ++	-	-	-	-	-	-	-	-	-
12113 ++	-	-	-	-	-	-	-	-	-
37030 ++	+	-	-	-	-	-	-	-	-
37144 ++	+++	-	-	-	-	-	-	-	-
37132 ++	+++	–	+	+	+	-	-	-	-
13526 ++	+++	-	-	-	-	-	-	-	-
37145 ++	-	--	-	-	-	-	-	-	-
14552 ++	+++	-	-	-	-	-	-	-	-
37146 ++	++	-	-	-	-	+	-	-	-
37147 ++	++	-	-	-	-	-	-	-	-
11296 ++	+++	-	-	-	-	-	-	-	-
37148 ++	-	--+	+	+++	+	-	-	+++	-
37149 ++	+++	--+	+++	+++	+++	+	–	-	-
13983 ++	++	-	-	-	-	-	-	-	-
14416 ++	++	-	-	-	+	-	-	-	-
36762 ++	-	--+	+	++	-	-	-	+++	++
37091 ++	+++	-	-	+	+	-	-	-	-
19755 ++	-	--+	+	-	-	-	-	-	-
37060 ++	++	-	-	+	-	-	-	-	-
11398 ++	+++	-	-	-	-	-	-	-	-
14035 ++	++	-	-	-	-	-	-	-	-
16217 ++	+++	-	-	-	-	-	-	-	-
11189 ++	+++	-	-	-	-	-	-	-	-
37012 ++	+++	-	-	-	+	-	–	-	-
37150 ++	++	-	-	-	-	-	-	-	-
36988 ++	+++	-	-	-	-	-	-	-	-
37151 ++	++	-	-	-	+	-	-	-	-
37152 ++	+	-	-	-	-	-	-	-	-
36875 ++	+++	-	-	-	+	-	-	-	-
37117 ++	+++	-	-	-	-	-	-	-	-
37076 ++	+	-	-	-	-	-	-	-	-

37153 ++	-	--+	+	+++	+	-	-	+++	-
11338 ++	-	-	-	-	-	-	-	-	-
17081 ++	+	–	+	+	+	+	–	-	-
37154 ++	+	-	-	-	-	-	-	-	-
37155 ++	+++	–	+	+	+	-	–	-	-
11516 ++	-	-	-	-	-	-	-	-	-
37156 ++	-	-	-	-	-	-	-	-	-
13752 ++	++	-	-	-	-	-	-	-	-
36606 ++	-	-	-	-	-	-	-	-	-
37100 ++	+++	-	-	-	-	-	-	-	-
37065 ++	-	--	-	-	-	-	-	-	-
14452 ++	++	-	-	-	-	-	-	-	-
36400 ++	+++	-	-	-	-	-	-	-	-
17493 ++	-	--+	+	+++	-	-	-	-	-
16025 ++	+++	-	-	-	-	-	-	-	-
37157 ++	++	-	-	-	-	-	-	-	-
36880 ++	+++	-	-	+	+	-	-	-	-
37158 ++	++	--+	+++	+++	+++	+	–	-	-
18112 ++	-	-	-	-	-	-	-	-	-
37159 ++	++	-	-	-	-	-	-	-	-
17890 ++	+	-	-	-	-	-	-	-	-
37160 ++	+	-	-	-	-	-	-	-	-
36947 ++	++	-	-	-	-	-	-	-	-
37161 ++	-	--+	+	+++	+	+	-	++	-
36663 ++	+	–	+	+	+	+	-	-	-
36955 ++	+++	-	-	+	-	-	-	-	-
17687 ++	+	-	-	-	-	-	-	-	-
36979 ++	+++	-	-	-	-	+	-	-	-
36985 ++	+++	–	+	+	-	+	–	-	-
37162 ++	+++	-	-	+	+	-	-	-	-
37030 ++	+	-	-	-	-	-	-	-	-
36865 ++	-	-	-	-	-	-	-	-	-
37102 ++	+++	-	-	-	+	-	–	-	-

37163 ++	+++	-	-	-	-	-	-	-	-
37084 ++	-	--	-	-	-	-	-	-	-
37164 ++	-	--+	-	+	-	-	-	-	-
37015 ++	+	-	-	-	-	-	-	-	-
36734 ++	+	--+	++	+++	++	+	-	+++	-
37165 ++	+++	-	-	-	-	-	-	-	-
37166 ++	-	-	-	-	-	-	-	-	-
36515 ++	+++	-	-	-	-	-	-	-	-
37167 ++	-	--	-	-	-	+	-	-	-
11077 ++	+++	-	-	-	-	-	-	-	-
37168 ++	++	-	-	-	-	-	-	-	-
11238 ++	+++	-	-	-	-	-	-	-	-
18036 ++	+++	-	-	-	-	-	-	-	-
12426 ++	++	-	-	-	-	-	-	-	-
16004 ++	-	-	-	-	-	-	-	-	-
37169 ++	+++	-	-	-	-	-	-	-	-
11276 ++	+++	-	-	-	-	-	-	-	-
37170 ++	++	-	-	-	-	-	-	-	-
11115 ++	+++	-	-	-	-	-	-	-	-
11113 ++	++	-	-	-	-	-	-	-	-
14259 ++	+++	-	-	-	-	-	-	-	-
36960 ++	+	--+	+++	+++	+++	+++	---	+++	+++
37171 ++	+	-	+	+	+	+	–	-	-
16033 ++	++	-	-	-	-	-	-	-	-
11407 ++	++	-	-	-	-	-	-	-	-
11288 ++	-	-	-	-	-	-	-	-	-
36869 ++	+	--+	++	+++	+++	+++	–	-	-
37172 ++	++	-	-	-	-	-	-	-	-
37029 ++	+	-	-	-	-	-	-	-	-
11749 ++	++	-	-	-	-	-	-	-	-
37173 ++	-	-	-	-	-	-	-	-	-
36803 ++	-	-	-	-	-	-	-	-	-
36733 ++	+	-	-	+	-	+	–	-	-

12517 ++	+++	-	-	-	-	-	-	-	-
37174 ++	+++	–	+	+	+	+	–	-	-
36696 ++	-	–+	+	+++	+	-	-	+++	-
17593 ++	+++	-	-	-	-	-	-	-	-
36982 ++	++	-	-	-	-	-	-	-	-
37175 ++	+	–+	+++	+++	+++	-	-	-	-
37118 ++	+	-	-	-	-	-	-	-	-
11640 ++	++	-	-	-	-	-	-	-	-
36987 ++	++	-	-	-	-	-	-	-	-
13526 ++	+++	-	-	-	-	-	-	-	-
18358 ++	-	-	-	-	-	-	-	-	-
37140 ++	++	-	-	-	-	-	-	-	-
11860 ++	+++	-	-	-	-	-	-	-	-
37176 ++	+++	-	-	-	-	-	-	-	-
37177 ++	-	–+	+	+	-	-	-	-	-
36817 ++	+	–	++	+	+	+++	---	+++	+++
14200 ++	+++	-	-	-	-	-	-	-	-
37045 ++	+	-	-	-	-	-	-	-	-
16112 ++	+	-	-	-	-	-	-	-	-
37178 ++	-	–+	++	+++	+	+	–	-	-
37154 ++	+	-	-	-	-	-	-	-	-
11528 ++	+++	-	-	-	-	-	-	-	-
37179 ++	++	–+	+++	+++	+++	+	–	-	-
11543 ++	++	-	-	-	-	-	-	-	-
17558 ++	++	-	-	-	-	-	-	-	-
37023 ++	+++	-	-	-	-	-	-	-	-
13629 ++	+++	–	+	+	++	++	--	+++	+++
37180 ++	++	-	-	-	-	-	-	-	-
37181 ++	+++	-	-	-	-	-	-	-	-
36541 ++	++	-	-	-	-	-	-	-	-
37177 ++	-	–+	+	+	-	-	-	-	-
17535 ++	-	–+	+	+++	-	-	-	+++	-
37101 ++	++	-	-	-	-	-	-	-	-

36866 ++	+	-	-	-	-	+	-	-	-
17883 ++	++	-	-	-	-	-	-	-	-
13576 ++	++	-	-	-	-	-	-	-	-
14291 ++	+++	-	-	-	-	-	-	-	-
15967 ++	-	–	+	-	+	-	-	-	-
14392 ++	-	-	-	-	-	-	-	-	-
37182 ++	+++	-	-	-	-	-	-	-	++
37108 ++	-	–+	+	+++	-	-	-	+++	-
37079 ++	++	-	-	-	-	-	-	-	-
37183 ++	-	–+	+	+++	+	+	-	+++	+++
13614 ++	-	-	+	+	+	+	-	-	-
11306 ++	++	-	-	-	-	-	-	-	-
37068 ++	++	-	-	-	-	-	-	-	-
37184 ++	-	–+	+	++	-	-	-	+++	-
36628 ++	-	-	-	-	-	-	-	-	-
11866 ++	-	-	-	-	-	-	-	-	-
37185 ++	-	-	+	-	+	-	-	-	-
37186 ++	+	-	-	-	-	-	–	-	-
37187 ++	++	-	-	-	+	-	-	-	-
37188 ++	+++	-	-	-	-	-	-	-	-
16580 ++	+++	-	+	-	+	-	-	-	-
16612 ++	+++	-	-	-	+	-	-	-	-
36662 ++	+++	–	+	++	++	-	-	-	-
19988 ++	+	-	-	-	-	-	-	-	-
37083 ++	++	-	-	-	-	-	-	-	-
15967 ++	-	–	+	+	+	-	-	-	-
16045 ++	+++	-	-	-	-	-	-	-	-
36897 ++	-	-	-	-	-	-	-	-	-
36975 ++	+++	–	+	+	+	+	–	-	-
37189 ++	-	-	+	-	-	-	-	-	-
37190 ++	++	-	-	-	-	-	-	-	-
36982 ++	++	-	-	-	-	-	-	-	-
12481 ++	-	-	-	-	-	-	-	-	-

36612 ++	+	-	-	-	-	-	-	-	-
37191 ++	++	–	+	++	++	-	-	-	-
37013 ++	-	-	-	-	-	-	-	-	-
11866 ++	-	-	-	-	-	-	-	-	-
36986 ++	+++	-	-	-	-	-	-	-	-
16121 ++	+++	-	-	-	-	-	-	-	-
37192 ++	-	-	-	-	-	-	-	-	-
37193 ++	+++	-	-	-	-	-	-	-	-
37039 ++	-	-	-	-	-	-	-	-	-
37194 ++	+	-	-	+	-	-	-	-	-
36668 ++	-	–+	+	+++	+	-	-	+++	-
37195 ++	++	–+	+++	+++	+++	-	-	-	-
11572 ++	++	-	-	-	-	-	-	-	-
18056 ++	++	-	-	-	-	-	-	-	-
37100 ++	+++	-	-	-	-	-	-	-	-
37156 ++	+	-	-	-	-	-	-	-	-
36854 ++	+++	-	-	-	-	-	-	-	-
37196 ++	-	-	-	-	-	-	-	-	-
37197 ++	+	-	-	-	-	-	-	-	-
11189 ++	++	-	-	-	-	-	-	-	-
36722 ++	-	–	-	++	-	+	-	-	-
12113 ++	-	-	-	-	-	-	-	-	-
36736 ++	+++	-	-	+	+	-	-	-	-
16566 ++	+++	-	-	-	-	-	-	-	-
36507 ++	-	–+	+	+++	+	-	-	+++	-
17937 ++	+++	-	-	-	-	-	-	-	-
12481 ++	-	-	-	-	-	-	-	-	-
37198 ++	+++	-	-	-	-	-	-	-	-
37117 ++	+++	-	-	-	-	-	-	-	-
11840 ++	-	-	-	-	-	-	-	-	-
11338 ++	+	-	-	-	-	-	-	-	-
37199 ++	-	–+	-	-	-	-	-	-	-
37180 ++	++	-	-	-	-	-	-	-	-

16038 ++	+++	-	-	-	-	-	-	-	-
37200 ++	+++	-	-	-	-	-	-	-	-
37201 ++	+	-	-	-	-	-	-	-	-
37202 ++	+	-	-	-	-	-	-	-	-
14081 ++	++	-	-	-	-	-	-	-	-
17725 ++	++	-	-	-	-	-	-	-	-
37203 ++	+	-	-	-	-	-	-	-	-
37089 ++	+++	-	+	-	-	-	-	-	-
37098 ++	+++	-	-	-	-	-	-	-	-
36904 ++	+++	-	-	-	-	-	-	-	-
37204 ++	++	-	-	-	-	-	-	-	-
36644 ++	+++	-	-	-	-	-	-	-	-
37205 ++	+++	--+	+++	+++	+++	+	-	+++	-
11549 ++	+++	-	-	-	-	-	-	-	-
37206 ++	-	-	-	-	-	-	-	-	-
37207 ++	-	-	-	++	-	-	-	-	-
37208 ++	+	-	-	-	-	-	-	-	-
14290 ++	+++	-	-	-	-	-	-	-	-
37209 ++	+++	-	+	++	++	-	-	-	-
37210 ++	+++	-	+	++	+	+++	---	-	-
17637 ++	+	--	+	-	-	+	-	-	-
36787 ++	-	-	-	-	-	-	-	-	-
37211 ++	+++	-	-	-	-	-	-	-	-
37212 ++	+	-	-	-	-	-	-	-	-
13833 ++	++	-	-	-	-	-	-	-	-
36907 ++	+++	-	-	-	-	-	-	-	-
37187 ++	++	-	-	-	-	-	-	-	-
37213 ++	++	-	-	-	-	-	-	-	-
16593 ++	-	--+	++	+++	++	++	-	-	-
17809 ++	-	-	-	-	-	-	-	-	-
37214 ++	+	-	-	-	-	-	-	-	-
14200 ++	+++	-	+	-	+	-	-	-	-
37215 ++	+++	-	-	-	-	-	-	-	-

37216 ++	++	-	-	+	+	-	–	-	-
18385 ++	-	-	-	-	-	-	-	-	-
37217 ++	+	–	+	+	+	-	–	-	-
37218 ++	+	-	-	-	-	-	-	-	-
37219 ++	-	-	-	-	-	-	-	-	-
37202 ++	+	-	-	-	-	-	-	-	-
37220 ++	+++	-	-	-	-	-	-	-	-
37221 ++	+	–+	+	++	+	+++	–	+++	-
37222 ++	++	-	-	-	-	-	-	-	-
37223 ++	++	-	-	-	-	-	-	-	-
36963 ++	-	–+	+	+++	+	+	-	+++	-
37224 ++	-	–+	+	+	-	-	-	-	-
37225 ++	++	-	-	+	+	+	-	-	-
37226 ++	+	-	-	-	-	-	-	-	-
17416 ++	++	-	+	+	+	-	-	-	-
17874 ++	-	–+	+	+	-	-	–	-	-
11573 ++	++	-	-	-	-	-	-	-	-
37227 ++	++	-	+	-	-	-	-	-	-
37228 ++	+	-	-	-	-	+	-	-	-
37229 ++	++	-	-	-	-	-	-	-	-
37230 ++	-	–+	+	+++	+	-	-	-	-
37165 ++	+++	-	-	-	-	-	-	-	-
37084 ++	-	––	-	-	-	-	-	-	-
12055 ++	++	-	-	-	-	-	-	-	-
36952 ++	+++	-	-	-	-	-	-	-	-
17605 ++	-	-	-	-	-	-	-	-	-
37231 ++	+++	-	-	-	-	-	-	-	-
11549 ++	++	-	-	-	-	-	-	-	-
37232 ++	-	–+	+++	+++	+++	-	-	-	-
37233 ++	+	-	-	-	-	-	-	-	-
37234 ++	++	-	-	-	-	-	-	-	-
11661 ++	++	-	-	-	-	-	-	-	-
37208 ++	+	-	-	-	-	-	-	-	-

37190 ++	+++	-	-	-	-	-	-	-	-
17411 ++	++	-	+	+	+	-	-	-	-
37235 ++	+++	-	-	-	-	-	-	-	-
37236 ++	++	-	-	-	-	-	-	-	-
37008 ++	++	-	-	-	-	-	-	-	-
37237 ++	++	-	-	-	-	-	-	-	-
37238 ++	+	-	-	-	-	-	-	-	-
37239 ++	+++	-	-	-	-	-	-	-	-
37185 ++	-	–	+	+	+	-	–	-	-
37240 ++	+++	-	-	-	-	-	-	-	-
37082 ++	+++	-	-	-	+	-	-	-	-
37241 ++	+++	-	-	-	-	-	-	-	-
37242 ++	+	-	-	-	-	-	-	-	-
37243 ++	-	-	-	-	-	-	-	-	-
36832 ++	-	––+	-	-	-	-	-	-	-
36352 ++	++	-	-	-	-	-	-	-	-
16592 ++	+	–	+	+	+	-	-	++	-
37244 ++	++	-	-	-	-	-	-	-	-
36872 ++	+++	-	-	-	-	-	-	-	-
14097 ++	+++	-	-	-	+	-	-	-	-
37197 ++	+	-	-	-	-	-	-	-	-
12426 ++	+++	-	-	-	-	-	-	-	-
18225 ++	-	–	-	+	-	-	-	-	-
13657 ++	++	-	-	-	-	-	-	-	-
37245 ++	+++	-	-	-	-	-	-	-	-
37246 ++	+++	-	-	-	+	-	-	-	-
37204 ++	+++	-	-	-	-	-	-	-	-
37201 ++	+	-	-	-	-	-	-	-	-
37247 ++	-	-	-	-	-	-	-	-	-
36949 ++	+++	-	-	-	-	+	-	-	-
36942 ++	++	-	-	-	-	-	-	-	-
37248 ++	++	-	-	-	-	-	-	-	-
11188 ++	++	-	-	-	-	-	-	-	-

37249 ++	++	-	-	-	-	-	-	-	-
37025 ++	++	-	-	-	-	-	-	-	-
37100 ++	+++	-	-	-	-	-	-	-	-
37103 ++	++	--+	+++	+++	+++	-	-	-	-
36475 ++	+++	-	-	-	-	-	–	-	-
37007 ++	++	-	-	-	-	-	-	-	-
37250 ++	+++	--+	+++	+++	+++	+	–	-	-
37080 ++	++	-	-	-	-	-	-	-	-
36482 ++	+++	-	+	+	+	-	-	-	-
37197 ++	+	-	-	-	-	-	-	-	-
14004 ++	++	-	-	-	-	-	-	-	-
37251 ++	+	-	-	+	-	-	-	-	-
11765 ++	-	-	-	-	-	-	-	-	-
37252 ++	+++	-	+	+	+	+	–	-	-
37135 ++	+++	-	-	-	-	-	-	-	-
37184 ++	-	--+	++	++	-	-	-	-	-
17826 ++	-	--+	+	+++	+	-	-	-	-
36901 ++	+++	-	-	-	-	-	-	-	-
36698 ++	-	--+	+	+++	-	-	-	-	-
17704 ++	-	-	-	-	-	-	-	-	-
37016 ++	+++	--+	+++	+++	+++	+	–	-	-
14269 ++	++	-	-	-	-	-	-	-	-
36957 ++	++	-	-	-	-	-	-	-	-
18036 ++	++	-	-	-	-	-	-	-	-
36743 ++	-	--+	+	+	+	-	-	-	-
11079 ++	++	-	-	-	-	-	-	-	-
37253 ++	++	-	-	-	-	-	-	-	-
37235 ++	++	-	-	-	-	-	-	-	-
37254 ++	-	-	-	-	-	-	-	-	-
11891 ++	++	-	-	-	-	-	-	-	-
17048 ++	-	-	-	-	-	-	-	-	-
37255 ++	+++	-	-	+	+	-	-	-	-
37256 ++	++	-	+	+	+	-	-	-	-

37165 ++	+++	-	-	-	-	-	-	-	-
15945 ++	++	-	-	-	-	-	-	-	-
36671 ++	++	-	-	-	-	-	-	-	-
18116 ++	++	-	-	-	+	-	-	-	-
36716 ++	-	--+	+	+++	+	+	-	+++	-
14269 ++	++	-	-	-	-	-	-	-	-
36867 ++	+++	-	-	-	-	-	-	-	-
37245 ++	+++	-	-	-	-	-	-	-	-
11355 ++	++	-	-	-	-	-	-	-	-
37257 ++	+++	-	+	+++	+++	-	-	-	-
11265 ++	+++	-	-	-	-	-	-	-	-
36917 ++	-	--+	+	+++	+	-	-	-	-
37258 ++	++	-	-	-	-	-	-	-	-
37259 ++	-	-	+	-	-	-	-	-	-
37260 ++	-	-	-	-	-	-	-	-	-
36921 ++	+++	-	-	-	-	-	-	-	-
36766 ++	++	-	-	-	-	-	-	-	-
37261 ++	+++	-	-	-	-	-	-	-	-
11707 ++	+	-	-	-	-	-	-	-	-
37262 ++	-	-	-	-	-	-	-	-	-
11065 ++	+++	-	-	-	-	-	-	-	-
11212 ++	++	-	-	-	-	-	-	-	-
11920 ++	-	-	-	-	-	-	-	-	-
11106 ++	-	-	-	-	-	-	-	-	-
36870 ++	-	--	+	-	-	+	-	-	-
37263 ++	+++	-	+	++	++	-	-	-	-
37264 ++	++	--+	+++	+++	+++	-	-	-	-
12006 ++	+++	-	-	-	-	-	-	-	-
36922 ++	+	-	-	-	-	-	-	-	-
37265 ++	+++	-	-	-	-	-	-	-	-
37063 ++	++	-	-	-	+	+	-	-	-
37159 ++	++	-	-	-	-	-	-	-	-
11221 ++	+++	-	-	-	-	-	-	-	-

37266 ++	+	-	-	-	-	-	-	-	-
15947 ++	++	-	-	+	-	-	-	-	-
36782 ++	+	--+	++	+++	++	++	-	-	-
37267 ++	++	-	-	-	-	-	-	-	-
14085 ++	+++	-	-	-	+	-	-	-	-
11690 ++	-	-	-	-	-	-	-	-	-
13593 ++	+++	-	-	-	-	-	-	-	-
14600 ++	-	-	-	-	-	-	-	-	-
14026 ++	++	-	-	-	-	-	-	-	-
12109 ++	++	-	+	+	+	-	-	-	-
11423 ++	-	-	-	-	-	-	-	-	-
36752 ++	+++	-	-	-	-	-	-	-	-
11749 ++	++	-	-	-	-	-	-	-	-
37268 ++	-	-	-	-	-	-	-	-	-
36625 ++	-	-	-	-	-	-	-	-	-
37269 ++	++	-	-	-	-	-	-	-	-
37155 ++	+++	-	+	+	+	+	-	-	-
37176 ++	+++	-	-	-	-	-	-	-	-
19253 ++	+++	-	-	-	-	-	-	-	-
37087 ++	-	--+	+	+++	+	+	-	-	-
36809 ++	++	-	-	-	-	-	-	-	-
37244 ++	++	-	-	-	-	-	-	-	-
17515 ++	++	-	-	-	-	-	-	-	-
37270 ++	++	-	-	-	-	-	-	-	-
37271 ++	++	-	-	-	-	-	-	-	-
36700 ++	-	--+	+	+++	+	-	-	+++	-
17032 ++	+	--+	+++	+++	+++	++	-	+++	-
37046 ++	++	-	-	+	+	-	-	-	-
36861 ++	+++	-	+	+	+	+	-	-	-
37237 ++	++	-	-	-	-	-	-	-	-
37272 ++	-	--+	++	+++	+	-	-	+++	-
37273 ++	-	--+	+	-	-	-	-	-	-
37274 ++	++	-	-	-	-	-	-	-	-

37275 ++	++	-	-	-	-	-	-	-	-
16595 ++	+++	-	-	-	-	-	-	-	-
37276 ++	+++	-	-	-	-	-	-	-	-
37277 ++	++	-	+	+	+	-	–	-	-
37278 ++	-	–-+	+	+++	+	-	-	+++	-
18663 ++	++	-	-	-	-	-	-	-	-
13952 ++	++	-	-	-	-	-	-	-	-
17048 ++	-	-	-	-	-	-	-	-	-
37078 ++	++	–	+	-	+	-	-	-	-
37279 ++	++	-	-	-	-	-	-	-	-
36984 ++	+	-	-	-	-	-	-	-	-
36831 ++	+++	-	-	+	+	-	-	-	-
37280 ++	+	-	-	-	-	-	-	-	-
37116 ++	+	-	-	-	-	-	-	-	-
37281 ++	++	-	-	-	-	-	-	-	-
11350 ++	+++	-	-	-	-	-	-	-	-
37022 ++	-	–-+	+	+++	+	+	–	+++	-
36853 ++	-	–-+	-	-	-	-	-	-	-
37282 ++	-	-	-	-	-	-	-	-	-
36657 ++	+++	-	-	-	-	-	-	-	-
17576 ++	-	–-+	+	+++	+	-	–	-	-
37033 ++	+++	-	-	-	-	-	-	-	-
19688 ++	++	-	-	-	-	-	-	-	-
37167 ++	-	––	+	+	+	-	-	-	-
37283 ++	+	-	-	-	-	-	-	-	-
37284 ++	-	–-+	+	+	-	-	-	++	-
37285 ++	-	-	-	-	-	-	-	-	-
37286 ++	+++	–-+	+++	+++	+++	+	-	-	-
37161 ++	-	–-+	+	+++	-	+	-	+++	-
37287 ++	++	-	-	-	-	-	-	-	-
16127 ++	-	-	-	-	-	-	-	-	-
36995 ++	+++	-	-	-	-	-	-	-	-
14174 ++	+++	-	-	-	-	-	-	-	-

37288 ++	+	-	-	-	-	-	-	-	-
36616 ++	+++	-	-	-	-	-	–	-	-
11079 ++	++	-	-	-	-	-	-	-	-
15974 ++	+++	-	-	-	-	-	-	-	-
37289 ++	-	–-+	++	+++	+	+	-	-	-
37290 ++	-	–-+	+	-	+	-	-	-	-
36773 ++	-	-	-	-	-	-	-	-	-
37239 ++	+++	-	-	-	-	-	-	-	-
37291 ++	++	-	-	-	-	-	-	-	-
37292 ++	+++	-	-	-	-	-	–	-	-
36940 ++	+++	-	-	-	-	-	-	-	-
36968 ++	+++	-	-	-	-	-	-	-	-
11111 ++	+++	-	-	-	-	-	-	-	-
37202 ++	+	-	-	-	-	-	-	-	-
37293 ++	++	-	-	-	-	-	-	-	-
37294 ++	++	-	-	-	-	-	-	-	-
36881 ++	-	-	-	-	-	-	-	-	-
37295 ++	++	-	-	-	-	-	-	-	-
17416 ++	++	-	+	+	+	-	-	-	-
37296 ++	++	-	-	-	-	-	-	-	-
14392 ++	-	-	-	-	-	-	-	-	-
37297 ++	-	–-+	++	+++	+	+	-	+++	+++
16628 ++	+++	-	-	-	+	+	–	-	-
36547 ++	-	-	-	-	-	-	-	-	-
37223 ++	++	-	-	-	-	-	-	-	-
14181 ++	++	-	-	-	-	-	-	-	-
36780 ++	++	-	-	-	-	-	-	-	-
17878 ++	+++	-	-	-	-	-	-	-	-
12011 ++	++	-	-	-	-	-	-	-	-
37298 ++	+	–-+	+	+++	+	+++	---	-	+++
37299 ++	++	-	-	-	-	-	-	-	-
11955 ++	-	-	-	-	-	-	-	-	-
37300 ++	-	-	-	-	+	+	-	-	-

11692 ++	-	-	-	-	-	-	-	-	-
37301 ++	-	-	-	-	-	-	-	-	-
37241 ++	+++	-	-	-	-	-	-	-	-
17883 ++	++	-	-	-	-	-	-	-	-
37302 ++	++	-	-	-	-	-	-	-	-
36524 ++	+	–	+	+	+	+++	---	+++	-
37303 ++	+++	--+	+++	+++	+++	-	-	-	-
37255 ++	+++	-	-	+	+	-	-	-	-
37302 ++	+++	-	-	-	-	-	-	-	-
36995 ++	+++	-	-	-	-	-	-	-	-
11199 ++	+++	-	-	-	-	-	-	-	-
37304 ++	++	-	-	-	-	-	-	-	-
14219 ++	+++	–	-	-	+	-	-	-	-
37297 ++	-	--+	+	+++	+	+	-	-	-
36746 ++	++	-	-	-	-	-	-	-	-
16027 ++	-	-	-	-	-	-	-	-	-
36846 ++	+++	-	-	-	-	-	-	-	-
37072 ++	-	--	+	+++	+	+	-	-	-
37305 ++	+	--+	+++	+++	+++	++	-	-	-
37306 ++	-	--+	+	+++	+	-	-	+++	-
16008 ++	++	-	-	-	-	-	-	-	-
37307 ++	-	-	-	-	-	-	-	-	-
13745 ++	+++	-	+	+	-	++	--	-	-
37235 ++	+++	-	-	-	-	-	-	-	-
37308 ++	++	-	-	+	-	-	-	-	-
37309 ++	-	--+	+	+++	+	-	-	-	-
37310 ++	+	-	-	-	-	-	-	-	-
37311 ++	+++	-	-	-	-	-	-	-	-
37278 ++	-	--+	+	+++	+	-	-	-	-
12229 ++	-	-	-	-	-	-	-	-	-
36703 ++	-	–	+	+	-	-	-	-	-
13934 ++	+++	-	-	-	-	-	-	-	-
16027 ++	-	-	-	-	-	-	-	-	-

12543 ++	++	-	-	-	-	-	-	-	-
37312 ++	++	–	+	+	+	+++	---	-	-
37008 ++	++	-	-	-	-	-	-	-	-
12482 ++	++	-	-	-	-	-	-	-	-
36794 ++	+++	-	-	-	-	-	-	-	-
17037 ++	-	--+	+	+++	+	+	-	-	-
37313 ++	++	-	-	-	-	-	-	-	-
37314 ++	-	--+	+	+++	+	+	-	+++	-
36625 ++	-	-	-	-	-	-	-	-	-
37315 ++	+++	--+	+++	+++	+++	+	–	+++	-
11875 ++	++	-	-	-	-	-	-	-	-
37280 ++	+	-	-	-	-	-	-	-	-
37316 ++	+++	-	-	-	-	-	-	-	-
14269 ++	+++	-	-	-	-	-	-	-	-
18899 ++	+	--+	+	+++	+	-	-	-	-
37096 ++	++	-	-	-	-	-	-	-	-
37317 ++	++	--+	+++	+++	+++	+	-	-	-
36667 ++	+	-	-	-	-	-	-	-	-
14079 ++	+++	-	-	-	-	-	-	-	-
14780 ++	++	--+	+++	+++	+++	+	-	-	-
37318 ++	+	--+	++	+++	+++	++	-	-	-
17032 ++	+	--+	++	+++	+++	++	-	-	-
18231 ++	-	--+	+	+++	+	+	-	-	-
18011 ++	++	-	-	-	-	-	-	-	-
36896 ++	+	-	-	-	-	-	-	-	-
11207 ++	+++	-	-	-	-	-	-	-	-
37310 ++	+	-	-	-	-	-	-	-	-
36994 ++	+++	-	+	-	+	-	-	-	-
37133 ++	+++	-	-	-	-	-	-	-	-
37319 ++	-	--+	+	+++	-	-	-	+++	-
37218 ++	+	-	-	-	-	-	-	-	-
37142 ++	+	-	-	-	-	-	-	-	-
37110 ++	+	–	+	+	+	+	–	-	-

16113 ++	-	-	-	-	-	-	-	-	-
37034 ++	+++	-	-	-	-	-	-	-	-
17662 ++	++	-	-	-	+	-	-	-	-
12179 ++	-	-	-	-	-	-	-	-	-
37320 ++	-	-	-	-	-	-	-	-	-
16567 ++	++	-	-	-	-	-	-	-	-
18173 ++	-	--+	+	+++	+	-	-	-	-
37321 ++	+	--+	+++	+++	+++	-	-	-	-
37225 ++	++	-	-	+	+	-	-	-	-
37322 ++	-	-	-	-	-	-	-	-	-
36883 ++	-	-	-	-	-	-	-	-	-
37323 ++	-	--+	+	+	-	-	-	-	-
12009 ++	-	-	-	-	-	-	-	-	-
37324 ++	+++	-	-	-	+	-	-	-	-
37325 ++	++	-	-	-	-	-	-	-	-
37108 ++	-	--+	+	+++	-	-	-	-	-
37326 ++	-	-	-	-	-	-	-	-	-
37327 ++	-	-	+	-	-	-	-	-	-
37273 ++	-	--+	+	-	-	-	-	-	-
36470 ++	+++	-	-	-	-	-	-	-	-
37328 ++	-	-	-	-	-	-	-	-	-
37329 ++	+++	-	+	-	-	-	-	-	-
37330 ++	-	--+	+	+++	+	-	-	+++	-
37331 ++	+	--+	++	+++	++	+	-	+++	-
14174 ++	+++	-	-	-	-	-	-	-	-
18566 ++	-	-	-	-	-	-	-	-	-
37332 ++	+	-	-	-	-	-	-	-	-
36754 ++	+++	-	-	-	-	-	-	-	-
11879 ++	++	-	-	-	-	-	-	-	-
37333 ++	-	-	-	-	-	-	-	-	-
18066 ++	-	-	-	-	-	-	-	-	-
37334 ++	-	-	-	-	-	-	-	-	-
37183 ++	-	--+	++	+++	+	-	-	+++	-

16087 ++	++	-	-	-	-	-	-	-	-
36956 ++	+	-	-	-	-	-	-	-	-
37117 ++	+++	-	-	-	-	-	-	-	-
37335 ++	-	--+	+	+++	++	-	-	+++	-
17049 ++	+	--+	++	+++	+	+	–	-	-
37336 ++	++	-	-	-	-	-	-	-	-
37058 ++	++	-	-	-	-	-	-	-	-
37235 ++	+++	-	-	-	-	-	-	-	-
37197 ++	+	-	-	-	-	-	-	-	-
14290 ++	+++	-	-	-	-	-	-	-	-
36821 ++	+	-	-	-	-	-	-	-	-
37337 ++	++	-	-	-	-	-	-	-	-
37338 ++	-	-	-	-	-	-	-	-	-
36855 ++	+++	-	-	-	-	-	-	-	-
11845 ++	++	-	-	-	-	-	-	-	-
37144 ++	+++	-	-	-	-	-	-	-	-
19988 ++	+	-	-	-	-	-	-	-	-
37008 ++	++	-	-	-	-	-	-	-	-
37339 ++	-	–	+	-	-	-	-	-	-
15956 ++	+++	-	-	-	-	-	-	-	-
37340 ++	-	--+	+	+++	+	-	-	+++	++
37261 ++	+++	-	-	-	-	-	-	-	-
37148 ++	-	--+	+	+++	++	-	-	+++	-
37235 ++	++	-	-	-	-	-	-	-	-
37341 ++	++	-	-	-	-	-	-	-	-
37198 ++	++	-	-	-	-	-	-	-	-
36791 ++	++	-	-	-	-	-	-	-	-
37342 ++	++	-	-	-	-	-	-	-	-
37343 ++	++	-	-	-	-	-	-	-	-
37344 ++	-	-	-	-	-	-	-	-	-
37226 ++	+	-	-	-	-	-	-	-	-
37345 ++	-	–	+	+	-	-	-	-	-
11338 ++	+	-	-	-	-	-	-	-	-

37064 ++	++	-	-	-	-	-	-	-	-
37092 ++	++	-	-	-	-	-	-	-	-
37346 ++	+	–	+	+	+	-	-	-	-
37347 ++	++	-	-	-	-	-	-	-	-
37348 ++	+	–+	+++	+++	+++	++	–	-	-
37349 ++	+	-	-	-	-	+	-	-	-
37188 ++	+++	-	-	-	-	-	-	-	-
36942 ++	++	-	-	-	-	-	-	-	-
37350 ++	+	–	+	+	+	++	––	-	-
37351 ++	+++	-	-	-	-	-	-	-	-
12064 ++	-	-	-	-	-	-	-	-	-
36531 ++	+++	-	-	-	-	-	-	-	-
37067 ++	-	-	-	-	-	-	-	-	-
36856 ++	+++	-	-	-	-	-	-	-	-
11707 ++	+	-	-	-	-	-	-	-	-
37352 ++	-	–+	+	++	-	-	-	+++	-
16620 ++	+++	-	-	-	-	-	-	-	-
37353 ++	++	-	-	-	-	-	-	-	-
37231 ++	+++	-	-	-	-	-	-	-	-
11074 ++	++	-	-	-	-	-	-	-	-
37354 ++	++	-	+	+	+	-	-	-	-
37355 ++	-	–+	++	+	+	-	-	-	-
11106 ++	-	-	-	-	-	-	-	-	-
37356 ++	-	-	-	-	-	-	-	-	-
37351 ++	++	-	-	-	-	-	-	-	-
37357 ++	++	-	-	-	-	-	-	-	-
11424 ++	++	-	-	-	-	-	-	-	-
37358 ++	+	-	-	-	-	-	-	-	-
37359 ++	-	–+	+	+++	+	-	-	-	-
17626 ++	+++	-	-	-	-	-	-	-	-
36823 ++	++	-	-	-	-	-	-	-	-
36929 ++	++	-	+	+	+	-	-	-	-
36653 ++	-	–+	+	+++	-	-	-	-	-

36427 ++	+	-	-	-	-	-	-	-	-
37360 ++	++	-	-	-	-	-	-	-	-
37361 ++	++	-	-	-	-	-	-	-	-
14552 ++	++	-	+	-	-	-	-	-	-
37362 ++	++	-	-	-	-	-	-	-	-
37090 ++	+++	-	-	-	-	-	-	-	-
13546 ++	+++	-	-	-	-	-	-	-	-
12100 ++	-	-	-	-	-	-	-	-	-
37012 ++	+++	-	-	-	-	-	-	-	-
16033 ++	++	-	-	+	-	-	-	-	-
12101 ++	++	-	+	-	+	-	-	-	-
37363 ++	+++	-	-	-	+	-	-	-	-
16058 ++	++	-	-	-	-	-	-	-	-
37364 ++	++	-	-	-	+	-	-	-	-
18079 ++	++	-	-	-	-	-	-	-	-
11783 ++	-	-	-	-	-	-	-	-	-
36643 ++	-	--+	+	+++	+	-	-	-	-
37365 ++	-	--+	-	+++	-	-	-	-	-
37054 ++	+	--	++	++	++	+++	---	-	+++
16569 ++	+++	-	+	++	+++	-	-	-	-
36936 ++	++	--+	+++	+++	+++	-	-	-	-
17601 ++	-	-	-	+	+	-	-	-	-
37366 ++	-	--+	++	+++	++	+	-	+++	+++
37030 ++	+	-	-	-	-	-	-	-	-
37151 ++	+++	-	-	-	-	-	-	-	-
13877 ++	++	-	+	-	-	-	-	-	-
37367 ++	++	-	-	-	-	-	-	-	-
37368 ++	-	-	-	-	-	-	-	-	-
15352 ++	+++	-	++	+	+	+++	---	-	-
37369 ++	+	--+	+++	+++	+++	-	-	-	-
37157 ++	++	-	-	-	-	-	-	-	-
37370 ++	++	-	-	-	-	-	-	-	-
37024 ++	+	-	+	+	+	+	-	-	-

36909 ++	++	-	-	-	-	-	-	-	-
36671 ++	++	-	-	-	-	-	-	-	-
37329 ++	+++	-	-	-	+	-	-	-	-
37371 ++	-	--+	+	+++	-	-	-	-	-
16676 ++	-	-	-	-	-	+	-	-	-
37372 ++	++	-	-	-	-	-	-	-	-
36971 ++	++	-	-	-	-	-	-	-	-
37108 ++	-	--+	+	+++	-	-	-	-	-
37373 ++	+++	-	-	-	-	-	-	-	-
37374 ++	++	-	-	-	+	-	-	-	-
37163 ++	+++	-	-	-	-	-	-	-	-
14327 ++	++	-	-	-	-	-	-	-	-
11586 ++	-	-	-	-	-	-	-	-	-
16008 ++	+++	-	-	-	-	-	-	-	-
37375 ++	-	-	-	-	-	-	-	-	-
17576 ++	-	--+	+	+++	+	+	-	-	-
37376 ++	++	-	-	-	-	-	-	-	-
37377 ++	++	-	-	-	-	-	-	-	-
11293 ++	+++	-	-	-	-	-	-	-	-
37378 ++	++	-	-	-	-	-	-	-	-
37379 ++	-	-	-	-	-	-	-	-	-
37140 ++	+++	-	-	-	-	-	-	-	-
37380 ++	+	-	-	-	-	-	-	-	-
37381 ++	-	--+	+	+++	-	-	-	+++	-
37186 ++	+	-	-	+	+	+	-	-	-
14860 ++	++	-	-	-	-	-	-	-	-
37113 ++	-	--+	+	-	-	-	-	-	++
37053 ++	-	-	-	-	-	-	-	-	-
37284 ++	-	--+	+	+	-	-	-	+++	-
36953 ++	-	-	-	-	-	-	-	-	-
36990 ++	++	-	+	-	+	-	-	-	-
36918 ++	-	--+	+	++	+	+	-	+++	-
36844 ++	+++	-	+	+	+	+	-	-	-

37351 ++	++	-	-	-	-	-	-	-	-
37382 ++	++	-	-	-	-	-	-	-	-
37045 ++	+	-	-	-	-	-	-	-	-
11293 ++	+++	-	-	-	-	-	-	-	-
36913 ++	-	--+	++	+++	+++	+	–	+++	-
37383 ++	++	-	-	-	-	-	-	-	-
37141 ++	-	--+	+	+++	+	-	-	-	-
37384 ++	-	-	-	-	-	-	-	-	-
11111 ++	+++	-	-	-	-	-	-	-	-
14359 ++	+++	–	+	-	+	-	-	-	-
37302 ++	++	-	-	-	-	-	-	-	-
37385 ++	+	-	-	-	-	-	–	-	-
37386 ++	+	-	-	-	-	-	-	-	-
37387 ++	+++	-	-	-	-	-	-	-	-
37388 ++	+	--+	+++	+++	+++	+++	---	-	-
37389 ++	-	–	+	+	+	-	–	-	-
37390 ++	-	-	+	++	-	-	-	-	-
37391 ++	++	-	-	-	-	-	-	-	-
37182 ++	++	-	-	-	-	-	-	-	-
11130 ++	++	-	-	-	-	-	-	-	-
37173 ++	-	-	-	-	-	-	-	-	-
13913 ++	+++	-	-	-	-	-	-	-	-
37193 ++	+++	-	-	-	-	-	-	-	-
36573 ++	+	--+	+	+++	+	+	-	+++	-
37392 ++	-	-	-	-	-	-	-	-	-
37393 ++	-	-	-	-	-	-	-	-	-
11292 ++	+	-	-	-	-	-	-	-	-
13523 ++	++	-	-	-	-	-	-	-	-
12342 ++	-	-	-	-	-	-	-	-	-
37394 ++	+	-	-	-	-	-	-	-	-
16088 ++	++	-	-	-	-	-	-	-	-
16019 ++	++	-	-	-	-	-	-	-	-
11735 ++	++	-	-	-	-	-	-	-	-

37062 ++	+++	–	+	+	+	+	–	-	-
36780 ++	+++	-	-	-	-	-	-	-	-
36951 ++	+++	-	-	-	-	-	-	-	-
37395 ++	-	-	-	-	-	-	–	-	-
19761 ++	+	-	-	-	-	-	-	-	-
37396 ++	++	-	-	-	+	-	-	-	-
11930 ++	-	-	-	-	-	-	-	-	-
17023 ++	-	-	-	-	-	-	-	-	-
37373 ++	++	-	-	-	-	-	-	-	-
37397 ++	+++	-	+	+	+	-	-	-	-
37012 ++	++	-	-	-	-	-	-	-	-
19906 ++	-	-	-	-	-	-	-	-	-
37398 ++	++	–+	+++	+++	+++	+	–	-	-
37399 ++	-	–	+	-	+	-	-	-	-
17824 ++	-	-	-	-	-	-	-	-	-
37400 ++	++	-	-	-	-	-	-	-	-
37383 ++	+++	-	-	-	-	-	-	-	-
36945 ++	-	-	-	-	-	-	-	-	-
37073 ++	+	–+	++	+++	++	++	––	+++	-
37401 ++	-	–+	++	+++	++	+	–	-	-
17540 ++	-	–+	-	++	-	-	-	-	-
37402 ++	++	-	-	-	-	-	-	-	-
37152 ++	-	-	-	-	-	-	-	-	-
37403 ++	++	-	-	-	-	-	-	-	-
37191 ++	++	–	+	++	++	-	-	-	-
11130 ++	++	-	-	-	-	-	-	-	-
37404 ++	-	-	-	-	-	-	-	-	-
37405 ++	+++	-	-	-	-	-	-	-	-
36982 ++	++	-	-	-	-	-	-	-	-
37406 ++	++	-	-	-	-	+	–	-	-
11564 ++	++	-	-	-	-	-	-	-	-
37407 ++	++	-	-	-	-	-	-	-	-
37408 ++	++	-	-	-	-	-	-	-	-

37009 ++	++	-	-	-	-	-	-	-	-
37409 ++	-	-	-	-	-	-	-	-	-
37222 ++	++	-	-	-	-	-	-	-	-
37410 ++	++	-	-	-	-	-	-	-	-
37411 ++	+++	--+	+++	+++	+++	+	–	-	-
36699 ++	-	--+	++	+++	+	+	-	+++	-
37412 ++	-	--+	+	+++	+	+	-	+++	-
37413 ++	-	--+	+	++	-	+	-	-	-
19125 ++	-	--+	+	++	-	-	-	-	-
37277 ++	+++	-	+	+	+	+	–	-	-
37310 ++	+	-	-	-	-	-	-	-	-
11199 ++	+++	-	-	-	-	-	-	-	-
37296 ++	+++	-	-	-	-	-	-	-	-
36577 ++	++	-	-	-	-	-	-	-	-
12229 ++	-	-	-	-	-	-	-	-	-
18210 ++	-	-	-	-	-	-	-	-	-
37414 ++	-	--+	+	+	-	-	-	-	-
37415 ++	++	-	-	-	-	-	-	-	-
36984 ++	+	-	-	-	-	-	-	-	-
37052 ++	+++	-	-	-	-	-	-	-	-
37416 ++	-	-	-	-	-	-	-	-	-
37027 ++	++	-	-	-	-	-	-	-	-
12239 ++	++	-	-	-	-	-	-	-	-
37417 ++	+++	-	-	-	-	-	-	-	-
11376 ++	++	-	-	-	-	-	-	-	-
36800 ++	-	--+	+	++	-	-	-	-	-
37418 ++	+	-	-	-	-	+	–	-	-
37419 ++	++	-	-	-	-	-	-	-	-
36544 ++	-	--+	+	+++	+	+	–	+++	-
36804 ++	+	–	+	+	+	+++	---	-	-
16134 ++	+	-	-	-	-	-	-	-	-
37420 ++	-	--+	+	+++	+	-	-	-	-
18966 ++	-	-	-	-	-	-	-	-	-

37421 ++	++	-	-	-	-	-	-	-	-
37422 ++	+++	-	-	+	+	+	-	-	-
36690 ++	-	--+	+	+++	+	-	-	+++	-
37217 ++	+	–	+	+	+	-	-	+++	-
37423 ++	+	-	-	-	-	-	-	-	-
37289 ++	+	--+	++	+++	++	+	–	-	-
37424 ++	+	-	-	-	+	+	-	-	-
18210 ++	-	-	-	-	-	-	-	-	-
37425 ++	+	-	-	-	-	-	-	-	-
14004 ++	++	-	-	-	-	-	-	-	-
37150 ++	+++	-	-	-	-	-	-	-	-
37425 ++	+	-	-	-	-	-	-	-	-
37260 ++	-	-	-	-	-	-	-	-	-
36750 ++	-	-	-	+	+	-	-	-	-
37426 ++	+	-	-	-	-	+	-	-	-
37373 ++	++	-	-	-	-	-	-	-	-
14150 ++	++	-	-	-	-	-	-	-	-
36948 ++	-	-	-	-	-	-	-	-	-
37427 ++	+	-	-	-	-	-	-	-	-
37428 ++	-	-	-	+	-	-	-	-	-
36613 ++	+++	-	-	-	-	-	-	-	-
37429 ++	-	--+	+	+++	++	-	–	-	-
14549 ++	+++	–	-	-	-	+	–	-	-
36957 ++	++	-	-	-	-	-	-	-	-
36882 ++	-	-	-	-	-	-	-	-	-
36927 ++	++	-	-	-	-	-	-	-	-
37430 ++	++	-	-	-	-	-	-	-	-
37431 ++	-	-	-	-	-	-	-	-	-
36964 ++	+++	-	-	-	-	-	-	-	-
37432 ++	+++	--+	+++	+++	+++	-	-	-	-
37433 ++	++	--+	+++	+++	+++	-	-	-	-
37434 ++	++	-	-	-	-	-	-	-	-
11979 ++	-	-	-	-	-	-	-	-	-

37435 ++	++	-	-	-	-	-	-	-	-
11455 ++	-	-	-	-	-	-	-	-	-
37373 ++	++	-	-	-	-	-	-	-	-
37101 ++	+++	-	-	-	-	-	-	-	-
36965 ++	+++	-	-	-	-	-	-	-	-
12144 ++	-	-	-	-	-	-	-	-	-
36802 ++	-	-	+	-	+	+	-	-	-
37256 ++	+++	–	+	+	+	-	-	-	-
13532 ++	++	-	-	+	+	-	-	-	-
16629 ++	++	–+	+++	+++	+++	-	–	-	-
37336 ++	+	-	-	-	-	-	-	-	-
11661 ++	++	-	-	-	-	-	-	-	-
37385 ++	-	-	+	+	+	-	–	-	-
37436 ++	-	-	-	-	-	-	-	-	-
11817 ++	+++	-	-	-	-	-	-	-	-
37437 ++	-	–+	+	+	-	-	-	-	-
11720 ++	-	-	-	-	-	-	-	-	-
37213 ++	++	-	-	-	-	-	-	-	-
37438 ++	-	–+	+	+	+	+	–	-	-
12009 ++	-	-	-	-	-	-	-	-	-
16573 ++	+	-	-	-	-	-	-	-	-
37300 ++	-	-	+	-	-	-	-	-	-
37079 ++	++	-	-	-	-	-	-	-	-
37439 ++	-	–+	+	+	-	-	-	-	+
37328 ++	-	-	-	-	-	-	-	-	-
11472 ++	-	-	-	-	-	-	-	-	-
17626 ++	+++	-	-	-	-	-	-	-	-
37440 ++	-	-	-	-	-	-	-	-	-
37218 ++	+	-	-	-	-	-	-	-	-
37337 ++	++	-	-	-	-	-	-	-	-
37265 ++	+++	-	-	-	-	-	-	-	-
16023 ++	++	-	-	-	-	-	-	-	-
18116 ++	++	-	-	-	+	-	-	-	-

13698 ++	++	-	+	-	+	-	-	-	-
37441 ++	++	-	-	-	-	-	-	-	-
37442 ++	-	–	+	-	+	-	-	-	-
37165 ++	++	-	-	-	-	-	-	-	-
37443 ++	+	–-+	+++	+++	+++	-	–	-	-
37064 ++	++	-	-	-	-	-	-	-	-
37444 ++	-	-	+	+	-	-	-	-	-
37159 ++	++	-	-	-	-	-	-	-	-
37032 ++	++	–-+	+++	+++	+++	+	–	-	-
17751 ++	++	-	-	-	-	-	-	-	-
37445 ++	+	-	-	+	-	-	-	-	-
37236 ++	++	-	-	-	-	-	-	-	-
18011 ++	++	-	-	-	-	-	-	-	-
17123 ++	+	–-+	+++	+++	+++	-	-	-	-
37446 ++	+	-	-	-	-	+	-	-	-
37200 ++	++	-	-	-	-	-	-	-	-
37447 ++	++	-	-	-	-	-	-	-	-
37315 ++	+++	–-+	+++	+++	+++	+	–	-	-
17127 ++	+	–-+	++	+++	++	-	-	-	-
37448 ++	-	-	-	-	-	-	-	-	-
16652 ++	++	–-+	+++	+++	+++	+	–	-	-
37145 ++	-	––	-	-	-	-	-	-	-
37449 ++	++	-	-	-	-	+	-	-	-
37450 ++	++	-	-	-	-	-	-	-	-
14050 ++	++	-	-	-	-	-	-	-	-
17596 ++	++	-	-	-	-	-	-	-	-
37451 ++	++	-	-	-	-	-	–	-	-
37275 ++	++	-	-	-	-	-	-	-	-
37327 ++	-	––	-	-	-	-	-	-	-
37409 ++	-	-	+	-	-	-	-	-	-
37194 ++	+	–	+	+	+	-	-	-	-
37204 ++	++	-	-	-	-	-	-	-	-
36998 ++	-	–-+	+	+	-	-	-	-	-

16609 ++	+	-	-	-	-	+	–	-	-
11615 ++	-	-	-	-	-	-	-	-	-
17039 ++	+	-	-	-	-	-	-	-	-
37452 ++	-	-	-	-	-	-	-	-	-
37214 ++	+	-	-	-	-	-	-	-	-
37453 ++	-	–+	+	+	+	-	-	-	-
16043 ++	++	-	-	-	-	-	-	-	-
13770 ++	++	-	+	+	+	+++	---	-	-
37454 ++	-	-	-	-	-	-	-	-	-
37455 ++	++	-	-	-	-	-	-	-	-
37456 ++	+	-	-	-	-	-	-	-	-
37457 ++	-	–	+	-	-	-	-	-	-
15352 ++	+++	–	++	+	++	+++	---	-	-
37458 ++	-	–+	+	+++	+	-	-	+++	-
37295 ++	++	-	-	-	-	-	-	-	-
37311 ++	+++	-	-	-	-	-	-	-	-
36717 ++	-	-	-	-	-	-	-	-	-
16620 ++	++	-	-	-	-	-	-	-	-
11740 ++	+++	-	-	-	-	-	-	-	-
37459 ++	+++	-	-	-	-	-	–	-	-
37460 ++	-	–+	+	+++	+	+	–	-	-
37342 ++	++	-	-	-	-	-	-	-	-
37461 ++	++	-	-	-	-	-	-	-	-
37362 ++	++	-	-	-	-	-	-	-	-
37462 ++	-	–+	+++	+++	+++	-	-	-	-
12064 ++	-	-	-	-	-	-	-	-	-
37463 ++	+	–	+	+	+	+++	---	-	-
37464 ++	++	-	-	-	-	-	-	-	-
16046 ++	++	-	-	-	-	-	-	-	-
20014 ++	-	–+	+	++	-	-	-	-	-
37465 ++	+++	-	-	-	-	-	-	-	-
37466 ++	+	-	-	-	+	-	-	-	-
11338 ++	-	-	-	-	-	-	-	-	-

37140 ++	+++	-	-	-	+	-	-	-	-
10995 ++	++	-	-	-	-	-	-	-	-
14007 ++	+++	--+	+++	+++	+++	+	-	-	-
18087 ++	+++	-	-	+	+	-	-	-	-
16607 ++	-	--+	+	+++	+	-	-	-	-
37363 ++	+++	-	-	-	+	-	-	-	-
37467 ++	++	-	-	-	-	+	-	-	-
13934 ++	+++	-	-	-	-	-	-	-	-
37463 ++	+	-	+	+	+	+++	---	+++	-
37468 ++	-	-	-	-	-	-	-	-	-
37371 ++	-	--+	+	+++	-	-	-	-	-
11648 ++	++	-	-	-	-	-	-	-	-
11787 ++	-	-	-	-	-	-	-	-	-
37469 ++	++	-	+	+	-	-	-	-	-
15996 ++	+++	-	-	-	-	-	-	-	-
37470 ++	++	-	-	-	-	-	-	-	-
13998 ++	++	-	-	-	-	-	-	-	-
37471 ++	++	-	-	-	-	-	-	-	-
37472 ++	-	-	-	-	-	-	-	-	-
37291 ++	++	-	-	-	-	-	-	-	-
36809 ++	+++	-	-	-	-	-	-	-	-
37473 ++	++	-	-	-	-	-	-	-	-
14958 ++	++	-	-	-	+	-	-	-	-
11660 ++	+++	-	-	-	-	-	-	-	-
11640 ++	++	-	-	-	-	-	-	-	-
36928 ++	++	-	-	+	+	+	-	-	-
37456 ++	+	-	-	-	-	-	-	-	-
37474 ++	++	-	-	-	-	-	-	-	-
37235 ++	++	-	-	-	-	-	-	+	-
37303 ++	++	--+	+++	+++	+++	-	-	-	-
36891 ++	-	-	+	+	+	-	-	-	-
37475 ++	-	--+	+	+++	+	+	-	+++	-
11980 ++	++	-	+	-	-	-	-	-	-

37476 ++	+	-	-	-	-	-	-	-	-
36984 ++	+	-	-	-	-	-	-	-	-
37101 ++	+++	-	-	-	-	-	-	-	-
37477 ++	-	–	-	+	-	-	-	-	-
37478 ++	++	–-+	+++	+++	+++	+	-	-	-
37416 ++	-	-	-	-	-	-	-	-	-
37479 ++	-	–-+	+++	+++	+++	-	-	-	-
37430 ++	++	-	-	-	-	-	-	-	-
14367 ++	++	-	-	-	+	-	-	-	-
37480 ++	-	-	-	-	-	-	-	-	-
36884 ++	+++	-	-	-	-	-	-	-	-
37481 ++	++	-	-	-	-	-	-	-	-
37482 ++	++	-	-	-	-	-	-	-	-
37389 ++	-	-	-	+	+	-	–	-	-
11531 ++	-	-	-	-	-	-	-	-	-
37483 ++	+	-	-	-	-	-	-	-	-
37484 ++	++	-	-	-	-	+	-	-	-
11212 ++	++	-	-	-	-	-	-	-	-
18772 ++	+	––	++	++	++	-	-	-	-
37391 ++	++	-	-	-	-	-	-	-	-
37435 ++	++	-	-	-	-	-	-	-	-
37253 ++	++	-	-	-	-	-	-	-	-
37485 ++	-	–-+	+++	+++	+++	-	-	-	-
37114 ++	-	––	+	+	+	+	–	-	-
37486 ++	++	-	-	-	-	-	-	-	-
13795 ++	+	-	-	-	-	-	-	-	-
16579 ++	+++	-	-	-	-	-	-	-	-
37042 ++	++	-	-	-	-	-	-	-	-
37125 ++	-	–-+	+	++	+	-	-	-	-
36908 ++	+	-	-	-	-	-	-	-	-
37487 ++	+	-	-	-	-	-	-	-	-
37419 ++	++	-	-	-	-	-	-	-	-
36599 ++	-	–-+	+	+++	-	-	-	-	-

11113	++	++	-	-	-	+	-	-	-	-
37488	++	++	-	-	-	-	-	-	-	-
37054	++	+	–	++	+	++	+++	---	+++	-
14461	++	++	-	-	-	-	-	-	-	-
37056	++	++	-	-	-	-	-	-	-	-
11732	++	-	-	-	-	-	-	-	-	-
16112	++	+	-	-	-	-	-	-	-	-
37489	++	-	-	-	-	-	-	-	-	-
12125	++	++	--+	+++	+++	+++	+	–	-	-
17968	++	+	-	-	-	-	-	-	-	-
37025	++	++	-	-	-	-	-	-	-	-
37310	++	+	-	-	-	-	-	-	-	-
37160	++	+	-	-	-	-	-	-	-	-
11746	++	++	-	-	-	+	-	-	-	-
37298	++	+	--+	+	+++	+	+++	---	-	-
37473	++	+++	-	-	-	-	+	–	-	-
37306	++	-	--+	+	+++	+	-	-	+++	-
37215	++	+++	-	-	-	-	-	-	-	-
37070	++	-	-	-	-	-	-	-	-	-
37490	++	++	-	-	-	-	-	-	-	-
37491	++	+	--+	++	+++	+	+++	---	+++	-
37492	++	++	-	-	-	-	-	-	-	-
37493	++	+	–	-	-	-	-	-	-	-
37179	++	++	--+	+++	+++	+++	+	–	-	-
14097	++	++	-	-	-	-	-	-	-	-
37494	++	-	--+	+	+++	-	+	-	-	-
37059	++	++	-	-	-	-	-	–	-	-
37106	++	+	-	-	-	-	-	-	-	-
15204	++	++	-	-	-	+	+	–	-	-
37495	++	++	-	-	-	-	-	-	-	-
16023	++	++	-	-	-	+	-	-	-	-
37288	++	+	-	-	-	-	-	-	-	-
14287	++	++	-	-	-	-	-	-	-	-

37481 ++	++	-	-	-	-	-	-	-	-
37496 ++	++	-	-	-	-	-	-	-	-
12005 ++	++	-	-	-	-	-	-	-	-
37497 ++	-	--+	+	++	-	-	-	-	-
37498 ++	-	-	-	-	-	-	-	-	-
12034 ++	-	-	-	-	-	-	-	-	-
11398 ++	+++	-	-	-	-	-	-	-	-
37499 ++	+	–	+	+++	+	++	--	-	-
37500 ++	++	-	-	-	-	-	-	-	-
14094 ++	+++	-	-	-	-	-	-	-	-
37501 ++	-	--+	++	+++	++	+++	---	+++	++
37270 ++	++	-	-	-	-	-	-	-	-
37438 ++	-	--+	+	+	-	-	-	-	-
36531 ++	+++	-	-	-	-	-	-	-	-
12013 ++	+	-	-	-	-	-	-	-	-
36940 ++	++	-	-	-	-	-	-	-	-
37027 ++	+++	-	-	-	-	-	-	-	-
37147 ++	++	-	-	-	-	-	-	-	-
37382 ++	++	-	-	-	-	-	–	-	-
37502 ++	-	-	-	-	-	-	-	-	-
37334 ++	-	–	-	-	-	-	-	-	-
37503 ++	-	-	-	-	-	-	-	-	-
13778 ++	++	-	-	-	-	-	-	-	-
37504 ++	+	--+	+++	+++	+++	-	-	-	-
17675 ++	-	--+	+	+++	+++	+	-	-	-
37204 ++	+++	-	-	-	-	-	-	-	-
14104 ++	++	-	-	-	-	-	-	-	-
37505 ++	++	-	-	-	-	-	-	-	-
37506 ++	-	--+	+	+++	-	-	-	-	-
37507 ++	+++	-	-	-	-	-	-	-	-
37508 ++	++	--+	+++	+++	+++	-	-	-	-
37509 ++	++	-	-	-	-	-	-	-	-
37510 ++	-	--+	+	+++	+	+	-	+++	-

37262 ++	-	-	-	-	-	-	-	-	-
37511 ++	++	-	-	-	-	-	-	-	-
37218 ++	+	-	-	-	-	-	-	-	-
11316 ++	++	-	-	-	-	-	-	-	-
36824 ++	++	-	-	-	-	-	-	-	-
37512 ++	++	-	-	-	-	-	-	-	-
37482 ++	++	-	-	-	-	-	-	-	-
17939 ++	-	-	-	-	-	-	-	-	-
37513 ++	+	-	-	-	-	+	-	-	-
37514 ++	-	--+	+	++	-	-	-	-	-
13788 ++	++	-	-	-	-	-	-	-	-
37281 ++	++	-	-	-	+	-	-	-	-
37412 ++	-	--+	+	+++	+	-	-	-	-
16578 ++	++	-	-	-	-	-	-	-	-
37410 ++	++	-	-	-	-	-	-	-	-
37515 ++	++	-	-	-	-	-	-	-	-
36942 ++	++	-	-	-	-	-	-	-	-
36786 ++	-	-	-	-	-	+	-	-	-
37516 ++	+	-	-	-	-	-	-	-	-
17873 ++	++	-	-	-	-	-	-	-	-
37517 ++	++	-	-	-	-	-	-	-	-
17937 ++	++	-	-	-	-	-	-	-	-
37518 ++	+++	-	-	-	-	-	-	-	-
37519 ++	++	-	-	-	-	-	-	-	-
37520 ++	-	--+	+	+++	-	-	-	+++	-
36818 ++	+++	-	-	-	-	-	-	-	-
36618 ++	-	-	-	-	-	-	-	-	-
37521 ++	++	--+	+++	+++	+++	+	-	-	-
36993 ++	++	-	-	-	-	-	-	-	-
18996 ++	+	-	+	-	+	-	-	-	-
17928 ++	++	-	-	+	-	-	-	-	-
14247 ++	++	-	-	-	-	-	-	-	-
37522 ++	-	--+	+	+++	++	+	-	-	-

37050 ++	+	-	+	+	+	+	-	-	-
37523 ++	++	-	-	-	-	-	-	-	-
11368 ++	+++	-	-	-	-	-	-	-	-
37524 ++	+	--+	+	+++	+++	-	-	+++	-
11476 ++	++	-	-	-	-	-	-	-	-
37525 ++	-	-	-	+	-	-	-	-	-
37526 ++	+++	-	-	-	-	-	-	-	-
37527 ++	++	-	+	+	+	++	--	-	-
37528 ++	-	--+	+	+++	+	-	-	++	-
12503 ++	++	-	-	-	-	-	-	-	-
37064 ++	++	-	-	-	-	-	-	-	-
37529 ++	-	-	-	+	-	-	-	-	-
37316 ++	++	-	-	-	-	-	-	-	-
37530 ++	++	-	+	+++	+++	-	-	-	+
37219 ++	-	-	-	-	-	-	-	-	-
16570 ++	++	-	+	+	+	-	-	-	-
37531 ++	+++	-	-	-	-	-	-	-	-
37532 ++	-	-	-	-	-	-	-	-	-
37461 ++	++	-	-	-	-	-	-	-	-
11188 ++	++	-	-	-	-	-	-	-	-
18231 ++	-	--+	+	+++	-	-	-	-	-
37313 ++	++	-	-	-	-	-	-	-	-
37429 ++	-	--+	+	+++	++	+	-	+++	-
37048 ++	-	-	+	++	+	-	-	-	-
11418 ++	+	-	-	-	-	-	-	-	-
37533 ++	-	-	-	-	-	-	-	-	-
37534 ++	++	-	-	-	-	-	-	-	-
37258 ++	++	-	-	-	-	-	-	-	-
17792 ++	-	-	-	-	-	-	-	-	-
37302 ++	++	-	-	-	-	-	-	-	-
12434 ++	-	-	-	-	-	-	-	-	-
11458 ++	+++	-	-	-	-	-	-	-	-
16112 ++	+	-	-	-	-	-	-	-	-

16116 ++	++	-	-	-	-	-	-	-	-
37535 ++	++	-	-	-	-	-	-	-	-
14227 ++	++	-	-	-	-	-	-	-	-
37536 ++	++	-	-	-	-	-	-	-	-
37537 ++	+	-	-	-	-	-	-	-	-
37538 ++	++	-	-	-	-	-	-	-	-
13814 ++	+++	-	-	-	-	-	–	-	-
37539 ++	++	––	+	-	-	-	-	-	-
37540 ++	-	–	-	+	-	+	––	-	-
11087 ++	++	-	-	-	-	-	-	-	-
37541 ++	-	-	-	-	-	-	-	-	-
37542 ++	++	-	-	-	-	-	-	-	-
37543 ++	-	-	-	-	-	-	-	-	-
36739 ++	+	-	-	-	-	-	-	-	-
37544 ++	++	-	-	-	-	-	-	-	-
17515 ++	+++	-	-	-	-	-	-	-	-
16667 ++	++	–	+	+	+	+	–	-	-
11688 ++	++	-	-	-	-	-	-	-	-
37545 ++	+	-	-	-	-	-	-	-	-
18899 ++	+	––+	++	+++	+	-	-	+++	-
36933 ++	++	––+	+++	+++	+++	+	–	-	-
18442 ++	++	-	-	-	-	-	-	-	-
37546 ++	-	-	-	-	-	-	–	-	-
37547 ++	-	-	-	+++	-	-	-	-	-
11664 ++	-	-	-	-	-	-	-	-	-
37548 ++	++	-	-	-	-	-	-	-	-
37549 ++	-	––+	+++	+++	+++	+	–	-	-
37550 ++	+	–	+	+	++	+	–	-	-
37471 ++	++	-	-	-	-	-	-	-	-
18659 ++	+++	-	-	-	-	-	-	-	-
37551 ++	+	––+	+++	+++	+++	-	-	-	-
37274 ++	++	-	-	-	-	-	-	-	-
37552 ++	++	-	-	-	-	-	-	-	-

37553 ++	-	-	-	-	-	-	-	-	-
37554 ++	+	–	+	+	+	-	-	-	-
11147 ++	++	-	-	-	-	-	-	-	-
37555 ++	-	-	-	-	-	-	-	-	-
11147 ++	++	-	-	-	-	-	-	-	-
37556 ++	-	–+	+	+++	+	-	-	-	-
37528 ++	-	–+	+	+++	+	-	-	+++	-
37557 ++	++	-	-	-	-	-	-	-	-
17437 ++	++	-	-	-	-	-	-	-	-
37558 ++	++	–	+	-	-	-	-	-	-
11572 ++	++	-	-	-	-	-	-	-	-
37559 ++	-	–+	+	+++	+	-	-	+++	-
37154 ++	+	-	-	-	-	-	-	-	-
37237 ++	++	-	-	-	-	-	-	-	-
37040 ++	++	-	-	-	-	-	-	-	-
12113 ++	-	-	-	-	-	-	-	-	-
11516 ++	-	-	-	-	-	-	-	-	-
37036 ++	-	–+	+	+++	+	-	-	-	-
37560 ++	++	-	-	-	-	-	-	-	-
37454 ++	-	-	-	-	-	-	-	-	-
37561 ++	-	-	-	-	-	-	-	-	-
37481 ++	++	-	-	-	-	-	-	-	-
37562 ++	++	-	+	+	+	+	–	-	-
37174 ++	+++	–	+	+	+	+	–	-	-
37563 ++	-	-	-	-	-	-	-	-	-
37238 ++	+	-	-	-	-	-	-	-	-
19221 ++	-	–+	+	+	-	+	–	-	-
36944 ++	+	–+	+	+++	-	-	–	-	-
37564 ++	++	–+	+++	+++	+++	-	-	-	-
37272 ++	-	–+	++	+++	+	-	-	-	-
37565 ++	++	-	-	-	-	-	-	-	-
36938 ++	-	–+	+	+++	+	-	-	+++	-
36854 ++	+++	-	-	-	-	-	-	-	-

37566 ++	++	-	-	-	-	-	-	-	-
37133 ++	++	-	-	-	-	-	-	-	-
37567 ++	-	-	-	-	-	-	-	-	-
37203 ++	+	-	-	-	-	-	-	-	-
17852 ++	+++	-	-	+	+	-	-	-	-
36976 ++	+++	-	-	-	-	-	-	-	-
17830 ++	+++	-	-	-	-	-	-	-	-
37568 ++	+	-	-	-	-	-	-	-	-
37569 ++	++	--+	++	-	-	-	-	-	-
37331 ++	-	--+	++	+++	++	++	-	+++	++
37570 ++	++	-	-	-	+	-	-	-	-
37280 ++	+	-	-	-	-	-	-	-	-
37061 ++	+++	-	-	-	-	-	-	-	-
37064 ++	+++	-	-	-	-	-	-	-	-
12073 ++	-	-	-	-	-	-	-	-	-
37486 ++	++	-	-	-	-	-	-	-	-
37569 ++	++	--+	++	-	-	-	-	++	-
14121 ++	++	-	-	-	-	-	-	-	-
37028 ++	++	-	-	-	-	-	-	-	-
37538 ++	++	-	-	-	-	-	-	-	-
37571 ++	+	-	-	-	-	-	-	-	-
18202 ++	-	-	-	-	-	-	-	-	-
37572 ++	-	--+	+	+++	+	-	-	-	-
13837 ++	++	-	-	-	+	-	-	-	-
37093 ++	+++	-	-	-	-	-	-	-	-
37524 ++	-	--+	+	+++	+++	-	-	+++	-
37282 ++	-	-	-	-	-	-	-	-	-
37043 ++	+++	-	-	-	-	-	-	-	-
37218 ++	+	-	-	-	-	-	-	-	-
37417 ++	+++	-	-	-	-	-	-	-	-
37573 ++	++	-	-	-	+	-	-	-	-
37461 ++	+++	-	-	-	-	-	-	-	-
36978 ++	+	-	-	-	-	-	-	-	-

37574 ++	-	--+	+	++	-	-	-	-	-
17888 ++	-	--+	+	+	+	-	-	+++	+++
19125 ++	-	--+	+	++	-	-	-	-	-
37575 ++	++	-	-	-	-	-	-	-	-
37576 ++	+	-	-	-	-	-	-	-	-
11014 ++	++	-	-	-	-	-	-	-	-
11411 ++	+++	-	-	-	-	-	-	-	-
12100 ++	-	-	-	-	-	-	-	-	-
37077 ++	+++	-	-	-	-	-	-	-	-
17607 ++	-	--	-	-	-	-	-	-	-
37577 ++	-	-	-	-	-	-	-	-	-
36643 ++	-	--+	+	+++	+	+	-	-	-
37131 ++	-	-	+	-	+	-	-	-	-
37228 ++	+	-	-	-	-	-	-	-	-
12113 ++	-	-	-	-	-	-	-	-	-
37578 ++	+	-	-	-	-	+	–	-	-
37349 ++	+	-	-	-	-	-	-	-	-
37370 ++	+++	-	-	-	-	-	-	-	-
11490 ++	+	-	-	-	-	-	-	-	-
36987 ++	++	-	-	-	-	-	-	-	-
16602 ++	+	–	+	+	+	-	-	-	-
37579 ++	-	--+	+++	+++	+++	-	-	-	-
37580 ++	++	-	-	-	-	-	-	-	-
12294 ++	-	-	-	-	-	-	-	-	-
37581 ++	-	--+	+	+++	-	-	-	-	-
11419 ++	-	-	-	-	-	-	-	-	-
37582 ++	++	-	-	-	-	-	-	-	-
37171 ++	+	-	-	-	+	+	–	-	-
12013 ++	+	-	-	-	-	-	-	-	-
37304 ++	++	-	-	-	-	-	-	-	-
37465 ++	++	-	-	-	-	-	-	-	-
37304 ++	++	-	-	-	-	-	-	-	-
37583 ++	++	-	-	-	-	-	-	-	-

12426 ++	++	-	-	-	-	-	-	-	-
37137 ++	-	--+	-	-	-	-	-	-	-
37584 ++	++	-	-	-	-	-	-	-	-
17946 ++	-	-	-	-	-	-	-	-	-
14247 ++	++	-	-	-	-	-	-	-	-
11383 ++	++	-	-	-	-	-	-	-	-
37585 ++	-	-	-	-	-	-	-	-	-
37575 ++	++	-	-	-	-	-	-	-	-
37092 ++	++	-	-	-	-	-	-	-	-
36763 ++	+	-	-	-	-	-	-	-	-
37407 ++	++	-	-	-	-	-	-	-	-
37555 ++	-	-	-	-	-	-	-	-	-
14574 ++	++	-	-	-	+	+	-	-	-
37586 ++	++	--+	+++	+++	+++	-	-	-	-
37587 ++	+	-	-	-	-	-	-	-	-
37439 ++	-	--+	+	+	-	-	-	-	-
37588 ++	++	-	+	+	+	-	-	-	-
37589 ++	-	-	-	-	-	-	-	-	-
11547 ++	++	-	-	-	-	-	-	-	-
11346 ++	++	-	-	-	-	-	-	-	-
37518 ++	++	-	-	-	-	-	-	-	-
17675 ++	-	--+	+	+++	+++	+	-	-	-
37324 ++	++	-	-	-	+	-	-	-	-
17966 ++	++	--+	+	-	-	-	-	-	-
37350 ++	+	-	+	+	+	++	--	-	-
37590 ++	++	-	-	-	-	-	-	-	-
37591 ++	+	-	-	-	-	-	-	-	-
18385 ++	-	-	-	-	-	-	-	-	-
36902 ++	-	--+	+	+++	+	-	-	+++	-
11096 ++	++	-	-	-	-	-	-	-	-
37484 ++	++	-	-	-	-	-	-	-	-
37014 ++	-	--+	+	+++	-	-	-	-	-
11633 ++	-	-	-	-	-	-	-	-	-

11391 ++	+++	-	+	-	-	-	-	-	-
37489 ++	+	-	-	-	-	-	-	-	-
36643 ++	-	--+	+	+++	+	-	-	-	-
18704 ++	++	-	-	-	-	-	-	-	-
37357 ++	++	-	-	-	-	-	-	-	-
37540 ++	+	–	+	+	+	+	–	-	-
36981 ++	-	-	-	-	-	-	-	-	-
37408 ++	++	-	-	-	-	-	-	-	-
36701 ++	++	-	+	-	+	-	-	-	-
37592 ++	+	-	-	+	-	-	-	-	-
36868 ++	-	-	-	-	-	-	-	-	-
37593 ++	-	--+	+	++	-	-	-	-	-
37172 ++	++	-	-	-	-	-	-	-	-
37362 ++	++	-	-	-	-	-	-	-	-
37490 ++	++	-	-	-	-	-	-	-	-
20420 ++	-	--+	+	+++	-	-	–	-	-
13795 ++	+	-	-	-	-	-	-	-	-
37496 ++	++	-	-	-	-	-	-	-	-
37594 ++	+	--+	+++	+++	+++	-	-	-	-
37533 ++	-	-	-	-	-	-	-	-	-
18089 ++	-	--	-	-	-	-	-	-	-
37595 ++	++	-	-	-	-	-	-	-	-
37027 ++	++	-	-	-	-	-	-	-	-
37593 ++	-	--+	+	+++	-	-	-	-	-
37596 ++	++	-	-	-	-	-	-	-	-
17675 ++	-	--+	++	+++	+++	+	–	-	-
14540 ++	++	-	-	-	-	-	-	-	-
17857 ++	++	-	-	-	-	-	-	-	-
11573 ++	++	-	-	-	-	-	-	-	-
16088 ++	++	-	-	-	-	-	-	-	-
37580 ++	++	-	-	-	-	-	-	-	-
37507 ++	+++	-	-	-	-	-	-	-	-
37597 ++	++	-	-	-	-	+	-	-	-

37598 ++	+	--+	++	+++	++	++	-	+++	-
37599 ++	++	-	-	-	-	-	-	-	-
37600 ++	++	-	-	-	-	-	-	-	-
37601 ++	+++	-	-	-	-	-	-	-	-
37602 ++	++	-	-	-	-	-	-	-	-
37603 ++	+++	-	-	-	-	-	-	-	-
37423 ++	+	-	-	-	-	-	-	-	-
37604 ++	++	-	-	-	-	-	-	-	-
37605 ++	++	-	-	-	-	-	-	-	-
37606 ++	+	-	-	-	-	-	-	-	-
37607 ++	++	-	+	-	-	-	-	-	-
37608 ++	++	-	-	-	-	-	-	-	-
11421 ++	-	-	-	-	-	-	-	-	-
37609 ++	++	–	+	-	-	+	–	-	-
36756 ++	-	--+	+	-	-	-	-	+++	-
37610 ++	-	--+	+	+++	+	+	-	-	-
37181 ++	++	-	-	-	-	-	-	-	-
37611 ++	+	-	-	-	-	-	-	-	-
11738 ++	-	-	-	-	-	-	-	-	-
37546 ++	+	-	+	-	-	-	–	-	-
37269 ++	++	-	-	-	-	-	-	-	-
37612 ++	++	-	-	-	-	-	-	-	-
12025 ++	-	-	-	-	-	-	-	-	-
37552 ++	++	-	-	-	-	-	-	-	-
11819 ++	-	-	-	-	-	-	-	-	-
11660 ++	++	-	-	-	-	-	-	-	-
14104 ++	+++	-	-	-	-	-	-	-	-
37613 ++	-	-	-	++	-	-	-	-	-
17903 ++	++	-	-	-	-	-	-	-	-
37571 ++	+	-	-	-	-	-	-	-	-
37045 ++	+	-	-	-	-	-	-	-	-
37614 ++	++	-	-	-	-	-	-	-	-
37470 ++	++	-	-	-	-	-	-	-	-

37124 ++	++	-	-	-	-	-	-	-	-
37615 ++	++	-	-	-	-	-	-	-	-
17578 ++	-	--+	+	+	-	-	-	+++	-
17034 ++	+	-	-	-	-	-	-	-	-
37363 ++	++	-	-	-	+	-	-	-	-
37001 ++	-	--+	+	+	+	+	-	-	-
37616 ++	-	-	-	-	-	-	-	-	-
37457 ++	-	-	+	-	+	-	-	-	-
17184 ++	-	--+	+++	+++	+++	-	-	-	-
11220 ++	++	-	-	-	-	-	-	-	-
18291 ++	++	-	-	-	-	-	-	-	-
16613 ++	++	-	-	-	-	-	-	-	-
37617 ++	++	-	-	-	+	+	-	-	-
17704 ++	-	-	-	-	-	-	-	-	-
37390 ++	-	-	-	++	-	-	-	-	-
37267 ++	++	-	-	-	-	-	-	-	-
37403 ++	++	-	-	-	-	-	-	-	-
37599 ++	++	-	-	-	-	-	-	-	-
37153 ++	-	--+	+	+++	+	-	-	+++	-
37234 ++	++	-	-	-	-	-	-	-	-
37615 ++	++	-	-	-	-	-	-	-	-
37203 ++	+	-	-	-	-	-	-	-	-
37618 ++	-	-	-	-	-	-	-	-	-
37619 ++	-	--+	+	+++	++	+	-	-	-
37620 ++	++	-	-	-	-	-	-	-	-
37621 ++	-	-	-	-	-	+	-	-	-
37527 ++	++	-	+	+	+	++	--	-	-
37169 ++	++	-	-	-	-	-	-	-	-
36808 ++	-	--+	+	++	+	+	-	-	-
37622 ++	++	-	-	-	-	-	-	-	-
11003 ++	++	-	-	-	-	-	-	-	-
37623 ++	-	--+	+	+++	-	+	-	+++	-
37624 ++	+	-	-	-	-	-	-	-	-

36836 ++	+++	-	-	-	-	-	-	-	-
37625 ++	-	--+	+	+++	+	-	-	-	-
37257 ++	+++	-	+	+++	+++	+	-	-	-
37626 ++	-	-	-	-	-	-	-	-	-
16030 ++	++	-	-	-	-	-	-	-	-
17613 ++	-	-	-	-	-	-	-	-	-
37567 ++	-	-	-	-	-	-	-	-	-
37590 ++	++	-	-	-	-	-	-	-	-
37307 ++	-	-	-	-	-	-	-	-	-
37448 ++	-	-	-	-	-	-	-	-	-
37218 ++	+	-	-	-	-	-	-	-	-
37627 ++	++	--+	+++	+++	+++	+	-	-	-
37628 ++	+++	-	-	-	-	-	-	-	-
37196 ++	-	-	-	-	-	-	-	-	-
36757 ++	-	-	-	-	-	-	-	-	-
37629 ++	-	--+	+++	+++	+++	-	-	-	-
13884 ++	-	-	-	-	-	-	-	-	-
18015 ++	+++	-	-	-	-	-	-	-	-
11144 ++	++	-	-	-	-	-	-	-	-
37630 ++	++	-	-	-	-	-	-	-	-
37029 ++	+	-	-	-	-	-	-	-	-
37631 ++	+	-	-	-	-	-	-	-	-
20376 ++	+	-	-	-	-	-	-	-	-
37458 ++	-	--+	+	+++	+	-	-	+++	+++
11714 ++	-	-	-	-	-	-	-	-	-
13530 ++	++	-	-	-	-	-	-	-	-
11995 ++	++	-	-	-	-	-	-	-	-
37632 ++	-	--+	-	+	-	-	-	-	-
14574 ++	++	-	-	-	+	-	-	-	-
37268 ++	-	-	-	-	-	-	-	-	-
37488 ++	++	-	-	-	-	-	-	-	-
37381 ++	-	--+	+	+++	+	-	-	+++	-
37633 ++	++	-	-	-	-	-	-	-	-

36611 ++	+	–	+	+	+	+	-	-	-
37634 ++	++	-	-	-	-	-	-	-	-
37635 ++	+	–	+	+++	+	+++	---	-	-
37636 ++	+	-	-	-	-	-	-	-	-
37637 ++	++	–	-	-	-	-	-	-	-
37492 ++	++	-	-	-	-	-	-	-	-
37638 ++	++	-	-	-	-	-	-	-	-
36980 ++	+	-	-	-	-	-	-	-	-
37279 ++	+++	-	-	-	-	-	-	-	-
37588 ++	++	-	+	+	+	-	-	-	-
13998 ++	++	-	-	-	-	-	-	-	-
37639 ++	++	-	-	-	-	-	-	-	-
37640 ++	++	--+	+++	+++	+++	-	-	-	-
37400 ++	++	-	-	-	-	-	-	-	-
17736 ++	++	-	-	-	-	-	-	-	-
37635 ++	+	–	+	++	+	+++	---	-	-
37583 ++	++	-	-	-	-	-	-	-	-
12125 ++	++	--+	+++	+++	+++	-	-	-	-
12229 ++	-	-	-	-	-	-	-	-	-
14208 ++	++	-	-	-	-	-	-	-	-
36801 ++	++	-	-	-	-	-	-	-	-
36996 ++	+	-	-	-	-	-	-	-	-
36776 ++	+++	-	-	+	-	-	-	-	-
19016 ++	++	-	-	-	-	-	-	-	-
37511 ++	++	-	-	-	-	-	-	-	-
37557 ++	++	-	-	-	-	-	-	-	-
37641 ++	+	-	-	-	-	-	-	-	-
37642 ++	+	-	-	-	+	-	-	-	-
37314 ++	-	--+	+	+++	+	-	-	+++	-
37643 ++	+	-	-	-	-	-	-	-	-
17671 ++	-	-	-	-	-	-	-	-	-
37377 ++	++	-	-	-	-	-	-	-	-
37420 ++	-	--+	+	+++	+	+	-	-	-

11819 ++	-	-	-	-	-	-	-	-	-
37348 ++	+	--+	++	+++	++	++	-	-	-
12224 ++	++	-	-	-	-	-	-	-	-
11096 ++	++	-	-	-	-	-	-	-	-
14224 ++	+++	-	-	-	-	-	-	-	-
11841 ++	+	-	-	-	-	-	-	-	-
37192 ++	-	-	-	-	-	-	-	-	-
13843 ++	++	-	+	-	-	-	-	-	-
36823 ++	++	-	-	-	-	-	-	-	-
11864 ++	-	-	-	-	-	-	-	-	-
37460 ++	-	--+	+	+++	++	+	-	+++	-
14026 ++	++	-	-	-	-	-	-	-	-
37644 ++	++	-	-	-	-	-	-	-	-
37402 ++	+++	-	-	-	-	-	-	-	-
17775 ++	+	-	-	-	-	-	-	-	-
37149 ++	+++	--+	+++	+++	+++	+	-	-	-
37411 ++	++	--+	+++	+++	+++	+	-	-	-
37328 ++	-	-	-	-	-	-	-	-	-
11055 ++	+	-	-	-	-	-	-	-	-
36634 ++	+++	-	-	-	-	-	-	-	-
37490 ++	++	-	-	-	-	-	-	-	-
18566 ++	-	-	-	-	-	-	-	-	-
37612 ++	++	-	-	-	-	-	-	-	-
37394 ++	+	-	-	-	-	-	-	-	-
37426 ++	+	-	-	-	-	-	-	-	-
37281 ++	++	-	-	-	-	-	-	-	-
37643 ++	+	-	-	-	-	-	-	-	-
20014 ++	-	--+	+	+++	-	-	-	-	-
37127 ++	+	-	-	-	-	-	-	-	-
37606 ++	+	-	-	-	-	-	-	-	-
37645 ++	++	-	-	-	-	-	-	-	-
37084 ++	-	--	-	-	-	-	-	-	-
37641 ++	+	-	-	-	-	-	-	-	-

17775 ++	+	-	-	-	-	-	-	-	-
37646 ++	++	-	-	-	-	-	-	-	-
19261 ++	-	-	-	-	-	-	-	-	-
37647 ++	+	-	-	-	-	-	-	-	-
37648 ++	++	-	-	-	-	-	-	-	-
13698 ++	++	-	-	+	+	-	-	-	-
17946 ++	-	-	-	-	-	-	-	-	-
16613 ++	++	-	-	-	-	-	-	-	-
17754 ++	-	–	-	+	-	-	-	-	-
11648 ++	++	-	-	-	-	-	-	-	-
37410 ++	++	-	-	-	-	-	-	-	-
36624 ++	-	–+	+	+++	++	-	–	-	-
37341 ++	++	-	-	-	-	-	-	-	-
37088 ++	++	-	-	-	-	+	-	-	-
16593 ++	+	–+	+	+++	++	+	–	-	-
14958 ++	++	-	-	-	+	-	–	-	-
17736 ++	++	-	-	-	-	-	-	-	-
37410 ++	++	-	-	-	-	-	-	-	-
16581 ++	+++	-	-	-	+	-	–	-	-
37493 ++	+	-	-	-	-	-	-	-	-
11574 ++	++	-	-	-	-	-	-	-	-
37649 ++	++	-	-	-	-	-	-	-	-
36987 ++	++	-	-	-	-	-	-	-	-
11864 ++	-	-	-	-	-	-	-	-	-
12707 ++	-	-	-	-	-	-	-	-	-
37026 ++	++	-	-	-	-	-	-	-	-
37646 ++	++	-	-	-	-	-	-	-	-
37650 ++	++	-	-	-	-	-	-	-	-
37328 ++	-	-	-	-	-	-	-	-	-
37651 ++	+++	-	-	-	-	-	-	-	-
13833 ++	++	-	-	-	-	-	-	-	-
37652 ++	++	-	-	-	-	-	-	-	-
37366 ++	-	–+	++	+++	++	+	–	+++	-

13748 ++	++	–	-	-	-	-	-	-	-
37653 ++	++	-	-	-	-	-	-	-	-
37654 ++	++	–+	+++	+++	+++	-	-	-	-
37521 ++	+++	–+	+++	+++	+++	-	-	-	-
36784 ++	+	–+	++	+++	+++	+++	–	+++	+++
37401 ++	-	–+	++	+++	++	+	–	-	-
17596 ++	++	-	-	-	-	-	-	-	-
37655 ++	++	-	-	-	-	-	-	-	-
37285 ++	-	-	-	-	-	-	-	-	-
37591 ++	+	-	-	-	-	-	-	-	-
37656 ++	++	-	-	-	-	-	-	-	-
36767 ++	-	–+	+	+++	-	-	-	-	-
17025 ++	-	-	-	-	-	-	-	-	-
37373 ++	++	-	-	-	-	-	-	-	-
37367 ++	++	-	-	-	-	-	-	-	-
37326 ++	+	-	-	-	-	-	-	-	-
37242 ++	-	-	-	-	-	-	-	-	-
17543 ++	+++	-	-	+	+	-	-	-	-
15961 ++	++	-	-	-	-	-	-	-	-
37036 ++	-	–+	+	+++	+	+	-	-	-
17903 ++	++	-	-	-	-	-	-	-	-
11346 ++	++	-	+	-	+	+	-	-	-
17231 ++	+	–+	+++	+++	+++	-	-	-	-
37129 ++	++	-	-	-	-	-	-	-	-
36646 ++	++	-	-	-	+	-	-	-	-
37040 ++	++	-	-	-	-	-	-	-	-
37657 ++	-	–	-	-	-	-	-	-	-
36980 ++	+	-	-	-	-	-	-	-	-
37658 ++	++	-	-	+	-	-	-	-	-
17848 ++	-	-	-	-	-	-	-	-	-
36785 ++	-	-	-	-	-	-	-	-	-
37592 ++	+	-	-	-	+	+	–	-	-
37659 ++	-	-	-	-	-	-	-	-	-

37660 ++	-	-	-	-	-	-	-	-	-
37341 ++	++	-	-	-	-	-	-	-	-
11371 ++	++	-	-	-	-	-	-	-	-
37661 ++	-	-	-	-	-	-	-	-	-
37662 ++	++	-	-	-	-	-	-	-	-
37663 ++	++	-	-	-	-	-	-	-	-
17755 ++	-	-	+	-	-	-	-	-	-
10981 ++	+++	−−+	+++	+++	+++	-	-	-	-
37664 ++	-	−−+	+	++	-	-	-	-	-
12011 ++	++	-	-	-	-	-	-	-	-
37665 ++	++	-	-	-	-	-	-	-	-
11915 ++	-	-	-	-	-	-	-	-	-
37424 ++	+	-	-	+	-	-	−	-	-
37618 ++	-	-	-	-	-	-	-	-	-
37092 ++	++	-	-	-	-	-	-	-	-
37666 ++	+	-	-	-	-	+	-	-	-
37040 ++	++	-	-	-	-	-	-	-	-
37667 ++	-	−−+	+	++	-	-	-	-	-
37209 ++	++	−	+	++	++	-	-	-	-
37139 ++	-	−−+	+	++	-	-	-	+++	-
17680 ++	-	−−+	-	+++	+	-	−	-	-
11418 ++	++	-	-	-	-	-	-	-	-
37668 ++	++	-	-	-	-	-	-	-	-
37669 ++	+	-	-	-	-	-	-	-	-
37233 ++	+	-	-	-	-	-	-	-	-
36973 ++	++	-	-	-	-	-	-	-	-
12146 ++	++	-	-	-	-	-	-	-	-
37482 ++	++	-	-	-	-	-	-	-	-
37064 ++	++	-	-	-	-	-	-	-	-
37670 ++	++	-	-	-	-	-	-	-	-
37115 ++	++	-	-	-	-	-	-	-	-
37126 ++	+++	-	-	-	-	-	-	-	-
37006 ++	++	-	-	-	-	-	-	-	-

37636 ++	+	-	-	-	-	-	-	-	-
37308 ++	++	-	-	-	-	-	-	-	-
37671 ++	++	-	-	-	-	-	-	-	-
37672 ++	-	–	-	-	-	-	-	-	-
37585 ++	-	-	-	-	-	-	-	-	-
14502 ++	++	-	-	-	-	-	-	-	-
16080 ++	++	-	-	-	-	-	-	-	-
37673 ++	++	-	-	-	-	-	-	-	-
11493 ++	-	-	-	-	-	-	-	-	-
37227 ++	++	-	-	-	-	-	-	-	-
17728 ++	++	-	-	-	-	-	-	-	-
37491 ++	+	–+	++	+++	++	+++	---	+++	-
37655 ++	++	-	-	-	-	-	-	-	-
14082 ++	++	-	-	-	-	-	-	-	-
37674 ++	-	-	-	-	-	-	-	-	-
37561 ++	-	-	-	+	-	-	-	-	-
17888 ++	-	–+	+	+	-	-	-	-	-
12025 ++	-	-	-	-	-	-	-	-	-
37045 ++	+	-	-	-	-	-	-	-	-
37566 ++	++	-	-	-	-	-	-	-	-
37545 ++	+	-	-	-	-	-	-	-	-
36924 ++	++	–	+	+++	+++	-	-	-	-
37675 ++	-	–+	+	+++	-	-	-	-	-
17535 ++	-	–+	+	++	+	+	-	+++	-
37676 ++	+	-	-	-	-	-	-	-	-
37323 ++	-	–+	+	+	-	-	-	-	-
37202 ++	+	-	-	-	-	-	-	-	-
37677 ++	+++	-	-	-	-	-	–	-	-
11930 ++	+	-	-	-	-	-	-	-	-
37455 ++	++	-	-	-	-	-	-	-	-
37343 ++	++	-	-	-	-	-	-	-	-
37678 ++	++	-	-	-	-	-	-	-	-
37679 ++	-	–+	+	+	-	-	–	-	-

37415 ++	++	-	-	-	-	-	-	-	-
37680 ++	++	-	-	-	-	+	–	-	-
17590 ++	-	–+	+	+	-	-	-	-	-
37681 ++	-	-	-	-	-	-	-	-	-
37588 ++	++	-	+	+	+	-	-	-	-
37682 ++	+++	–	+	+	+	-	-	-	-
16639 ++	+	–+	++	+++	++	+++	––	-	-
37683 ++	-	–+	+++	+++	+++	-	-	-	-
37684 ++	++	–+	+++	+++	+++	-	-	-	-
37685 ++	++	-	-	-	-	-	-	-	-
37219 ++	-	-	-	-	-	-	-	-	-
16572 ++	++	-	-	-	-	-	-	-	-
13623 ++	++	-	-	-	-	-	-	-	-
37159 ++	++	-	-	-	-	-	-	-	-
36732 ++	-	-	-	-	-	-	-	-	-
17018 ++	+	-	+	-	-	++	––	-	-
37686 ++	++	–+	+++	+++	+++	+	-	-	-
17571 ++	-	–+	+	-	-	-	-	-	-
37687 ++	++	-	-	-	-	-	-	-	-
14102 ++	++	-	-	-	-	-	-	-	-
37688 ++	++	-	-	-	-	-	-	-	-
37689 ++	++	-	-	-	-	+	-	-	-
37690 ++	++	-	-	-	-	-	-	-	-
37477 ++	-	–	+	+	-	-	-	-	-
37691 ++	+	-	-	-	-	-	-	-	-
37617 ++	++	-	-	-	+	-	-	-	-
37671 ++	++	-	-	-	-	-	-	-	-
37692 ++	++	-	-	-	-	-	-	-	-
37431 ++	-	-	-	-	-	-	-	-	-
37693 ++	+	–	+	+	+	-	-	-	-
37694 ++	++	-	-	-	-	-	-	-	-
37437 ++	-	–+	+	-	-	-	-	-	-
37695 ++	++	-	-	-	-	-	-	-	-

37696 ++	++	–	+	+++	+++	-	-	-	-
37247 ++	-	-	-	-	-	-	-	-	-
20368 ++	++	-	-	-	-	-	-	-	-
37614 ++	++	-	-	-	-	-	-	-	-
37355 ++	-	–+	+	++	+	-	-	-	-
37349 ++	+	-	-	-	-	-	-	-	-
37697 ++	++	–+	+++	+++	+++	-	-	-	-
11561 ++	++	-	-	-	-	+	-	-	-
11615 ++	-	-	-	-	-	-	-	-	-
37698 ++	++	-	-	-	-	-	-	-	-
37699 ++	++	-	-	-	-	-	-	-	-
37700 ++	++	-	-	-	-	-	-	-	-
11424 ++	++	-	-	-	-	-	-	-	-
37645 ++	++	-	-	-	-	-	-	-	-
37701 ++	++	-	-	-	-	-	-	-	-
37702 ++	-	–	-	-	-	-	-	-	-
37703 ++	++	-	-	-	-	-	-	-	-
37330 ++	-	–+	+	+++	+	-	-	+++	++
11017 ++	+++	-	-	-	-	-	-	-	-
13564 ++	++	-	-	-	-	+	–	-	-
12073 ++	-	-	-	-	-	-	-	-	-
37663 ++	++	-	-	-	-	-	-	-	-
16581 ++	++	-	-	-	+	-	-	-	-
11188 ++	++	-	-	-	-	-	-	-	-
13523 ++	++	-	-	-	-	-	-	-	-
37704 ++	++	-	-	-	-	+	–	-	-
36806 ++	++	-	-	-	-	-	-	-	-
18966 ++	-	-	-	-	-	-	-	-	-
19304 ++	-	–+	-	+	-	-	-	-	-
37374 ++	++	-	-	-	+	-	-	-	-
37705 ++	-	-	-	-	-	-	-	-	-
14121 ++	++	-	-	-	-	-	-	-	-
37532 ++	-	-	-	-	-	-	-	-	-

13629 ++	++	–	+	+	+	++	––	+++	+++
37706 ++	++	-	-	-	-	-	-	-	-
37271 ++	++	-	-	-	-	-	-	-	-
37707 ++	++	-	-	-	-	-	-	-	-
11760 ++	++	-	-	-	-	-	-	-	-
37122 ++	++	-	-	-	-	-	-	-	-
37514 ++	-	–+	+	++	-	-	-	-	-
37644 ++	++	-	-	-	-	-	-	-	-
37708 ++	-	–+	-	-	-	-	-	-	-
37211 ++	++	-	-	-	-	-	-	-	-
37472 ++	-	-	-	-	-	-	-	-	-
36629 ++	++	–+	+++	+++	+++	-	-	-	-
37556 ++	-	–+	+	+++	+	-	-	+++	++
37709 ++	++	–	+	++	++	+++	––	-	-
37710 ++	++	–+	+	-	-	-	-	-	-
19230 ++	+	-	-	-	-	-	-	-	-
17666 ++	-	-	-	-	-	-	-	-	-
37025 ++	++	-	-	-	-	-	-	-	-
17159 ++	-	–+	+++	+++	+++	-	-	-	-
37711 ++	++	-	-	-	-	-	-	-	-
37712 ++	-	–+	+	+++	+	-	–	-	-
37713 ++	-	-	-	-	-	-	-	-	-
36809 ++	+++	-	-	-	-	-	-	-	-
37130 ++	-	-	-	-	-	-	-	-	-
37319 ++	-	–+	+	+++	+	-	-	+++	-
13623 ++	++	-	-	+	+	-	-	-	-
37714 ++	-	–+	+++	+++	+++	-	-	-	-
37715 ++	-	-	-	-	-	-	-	-	-
37572 ++	-	–+	+	+++	+	-	-	-	-
37643 ++	+	-	-	-	-	-	-	-	-
37643 ++	+	-	-	-	-	-	-	-	-
37716 ++	-	–+	+	+	-	-	-	-	-
37252 ++	++	-	-	-	+	+	–	-	-

17714 ++	-	--+	+	+++	+	+	-	+++	-
37672 ++	-	-	-	-	-	-	-	-	-
11316 ++	++	-	-	-	-	-	-	-	-
37717 ++	+	--+	++	+++	+++	+++	---	+++	-
37517 ++	++	-	-	-	-	-	-	-	-
37489 ++	-	-	-	-	-	-	-	-	-
37718 ++	-	--+	++	+++	+++	+	-	+++	-
37489 ++	-	-	-	-	-	-	-	-	-
36578 ++	++	-	-	-	-	-	-	-	-
37534 ++	+++	-	-	-	-	-	-	-	-
37367 ++	++	-	-	-	-	-	-	-	-
37547 ++	-	-	+	+++	-	-	-	-	-
37719 ++	-	-	-	-	-	-	-	-	-
17686 ++	-	--+	+	-	-	-	-	-	-
17016 ++	++	-	+	+	+	-	-	-	-
37575 ++	++	-	-	-	-	-	-	-	-
37720 ++	++	-	-	-	-	-	-	-	-
37471 ++	++	-	-	-	-	-	-	-	-
11419 ++	-	-	-	-	-	-	-	-	-
37721 ++	++	-	-	-	-	-	-	-	-
37276 ++	++	-	-	-	-	-	-	-	-
37722 ++	++	-	+	-	-	-	-	-	-
37490 ++	++	-	-	-	-	-	-	-	-
37723 ++	++	-	-	-	+	-	-	-	-
37724 ++	++	-	-	-	-	-	-	-	-
37725 ++	+	-	-	-	-	-	-	-	-
37036 ++	-	--+	+	+++	+	+	-	-	-
37726 ++	++	-	+	+	++	+	-	-	-
17759 ++	++	-	-	-	-	-	-	-	-
37727 ++	++	-	-	-	+	-	-	-	-
16004 ++	-	-	-	-	-	-	-	-	-
37643 ++	+	-	-	-	-	-	-	-	-
37728 ++	++	-	-	+	-	+	-	-	-

37580 ++	++	-	-	-	-	-	-	-	-
14139 ++	++	-	-	-	-	-	-	-	-
37729 ++	++	-	-	-	-	-	-	-	-
37730 ++	++	-	-	-	-	-	-	-	-
37646 ++	++	-	-	-	-	-	-	-	-
37731 ++	++	-	-	-	-	-	-	-	-
16610 ++	++	-	-	-	-	-	-	-	-
37732 ++	++	-	-	-	-	-	-	-	-
37733 ++	++	-	-	-	+	-	-	-	-
37645 ++	++	-	-	-	-	-	-	-	-
37734 ++	++	--	+++	++	+++	-	-	-	-
37735 ++	++	--+	+++	+++	+++	-	-	-	-
37736 ++	+	--+	+	+++	+++	+	-	+++	-
37335 ++	-	--+	+	+++	+	+	-	+++	-
37643 ++	+	-	-	-	-	-	-	-	-
11910 ++	++	-	-	-	-	-	-	-	-
36992 ++	+++	-	-	-	-	-	-	-	-
37737 ++	++	-	-	-	-	-	-	-	-
37531 ++	++	-	-	-	-	-	-	-	-
37603 ++	+++	-	-	-	-	-	-	-	-
37004 ++	-	--+	+	+	-	-	-	-	-
18295 ++	-	-	-	-	-	-	-	-	-
37706 ++	++	-	-	-	-	-	-	-	-
36943 ++	+	-	-	-	-	-	-	-	-
14242 ++	++	-	+	+	+	-	-	-	-
37085 ++	++	-	-	-	-	-	-	-	-
36624 ++	-	--+	+	+++	++	+	–	-	-
37362 ++	++	-	-	-	-	-	-	-	-
37631 ++	-	-	-	-	-	-	-	-	-
37738 ++	-	–	+	++	-	+	-	-	-
14502 ++	+	-	-	-	-	-	-	-	-
17681 ++	+++	-	-	-	-	-	-	-	-
36863 ++	++	-	-	-	-	-	-	-	-

37739 ++	++	-	-	-	-	-	-	-	-
17687 ++	+	-	-	-	-	-	-	-	-
37664 ++	-	--+	+	+++	-	-	-	+++	-
37740 ++	+	-	+	-	+	-	-	-	-
37741 ++	-	--+	+	+	-	-	-	-	-
37481 ++	++	-	-	-	-	-	-	-	-
37121 ++	++	-	-	-	-	-	-	-	-
37554 ++	-	-	+	+	+	-	-	-	-
37742 ++	++	-	-	-	-	-	-	-	-
37743 ++	++	--+	+++	+++	+++	+	-	-	-
37526 ++	+++	-	-	-	-	-	-	-	-
37744 ++	+	-	+	-	-	-	-	-	-
37745 ++	-	-	-	-	-	-	-	-	-
18704 ++	++	-	-	-	-	-	-	-	-
36969 ++	+++	-	-	-	-	-	-	-	-
11720 ++	-	-	-	-	-	-	-	-	-
37347 ++	++	-	-	-	-	-	-	-	-
36854 ++	+++	-	-	-	-	-	-	-	-
11483 ++	++	-	-	-	-	-	-	-	-
37248 ++	++	-	-	-	-	-	-	-	-
37746 ++	++	-	-	-	+	-	-	-	-
37747 ++	-	-	-	-	-	-	-	-	-
37748 ++	++	--+	+++	+++	+++	+	-	-	-
37563 ++	-	-	-	-	-	-	-	-	-
37027 ++	++	-	-	-	-	-	-	-	-
37749 ++	++	-	-	-	+	-	-	-	-
37206 ++	-	-	-	-	-	-	-	-	-
37750 ++	++	--+	+++	+++	+++	+	-	-	-
37751 ++	++	--+	+++	+++	+++	+	-	-	-
37742 ++	++	-	-	-	-	-	-	-	-
37752 ++	+	-	-	-	-	-	-	-	-
37668 ++	++	-	-	-	-	-	-	-	-
37753 ++	+	-	-	-	-	-	-	-	-

37754 ++	-	-	-	+	+	-	-	-	-
37376 ++	++	-	-	-	-	-	-	-	-
37755 ++	-	--+	+	+++	+	+	-	++	-
37475 ++	-	--+	+	+++	+	+	-	-	-
37756 ++	-	-	-	-	-	-	-	-	-
37638 ++	++	-	-	-	-	-	-	-	-
37386 ++	-	-	-	-	-	-	-	-	-
37757 ++	++	-	-	-	-	-	-	-	-
37758 ++	-	-	-	-	-	-	-	-	-
15954 ++	++	-	-	-	-	-	-	-	-
37759 ++	++	--+	+++	+++	+++	+	-	-	-
37701 ++	++	-	-	-	-	-	-	-	-
37760 ++	++	-	-	-	-	-	-	-	-
37761 ++	++	-	-	-	-	-	-	-	-
37136 ++	+	-	-	-	-	-	-	-	-
16571 ++	++	-	-	-	-	-	-	-	-
37762 ++	++	--+	+++	+++	+++	-	-	-	-
37380 ++	+	-	-	-	-	-	-	-	-
37763 ++	-	-	-	-	-	+	-	-	-
37764 ++	+	-	-	-	-	-	-	-	-
11879 ++	++	-	-	-	-	-	-	-	-
37765 ++	++	-	-	-	-	-	-	-	-
13928 ++	++	-	-	-	-	-	-	-	-
37625 ++	-	--+	+	+++	+	-	-	-	-
37559 ++	-	--+	+	+++	+	-	-	+++	-
37766 ++	-	--+	+	+++	+	-	-	+++	++
37682 ++	+++	-	+	+	+	-	-	-	-
11480 ++	-	-	-	-	-	-	-	-	-
15352 ++	++	--	+	++	+	+++	---	-	-
13530 ++	++	-	-	-	-	-	-	-	-
37754 ++	-	-	+	+	+	-	-	-	-
12348 ++	++	-	-	-	-	-	-	-	-
37767 ++	++	-	-	-	-	-	-	-	-

37768 ++	++	--+	+++	+++	+++	-	-	-	-
37761 ++	++	-	-	-	-	-	-	-	-
37505 ++	++	-	-	-	-	-	-	-	-
37133 ++	+++	-	-	-	-	-	-	-	-
37769 ++	++	-	-	-	-	-	-	-	-
37770 ++	-	-	-	-	-	-	-	-	-
37287 ++	++	-	-	-	-	-	-	-	-
37771 ++	-	-	-	-	-	-	-	-	-
37702 ++	-	-	-	-	-	-	-	-	-
17910 ++	-	--	+	++	-	-	-	-	-
37440 ++	-	-	-	-	-	-	-	-	-
37772 ++	-	-	+	-	-	+	-	-	-
37384 ++	-	-	-	-	-	-	-	-	-
37638 ++	++	-	-	-	-	-	-	-	-
37773 ++	+++	--+	+++	+++	+++	+	-	-	-
37774 ++	-	--+	+++	+++	+++	-	-	-	-
37548 ++	++	-	-	-	-	-	-	-	-
37775 ++	++	-	-	-	-	-	-	-	-
37776 ++	++	-	-	-	-	-	-	-	-
37525 ++	-	-	+	+	-	-	-	-	-
37777 ++	-	-	-	-	-	-	-	-	-
37778 ++	-	--+	+	+++	-	-	-	++	-
37290 ++	-	--+	+	-	-	-	-	-	-
37779 ++	++	-	-	-	+	-	-	-	-
37325 ++	++	-	-	-	-	-	-	-	-
14066 ++	+++	-	+	-	+	-	-	-	-
37780 ++	++	-	-	-	-	-	-	-	-
37781 ++	-	-	-	-	-	-	-	-	-
37500 ++	++	-	-	-	-	-	-	-	-
37442 ++	-	-	+	-	+	-	-	-	-
37641 ++	+	-	-	-	-	-	-	-	-
37782 ++	-	--+	++	+++	+	+++	---	+++	-
37309 ++	-	--+	+	+++	-	-	-	-	-

11087 ++	++	-	-	-	-	-	-	-	-
11774 ++	-	-	-	-	-	-	-	-	-
37292 ++	++	-	-	-	-	-	-	-	-
37783 ++	-	-	-	-	-	-	-	-	-
37729 ++	++	-	-	-	-	-	-	-	-
19263 ++	-	--+	-	-	-	-	-	-	-
11692 ++	-	-	-	-	-	-	-	-	-
37784 ++	++	-	-	-	-	-	-	-	-
37665 ++	++	-	-	-	-	-	-	-	-
11455 ++	-	-	-	-	-	-	-	-	-
37349 ++	+	-	-	-	-	-	-	-	-
13565 ++	++	-	+	+	+	+++	---	+++	-
37229 ++	++	-	-	-	-	-	-	-	-
37392 ++	-	-	-	-	-	-	-	-	-
37785 ++	++	-	-	-	-	-	-	-	-
37786 ++	+	--+	+++	+++	+++	-	-	-	-
37787 ++	+	--+	+++	+++	+++	+	-	-	-
37788 ++	++	--+	++	+	-	-	-	-	-
37601 ++	++	-	-	-	-	-	-	-	-
37789 ++	-	--+	+++	+++	+++	-	-	-	-
36843 ++	+	-	-	-	-	-	-	-	-
36797 ++	-	--+	+	-	-	-	-	-	-
37790 ++	++	--+	+++	+++	+++	-	-	-	-
37352 ++	-	--+	+	++	-	-	-	-	-
37542 ++	++	-	-	-	-	-	-	-	-
37791 ++	++	-	-	-	-	-	-	-	-
37652 ++	++	-	-	-	-	-	-	-	-
37792 ++	++	-	-	-	-	-	-	-	-
16108 ++	++	-	-	-	-	-	-	-	-
37793 ++	-	-	+	-	-	-	-	-	-
37794 ++	++	-	-	-	-	-	-	-	-
11853 ++	+	-	-	-	-	-	-	-	-
37795 ++	++	-	-	-	-	-	-	-	-

37725 ++	+	-	-	-	-	-	-	-	-
37796 ++	++	--+	+++	+++	+++	+	-	-	-
37699 ++	++	-	-	-	-	-	-	-	-
37680 ++	++	-	+	-	-	+	–	-	-
14743 ++	++	-	-	-	-	-	-	-	-
37495 ++	++	-	-	-	-	-	-	-	-
37797 ++	++	--+	+++	+++	+++	+	–	-	-
37478 ++	+++	--+	+++	+++	+++	+	–	+++	-
37798 ++	++	-	-	-	-	-	-	-	-
37799 ++	++	-	-	-	-	-	-	-	-
13835 ++	++	-	-	-	-	-	-	-	-
37566 ++	++	-	-	-	-	-	-	-	-
37586 ++	++	--+	+++	+++	+++	+	-	-	-
37765 ++	++	-	-	-	-	-	-	-	-
37378 ++	++	-	-	-	-	-	-	-	-
37281 ++	++	-	-	-	-	-	-	-	-
37800 ++	++	-	-	-	-	-	-	-	-
37801 ++	++	-	-	-	-	-	-	-	-
37301 ++	-	-	-	-	-	-	-	-	-
37480 ++	-	-	-	-	-	-	-	-	-
37802 ++	++	-	-	-	-	-	-	-	-
18056 ++	+++	-	-	-	-	-	-	-	-
37051 ++	++	–	+	-	+	-	–	-	-
37803 ++	++	-	-	-	+	-	-	-	-
37804 ++	+	--+	+++	+++	+++	-	–	-	-
11578 ++	++	-	-	-	-	-	-	-	-
37805 ++	+	--+	+++	+++	+++	+	–	-	-
37429 ++	-	--+	+	+++	++	+	-	+++	-
16217 ++	++	-	-	-	-	-	-	-	-
37806 ++	++	-	-	-	-	-	-	-	-
36607 ++	++	-	-	+	+	-	-	-	-
11483 ++	++	-	-	-	-	-	-	-	-
11423 ++	-	-	-	-	-	-	-	-	-

37807 ++	+	-	-	-	-	-	-	-	-
37808 ++	-	-	-	-	-	-	-	-	-
36925 ++	+	-	-	-	-	-	-	-	-
37240 ++	++	-	-	-	-	-	-	-	-
37598 ++	+	--+	+	+++	++	++	-	-	-
37809 ++	+	-	-	-	-	-	-	-	-
37810 ++	++	-	-	-	+	-	-	-	-
37673 ++	++	-	-	-	-	-	-	-	-
37773 ++	++	--+	+++	+++	+++	+	-	-	-
37237 ++	++	-	-	-	-	-	-	-	-
11177 ++	++	-	-	-	-	-	-	-	-
37811 ++	++	-	-	-	-	-	-	-	-
37717 ++	+	--+	++	+++	++	+++	--	+++	-
37812 ++	-	-	-	-	-	-	-	-	-
37674 ++	-	-	-	-	-	-	-	-	-
37813 ++	-	-	-	-	-	-	-	-	-
37814 ++	++	-	+	+	+	+++	---	-	-
37815 ++	++	-	-	-	-	-	-	-	-
37811 ++	++	-	-	-	-	-	-	-	-
37807 ++	+	-	-	-	-	+	-	-	-
37816 ++	++	-	-	-	-	-	-	-	-
37817 ++	-	--+	+	+	-	-	-	++	-
37283 ++	-	-	-	-	-	-	-	-	-
37818 ++	++	--+	+++	+++	+++	+	-	-	-
37294 ++	++	-	-	-	-	-	-	-	-
37447 ++	++	-	-	-	-	-	-	-	-
37557 ++	++	-	-	-	-	-	-	-	-
13924 ++	++	-	-	-	-	-	-	-	-
13565 ++	++	-	+	+	-	+++	---	-	-
37819 ++	++	-	-	-	-	-	-	-	-
37820 ++	++	-	-	-	-	-	-	-	-
37821 ++	++	--+	+++	+++	+++	+	-	-	-
37822 ++	++	-	-	-	+	-	-	-	-

37557 ++	++	-	-	-	-	+	-	-	-
37658 ++	++	-	-	-	-	-	-	-	-
17694 ++	-	-	-	-	-	-	-	-	-
17607 ++	-	--	+	-	-	-	-	-	-
37823 ++	-	--+	+	+++	+	-	-	-	-
18232 ++	++	-	-	-	-	-	-	-	-
37824 ++	++	-	-	-	-	-	-	-	-
37733 ++	++	-	-	-	+	-	-	-	-
11182 ++	++	-	-	-	-	-	-	-	-
36914 ++	-	--+	+	+++	+	-	-	-	-
37612 ++	++	-	-	-	-	-	-	-	-
18232 ++	++	-	-	-	-	-	-	-	-
37825 ++	+	--+	+++	+++	+++	-	-	-	-
37535 ++	++	-	-	-	-	-	-	-	-
17863 ++	-	-	-	-	+	+	-	-	-
37826 ++	++	-	-	-	-	-	-	-	-
14418 ++	++	-	-	-	-	-	-	-	-
37827 ++	+	-	-	-	-	-	-	-	-
37828 ++	++	-	-	-	-	-	-	-	-
37829 ++	++	-	+	+	+	+	-	-	-
37830 ++	++	-	+	+	+	+	-	-	-
37831 ++	++	-	-	-	-	-	-	-	-
37710 ++	++	--+	+	-	-	-	-	-	-
37020 ++	++	-	-	-	-	-	-	-	-
37832 ++	++	-	-	-	-	-	-	-	-
37833 ++	-	--	+	-	-	+	-	-	-
37834 ++	++	-	-	-	-	-	-	-	-
37577 ++	-	-	-	-	-	-	-	-	-
37835 ++	++	-	-	-	-	-	-	-	-
37836 ++	++	-	-	-	-	+	-	-	-
37837 ++	+	-	-	-	-	-	-	-	-
37275 ++	++	-	-	-	-	-	-	-	-
11841 ++	+	-	-	-	-	-	-	-	-

37838 ++	++	-	-	-	-	-	-	-	-
37212 ++	+	-	-	-	-	-	-	-	-
37839 ++	++	–	+	+	+	+++	---	-	-
37840 ++	-	-	-	-	-	-	-	-	-
37767 ++	++	-	-	-	-	-	-	-	-
37841 ++	++	-	-	-	-	-	-	-	-
19221 ++	-	--+	-	+	-	-	–	-	-
37802 ++	++	-	-	-	-	-	-	-	-
37088 ++	++	-	-	-	-	-	-	-	-
37842 ++	-	–	-	-	-	-	-	-	-
17918 ++	-	-	-	-	-	-	-	-	-
37843 ++	+	--+	+++	+++	+++	-	–	-	-
37788 ++	++	--+	++	-	-	-	-	-	-
20368 ++	++	-	-	-	-	-	-	-	-
17197 ++	++	--+	+++	+++	+++	++	--	-	-
37844 ++	-	-	-	-	-	-	-	-	-
37845 ++	++	-	-	-	-	-	-	-	-
11735 ++	++	-	-	-	-	-	-	-	-
37846 ++	+	-	-	-	-	-	-	-	-
37730 ++	++	-	-	-	-	-	-	-	-
37461 ++	++	-	-	-	-	-	-	-	-
37632 ++	-	--+	+	-	-	-	-	-	-
37847 ++	++	-	-	-	-	-	-	-	-
18597 ++	++	-	-	-	-	-	-	-	-
17065 ++	+	--+	++	+++	+	+	–	-	-
37848 ++	-	-	-	-	-	-	-	-	-
37429 ++	-	--+	+	+++	+	-	-	-	-
37304 ++	++	-	-	-	-	-	-	-	-
37474 ++	++	-	-	-	-	-	-	-	-
14231 ++	++	-	-	-	-	-	-	-	-
11776 ++	-	-	-	-	-	-	-	-	-
37849 ++	++	-	+	-	-	+	-	-	-
37219 ++	-	-	-	-	-	-	-	-	-

37850 ++	+	-	-	-	-	-	-	-	-
37731 ++	++	-	-	-	-	-	-	-	-
37851 ++	++	–	+	+	+	-	-	-	-
37852 ++	++	-	-	-	-	-	-	-	-
37853 ++	++	-	-	-	-	-	-	-	-
11875 ++	+	-	-	-	-	-	-	-	-
11192 ++	++	-	-	-	+	-	-	-	-
37119 ++	+	-	-	-	-	-	-	-	-
36732 ++	-	-	-	-	-	-	-	-	-
36732 ++	-	-	-	-	-	-	-	-	-
37854 ++	++	-	+	+	+	-	-	-	-
37855 ++	++	-	-	-	-	-	-	-	-
37856 ++	++	-	-	-	-	-	-	-	-
14618 ++	+++	–	+	+	+	+++	---	-	-
17571 ++	-	--+	+	+	-	+	-	-	-
37857 ++	+	-	-	-	-	-	-	-	-
37816 ++	++	-	-	-	-	-	-	-	-
18089 ++	-	--	-	-	-	-	-	-	-
37363 ++	++	-	-	-	+	-	-	-	-
37249 ++	++	-	-	-	-	-	-	-	-
11757 ++	-	-	-	-	-	-	-	-	-
37749 ++	++	-	-	-	-	-	-	-	-
37544 ++	++	-	-	-	-	-	-	-	-
37651 ++	+++	-	-	-	-	-	-	-	-
11910 ++	++	-	-	-	-	-	-	-	-
17308 ++	++	--+	+++	+++	+++	+	–	-	-
37373 ++	+++	-	-	-	-	-	-	-	-
17049 ++	-	--+	++	+++	+	-	-	-	-
11285 ++	++	-	-	-	-	-	-	-	-
37858 ++	-	-	-	-	-	-	-	-	-
37250 ++	++	--+	+++	+++	+++	+	–	-	-
37859 ++	++	–	+	+	+	-	-	-	-
37860 ++	++	-	-	-	-	-	-	-	-

37832 ++	++	-	-	-	-	-	-	-	-
37249 ++	++	-	-	-	-	-	-	-	-
37455 ++	++	-	-	-	-	-	-	-	-
37861 ++	++	-	-	-	-	-	-	-	-
37421 ++	++	-	-	-	-	-	-	-	-
37360 ++	++	-	-	-	-	-	-	-	-
37861 ++	++	-	-	-	-	-	-	-	-
11285 ++	++	-	-	-	-	-	-	-	-
37862 ++	+	-	-	-	-	-	-	-	-
37863 ++	++	-	-	-	-	-	-	-	-
11816 ++	+++	-	-	-	-	-	-	-	-
14208 ++	++	-	-	-	-	-	-	-	-
36751 ++	+++	–	++	++	++	+++	---	-	-
37864 ++	++	-	-	-	-	-	-	-	-
37376 ++	++	-	-	-	-	-	-	-	-
37170 ++	++	-	-	-	-	-	-	-	-
17780 ++	++	-	-	-	-	-	-	-	-
37865 ++	++	-	-	-	-	-	-	-	-
37866 ++	++	–	+	++	+++	+	–	-	-
37737 ++	++	-	-	-	-	-	-	-	-
37867 ++	-	--	+	+	+	-	-	-	-
37868 ++	++	-	-	-	-	-	-	-	-
37869 ++	+	-	-	-	-	-	-	-	-
37870 ++	-	-	-	-	-	-	-	-	-
37871 ++	-	--+	+	-	-	-	-	-	-
37864 ++	++	-	-	-	-	-	-	-	-
37872 ++	++	-	-	-	-	-	-	-	-
37709 ++	++	–	+	++	++	++	--	-	-
37873 ++	++	-	-	-	-	-	-	-	-
37275 ++	++	-	-	-	-	-	-	-	-
37727 ++	++	-	-	-	+	-	–	-	-
12101 ++	++	-	-	-	-	-	-	-	-
37375 ++	-	-	-	-	-	-	-	-	-

17686 ++	-	--+	-	-	-	-	-	-	-
11177 ++	++	-	-	-	-	-	-	-	-
37874 ++	+	-	-	+	+	-	-	-	-
11916 ++	-	-	-	-	-	-	-	-	-
37875 ++	-	-	-	-	-	-	-	-	-
37876 ++	++	-	-	-	-	-	-	-	-
12667 ++	++	-	-	-	+	-	-	-	-
37645 ++	++	-	-	-	-	-	-	-	-
37693 ++	+	–	+	+	+	-	-	-	-
37730 ++	++	-	-	-	-	-	-	-	-
11732 ++	-	-	-	-	-	-	-	-	-
37732 ++	++	-	-	-	-	-	-	-	-
37877 ++	++	--+	+++	+++	+++	+	–	-	-
37878 ++	-	-	-	-	-	-	-	-	-
37351 ++	++	-	-	-	-	-	-	-	-
37879 ++	-	--+	++	+++	+	++	--	-	-
37880 ++	++	-	-	-	-	-	-	-	-
37622 ++	++	-	-	-	-	-	-	-	-
37881 ++	++	-	-	-	-	-	-	-	-
37512 ++	++	-	-	-	-	-	-	-	-
36827 ++	-	--	+	+++	+	-	-	-	-
37882 ++	++	-	+	-	-	+++	---	-	-
36937 ++	-	--+	+	+++	+	-	-	-	-
37806 ++	++	-	-	-	-	-	-	-	-
36966 ++	++	-	-	-	-	-	-	-	-
37883 ++	++	-	-	-	-	-	-	-	-
16057 ++	++	-	-	-	-	-	-	-	-
37783 ++	-	-	-	-	+	-	-	-	-
37557 ++	++	-	-	-	-	+	–	-	-
37667 ++	-	--+	+	++	-	-	–	-	-
36980 ++	+	-	-	-	-	-	-	-	-
37628 ++	++	-	-	-	-	-	-	-	-
16572 ++	+++	-	-	-	-	-	-	-	-

37884 ++	-	-	-	-	-	-	-	-	-
37885 ++	++	-	-	-	-	-	-	-	-
37405 ++	++	-	-	-	-	-	-	-	-
37886 ++	++	–	+	+++	+++	+	–	-	-
37684 ++	++	---+	+++	+++	+++	-	-	+++	+++
37441 ++	++	-	-	-	-	-	-	-	-
37263 ++	++	-	+	++	++	-	-	-	-
37887 ++	++	-	-	-	-	-	-	-	-
11797 ++	++	-	-	-	-	-	-	-	-
37888 ++	++	-	-	-	-	-	-	-	-
36873 ++	+++	-	-	-	-	-	-	-	-
37158 ++	++	---+	+++	+++	+++	-	-	-	-
37780 ++	++	-	-	-	-	-	-	-	-
37889 ++	-	-	-	-	-	-	-	-	-
37890 ++	++	-	-	-	-	-	-	-	-
37891 ++	+	---+	+++	+++	+++	-	--	-	-
36950 ++	++	-	-	-	-	-	-	-	-
37892 ++	+	---+	++	+++	++	-	-	+++	-
37705 ++	-	-	-	-	-	-	-	-	-
16043 ++	++	-	-	-	-	-	-	-	-
37893 ++	-	-	-	-	-	-	-	-	-
37482 ++	++	-	-	-	-	-	-	-	-
11667 ++	++	-	-	-	-	-	-	-	-
18673 ++	++	-	-	-	-	-	-	-	-
37812 ++	-	-	-	-	-	-	-	-	-
37894 ++	++	-	-	-	-	+	-	-	-
37719 ++	+	-	-	-	-	-	-	-	-
37895 ++	+	-	-	-	+	-	-	-	-
11796 ++	++	-	-	-	-	-	-	-	-
37896 ++	+	-	-	-	-	-	-	-	-
37897 ++	+	-	-	-	-	-	-	-	-
37844 ++	-	-	-	-	-	-	-	-	-
17446 ++	++	-	-	-	-	-	-	-	-

17652 ++	++	-	-	-	-	-	-	-	-
18772 ++	+	--	++	++	++	-	-	-	-
37249 ++	++	-	-	-	-	-	-	-	-
37898 ++	+	-	+	-	-	-	-	-	-
11172 ++	++	-	-	-	-	-	-	-	-
37899 ++	++	-	-	-	-	-	-	-	-
37900 ++	-	--+	+	+++	+	-	-	+++	-
19485 ++	++	-	-	-	-	-	-	-	-
16634 ++	++	-	-	-	-	-	-	-	-
18112 ++	-	-	-	-	-	-	-	-	-
37901 ++	++	-	-	-	-	-	-	-	-
37757 ++	++	-	-	-	-	-	-	-	-
37595 ++	++	-	-	-	-	-	-	-	-
37280 ++	+	-	-	-	-	-	-	-	-
36843 ++	+	-	-	-	+	-	–	-	-
37902 ++	-	-	-	-	-	-	-	-	-
37903 ++	+	-	-	-	-	-	-	-	-
37574 ++	-	--+	+	+	-	-	-	-	-
36799 ++	+	-	-	-	-	-	-	-	-
11389 ++	++	-	-	-	-	-	-	-	-
37372 ++	++	-	-	-	-	-	-	-	-
37785 ++	++	-	-	-	-	-	-	-	-
37904 ++	-	-	-	-	-	-	-	-	-
37905 ++	+	-	-	-	-	-	-	-	-
37906 ++	++	-	-	-	-	-	-	-	-
37340 ++	-	--+	+	+++	+	-	-	+++	++
37907 ++	+	-	-	-	-	-	-	-	-
37698 ++	++	-	-	-	-	-	-	-	-
37566 ++	++	-	-	-	-	-	-	-	-
37908 ++	++	-	-	-	-	-	-	-	-
37909 ++	++	-	-	-	-	-	-	-	-
37910 ++	++	-	-	-	-	-	-	-	-
37911 ++	+	-	+	-	-	+	-	-	-

37328 ++	-	-	-	-	-	-	-	-	-
13181 ++	++	-	-	-	-	-	-	-	-
37705 ++	-	-	-	-	-	-	-	-	-
37784 ++	++	-	-	-	-	-	-	-	-
37397 ++	++	-	+	+	+	-	-	-	-
13596 ++	++	-	-	-	-	+++	--	-	-
16597 ++	+++	-	-	-	+	-	-	-	-
37345 ++	-	-	+	-	-	-	-	-	-
37912 ++	++	-	-	-	-	-	-	-	-
37260 ++	-	-	-	-	-	-	-	-	-
37620 ++	++	-	-	-	-	-	-	-	-
37913 ++	+	--+	+++	+++	+++	-	-	-	-
14281 ++	++	-	-	-	-	-	-	-	-
37914 ++	+	-	-	-	-	-	-	-	-
37915 ++	++	-	-	-	-	-	-	-	-
17808 ++	+	-	-	-	-	-	-	-	-
37916 ++	++	-	-	-	+	-	-	-	-
37917 ++	++	-	+	-	-	-	-	-	-
37589 ++	-	-	-	-	-	-	-	-	-
37739 ++	++	-	-	-	-	-	-	-	-
37840 ++	-	-	-	-	-	-	-	-	-
37918 ++	+	--+	+++	+++	+++	-	-	-	-
37824 ++	++	-	-	-	-	-	-	-	-
37573 ++	++	-	-	-	-	-	-	-	-
17722 ++	++	-	-	-	-	-	-	-	-
37919 ++	++	-	-	-	-	-	-	-	-
37216 ++	++	-	-	-	-	-	-	-	-
37920 ++	-	-	-	-	-	-	-	-	-
11688 ++	++	-	-	-	-	-	-	-	-
37921 ++	++	-	+	+	+	-	-	-	-
37922 ++	++	-	-	-	-	-	-	-	-
37923 ++	+	-	-	-	-	-	-	-	-
12913 ++	-	-	-	-	-	-	-	-	-

37924 ++	++	–	+	+	+	+++	---	-	-
16563 ++	++	-	-	-	+	-	-	-	-
12294 ++	-	-	-	-	-	-	-	-	-
37728 ++	++	-	-	-	+	+	–	-	-
37925 ++	-	-	-	-	-	-	-	-	-
11306 ++	++	-	-	-	-	-	-	-	-
37665 ++	++	-	-	-	-	-	-	-	-
37926 ++	++	-	-	-	-	-	-	-	-
13877 ++	++	-	-	-	+	-	-	-	-
37927 ++	-	-	-	-	-	-	-	-	-
11848 ++	-	-	-	-	-	-	-	-	-
11206 ++	++	-	-	-	-	-	-	-	-
37928 ++	++	-	-	-	-	-	-	-	-
37565 ++	++	-	-	-	-	-	-	-	-
36732 ++	-	-	-	-	-	-	-	-	-
37929 ++	+	-	-	-	-	-	-	-	-
14924 ++	++	–	+	+	+	+++	---	-	-
37880 ++	++	-	-	-	-	-	-	-	-
37626 ++	-	–	-	-	-	-	-	-	-
37450 ++	++	-	-	-	-	-	-	-	-
37930 ++	++	-	-	-	-	-	-	-	-
37921 ++	++	–	+	+	+	-	-	-	-
37931 ++	-	-	-	-	-	-	-	-	-
17717 ++	-	-	-	-	-	-	-	-	-
11486 ++	++	-	-	-	-	-	-	-	-
18345 ++	-	-	-	-	-	-	-	-	-
14464 ++	++	-	-	-	-	-	-	-	-
37616 ++	-	-	-	-	-	-	-	-	-
11644 ++	-	-	-	-	-	-	-	-	-
37932 ++	+	-	-	-	+	-	-	-	-
14860 ++	++	-	-	-	-	-	-	-	-
37933 ++	-	--+	+	+++	+	-	-	+++	-
18460 ++	++	-	-	-	-	-	-	-	-

37704 ++	++	-	-	-	-	-	-	-	-
37934 ++	-	–	-	-	-	-	-	-	-
37832 ++	++	-	-	-	-	-	-	-	-
37616 ++	-	-	-	-	-	-	-	-	-
37020 ++	++	-	-	-	+	-	-	-	-
12025 ++	-	-	-	-	-	-	-	-	-
37333 ++	-	-	-	-	-	-	-	-	-
37734 ++	++	––	+++	+++	+++	-	-	-	-
37826 ++	++	-	-	-	-	-	-	-	-
37820 ++	++	-	-	-	-	-	-	-	-
37935 ++	++	-	-	-	-	-	-	-	-
37936 ++	++	-	-	-	-	-	-	-	-
37776 ++	++	-	-	-	-	-	-	-	-
37610 ++	-	––+	+	+++	+	-	-	-	-
37869 ++	+	-	-	-	-	-	-	-	-
37884 ++	-	-	-	-	-	-	-	-	-
17023 ++	-	-	-	-	-	-	-	-	-
15954 ++	++	-	-	-	-	-	-	-	-
37666 ++	-	-	-	-	+	+	-	-	-
37509 ++	++	-	-	-	-	-	-	-	-
37509 ++	++	-	-	-	-	-	-	-	-
37937 ++	+	-	-	-	-	-	-	-	-
37938 ++	++	-	-	-	-	-	-	-	-
17680 ++	-	––+	-	+++	-	-	-	-	-
37939 ++	+	-	-	-	-	-	-	-	-
13985 ++	++	-	-	-	-	-	-	-	-
37795 ++	++	-	-	-	-	-	-	-	-
37605 ++	++	-	-	-	-	-	-	-	-
14418 ++	++	-	-	-	-	-	-	-	-
37940 ++	-	––+	+	+++	-	-	-	-	-
15947 ++	++	-	-	-	-	-	-	-	-
37322 ++	-	-	-	-	-	-	-	-	-
14242 ++	++	-	+	-	+	-	-	-	-

37941 ++	++	-	-	-	-	-	-	-	-
37942 ++	-	-	-	-	-	-	-	-	-
37943 ++	++	-	-	-	-	-	-	-	-
37221 ++	+	--+	+	++	+	+++	---	-	-
37944 ++	+	-	-	-	-	-	-	-	-
37945 ++	++	-	-	-	-	-	-	-	-
11656 ++	-	-	-	-	-	-	-	-	-
37946 ++	++	--+	+++	+++	+++	-	-	-	-
11783 ++	-	-	-	-	-	-	-	-	-
37947 ++	++	-	-	-	-	-	-	-	-
13564 ++	++	-	-	-	+	+	-	-	+++
37948 ++	++	-	-	-	-	-	-	-	-
37299 ++	++	-	-	-	-	-	-	-	-
37912 ++	++	-	-	-	-	-	-	-	-
37949 ++	+	--+	+++	+++	+++	+	-	-	-
37950 ++	-	-	-	-	-	-	-	-	-
36961 ++	+++	-	-	-	-	-	-	-	-
37951 ++	-	-	-	-	-	-	-	-	-
11164 ++	-	-	-	-	-	-	-	-	-
36731 ++	+	-	-	-	-	-	-	-	-
37523 ++	++	-	-	-	-	-	-	-	-
17797 ++	-	-	-	-	-	-	-	-	-
37367 ++	++	-	-	-	-	-	-	-	-
37952 ++	++	-	-	-	-	-	-	-	-
17652 ++	++	-	-	-	-	-	-	-	-
36859 ++	+++	-	-	-	-	-	-	-	-
37910 ++	++	-	-	-	-	-	-	-	-
17578 ++	-	--+	+	+	-	-	-	-	-
37953 ++	-	--+	-	+	-	-	-	-	-
37895 ++	+	-	-	-	-	-	-	-	-
37954 ++	-	--+	+++	+++	+++	-	-	-	-
37955 ++	++	-	-	-	-	-	-	-	-
37956 ++	-	--+	+	-	-	-	-	-	-

37747	++	-	-	-	-	-	-	-	-
37580	++	++	-	-	-	-	-	-	-
37259	++	-	-	-	-	-	-	-	-
37646	++	++	-	-	-	-	-	–	-
37957	++	++	–+	+++	+++	+++	-	-	-
37553	++	-	-	-	-	-	-	-	-
11683	++	++	-	-	-	-	-	-	-
37958	++	++	-	-	-	-	-	-	-
11596	++	+	-	-	-	-	-	-	-
37959	++	+	-	-	-	-	-	-	-
37078	++	++	-	-	-	-	-	–	-
20373	++	++	-	-	-	-	-	-	-
12392	++	-	-	-	-	-	-	-	-
37055	++	++	-	-	+	+	-	-	-
37049	++	-	–+	+	+++	+	-	-	+++
12543	++	++	-	-	-	-	-	-	-
12097	++	-	-	-	-	-	-	-	-
37960	++	++	-	-	-	-	-	-	-
14367	++	+++	-	-	-	-	-	-	-
37961	++	-	-	-	-	-	-	-	-
14219	++	++	-	-	-	-	-	-	-
12827	++	++	–+	+++	+++	+++	+	–	-
37962	++	++	-	-	-	-	-	-	-
37154	++	+	-	-	-	-	-	-	-
11615	++	-	-	-	-	-	-	-	-
14540	++	++	-	-	-	-	-	-	-
37963	++	++	-	-	-	-	-	-	-
37964	++	-	–+	+++	+	-	-	-	-
16038	++	++	-	-	-	-	-	-	-
36542	++	++	-	-	-	-	-	–	-
37965	++	+	-	-	-	-	+	–	-
37403	++	++	-	-	-	-	-	-	-
37791	++	++	-	-	-	-	-	-	-

16602 ++	+	-	+	-	+	-	-	-	-
19078 ++	-	-	-	-	-	-	-	-	-
37966 ++	+	--+	+	+++	+	-	-	+++	+++
37637 ++	++	-	-	-	-	-	-	-	-
37967 ++	-	–	+	-	-	-	–	-	-
37656 ++	++	-	-	-	-	-	-	-	-
37207 ++	+	–	+	++	+	+	–	-	-
17848 ++	-	-	-	-	-	-	-	-	-
37968 ++	-	--+	+++	+++	+++	+	–	-	-
16634 ++	++	-	-	-	-	-	-	-	-
37969 ++	++	-	-	-	-	-	-	-	-
37970 ++	++	-	-	-	-	-	-	-	-
37971 ++	++	--+	+	-	-	-	-	-	-
37653 ++	++	-	-	-	-	-	-	-	-
37471 ++	++	-	-	-	-	-	-	-	-
37685 ++	++	-	-	-	-	-	-	-	-
37972 ++	++	-	-	-	-	-	-	-	-
37973 ++	++	-	-	-	-	-	-	-	-
18878 ++	+++	-	-	-	-	-	-	-	-
37974 ++	-	--+	+	++	+	-	-	+++	-
37975 ++	++	-	-	-	-	-	-	-	-
37501 ++	-	--+	++	+++	++	+++	---	+++	+++
37490 ++	++	-	-	-	-	-	-	-	-
37069 ++	++	-	-	-	-	+	–	-	-
37736 ++	+	--+	+	+++	+++	+	-	-	-
37976 ++	+	--+	+++	+++	+++	-	–	-	-
37623 ++	-	--+	+	+++	-	+	-	+++	-
17739 ++	-	-	-	-	-	-	-	-	-
37654 ++	++	--+	+++	+++	+++	-	-	-	-
37977 ++	-	--	-	++	-	-	-	-	-
15977 ++	++	-	-	-	-	-	-	-	-
37978 ++	+	-	-	-	+	-	–	-	-
16609 ++	+	-	-	-	+	+	–	-	-

37979 ++	++	-	-	-	-	-	-	-	-
37887 ++	++	-	-	-	-	-	-	-	-
17059 ++	++	-	-	-	-	-	-	-	-
37980 ++	++	-	-	-	-	-	-	-	-
11133 ++	++	-	-	-	+	-	-	-	-
36851 ++	+++	--+	+++	+++	+++	+	-	-	-
37981 ++	+	--+	+	-	-	-	-	-	-
37961 ++	-	-	-	-	-	-	-	-	-
37971 ++	++	--+	+	-	-	-	-	-	-
37578 ++	+	-	-	-	-	+	-	-	-
37982 ++	++	-	-	-	-	-	-	-	-
37529 ++	-	-	-	+	-	-	-	-	-
17535 ++	-	--+	+	++	-	-	-	+++	-
37983 ++	-	-	-	-	-	-	-	-	-
37984 ++	-	-	-	-	-	-	-	-	-
37985 ++	-	-	-	-	-	-	-	-	-
37986 ++	++	-	+	-	-	-	-	-	-
37890 ++	++	-	-	-	-	-	-	-	-
17660 ++	++	-	-	-	-	-	-	-	-
37987 ++	++	-	-	-	-	-	-	-	-
17034 ++	++	-	-	-	-	-	-	-	-
37892 ++	+	--+	++	+++	++	+	-	+++	+
37988 ++	++	-	+	-	-	+	-	-	-
37711 ++	++	-	-	-	-	-	-	-	-
37989 ++	-	-	-	-	-	-	-	-	-
37966 ++	+	--+	+	+++	+	+	-	+++	-
37990 ++	+	-	-	-	-	-	-	-	-
17139 ++	++	--+	+++	+++	+++	+	-	-	-
14607 ++	++	-	-	-	-	-	-	-	-
37991 ++	+++	--+	+++	+++	+++	+	-	-	-
37575 ++	++	-	-	-	-	-	-	-	-
37992 ++	-	--+	+++	+++	+++	-	-	-	-
37993 ++	++	-	+	+	+	-	-	-	-

37994 ++	+	-	-	-	+	+++	---	-	-
37995 ++	++	-	-	-	-	-	-	-	-
37695 ++	++	-	-	-	-	-	-	-	-
37834 ++	++	-	-	-	-	-	-	-	-
37910 ++	++	-	-	-	-	-	-	-	-
13589 ++	++	-	-	-	-	+	-	-	-
37996 ++	++	-	-	-	-	-	-	-	-
37972 ++	++	-	-	-	-	-	-	-	-
37624 ++	+	-	-	-	-	-	-	-	-
37997 ++	++	-	-	-	-	-	-	-	-
37998 ++	-	–	-	-	-	+	–	-	-
37999 ++	++	-	-	-	-	-	-	-	-
38000 ++	++	-	-	-	-	-	-	-	-
38001 ++	-	-	-	-	-	-	-	-	-
37224 ++	-	--+	+	+	-	-	-	+++	-
38002 ++	-	-	-	-	-	-	-	-	-
37568 ++	+	-	-	-	-	-	-	-	-
38003 ++	++	-	-	-	-	-	-	-	-
37865 ++	++	-	-	-	-	-	-	-	-
37243 ++	-	-	-	-	-	-	-	-	-
37600 ++	++	-	-	-	-	-	-	-	-
16151 ++	++	-	+	+	+	-	-	-	-
37665 ++	++	-	-	-	-	-	-	-	-
37902 ++	-	-	-	-	-	-	-	-	-
37616 ++	-	-	-	-	-	-	-	-	-
38004 ++	-	-	-	-	-	-	-	-	-
38005 ++	++	-	-	-	-	-	–	-	-
37756 ++	-	-	-	-	-	-	-	-	-
12523 ++	-	-	-	-	-	-	-	-	-
38006 ++	++	-	-	-	-	-	-	-	-
37361 ++	++	-	-	-	-	-	-	-	-
36843 ++	+	-	-	-	-	-	-	-	-
16570 ++	++	-	+	+	+	-	-	-	-

38007	++	+	--+	+++	+++	+++	-	-	-	-
17708	++	-	--+	+	+++	+	+	-	-	-
14023	++	++	-	-	-	-	-	-	-	-
38008	++	+	-	-	-	-	-	-	-	-
37088	++	++	-	-	-	-	-	-	-	-
18040	++	-	-	-	-	-	-	-	-	-
38009	++	++	--+	+++	+++	+++	+	-	-	-
37862	++	+	-	-	-	-	-	-	-	-
37962	++	++	-	-	-	-	-	-	-	-
38010	++	++	-	-	-	-	-	-	-	-
38011	++	+	-	-	-	-	-	-	-	-
38012	++	-	-	-	-	-	+	-	-	-
36846	++	+++	-	-	-	-	-	-	-	-
37809	++	+	-	-	-	-	-	-	-	-
37761	++	++	-	-	-	-	-	-	-	-
37367	++	++	-	-	-	-	-	-	-	-
18932	++	-	-	-	+	-	+	-	-	-
38013	++	++	-	-	-	-	-	-	-	-
38014	++	-	--+	+	+	+	-	-	+++	-
38015	++	++	-	-	+	+	-	-	-	-
38016	++	++	--+	+++	+++	+++	-	-	-	-
37856	++	++	-	-	-	-	-	-	-	-
13546	++	++	-	-	-	-	-	-	-	-
37808	++	-	-	-	+	-	-	-	-	-
17784	++	-	-	-	-	-	-	-	-	-
13995	++	++	-	-	-	-	-	-	-	-
38017	++	-	-	-	-	-	-	-	-	-
38018	++	+	-	-	-	-	-	-	-	-
38019	++	-	-	-	-	-	-	-	-	-
38020	++	++	-	-	-	-	-	-	-	-
38021	++	+	-	-	-	-	-	-	-	-
38022	++	++	--+	+++	+++	+++	-	-	-	-
38023	++	++	-	-	-	-	-	-	-	-

38024 ++	-	-	-	-	-	+	-	-	-
37396 ++	+++	-	-	-	+	+	-	-	-
37818 ++	++	--+	+++	+++	+++	+	-	-	+++
18445 ++	++	-	-	-	-	-	-	-	-
17732 ++	++	-	-	-	-	-	-	-	-
38025 ++	+	--+	++	+	+	+++	---	++	++
37761 ++	++	-	-	-	-	-	-	-	-
38026 ++	+	-	+	+	+	+	-	-	-
37761 ++	++	-	-	-	-	-	-	-	-
37761 ++	++	-	-	-	-	-	-	-	-
37811 ++	++	-	-	-	-	-	-	-	-
37831 ++	++	-	-	-	-	-	-	-	-
38027 ++	+	--+	+++	+++	+++	+	-	-	-
37811 ++	++	-	-	-	-	-	-	-	-
13899 ++	++	-	+	-	-	-	-	-	-
37989 ++	+	-	-	-	-	-	-	-	-
10955 ++	++	-	-	-	-	-	-	-	-
37858 ++	-	-	-	-	-	-	-	-	-
37864 ++	++	-	-	-	-	-	-	-	-
14333 ++	++	-	-	-	-	-	-	-	-
17035 ++	+	--	++	+	++	-	-	-	-
37817 ++	-	--+	-	+	-	-	-	-	-
17648 ++	++	-	-	-	+	-	-	-	-
37649 ++	++	-	-	-	-	-	-	-	-
37910 ++	++	-	-	-	-	-	-	+	-
37608 ++	++	-	-	-	-	-	-	-	-
38028 ++	+	--+	+++	+++	+++	+	-	-	-
38029 ++	-	-	-	-	-	-	-	-	-
11009 ++	-	-	-	-	-	-	-	-	-
37515 ++	++	-	-	-	-	-	-	-	-
10955 ++	++	-	-	-	-	-	-	-	-
38030 ++	+	-	-	-	-	-	-	-	-
37886 ++	++	-	+	+++	+++	+	-	-	-

37455 ++	++	-	-	-	-	-	-	-	-
17711 ++	-	--+	+	+++	-	-	-	+++	-
38031 ++	++	-	-	-	-	-	-	-	-
38032 ++	++	-	-	-	-	-	-	-	-
38019 ++	-	-	-	-	-	-	-	-	-
37876 ++	++	-	-	-	-	-	-	-	-
38033 ++	++	-	-	-	-	-	-	-	-
38034 ++	+	--+	++	+	+	+++	---	-	-
38035 ++	++	-	-	-	-	-	-	-	-
38036 ++	++	-	-	-	-	-	-	-	-
38037 ++	++	-	-	-	-	-	-	-	-
38038 ++	++	-	-	-	-	-	-	-	-
18903 ++	+	-	-	-	-	-	-	-	-
38039 ++	-	--+	+	+++	+	-	-	+++	-
38040 ++	++	-	-	-	-	-	-	-	-
37530 ++	++	-	+	+++	+++	-	-	-	-
37995 ++	++	-	-	-	-	-	-	-	-
38041 ++	+	-	-	-	-	+	-	-	-
38042 ++	++	-	-	-	-	-	-	-	-
37220 ++	++	-	-	-	-	-	-	-	-
38043 ++	+	-	-	-	-	-	-	-	-
38044 ++	-	--+	+++	+++	+++	+	-	-	-
37199 ++	-	--+	-	-	-	-	-	-	-
38045 ++	-	-	-	-	-	-	-	-	-
37904 ++	-	-	-	-	-	-	-	-	-
38046 ++	++	-	-	-	+	+	-	-	-
37841 ++	++	-	-	-	-	-	-	-	-
37557 ++	++	-	-	-	-	-	-	-	-
38047 ++	+	--+	+++	+++	+++	-	-	-	-
38048 ++	++	-	-	-	-	-	-	-	-
37893 ++	-	-	-	-	-	-	-	-	-
13795 ++	+	-	-	-	-	-	-	-	-
37027 ++	++	-	-	-	-	-	-	-	-

37878 ++	-	-	-	-	-	-	-	-	-
37119 ++	+	-	-	-	-	-	-	-	-
38049 ++	++	--+	+++	+++	+++	-	-	-	-
38050 ++	++	-	-	-	-	-	-	-	-
38051 ++	++	-	-	-	-	-	-	-	-
16655 ++	++	-	-	-	-	+	-	-	-
37924 ++	++	-	+	+	+	+++	---	+++	-
38052 ++	-	-	-	-	-	-	-	-	-
37086 ++	-	-	-	-	-	-	-	-	-
37694 ++	++	-	-	-	-	-	-	-	-
38053 ++	++	--+	+++	+++	+++	-	-	-	-
17595 ++	-	-	-	-	-	-	-	-	-
11707 ++	+	-	-	-	-	-	-	-	-
37446 ++	+	-	-	-	-	-	-	-	-
38054 ++	++	-	-	-	-	-	-	-	-
37422 ++	+++	-	-	-	-	-	-	-	-
37354 ++	++	-	-	+	+	-	-	-	-
11053 ++	++	--+	+++	+++	+++	+	-	-	-
38053 ++	++	--+	+++	+++	+++	-	-	-	-
38055 ++	+	--+	+++	+++	+++	-	-	-	-
38056 ++	++	-	-	-	-	-	-	-	-
16667 ++	++	-	+	-	+	+	-	-	-
17950 ++	++	--+	+++	+++	+++	-	-	-	-
13770 ++	++	-	+	+	+	+++	---	-	-
37934 ++	-	--	+	-	-	-	-	-	-
37985 ++	-	-	-	-	-	-	-	-	-
17106 ++	+	--+	+++	+++	+++	-	-	-	-
38057 ++	++	-	-	-	-	-	-	-	-
11724 ++	++	-	-	-	-	-	-	-	-
38058 ++	-	-	-	-	-	-	-	-	-
38059 ++	-	-	-	-	-	-	-	-	-
38060 ++	++	-	-	-	-	-	-	-	-
38061 ++	++	-	-	-	-	-	-	-	-

13605 ++	+	-	-	-	-	-	-	-	-
20373 ++	++	-	-	-	-	-	-	-	-
11014 ++	++	-	-	-	-	-	-	-	-
37112 ++	++	-	+	-	-	-	-	-	-
38060 ++	++	-	-	-	-	-	-	-	-
38062 ++	-	-	-	-	-	-	-	-	-
37516 ++	+	-	-	-	-	-	-	-	-
38063 ++	++	-	-	-	-	-	-	-	-
38064 ++	-	--+	+	+++	-	-	-	-	-
37020 ++	++	-	+	-	-	-	-	-	-
38065 ++	+	-	-	-	-	-	-	-	-
38040 ++	++	-	-	-	-	-	-	-	-
38066 ++	++	-	-	-	-	-	-	-	-
17268 ++	+	--+	+++	+++	+++	-	-	-	-
37691 ++	-	-	-	-	-	-	-	-	-
17729 ++	-	-	-	-	-	-	-	-	-
37801 ++	++	-	-	-	-	-	-	-	-
37476 ++	+	-	-	-	-	-	-	-	-
17849 ++	-	-	-	-	-	-	-	-	-
37203 ++	+	-	-	-	-	-	-	-	-
13181 ++	++	-	-	-	-	-	-	-	-
38067 ++	++	-	-	-	-	-	-	-	-
11371 ++	++	-	-	-	-	-	-	-	-
38068 ++	+	-	-	-	-	-	-	-	-
38023 ++	++	-	-	-	-	-	-	-	-
38069 ++	++	-	-	-	-	-	-	-	-
16112 ++	+	-	-	-	-	-	-	-	-
17669 ++	++	-	-	-	-	-	-	-	-
38070 ++	+	--+	+++	+++	+++	-	-	-	-
37638 ++	++	-	-	-	-	-	-	-	-
17018 ++	+	-	+	-	-	++	--	-	-
17119 ++	-	-	-	-	-	+	-	-	-
37939 ++	+	-	-	-	-	-	-	-	-

38071 ++	-	-	-	-	-	-	-	-	-
14139 ++	++	-	-	-	-	-	-	-	-
37607 ++	++	-	+	-	-	-	-	-	-
38013 ++	++	-	-	-	-	-	-	-	-
14632 ++	++	-	-	-	+	-	-	-	-
38072 ++	++	-	-	-	-	-	-	-	-
37445 ++	+	-	-	-	-	-	-	-	-
37612 ++	++	-	-	-	-	-	-	-	-
38073 ++	-	-	-	-	+	-	-	-	-
37459 ++	+++	-	-	-	-	-	-	-	-
38074 ++	++	-	-	-	-	-	-	-	-
37715 ++	-	-	-	-	-	-	-	-	-
16664 ++	+	-	+	+	+	+	–	-	-
37641 ++	+	-	-	-	-	-	-	-	-
38075 ++	+	–+	+++	+++	+++	-	-	-	-
37562 ++	++	-	+	+	+	+	–	-	-
37847 ++	++	-	-	-	-	-	-	-	-
37120 ++	+	–+	++	+++	++	+++	–––	-	-
38076 ++	++	-	-	-	-	-	-	-	-
11411 ++	++	-	-	-	-	-	-	-	-
38077 ++	+	–+	+++	+++	+++	-	-	-	-
12596 ++	-	-	-	-	-	-	-	-	-
38078 ++	++	-	-	-	-	-	-	-	-
37376 ++	++	-	-	-	-	-	-	-	-
17708 ++	-	–+	+	+++	+	-	–	-	-
38079 ++	-	-	-	-	-	-	-	-	-
38080 ++	++	–+	++	-	-	-	-	-	-
16059 ++	-	-	-	-	-	-	-	-	-
38064 ++	-	–+	+	+++	-	-	-	-	-
37909 ++	++	-	-	-	-	-	-	-	-
13874 ++	++	-	-	-	-	-	-	-	-
37989 ++	-	-	-	-	-	-	-	-	-
38081 ++	-	––	-	-	-	-	-	-	-

17016 ++	++	–	+	+	+	-	-	-	-
37467 ++	++	-	-	-	-	-	-	-	-
37872 ++	++	-	-	-	-	-	-	-	-
38082 ++	+	–+	+++	+++	+++	-	–	-	-
17918 ++	-	-	-	-	-	-	-	-	-
11690 ++	-	-	-	-	-	-	-	-	-
37974 ++	-	–+	+	++	-	-	-	+++	+++
37230 ++	-	–+	+	+++	-	-	-	-	-
37794 ++	++	-	-	-	-	-	-	-	-
38083 ++	++	-	-	-	-	-	-	-	-
36892 ++	-	-	-	-	-	+	-	-	-
38084 ++	++	-	-	-	-	-	-	-	-
37104 ++	++	-	-	+	-	-	-	-	-
37544 ++	++	-	-	-	-	-	-	-	-
37775 ++	++	-	-	-	-	-	-	-	-
38085 ++	+	–+	+++	+++	+++	+	-	-	-
12052 ++	-	-	-	-	-	-	-	-	-
12342 ++	-	-	-	-	-	-	-	-	-
38086 ++	++	-	-	-	-	-	-	-	-
17230 ++	++	–+	+++	+++	+++	-	-	-	-
38087 ++	+	–+	+++	+++	+++	-	–	-	-
20373 ++	++	-	-	-	-	-	-	-	-
14333 ++	++	-	-	-	+	-	-	-	-
37903 ++	+	-	-	-	-	-	-	-	-
37841 ++	++	-	-	-	-	-	-	-	-
17745 ++	++	-	-	-	-	-	-	-	-
37332 ++	+	-	-	-	-	-	-	-	-
37930 ++	++	-	-	-	-	-	-	-	-
38088 ++	++	–	+	+++	+++	+++	---	-	-
37713 ++	-	-	-	-	-	-	-	-	-
38042 ++	++	-	-	-	-	-	-	-	-
37971 ++	++	–+	+	-	-	-	-	-	-
15480 ++	+++	-	+	+	+	++	--	-	-

37205	++	++	--+	+++	+++	+++	+	-	-	-
37678	++	++	-	-	-	-	-	-	-	-
38089	++	-	-	-	-	-	-	-	-	-
11226	++	++	-	-	-	-	-	-	-	-
37648	++	++	-	-	-	-	-	-	-	-
38090	++	-	-	-	-	-	-	-	-	-
37687	++	++	-	-	-	-	-	-	-	-
38091	++	-	-	-	-	-	-	-	-	-
17528	++	-	-	-	-	-	-	-	-	-
38092	++	-	-	+	-	-	-	-	-	-
38093	++	++	-	-	-	-	-	-	-	-
38094	++	++	-	-	-	-	-	-	-	-
37452	++	-	-	-	-	-	-	-	-	-
14082	++	++	-	-	-	-	-	-	-	-
37993	++	++	-	+	+	+	-	-	-	-
14556	++	+	-	-	+	-	++	--	-	-
37708	++	-	--+	-	-	-	-	-	-	-
38095	++	-	-	-	-	-	-	-	-	-
37403	++	++	-	-	-	-	-	-	-	-
38096	++	++	--+	+++	+++	+++	+	-	-	-
38097	++	++	-	-	+	-	-	-	-	-
17694	++	-	-	-	-	-	-	-	-	-
37756	++	-	-	-	-	-	-	-	-	-
37677	++	++	-	-	-	+	-	-	-	-
38098	++	+	--+	+++	+++	+++	+	-	-	-
38099	++	++	-	-	-	-	-	-	-	-
13807	++	+	-	-	-	-	-	-	-	-
38100	++	+	-	-	-	-	-	-	-	-
37945	++	++	-	-	-	-	-	-	-	-
12553	++	++	-	+	+	+	-	-	-	-
37982	++	++	-	-	-	-	-	-	-	-
38101	++	++	-	-	-	-	-	-	-	-
37578	++	+	-	-	-	-	+	-	-	-

38102 ++	-	-	-	-	-	-	-	-	-
36900 ++	++	-	-	-	-	-	-	-	-
37705 ++	-	-	-	-	-	-	-	-	-
36727 ++	++	--+	+++	+++	+++	-	-	-	-
38103 ++	++	-	+	+++	+++	+	-	-	-
37973 ++	++	-	-	-	-	-	-	-	-
36731 ++	+	-	-	-	-	-	-	-	-
37634 ++	++	-	-	-	-	-	-	-	-
37864 ++	++	-	-	-	-	-	-	-	-
37997 ++	++	-	-	-	-	-	-	-	-
38104 ++	-	-	-	-	-	+	-	-	-
11334 ++	-	-	-	-	-	-	-	-	-
38105 ++	++	-	-	-	-	-	-	-	-
38106 ++	++	-	-	-	-	-	-	-	-
38107 ++	-	-	-	-	-	-	-	-	-
38108 ++	-	-	-	-	-	-	-	-	-
13580 ++	++	-	-	-	-	-	-	-	-
38109 ++	++	-	+	-	-	-	-	-	-
37581 ++	-	--+	+	+++	-	-	-	+++	-
38110 ++	+	-	-	-	-	-	-	-	-
37722 ++	++	-	+	-	-	-	-	-	-
37771 ++	-	-	-	-	-	-	-	-	-
18179 ++	++	-	-	-	-	-	-	-	-
38072 ++	++	-	-	-	-	-	-	-	-
38111 ++	++	-	-	-	-	-	-	-	-
38112 ++	++	-	+	-	-	-	-	-	-
11913 ++	-	-	-	-	-	-	-	-	-
37852 ++	++	-	-	-	-	-	-	-	-
38113 ++	++	-	+	+	-	-	-	-	-
16019 ++	++	-	-	-	-	-	-	-	-
38114 ++	++	-	-	-	-	-	-	-	-
38115 ++	++	-	-	-	-	-	-	-	-
37449 ++	++	-	-	-	-	-	-	-	-

37692 ++	++	-	-	-	-	-	-	-	-
38116 ++	-	-	-	-	-	-	-	-	-
17037 ++	-	--+	+	+++	+	-	-	-	-
37483 ++	+	-	-	-	-	-	-	-	-
38117 ++	++	-	-	-	-	-	-	-	-
37990 ++	+	-	-	-	-	-	-	-	-
38118 ++	++	-	-	-	-	-	-	-	-
38119 ++	++	-	-	-	-	-	-	-	-
38120 ++	++	-	-	-	-	-	–	-	-
38121 ++	++	-	-	-	-	-	-	-	-
17619 ++	-	--+	-	+++	-	-	-	-	-
16046 ++	++	-	-	-	+	-	-	-	-
38002 ++	-	-	-	-	-	-	-	-	-
37944 ++	-	-	-	-	-	-	-	-	-
13642 ++	++	-	-	-	+	++	--	-	-
38122 ++	++	-	-	-	-	-	-	-	-
12827 ++	++	--+	+++	+++	+++	-	-	-	-
14858 ++	++	-	-	-	-	-	-	-	-
37741 ++	-	--+	+	+	-	-	-	-	-
37880 ++	++	-	-	-	-	-	-	-	-
13796 ++	++	-	-	-	-	-	-	-	-
13899 ++	++	-	-	-	-	-	-	-	-
38123 ++	+	-	-	-	-	-	-	-	-
38124 ++	++	-	+	+	+	+	–	-	-
38125 ++	++	-	-	-	-	-	-	-	-
38068 ++	+	-	-	-	-	-	-	-	-
11144 ++	++	-	-	-	-	-	-	-	-
38126 ++	-	--	+	++	+	-	-	-	-
38127 ++	++	-	-	-	-	-	-	-	-
37081 ++	+++	-	+	+	+	-	-	-	-
38128 ++	++	-	-	-	-	-	-	-	-
37621 ++	+	-	-	-	-	+	–	-	-
37246 ++	++	–	+	-	-	-	-	-	-

37697	++	++	--+	+++	+++	+++	-	-	-	-
38129	++	+	-	-	-	-	-	-	-	-
17270	++	+	--+	+++	+++	+++	+	-	-	-
37162	++	++	-	-	-	+	-	-	-	-
38069	++	++	-	-	-	-	-	-	-	-
11757	++	-	-	-	-	-	-	-	-	-
11866	++	-	-	-	-	-	-	-	-	-
37054	++	+	–	++	+	++	+++	---	+++	+++
37544	++	++	-	-	-	-	-	-	-	-
38130	++	-	-	-	+++	+	-	-	-	-
38131	++	-	-	-	-	-	-	-	-	-
36403	++	+	-	-	-	-	+	-	-	-
38132	++	-	-	-	-	-	-	-	-	-
38012	++	+	-	-	-	-	+	–	-	-
38133	++	-	–	+	+	+	+	–	-	-
38134	++	++	--+	+++	-	-	-	-	+++	-
38135	++	++	-	-	-	-	-	-	-	-
37720	++	++	-	-	-	-	-	-	-	-
38136	++	++	-	-	-	-	-	-	-	-
37917	++	++	-	-	-	-	-	-	-	-
37841	++	++	-	-	-	-	-	-	-	-
15972	++	++	-	-	-	-	-	-	-	-
38137	++	++	-	-	-	-	-	-	-	-
37820	++	++	-	-	-	-	-	-	-	-
38138	++	++	-	-	-	-	-	-	-	-
38139	++	-	-	-	-	-	-	–	-	-
38140	++	++	--+	+++	+++	+++	+	--	-	-
38141	++	+	-	-	-	-	-	-	-	-
17666	++	-	-	-	-	-	-	-	-	-
38062	++	-	-	-	-	-	-	-	-	-
16664	++	+	-	-	+	+	+	–	-	-
38142	++	-	--+	+++	+++	+++	+	-	-	-
37353	++	++	-	-	-	-	-	-	-	-

38143 ++	+	-	-	-	-	-	-	-	-
11860 ++	++	-	-	-	-	-	-	-	-
37923 ++	+	-	-	-	-	-	-	-	-
38023 ++	++	-	-	-	-	-	-	-	-
38144 ++	+	-	-	-	-	-	-	-	-
37745 ++	-	-	-	-	-	-	-	-	-
19253 ++	++	-	-	-	-	-	-	-	-
12348 ++	++	-	-	-	-	-	-	-	-
14925 ++	++	-	-	-	+	-	-	-	-
37936 ++	++	-	-	-	-	-	-	-	-
37987 ++	++	-	-	-	-	-	-	-	-
37928 ++	++	-	-	-	-	-	-	-	-
16613 ++	++	-	-	-	-	-	-	-	-
38145 ++	++	--+	+++	+++	+++	-	-	-	-
38146 ++	++	-	-	-	-	-	-	-	-
37945 ++	++	-	-	-	-	-	-	-	-
38147 ++	-	-	-	-	-	-	-	-	-
16630 ++	++	-	-	-	-	+	-	++	-
11955 ++	-	-	-	-	-	-	-	-	-
38148 ++	++	-	-	-	-	-	-	-	-
38149 ++	++	-	-	-	-	-	-	-	-
11358 ++	++	-	-	-	-	-	-	-	-
37588 ++	++	-	-	+	+	-	-	-	-
13800 ++	++	--+	+++	+++	+++	+	-	-	-
19182 ++	++	-	-	-	-	-	-	-	-
37700 ++	++	-	-	-	-	-	-	-	-
38150 ++	-	--+	+	+++	++	-	-	-	-
38151 ++	++	-	-	-	-	-	-	-	-
38050 ++	++	-	-	-	-	-	-	-	-
38094 ++	++	-	-	-	-	-	-	-	-
38025 ++	+	--+	++	+	+	+++	---	-	++
11475 ++	++	-	-	-	-	-	-	-	-
17446 ++	++	-	-	-	-	-	-	-	-

37915 ++	++	-	-	-	-	-	-	-	-
37969 ++	++	-	-	-	-	-	-	-	-
37045 ++	+	-	-	-	-	-	-	-	-
38152 ++	++	-	-	-	-	-	-	-	-
38153 ++	+	--+	+++	+++	+++	-	-	-	-
38004 ++	-	-	-	-	-	-	-	-	-
18303 ++	-	-	-	-	-	-	-	-	-
37434 ++	+++	-	-	-	-	-	-	-	-
15051 ++	-	--+	+++	+++	+++	-	-	-	-
14502 ++	+	-	-	-	-	-	-	-	-
38154 ++	++	-	-	-	-	-	-	-	-
18518 ++	++	-	-	-	-	-	-	-	-
37971 ++	++	--+	+	-	-	-	-	-	-
37885 ++	++	-	-	-	-	-	-	-	-
37957 ++	++	--+	+++	+++	+++	-	-	-	-
38155 ++	++	-	-	-	-	-	-	-	-
38156 ++	-	--	-	+	+	-	-	-	-
38157 ++	-	--+	+	+++	+	-	-	+++	-
37853 ++	++	-	-	-	-	-	-	-	-
38121 ++	++	-	-	-	-	-	-	-	-
38158 ++	-	-	-	-	-	-	-	-	-
37597 ++	++	-	-	-	-	-	-	-	-
37647 ++	+	-	-	-	-	-	-	-	-
15976 ++	++	-	-	-	-	-	-	-	-
38128 ++	++	-	-	-	-	-	-	-	-
38159 ++	+	-	-	-	-	-	-	-	-
38160 ++	++	-	-	-	-	-	-	-	-
38039 ++	-	--+	+	+++	+	-	-	+++	-
13961 ++	++	-	-	-	-	-	-	-	-
11898 ++	-	-	-	-	-	-	-	-	-
38084 ++	++	-	-	-	-	-	-	-	-
16151 ++	++	-	+	+	+	-	-	-	-
37824 ++	++	-	-	-	-	-	-	-	-

17751 ++	++	-	-	-	-	-	-	-	-
37368 ++	-	-	-	-	-	-	–	-	-
17590 ++	-	–+	+	+	-	+	-	-	-
11204 ++	+	-	-	-	-	-	-	-	-
37687 ++	++	-	-	-	-	-	-	-	-
38161 ++	+	–	-	+	+	-	-	-	-
13961 ++	++	-	-	-	-	-	-	-	-
38162 ++	-	-	-	-	-	-	-	-	-
37519 ++	++	-	-	-	-	-	-	-	-
13985 ++	++	-	-	-	-	-	-	-	-
38163 ++	-	–	+	+	-	-	-	-	-
15940 ++	+	-	-	-	-	-	-	-	-
11785 ++	+	-	-	-	-	-	-	-	-
37881 ++	++	-	-	-	-	-	-	-	-
37933 ++	-	–+	+	+++	+	-	-	+++	-
38164 ++	++	-	-	-	-	-	-	-	-
37659 ++	-	-	-	-	-	-	-	-	-
17039 ++	+	-	-	-	-	-	-	-	-
38165 ++	++	-	-	-	-	-	-	-	-
38166 ++	-	-	-	-	+	-	-	-	-
17496 ++	-	-	-	-	-	-	-	-	-
11973 ++	-	-	-	-	-	-	-	-	-
37914 ++	+	-	-	-	-	-	-	-	-
37905 ++	+	-	-	-	-	-	-	-	-
38167 ++	-	-	-	-	-	-	-	-	-
37630 ++	++	-	-	-	-	-	-	-	-
37755 ++	-	–+	+	+++	+	+	-	-	-
38168 ++	++	-	-	-	-	-	-	-	-
10963 ++	++	-	-	-	-	-	-	-	-
38112 ++	++	–	+	-	-	-	-	-	-
11475 ++	++	-	-	-	-	-	-	-	-
11668 ++	++	-	-	-	+	+	–	-	-
38169 ++	-	––	+	-	-	-	-	-	-

36821 ++	+	-	-	-	-	-	-	-	-
38170 ++	++	--+	+++	+++	+++	+	-	-	-
38171 ++	-	--+	+++	+++	+++	-	-	-	-
37968 ++	++	--+	+++	+++	+++	+	-	-	-
38172 ++	+	-	-	-	-	-	-	-	-
38078 ++	++	-	-	-	-	-	-	-	-
38173 ++	++	--+	+++	+++	+++	+	-	-	-
38174 ++	++	-	-	-	-	-	-	-	-
38175 ++	++	-	-	-	-	-	-	-	-
38176 ++	+	--+	+++	+++	+++	-	-	-	-
38177 ++	++	-	-	-	-	-	-	-	-
14464 ++	++	-	-	-	-	-	-	-	-
37585 ++	-	-	-	-	-	-	-	-	-
38121 ++	++	-	-	-	-	-	-	-	-
37951 ++	-	-	-	-	-	-	-	-	-
38178 ++	++	-	-	-	-	-	-	-	-
38111 ++	++	-	-	-	-	-	-	-	-
38048 ++	++	-	-	-	-	-	-	-	-
37444 ++	-	-	-	-	-	-	-	-	-
38179 ++	+++	-	-	-	-	-	-	-	-
37802 ++	++	-	-	-	-	-	-	-	-
14326 ++	+	-	-	-	-	-	-	-	-
11430 ++	++	-	-	-	-	-	-	-	-
38083 ++	++	-	-	-	-	-	-	-	-
38061 ++	++	-	-	-	-	-	-	-	-
37687 ++	++	-	-	-	-	-	-	-	-
17186 ++	++	--+	+++	+++	+++	-	-	-	-
16056 ++	-	-	-	-	-	-	-	-	-
37827 ++	-	-	-	-	-	-	-	-	-
37545 ++	+	-	-	-	-	-	-	-	-
37689 ++	++	-	+	-	-	+	-	-	-
38108 ++	-	-	-	-	-	-	-	-	-
37820 ++	++	-	-	-	-	-	-	-	-

37686 ++	+++	--+	+++	+++	+++	-	-	-	-
14655 ++	++	-	-	-	-	-	-	-	-
12224 ++	++	-	-	-	-	-	-	-	-
38180 ++	-	-	-	-	-	-	-	-	-
11840 ++	-	-	-	-	-	-	-	-	-
13796 ++	++	-	-	-	-	-	-	-	-
38106 ++	++	-	-	-	-	-	-	-	-
17797 ++	-	-	-	+	-	-	-	-	-
37943 ++	++	-	-	-	-	-	-	-	-
37906 ++	++	-	-	-	-	-	-	-	-
38181 ++	++	-	-	-	-	-	-	-	-
38182 ++	+	-	-	-	+	-	-	-	-
16088 ++	++	-	-	-	-	-	-	-	-
37916 ++	++	-	-	-	-	-	-	-	-
14270 ++	++	-	-	-	-	-	-	-	-
37802 ++	++	-	-	-	-	-	-	-	-
38183 ++	++	-	+	+	+	+	--	+++	-
16578 ++	++	-	-	-	-	-	-	-	-
14394 ++	-	-	-	-	-	-	-	-	-
38184 ++	++	-	-	-	-	-	-	-	-
18058 ++	-	-	-	-	-	-	-	-	-
37747 ++	-	-	-	-	-	-	-	-	-
18597 ++	++	-	-	-	-	-	-	-	-
37365 ++	-	--+	+	+++	+	-	-	-	-
38185 ++	+	--+	+++	+++	+++	-	-	-	-
19230 ++	+	-	-	-	-	-	-	-	-
13762 ++	++	-	-	+	+	-	-	-	-
38186 ++	-	--+	+	++	+	-	-	-	-
38187 ++	+	-	-	-	-	-	-	-	-
17669 ++	++	-	-	-	-	-	-	-	-
37845 ++	++	-	-	-	-	-	-	-	-
36623 ++	-	-	-	-	-	+	-	-	-
38114 ++	++	-	-	-	-	-	-	-	-

37941 ++	++	-	-	-	-	-	-	-	-
37328 ++	-	-	-	-	-	-	-	-	-
12176 ++	-	-	-	-	-	-	-	-	-
38188 ++	-	-	-	-	-	-	-	-	-
11791 ++	++	-	-	-	-	-	-	-	-
37885 ++	++	-	-	-	-	-	-	-	-
38189 ++	++	-	-	-	-	-	-	-	-
13807 ++	+	-	-	-	-	-	-	-	-
38190 ++	+	-	-	-	-	-	–	-	-
13737 ++	++	-	-	-	-	-	-	-	-
38191 ++	++	--	++	+++	+++	-	-	-	-
37766 ++	-	--+	+	+++	+	-	-	+++	-
19982 ++	-	-	-	-	-	-	-	-	-
11218 ++	++	-	-	-	-	-	-	-	-
11629 ++	++	-	+	-	+	-	-	-	-
38192 ++	+	--+	+++	+++	+++	-	–	-	-
37560 ++	++	-	-	-	-	-	-	-	-
17540 ++	-	--+	-	++	-	-	-	-	-
11791 ++	++	-	-	-	-	-	-	-	-
14861 ++	++	-	-	-	-	-	-	-	-
17695 ++	-	-	-	-	-	-	-	-	-
17752 ++	+	-	-	-	-	-	–	-	-
38193 ++	++	-	-	-	-	-	-	-	-
38194 ++	++	-	-	-	+	-	-	-	-
37487 ++	+	-	-	-	-	-	-	-	-
38101 ++	++	-	-	-	-	-	-	-	-
37341 ++	++	-	-	-	-	-	-	-	-
13908 ++	++	–	+	+	+	+++	---	-	-
38065 ++	++	-	-	-	-	-	-	-	-
12391 ++	-	-	-	-	-	-	-	-	-
37570 ++	++	-	-	-	-	-	-	-	-
37718 ++	-	--+	+	+++	+++	+	-	-	-
38195 ++	+	--	+	-	-	-	-	-	-

16062	++	++	–	+	+	+	-	–	-	-
37520	++	-	–-+	+	+++	-	-	-	+++	-
38196	++	++	-	-	-	+	-	–	-	-
17728	++	++	-	-	-	-	-	-	-	-
37926	++	++	-	-	-	-	-	-	-	-
37898	++	+	-	+	-	-	-	-	-	-
38197	++	++	-	-	-	-	-	-	-	-
38198	++	+	-	-	-	-	-	-	-	-
17281	++	++	-	-	-	-	-	-	-	-
37711	++	++	-	-	-	-	-	-	-	-
38109	++	++	–	+	-	-	-	-	-	-
38012	++	+	-	-	-	-	+	–	-	-
18956	++	++	-	-	-	-	-	-	-	-
37143	++	-	–-+	+	+	-	-	-	-	-
38199	++	-	–	-	-	-	-	-	-	-
38175	++	++	-	-	-	-	-	-	-	-
37897	++	++	-	-	-	-	-	-	-	-
11787	++	-	-	-	-	-	-	-	-	-
38032	++	++	-	-	-	-	-	-	-	-
18270	++	+	-	-	-	-	-	-	-	-
36931	++	+	-	-	-	-	-	-	-	-
17939	++	-	-	-	-	-	-	-	-	-
14003	++	++	-	-	-	-	-	-	-	-
37938	++	++	-	-	-	-	-	-	-	-
38200	++	+	-	-	-	-	-	-	-	-
38201	++	-	-	-	-	-	-	-	-	-
38202	++	++	-	-	-	-	-	-	-	-
38203	++	+	-	-	+	+	++	––	-	-
37716	++	-	–-+	+	+	-	-	-	-	-
38204	++	++	–-+	+++	+++	+++	-	––	-	-
38205	++	-	–-+	+	-	-	+	–	-	-
38206	++	++	-	-	-	-	-	-	-	-
12146	++	++	-	-	-	-	-	-	-	-

13310 ++	++	-	-	-	-	-	-	-	-
12381 ++	-	-	-	-	-	-	-	-	-
37863 ++	++	-	-	-	-	-	-	-	-
14145 ++	++	-	-	-	-	-	-	-	-
14059 ++	++	-	-	-	-	-	-	-	-
38207 ++	++	-	+	-	-	-	-	-	-
38208 ++	++	-	-	-	-	+	–	-	-
20373 ++	++	-	-	-	-	-	-	-	-
37747 ++	-	-	-	-	-	-	-	-	-
38209 ++	-	–+	+	+	-	-	-	+++	-
13767 ++	++	-	-	-	-	-	-	-	-
37712 ++	-	–+	+	+++	+	-	-	+++	-
37675 ++	-	–+	+	+++	-	-	-	-	-
37642 ++	+	–	-	-	+	+	–	-	-
38210 ++	++	-	-	-	-	-	-	-	-
38211 ++	+	-	-	-	-	-	-	-	-
13181 ++	++	-	-	-	-	-	-	-	-
38212 ++	+	–+	+++	+++	+++	-	–	-	-
13605 ++	+	-	-	-	-	-	-	-	-
37842 ++	-	–	-	-	-	-	-	-	-
14925 ++	++	-	-	-	+	-	-	-	-
38213 ++	++	-	-	-	-	-	-	-	-
36306 ++	++	–	+++	-	++	+++	–––	-	-
38214 ++	-	––	-	-	-	+	–	-	-
38215 ++	++	-	-	-	-	-	-	-	-
38216 ++	-	–+	+	-	-	-	-	-	-
14269 ++	++	-	+	+	-	-	-	-	-
38217 ++	++	-	-	-	-	-	-	-	-
11629 ++	++	–	-	-	+	-	-	-	-
38012 ++	+	-	-	-	-	+	–	-	-
11323 ++	+	-	-	-	-	-	-	-	-
36665 ++	+++	-	-	-	-	-	-	-	-
14045 ++	++	–+	+++	+++	+++	+	-	-	-

19924 ++	-	-	-	-	-	-	-	-	-
14092 ++	++	-	-	-	-	-	-	-	-
17308 ++	++	--+	+++	+++	+++	-	-	-	-
11812 ++	++	-	+	-	-	-	-	-	-
17399 ++	++	-	-	-	-	-	-	-	-
12602 ++	+	-	-	-	+	-	-	-	-
38218 ++	++	-	-	-	-	-	-	-	-
38118 ++	++	-	-	-	-	-	-	-	-
37790 ++	++	--+	+++	+++	+++	-	-	-	-
11358 ++	++	-	-	-	-	-	-	-	-
14256 ++	++	-	+	-	-	-	-	-	-
38219 ++	-	-	-	-	-	+	-	-	-
37639 ++	++	-	-	-	-	-	-	-	-
38220 ++	++	-	-	-	-	+	-	-	-
38080 ++	++	--+	++	-	-	-	-	-	-
38221 ++	++	-	+	-	-	-	-	-	-
38081 ++	-	--	-	-	-	-	-	-	-
38222 ++	++	-	-	-	-	-	-	-	-
38139 ++	-	-	-	-	-	-	-	-	-
37859 ++	++	-	+	+	+	-	-	-	-
38223 ++	++	-	-	-	-	-	-	-	-
38224 ++	+	-	-	-	-	-	-	-	-
38225 ++	++	-	-	-	+	-	-	-	-
38146 ++	++	-	-	-	-	-	-	-	-
38226 ++	++	-	-	-	-	-	-	-	-
37925 ++	-	-	-	-	-	-	-	-	-
38170 ++	+	--+	+++	+++	+++	+	-	-	-
38031 ++	++	-	-	-	-	-	-	-	-
14231 ++	++	-	-	-	-	-	-	-	-
37854 ++	++	-	+	+	++	-	-	-	-
37979 ++	++	-	-	-	-	-	-	-	-
37498 ++	-	-	-	-	-	-	-	-	-
37867 ++	-	--	+	+	-	-	-	-	-

38227	++	+	--+	+++	+++	+++	-	-	-	-
38158	++	-	-	-	-	-	-	-	-	-
16584	++	++	-	-	-	-	-	-	-	-
38228	++	++	-	-	-	-	-	-	-	-
16589	++	++	-	-	-	-	-	-	-	-
38229	++	+	-	+	+	+	+++	---	-	-
37650	++	++	-	-	-	-	-	-	-	-
37660	++	+	-	-	-	-	-	-	-	-
37931	++	-	-	-	-	-	-	-	-	-
37822	++	++	-	-	-	-	-	-	-	-
38230	++	-	--+	+++	+++	+++	-	-	-	-
38231	++	-	-	-	-	-	-	-	-	-
38232	++	+	-	-	+++	+	-	-	-	-
38233	++	++	-	-	-	-	-	-	-	-
38234	++	+	--+	+++	+++	+++	+	-	-	-
38235	++	++	-	-	-	-	-	-	-	-
38172	++	+	-	-	-	-	-	-	-	-
38236	++	++	--+	+++	+++	+++	-	-	-	-
38237	++	+	-	-	-	-	-	-	-	-
12503	++	++	-	-	-	-	-	-	-	-
38238	++	-	--+	+++	+++	+++	-	-	-	-
38239	++	++	--+	+++	+++	+++	+	-	-	-
38099	++	++	-	-	-	-	-	-	-	-
11121	++	+	-	-	-	-	-	-	-	-
12289	++	-	-	-	-	-	-	-	-	-
38240	++	++	-	-	-	-	-	-	-	-
38206	++	++	-	-	-	-	-	-	-	-
37166	++	-	-	-	-	-	-	-	-	-
37940	++	-	--+	+	+++	-	-	-	-	-
38241	++	++	-	-	-	-	-	-	-	-
13961	++	++	-	-	-	-	-	-	-	-
38242	++	++	-	-	-	-	-	-	-	-
11182	++	++	-	-	-	-	-	-	-	-

11226 ++	++	-	-	-	-	-	-	-	-
37848 ++	-	-	-	-	-	-	-	-	-
38243 ++	++	-	-	-	-	-	-	-	-
38244 ++	++	-	-	-	-	-	-	-	-
38245 ++	+	-	-	-	-	-	-	-	-
19543 ++	+	-	-	-	-	-	-	-	-
18225 ++	-	-	-	+	-	-	-	-	-
38246 ++	++	-	-	-	-	-	-	-	-
37880 ++	++	-	-	-	-	-	-	-	-
38024 ++	-	-	+	-	-	-	-	-	-
17657 ++	-	-	-	-	-	-	-	-	-
17625 ++	-	–	-	-	-	-	-	-	-
37359 ++	-	–-+	+	+++	+	-	-	-	-
38247 ++	++	-	-	-	-	-	-	-	-
11724 ++	++	-	-	-	-	-	-	-	-
13961 ++	++	-	-	-	-	-	-	-	-
38058 ++	-	-	-	-	-	-	-	-	-
11067 ++	++	-	-	-	-	-	-	-	-
37344 ++	-	-	-	-	-	-	-	-	-
38248 ++	++	-	+	-	-	-	-	-	-
38249 ++	++	––	+++	+++	+++	-	-	-	-
12913 ++	-	-	-	-	-	-	-	-	-
37782 ++	-	–-+	+	+++	+	+++	––	+++	-
13864 ++	++	-	-	-	-	-	-	-	-
11983 ++	-	-	-	-	-	-	-	-	-
37950 ++	-	-	-	-	-	-	-	-	-
11376 ++	++	-	-	-	-	-	-	-	-
18445 ++	++	-	-	-	-	-	-	-	-
12152 ++	++	-	-	-	+	-	-	-	-
38250 ++	++	-	-	-	-	-	-	-	-
13763 ++	++	-	-	-	+	-	-	-	-
38251 ++	-	–	-	+	-	-	-	-	-
15976 ++	++	-	-	-	-	-	-	-	-

38252 ++	+	–	+	-	+	-	–	-	-
38253 ++	-	-	-	-	-	-	-	-	-
38254 ++	++	-	-	-	-	-	-	-	-
38255 ++	++	-	-	-	-	-	-	-	-
37945 ++	++	-	-	-	-	-	-	-	-
37903 ++	+	-	-	-	-	+	–	-	-
38256 ++	+	-	-	-	-	-	-	-	-
18625 ++	-	-	-	-	-	-	-	-	-
38196 ++	++	-	-	-	-	+	–	-	-
37128 ++	++	-	-	-	-	-	-	-	-
11633 ++	-	-	-	-	-	-	-	-	-
38257 ++	++	-	-	-	-	-	-	-	-
38258 ++	++	-	+	+	+	-	-	-	-
38222 ++	++	-	-	-	-	-	-	-	-
16655 ++	++	-	-	-	-	+	–	-	++
38259 ++	++	-	-	-	-	-	-	-	-
11346 ++	++	-	-	-	-	-	-	-	-
14227 ++	++	-	-	-	-	-	-	-	-
38141 ++	++	-	-	-	-	-	-	-	-
38260 ++	++	-	-	-	-	+	-	-	-
19676 ++	++	-	-	-	-	-	-	-	-
38261 ++	-	-	-	-	-	-	-	-	-
38225 ++	++	-	-	-	-	+	-	-	-
37681 ++	-	-	-	-	-	-	-	-	-
37497 ++	-	–+	+	++	-	-	-	-	-
38084 ++	++	-	-	-	-	-	-	-	-
38262 ++	+	–+	+++	+++	+++	-	-	-	-
37947 ++	++	-	-	-	-	-	-	-	-
37873 ++	++	-	-	-	-	-	-	-	-
38000 ++	++	-	-	-	-	-	-	-	-
38217 ++	++	-	-	-	-	-	-	-	-
11844 ++	-	-	-	-	-	-	-	-	-
38112 ++	+	–	+	-	-	-	–	-	-

14628 ++	++	-	-	-	-	-	-	-	-
14187 ++	++	-	-	-	-	-	-	-	-
38263 ++	++	-	-	-	-	-	–	-	-
11480 ++	-	-	-	-	-	-	-	-	-
37409 ++	+	-	-	-	-	-	-	-	-
38264 ++	-	-	-	-	-	-	-	-	-
38154 ++	++	-	-	-	-	-	-	-	-
14502 ++	+	-	-	-	-	-	-	-	-
38265 ++	+	-	-	-	-	-	-	-	-
38266 ++	++	–+	+++	+++	+++	-	-	-	-
37832 ++	++	-	-	-	-	-	-	-	-
38267 ++	+	–+	+++	+++	+++	+	–	+	-
37455 ++	++	-	-	-	-	-	-	-	-
17826 ++	-	–+	+	+++	+	-	-	-	-
37119 ++	+	-	-	-	-	-	-	-	-
38253 ++	-	-	-	-	-	-	-	-	-
37134 ++	++	–+	+++	+++	+++	-	–	-	-
37035 ++	++	-	-	-	-	-	-	-	-
17590 ++	-	–+	+	+	-	-	-	-	-
37845 ++	++	-	-	-	-	-	-	-	-
38268 ++	++	–+	+++	+++	+++	-	-	-	-
17087 ++	+	–+	+++	+++	+++	-	-	-	-
38157 ++	-	–+	+	+++	+	-	-	+++	-
38269 ++	++	-	-	-	-	-	-	-	-
11133 ++	++	-	-	-	-	-	-	-	-
37545 ++	+	-	-	-	-	-	-	-	-
17604 ++	+	-	-	-	-	-	-	-	-
38079 ++	-	-	-	-	-	-	-	-	-
38270 ++	++	-	-	-	-	-	-	-	-
38154 ++	++	-	-	-	-	-	-	-	-
37983 ++	-	––	-	-	-	-	-	-	-
38271 ++	-	-	-	-	-	-	-	-	-
17281 ++	++	-	-	-	-	-	-	-	-

38272 ++	-	-	-	-	-	-	-	-	-
14502 ++	+	-	-	-	-	-	-	-	-
14473 ++	++	-	-	-	-	-	-	-	-
38273 ++	+++	–	+	-	+	-	-	-	-
11738 ++	-	-	-	-	-	-	-	-	-
38021 ++	-	-	-	-	-	-	-	-	-
17584 ++	-	–-+	+	+	-	-	-	-	-
38274 ++	+	-	-	-	-	-	-	-	-
37688 ++	++	-	-	-	-	+	–	-	-
18766 ++	++	-	-	-	-	+	–	-	-
37989 ++	-	-	-	-	-	-	-	-	-
38014 ++	-	–-+	+	++	-	-	-	-	-
38235 ++	++	-	-	-	-	+	-	-	-
38275 ++	+	-	-	-	-	-	-	-	-
38276 ++	++	-	-	-	-	+	–	-	-
38277 ++	++	-	-	-	-	-	-	-	-
19676 ++	++	-	-	-	-	-	-	-	-
38197 ++	++	-	-	-	-	-	-	-	-
38278 ++	-	–	-	-	-	-	-	-	-
38074 ++	++	-	+	-	-	-	-	-	-
38056 ++	++	-	-	-	-	-	-	-	-
38269 ++	++	-	-	-	-	-	-	-	-
38279 ++	-	-	-	-	-	-	-	-	-
38280 ++	++	-	-	-	-	-	-	-	-
37901 ++	++	-	-	-	-	-	-	-	-
12056 ++	+	-	-	-	-	-	-	-	-
37951 ++	-	-	-	-	-	-	-	-	-
11206 ++	++	-	-	-	-	-	-	-	-
37633 ++	++	-	-	-	-	-	-	-	-
38281 ++	++	-	-	-	-	-	-	-	-
38282 ++	-	-	-	-	-	+	-	-	-
38154 ++	++	-	-	-	-	-	-	-	-
37094 ++	-	-	-	-	-	-	-	-	-

19089 ++	++	-	-	-	-	-	-	-	-
37873 ++	++	-	-	-	-	-	-	-	-
14150 ++	++	-	-	-	-	-	-	-	-
38283 ++	++	-	-	-	-	-	-	-	-
38284 ++	-	–	++	-	+++	+++	---	-	-
13589 ++	++	-	-	-	-	-	-	-	-
17739 ++	-	-	-	-	-	-	-	-	-
38285 ++	++	–	-	-	-	-	-	-	-
38286 ++	-	–	-	-	-	-	-	-	-
14185 ++	++	-	-	-	-	+	–	-	-
37751 ++	++	--+	+++	+++	+++	-	-	-	-
37838 ++	++	-	-	-	-	-	-	-	-
37506 ++	-	--+	+	+++	-	-	-	-	-
37937 ++	+	-	-	-	-	-	-	-	-
11421 ++	-	-	-	-	-	-	-	-	-
16097 ++	++	-	-	-	-	-	-	-	-
37835 ++	++	-	-	-	-	-	-	-	-
37510 ++	-	--+	+	+++	+	-	-	-	-
37833 ++	-	--	+	-	-	+	–	-	-
38287 ++	++	-	-	-	-	-	-	-	-
38080 ++	++	--+	++	-	-	-	-	+++	-
12005 ++	++	-	-	-	-	-	-	-	-
38288 ++	++	-	-	-	-	-	-	-	-
37744 ++	+	-	+	-	-	-	-	-	-
37047 ++	+	--+	++	+++	++	++	-	+++	-
11218 ++	++	-	-	-	-	-	-	-	-
38289 ++	++	-	-	-	-	-	-	-	-
14058 ++	++	-	-	-	-	-	-	-	-
14185 ++	++	-	+	+	-	+	–	-	-
38290 ++	++	--+	+++	+++	+++	-	-	-	-
38291 ++	++	-	-	-	-	-	-	-	-
38165 ++	++	-	-	-	-	-	-	-	-
36658 ++	++	-	-	-	-	-	-	-	-

38292 ++	-	--	+	++	-	+	-	-	-
37367 ++	++	-	+	-	-	-	-	-	-
38249 ++	++	--+	+++	+++	+++	-	-	-	-
37611 ++	+	-	-	-	-	-	-	-	-
38293 ++	-	-	-	-	-	-	-	-	-
14576 ++	++	-	-	-	-	-	-	-	-
17752 ++	+	-	-	-	-	-	-	-	-
37859 ++	++	-	+	+	+	-	-	-	-
38107 ++	-	-	-	-	-	-	-	-	-
13731 ++	++	-	-	+	+	++	-	-	-
38294 ++	-	--	-	++	-	-	-	-	-
37720 ++	++	-	-	-	-	-	-	-	-
37670 ++	+	-	-	-	-	-	-	-	-
38295 ++	-	--+	+	+++	+	-	-	-	-
17662 ++	++	-	-	-	-	-	-	-	-
37929 ++	+	-	-	-	-	-	-	-	-
38240 ++	++	-	-	-	-	-	-	-	-
11774 ++	-	-	-	-	-	-	-	-	-
37846 ++	+	-	-	-	-	-	-	-	-
37883 ++	++	-	-	-	-	-	-	-	-
17426 ++	++	-	-	-	-	-	-	-	-
38296 ++	+++	-	+	+	+	+++	---	+++	-
18265 ++	-	-	-	-	-	-	-	-	-
38297 ++	+	-	+	+	+	+++	---	+++	+++
11344 ++	+	-	-	-	-	-	-	-	-
38298 ++	+	-	-	-	-	-	-	-	-
37595 ++	++	-	-	-	-	-	-	-	-
38034 ++	-	--+	++	++	+	+++	---	-	-
37539 ++	++	--	+	-	-	-	-	-	-
13859 ++	+	-	-	+	-	+	-	-	-
14098 ++	++	-	-	-	-	-	-	-	-
18058 ++	-	-	-	-	-	-	-	-	-
11578 ++	++	-	-	-	-	-	-	-	-

11334 ++	-	-	-	-	-	-	-	-	-
38299 ++	++	-	-	-	-	-	-	-	-
38300 ++	++	-	-	-	-	-	-	-	-
38301 ++	++	-	-	-	-	-	-	-	-
38018 ++	-	-	-	-	-	-	-	-	-
38302 ++	+	-	-	-	-	-	-	-	-
17547 ++	-	-	-	-	-	-	–	-	-
12602 ++	++	-	-	-	-	-	-	-	-
38303 ++	++	-	-	-	-	-	-	-	-
38304 ++	-	--	+	-	+	-	-	-	-
13636 ++	++	-	-	-	-	-	-	-	-
38169 ++	-	--	+	-	-	-	-	-	-
38207 ++	++	-	-	-	-	-	-	-	-
38240 ++	++	-	-	-	-	-	-	-	-
37917 ++	++	-	+	-	-	-	-	-	-
37810 ++	++	-	-	-	-	-	-	-	-
38066 ++	++	-	-	-	-	-	-	-	-
37406 ++	++	-	-	-	-	-	-	-	-
37994 ++	+	-	-	-	+	+++	---	-	-
16611 ++	++	-	-	-	-	-	-	-	-
14359 ++	++	-	-	-	-	-	-	-	-
38122 ++	++	-	-	-	-	-	-	-	-
38305 ++	+	-	-	-	-	-	-	-	-
38306 ++	+	--+	+++	+++	+++	+	-	-	-
12596 ++	-	-	-	-	-	-	-	-	-
18835 ++	-	--	+	+++	+	-	-	-	-
36835 ++	-	--+	+	+	-	-	-	-	-
11626 ++	-	-	-	-	-	-	-	-	-
18460 ++	++	-	-	-	-	-	-	-	-
38307 ++	-	-	-	-	-	-	-	-	-
38223 ++	++	-	-	-	-	-	-	-	-
38308 ++	+	-	-	-	-	-	-	-	-
17759 ++	++	-	-	-	-	-	-	-	-

38112	++	++	-	+	-	-	+	-	-	-
38309	++	++	--+	+++	+++	+++	+	-	-	-
17786	++	++	-	-	-	-	-	-	-	-
38310	++	-	-	-	-	-	-	-	-	-
37464	++	++	-	-	-	-	-	-	-	-
17900	++	-	-	-	-	-	-	-	-	-
14861	++	++	-	-	-	-	-	-	-	-
38311	++	++	-	-	-	-	-	-	-	-
37164	++	-	--	-	+	+	-	-	-	-
38312	++	-	--+	+	+++	+	-	-	-	-
37743	++	++	--+	+++	+++	+++	-	-	-	-
18295	++	-	-	-	-	-	-	-	-	-
37958	++	++	-	-	-	-	-	-	-	-
37888	++	++	-	-	-	-	-	-	-	-
38313	++	+	-	+	+	-	-	--	-	-
38264	++	-	-	-	-	-	-	-	-	-
37824	++	++	-	-	-	-	-	-	-	-
38058	++	-	-	-	-	-	-	-	-	-
14187	++	++	-	-	-	-	-	-	-	-
14010	++	++	-	-	-	-	-	-	-	-
38314	++	++	-	-	-	-	-	-	-	-
38315	++	++	-	+	-	-	+	-	-	-
38316	++	++	-	-	-	-	-	-	-	-
38095	++	-	-	-	-	-	-	-	-	-
37582	++	+	-	-	-	-	-	-	-	-
14167	++	++	-	-	-	-	-	-	-	-
15992	++	++	-	-	-	-	-	-	-	-
38043	++	+	-	-	-	-	-	-	-	-
17220	++	++	-	+	+	+	-	-	-	++
38317	++	++	-	-	-	-	-	-	-	-
37696	++	++	-	+	+++	+++	+	-	-	-
38081	++	-	--	-	-	-	-	-	-	-
38318	++	++	-	-	-	-	-	-	-	-

37349 ++	+	-	-	-	-	-	-	-	-
38319 ++	-	-	-	-	-	+	–	-	-
38320 ++	+	-	-	-	-	-	-	-	-
18531 ++	-	-	-	-	-	-	-	-	-
37541 ++	-	-	+	+	-	-	-	-	-
38321 ++	-	-	-	-	-	-	-	-	-
13748 ++	++	-	-	-	-	-	-	-	-
38322 ++	+	–+	+++	+++	+++	-	-	-	-
38323 ++	+++	–+	+++	+++	+++	+	––	-	-
38324 ++	-	-	-	-	-	-	-	-	-
38325 ++	+	-	-	-	-	-	-	-	-
38218 ++	++	-	-	-	-	-	-	-	-
37902 ++	-	-	-	-	-	-	-	-	-
37490 ++	++	-	-	-	-	-	-	-	-
37772 ++	-	-	-	-	-	+	-	-	-
16029 ++	++	-	-	-	-	-	-	-	-
38318 ++	++	-	-	-	-	-	-	-	-
20420 ++	-	–+	+	++	-	-	-	-	-
37997 ++	++	-	-	-	-	-	-	-	-
38326 ++	++	–+	+++	+++	+++	+	––	-	-
38327 ++	+	-	-	-	-	-	–	-	-
18956 ++	++	-	-	-	-	+	-	-	-
37723 ++	++	-	-	-	-	-	–	-	-
18013 ++	++	-	+	-	-	-	-	-	-
38328 ++	++	-	-	-	-	-	-	-	-
38021 ++	+	-	-	-	-	-	-	-	-
37970 ++	++	-	-	-	-	-	-	-	-
38329 ++	-	-	-	-	-	-	-	-	-
38330 ++	+	-	+	++	-	-	-	-	-
38320 ++	+	-	-	-	-	-	-	-	-
17808 ++	+	-	-	-	-	-	-	-	-
38331 ++	-	–+	+	+++	-	-	-	+++	++
37414 ++	-	–+	+	+	+	-	-	-	-

38332 ++	-	--+	+++	+++	-	-	-	-	-
14023 ++	++	-	-	-	-	-	-	-	-
12239 ++	+	-	-	-	-	-	-	-	-
13764 ++	++	-	-	-	-	-	-	-	-
37763 ++	-	-	-	-	-	-	-	-	-
38333 ++	++	--+	+++	+++	+++	-	–	-	-
38334 ++	++	-	-	-	-	-	-	-	-
37955 ++	+	-	-	-	-	-	-	-	-
38335 ++	++	-	-	-	-	-	-	-	-
11776 ++	-	-	-	-	-	-	-	-	-
38067 ++	++	-	-	-	-	-	-	-	-
16567 ++	++	-	-	-	-	-	-	-	-
38336 ++	++	-	-	-	-	-	-	-	-
37720 ++	++	-	-	-	-	-	-	-	-
38337 ++	-	-	-	-	-	-	-	-	-
14273 ++	++	-	-	-	-	-	-	-	-
38338 ++	++	-	-	-	-	-	-	-	-
38339 ++	-	-	+	+	+	+	–	-	-
37870 ++	-	-	-	-	-	-	-	-	-
14013 ++	+	-	-	+	-	-	-	-	-
11928 ++	++	-	-	-	-	-	-	-	-
15098 ++	++	–	-	-	+	+++	---	-	-
16005 ++	++	-	-	-	-	-	-	-	-
38340 ++	++	-	-	-	-	-	-	-	-
38307 ++	-	-	-	-	-	-	-	-	-
38341 ++	++	-	-	-	-	-	-	-	-
38342 ++	++	-	+	-	-	-	-	-	-
38343 ++	-	--+	++	+++	+	+	–	+++	-
38344 ++	++	-	-	-	-	-	-	-	-
11057 ++	++	-	-	-	-	-	-	-	-
38345 ++	+	--+	+++	+++	+++	-	-	-	-
38346 ++	++	-	-	-	-	-	-	-	-
37800 ++	++	-	-	-	-	-	-	-	-

17601 ++	-	–	-	+	-	-	-	-	-
37850 ++	+	-	-	-	-	-	-	-	-
17730 ++	++	-	-	-	-	-	-	-	-
38347 ++	++	-	-	-	-	-	-	-	-
37871 ++	-	–+	+	-	-	+	–	-	-
13580 ++	++	-	-	-	-	-	-	-	-
17671 ++	-	-	-	-	-	-	-	-	-
17520 ++	++	-	-	-	-	-	-	-	-
38348 ++	-	–	-	+	-	-	-	-	-
38178 ++	++	-	-	-	-	-	-	-	-
38080 ++	++	–+	++	-	-	-	-	++	-
12602 ++	++	-	-	-	-	-	-	-	-
37394 ++	+	-	-	-	-	-	-	-	-
38059 ++	-	-	-	-	-	-	-	-	-
37661 ++	+	-	-	-	-	-	-	-	-
14122 ++	++	-	-	-	-	-	-	-	-
17822 ++	++	-	-	-	-	-	-	-	-
38337 ++	-	-	-	-	-	-	-	-	-
11206 ++	++	-	-	-	-	-	-	-	-
38349 ++	++	-	-	-	-	-	-	-	-
37781 ++	-	-	-	-	-	-	-	-	-
18928 ++	+	–+	+++	+++	+++	-	-	-	-
38350 ++	-	-	-	-	-	-	-	-	-
18420 ++	+	-	-	-	-	-	-	-	-
38351 ++	++	-	-	-	-	-	-	-	-
38352 ++	+	-	-	-	-	-	-	-	-
38353 ++	++	-	-	-	-	+	–	-	-
38354 ++	+	–+	+++	+++	+++	-	-	-	-
38260 ++	++	-	-	-	-	-	-	-	-
38261 ++	-	-	-	-	-	-	-	-	-
17636 ++	++	-	-	-	-	-	-	-	-
38355 ++	++	-	-	-	+	-	-	-	-
38254 ++	++	-	-	-	-	-	-	-	-

38356	++	++	--+	+++	+++	+++	-	-	-	-
38357	++	-	-	-	-	+	-	-	-	-
37950	++	-	-	-	-	-	-	-	-	-
38358	++	++	-	-	-	-	-	-	-	-
38359	++	-	-	-	-	-	-	-	-	-
38360	++	++	-	-	-	-	-	-	-	-
18013	++	++	-	+	-	-	-	-	-	-
14231	++	++	-	-	-	-	-	-	-	-
11866	++	-	-	-	-	-	-	-	-	-
38361	++	++	-	-	-	-	-	-	-	-
38362	++	++	--+	+++	+++	+++	-	-	-	-
38363	++	-	-	-	-	-	-	-	-	-
38364	++	-	-	-	-	-	-	-	-	-
38365	++	++	-	+	+	+	++	---	-	-
38097	++	++	-	-	-	-	-	-	-	-
38366	++	++	-	-	-	-	-	-	-	-
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38367	++	++	-	-	-	-	-	-	-	-
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37963	++	++	-	-	-	-	-	-	-	-
13181	++	++	-	-	-	-	-	-	-	-
17729	++	-	-	-	-	-	-	-	-	-
38368	++	++	-	-	-	-	-	-	-	-
37254	++	-	-	-	-	-	-	-	-	-
14542	++	++	-	-	+	+	-	-	-	-
38369	++	++	-	-	-	-	-	-	-	-
37845	++	++	-	-	-	-	-	-	-	-
38147	++	-	-	-	-	-	-	-	-	-
17642	++	++	-	-	-	-	-	-	-	-
37994	++	+	-	-	-	+	+++	---	-	-
38297	++	+	-	+	+	+	+++	---	+++	-
13532	++	++	-	-	+	+	-	-	-	-

38135 ++	++	-	-	-	-	-	-	-	-
38370 ++	-	--+	+++	+++	+++	-	-	-	-
38371 ++	-	--+	+	+	-	-	-	-	-
38282 ++	-	-	-	-	-	-	-	-	-
11989 ++	+	-	-	-	-	-	-	-	-
38372 ++	-	--+	+++	+++	+++	-	-	-	-
38076 ++	++	-	-	-	-	-	-	-	-
38373 ++	++	-	-	-	-	-	-	-	-
37935 ++	++	-	-	-	-	-	-	-	-
14542 ++	++	-	-	-	-	-	-	-	-
17842 ++	-	-	-	-	-	-	-	-	-
38276 ++	++	-	-	-	-	+	-	-	-
38374 ++	+	--+	+++	+++	+++	-	-	-	-
38375 ++	++	-	-	-	-	-	-	-	-
38376 ++	++	-	-	-	-	-	-	-	-
37810 ++	++	-	-	-	-	-	-	-	-
38377 ++	+	-	+	+	-	-	-	-	-
38029 ++	-	-	-	-	-	-	-	-	-
14287 ++	++	-	-	-	-	-	-	-	-
38166 ++	+	-	+	+	-	-	-	-	-
38378 ++	+	-	-	-	-	-	-	-	-
38379 ++	++	-	-	-	-	-	-	-	-
38380 ++	++	-	-	-	-	-	-	-	-
37758 ++	-	-	-	-	-	-	-	-	-
38381 ++	++	-	-	-	-	-	-	-	-
38382 ++	-	-	-	-	-	-	-	-	-
38383 ++	-	-	-	-	-	+	-	-	-
38384 ++	-	-	-	-	-	-	-	-	-
38385 ++	-	--+	+++	+++	+++	-	-	-	-
38211 ++	+	-	-	-	-	-	-	-	-
38036 ++	++	-	-	-	-	-	-	-	-
17810 ++	+	-	-	-	-	-	-	-	-
38126 ++	-	--	+	++	+	-	-	-	-

37824 ++	++	-	-	-	-	-	-	-	-
11460 ++	+	-	-	-	-	-	-	-	-
38386 ++	++	-	-	-	-	-	-	-	-
38359 ++	-	-	-	-	-	-	-	-	-
16097 ++	++	-	-	-	-	-	-	-	-
11841 ++	+	-	-	-	-	-	-	-	-
38387 ++	+	-	-	-	-	-	-	-	-
38062 ++	-	-	-	-	-	-	-	-	-
11210 ++	++	-	-	-	-	-	-	-	-
13763 ++	++	-	-	-	-	-	-	-	-
38388 ++	++	-	-	-	-	-	-	-	-
38389 ++	-	--	-	+	-	+	-	-	-
38168 ++	++	-	-	-	-	-	-	-	-
38390 ++	++	-	-	-	-	-	-	-	-
38391 ++	-	--+	-	-	-	-	-	-	-
38392 ++	++	-	-	-	-	-	-	-	-
38393 ++	-	-	-	-	-	-	-	-	-
37792 ++	++	-	-	-	-	-	-	-	-
37798 ++	++	-	-	-	-	-	-	-	-
38394 ++	++	-	-	-	-	-	-	-	-
38395 ++	-	-	-	-	-	-	-	-	-
38396 ++	-	-	-	-	-	-	-	-	-
37418 ++	+	-	-	-	+	+	-	-	-
16613 ++	++	-	-	-	-	-	-	-	-
38397 ++	-	-	-	-	-	-	-	-	-
38398 ++	++	-	-	-	-	-	-	-	-
38191 ++	++	--	++	+++	++	-	-	-	-
38399 ++	++	-	-	-	-	-	-	-	-
38400 ++	++	--+	+++	+++	+++	+	-	-	-
38401 ++	++	-	-	-	-	-	-	-	-
38402 ++	++	-	-	-	-	-	-	-	-
36732 ++	-	-	-	-	-	-	-	-	-
38403 ++	++	-	-	-	-	-	-	-	-

38404 ++	++	--+	+++	+++	+++	+	-	-	-
38405 ++	-	-	-	-	-	-	-	-	-
38406 ++	++	--+	+++	+++	+++	-	-	-	+++
38407 ++	++	-	-	-	-	-	-	-	-
38408 ++	++	-	-	-	-	-	-	-	-
16062 ++	++	-	+	+	+	-	-	-	-
36890 ++	-	--+	+	+++	++	+	-	-	-
14179 ++	++	-	-	-	-	-	-	-	-
38409 ++	++	--+	+++	+++	+++	-	-	-	-
37894 ++	++	-	-	-	-	-	-	-	-
38003 ++	++	-	-	-	-	-	-	-	-
38410 ++	+	-	-	-	-	-	-	-	-
13928 ++	++	-	-	-	-	-	-	-	-
38224 ++	-	-	-	-	-	-	-	-	-
37312 ++	+	-	+	+	+	+++	---	-	-
38411 ++	-	-	-	-	-	+	-	-	-
38412 ++	+	--+	+++	+++	+++	+	-	-	-
14533 ++	++	-	-	-	+	+	-	-	-
37856 ++	++	-	-	-	-	-	-	-	-
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13673 ++	++	-	+	+	+	-	-	-	++
17608 ++	++	-	-	-	-	-	-	-	-
38414 ++	+	-	-	-	-	+	-	-	-
38010 ++	++	-	-	-	-	-	-	-	-
38057 ++	++	-	-	-	-	-	-	-	-
38415 ++	+	-	-	-	-	-	-	-	-
19016 ++	++	-	-	-	+	-	-	-	-
38416 ++	+	--+	+++	+++	+++	+	-	-	-
14743 ++	++	-	-	-	-	-	-	-	-
12056 ++	+	-	-	-	-	-	-	-	-
38417 ++	++	-	-	-	-	-	-	-	-
38418 ++	+	-	-	-	-	-	-	-	-
37917 ++	++	-	-	-	-	-	-	-	-

38419	++	++	-	+	+	+	-	-	-	-
37587	++	+	-	-	-	-	-	-	-	-
38420	++	++	-	+	+	+	+	–	-	-
38421	++	++	-	-	-	-	-	-	-	-
38422	++	-	–	+	-	-	-	-	-	-
17722	++	++	-	-	-	-	-	-	-	-
38355	++	++	-	+	+	+	-	-	-	-
38423	++	++	-	-	-	-	-	-	-	-
38312	++	-	–+	+	+++	-	-	-	-	-
38424	++	++	-	-	-	-	-	-	-	-
11880	++	++	-	-	-	-	-	-	-	-
17503	++	-	-	-	-	-	-	–	-	-
38425	++	++	-	-	-	-	-	-	-	-
38394	++	++	-	-	-	-	-	-	-	-
17499	++	-	–+	+	+	-	-	-	-	-
38426	++	++	-	-	-	-	-	-	-	-
38427	++	+	-	-	-	-	-	-	-	-
37879	++	+	–+	++	+++	+	++	––	-	-
38343	++	-	–+	++	+++	+	+	-	+++	-
14628	++	++	-	-	-	-	-	-	-	-
38428	++	+	-	-	-	-	-	-	-	-
37661	++	+	-	-	-	-	-	-	-	-
37952	++	++	-	-	-	-	-	-	-	-
17648	++	++	-	-	-	-	-	-	-	-
38299	++	++	-	-	-	+	-	-	-	-
38429	++	++	–+	+++	-	-	-	-	-	-
38430	++	++	-	-	-	-	-	-	-	-
38431	++	++	-	-	+	-	-	–	-	-
38026	++	-	-	-	+	+	-	-	-	-
38292	++	-	––	-	++	-	-	-	-	-
38432	++	++	-	-	-	-	-	–	-	-
38351	++	++	-	-	-	-	-	-	-	-
38433	++	++	-	-	-	-	-	-	-	-

37613 ++	-	-	-	++	-	-	-	-	-
14378 ++	++	-	-	-	-	-	-	-	-
37960 ++	+	-	-	-	-	-	-	-	-
37364 ++	++	-	-	-	-	-	-	-	-
38434 ++	++	-	-	-	-	-	-	-	-
38410 ++	-	-	-	-	-	-	-	-	-
10968 ++	++	-	-	-	-	-	–	-	-
17784 ++	-	–	+	-	+	-	-	-	-
38221 ++	++	-	+	-	-	-	-	-	-
38435 ++	++	–+	++	-	-	-	-	++	+
38436 ++	++	-	-	-	+	-	-	-	-
17564 ++	-	-	-	-	-	-	-	-	-
37690 ++	++	-	-	-	-	-	-	-	-
37707 ++	++	-	-	-	-	-	-	-	-
14253 ++	++	–	+	+	+	+++	–––	-	-
38017 ++	-	-	-	-	-	-	-	-	-
38437 ++	++	-	-	-	-	-	-	-	-
11956 ++	-	-	-	-	-	-	-	-	-
38438 ++	-	-	-	-	-	-	-	-	-
11070 ++	++	-	-	-	-	-	-	-	-
38439 ++	++	-	-	-	-	-	-	-	-
38440 ++	++	–+	+++	+++	+++	+	-	-	-
37911 ++	+	-	-	-	-	-	–	-	-
37726 ++	++	–	+	++	++	+	–	-	-
38441 ++	-	-	-	-	-	-	-	-	-
38442 ++	-	–+	-	-	-	-	-	-	-
38443 ++	+	-	-	-	-	-	-	-	-
37499 ++	+	–	+	+++	+	++	––	-	-
38444 ++	++	–+	+++	+++	+++	+	-	-	-
38445 ++	++	-	-	-	-	-	-	-	-
11651 ++	++	-	-	-	-	-	-	-	-
38446 ++	-	–+	+	+++	+	-	-	-	-
38321 ++	-	-	-	-	-	-	-	-	-

38447 ++	+	--+	+++	+++	+++	-	-	-	-
38448 ++	++	-	-	-	-	+	-	-	-
38288 ++	++	-	-	-	-	-	-	-	-
38449 ++	-	-	-	-	-	+	-	-	-
38450 ++	++	--+	+++	+++	+++	-	--	-	-
38451 ++	-	--+	+++	+++	+++	-	-	-	-
38243 ++	++	-	-	-	-	-	-	-	-
37146 ++	+	-	-	-	-	-	-	-	-
38452 ++	++	-	-	-	-	-	-	-	-
38453 ++	-	-	-	-	-	-	-	-	-
37595 ++	++	-	-	-	-	-	-	-	-
38454 ++	-	-	-	+	-	-	-	-	-
38455 ++	-	--	-	+	-	-	-	-	-
38456 ++	++	-	-	-	-	-	-	-	-
37681 ++	-	-	-	-	-	-	-	-	-
38457 ++	++	-	-	-	-	-	-	-	-
13769 ++	++	-	-	-	-	-	-	-	-
38458 ++	++	-	-	-	-	-	-	-	-
18068 ++	++	-	-	-	-	-	-	-	-
38459 ++	++	--+	+++	+++	+++	+	-	-	-
14063 ++	+	-	-	-	-	-	-	-	-
37770 ++	-	-	-	-	-	-	-	-	-
14542 ++	++	-	-	-	+	-	-	-	-
16016 ++	++	-	-	-	-	-	-	-	-
14204 ++	++	-	-	-	+	-	-	-	-
14028 ++	-	-	-	-	-	-	-	-	-
38439 ++	++	-	-	-	-	-	-	-	-
16016 ++	++	-	-	-	-	-	-	-	-
38460 ++	++	--+	+++	+++	+++	+	-	-	-
38435 ++	++	--+	++	-	-	-	-	-	-
38349 ++	++	-	-	-	-	-	-	-	-
11973 ++	-	-	-	-	-	-	-	-	-
38461 ++	++	-	-	-	-	+	-	-	-

37703 ++	++	-	-	-	-	-	-	-	-
37835 ++	++	-	-	-	-	-	-	-	-
38300 ++	++	-	-	-	-	-	-	-	-
38462 ++	++	-	-	-	-	-	-	-	-
17844 ++	++	-	-	-	-	-	-	-	-
38463 ++	++	-	-	-	-	-	-	-	-
38464 ++	++	-	-	-	-	-	-	-	-
38134 ++	++	--+	+++	-	-	-	-	++	-
38465 ++	++	-	-	-	-	-	-	-	-
38466 ++	-	-	-	-	-	-	-	-	-
38136 ++	++	-	-	-	-	-	-	-	-
38120 ++	++	-	-	-	-	-	-	-	-
19608 ++	+	-	-	-	-	-	-	-	-
38467 ++	++	-	+	-	-	+	−	-	-
13773 ++	++	-	-	-	-	-	-	-	-
38465 ++	++	-	-	-	-	-	-	-	-
38297 ++	+	−	+	+	+	+++	---	-	-
37379 ++	-	-	-	-	-	-	-	-	-
18152 ++	-	-	-	-	-	-	-	-	-
38468 ++	+	−	++	++	++	+++	---	-	-
19945 ++	-	--+	-	+	-	-	-	-	-
38392 ++	++	-	-	-	-	-	-	-	-
38469 ++	++	-	-	-	-	-	-	-	-
38342 ++	++	-	-	-	-	-	-	-	-
38470 ++	++	--+	+++	+++	+++	+	−	-	-
16635 ++	-	-	+	-	+	+	−	-	++
12120 ++	-	-	-	-	-	-	-	-	-
37896 ++	+	-	-	-	-	-	-	-	-
38471 ++	++	--+	+++	+++	+++	-	-	-	-
37021 ++	++	-	-	-	-	-	-	-	-
11880 ++	++	-	-	-	-	-	-	-	-
38472 ++	-	−	-	-	-	-	-	-	-
37798 ++	++	-	-	-	-	-	-	-	-

11785 ++	+	-	-	-	-	-	-	-	-
38473 ++	-	-	-	-	-	-	-	-	-
38474 ++	++	-	-	-	-	-	-	-	-
37951 ++	-	-	-	-	-	-	-	-	-
38475 ++	++	-	-	-	-	-	-	-	-
37856 ++	++	-	-	-	-	-	-	-	-
19182 ++	++	-	-	-	-	-	-	-	-
38476 ++	-	-	-	-	-	-	-	-	-
37358 ++	+	-	-	-	-	-	-	-	-
38477 ++	++	-	-	-	-	-	-	-	-
16647 ++	+++	-	-	-	-	-	-	-	-
11776 ++	-	-	-	-	-	-	-	-	-
18202 ++	-	-	-	-	-	-	-	-	-
37578 ++	+	-	-	-	-	+	−	-	-
38160 ++	++	-	-	-	-	-	-	-	-
38478 ++	+	-	-	-	-	-	-	-	-
17874 ++	-	−−+	+	-	-	-	-	-	-
19089 ++	++	-	-	-	-	-	-	-	-
38479 ++	++	-	-	-	-	-	-	-	-
38480 ++	++	-	-	-	-	-	-	-	-
38437 ++	++	-	-	-	-	-	-	-	-
37730 ++	++	-	-	-	-	-	-	-	-
38341 ++	++	-	-	-	-	-	-	-	-
38481 ++	++	-	-	-	-	-	-	-	-
16562 ++	++	-	-	+	+	+	−	-	-
11583 ++	++	-	-	-	-	-	-	-	-
37711 ++	++	-	-	-	-	-	-	-	-
37928 ++	++	-	-	-	-	-	-	-	-
38202 ++	++	-	-	-	-	-	-	-	-
38482 ++	+	−−+	+++	+++	+++	+	−	-	-
38483 ++	++	-	-	-	-	-	-	-	-
11844 ++	-	-	-	-	-	-	-	-	-
14576 ++	++	-	-	-	-	-	-	-	-

37889 ++	-	-	-	-	-	-	-	-	-
38484 ++	+	-	-	-	-	+	–	-	-
13514 ++	++	-	-	-	-	-	-	-	-
38485 ++	++	-	-	-	+	-	-	-	-
38362 ++	+	–+	+++	+++	+++	-	–	-	-
38375 ++	++	-	-	-	-	-	-	-	-
38486 ++	+	-	-	-	-	-	-	-	-
14873 ++	++	–	+	+	+	+++	–––	-	-
38487 ++	++	-	-	-	-	-	-	-	-
37619 ++	-	–+	+	+++	++	-	–	-	-
38488 ++	++	-	-	-	-	-	-	-	-
38477 ++	++	-	-	-	-	-	-	-	-
15992 ++	++	-	-	-	-	-	-	-	-
38489 ++	+	–+	+++	+++	+++	-	–	-	-
38300 ++	++	-	-	-	-	-	-	-	-
13860 ++	++	-	-	-	-	-	-	-	-
12919 ++	+	-	-	-	-	+	-	-	-
38103 ++	++	–	+	+++	+++	+	–	-	-
15942 ++	++	-	-	-	-	-	-	-	-
18518 ++	++	-	-	-	-	-	-	-	-
38174 ++	++	-	-	-	-	-	-	-	-
38490 ++	++	-	-	-	-	-	-	-	-
38265 ++	+	-	-	-	-	-	-	-	-
13617 ++	++	-	-	-	-	-	-	-	-
38481 ++	++	-	-	-	-	-	-	-	-
38491 ++	+	-	-	-	-	-	-	-	-
38492 ++	+	-	-	-	+	-	-	-	-
38493 ++	++	-	-	-	-	-	-	-	-
15972 ++	++	-	-	-	-	-	-	-	-
20423 ++	-	–+	-	-	-	-	-	-	-
38494 ++	+	–+	+++	+++	+++	+	–	-	-
38495 ++	++	-	-	-	-	-	-	-	-
38496 ++	+	–+	+++	+++	+++	-	-	-	-

19269 ++	-	-	-	-	-	-	-	-	-
13863 ++	++	-	-	-	-	-	-	-	-
38497 ++	+	--+	+++	+++	+++	+	-	-	-
12255 ++	-	-	-	-	-	-	-	-	-
38498 ++	++	-	-	-	-	-	-	-	-
38499 ++	+	-	-	-	-	-	-	-	-
38429 ++	++	--+	+++	-	-	-	-	+++	-
38500 ++	+	-	++	++	++	+++	---	-	-
16644 ++	+	-	-	-	-	-	-	-	-
38200 ++	++	-	-	-	-	-	-	-	-
38501 ++	+	-	-	-	-	-	-	-	-
38051 ++	++	-	-	-	-	-	-	-	-
38331 ++	-	--+	+	+++	+	-	-	+++	+
15942 ++	++	-	-	-	-	-	-	-	-
38502 ++	++	--+	+++	+++	+++	+	-	-	-
38503 ++	-	-	-	-	-	-	-	-	-
37900 ++	-	--+	+	+++	+	-	-	+++	-
14062 ++	++	-	-	-	-	-	-	-	-
16611 ++	++	-	-	-	-	-	-	-	-
38504 ++	-	-	-	-	-	-	-	-	-
16029 ++	++	-	-	-	-	-	-	-	-
37984 ++	-	-	-	-	-	-	-	-	-
38505 ++	++	-	-	+	-	-	-	-	-
38506 ++	-	-	-	-	-	-	-	-	-
38507 ++	-	-	-	-	-	-	-	-	-
38508 ++	++	-	-	-	-	-	-	-	-
38509 ++	+	--+	+++	+++	+++	-	-	-	-
38510 ++	++	-	-	-	-	-	-	-	-
37948 ++	++	-	-	-	-	+	-	-	-
38511 ++	++	-	-	-	-	-	-	-	-
38512 ++	++	-	-	-	-	-	-	-	-
38513 ++	++	-	-	-	-	-	-	-	-
38384 ++	-	-	-	-	-	-	-	-	-

37903 ++	+	-	-	-	-	-	-	-	-
17426 ++	++	-	-	-	-	-	-	-	-
38514 ++	-	-	-	-	-	-	-	-	-
11496 ++	++	-	-	-	-	-	-	-	-
38515 ++	-	-	-	-	-	-	-	-	-
38516 ++	+	-	-	-	-	-	-	-	-
38517 ++	++	-	-	-	-	-	-	-	-
38518 ++	-	--	+	++	+	+	-	-	-
11611 ++	++	-	-	-	-	-	-	-	-
12152 ++	++	-	+	+	+	-	-	-	-
38519 ++	-	--+	+++	+++	+++	-	-	-	-
14305 ++	++	-	-	-	-	+	-	-	-
38520 ++	-	-	-	+	-	-	-	-	-
18708 ++	+	-	-	-	-	-	-	-	-
38420 ++	++	-	+	+	+	+	-	-	-
17399 ++	++	-	-	-	-	-	-	-	-
38194 ++	++	-	-	-	-	-	-	-	-
38521 ++	++	--+	+++	+++	+++	-	-	-	-
38522 ++	+	--+	+++	+++	+++	+	-	-	+++
37943 ++	++	-	-	-	-	-	-	-	-
13517 ++	++	-	-	-	-	-	-	-	-
38523 ++	++	-	+	+	+	+	-	-	-
38052 ++	-	-	-	-	-	-	-	-	-
37839 ++	++	-	+	-	+	+++	---	-	-
38524 ++	++	-	-	-	-	-	-	-	-
38501 ++	-	-	-	-	-	-	-	-	-
36522 ++	+	-	-	-	-	-	-	-	-
38525 ++	-	-	-	-	-	-	-	-	-
38526 ++	-	-	-	-	-	-	-	-	-
38527 ++	+	--+	+++	+++	+++	-	-	-	-
38373 ++	++	-	-	-	-	-	-	-	-
37920 ++	-	-	-	-	-	-	-	-	-
38528 ++	-	-	-	+	-	-	-	-	-

18161 ++	+	-	-	-	-	-	-	-	-
38529 ++	+	---+	+++	+++	+++	-	-	-	-
38530 ++	+	-	-	-	-	-	-	-	-
38531 ++	++	-	-	-	-	-	-	-	-
37959 ++	+	-	-	-	-	-	-	-	-
38532 ++	++	-	-	-	-	-	-	-	-
11220 ++	++	-	-	-	-	-	-	-	-
17417 ++	++	-	+	+	+	-	-	-	-
37935 ++	++	-	-	-	-	-	-	-	-
38533 ++	++	-	-	-	-	-	-	-	-
38534 ++	-	---+	+	+	-	-	-	-	-
38216 ++	-	---+	+	-	-	-	-	-	-
38324 ++	-	-	-	-	-	-	-	-	-
38535 ++	+	-	-	-	-	-	-	-	-
37539 ++	++	--	+	-	-	-	-	-	-
13642 ++	++	-	+	+	+	++	--	-	-
38536 ++	++	-	-	-	-	-	-	-	-
37819 ++	++	-	-	-	-	-	-	-	-
38537 ++	++	-	-	-	-	-	-	-	-
38117 ++	++	-	-	-	-	-	-	-	-
38129 ++	+	-	-	-	-	-	-	-	-
38538 ++	++	-	-	-	-	-	-	-	-
38539 ++	++	-	-	-	-	-	-	-	-
38540 ++	-	-	-	-	-	-	-	-	-
38541 ++	++	-	-	-	-	-	-	-	-
38119 ++	++	-	-	-	-	-	-	-	-
38542 ++	+	---+	+++	+++	+++	-	-	-	-
14122 ++	++	-	-	-	-	-	-	-	-
38543 ++	+	---+	+++	+++	+++	-	--	-	-
38544 ++	+	-	+	+	+	+++	---	-	-
17086 ++	-	---+	+++	+++	+++	-	-	-	-
38545 ++	++	-	-	-	-	-	-	-	-
38516 ++	+	-	-	-	-	-	-	-	-

38546 ++	+	--+	+++	+++	+++	-	-	-	-
38547 ++	+	-	-	-	-	-	-	-	-
11103 ++	++	-	-	-	-	-	-	-	-
38548 ++	++	-	-	-	-	+	-	-	-
38549 ++	+	-	-	-	-	-	-	-	-
17220 ++	++	-	+	+	+	+	-	-	-
38550 ++	+	--+	+++	+++	+++	-	-	-	-
38551 ++	++	-	-	-	-	-	-	-	-
11797 ++	++	-	-	-	-	-	-	-	-
37584 ++	++	-	-	-	-	-	-	-	-
38487 ++	++	-	-	-	-	-	-	-	-
16565 ++	+	-	-	+	+	-	-	-	-
38552 ++	-	-	-	-	-	-	-	-	-
38553 ++	+	-	-	-	-	-	-	-	-
38143 ++	+	-	-	-	-	-	-	-	-
38554 ++	-	--	+	-	-	+	-	-	-
37944 ++	-	-	-	-	-	-	-	-	-
38555 ++	-	-	+	-	-	-	-	-	-
38556 ++	+	--+	++	+++	+	+++	---	+++	+++
37952 ++	++	-	-	-	-	-	-	-	-
38557 ++	-	-	+	-	+	-	-	-	-
11224 ++	-	-	-	-	-	-	-	-	-
38558 ++	+	-	+	+++	+	++	---	-	-
38179 ++	++	-	-	-	-	-	-	-	-
16603 ++	++	-	-	+	+	+	-	-	-
38559 ++	-	-	+	-	-	-	-	-	-
38219 ++	-	-	-	-	-	+	-	-	-
38510 ++	++	-	-	-	-	-	-	-	-
14230 ++	++	-	-	-	-	-	-	-	-
38560 ++	-	-	-	-	-	-	-	-	-
38162 ++	+	-	-	-	-	-	-	-	-
17119 ++	-	-	-	-	-	-	-	-	-
17919 ++	-	-	-	-	-	-	-	-	-

38561 ++	++	-	-	-	-	-	-	-	-
38562 ++	++	-	-	-	-	-	-	-	-
38563 ++	-	–	+	+	+	-	-	-	-
16057 ++	++	-	-	-	-	-	-	-	-
37835 ++	++	-	-	-	-	-	-	-	-
11019 ++	-	–	+	-	+	-	-	-	-
37975 ++	++	-	-	-	-	-	-	-	-
37539 ++	++	––	+	-	-	-	-	-	-
14607 ++	++	-	-	-	-	-	-	-	-
38564 ++	++	-	-	-	-	-	-	-	-
11479 ++	++	-	-	-	-	-	-	-	-
16577 ++	++	-	-	-	-	-	-	-	-
37821 ++	+++	––+	+++	+++	+++	-	–	-	-
12381 ++	-	-	-	-	-	-	-	-	-
38218 ++	++	-	-	-	-	-	-	-	-
11853 ++	+	-	-	-	-	-	-	-	-
11279 ++	-	-	-	-	-	-	-	-	-
37994 ++	+	-	-	-	+	+++	–––	-	+++
38565 ++	+	-	-	-	-	-	-	-	-
14542 ++	++	-	-	-	-	-	-	-	-
11206 ++	++	-	-	-	-	-	-	-	-
11683 ++	++	-	-	-	-	-	-	-	-
38566 ++	+	-	-	-	-	-	-	-	-
13874 ++	++	-	-	-	+	-	-	-	-
38567 ++	++	-	-	-	-	-	-	-	-
38518 ++	-	––	+	++	+	+	–	-	-
38164 ++	++	-	-	-	-	-	-	-	-
11103 ++	++	-	-	-	-	-	-	-	-
38005 ++	++	-	-	-	-	-	-	-	-
38480 ++	++	-	-	-	-	-	-	-	-
38568 ++	-	-	-	-	-	-	-	-	-
38569 ++	++	-	-	-	-	-	–	-	-
19720 ++	+	––+	+++	+++	+++	-	–	-	-

13603 ++	++	-	-	-	-	-	-	-	-
38163 ++	-	–	-	+	-	-	-	-	-
38294 ++	-	––	-	++	-	-	-	-	-
38570 ++	+	––+	+++	+++	+++	-	–	-	-
38571 ++	++	-	-	-	-	-	-	-	-
38455 ++	-	––	+	+	-	-	-	-	-
11704 ++	+	-	-	-	-	-	-	-	-
11867 ++	-	-	-	-	-	-	-	-	-
38407 ++	++	-	-	-	-	-	-	-	-
38572 ++	++	-	-	-	-	-	-	-	-
38573 ++	++	––+	+++	+++	+++	-	–	-	-
38574 ++	++	-	-	-	-	-	-	-	-
38575 ++	-	-	-	-	-	-	-	-	-
38576 ++	+	-	-	-	-	-	-	-	-
38577 ++	++	-	-	-	-	-	-	-	-
37919 ++	++	-	-	-	-	-	-	-	-
37828 ++	++	-	-	-	-	-	-	-	-
38177 ++	++	-	-	-	-	-	-	-	-
37799 ++	++	-	-	-	-	-	-	-	-
15352 ++	++	–	+	+	+	+++	–––	-	+++
17590 ++	-	––+	+	+	-	-	-	-	-
38578 ++	-	-	-	-	-	-	-	-	-
37849 ++	++	-	-	-	-	-	-	-	-
38579 ++	-	-	-	-	-	-	-	-	-
38208 ++	++	-	-	-	+	+	–	-	-
38105 ++	++	-	-	-	-	-	-	-	-
12667 ++	++	-	-	-	-	-	-	-	-
38461 ++	++	-	-	-	-	+	-	-	-
38580 ++	+	-	+	-	-	-	-	-	-
11236 ++	+	-	-	-	-	-	-	-	-
38456 ++	++	-	-	-	-	-	-	-	-
38224 ++	-	-	-	-	-	-	-	-	-
37616 ++	-	-	-	-	-	-	-	-	-

38581	++	++	--+	+++	+++	+++	+	-	.	.
38582	++	.	.	.	.	.	.	.	.	.
14059	++	++	.	.	.	+	.	.	.	.
38430	++	++	.	.	.	.	.	.	.	.
38531	++	++	.	.	.	.	.	.	.	.
17700	++	++	.	.	.	.	.	.	.	.
38583	++	++	--+	+++	+++	+++	+	-	.	.
38584	++	.	.	+	.	.	.	.	.	.
38585	++	++	.	.	.	.	.	.	.	.
38586	++	++	.	.	.	.	.	.	.	.
16630	++	++	.	.	.	.	+	-	.	.
15958	++	++	.	.	.	.	.	.	.	.
18375	++	++	.	.	.	.	.	.	.	.
37695	++	++	.	.	.	.	.	.	.	.
38525	++	.	.	.	.	.	.	.	.	.
38587	++	++	.	.	.	.	+	-	.	.
11027	++	++	.	.	.	.	.	.	.	.
38588	++	++	.	.	.	.	.	.	.	.
11594	++	.	.	.	.	.	.	.	.	.
38589	++	++	.	.	.	.	.	.	.	.
38590	++	+	.	.	.	.	.	.	.	.
38591	++	+	-	+	+	+	+++	---	.	.
17417	++	++	.	+	+	+	+	-	.	.
38381	++	++	.	.	.	.	.	.	.	.
13864	++	++	.	.	.	.	.	.	.	.
38592	++	++	.	.	.	.	.	.	.	.
38593	++	+	-	+	+	+	+++	---	.	.
13892	++	++	.	.	.	.	.	.	.	.
38594	++	.	.	.	.	.	.	.	.	.
38258	++	++	-	+	+	+	.	.	.	.
37596	++	++	.	.	.	.	.	.	.	.
37978	++	+	.	.	.	.	.	-	.	.
13884	++	.	.	.	.	.	.	.	.	.

38595 ++	++	-	-	-	-	-	-	-	-
13517 ++	++	-	-	-	-	-	-	-	-
38596 ++	+	--+	+++	+++	+++	-	-	-	-
38406 ++	++	--+	+++	+++	+++	-	-	-	-
38597 ++	-	-	-	-	-	-	-	-	-
38598 ++	++	-	-	-	+	-	-	-	-
17637 ++	+	-	+	-	-	-	-	-	-
37917 ++	++	-	+	-	-	-	-	-	-
38213 ++	++	-	-	-	-	-	-	-	-
38599 ++	-	-	-	-	-	-	-	-	-
18903 ++	+	-	-	-	-	+	-	-	-
12135 ++	+	--+	+++	+++	+++	-	-	-	-
38600 ++	-	--+	+++	+++	+++	++	-	-	-
38601 ++	-	--+	+++	+++	+++	-	-	-	-
38602 ++	++	-	-	-	-	-	-	-	-
38013 ++	++	-	-	-	-	-	-	-	-
38503 ++	-	-	-	-	-	-	-	-	-
38338 ++	++	-	-	-	-	-	-	-	-
38305 ++	+	-	-	-	-	-	-	-	-
37875 ++	-	-	-	-	-	-	-	-	-
38603 ++	-	-	-	-	-	-	-	-	-
37690 ++	++	-	-	-	-	-	-	-	-
37349 ++	+	-	-	-	-	-	-	-	-
14230 ++	++	-	-	-	-	-	-	-	-
17949 ++	+	-	-	-	-	-	-	-	-
12523 ++	-	-	-	-	-	-	-	-	-
11002 ++	-	-	-	-	-	-	-	-	-
37395 ++	-	-	-	-	-	-	-	-	-
38604 ++	++	-	-	-	-	-	-	-	-
14628 ++	++	-	-	-	-	-	-	-	-
38062 ++	-	-	-	-	-	-	-	-	-
11194 ++	+	-	-	-	-	-	-	-	-
13592 ++	++	-	-	-	-	-	-	-	-

14393 ++	++	-	-	-	-	-	-	-	-
38023 ++	++	-	-	-	-	-	-	-	-
17493 ++	-	--+	+	+++	-	-	-	-	-
38605 ++	+	-	-	-	-	+	--	-	-
38606 ++	++	-	-	-	-	-	-	-	-
38607 ++	++	-	-	-	-	-	-	-	-
18173 ++	-	--+	+	+++	-	-	-	-	-
38578 ++	-	-	-	-	-	-	-	-	-
12392 ++	-	-	-	-	-	-	-	-	-
13950 ++	++	-	-	-	-	-	-	-	-
37996 ++	++	-	-	-	-	-	-	-	-
38608 ++	++	--+	+	+	+	-	-	-	-
38609 ++	+	-	-	-	-	-	-	-	-
38293 ++	-	-	-	-	-	-	-	-	-
38610 ++	+	--+	++	+++	++	+++	---	+++	+++
18244 ++	++	-	-	-	-	-	-	-	-
14473 ++	++	-	-	-	-	-	-	-	-
38013 ++	++	-	-	-	-	-	-	-	-
38581 ++	+	--+	+++	+++	+++	+	-	-	-
36757 ++	+	-	-	-	-	-	-	-	-
38611 ++	++	-	-	-	-	-	-	-	-
12441 ++	-	-	-	-	-	-	-	-	-
38283 ++	++	-	-	-	-	-	-	-	-
38612 ++	++	-	-	-	-	-	-	-	-
38511 ++	++	-	-	-	-	-	-	-	-
17405 ++	++	-	-	-	-	-	-	-	-
37978 ++	-	-	-	-	+	+	-	-	-
14607 ++	++	-	-	-	-	-	-	-	-
38613 ++	++	--+	+++	+++	+++	+	-	-	-
38058 ++	-	-	-	-	-	-	-	-	-
37944 ++	-	-	-	-	-	-	-	-	-
38614 ++	++	-	-	-	-	-	-	-	-
11928 ++	++	-	-	-	-	-	-	-	-

38615 ++	+	-	-	-	-	-	-	-	-
37558 ++	++	–	+	-	-	-	-	-	-
38616 ++	-	–	-	-	-	-	-	-	-
16059 ++	-	-	-	-	-	-	-	-	-
38617 ++	-	–+	+++	+++	+++	-	-	-	-
37922 ++	++	-	-	-	-	-	-	-	-
38184 ++	++	-	-	-	-	-	-	-	-
12172 ++	++	-	-	-	-	-	-	-	-
38618 ++	++	-	-	-	-	-	-	-	-
38619 ++	++	–+	+++	+	+	+++	---	-	+++
14393 ++	++	-	-	-	-	-	-	-	-
14109 ++	++	-	-	-	-	-	-	-	-
16145 ++	++	-	-	-	-	-	-	-	-
38488 ++	++	-	-	-	-	-	-	-	-
38620 ++	++	-	-	-	-	-	-	-	-
36267 ++	++	-	-	-	+	-	-	-	-
17863 ++	+	-	-	+	-	-	-	-	-
11913 ++	-	-	-	-	-	-	-	-	-
38584 ++	+	-	-	-	-	-	-	-	-
11308 ++	+	-	-	-	-	-	-	-	-
38621 ++	++	-	-	-	-	-	-	-	-
37000 ++	-	-	+	-	-	+	–	-	-
38622 ++	+	–+	+++	+++	+++	+	-	-	-
12391 ++	-	-	-	-	-	-	-	-	-
38623 ++	++	-	-	-	-	-	-	-	-
17564 ++	-	-	-	-	-	-	-	-	-
37927 ++	-	-	-	-	-	-	-	-	-
38624 ++	++	–+	+++	+++	+++	-	-	-	-
38295 ++	-	–+	+	+++	+	-	-	-	-
14391 ++	++	-	-	-	-	-	-	-	-
38625 ++	++	–	+	+	+	++	--	-	-
38626 ++	-	-	+	+	+	-	-	-	-
37550 ++	+	–	+	+	+	+	–	-	-

17718 ++	-	-	-	-	-	-	-	-	-
38547 ++	++	-	-	-	-	-	-	-	-
38360 ++	++	-	-	-	-	-	-	-	-
38352 ++	+	-	-	-	-	-	-	-	-
38627 ++	++	-	-	-	-	-	-	-	-
38628 ++	++	--+	+++	+++	+++	-	-	-	-
38629 ++	++	-	-	-	-	-	-	-	-
37178 ++	-	--+	++	+++	+	-	-	-	-
37967 ++	-	–	+	-	-	+	–	-	-
38478 ++	+	-	-	-	-	-	-	-	-
38630 ++	++	-	-	-	-	-	-	-	-
38401 ++	++	-	-	-	-	-	-	-	-
38610 ++	+	--+	++	+++	++	+++	---	+++	++
14704 ++	++	-	-	-	-	-	-	-	-
16592 ++	+	–	+	+	-	-	–	-	-
38054 ++	++	-	-	-	-	-	-	-	-
38456 ++	++	-	-	-	-	-	-	-	-
38071 ++	-	-	-	-	-	-	-	-	-
14190 ++	++	-	-	-	-	-	–	-	-
38463 ++	++	-	-	-	-	-	-	-	-
38631 ++	++	-	-	-	-	-	-	-	-
38632 ++	+	–	++	++	++	+++	---	-	+++
38310 ++	-	-	-	-	-	-	-	-	-
38633 ++	++	-	-	-	-	-	-	-	-
37866 ++	++	–	+	++	+++	+	--	-	-
13947 ++	++	-	-	-	-	-	-	-	-
38634 ++	+	-	-	-	-	-	-	-	-
38571 ++	++	-	-	-	-	-	-	-	-
38299 ++	++	-	-	-	-	-	-	-	-
11592 ++	-	-	-	-	-	-	-	-	-
14030 ++	++	-	-	+	-	+	–	-	-
38635 ++	++	-	-	-	+	-	-	-	-
38636 ++	++	--+	+++	+++	+++	+	–	-	-

38637 ++	-	-	-	-	-	-	-	-	-
11867 ++	-	-	-	-	-	-	-	-	-
38638 ++	++	-	-	-	+	+	–	-	-
14003 ++	++	-	-	-	-	-	-	-	-
12667 ++	++	-	-	-	+	-	-	-	-
38639 ++	-	–+	+++	+++	+++	-	–	-	-
38640 ++	+	–	+	+	+	-	-	-	-
38452 ++	++	-	-	-	-	-	-	-	-
38641 ++	+	–+	+++	+++	+++	+	–	-	-
14024 ++	++	-	-	-	-	++	––	-	-
38642 ++	++	-	-	-	-	-	-	-	-
38612 ++	++	-	-	-	-	-	-	-	-
38643 ++	++	-	-	-	-	-	-	-	-
13843 ++	++	-	-	-	-	-	-	-	-
37138 ++	-	-	-	-	-	-	-	-	-
36641 ++	+	-	-	-	-	-	-	-	-
38555 ++	-	–	-	-	-	-	-	-	-
38393 ++	-	-	-	-	-	-	-	-	-
38159 ++	+	-	-	-	-	-	-	-	-
11588 ++	-	-	-	-	-	-	-	-	-
38305 ++	+	-	-	-	-	-	-	-	-
38499 ++	++	-	-	-	-	-	-	-	-
38367 ++	++	-	-	-	-	-	-	-	-
37793 ++	-	-	-	-	-	-	-	-	-
38552 ++	-	-	-	-	-	-	-	-	-
37778 ++	-	–+	+	++	-	-	-	-	-
38263 ++	++	-	-	-	-	-	-	-	-
38431 ++	++	-	-	-	-	+	-	-	-
16037 ++	++	-	-	-	+	-	–	-	-
38259 ++	++	-	-	-	-	-	-	-	-
37109 ++	+	–	-	-	-	+	-	-	-
38443 ++	+	-	-	-	-	-	-	-	-
18265 ++	+	-	-	-	-	-	-	-	-

38524 ++	++	-	-	-	-	-	-	-	-
38149 ++	++	-	-	-	-	-	-	-	-
38464 ++	++	-	-	-	-	-	-	-	-
11867 ++	-	-	-	-	-	-	-	-	-
38091 ++	-	-	-	-	-	-	-	-	-
37873 ++	++	-	-	-	-	-	-	-	-
13552 ++	++	-	+	+	+	+	–	-	-
17754 ++	-	–	+	+	-	-	-	-	-
11206 ++	++	-	-	-	-	-	-	-	-
38644 ++	+	–+	+++	+++	+++	+	–	-	-
38366 ++	++	-	-	-	-	-	-	-	-
38305 ++	+	-	-	-	-	-	-	-	-
37502 ++	-	-	-	-	-	-	-	-	-
12020 ++	-	-	-	-	-	-	-	-	-
38278 ++	-	–	-	-	-	-	-	-	-
37796 ++	+	–+	+++	+++	+++	+	-	-	-
38645 ++	-	-	-	-	-	-	-	-	-
38011 ++	+	-	-	-	-	-	-	-	-
36877 ++	+	–+	++	+++	++	+	-	+++	-
38646 ++	-	-	-	-	-	-	-	-	-
38408 ++	++	-	-	-	-	+	-	-	-
38647 ++	+	-	-	-	-	-	-	-	-
38648 ++	-	-	-	-	-	-	-	-	-
38379 ++	++	-	-	-	-	-	-	-	-
38209 ++	-	–+	+	+	-	-	-	+++	++
37978 ++	+	-	+	-	-	-	-	-	-
38649 ++	+	–+	+++	+++	+++	-	-	-	-
38650 ++	++	-	-	-	-	-	–	-	-
38651 ++	+	-	-	-	-	-	-	-	-
38652 ++	+	–	+	+	+	+	–	-	-
11164 ++	-	-	-	-	-	-	-	-	-
14607 ++	++	-	-	-	-	-	-	-	-
38653 ++	-	-	-	-	-	-	-	-	-

38654 ++	++	-	-	-	-	-	-	-	-
17690 ++	-	-	-	-	-	-	-	-	-
38655 ++	-	-	+	+	-	-	-	-	-
38381 ++	++	-	-	-	-	-	-	-	-
38656 ++	++	-	-	-	-	-	-	-	-
17529 ++	+	--+	+++	+++	+++	+	-	-	-
38657 ++	++	-	-	-	-	++	-	-	-
38514 ++	-	-	-	-	-	-	-	-	-
37845 ++	++	-	-	-	-	-	-	-	-
37810 ++	++	-	-	-	-	-	-	-	-
20379 ++	-	-	+	+	+	-	-	-	-
38658 ++	++	-	+	+	+	-	-	-	-
38551 ++	++	-	-	-	-	-	-	-	-
11741 ++	++	-	-	-	-	-	-	-	-
38659 ++	++	-	-	-	-	-	-	-	-
38278 ++	-	-	-	-	-	-	-	-	-
38541 ++	+	-	-	-	-	-	-	-	-
38605 ++	+	-	-	-	-	++	--	-	-
38660 ++	+	--	+	+	+	+++	---	-	-
13720 ++	++	-	-	-	-	+	-	-	-
37870 ++	-	-	-	-	-	-	-	-	-
11626 ++	-	-	-	-	-	-	-	-	-
17033 ++	++	-	-	-	-	-	-	-	-
14092 ++	++	-	-	-	-	-	-	-	-
14204 ++	++	-	-	-	-	-	-	-	-
12300 ++	++	-	-	-	-	-	-	-	-
38661 ++	+	--+	+++	+++	+++	+	-	-	-
17205 ++	+	--+	+++	+++	+++	+	-	-	-
38662 ++	++	-	-	-	-	-	-	-	-
38663 ++	+	--+	+++	+++	+++	-	-	-	-
38664 ++	++	-	-	-	-	-	-	-	-
13924 ++	++	-	-	-	-	-	-	-	-
38665 ++	-	-	+	+++	+	-	-	-	-

38435 ++	++	--+	++	-	-	-	-	-	-
38666 ++	-	--+	++	+++	++	+	–	-	-
16569 ++	++	–	+	++	++	-	-	-	-
37951 ++	-	-	-	-	-	-	-	-	-
11121 ++	++	-	-	-	-	-	-	-	-
13732 ++	++	-	-	-	-	-	-	-	-
38662 ++	++	-	-	-	-	-	-	-	-
38602 ++	++	-	-	-	-	-	-	-	-
37576 ++	++	-	-	-	-	-	-	-	-
38591 ++	+	–	+	+	+	+++	---	++	++
14016 ++	-	-	-	-	-	-	-	-	-
37338 ++	+	-	-	-	-	-	-	-	-
11157 ++	++	-	-	-	-	-	-	-	-
38667 ++	++	-	-	-	-	-	-	-	-
38668 ++	-	-	-	-	-	-	–	-	-
38669 ++	++	-	-	-	-	-	-	-	-
37850 ++	+	-	-	-	-	-	-	-	-
38658 ++	++	-	+	+	+	-	-	-	-
13731 ++	++	-	-	+	+	+	–	-	++
38670 ++	+	-	-	-	-	-	-	-	-
11490 ++	+	-	-	-	-	-	-	-	-
37950 ++	-	-	-	-	-	-	-	-	-
18713 ++	-	-	-	-	-	-	-	-	-
38231 ++	-	-	-	-	-	-	-	-	-
36607 ++	++	-	+	-	+	-	-	-	-
12458 ++	+	-	-	-	-	-	-	-	-
18198 ++	-	-	-	-	+	-	-	-	-
38671 ++	+	-	-	-	-	-	–	-	-
12027 ++	+	-	-	-	-	-	-	-	-
38618 ++	++	-	-	-	-	-	-	-	-
38672 ++	++	--+	+++	+++	+++	+	–	-	-
38673 ++	++	-	-	-	-	-	-	-	-
38438 ++	-	-	-	-	-	-	-	-	-

38674 ++	-	-	-	-	-	-	-	-	-
38675 ++	+	--+	+++	+++	+++	+	-	-	-
38271 ++	-	-	-	-	-	-	-	-	-
14218 ++	++	-	-	-	-	-	-	-	-
38676 ++	+	-	+	-	-	-	-	-	-
38185 ++	++	--+	+++	+++	+++	+	-	-	-
11776 ++	-	-	-	-	-	-	-	-	-
38195 ++	+	-	-	-	-	-	-	-	-
38167 ++	-	-	-	-	-	-	-	-	-
38615 ++	+	-	-	-	-	-	-	-	-
11841 ++	+	-	-	-	-	-	-	-	-
38677 ++	++	-	-	-	-	-	-	-	-
38678 ++	++	-	-	-	-	-	-	-	-
14264 ++	++	-	-	-	-	-	-	-	-
37752 ++	+	-	-	+	-	-	-	-	-
38250 ++	++	-	-	-	-	-	-	-	-
38387 ++	+	-	-	-	-	-	-	-	-
38679 ++	++	-	+	-	-	-	-	-	-
38251 ++	-	-	-	+	-	-	-	-	-
11560 ++	++	-	-	-	-	-	-	-	-
38680 ++	++	-	-	-	-	-	-	-	-
38681 ++	++	-	-	-	-	-	-	-	-
38682 ++	++	-	-	-	-	-	-	-	-
38683 ++	+	--+	+++	+++	+++	+	-	-	-
38684 ++	+	--+	+++	+++	+++	+	-	-	-
11479 ++	++	-	-	-	-	-	-	-	-
13869 ++	++	-	-	-	+	-	-	-	-
38316 ++	++	-	-	-	-	-	-	-	-
37953 ++	-	--+	-	-	-	-	-	-	-
38549 ++	-	-	-	-	-	-	-	-	-
38544 ++	+	-	+	+	+	+++	---	-	+++
38685 ++	-	--	-	++	-	-	-	-	-
13732 ++	++	-	-	-	-	-	-	-	-

37451 ++	++	-	-	-	-	-	-	-	-
38686 ++	+	--+	+++	+++	+++	+	-	-	-
38127 ++	++	-	-	-	+	-	-	-	-
38687 ++	++	-	-	-	-	-	-	-	-
38620 ++	++	-	-	-	-	-	-	-	-
37803 ++	++	-	-	-	-	-	-	-	-
11577 ++	++	-	+	-	+	-	-	-	-
38478 ++	+	-	-	-	-	-	-	-	-
38688 ++	+	--+	+++	+++	+++	-	-	-	-
37509 ++	++	-	-	-	-	-	-	-	-
15995 ++	++	-	-	-	-	-	-	-	-
14344 ++	++	-	-	-	-	-	-	-	-
38569 ++	++	-	-	-	-	-	-	-	-
38689 ++	-	--+	+	+++	-	-	-	+++	-
18102 ++	+	-	-	-	-	-	-	-	-
37859 ++	++	–	+	+	+	-	–	-	-
13673 ++	++	–	+	+	+	-	-	-	++
38317 ++	++	-	-	-	-	-	-	-	-
11512 ++	-	-	-	-	-	+	–	-	-
37847 ++	++	-	-	-	-	-	-	-	-
38021 ++	-	-	-	-	-	-	-	-	-
38690 ++	++	-	-	-	-	-	-	-	-
14190 ++	++	-	-	-	-	-	-	-	-
18354 ++	-	-	-	-	-	-	-	-	-
38449 ++	-	-	-	-	-	-	-	-	-
38691 ++	++	-	-	-	-	-	-	-	-
38692 ++	-	-	-	-	-	-	-	-	-
38291 ++	++	-	-	-	-	-	-	-	-
37970 ++	++	-	-	-	-	-	-	-	-
18395 ++	+	-	-	-	-	-	-	-	-
38445 ++	++	-	-	-	-	-	-	-	-
37455 ++	++	-	-	-	-	-	-	-	-
17563 ++	-	--+	+	+	-	-	-	-	-

38693 ++	-	-	+	-	-	-	-	-	-
17900 ++	-	-	-	-	-	-	-	-	-
38694 ++	++	-	-	-	+	-	-	-	-
16111 ++	++	–	+	+	+	-	-	-	++
37902 ++	+	-	-	-	-	-	-	-	-
38695 ++	++	-	-	-	-	-	-	-	-
37855 ++	++	-	-	-	-	-	-	-	-
13930 ++	++	-	-	-	-	-	-	-	-
14640 ++	++	-	+	+	+	-	-	-	-
11942 ++	-	-	-	-	-	-	–	-	-
18831 ++	-	-	-	-	-	-	-	-	-
38681 ++	++	-	-	-	-	-	-	-	-
38696 ++	++	-	-	-	-	-	-	-	-
38081 ++	-	––	-	-	-	-	-	++	-
38697 ++	+	-	-	-	-	-	-	-	-
38698 ++	++	-	-	-	-	-	–	-	-
18132 ++	+	-	-	-	-	-	-	-	-
38699 ++	++	-	-	-	-	-	-	-	-
38700 ++	++	-	-	-	-	-	-	-	-
38483 ++	++	-	-	-	-	-	-	-	-
38701 ++	+	-	-	-	-	-	-	-	-
13874 ++	++	-	-	-	-	-	-	-	-
38389 ++	-	––+	+	+	-	-	-	-	-
38702 ++	-	-	-	-	-	-	-	-	-
38703 ++	++	-	-	-	-	-	-	-	-
16605 ++	-	––+	+	+++	+	+	-	-	-
38301 ++	++	-	-	-	-	-	-	-	-
11583 ++	++	-	-	-	-	-	-	-	-
38704 ++	+	-	-	-	-	-	-	-	-
38705 ++	+	-	-	-	-	+	–	-	-
38369 ++	++	-	-	-	-	-	-	-	-
38706 ++	++	-	-	-	-	-	-	-	-
38707 ++	-	–	+	+	+	-	-	-	-

38708 ++	++	-	-	-	-	-	-	-	-
38709 ++	+	--+	+++	+++	+++	-	-	-	-
38710 ++	-	-	+	+	+	-	-	-	-
38711 ++	-	-	+	+++	+	-	-	-	-
13917 ++	++	-	-	-	-	-	-	-	-
14533 ++	++	-	-	-	-	+	-	-	-
37676 ++	+	-	+	-	-	-	-	-	-
37980 ++	++	-	-	-	-	-	-	-	-
16594 ++	+	-	-	-	-	-	-	-	-
14146 ++	++	-	-	-	-	+	-	-	-
37944 ++	-	-	-	-	-	-	-	-	-
11461 ++	-	-	-	-	-	-	-	-	-
17717 ++	-	-	-	-	-	-	-	-	-
11684 ++	-	-	-	-	-	-	-	-	-
17606 ++	++	-	-	-	-	-	-	-	-
38587 ++	++	-	-	-	-	+	-	-	-
38392 ++	++	-	-	-	-	-	-	-	-
14344 ++	++	-	-	-	-	-	-	-	-
38712 ++	++	-	-	-	-	-	-	-	-
38381 ++	++	-	-	-	-	-	-	-	-
38255 ++	++	-	-	-	-	-	-	-	-
38713 ++	++	-	-	-	-	+	-	-	-
38378 ++	++	-	-	-	-	-	-	-	-
38714 ++	++	-	-	-	-	-	-	-	-
17631 ++	+	-	-	-	-	-	-	-	-
38715 ++	++	-	+	-	-	-	-	-	-
38579 ++	-	-	-	-	-	-	-	-	-
20379 ++	-	-	+	-	+	-	-	-	-
15970 ++	++	-	-	-	-	+	-	-	-
38716 ++	+	--+	+++	+++	+++	-	-	-	-
38658 ++	++	-	+	+	+	-	-	-	-
38717 ++	++	-	-	-	-	-	-	-	-
38168 ++	++	-	-	-	-	-	-	-	-

37943 ++	++	-	-	-	-	-	-	-	-
14253 ++	++	–	+	+	+	+++	---	-	-
38718 ++	+	-	-	-	-	-	-	-	-
17636 ++	++	-	-	-	-	-	-	-	-
17949 ++	++	-	-	-	-	-	–	-	-
11563 ++	-	-	-	-	-	+	-	-	-
16127 ++	-	-	-	-	-	-	-	-	-
36317 ++	+	-	-	-	-	-	-	-	-
11279 ++	-	-	-	-	-	-	-	-	-
37979 ++	++	-	-	-	-	-	-	-	-
38562 ++	++	-	-	-	-	-	-	-	-
37830 ++	++	–	+	+	+	+	–	-	-
36631 ++	-	-	-	-	-	-	-	-	-
19603 ++	++	-	-	-	-	-	-	-	-
38438 ++	-	-	-	-	-	-	-	-	-
38321 ++	-	-	-	-	-	-	-	-	-
38297 ++	+	–	+	+	+	+++	---	-	+++
38719 ++	++	-	+	+	+	+	–	-	-
38720 ++	-	–	-	++	+	-	-	-	-
14576 ++	++	-	-	-	-	-	-	-	-
14045 ++	++	--+	+++	+++	+++	+	–	-	-
11699 ++	++	-	-	-	-	-	-	-	-
38498 ++	++	-	-	-	-	-	-	-	-
37991 ++	++	--+	+++	+++	+++	-	–	-	-
38721 ++	+	--+	+++	+++	+++	+	-	-	-
18354 ++	-	-	-	-	-	-	-	-	-
38218 ++	++	-	-	-	-	-	-	-	-
38361 ++	++	-	-	-	-	-	-	-	-
14145 ++	++	-	-	-	-	-	-	-	-
38037 ++	++	-	-	-	-	-	-	-	-
38722 ++	+	-	-	-	+	-	-	-	-
12179 ++	-	-	-	-	-	-	-	-	-
16589 ++	++	-	-	-	-	-	-	-	-

17300	++	++	--+	+++	+++	+++	-	-	-	-
38723	++	++	-	-	-	-	-	-	-	-
12361	++	-	-	-	-	-	-	-	-	-
38724	++	++	-	-	-	-	-	-	-	-
16624	++	-	-	-	-	-	+	-	-	-
17584	++	-	--+	-	-	-	-	-	-	-
12109	++	++	-	-	-	-	-	-	-	-
37935	++	++	-	-	-	-	-	-	-	-
13859	++	+	-	-	-	-	+	-	-	-
38172	++	+	-	-	-	-	-	-	-	-
11172	++	++	-	-	-	-	-	-	-	-
38725	++	+	-	-	-	-	-	-	-	-
38726	++	+	-	+	+	+	++	--	-	++
38727	++	+	-	-	-	-	-	-	-	-
37690	++	++	-	-	-	-	-	-	-	-
38728	++	+	--+	+++	+++	+++	-	-	-	-
38729	++	-	-	-	-	-	-	-	-	-
38730	++	++	-	-	-	-	-	-	-	-
18714	++	+	-	-	-	-	-	-	-	-
38731	++	++	-	-	-	-	-	-	-	-
37168	++	++	-	-	-	-	-	-	-	-
16563	++	++	-	-	-	-	-	-	-	-
38732	++	++	-	-	-	-	-	-	-	-
17171	++	+	--+	+++	+++	+++	+	-	-	-
13552	++	++	-	+	-	+	+	-	-	-
38457	++	+	-	-	-	-	-	-	-	-
37838	++	++	-	-	-	-	-	-	-	-
38286	++	-	-	-	-	-	-	-	-	-
11675	++	+	-	-	-	-	-	-	-	-
38733	++	+	--+	+++	+++	+++	-	-	-	-
38734	++	-	--+	+++	+++	+++	-	--	-	-
12020	++	-	-	-	-	-	-	-	-	-
38567	++	++	-	-	-	-	-	-	-	-

37885 ++	++	-	-	-	-	-	-	-	-
38735 ++	+	--+	+++	+++	+++	-	-	-	-
38736 ++	++	-	-	-	-	-	-	-	-
38340 ++	+	-	-	-	-	-	-	-	-
11476 ++	++	-	-	-	-	-	-	-	-
17197 ++	++	--+	+++	+++	+++	++	--	-	-
11668 ++	++	-	+	+	+	+	-	-	-
14344 ++	++	-	-	-	-	-	-	-	-
13995 ++	++	-	-	-	-	-	-	-	-
37604 ++	++	-	-	-	-	-	-	-	-
17730 ++	++	-	-	-	-	-	-	-	-
18558 ++	-	-	-	-	-	-	-	-	-
38737 ++	+	--+	+++	+++	+++	-	-	-	-
11464 ++	+	-	-	-	-	-	-	-	-
38738 ++	++	--+	+++	+++	+++	+	-	-	-
38739 ++	++	-	-	-	-	-	-	-	-
38740 ++	++	-	-	-	-	-	-	-	-
14013 ++	++	-	-	-	-	-	-	-	-
38741 ++	-	-	-	-	-	-	-	-	-
38742 ++	-	--+	+++	+++	+++	+	-	-	-
38626 ++	-	-	+	+	+	-	-	-	-
38743 ++	++	-	-	-	-	-	-	-	-
20368 ++	++	-	-	-	-	-	-	-	-
38182 ++	+	-	+	+	+	-	-	-	-
14225 ++	++	-	-	-	-	-	-	-	-
38744 ++	+	-	-	-	-	-	-	-	-
38677 ++	++	-	-	-	-	-	-	-	-
38745 ++	++	-	-	-	-	-	-	-	-
38746 ++	++	--+	+++	+++	+++	+	-	-	-
38533 ++	++	-	-	-	-	-	-	-	-
16005 ++	++	-	-	-	-	-	-	-	-
37111 ++	++	-	-	-	-	-	-	-	-
38747 ++	+	--	+++	+++	+++	+++	---	-	-

14030 ++	++	-	-	-	-	+	−	-	-
17038 ++	-	−−+	+	+++	-	-	-	+++	+
12458 ++	+	-	-	-	-	-	-	-	-
20368 ++	++	-	-	-	-	-	-	-	-
38748 ++	++	-	-	-	-	-	-	-	-
38749 ++	++	−−+	+++	+++	+++	+	-	-	-
38750 ++	-	-	-	-	-	-	-	-	-
17503 ++	-	-	-	-	-	-	-	-	-
13989 ++	++	-	-	-	-	-	-	-	-
38751 ++	+	−	+	+	+	-	−	-	-
38388 ++	++	-	-	-	-	-	-	-	-
38590 ++	+	-	-	-	-	-	-	-	-
38752 ++	+	−−+	++	+++	++	+	−	-	-
38433 ++	++	-	-	-	-	-	-	-	-
11560 ++	++	-	-	-	-	-	-	-	-
38478 ++	+	-	-	-	-	-	-	-	-
38272 ++	-	-	-	-	-	-	-	-	-
38280 ++	+	-	-	-	-	-	-	-	-
38753 ++	++	-	-	-	-	-	-	-	-
38754 ++	+	-	-	-	-	-	-	-	-
38325 ++	+	-	-	-	-	-	-	-	-
38670 ++	-	-	-	-	-	-	-	-	-
38755 ++	+	-	-	-	-	+	-	-	-
38756 ++	+	−−+	++	+++	++	+++	−−	-	-
11430 ++	++	-	-	-	+	-	-	-	-
38708 ++	++	-	-	-	-	-	-	-	-
14632 ++	++	-	-	-	-	-	-	-	-
19081 ++	++	-	-	-	-	-	-	-	-
38757 ++	++	-	-	-	-	-	-	-	-
38210 ++	++	-	-	-	-	-	-	-	-
38758 ++	++	−	+	+	+	-	-	-	-
38566 ++	+	-	-	-	-	-	-	-	-
37393 ++	-	-	-	-	-	-	-	-	-

38759 ++	++	-	-	-	-	-	-	-	-
38335 ++	++	-	-	-	-	-	-	-	-
38760 ++	-	-	-	-	-	-	-	-	-
17839 ++	+	-	-	-	-	-	-	-	-
38740 ++	++	-	-	-	-	-	-	-	-
38659 ++	++	-	-	-	-	-	-	-	-
38537 ++	++	-	-	-	-	-	-	-	-
38761 ++	++	-	-	-	-	-	-	-	-
38762 ++	++	-	-	-	-	+	–	-	-
38506 ++	-	-	-	-	-	-	-	-	-
38373 ++	++	-	-	-	-	-	-	-	-
38763 ++	++	-	+	-	-	+	–	-	-
38479 ++	++	-	-	-	-	-	-	-	-
38413 ++	+	–-+	++	+++	++	+++	––	-	-
38764 ++	++	-	-	-	-	-	-	-	-
38765 ++	+	-	-	-	-	+++	---	-	-
38757 ++	++	-	-	-	-	-	-	-	-
13947 ++	++	-	-	-	-	-	-	-	-
16071 ++	+	-	-	-	-	-	-	-	-
38766 ++	++	-	-	-	+	+	-	-	-
17646 ++	+	-	-	-	-	-	-	-	-
38713 ++	++	-	-	-	-	-	-	-	-
38767 ++	-	-	-	+	-	-	-	-	-
12596 ++	-	-	-	-	-	-	-	-	-
17800 ++	+	-	-	-	-	-	-	-	-
16092 ++	-	-	-	-	-	-	-	-	-
38744 ++	+	-	-	-	-	-	-	-	-
38768 ++	+	–-+	+++	+++	+++	+	-	-	-
37679 ++	-	–-+	+	+	-	-	-	-	-
17649 ++	-	-	-	-	-	-	–	-	-
38380 ++	++	-	-	-	-	-	-	-	-
38769 ++	++	–	+	+	+	++	––	-	-
38770 ++	++	-	-	-	-	-	-	-	-

38315	++	++	-	-	-	-	+	–	-	-
16603	++	++	-	-	+	+	+	–	-	-
38771	++	++	–+	+++	+++	+++	+	-	-	-
38772	++	+	-	-	-	-	-	-	-	-
38773	++	-	-	-	-	-	-	-	-	-
19261	++	-	-	-	-	-	-	-	-	-
38774	++	++	–+	+++	+++	+++	+	–	-	-
38775	++	-	–	+	+	-	-	-	-	-
11157	++	++	-	-	-	-	-	-	-	-
38776	++	+	–+	+++	+++	+++	+	–	-	-
37978	++	+	-	-	-	-	+	–	-	-
14003	++	++	-	-	-	-	-	-	-	-
38777	++	++	-	-	-	-	-	-	-	-
38008	++	-	-	-	-	-	-	-	-	-
38778	++	++	-	-	-	-	-	-	-	-
38779	++	+	–+	+++	+++	+++	-	–	-	-
38780	++	++	-	-	-	-	-	-	-	-
38130	++	-	-	-	+++	+	-	-	-	-
17645	++	-	-	-	-	-	-	-	-	-
37681	++	-	-	-	-	-	-	-	-	-
37813	++	-	-	-	-	-	-	-	-	-
38781	++	++	-	-	-	-	-	-	-	-
38782	++	++	-	-	-	-	-	-	-	-
16054	++	-	-	-	-	-	-	-	-	-
37932	++	+	-	-	-	-	-	-	-	-
18303	++	-	-	-	-	-	-	-	-	-
38753	++	++	-	-	-	-	-	-	-	-
38783	++	+	––	+	-	-	-	-	-	-
38784	++	++	-	-	-	-	-	-	-	-
38785	++	++	-	-	-	-	-	-	-	-
38648	++	-	-	-	-	-	-	-	-	-
38606	++	++	-	-	-	-	-	-	-	-
38786	++	+	-	-	-	-	+	–	-	-

37908 ++	++	-	-	-	-	-	-	-	-
38787 ++	+	-	-	-	-	-	-	-	-
38020 ++	++	-	-	-	-	-	-	-	-
38528 ++	-	–	-	+	-	+	-	-	-
38788 ++	++	-	-	-	-	-	-	-	-
11252 ++	++	-	-	-	-	-	-	-	-
38283 ++	++	-	-	-	-	-	-	-	-
38619 ++	++	–+	+++	+	+	+++	–	+++	+++
14607 ++	++	-	-	-	-	-	-	-	-
38789 ++	+	–+	+++	+++	+++	-	-	-	-
37394 ++	+	-	-	-	-	-	-	-	-
38790 ++	++	-	-	-	-	-	-	-	-
38791 ++	+	–+	+++	+++	+++	+	-	-	-
38792 ++	++	-	-	-	+	+	-	-	-
38793 ++	-	–	++	++	-	-	-	-	-
38423 ++	++	-	-	-	-	-	-	-	-
38794 ++	++	-	-	-	-	-	-	-	-
38781 ++	++	-	-	-	-	-	-	-	-
38795 ++	++	-	-	-	-	-	-	-	-
38740 ++	++	-	-	-	-	-	-	-	-
13989 ++	++	-	-	-	-	-	-	-	-
17931 ++	+	-	-	-	-	-	-	-	-
38796 ++	++	-	-	-	-	-	-	-	-
12361 ++	-	-	-	-	-	-	-	-	-
13999 ++	++	-	-	-	-	-	-	-	-
38797 ++	++	-	-	-	-	-	-	-	-
38798 ++	-	-	-	-	-	-	-	-	-
17221 ++	+	–+	+++	+++	+++	-	-	-	-
38275 ++	+	-	-	-	-	-	-	-	-
38015 ++	++	-	-	+	-	-	-	-	-
38799 ++	++	–+	+++	+++	+++	-	–	-	-
38399 ++	++	-	-	-	-	-	-	-	-
11704 ++	+	-	-	-	-	-	-	-	-

38800 ++	++	-	-	-	-	-	-	-	-
11721 ++	++	–	+	+	+	-	–	-	-
38801 ++	++	-	-	-	-	-	-	-	-
38802 ++	-	-	-	-	-	-	-	-	-
14343 ++	++	-	-	-	-	-	-	-	-
38712 ++	++	-	-	-	-	-	-	-	-
37065 ++	-	–	+	-	-	-	-	-	-
38665 ++	-	–	+	+++	+	-	–	-	-
14216 ++	++	-	-	-	-	-	-	-	-
11894 ++	+	-	+	-	-	-	-	-	-
38803 ++	++	-	+	-	+	+	–	-	-
19924 ++	-	-	+	-	-	-	-	-	-
36939 ++	++	-	-	-	-	-	-	-	-
14216 ++	++	-	-	-	-	-	-	-	-
11684 ++	-	-	-	-	-	-	-	-	-
38554 ++	-	––	+	-	-	-	–	-	-
38804 ++	++	–-+	+++	+++	+++	-	–	-	-
11173 ++	++	-	-	-	-	-	-	-	-
17035 ++	+	––	+++	++	++	-	-	-	-
38805 ++	+	–-+	+++	+++	+++	+	-	-	-
38806 ++	-	-	-	-	-	-	-	-	-
14273 ++	++	-	-	-	-	-	-	-	-
37210 ++	++	–	+	+	+	+++	---	-	-
38807 ++	++	-	-	-	-	-	-	-	-
38808 ++	++	-	-	-	-	-	-	-	-
38645 ++	-	-	-	-	-	-	-	-	-
38809 ++	++	-	-	-	-	-	-	-	-
12061 ++	+	-	-	-	-	-	-	-	-
38810 ++	++	-	-	-	-	-	-	-	-
38811 ++	+	–-+	+++	+++	+++	+	–	-	-
38812 ++	+	-	-	-	-	-	–	-	-
16585 ++	++	-	-	+	+	-	-	-	-
38495 ++	++	-	-	-	-	-	-	-	-

14179 ++	++	-	-	-	-	-	-	-	-
38155 ++	++	-	-	-	-	-	-	-	-
38373 ++	++	-	-	-	-	-	-	-	-
17663 ++	-	--	-	++	+	-	-	-	-
38792 ++	++	-	-	-	-	-	-	-	-
38813 ++	-	--+	+++	+++	+++	-	-	-	-
38355 ++	++	-	+	+	+	-	-	-	-
13824 ++	++	-	-	-	-	-	-	-	-
38029 ++	-	-	-	-	-	-	-	-	-
38611 ++	++	-	-	-	-	-	-	-	-
38814 ++	+	-	+	+	++	+++	---	-	-
38815 ++	+	--+	++	+++	++	+++	---	+++	+++
38782 ++	++	-	-	-	-	-	-	-	-
38215 ++	++	-	-	-	-	-	-	-	-
38745 ++	++	-	-	-	-	-	-	-	-
12489 ++	+	-	-	-	-	-	-	-	-
38816 ++	++	-	-	-	+	-	-	-	-
38608 ++	++	--+	+	-	-	-	-	-	-
38817 ++	-	-	-	-	+	+	-	-	-
38818 ++	-	-	-	-	-	-	-	-	-
38819 ++	++	-	-	-	-	-	-	-	-
17711 ++	-	--+	+	+++	-	-	-	-	-
38820 ++	++	-	-	-	-	-	-	-	-
38821 ++	+	-	+	+	+	+++	---	-	++
38687 ++	++	-	-	-	-	-	-	-	-
38512 ++	++	-	-	-	-	-	-	-	-
38586 ++	++	-	-	-	-	-	-	-	-
13551 ++	++	-	-	-	-	+	-	-	-
13948 ++	++	-	-	-	-	-	-	-	-
38822 ++	+	-	-	-	-	-	-	-	-
38821 ++	+	-	+	+	+	+++	---	+++	++
17817 ++	+	-	-	-	-	-	-	-	-
37356 ++	-	-	-	-	-	-	-	-	-

14443 ++	++	-	-	-	-	-	-	-	-
38823 ++	+	--+	+++	+++	+++	+	-	-	-
18345 ++	-	-	-	-	-	-	-	-	-
37404 ++	+	-	-	-	-	-	-	-	-
38001 ++	-	-	-	-	-	-	-	-	-
38798 ++	-	-	-	-	-	-	-	-	-
38824 ++	-	--+	+	++	-	-	-	-	-
38825 ++	-	-	-	-	-	-	-	-	-
38826 ++	-	-	-	-	-	-	-	-	-
38226 ++	++	-	-	-	-	-	-	-	-
38699 ++	++	-	-	-	-	-	-	-	-
38827 ++	++	-	-	-	-	+	-	-	-
13815 ++	++	-	+	+	+	++	--	-	-
38828 ++	+	-	-	-	-	-	-	-	-
38286 ++	-	-	-	-	-	-	-	-	-
38829 ++	++	-	-	-	-	-	-	-	-
37762 ++	++	--+	+++	+++	+++	-	-	-	-
37870 ++	-	-	-	-	-	-	-	-	-
38830 ++	+	--+	+++	+++	+++	++	-	-	-
17485 ++	-	-	-	-	-	-	-	-	-
17555 ++	++	-	-	-	-	-	-	-	-
38831 ++	+	--+	++	+++	++	+++	---	-	-
17781 ++	++	-	-	-	-	-	-	-	-
14704 ++	++	-	-	-	-	-	-	-	-
17520 ++	++	-	-	-	-	-	-	-	-
37616 ++	-	-	-	-	-	-	-	-	-
38832 ++	++	-	-	-	+	-	-	-	-
37951 ++	-	-	-	-	-	-	-	-	-
38833 ++	+	-	+	+	+	+	--	-	-
38834 ++	+	-	-	-	-	-	-	-	-
14858 ++	++	-	-	-	-	-	-	-	-
12172 ++	++	-	-	-	-	-	-	-	-
38228 ++	++	-	-	-	-	-	-	-	-

38305 ++	+	-	-	-	-	-	-	-	-
38435 ++	+	--+	++	-	-	-	-	-	-
38712 ++	++	-	-	-	-	-	-	-	-
38474 ++	++	-	-	-	-	-	-	-	-
38807 ++	++	-	-	-	-	-	-	-	-
38835 ++	-	-	-	-	-	-	-	-	-
38836 ++	+	--+	+++	+++	+++	+	–	-	-
36645 ++	+	–	-	-	-	-	-	-	-
13540 ++	++	-	-	-	-	-	-	-	-
16064 ++	++	-	-	-	-	-	-	-	-
11210 ++	++	-	-	-	-	-	-	-	-
38405 ++	-	-	-	-	-	-	-	-	-
14192 ++	++	-	-	-	-	-	-	-	-
38346 ++	++	-	-	-	-	-	-	-	-
38724 ++	++	-	-	-	-	-	-	-	-
38837 ++	-	-	-	+	-	+	–	-	-
38838 ++	++	-	-	-	-	-	-	-	-
38839 ++	+	-	-	-	-	-	-	-	-
38840 ++	-	–	-	+	-	-	-	-	-
38469 ++	++	-	-	-	-	-	-	-	-
38841 ++	+	--+	+++	+++	+++	+	-	-	-
38842 ++	+	--+	+++	+++	+++	+	-	-	-
37838 ++	+	-	-	-	-	-	-	-	-
14167 ++	++	-	-	-	-	-	-	-	-
13827 ++	+	-	-	-	-	-	-	-	-
38843 ++	++	-	-	-	+	+	–	-	-
38844 ++	+	--+	+++	+++	+++	+	–	-	+++
38305 ++	+	-	-	-	-	-	-	-	-
38845 ++	-	--+	-	-	-	-	-	-	-
14640 ++	++	-	+	+	+	-	-	-	-
38674 ++	-	-	-	-	-	-	-	-	-
36876 ++	-	--	+	+	-	-	–	-	-
13636 ++	++	-	-	-	-	-	-	-	-

16186 ++	-	-	-	-	-	-	-	-	-
37428 ++	-	-	-	+	-	-	-	-	-
38846 ++	+	-	-	-	-	-	-	-	-
38847 ++	++	-	-	-	-	-	–	-	-
38848 ++	+	–+	+++	+++	+++	-	-	-	-
38849 ++	++	-	-	-	-	-	-	-	-
37494 ++	-	–+	++	+++	+	+	–	-	-
38701 ++	+	-	-	-	-	-	-	-	-
19310 ++	++	-	-	-	-	-	-	-	-
38850 ++	-	–	+	+	+	++	––	-	-
38236 ++	+	–+	+++	+++	+++	+	–	-	-
38046 ++	++	-	+	+	+	+	–	-	-
16611 ++	++	-	-	-	-	-	-	-	-
17913 ++	+	-	-	-	-	-	-	-	-
13603 ++	++	-	-	-	-	-	-	-	-
11253 ++	+	-	-	-	-	-	-	-	-
38851 ++	+	–+	+++	+++	+++	-	-	-	-
38852 ++	+	–+	+++	+++	+++	-	-	-	-
38168 ++	++	-	-	-	-	-	-	-	-
38336 ++	++	-	-	-	-	-	-	-	-
38853 ++	+	–+	+	++	+	++	––	-	-
11197 ++	++	-	-	-	-	-	-	-	-
38854 ++	++	-	-	-	-	+	–	-	-
38855 ++	-	-	-	-	-	-	-	-	-
38856 ++	+	-	-	-	-	-	-	-	-
17589 ++	+	-	-	-	-	-	-	-	-
38857 ++	-	-	-	-	+	-	-	-	-
38508 ++	++	-	-	-	-	-	-	-	-
38858 ++	-	-	-	-	-	-	-	-	-
38859 ++	+	–+	+++	+++	+++	-	-	-	-
38808 ++	++	-	-	-	-	-	-	-	-
37874 ++	+	-	-	+	+	-	-	-	-
11812 ++	++	-	+	+	+	-	-	-	-

38810 ++	++	-	-	-	-	-	-	-	-
38084 ++	++	-	-	-	-	-	-	-	-
38193 ++	++	-	-	-	-	-	-	-	-
38086 ++	++	-	-	-	-	-	-	-	-
16054 ++	-	-	-	-	-	-	-	-	-
38860 ++	++	--+	+++	+++	+++	-	-	-	-
38847 ++	++	-	-	-	+	+	-	-	-
38861 ++	++	-	-	-	-	-	-	-	-
38512 ++	++	-	-	-	-	-	-	-	-
38862 ++	-	-	-	-	-	-	-	-	-
38740 ++	++	-	-	-	-	-	-	-	-
38582 ++	-	-	-	-	-	-	-	-	-
38125 ++	++	-	-	-	-	-	-	-	-
12015 ++	+	-	-	-	-	-	-	-	-
11253 ++	+	-	-	-	-	-	-	-	-
11684 ++	-	-	-	-	-	-	-	-	-
37693 ++	+	-	+	+	++	-	-	-	-
38863 ++	++	-	-	-	-	-	-	-	-
38199 ++	-	-	-	-	-	-	-	-	-
38864 ++	++	-	-	-	-	-	-	-	-
38438 ++	-	-	-	-	-	-	-	-	-
38865 ++	++	-	-	-	-	-	-	-	-
37662 ++	++	-	-	-	-	-	-	-	-
38727 ++	+	-	-	-	-	-	-	-	-
38866 ++	++	-	-	-	-	-	-	-	-
14010 ++	++	-	-	-	-	-	-	-	-
38867 ++	-	-	-	-	-	-	-	-	-
38868 ++	-	--+	+	+++	-	-	-	++	+
37845 ++	++	-	-	-	-	-	-	-	-
10964 ++	-	-	-	-	-	-	-	-	-
38869 ++	++	-	-	-	-	-	-	-	-
19011 ++	-	-	+	-	-	-	-	-	-
38561 ++	++	-	-	-	-	-	-	-	-

17834 ++	-	-	-	-	-	-	-	-	-
38870 ++	-	–	+	+	-	-	-	-	-
38371 ++	-	–+	+	-	-	-	-	-	-
14109 ++	++	-	-	-	-	-	-	-	-
38871 ++	++	-	-	-	-	-	-	-	-
38872 ++	++	-	-	-	-	-	-	-	-
38398 ++	++	-	-	-	-	-	-	-	-
11000 ++	++	-	-	-	-	-	-	-	-
38873 ++	-	–+	+	+++	+	-	-	-	-
38874 ++	++	-	-	-	-	-	-	-	-
17819 ++	+	-	-	-	-	-	-	-	-
38856 ++	+	-	-	-	-	-	-	-	-
17637 ++	+	–	+	-	+	-	-	-	-
38875 ++	++	-	-	-	-	-	-	-	-
11760 ++	++	-	-	-	-	-	-	-	-
38876 ++	-	-	-	-	-	-	-	-	-
38877 ++	-	–+	+	+	-	-	-	-	-
38424 ++	++	-	-	-	-	-	-	-	-
17675 ++	-	–+	+	+++	+++	+	–	-	-
17710 ++	-	-	-	-	-	-	–	-	-
38878 ++	+	–+	+++	+++	+++	+	–	-	-
38869 ++	++	-	-	-	-	-	-	-	-
13892 ++	++	-	-	-	-	-	-	-	-
38759 ++	++	-	-	-	-	-	-	-	-
38089 ++	-	-	-	-	-	-	-	-	-
11527 ++	-	-	-	-	-	-	-	-	-
37997 ++	++	-	-	-	-	-	-	-	-
38879 ++	++	-	-	-	-	-	-	-	-
38880 ++	-	–+	+	+	-	-	-	-	-
13961 ++	++	-	-	-	-	-	-	-	-
38881 ++	-	-	-	-	-	-	-	-	-
14126 ++	++	-	-	-	-	+	-	-	-
18070 ++	-	-	-	-	-	-	-	-	-

38882 ++	++	-	-	-	-	-	-	-	-
38690 ++	++	-	-	-	-	-	-	-	-
38883 ++	-	--+	+	+++	-	-	-	-	-
11799 ++	++	-	-	-	-	-	-	-	-
38436 ++	++	-	-	-	-	-	-	-	-
38640 ++	+	-	+	+	+	-	-	-	-
38884 ++	++	-	-	-	-	-	-	-	-
16647 ++	++	-	-	-	-	-	-	-	-
36702 ++	++	--+	+++	+++	+++	+	-	-	-
38669 ++	++	-	-	-	-	-	-	-	-
17657 ++	-	-	-	-	-	-	-	-	-
38885 ++	++	-	-	-	-	-	-	-	-
38886 ++	-	-	+	-	+	-	-	-	-
38121 ++	++	-	-	-	-	-	-	-	-
19627 ++	-	--	-	+	-	-	-	-	-
11721 ++	++	-	+	+	+	+	-	-	-
19355 ++	-	-	-	-	-	-	-	-	-
38887 ++	+	--+	+++	+++	+++	-	-	-	-
38888 ++	++	-	-	-	-	+	-	-	-
38604 ++	++	-	-	-	-	-	-	-	-
37829 ++	+	-	+	+	+	+	-	-	-
11033 ++	++	-	-	-	-	-	-	-	-
38256 ++	+	-	-	-	-	-	-	-	-
17444 ++	++	-	-	-	-	-	-	-	-
38704 ++	+	-	-	-	-	-	-	-	-
13818 ++	++	-	-	-	-	-	-	-	-
14576 ++	++	-	-	-	-	-	-	-	-
37999 ++	++	-	-	-	-	-	-	-	-
38889 ++	++	-	-	-	-	-	-	-	-
13949 ++	++	-	-	-	-	-	-	-	-
38890 ++	++	-	-	-	-	+	-	-	-
38517 ++	++	-	-	-	-	-	-	-	-
38102 ++	-	-	-	-	-	-	-	-	-

38891 ++	++	-	-	-	-	-	-	-	-
13841 ++	+	-	-	+	+	+	-	-	-
38577 ++	++	-	-	-	-	-	-	-	-
38892 ++	++	-	-	-	-	-	-	-	-
38752 ++	-	--+	+	+++	+	+	–	-	-
38867 ++	-	-	-	-	-	+	–	-	-
38893 ++	-	--+	+++	+++	+++	-	-	-	-
17938 ++	-	–	+	-	+	-	-	-	-
38894 ++	++	--+	+++	+++	+++	+	-	-	-
38895 ++	-	--+	+++	+++	+++	-	-	-	-
20376 ++	+	-	-	-	-	-	-	-	-
38896 ++	+	--+	+++	+++	+++	+	–	-	-
13960 ++	++	-	-	-	-	-	-	-	-
38897 ++	++	-	-	-	-	-	-	-	-
11206 ++	++	-	-	-	-	-	-	-	-
11508 ++	++	-	-	-	-	-	-	-	-
16629 ++	++	--+	+++	+++	+++	-	-	-	-
38898 ++	++	-	-	-	-	-	-	-	-
38180 ++	-	-	-	-	-	-	-	-	-
38899 ++	+	-	-	-	-	-	-	-	-
38900 ++	++	-	-	-	-	-	-	-	-
38901 ++	+	-	-	-	-	-	-	-	-
18270 ++	+	-	-	-	-	-	-	-	-
13858 ++	++	-	-	-	-	-	-	-	-
38902 ++	-	-	-	-	-	-	-	-	-
38903 ++	+	-	-	-	-	-	-	-	-
38806 ++	-	-	-	-	-	-	-	-	-
38904 ++	++	-	-	+	+	-	-	-	-
38346 ++	++	-	-	-	-	-	-	-	-
37616 ++	-	-	-	-	-	-	-	-	-
13950 ++	++	-	-	-	-	-	-	-	-
38905 ++	++	-	-	-	-	-	–	-	-
38906 ++	++	-	-	-	-	+	–	-	-

38907 ++	+	-	-	-	-	-	-	-	-
38908 ++	-	–	+	+	+	+	–	-	-
12294 ++	-	-	-	-	-	-	-	-	-
11204 ++	+	-	-	-	-	-	-	-	-
38691 ++	++	-	-	-	-	-	-	-	-
38909 ++	-	–-+	+++	+++	+++	+	–	-	-
11742 ++	++	-	+	+	+	+	-	-	-
38910 ++	++	-	-	-	-	+	-	-	-
38462 ++	++	-	-	-	-	-	-	-	-
38612 ++	++	-	-	-	-	-	-	-	-
38911 ++	++	-	-	-	-	-	-	-	-
17329 ++	-	–-+	+++	+++	++	-	-	-	-
38843 ++	++	-	-	+	+	+	–	+	-
38912 ++	-	–	-	+++	+	-	-	-	-
38913 ++	++	-	-	-	-	-	-	-	-
11788 ++	+	-	-	-	-	-	-	-	-
16635 ++	-	-	-	-	-	+	–	-	-
38607 ++	++	-	-	-	-	-	-	-	-
38832 ++	++	-	-	-	-	-	-	-	-
11741 ++	++	-	-	-	-	-	-	-	-
38837 ++	-	-	-	+	-	-	-	-	-
11052 ++	-	-	-	-	-	-	-	-	-
16615 ++	-	-	-	-	-	-	-	-	-
38682 ++	+	-	-	-	-	-	-	-	-
38914 ++	++	-	-	-	-	+	–	-	-
38915 ++	-	–	-	+	-	-	–	-	-
38916 ++	+	–-+	+++	+++	+++	+	–	-	+++
38917 ++	++	-	-	-	+	+	–	-	-
17405 ++	++	-	-	-	-	-	-	-	-
38467 ++	++	-	-	-	-	+	–	-	-
38918 ++	+	–-+	+++	+++	+++	+	-	-	-
38919 ++	+	–-+	+++	+++	+++	+	-	-	-
38920 ++	++	-	-	-	-	-	-	-	-

16064 ++	++	-	-	-	-	-	-	-	-
16034 ++	++	-	-	-	-	-	-	-	-
38921 ++	-	--+	+++	+++	+++	-	-	-	-
38922 ++	-	--+	+++	+++	+++	-	-	-	-
17300 ++	+	--+	+++	+++	+++	-	-	-	-
38923 ++	+	--+	+++	+++	+++	-	-	-	-
38924 ++	-	-	-	-	-	-	-	-	-
38198 ++	+	-	-	-	-	-	-	-	-
38925 ++	+	--+	+++	+++	+++	-	-	-	-
38843 ++	++	-	-	-	+	+	-	-	-
38926 ++	++	-	-	-	-	-	-	-	-
13778 ++	++	-	-	-	-	-	-	-	-
38073 ++	+	-	-	-	-	-	-	-	-
38785 ++	++	-	-	-	-	-	-	-	-
14058 ++	++	-	-	-	-	-	-	-	-
17719 ++	++	-	-	-	-	-	-	-	-
12176 ++	-	-	-	-	-	-	-	-	-
17967 ++	++	-	-	-	-	-	-	-	-
38685 ++	-	--	-	++	-	-	-	-	-
17838 ++	+	-	+	-	-	-	-	-	-
38927 ++	++	-	-	-	-	-	-	-	-
36905 ++	++	-	-	-	-	-	-	-	-
38928 ++	-	-	-	-	-	-	-	-	-
15098 ++	++	-	-	+	+	+++	---	-	-
11560 ++	++	-	-	-	-	-	-	-	-
38576 ++	-	-	-	-	-	-	-	-	-
37695 ++	++	-	-	-	-	-	-	-	-
17732 ++	++	-	-	-	-	-	-	-	-
38929 ++	++	--+	+++	+++	+++	-	-	-	-
38530 ++	+	-	-	-	-	-	-	-	-
38930 ++	+	--+	+++	+++	+++	+	-	-	-
38358 ++	++	-	-	-	-	-	-	-	-
38931 ++	+	--+	++	++	+	+++	---	-	-

38699 ++	++	-	-	-	-	-	-	-	-
11718 ++	-	-	-	-	-	-	-	-	-
38560 ++	-	-	-	-	-	-	-	-	-
14146 ++	++	-	-	-	+	+	--	-	-
38932 ++	-	--+	+++	+++	+++	-	-	-	-
17700 ++	++	-	-	-	-	-	-	-	-
38458 ++	++	-	-	-	-	-	-	-	-
38933 ++	-	-	-	-	-	-	-	-	-
38934 ++	-	--+	++	+++	+++	++	--	-	+++
38668 ++	-	-	-	-	-	-	-	-	-
37952 ++	++	-	-	-	-	-	-	-	-
38731 ++	++	-	-	-	-	-	-	-	-
38935 ++	-	-	+	+	+	-	-	-	-
17606 ++	++	-	-	-	-	-	-	-	-
14593 ++	++	-	-	-	-	-	-	-	-
38696 ++	++	-	-	-	-	-	-	-	-
37814 ++	++	-	+	+	+	+++	---	-	-
11763 ++	++	-	-	-	-	-	-	-	-
38902 ++	-	-	-	-	-	-	-	-	-
38936 ++	++	-	-	-	-	-	-	-	-
38905 ++	++	-	+	-	-	-	-	-	-
19350 ++	+	-	-	-	-	-	-	-	-
14344 ++	++	-	-	-	-	-	-	-	-
38303 ++	++	-	-	-	-	-	-	-	-
11252 ++	+	-	-	-	-	-	-	-	-
38937 ++	-	-	-	-	-	-	-	-	-
38938 ++	++	-	-	-	-	-	-	-	-
38939 ++	++	-	-	+	-	+	-	-	-
14305 ++	++	-	-	-	-	-	-	-	-
38115 ++	++	-	-	-	-	-	-	-	-
38329 ++	-	-	-	-	-	-	-	-	-
17814 ++	++	-	-	-	-	-	-	-	-
38780 ++	++	-	-	-	-	-	-	-	-

38764 ++	++	-	-	-	-	-	-	-	-
17079 ++	+	-	-	-	-	-	-	-	-
38940 ++	++	-	-	-	-	-	-	-	-
12255 ++	-	-	-	-	-	-	-	-	-
11894 ++	+	-	-	-	-	-	-	+	-
38941 ++	++	-	-	-	-	-	-	-	-
17572 ++	-	-	-	-	-	-	-	-	-
38934 ++	+	--+	++	+++	++	+++	--	+++	-
17780 ++	++	-	-	-	-	-	-	-	-
38714 ++	++	-	-	-	-	-	-	-	-
38942 ++	+	--+	+++	+++	+++	-	-	-	-
38943 ++	++	-	-	-	-	-	-	-	-
38719 ++	++	-	-	+	+	+	-	-	-
38761 ++	++	-	-	-	-	-	-	-	-
14048 ++	++	-	-	-	-	-	-	-	-
17066 ++	+	-	-	-	-	-	-	-	-
38030 ++	+	-	-	-	-	-	-	-	-
38944 ++	-	-	-	-	-	-	-	-	-
17691 ++	++	-	-	-	-	-	-	-	-
16624 ++	-	-	-	-	-	-	-	-	-
38945 ++	++	-	-	-	-	-	-	-	-
38220 ++	++	-	-	-	-	-	-	-	-
38946 ++	++	-	-	-	-	-	-	-	-
38589 ++	++	-	-	-	-	-	-	-	-
17653 ++	++	-	-	-	-	-	-	-	-
19355 ++	-	-	-	-	-	-	-	-	-
38947 ++	-	-	-	-	-	-	-	-	-
38743 ++	++	-	-	-	-	-	-	-	-
13914 ++	+	-	-	-	-	-	-	-	-
16032 ++	-	-	-	-	-	-	-	-	-
38063 ++	++	-	-	-	-	-	-	-	-
38642 ++	++	-	-	-	-	-	-	-	-
38871 ++	++	-	-	-	-	-	-	-	-

38536 ++	++	-	-	-	-	-	-	-	-
38537 ++	++	-	-	-	-	-	-	-	-
38948 ++	-	---+	+++	+++	+++	-	-	-	-
14016 ++	-	-	-	-	-	-	-	-	-
12327 ++	++	---+	+++	+++	+++	+	-	-	-
38949 ++	+	---+	+++	+++	+++	-	-	-	-
11214 ++	-	-	-	-	-	-	-	-	-
38950 ++	++	-	-	-	-	-	-	-	-
17591 ++	++	-	-	-	-	-	-	-	-
38327 ++	-	-	-	-	-	-	-	-	-
38951 ++	++	-	-	-	-	-	-	-	-
16186 ++	-	-	-	-	-	-	-	-	-
38252 ++	+	-	-	-	+	-	-	-	-
13863 ++	++	-	-	-	-	-	-	-	-
38248 ++	++	-	-	-	-	-	-	-	-
13834 ++	++	-	-	-	-	-	-	-	-
38952 ++	++	---+	+++	+++	+++	+	-	-	-
38505 ++	++	-	-	-	-	-	-	-	-
11684 ++	-	-	-	-	-	-	-	-	-
38953 ++	++	-	-	-	-	-	-	-	-
38237 ++	-	-	-	-	-	-	-	-	-
37251 ++	+	-	+	-	-	-	-	-	-
38172 ++	+	-	-	-	-	-	-	-	-
37856 ++	++	-	-	-	-	-	-	-	-
16088 ++	++	-	-	-	-	-	-	-	-
11812 ++	++	-	-	-	+	-	-	-	-
12501 ++	-	-	-	-	-	-	-	-	-
12796 ++	-	-	-	-	-	-	-	-	-
14445 ++	++	-	-	-	-	-	-	-	-
38530 ++	+	-	-	-	-	-	-	-	-
11476 ++	++	-	-	-	-	-	-	-	-
38772 ++	+	-	-	+	-	-	-	-	-
16615 ++	-	-	-	-	-	-	-	-	-

38954 ++	++	-	-	-	+	+	-	-	-
36516 ++	-	--+	+++	+++	+++	-	-	-	-
38244 ++	+	-	-	-	-	-	-	-	-
38955 ++	-	-	-	+	+	+	-	-	-
38956 ++	-	--	+	+	+	++	--	-	-
38957 ++	-	-	-	-	-	-	-	-	-
38958 ++	++	-	-	-	-	-	-	-	-
38753 ++	++	-	-	-	-	-	-	-	-
12518 ++	++	-	++	++	++	+++	-	-	-
38959 ++	-	--+	+++	+++	+++	-	-	-	-
17085 ++	+	--+	+++	+++	+++	+	-	-	-
13869 ++	++	-	-	-	+	-	-	-	-
18573 ++	++	-	-	-	-	-	-	-	-
38960 ++	+	-	-	-	-	-	-	-	-
38961 ++	+	-	-	-	-	-	-	-	-
38167 ++	-	-	-	-	-	-	-	-	-
38906 ++	++	-	-	-	-	+	-	-	-
38962 ++	++	-	-	-	-	-	-	-	-
38963 ++	-	-	-	-	-	-	-	-	-
38964 ++	-	-	-	-	-	-	-	-	-
14087 ++	++	-	-	-	-	-	-	-	-
15970 ++	++	-	-	-	-	-	-	-	-
38965 ++	-	-	-	-	-	-	-	-	-
38723 ++	++	-	-	-	-	-	-	-	-
37669 ++	+	-	-	-	-	-	-	-	-
38609 ++	+	-	-	-	-	-	-	-	-
38863 ++	++	-	-	-	-	-	-	-	-
14295 ++	++	-	-	-	-	-	-	-	-
18713 ++	-	-	-	-	-	-	-	-	-
38966 ++	-	-	-	-	-	-	-	-	-
38967 ++	+	-	-	-	-	++	--	-	-
11651 ++	++	-	-	-	-	-	-	-	-
38853 ++	+	--+	+	++	+	++	--	+++	-

36729 ++	+	–	+	+	+	+	–	.	.
38233 ++	++	.	.	.	.	.	.	.	.
38968 ++	.	––	.	.	.	.	.	.	.
37738 ++	.	.	+	++	.	.	.	.	.
38969 ++	.	–	++	.	++	+++	–––	.	.
38970 ++	.	––+	+++	+++	+++	.	–	.	.
11036 ++	++	.	.	.	.	.	.	.	.
17924 ++	++	.	.	.	.	.	.	.	.
38689 ++	.	––+	+	+++	.	.	.	++	.
38630 ++	++	.	.	.	.	.	.	.	.
38426 ++	++	.	.	.	.	.	.	.	.
38971 ++	++	––+	+++	+++	+++	.	.	.	.
37585 ++	.	.	.	.	.	.	.	.	.
38786 ++	+	.	.	.	.	+	–	.	.
38653 ++	.	.	.	.	.	.	.	.	.
11053 ++	++	––+	+++	+++	+++	.	–	.	.
38972 ++	.	––+	.	.	.	.	.	.	.
37988 ++	++	.	.	.	.	.	.	.	.
38973 ++	+	––+	+++	+++	+++	+	–	.	.
38328 ++	++	.	.	.	.	.	.	.	.
17189 ++	.	––+	+++	+++	+++	.	.	.	.
38974 ++	++	.	.	.	.	.	.	.	.
37850 ++	+	.	.	.	.	.	.	.	.
38975 ++	++	––+	+++	+++	+++	+	.	.	.
38976 ++	++	––+	+++	+++	+++	+	–	.	.
17786 ++	++	.	.	.	.	.	.	.	.
38977 ++	.	.	+	.	.	.	.	.	.
38978 ++	+	––+	+++	+++	+++	+	–	.	.
19761 ++	+	.	.	.	.	.	.	.	.
38456 ++	++	.	.	.	.	.	.	.	.
20373 ++	++	.	.	.	.	.	.	.	.
38979 ++	++	.	.	.	.	+	.	.	.
38980 ++	++	.	.	.	.	+	–	.	.

38981 ++	++	-	-	-	-	-	-	-	-
38982 ++	+	-	-	-	-	++	−−	-	-
38983 ++	+	-	-	-	-	-	-	-	-
38984 ++	-	−−+	+++	+++	+++	+	-	-	-
38714 ++	++	-	-	-	-	-	-	-	-
38985 ++	++	-	-	-	-	-	-	-	-
11503 ++	-	-	-	-	-	-	-	-	-
38381 ++	++	-	-	-	-	-	-	-	-
14053 ++	++	-	-	-	-	-	-	-	-
38986 ++	++	-	-	-	-	-	-	-	-
38987 ++	-	-	-	+	-	+	−	-	-
38353 ++	++	-	-	-	-	+	−	-	-
38988 ++	++	−−+	+++	+++	+++	+	-	-	-
16107 ++	+	-	-	-	-	-	-	-	-
38989 ++	+	−−+	+++	+++	+++	-	-	-	-
38990 ++	-	-	-	-	-	-	-	-	-
11615 ++	-	-	-	-	-	-	-	-	-
38991 ++	+	-	-	-	-	-	-	-	-
13776 ++	++	-	-	-	-	-	-	-	-
18710 ++	-	−	-	-	-	-	−	-	-
38748 ++	++	-	-	-	-	-	-	-	-
38144 ++	+	-	-	-	-	-	-	-	-
38390 ++	++	-	-	-	-	-	-	-	-
14321 ++	++	-	-	-	-	-	-	-	-
38957 ++	-	-	-	-	-	-	-	-	-
38992 ++	+	−−+	+++	+++	+++	+	−	-	-
38561 ++	++	-	-	-	-	-	-	-	-
38993 ++	-	-	-	-	-	-	-	-	-
14074 ++	++	-	-	-	-	-	-	-	-
17822 ++	++	-	-	-	-	-	-	-	-
38994 ++	++	-	-	-	-	-	-	-	-
38283 ++	++	-	-	-	-	-	-	-	-
17114 ++	++	-	-	-	-	-	-	-	-

38755 ++	+	-	-	-	+	-	-	-	-
38731 ++	++	-	-	-	-	-	-	-	-
38995 ++	+	--+	+++	+++	+++	-	-	-	-
38218 ++	++	-	-	-	-	-	-	-	-
12501 ++	-	-	-	-	-	-	-	-	-
17852 ++	++	-	-	-	-	-	-	-	-
14768 ++	++	-	-	-	-	-	-	-	-
38996 ++	+	--+	+++	+++	+++	+	-	-	-
38997 ++	-	--+	+++	+++	+++	+	-	-	-
38998 ++	++	-	-	-	+	-	-	-	-
38999 ++	++	-	-	-	-	-	-	-	-
38877 ++	-	--+	-	-	-	-	-	-	-
39000 ++	++	-	-	-	-	-	-	-	-
38218 ++	++	-	-	-	-	-	-	-	-
13738 ++	++	-	-	-	-	-	-	-	-
38727 ++	+	-	-	-	-	-	-	-	-
38148 ++	++	-	-	-	-	-	-	-	-
39001 ++	++	-	-	-	-	+	–	-	-
39002 ++	-	--+	+++	+++	+++	-	-	-	-
38300 ++	++	-	-	-	-	-	-	-	-
38241 ++	+	-	-	-	-	-	-	-	-
39003 ++	+	-	-	-	-	-	-	-	-
38319 ++	-	-	-	-	-	-	–	-	-
39004 ++	++	-	-	-	-	-	-	-	-
38706 ++	++	-	-	-	-	-	-	-	-
38629 ++	++	-	-	-	-	-	-	-	-
38872 ++	++	-	-	-	-	-	-	-	-
38794 ++	++	-	-	-	-	-	-	-	-
12120 ++	-	-	-	-	-	-	-	-	-
18831 ++	-	-	-	-	-	-	-	-	-
39005 ++	+	-	-	-	-	-	-	-	-
39006 ++	+	-	-	-	-	-	-	-	-
17941 ++	-	-	-	-	-	-	-	-	-

38677 ++	++	-	-	-	-	-	-	-	-
39007 ++	++	-	-	-	-	-	-	-	-
39008 ++	+	-	-	-	-	-	-	-	-
11361 ++	-	-	-	-	-	-	-	-	-
38473 ++	-	-	-	-	-	-	-	-	-
37264 ++	++	--+	+++	+++	+++	-	-	-	-
38744 ++	+	-	-	-	-	-	-	-	-
38880 ++	-	--+	+	+	-	-	-	+++	-
38810 ++	++	-	-	-	-	-	-	-	-
38296 ++	++	–	+	+	-	+++	---	-	-
17870 ++	++	-	-	-	-	-	-	-	-
38441 ++	-	-	-	-	-	-	-	-	-
39009 ++	+	-	-	-	-	-	-	-	-
11066 ++	+	-	-	-	-	-	-	-	-
11450 ++	-	-	-	-	-	-	-	-	-
17867 ++	+	-	-	-	-	-	-	-	-
39010 ++	++	-	-	-	-	-	-	-	-
13860 ++	++	-	-	-	-	-	-	-	-
39011 ++	++	-	-	-	-	-	-	-	-
18040 ++	-	-	-	-	-	-	-	-	-
39012 ++	+	–	+	+	+	++	--	-	-
39013 ++	++	-	-	-	-	-	-	-	-
38879 ++	++	-	-	-	-	-	-	-	-
17547 ++	-	-	-	-	-	-	–	-	-
38616 ++	-	-	-	-	-	-	-	-	-
11033 ++	++	-	-	-	-	-	-	-	-
16590 ++	+	-	-	-	-	-	-	-	-
38986 ++	++	-	-	-	-	-	-	-	-
18880 ++	+	-	-	-	-	-	-	-	-
38908 ++	-	–	+	+	+	+	-	-	-
39014 ++	+	-	-	-	-	-	-	-	-
39015 ++	-	--+	+++	+++	+++	+	-	-	-
36912 ++	-	-	-	+	-	-	-	-	-

39016 ++	+	--+	+	-	-	-	-	-	+
14776 ++	++	-	-	-	-	-	-	-	-
39017 ++	+	-	-	-	-	-	-	-	-
11745 ++	++	-	-	-	-	+	–	-	-
39018 ++	-	--+	+++	+++	+++	+	–	-	-
38513 ++	++	-	-	-	-	-	-	-	-
17040 ++	+	-	-	-	-	-	-	-	-
38347 ++	++	-	-	-	-	-	-	-	-
11279 ++	-	-	-	-	-	-	-	-	-
11467 ++	-	-	-	-	-	-	-	-	-
13799 ++	++	-	-	-	+	-	-	-	-
38911 ++	++	-	-	-	-	-	-	-	-
39019 ++	+	-	-	-	-	-	-	-	-
39020 ++	+	-	-	-	-	-	-	-	-
39021 ++	++	-	-	-	-	-	-	-	-
18032 ++	-	-	-	-	-	+	–	-	-
39022 ++	++	-	-	-	+	-	-	-	-
13930 ++	++	-	-	-	-	-	-	-	-
38183 ++	++	–	+	+	+	+	–	-	-
38565 ++	+	-	-	-	-	-	-	-	-
38770 ++	++	-	-	-	-	-	-	-	-
39023 ++	+	-	-	-	-	-	-	-	-
39024 ++	-	-	-	-	-	-	-	-	-
38131 ++	-	-	-	-	-	-	-	-	-
38553 ++	+	-	-	-	-	-	-	-	-
16009 ++	+	-	-	-	-	-	-	-	-
37724 ++	++	-	-	-	-	-	-	-	-
16009 ++	+	-	-	-	-	-	-	-	-
13521 ++	++	-	+	+	-	-	-	-	-
38654 ++	++	-	-	-	-	-	-	-	-
39025 ++	+	--+	+++	+++	+++	-	-	-	-
39026 ++	++	--+	+++	+++	+++	-	–	-	-
39027 ++	++	-	-	-	-	-	-	-	-

38556 ++	+	--+	+	+++	+	+++	---	+++	+++
39028 ++	-	-	-	-	-	-	-	-	-
39029 ++	++	-	-	-	-	-	-	-	-
14354 ++	++	-	+	+	+	-	-	-	-
13939 ++	++	-	-	-	-	-	-	-	-
11581 ++	++	-	-	-	-	-	-	-	-
17924 ++	++	-	-	-	-	-	-	-	-
39030 ++	-	-	-	-	-	-	-	-	-
11158 ++	+	-	-	-	-	-	-	-	-
38414 ++	+	-	+	-	+	+	-	-	-
39031 ++	+	--+	+++	+++	+++	-	-	-	-
14046 ++	++	-	-	-	-	-	-	-	-
38190 ++	-	-	-	-	-	-	-	-	-
39032 ++	+	--+	+++	+++	+++	+	-	-	-
39033 ++	++	-	-	-	-	-	-	-	-
39034 ++	+	--+	+++	+++	+++	-	-	-	-
13901 ++	++	-	-	-	-	-	-	-	-
38762 ++	++	-	-	-	-	+	-	-	-
39035 ++	++	-	-	-	-	-	-	-	-
38201 ++	-	-	-	-	-	-	-	-	-
38579 ++	-	-	-	-	-	-	-	-	-
16593 ++	+	--+	+	+++	++	++	-	-	-
12508 ++	++	--+	+++	+++	+++	-	-	-	-
39036 ++	-	-	-	-	-	-	-	-	-
39028 ++	-	-	-	-	-	-	-	-	-
37907 ++	-	-	-	-	-	-	-	-	-
39037 ++	++	-	-	-	-	-	-	-	-
39013 ++	++	-	-	-	-	-	-	-	-
11503 ++	-	-	-	-	-	-	-	-	-
11009 ++	-	-	-	-	-	-	-	-	-
38819 ++	++	-	-	-	-	-	-	-	-
38304 ++	-	--	+	-	-	+	-	-	-
38643 ++	+	-	-	-	-	-	-	-	-

38278 ++	-	–	-	-	-	-	-	-	-
38388 ++	++	-	-	-	-	-	-	-	-
16137 ++	++	-	-	-	-	-	-	-	-
38530 ++	+	-	-	-	-	-	-	-	-
16032 ++	-	-	-	-	-	-	-	-	-
18651 ++	++	–+	+++	+++	+++	-	–	-	-
14262 ++	++	-	-	-	-	-	-	-	-
38727 ++	+	-	-	-	-	-	-	-	-
39038 ++	++	-	-	-	-	-	-	-	-
39039 ++	++	-	-	-	-	-	-	-	-
38363 ++	-	-	-	-	-	-	-	-	-
39040 ++	+	-	-	-	-	-	-	-	-
18375 ++	++	-	-	-	-	-	-	-	-
39041 ++	++	-	-	-	-	-	-	-	-
39042 ++	+	–+	+++	+++	+++	-	-	-	-
39043 ++	+	-	-	-	-	-	-	-	-
39044 ++	++	-	-	-	-	-	-	-	-
14502 ++	+	-	-	-	-	-	-	-	-
17913 ++	+	-	-	-	-	-	-	-	-
39045 ++	+	-	-	-	-	-	-	-	-
14263 ++	++	-	-	-	-	-	-	-	-
14346 ++	++	-	-	-	-	-	-	-	-
39046 ++	++	-	-	-	-	-	-	-	-
39047 ++	++	-	-	-	-	-	-	-	-
38627 ++	++	-	-	-	-	-	-	-	-
39048 ++	+	–+	+++	+++	+++	-	-	-	-
39049 ++	-	-	-	-	-	-	-	-	-
14025 ++	++	-	-	-	-	-	-	-	-
38638 ++	++	-	-	-	+	+	–	-	-
39050 ++	++	-	-	-	-	-	-	-	-
39016 ++	+	–+	+	-	-	-	-	++	-
38421 ++	++	-	-	-	-	-	-	-	-
39051 ++	++	-	-	-	-	-	-	-	-

39052	++	++	--+	+++	+++	+++	-	-	-	-
39053	++	+	--+	+++	+++	+++	++	-	-	-
38892	++	++	-	-	-	-	-	-	-	-
16606	++	-	-	-	-	-	+	-	-	-
39054	++	-	-	-	-	-	-	-	-	-
11948	++	+	-	-	-	-	-	-	-	-
14138	++	+	-	-	-	-	-	-	-	-
19078	++	-	-	-	-	-	-	-	-	-
39055	++	++	-	-	-	-	-	-	-	-
38783	++	++	--	+	-	-	-	-	-	-
16605	++	-	--+	+	+++	+	+	-	-	-
38732	++	++	-	-	-	-	+	-	-	-
39056	++	+	-	-	-	-	-	-	-	-
13595	++	++	-	-	-	-	+	–	-	-
39057	++	+	--+	+++	+++	+++	+	–	-	-
14270	++	++	-	-	-	-	-	-	-	-
38849	++	++	-	-	-	-	-	-	-	-
11664	++	-	-	-	-	-	-	-	-	-
37568	++	++	-	-	-	-	-	-	-	-
39058	++	+	--+	+++	+++	+++	+	-	-	-
12289	++	-	-	-	-	-	-	-	-	-
38650	++	++	-	-	-	-	-	-	-	-
38161	++	++	-	+	-	-	+	-	-	-
39059	++	++	-	-	-	-	-	-	-	-
14084	++	+	-	-	-	-	-	-	-	-
17910	++	-	--	+	++	-	-	-	-	-
18124	++	++	-	-	-	-	-	-	-	-
11346	++	++	-	-	-	-	-	-	-	-
16610	++	++	-	-	-	-	-	-	-	-
38033	++	++	-	-	-	-	-	-	-	-
38862	++	-	-	-	-	-	-	-	-	-
39060	++	-	-	-	+	-	-	-	-	-
39061	++	+	-	-	-	-	-	-	-	-

39062 ++	+	--+	+++	+++	+++	+	-	-	-
38137 ++	++	-	-	-	-	-	-	-	-
38110 ++	+	-	-	-	-	-	-	-	-
39063 ++	+	-	+	-	-	-	-	-	-
11426 ++	++	-	-	-	-	-	-	-	-
39064 ++	++	-	-	-	-	-	-	-	-
38884 ++	++	-	-	-	-	-	-	-	-
11478 ++	++	-	-	-	-	-	-	-	-
39065 ++	+	--+	+++	+++	+++	-	-	-	+
16627 ++	++	-	-	-	-	+	-	-	-
39066 ++	++	-	-	-	-	-	-	-	-
39067 ++	++	-	-	-	-	-	-	-	-
38574 ++	++	-	-	-	-	-	-	-	-
17060 ++	-	--+	+	++	-	-	-	+++	+
13738 ++	++	-	-	-	-	-	-	-	-
39068 ++	++	--+	+++	+++	+++	-	-	-	-
38928 ++	-	-	-	-	-	-	-	-	-
14674 ++	++	-	-	-	-	-	-	-	-
39069 ++	++	-	-	-	-	-	-	-	-
38637 ++	-	-	-	-	-	-	-	-	-
14325 ++	++	-	-	-	-	-	-	-	-
11224 ++	-	-	-	-	-	+	-	-	-
11308 ++	+	-	-	-	-	-	-	-	-
11867 ++	-	-	-	-	-	-	-	-	-
38677 ++	++	-	-	-	-	-	-	-	-
11964 ++	-	-	-	-	-	-	-	-	-
17437 ++	++	-	-	-	-	-	-	-	-
38700 ++	++	-	-	-	-	-	-	-	-
13851 ++	++	-	-	-	-	-	-	-	-
14532 ++	++	-	-	-	-	-	-	-	-
38897 ++	++	-	-	-	-	-	-	-	-
39035 ++	++	-	-	-	-	-	-	-	-
39070 ++	++	-	-	-	-	+	-	-	-

14267 ++	++	-	-	-	-	-	-	-	-
38631 ++	++	-	-	-	-	-	-	-	-
38864 ++	++	-	-	-	-	-	-	-	-
14399 ++	++	-	-	-	-	-	-	-	-
38574 ++	++	-	-	-	-	-	-	-	-
37824 ++	++	-	-	-	-	-	-	-	-
10963 ++	++	-	-	-	-	-	-	-	-
38891 ++	++	-	-	-	-	-	-	-	-
39071 ++	+	--+	+++	+++	+++	+	-	-	-
39072 ++	-	--	+	-	-	-	-	-	-
38865 ++	++	-	-	-	-	-	-	-	-
39073 ++	-	-	-	-	-	-	-	-	-
38712 ++	++	-	-	-	-	-	-	-	-
39074 ++	-	--+	-	+++	+	-	-	-	-
39075 ++	++	-	-	-	-	-	-	-	-
14292 ++	++	-	+	+	+	+++	---	-	-
17844 ++	++	-	-	-	-	-	-	-	-
11658 ++	++	-	-	-	-	-	-	-	-
39076 ++	+	-	+	-	-	++	---	-	-
39077 ++	-	--+	-	-	-	-	-	-	-
38245 ++	+	-	-	-	-	-	-	-	-
39078 ++	++	-	+	+	+	-	-	-	-
38192 ++	++	--+	+++	+++	+++	+	--	-	-
39079 ++	+	--+	+++	+++	+++	+	-	-	-
39080 ++	-	-	-	-	-	-	-	-	-
11988 +	++	-	-	-	-	-	-	-	-
38130 +	-	-	-	+++	+	-	-	-	-
13773 +	++	-	-	-	-	-	-	-	-
38277 +	++	-	-	-	-	-	-	-	-
17211 +	++	--+	+++	+++	+++	+	-	-	-
14140 +	++	-	-	-	-	-	-	-	-
39081 +	-	-	-	-	-	-	-	-	-
14527 +	++	-	-	-	-	-	-	-	-

38321 +	-	-	-	-	-	-	-	-	-
39082 +	++	-	-	-	-	-	-	-	-
38796 +	++	-	-	-	-	-	-	-	-
37750 +	+++	--+	+++	+++	+++	+	-	-	-
14405 +	++	-	-	-	-	-	-	-	-
39083 +	-	-	-	-	-	-	-	-	-
39084 +	+	-	-	-	-	-	-	-	-
12489 +	+	-	-	-	-	-	-	-	-
38585 +	++	-	-	-	-	-	-	-	-
12160 +	-	-	-	-	-	-	-	-	-
17838 +	++	-	-	-	-	-	-	-	-
39085 +	++	-	-	-	-	-	-	-	-
38281 +	+	-	-	-	-	-	-	-	-
11898 +	-	-	-	-	-	-	-	-	-
18102 +	+	-	-	-	-	-	-	-	-
38717 +	++	-	-	-	-	-	-	-	-
38758 +	++	-	+	+	+	-	-	-	-
39000 +	++	-	-	-	+	-	-	-	-
37760 +	++	-	-	-	-	-	-	-	-
16637 +	+	-	-	-	-	-	-	-	-
39086 +	+	-	-	-	-	-	-	-	-
39087 +	++	-	-	-	-	-	-	-	-
12269 +	-	-	-	-	-	-	-	-	-
39088 +	-	-	-	+	+	-	-	-	-
39089 +	++	-	-	-	-	+	-	-	-
37823 +	-	--+	+	+++	-	-	-	-	-
14447 +	++	-	-	-	-	-	-	-	-
39090 +	+	--+	+++	+++	+++	-	-	-	-
39091 +	+	--+	+++	+++	+++	+	-	-	-
38700 +	++	-	-	-	-	-	-	-	-
38572 +	++	-	-	-	-	-	-	-	-
13782 +	++	-	-	-	-	-	-	-	-
17591 +	++	-	-	-	-	-	-	-	-

17570 +	+	-	-	-	-	-	-	-	-
14073 +	+	-	-	-	-	-	-	-	-
39092 +	-	–	+	-	+	-	-	-	-
38540 +	-	–	-	-	-	-	-	-	-
14607 +	++	-	-	-	-	-	-	-	-
39093 +	++	-	-	-	-	-	-	-	-
13688 +	++	-	-	-	-	-	-	-	-
39094 +	-	-	-	-	-	-	-	-	-
38246 +	++	-	-	-	-	-	-	-	-
17967 +	++	-	-	-	-	-	-	-	-
38881 +	-	-	-	-	-	-	-	-	-
39095 +	+	–+	+++	+++	+++	+	–	-	-
39096 +	+	-	-	-	-	-	-	-	-
20423 +	-	–+	-	-	-	-	-	-	-
38535 +	+	-	-	-	-	-	-	-	-
38731 +	++	-	-	-	-	-	-	-	-
15958 +	++	-	-	-	-	+	–	-	-
39083 +	-	-	-	-	-	-	-	-	-
11940 +	-	-	-	-	-	-	-	-	-
11512 +	+	-	-	-	-	+	–	-	-
13982 +	++	-	-	-	-	-	-	-	-
39097 +	++	–+	+++	+++	+++	+	-	-	-
39098 +	++	-	-	-	-	-	-	-	-
38396 +	-	-	-	-	-	-	-	-	-
38474 +	++	-	-	-	-	-	-	-	-
39099 +	-	–+	+++	+++	+++	+	-	-	-
39100 +	-	–+	+++	+++	+++	-	-	-	-
13919 +	+	-	-	-	-	-	-	-	-
39101 +	-	–+	+++	+++	+++	-	-	-	-
39102 +	++	-	-	-	-	-	–	-	-
38442 +	-	–+	-	-	-	-	-	-	-
17901 +	++	-	-	-	-	-	-	-	-
13763 +	++	-	-	-	-	-	-	-	-

39103 +	+	–	+	+	++	-	-	-	-
37786 +	++	–+	+++	+++	+++	++	-	-	-
18395 +	+	-	-	-	-	-	-	-	-
38138 +	++	-	-	-	-	-	-	-	-
13894 +	++	-	-	-	-	+	–	-	-
38843 +	++	-	-	-	+	+	–	-	-
16577 +	++	-	-	-	-	-	-	-	-
39104 +	+	–+	+++	+++	+++	-	-	-	-
38029 +	-	-	-	-	-	-	-	-	-
38910 +	+	-	-	-	-	-	-	-	-
36962 +	+++	–	+	-	-	+	-	-	-
14301 +	++	-	-	-	-	-	-	-	-
16002 +	++	-	-	-	-	-	-	-	-
39105 +	+	-	-	-	-	-	-	-	-
17563 +	-	–+	+	+	-	-	-	-	-
12553 +	++	-	+	-	+	+	-	-	-
38422 +	-	–	+	-	-	-	-	-	-
11002 +	-	-	-	-	-	-	-	-	-
38751 +	-	–	+	+	+	+	–	-	-
38658 +	++	–	+	+	+	-	-	-	-
13688 +	++	-	-	-	-	-	-	-	-
38588 +	++	-	-	-	-	-	-	-	-
38937 +	-	-	-	-	-	-	-	-	-
39106 +	+	–+	+++	+++	+++	-	-	-	-
39107 +	+	–+	+++	-	-	-	-	+++	-
39108 +	++	-	-	-	-	-	-	-	-
39109 +	++	-	-	-	-	-	-	-	-
38815 +	-	–+	++	+++	++	+++	---	+++	+++
39110 +	+	–+	+++	+++	+++	-	–	-	-
39111 +	++	-	-	-	-	-	-	-	-
39112 +	++	-	-	-	-	-	-	-	-
14344 +	++	-	-	-	-	-	-	-	-
17660 +	++	-	-	-	-	-	-	-	-

38966 +	-	-	-	-	-	-	-	-	-
11161 +	-	-	-	-	-	-	-	-	-
38537 +	++	-	-	-	-	-	-	-	-
38698 +	++	-	-	-	-	-	–	-	-
16016 +	++	-	-	-	-	-	-	-	-
38507 +	-	-	-	-	-	-	-	-	-
39113 +	+	–+	+++	+++	+++	+	–	-	-
11496 +	++	-	-	-	-	-	-	-	-
18417 +	++	-	-	-	-	-	-	-	-
39114 +	++	-	-	-	-	-	-	-	-
13798 +	++	-	-	-	-	-	-	-	-
13894 +	++	-	-	-	-	+	–	-	-
39115 +	-	-	-	-	-	-	-	-	-
38561 +	++	-	-	-	-	-	-	-	-
38894 +	+	–+	+++	+++	+++	+	-	-	-
18714 +	+	-	-	-	-	-	-	-	-
17405 +	++	-	-	-	-	-	-	-	-
39116 +	-	-	-	-	-	-	-	-	-
39117 +	+	–+	+++	+++	+++	+	-	-	-
17186 +	++	–+	+++	+++	+++	+	-	-	-
14628 +	++	-	-	-	-	-	-	-	-
38559 +	+	-	+	-	-	-	-	-	-
17411 +	++	-	-	+	-	-	-	-	-
39118 +	++	–+	+++	+++	+++	+	–	-	-
17062 +	-	–+	+	+++	-	-	-	-	-
38545 +	++	-	-	-	-	-	-	-	-
39073 +	-	-	-	-	-	-	-	-	-
38773 +	-	-	-	-	-	-	-	-	-
39119 +	+	–+	+++	+++	+++	-	–	-	-
17519 +	++	-	-	-	-	-	-	-	-
39120 +	++	–+	+++	+++	+++	+	-	-	-
11351 +	++	-	-	-	-	-	-	-	-
12032 +	-	-	-	-	-	-	-	-	-

39121 +	-	-	-	-	-	-	-	-	-
39122 +	+	--+	+++	+++	+++	+++	---	-	-
39123 +	-	-	-	++	+++	-	-	-	-
13764 +	++	-	-	-	-	-	-	-	-
38667 +	++	-	-	-	-	-	-	-	-
38960 +	+	-	-	-	-	-	-	-	-
39124 +	-	-	-	-	-	+	–	-	-
38308 +	+	-	-	-	-	-	-	-	-
39125 +	++	-	-	-	-	-	-	-	-
14704 +	++	-	-	-	-	-	-	-	-
39126 +	++	-	-	-	-	-	-	-	-
39127 +	+	–	+	+	+	++	---	-	+++
18014 +	++	-	-	-	-	-	-	-	-
11742 +	++	-	+	-	-	+	-	-	-
39128 +	+	--+	+++	+++	+++	-	-	-	-
39129 +	++	-	+	-	-	+	–	-	-
39130 +	+	--+	+++	+++	+++	-	–	-	-
13578 +	++	-	-	-	+	+	–	-	-
38623 +	++	-	-	-	-	-	-	-	-
13580 +	++	-	-	-	-	-	-	-	-
38946 +	++	-	-	-	-	-	-	-	-
39131 +	+	--+	+++	+++	+++	+	–	-	-
14133 +	++	-	-	-	-	-	-	-	-
38491 +	+	-	-	-	-	-	-	-	-
39132 +	+	-	-	-	-	-	-	-	-
14025 +	++	-	-	-	-	-	-	-	-
17496 +	-	-	-	-	-	-	-	-	-
39046 +	++	-	-	-	-	-	-	-	-
38886 +	+	–	+	-	-	-	-	-	-
11658 +	++	-	-	-	-	-	-	-	-
39133 +	-	--	+	+	+	-	-	-	-
37777 +	-	-	-	-	-	-	-	-	-
11171 +	++	-	-	-	-	-	-	-	-

14607 +	++	-	-	-	-	-	-	-	-
39134 +	-	–	+	+	+	+	–	++	-
13578 +	++	-	-	-	+	+	–	-	-
16106 +	+	-	+	+	+	+++	---	-	-
38982 +	++	-	-	+	+	++	––	-	-
38797 +	++	-	-	-	-	-	-	-	-
38818 +	-	-	-	-	-	-	-	-	-
39135 +	++	–-+	+++	+++	+++	-	-	-	-
39136 +	++	-	-	+	+	++	––	-	+
39044 +	++	-	-	-	-	-	-	-	-
17792 +	-	-	-	-	-	-	-	-	-
14074 +	++	-	-	-	+	-	-	-	-
38289 +	++	-	-	-	-	-	-	-	-
39137 +	-	–-+	+	++	-	-	-	-	-
14338 +	++	-	-	-	-	-	-	-	-
38368 +	++	-	-	-	-	-	-	-	-
39138 +	++	–-+	++	+++	+++	+++	–	-	-
39139 +	-	-	-	-	-	-	-	-	-
39140 +	++	-	-	-	-	-	-	-	-
18913 +	-	–-+	+++	+++	+++	-	-	-	-
39141 +	++	-	-	-	-	-	-	-	-
38676 +	+	–	-	-	-	-	-	-	-
38376 +	++	-	-	-	-	-	-	-	-
38961 +	+	-	-	-	-	-	-	-	-
39142 +	++	-	-	-	-	-	-	-	-
13960 +	++	-	-	-	-	-	-	-	-
39143 +	++	-	-	-	-	-	-	-	-
11470 +	+	-	-	-	-	-	-	-	-
14003 +	+	-	-	-	-	-	-	-	-
39144 +	+	–	+	-	-	++	––	-	-
39145 +	-	-	-	-	-	-	-	-	-
39146 +	++	-	-	-	-	-	-	-	-
39147 +	+	-	-	-	-	-	-	-	-

39148 +	-	--+	+++	+++	+++	++	-	-	-
39149 +	-	--+	+++	+++	+++	-	-	-	-
39150 +	-	-	-	-	-	-	-	-	-
39089 +	++	-	-	-	-	+	–	-	-
20373 +	++	-	-	-	-	-	-	-	-
39151 +	+	-	-	-	-	-	-	-	-
38490 +	++	-	-	-	-	+	-	-	-
38714 +	++	-	-	-	-	-	-	-	-
14350 +	++	-	-	-	-	-	-	-	-
38838 +	+	-	-	-	+	-	-	-	-
14042 +	++	-	-	-	-	-	-	-	-
39152 +	++	-	-	-	-	-	-	-	-
11911 +	++	-	-	-	-	-	-	-	-
13999 +	++	-	-	-	-	-	-	-	-
39153 +	+	-	-	-	-	+	-	-	-
11718 +	-	-	-	-	-	-	-	-	-
14010 +	++	-	-	-	-	-	-	-	-
39154 +	+	--+	+++	+++	+++	+	–	-	-
38678 +	+	-	-	-	-	-	-	-	-
37942 +	-	-	-	-	-	-	-	-	-
39155 +	++	-	-	-	-	-	-	-	-
38718 +	+	-	-	-	-	-	-	-	-
39156 +	++	-	-	-	-	-	-	-	-
14330 +	+	-	-	-	-	-	-	-	-
39140 +	++	-	-	-	-	-	-	-	-
39157 +	++	-	-	-	-	-	-	-	-
39158 +	-	-	-	-	-	-	-	-	-
39159 +	++	-	-	-	-	-	-	-	-
39160 +	++	-	-	-	-	-	-	-	-
13943 +	++	-	-	-	-	-	-	-	-
39161 +	+	--+	+++	+++	+++	+	–	-	-
17155 +	++	-	-	-	-	-	-	-	-
39162 +	++	-	-	-	-	-	-	-	-

14376 +	+	-	-	-	-	-	-	-	-
38900 +	++	-	-	-	-	-	-	-	-
39163 +	-	-	-	-	-	-	-	-	-
39112 +	++	-	-	-	-	-	-	-	-
39164 +	++	--+	+++	+++	+++	-	-	-	-
13961 +	++	-	-	-	-	-	-	-	-
39165 +	-	--+	+++	+++	+++	-	-	-	-
38730 +	++	-	-	-	-	-	-	-	-
39166 +	++	-	-	-	-	-	-	-	-
38760 +	-	-	-	-	-	-	-	-	-
39167 +	-	-	-	-	-	-	-	-	-
39168 +	-	–	+	-	-	+	–	-	-
39169 +	+	--+	+++	+++	+++	+	-	-	-
38656 +	++	-	-	-	-	-	-	-	-
38530 +	+	-	-	-	-	-	-	-	-
39098 +	++	-	-	+	+	-	-	-	-
38711 +	-	–	-	++	-	-	-	-	-
11699 +	++	-	-	-	+	-	-	-	-
38133 +	-	-	-	+	+	+	–	-	-
39170 +	-	-	-	-	-	-	-	-	-
39171 +	++	-	-	-	-	-	-	-	-
38926 +	++	-	-	-	-	-	-	-	-
38946 +	++	-	-	-	-	-	-	-	-
18198 +	-	-	-	-	-	+	-	-	-
39172 +	+	-	-	-	-	-	-	-	-
38690 +	++	-	-	-	-	-	-	-	-
38355 +	++	-	-	-	-	-	-	-	-
38392 +	++	-	-	-	-	-	-	-	-
39173 +	-	--+	+	+++	+	-	-	-	-
38580 +	+	-	-	-	-	-	-	-	-
39174 +	-	-	-	-	-	-	-	-	-
17444 +	++	-	+	-	-	-	-	-	-
38910 +	++	-	-	-	-	-	-	-	-

38474 +	++	-	-	-	-	-	-	-	-
38950 +	++	-	-	-	-	-	-	-	-
38694 +	++	-	-	-	-	-	-	-	-
13517 +	++	-	-	-	-	-	-	-	-
39175 +	-	-	-	-	-	-	-	-	-
37537 +	+	-	-	-	-	-	-	-	-
14074 +	++	-	-	-	+	-	-	-	-
39176 +	++	-	-	-	-	-	-	-	-
11563 +	-	-	-	-	-	-	-	-	-
16037 +	++	-	-	-	-	-	-	-	-
19565 +	+	--+	+++	+++	+++	-	-	-	-
37453 +	-	--+	+	+	-	-	-	-	-
39177 +	++	-	-	-	-	-	-	-	-
39003 +	++	-	-	-	-	-	-	-	-
39178 +	++	-	-	-	-	-	-	-	-
39179 +	-	-	-	-	-	-	-	-	-
18240 +	-	-	-	-	-	-	-	-	-
39180 +	++	-	-	-	-	-	-	-	-
39181 +	-	-	-	-	-	-	-	-	-
13531 +	+	-	-	-	-	-	-	-	-
39182 +	++	-	-	-	-	-	-	-	-
39183 +	+	-	+	-	-	-	-	-	-
13604 +	++	-	-	-	-	-	-	-	-
39184 +	++	-	-	-	-	-	-	-	-
17691 +	++	-	-	-	-	-	-	-	-
39185 +	+	-	-	-	-	-	-	-	-
15995 +	++	-	-	-	-	-	-	-	-
39158 +	-	-	-	-	-	-	-	-	-
38664 +	++	-	-	-	-	-	-	-	-
39186 +	+	-	-	-	-	-	-	-	-
38915 +	-	–	-	+	-	-	-	-	-
39187 +	+	--+	+++	+++	+++	+	–	-	-
39188 +	+	-	-	-	-	-	-	-	-

19998 +	-	-	-	-	-	-	-	-	-
39189 +	++	–	+	+	+	-	-	-	-
13525 +	++	-	-	-	-	+	–	-	-
38690 +	++	-	-	-	-	-	-	-	-
14295 +	++	-	-	-	-	+	-	-	-
39190 +	++	-	-	-	-	+	-	-	-
39061 +	-	-	-	-	-	-	-	-	-
39191 +	+	-	-	-	-	+	––	-	-
18693 +	+	-	-	-	-	-	-	-	-
39192 +	+	-	-	-	-	-	-	-	-
14303 +	++	-	-	-	-	-	-	-	-
16594 +	-	-	-	-	-	-	-	-	-
14376 +	+	-	-	-	-	-	-	-	-
39193 +	-	-	-	-	-	-	-	-	-
39194 +	++	-	-	-	-	-	-	-	-
38700 +	++	-	-	-	-	-	-	-	-
39195 +	-	–+	+	++	-	-	-	-	-
13604 +	++	-	-	-	-	-	-	-	-
39196 +	+	–+	+++	+++	+++	-	-	-	-
39197 +	-	-	-	-	-	-	-	-	-
39198 +	+	-	-	-	-	-	–	-	-
39199 +	+	-	+	-	-	-	-	-	-
39200 +	+	–+	+++	+++	+++	-	–	-	-
39201 +	-	–	+	++	+	+	–	-	-
39202 +	+	–+	+++	+++	+++	+	–	-	-
14262 +	++	-	-	-	-	-	-	-	-
11377 +	++	-	-	-	-	-	-	-	-
18670 +	+	–+	+++	+++	+++	+	-	-	-
17114 +	++	-	-	-	-	-	-	-	-
38432 +	++	-	-	-	-	-	-	-	-
11415 +	-	-	-	-	-	-	-	-	-
10966 +	++	–+	+++	+++	+++	+	-	-	-
38745 +	++	-	-	-	-	-	-	-	-

38574 +	++	-	-	-	-	-	-	-	-
39203 +	-	-	-	-	-	-	-	-	-
17919 +	-	-	-	-	-	-	-	-	-
14074 +	++	-	-	-	-	-	–	-	-
13551 +	++	-	-	-	+	-	-	-	-
11462 +	-	-	-	-	-	-	-	-	-
39204 +	-	–	+	+	+	+	–	-	-
39056 +	+	-	-	-	-	-	-	-	-
39205 +	++	-	-	-	-	-	-	-	-
11452 +	-	-	-	-	-	-	-	-	-
38188 +	-	-	-	-	-	-	-	-	-
39206 +	++	–+	+++	+++	+++	-	-	-	-
38434 +	++	-	-	-	+	+	-	-	-
38817 +	-	-	-	-	-	+	–	-	-
13583 +	++	-	-	-	-	-	-	-	-
39085 +	++	-	-	-	-	-	-	-	-
39207 +	+	-	-	-	-	-	-	-	-
39208 +	++	-	-	-	-	-	-	-	-
39209 +	+	-	-	-	-	-	-	-	-
39068 +	+	–+	+++	+++	+++	-	-	-	-
38936 +	++	-	-	-	-	-	-	-	-
17684 +	+	-	-	-	-	-	-	-	-
39210 +	-	-	-	-	-	-	-	-	-
39115 +	-	-	-	-	-	-	-	-	-
39195 +	-	–+	-	++	-	-	-	-	-
38453 +	-	-	-	-	-	-	-	-	-
39211 +	-	-	-	-	-	-	-	-	-
39212 +	++	-	-	-	-	-	-	-	-
37469 +	++	-	-	-	-	-	-	-	-
39174 +	-	-	-	-	-	-	-	-	-
37095 +	++	–	+	+	-	-	-	-	-
38979 +	++	-	-	-	-	-	-	-	-
39213 +	+	–+	+++	+++	+++	-	-	-	-

38485 +	++	-	-	-	-	-	-	-	-
39102 +	++	-	-	-	-	+	–	-	-
17405 +	++	-	-	-	-	-	-	-	-
11855 +	-	-	-	-	-	-	-	-	-
11192 +	++	-	+	+	+	+	-	-	-
10968 +	++	-	-	-	-	-	-	-	-
38810 +	++	-	-	-	-	-	-	-	-
38621 +	++	-	-	-	-	-	-	-	-
38592 +	++	-	-	-	-	-	-	-	-
16145 +	++	-	-	-	-	-	-	-	-
17818 +	-	–	-	-	-	-	-	-	-
13737 +	++	-	-	-	-	-	-	-	-
39111 +	++	-	-	-	-	-	-	-	-
38715 +	++	-	-	-	-	-	-	-	-
38088 +	++	–	+	+++	+++	+++	---	-	-
10990 +	++	-	-	-	-	-	-	-	-
39214 +	+	--+	+++	+++	+++	+	-	-	-
38247 +	++	-	-	-	-	-	-	-	-
11464 +	+	-	-	-	-	-	-	-	-
18314 +	+	–	-	-	-	+	-	-	-
13540 +	++	-	-	-	-	-	-	-	-
13862 +	++	-	-	-	-	-	-	-	-
39215 +	+	--+	+++	+++	+++	+	-	-	-
39216 +	++	-	-	-	-	-	-	-	-
14087 +	++	-	-	-	-	-	-	-	-
38943 +	++	-	-	-	-	-	-	-	-
38700 +	++	-	-	-	-	-	-	-	-
14169 +	+	-	-	-	-	-	-	-	-
39217 +	+	--+	+++	+++	+++	+	-	-	-
38980 +	++	-	-	-	-	+	–	-	-
19998 +	-	-	-	-	-	-	-	-	-
39218 +	++	-	-	-	-	-	-	-	-
39219 +	++	--+	+++	+++	+++	-	-	+	-

39220 +	+	-	-	-	-	+	-	-	-
17854 +	-	-	-	-	-	-	-	-	-
39221 +	++	-	-	-	-	-	-	-	-
14529 +	++	-	-	-	-	-	-	-	-
17519 +	++	-	-	-	-	-	-	-	-
13664 +	++	-	-	-	-	-	-	-	-
19005 +	-	-	-	-	-	-	-	-	-
39222 +	+	-	-	-	-	-	-	-	-
39223 +	-	–	+	+	+	+++	---	-	+++
39224 +	+	--+	+++	+++	+++	+	–	-	+++
38903 +	+	-	-	-	-	-	-	-	-
13520 +	++	-	-	-	-	+	–	-	-
39225 +	+	–	++	+	++	-	-	-	-
39226 +	++	-	-	-	-	-	-	-	-
38580 +	+	-	-	-	-	-	-	-	-
38153 +	-	--+	+++	+++	+++	-	-	-	-
39173 +	-	--+	+	+++	+	-	-	+++	-
18835 +	-	–	+	+++	+	+	-	-	-
14495 +	++	-	-	-	-	-	-	-	-
39227 +	++	--+	+++	+++	+++	+	-	-	-
10960 +	+	-	-	-	-	-	-	-	-
14704 +	++	-	-	-	-	-	-	-	-
38409 +	++	--+	+++	+++	+++	-	-	-	-
11048 +	+	-	-	-	-	-	-	-	-
39228 +	+	--+	+++	+++	+++	+	–	-	-
39229 +	-	--+	-	+	-	-	-	-	-
11893 +	++	-	-	-	-	-	-	-	-
39230 +	++	-	-	-	-	-	-	-	-
37293 +	++	-	-	-	-	-	-	-	-
38795 +	++	-	-	-	-	-	-	-	-
38866 +	++	-	-	-	-	-	–	-	-
39231 +	+	--+	+++	+++	+++	+	-	-	-
39232 +	++	-	-	-	-	-	-	-	-

39233 +	-	-	-	-	-	-	-	-	-
39234 +	+	--+	+++	+++	+++	+	-	-	-
14093 +	+	-	-	-	-	-	-	-	-
38920 +	++	-	-	-	-	-	-	-	-
16638 +	+	-	-	-	-	-	-	-	-
37851 +	++	-	+	-	+	-	-	-	-
13850 +	++	-	-	-	-	-	-	-	-
39235 +	++	-	-	-	-	-	-	-	-
37979 +	++	-	-	-	-	-	-	-	-
38824 +	-	--+	+	++	-	-	-	-	-
38907 +	++	-	-	-	-	-	-	-	-
39236 +	+	--+	+++	+++	+++	-	-	-	-
39237 +	++	-	-	-	-	-	-	-	-
39238 +	-	--+	+++	+++	+++	-	-	-	-
19561 +	-	-	-	-	-	-	-	-	-
14620 +	++	-	-	-	-	-	-	-	-
36871 +	++	--+	+++	+++	+++	+	-	-	-
38874 +	++	-	-	-	-	-	-	-	-
11680 +	-	-	-	-	-	-	-	-	-
39239 +	+	-	-	-	-	-	-	-	-
39240 +	++	-	-	-	-	-	-	-	-
38433 +	++	-	-	-	-	-	-	-	-
12128 +	-	-	-	-	-	-	-	-	-
38739 +	++	-	-	-	-	-	-	-	-
13595 +	++	-	+	+	+	+	-	-	-
39241 +	+	--+	+++	+++	+++	+	-	-	-
38958 +	++	-	-	-	-	-	-	-	-
39029 +	++	-	-	-	-	-	-	-	-
37568 +	++	-	-	-	-	-	-	-	-
37756 +	-	-	-	-	-	-	-	-	-
39242 +	+	-	-	-	-	-	-	-	-
11983 +	-	-	-	-	-	-	-	-	-
11956 +	-	-	-	-	-	-	-	-	-

16136 +	+	-	-	-	-	-	-	-	-
17719 +	++	-	-	-	-	-	-	-	-
39243 +	++	-	-	-	-	-	-	-	-
39244 +	++	--+	+++	+++	+++	+++	---	-	-
13990 +	++	-	-	-	-	-	-	-	-
39245 +	+	--+	+++	+++	+++	+	-	-	-
38399 +	++	-	-	-	-	-	-	-	-
12015 +	+	-	-	-	+	-	-	-	-
39246 +	++	--+	+++	+++	+++	+	–	-	-
39125 +	++	-	-	-	-	-	-	-	-
39247 +	+	--+	+++	+++	+++	+	–	-	-
11624 +	+	-	+	-	+	-	-	-	-
18078 +	-	-	-	-	-	-	-	-	-
39248 +	++	-	-	-	-	-	-	-	-
14136 +	++	-	-	-	-	-	-	-	-
18493 +	-	-	-	-	-	-	-	-	-
16002 +	++	-	-	-	-	-	-	-	-
38446 +	-	--+	+	+++	+	-	-	-	-
39010 +	++	-	-	-	-	-	-	-	-
39249 +	++	-	-	-	-	+	-	-	-
39250 +	+	-	-	-	-	-	-	-	-
37856 +	++	-	-	-	-	-	-	-	-
38098 +	++	--+	+++	+++	+++	+	–	-	-
39116 +	-	-	-	-	-	-	-	-	-
38472 +	-	-	-	-	-	-	-	-	-
39251 +	-	-	-	+	-	-	-	-	-
14301 +	++	-	-	-	-	-	-	-	-
12513 +	-	-	-	-	-	-	-	-	-
39252 +	++	-	-	-	-	-	-	-	-
38898 +	++	-	-	-	-	-	-	-	-
13897 +	++	-	-	-	-	-	-	-	-
39253 +	++	--+	+++	+++	+++	+	–	-	-
14137 +	++	-	-	-	-	-	-	-	-

38381 +	++	-	-	-	-	-	-	-	-
39033 +	++	-	-	-	-	-	-	-	-
38425 +	++	-	-	-	-	-	-	-	-
38777 +	++	-	-	-	-	+	-	-	-
39254 +	-	–	-	-	-	-	--	-	-
39255 +	++	-	-	-	-	-	-	-	-
38153 +	+	--+	+++	+++	+++	+	-	-	-
39256 +	+	--+	+++	+++	+++	-	--	-	-
39257 +	+	-	-	-	-	-	-	-	-
39258 +	+	--+	+++	+++	+++	-	-	-	-
39259 +	-	--+	-	+	-	-	-	-	-
11152 +	++	-	-	-	+	-	-	-	-
11976 +	-	-	-	-	-	-	-	-	-
18417 +	++	-	-	-	-	-	-	-	-
12160 +	-	-	-	-	-	-	-	-	-
14047 +	+	-	-	-	-	-	-	-	-
13617 +	++	-	-	-	-	-	-	-	-
19136 +	-	–	-	-	-	-	-	-	-
37536 +	+	-	-	-	-	-	-	-	-
14391 +	++	-	-	-	-	-	-	-	-
38548 +	++	-	-	-	-	+	–	-	-
39260 +	++	-	-	-	-	-	-	-	-
38539 +	++	-	-	-	-	-	-	-	-
14293 +	++	-	-	-	-	-	-	-	-
11934 +	++	-	-	-	-	-	-	-	-
39261 +	+	-	-	-	-	-	-	-	-
14057 +	+	–	+	+	+	-	-	-	-
14080 +	+	-	+	+	+	++	--	-	-
39262 +	-	-	-	-	-	-	-	-	-
39263 +	++	-	-	-	-	-	-	-	-
38492 +	-	-	-	-	-	-	-	-	-
38276 +	++	-	-	+	+	+	–	-	-
39264 +	++	-	-	-	-	-	-	-	-

39265 +	++	-	-	-	-	-	-	-	-
14010 +	++	-	-	-	-	-	-	-	-
11447 +	-	-	-	-	-	-	-	-	-
11628 +	-	-	-	-	-	-	-	-	-
38953 +	++	-	-	-	-	-	-	-	-
39266 +	-	-	-	-	-	-	-	-	-
39267 +	+	-	-	-	-	-	-	-	-
11143 +	-	-	-	-	-	-	-	-	-
39268 +	++	-	-	-	-	-	-	-	-
39119 +	++	--+	+++	+++	+++	-	-	-	-
39269 +	++	--+	+++	+++	+++	+	-	-	-
39270 +	-	-	+	-	+	-	-	-	-
39271 +	++	-	-	-	-	-	-	-	-
38800 +	++	-	-	-	-	-	-	-	-
14588 +	+	-	-	-	-	-	-	-	-
39272 +	-	-	-	+	-	-	-	-	-
38411 +	-	-	-	-	-	-	-	-	-
39054 +	-	-	-	-	-	-	-	-	-
39273 +	++	-	-	-	+	-	-	-	-
12027 +	-	-	-	-	-	-	-	-	-
39274 +	++	-	-	-	-	-	-	-	-
38972 +	-	--+	-	-	-	-	-	-	-
39275 +	++	-	+	+	+	+	-	-	-
18066 +	-	-	-	-	-	-	-	-	-
39276 +	+	-	-	-	-	-	-	-	-
38287 +	++	-	-	-	-	-	-	-	-
39277 +	++	--+	+++	+++	+++	-	-	-	-
16016 +	++	-	-	-	-	-	-	-	-
14344 +	++	-	-	-	-	-	-	-	-
38974 +	++	-	-	-	-	-	-	-	-
39278 +	++	-	-	-	-	-	-	-	-
39064 +	++	-	-	-	-	-	-	-	-
13826 +	+	-	-	-	-	-	-	-	-

19945 +	-	--+	+	+	-	-	-	-	-
18688 +	-	-	-	-	-	+	-	-	-
39279 +	+	--+	+++	+++	+++	+	–	-	-
39280 +	+	-	-	-	-	+	-	-	-
13612 +	++	–	+	+	+	+++	---	++	-
20367 +	-	-	-	-	-	-	-	-	-
38586 +	++	-	-	-	-	-	-	-	-
14083 +	++	-	-	-	-	-	-	-	-
17545 +	-	-	-	-	-	-	-	-	-
11097 +	++	-	-	-	-	+	-	-	-
39281 +	+	--+	+++	+++	+++	-	-	-	-
38299 +	++	-	-	-	-	-	-	-	-
11117 +	+	-	-	-	-	-	-	-	-
14264 +	++	-	-	-	-	-	-	-	-
39208 +	++	-	-	-	-	-	-	-	-
38873 +	-	--+	+	+++	+	-	-	-	-
39089 +	++	-	+	+	+	+	-	-	-
14445 +	++	-	-	-	-	-	-	-	-
39282 +	++	-	-	-	-	-	-	-	-
36298 +	++	--+	+++	+++	+++	-	-	-	-
13834 +	++	-	-	-	-	-	-	-	-
39283 +	++	-	-	-	-	-	-	-	-
13948 +	++	-	-	-	-	-	-	-	-
11771 +	-	-	-	-	-	-	-	-	-
39284 +	++	--+	+++	+++	+++	-	-	-	-
39285 +	+	-	-	-	+	-	-	-	-
11206 +	+	-	-	-	-	-	-	-	-
39286 +	-	-	-	-	-	-	-	-	-
38586 +	++	-	-	-	-	-	-	-	-
17070 +	+	-	-	-	-	-	-	-	-
39266 +	-	-	-	-	-	-	-	-	-
39287 +	+	--+	+++	+++	+++	-	-	-	-
39288 +	-	-	-	-	-	-	-	-	-

39289 +	++	-	-	-	-	-	-	-	-
39290 +	-	-	-	-	-	-	-	-	-
39291 +	++	-	-	-	-	-	-	-	-
39292 +	+	---+	+++	+++	+++	-	-	-	-
17573 +	-	-	-	-	-	-	-	-	-
39293 +	++	---+	+++	+++	+++	+	-	-	-
11565 +	+	-	-	-	-	-	-	-	-
19914 +	-	-	-	-	-	-	-	-	-
11258 +	+	-	-	-	-	-	-	-	-
16149 +	++	-	-	-	-	-	-	-	-
38744 +	+	-	-	-	-	-	-	-	-
39294 +	++	-	-	-	-	-	-	-	-
37468 +	-	-	-	-	-	-	-	-	-
39295 +	+	--	++	++	-	-	-	-	-
39296 +	++	-	-	-	-	-	-	-	-
16022 +	+	-	-	-	-	-	-	-	-
38868 +	-	---+	+	+++	-	-	-	-	-
14048 +	++	-	-	-	-	-	-	-	-
14444 +	++	-	-	-	-	-	-	-	-
38580 +	+	-	-	-	-	-	-	-	-
38679 +	++	-	+	-	-	-	-	-	-
14074 +	++	-	-	-	-	-	-	-	-
39297 +	++	---+	+++	+++	+++	+	-	-	-
13624 +	++	-	-	-	-	-	-	-	-
39298 +	-	-	-	-	-	-	-	-	-
38123 +	-	-	-	-	-	-	-	-	-
39299 +	+	---+	+++	+++	+++	+	-	-	-
39300 +	-	-	-	-	-	-	-	-	-
39047 +	++	-	-	-	-	-	-	-	-
13696 +	++	-	-	-	-	-	-	-	-
14103 +	++	-	-	-	-	-	-	-	-
11889 +	-	-	-	-	-	-	-	-	-
38927 +	++	-	-	-	-	+	-	-	-

18739 +	-	-	-	-	-	-	-	-	-
13802 +	++	-	-	-	-	-	-	-	-
39256 +	++	--+	+++	+++	+++	-	-	-	-
39301 +	+	--+	+++	+++	+++	-	-	-	-
39260 +	++	-	-	-	-	-	-	-	-
38285 +	+	-	-	-	-	-	-	-	-
39006 +	++	-	-	-	-	-	-	-	-
39302 +	+	-	-	-	-	-	-	-	-
39127 +	+	-	+	+	+	++	--	-	-
39303 +	++	-	-	-	-	-	-	-	-
17059 +	++	-	-	-	-	-	-	-	-
20360 +	-	-	+	-	-	+	-	-	-
38167 +	-	-	-	-	-	-	-	-	-
11487 +	-	-	-	-	-	-	-	-	-
39304 +	-	--	+	+++	+	+	-	-	-
37917 +	++	-	-	-	-	-	-	-	-
11988 +	++	-	-	-	-	-	-	-	-
38966 +	-	-	-	-	-	-	-	-	-
13746 +	++	-	-	-	-	-	-	-	-
39278 +	++	-	-	-	-	-	-	-	-
13902 +	++	-	-	-	-	-	-	-	-
39305 +	++	-	-	-	-	-	-	-	-
38402 +	++	-	-	-	-	-	-	-	-
13596 +	++	-	-	+	-	+++	---	-	-
39038 +	++	-	-	-	-	-	-	-	-
11363 +	-	-	-	-	-	-	-	-	-
14132 +	++	-	-	-	-	-	-	-	-
39306 +	++	-	-	-	-	-	-	-	-
11385 +	++	-	-	-	-	+	-	-	-
14042 +	++	-	-	-	-	-	-	-	-
39307 +	+	-	+	-	-	+	-	-	-
11219 +	+	-	-	-	-	-	-	-	-
14389 +	++	-	-	-	-	-	-	-	-

38966 +	-	-	-	-	-	-	-	-	-
11460 +	+	-	-	-	-	-	-	-	-
39308 +	++	-	-	-	-	-	-	-	-
39309 +	++	-	-	-	-	-	-	-	-
39191 +	+	-	-	-	-	+	–	-	-
39310 +	++	-	-	-	-	+	–	-	-
39069 +	++	-	-	-	-	-	-	-	-
17104 +	-	–+	+++	+++	+++	-	-	-	-
16601 +	-	-	-	-	-	-	-	-	-
39311 +	++	–+	+++	+++	+++	+	–	-	-
39140 +	++	-	-	-	-	-	-	-	-
38232 +	-	-	-	+++	+	-	-	-	-
14256 +	+	-	-	-	-	-	-	-	-
38816 +	++	-	+	-	+	-	-	-	-
38641 +	+	–+	+++	+++	+++	-	–	-	-
14116 +	+	-	-	-	-	-	-	-	-
39312 +	-	-	-	-	-	-	-	-	-
17562 +	-	-	-	-	-	-	-	-	-
17509 +	+	–+	+++	+++	+++	+	–	-	-
12061 +	+	-	-	-	-	-	-	-	-
11555 +	+	-	-	-	-	-	-	-	-
39313 +	-	-	-	-	-	-	-	-	-
39314 +	++	-	-	-	-	-	-	-	-
39166 +	++	-	-	-	-	-	-	-	-
38981 +	++	-	-	-	-	-	-	-	-
14366 +	++	-	-	+	-	-	–	-	-
39315 +	+	–+	+++	+++	+++	-	––	-	-
39316 +	+	–+	+++	+++	+++	+	–	-	-
39317 +	+	-	-	-	-	-	-	-	-
39145 +	+	-	-	-	-	-	-	-	-
11908 +	+	-	-	-	-	-	-	-	-
39157 +	++	-	-	-	-	-	-	-	-
11236 +	+	-	-	-	-	-	-	-	-

38883 +	-	--+	+	+++	-	-	-	-	-
38861 +	++	-	-	-	-	-	-	-	-
39232 +	++	-	-	-	-	-	-	-	-
39318 +	+	-	-	-	-	-	-	-	-
17737 +	++	-	-	-	-	-	-	-	-
38280 +	++	-	-	-	-	-	-	-	-
39319 +	+	--+	+++	+++	+++	-	–	-	-
39320 +	+	-	-	-	-	-	-	-	-
11921 +	+	-	-	-	-	-	-	-	-
13972 +	++	-	-	+	+	++	--	-	-
39321 +	++	--+	+++	+++	+++	+	–	-	-
39322 +	+	–	+	++	++	-	-	-	-
39323 +	++	-	-	-	-	-	-	-	-
39039 +	++	-	-	-	-	-	-	-	-
38598 +	++	-	-	-	-	-	-	-	-
14674 +	++	-	-	-	-	-	-	-	-
39324 +	-	-	-	+	-	+	–	-	-
39011 +	++	-	-	-	-	-	-	-	-
39325 +	-	-	-	-	-	-	-	-	-
39221 +	++	-	-	-	-	-	-	-	-
11804 +	-	-	-	-	-	-	-	-	-
37868 +	++	-	-	-	-	-	-	-	-
37602 +	++	-	-	-	-	-	-	-	-
39326 +	+	-	-	-	-	-	-	-	-
38365 +	++	–	+	+	+	++	--	-	-
38695 +	++	-	-	-	-	-	-	-	-
39327 +	+	--+	+++	+++	+++	+	–	-	-
39328 +	++	-	-	-	-	-	-	-	-
38654 +	++	-	-	-	-	-	-	-	-
39329 +	++	-	-	-	-	-	-	-	-
39330 +	++	--+	+++	+++	+++	+	-	-	-
13827 +	+	-	-	-	-	-	-	-	-
38703 +	++	-	-	-	-	-	-	-	-

16077 +	++	-	-	-	-	-	-	-	-
11980 +	++	-	-	-	-	-	-	-	-
11750 +	-	-	-	-	-	-	-	-	-
13718 +	+	-	-	-	-	-	-	-	-
17521 +	+	-	-	-	-	-	-	-	-
38614 +	++	-	-	-	-	-	-	-	-
39331 +	+	–	+	+	+	+++	---	-	-
39205 +	++	-	-	-	-	-	-	-	-
38993 +	-	-	-	-	-	-	-	-	-
37095 +	++	-	-	-	-	-	-	-	-
39168 +	-	-	+	+	-	+	-	-	-
39332 +	+	–	+	-	-	+	–	-	-
39212 +	++	-	-	-	-	-	-	-	-
39333 +	++	-	-	-	-	-	-	-	-
19739 +	+	-	-	-	-	-	–	-	-
38130 +	-	-	-	+++	-	-	-	-	-
12185 +	-	-	-	-	-	-	-	-	-
39334 +	+	--+	+++	+++	+++	+	-	-	-
16637 +	+	-	-	-	-	-	-	-	-
38692 +	-	-	-	-	-	-	-	-	-
39335 +	++	-	-	-	-	-	-	-	-
38597 +	-	-	-	-	-	-	-	-	-
37609 +	++	–	+	-	-	-	-	-	-
39336 +	+	-	-	-	-	-	-	-	-
16646 +	-	-	-	-	-	+	–	-	-
39337 +	++	-	-	-	-	+	–	-	-
16600 +	++	--	+++	+++	+++	-	-	-	-
39338 +	++	-	-	-	-	-	-	-	-
39038 +	++	-	-	-	-	-	-	-	-
39318 +	++	-	-	-	-	-	-	-	-
14378 +	++	-	-	-	-	-	-	-	-
39339 +	++	-	-	-	-	-	-	-	-
38722 +	+	-	-	-	-	-	-	-	-

39340 +	++	-	-	-	-	-	-	-	-
39341 +	+	--+	+++	+++	+++	-	-	-	-
11277 +	-	-	-	-	-	-	-	-	-
38787 +	+	-	-	-	-	-	-	-	-
37721 +	++	-	-	-	-	-	-	-	-
38606 +	++	-	-	-	-	-	-	-	-
39342 +	+	-	+	-	-	-	-	-	-
14813 +	+	-	-	-	-	-	-	-	-
37522 +	+	--+	+	+++	+	-	-	-	-
38813 +	+	--+	+++	+++	+++	+	-	-	-
39343 +	++	-	-	-	-	-	-	-	-
38787 +	+	-	-	-	-	-	-	-	-
39294 +	++	-	-	-	-	-	-	-	-
14529 +	++	-	-	-	-	-	-	-	-
39344 +	+	-	-	-	-	-	-	-	-
39077 +	-	--+	-	-	-	-	-	-	-
38459 +	+	--+	+++	+++	+++	+	-	-	-
39345 +	+	-	-	-	-	-	-	-	-
13620 +	+	-	-	-	-	-	-	-	-
39346 +	+	-	+	-	+	-	-	-	-
17570 +	+	-	-	-	-	-	-	-	-
39347 +	++	-	+	+	+	+	--	-	-
14325 +	++	-	-	-	-	-	-	-	-
12033 +	++	-	-	-	-	-	-	-	-
38778 +	++	-	-	-	-	-	-	-	-
11470 +	++	-	-	-	-	-	-	-	-
39348 +	+	--+	+++	+++	+++	+	-	-	-
17251 +	++	-	-	-	-	-	-	-	-
14080 +	+	-	+	-	+	++	--	-	-
17040 +	+	-	-	-	-	-	-	-	-
39349 +	++	-	-	-	-	-	-	-	-
39305 +	++	-	-	-	-	-	-	-	-
39350 +	-	-	-	-	-	-	-	-	-

39351 +	++	--+	+++	+++	+++	-	-	-	-
39352 +	++	-	-	-	-	-	-	-	-
39353 +	++	-	-	-	-	-	-	-	-
39354 +	++	-	-	-	-	-	-	-	-
39355 +	+	--+	+++	+++	+++	+++	---	-	-
39356 +	+	--+	+++	+++	+++	-	-	-	-
38593 +	+	-	+	+	+	+++	---	-	-
13599 +	+	-	-	-	-	+	--	-	-
14074 +	++	-	-	-	-	-	-	-	-
38153 +	+	--+	+++	+++	+++	-	-	-	-
14136 +	++	-	-	-	-	-	-	-	-
39357 +	++	-	-	-	-	+	-	-	-
39358 +	-	-	-	-	-	-	-	-	-
11337 +	+	-	-	-	-	-	-	-	-
15959 +	+	-	-	-	-	-	-	-	-
39346 +	-	-	+	+	-	-	-	-	-
37260 +	-	-	-	-	-	-	-	-	-
14140 +	++	-	-	-	-	-	-	-	-
39359 +	+	-	-	-	-	-	-	-	-
11228 +	+	-	-	-	+	-	-	-	-
14123 +	++	--+	+++	+++	+++	-	-	-	-
39360 +	-	-	-	-	-	-	-	-	-
13664 +	++	-	-	-	-	-	-	-	-
39361 +	+	-	-	-	-	-	-	-	-
38803 +	++	-	+	-	-	+	-	-	-
14861 +	++	-	-	-	-	-	-	-	-
11057 +	+	-	-	-	-	-	-	-	-
39362 +	+	--+	+++	+++	+++	-	-	-	-
39229 +	-	--+	-	+	-	-	-	-	-
39363 +	+	--+	+++	+++	+++	-	-	-	-
38150 +	-	--+	++	+++	+++	+	-	-	-
39364 +	-	-	-	-	-	-	-	-	-
38334 +	++	-	-	-	-	-	-	-	-

39365 +	++	-	-	-	-	-	-	-	-
39366 +	+	--	+	++	++	++	--	-	-
39367 +	+	--+	+++	+++	+++	-	-	-	-
12692 +	-	-	-	-	-	-	-	-	-
39093 +	++	-	-	-	-	-	-	-	-
14115 +	++	-	-	-	-	-	-	-	-
13816 +	++	-	-	-	-	-	-	-	-
14542 +	++	-	-	-	-	-	-	-	-
39203 +	-	-	-	-	-	-	-	-	-
14084 +	++	-	-	-	-	-	-	-	-
12070 +	-	-	-	-	-	-	-	-	-
38647 +	-	-	-	-	-	-	-	-	-
38041 +	+	-	+	-	+	+	-	-	-
13990 +	++	-	-	-	-	-	-	-	-
17800 +	+	-	-	-	-	-	-	-	-
39082 +	++	-	-	-	-	-	-	-	-
39368 +	+	-	-	-	-	+	-	-	-
13798 +	++	-	-	-	-	-	-	-	-
37978 +	-	-	-	-	-	-	-	-	-
12438 +	++	-	-	-	-	-	-	-	-
39369 +	-	-	-	-	-	-	-	-	-
14105 +	++	-	-	-	-	-	-	-	-
37956 +	-	--+	+	-	-	+	-	-	-
13763 +	++	-	-	-	-	-	-	-	-
39353 +	++	-	-	-	-	-	-	-	-
11432 +	+	-	-	-	-	-	-	-	-
17167 +	+	--+	+++	+++	+++	+	-	-	-
39370 +	++	-	-	-	-	-	-	-	-
13943 +	++	-	-	-	-	-	-	-	-
11055 +	+	-	-	-	-	-	-	-	-
38504 +	-	-	-	-	-	-	-	-	-
14074 +	++	-	-	-	-	-	-	-	-
39305 +	++	-	-	-	-	-	-	-	-

39371	+	+	−+	+++	+++	+++	+	−	-	-
39372	+	+	−+	+++	+++	+++	-	-	-	-
39373	+	-	−+	+++	+++	+++	-	-	-	-
39374	+	++	-	-	-	-	-	-	-	-
38897	+	++	-	-	-	-	-	-	-	-
19891	+	+	−+	+++	+++	+++	+	−	-	-
11940	+	-	-	-	-	-	-	-	-	-
38133	+	-	-	-	-	-	+	−	-	-
38705	+	+	-	-	-	-	++	−−	-	-
17814	+	++	-	-	-	-	-	-	-	-
39375	+	+	-	-	-	-	-	-	-	-
39235	+	++	-	-	-	-	-	-	-	-
39376	+	+	−+	+++	+++	+++	+	−	-	-
39377	+	+	−+	+++	+++	+++	+	-	-	-
11911	+	++	-	-	-	-	-	-	-	-
39378	+	++	−+	+++	-	-	-	-	+	-
14098	+	++	-	-	-	-	-	−	-	-
11976	+	-	-	-	-	-	-	-	-	-
39379	+	-	-	-	-	-	+	−	-	-
39380	+	++	-	-	-	-	+	−	-	-
37798	+	++	-	-	-	-	-	-	-	-
14531	+	++	-	-	-	-	-	−	-	-
39381	+	+	-	-	-	-	-	-	-	-
17649	+	-	-	-	-	-	-	-	-	-
39382	+	+	−+	+++	+++	+++	+	−	-	-
39383	+	+	−+	+++	+++	+++	-	−	-	-
39384	+	+	−+	+++	+++	+++	-	−	-	-
39268	+	++	-	-	-	-	-	-	-	-
14071	+	+	-	+	+	+	+++	−−−	-	-
39385	+	++	-	-	-	-	-	-	-	-
39386	+	+	−+	+++	+++	+++	-	-	-	-
39387	+	+	-	-	-	-	-	-	-	-
39140	+	++	-	-	-	-	-	-	-	-

19751 +	+	--+	+++	+++	+++	-	-	-	-
39388 +	-	-	-	+	+	+	-	-	-
39389 +	+	-	-	-	-	-	-	-	-
38801 +	++	-	-	-	-	-	-	-	-
39390 +	++	-	-	-	-	-	-	-	-
39109 +	++	-	-	-	-	-	-	-	-
11197 +	++	-	-	-	-	-	-	-	-
39391 +	+	--+	+++	+++	+++	+	-	-	-
39392 +	+	--+	+++	+++	+++	+	-	-	-
11588 +	-	-	-	-	-	-	-	-	-
39370 +	+	-	-	-	-	-	-	-	-
39393 +	+	--+	+++	+++	+++	+	-	-	-
14292 +	++	-	+	+	+	+++	---	-	-
13521 +	++	-	+	+	+	+	-	-	-
17867 +	++	-	-	-	-	-	-	-	-
39394 +	-	-	-	-	-	-	-	-	-
39305 +	++	-	-	-	-	-	-	-	-
38882 +	++	-	-	-	-	-	-	-	-
39102 +	++	-	-	-	-	-	-	-	-
39180 +	++	-	-	-	-	-	-	-	-
39160 +	+	-	-	-	-	-	-	-	-
39306 +	++	-	-	-	-	-	-	-	-
39126 +	++	-	-	-	-	-	-	-	-
13181 +	++	-	-	-	-	-	-	-	-
39170 +	-	-	-	-	-	-	-	-	-
39242 +	+	-	-	-	-	-	-	-	-
38945 +	++	-	-	-	-	-	-	-	-
37399 +	+	-	+	+	+	-	-	-	-
17251 +	+	-	-	-	-	-	-	-	-
38274 +	+	-	-	-	+	-	-	-	-
14038 +	++	-	-	-	-	-	-	-	-
39395 +	++	-	-	-	-	-	-	-	-
17726 +	-	-	-	-	-	-	-	-	-

11066 +	++	-	-	-	+	-	-	-	-
16071 +	++	-	-	-	-	-	-	-	-
39396 +	+	-	-	-	-	-	-	-	-
11742 +	+	-	-	-	-	-	-	-	-
14123 +	++	--+	+++	+++	+++	+	-	-	-
14412 +	+	-	-	-	-	-	-	-	-
17079 +	+	-	-	-	-	-	-	-	-
39397 +	++	-	-	-	-	-	-	-	-
13720 +	++	-	-	-	-	-	-	-	-
39398 +	++	-	-	-	-	-	-	-	-
38825 +	-	-	-	-	-	-	-	-	-
39378 +	++	--+	++	-	-	-	-	-	-
39399 +	++	-	-	-	-	-	-	-	-
39400 +	+	--+	+++	+++	+++	-	–	-	-
37981 +	-	--+	-	-	-	-	-	-	-
38240 +	++	-	-	-	-	-	-	-	-
39401 +	+	-	-	-	-	-	-	-	-
38124 +	++	-	+	+	-	-	-	-	-
13901 +	++	-	-	-	-	-	-	-	-
39402 +	+	-	-	-	+	-	-	-	-
39216 +	++	-	-	-	-	-	-	-	-
38652 +	-	–	+	+	+	+	-	-	-
39344 +	++	-	-	-	-	-	-	-	-
11048 +	++	-	-	-	-	-	-	-	-
11452 +	-	-	-	-	-	-	-	-	-
39403 +	-	-	-	-	-	-	-	-	-
39404 +	++	-	-	-	-	-	-	-	-
14507 +	++	-	-	-	-	-	-	-	-
38428 +	+	-	-	-	-	-	-	-	-
17573 +	-	-	-	-	-	-	-	-	-
11214 +	-	-	-	-	-	-	-	-	-
38827 +	++	-	-	-	-	-	–	-	-
39405 +	++	-	-	-	-	-	-	-	-

13635 +	++	-	-	-	-	-	-	-	-
39406 +	-	-	-	-	-	-	-	-	-
38974 +	++	-	-	-	-	-	-	-	-
38854 +	++	-	-	-	-	+	–	-	-
13761 +	+	-	-	-	-	-	-	-	-
17528 +	-	-	-	-	+	-	–	-	-
14295 +	++	-	-	-	-	-	-	-	-
39407 +	++	-	-	-	-	-	-	-	-
11438 +	-	-	-	-	-	-	-	-	-
39408 +	+	-	-	-	-	-	-	-	-
39409 +	++	–+	+++	+++	+++	+	–	-	-
19220 +	+	–+	+++	+++	+++	-	-	-	-
17442 +	+	-	-	-	-	-	–	-	-
11942 +	-	-	-	-	-	-	-	-	-
39288 +	-	-	-	-	-	-	-	-	-
38820 +	++	-	-	-	-	-	-	-	-
39410 +	-	-	-	-	-	-	-	-	-
14083 +	++	-	-	-	-	-	-	-	-
19603 +	++	-	-	-	-	-	-	-	-
11989 +	+	-	-	-	-	-	-	-	-
39411 +	+	–+	+++	+++	+++	+	-	-	-
39412 +	++	–+	+++	+++	+++	+	–	-	-
39413 +	++	-	-	-	-	-	-	-	-
11311 +	+	-	-	-	-	-	-	-	-
36276 +	+	–+	+	+++	+	+	–	-	-
39414 +	+	–+	+++	+++	+++	-	-	-	-
39102 +	++	-	-	-	-	+	-	-	-
16576 +	+	-	-	-	-	-	-	-	-
39415 +	++	-	-	-	-	-	-	-	-
38668 +	-	-	-	-	-	-	-	-	-
39416 +	++	-	-	-	-	-	-	-	-
10990 +	++	-	-	-	-	-	-	-	-
12438 +	++	-	-	-	-	-	-	-	-

39417 +	+	-	-	-	-	-	-	-	-
39075 +	++	-	-	-	-	-	-	-	-
39418 +	++	--+	+++	+++	+++	-	-	-	-
39419 +	+	–	-	-	-	-	-	-	-
39237 +	++	-	-	-	-	-	-	-	-
38427 +	++	-	-	-	-	-	-	-	-
17467 +	+	-	-	-	-	-	-	-	-
11000 +	++	-	-	-	-	-	-	-	-
14593 +	++	-	-	-	-	-	-	-	-
38276 +	++	-	-	+	+	+	–	-	-
39420 +	-	--+	+++	+++	+++	-	-	-	-
17625 +	-	–	-	-	-	-	-	-	-
38779 +	++	--+	+++	+++	+++	-	-	-	-
39421 +	-	-	-	-	-	-	-	-	-
13510 +	++	-	-	-	-	+	–	-	-
39422 +	+	--+	+++	+++	+++	+	–	-	-
37998 +	-	–	-	+	+	+	-	-	-
39423 +	++	-	-	-	-	-	-	-	-
39309 +	++	-	-	-	-	-	-	-	-
39424 +	++	-	-	-	-	-	-	-	-
11250 +	-	-	-	-	-	-	-	-	-
11452 +	-	-	-	-	-	-	-	-	-
38403 +	++	-	-	-	-	-	-	-	-
39425 +	+	-	-	-	-	-	-	-	-
38286 +	-	–	-	-	-	-	-	-	-
20041 +	-	--+	+++	+++	+++	-	-	-	-
39426 +	+	--+	+++	+++	+++	-	-	-	-
39427 +	++	-	-	-	-	-	-	-	-
39193 +	-	-	-	-	-	-	-	-	-
39428 +	+	-	+	-	-	-	-	-	-
37387 +	++	-	-	-	+	-	-	-	-
39374 +	+	-	-	-	-	-	-	-	-
12128 +	-	-	-	-	-	-	-	-	-

39429 +	-	–	-	+++	-	-	-	-	-
39430 +	++	-	-	-	-	-	-	-	-
39431 +	-	-	-	-	-	-	-	-	-
13558 +	++	–+	+++	+++	+++	+	–	-	-
39394 +	-	-	-	-	-	-	-	-	-
15959 +	+	-	-	-	-	+	–	-	-
11684 +	-	-	-	-	-	-	-	-	-
38077 +	+	–+	+++	+++	+++	+	–	-	-
39432 +	+	-	+	+	+	++	––	-	-
39427 +	++	-	-	-	-	-	-	-	-
17644 +	-	-	-	+	-	+	-	-	-
17781 +	++	-	-	-	-	-	-	-	-
39433 +	+	–+	+++	+++	+++	-	-	-	-
14618 +	++	-	+	+	-	+++	–––	-	-
39024 +	-	-	-	-	-	-	-	-	-
13751 +	+	-	-	-	-	-	-	-	-
39402 +	++	-	-	-	-	-	-	-	-
15963 +	+	-	-	-	-	+	-	-	-
13637 +	++	-	-	-	-	+	–	-	-
39434 +	++	–	-	+	-	+++	–––	-	-
15994 +	++	-	-	-	-	-	-	-	-
38151 +	++	-	-	-	-	-	-	-	-
38100 +	+	-	-	-	-	-	-	-	-
39435 +	+	–+	+++	+++	+++	-	–	-	-
14006 +	+	-	-	-	-	-	-	-	-
19688 +	++	-	-	-	-	-	-	-	-
11187 +	+	-	-	-	-	-	-	-	-
39300 +	-	-	-	-	-	-	-	-	-
39436 +	-	-	-	-	-	-	-	-	-
38930 +	++	–+	+++	+++	+++	-	–	-	-
17212 +	++	–+	+++	+++	+++	+	-	-	+
17237 +	+	–+	+++	+++	+++	-	-	-	-
36317 +	+	-	-	-	-	-	-	-	-

39413 +	++	-	-	-	-	-	-	-	-
19681 +	+	-	-	-	-	-	-	-	-
13857 +	++	-	-	-	-	+	–	-	-
38855 +	-	-	-	-	-	-	-	-	-
38093 +	++	-	-	-	-	-	-	-	-
39437 +	+	–+	+++	+++	+++	-	–	-	-
17684 +	+	-	-	-	-	-	-	-	-
39438 +	++	-	-	-	-	-	-	-	-
39439 +	++	-	-	-	-	-	–	-	-
39440 +	+	-	-	-	-	-	-	-	-
39441 +	+	–	-	+	+	-	-	-	-
39442 +	++	-	-	-	-	-	-	-	-
20360 +	-	-	+	-	+	-	-	-	-
39443 +	++	-	-	-	-	-	-	-	-
16617 +	-	-	-	-	-	-	-	-	-
39390 +	+	-	-	-	-	-	-	-	-
39444 +	+	–+	+++	+++	+++	-	-	-	-
39445 +	+	–+	+++	+++	+++	-	-	-	-
38745 +	++	-	-	-	-	-	-	-	-
18048 +	++	-	-	-	-	-	-	-	-
14384 +	++	-	-	-	-	-	-	-	-
12692 +	-	-	-	-	-	-	-	-	-
14138 +	+	-	-	-	-	-	-	-	-
18314 +	-	–	-	-	-	+	-	-	-
39446 +	+	-	-	-	-	-	-	-	-
13620 +	++	-	-	-	-	-	-	-	-
13966 +	++	-	-	-	-	-	-	-	-
14191 +	++	-	-	-	-	+	–	-	+
38035 +	++	-	-	-	-	-	-	-	-
39385 +	++	-	-	-	-	-	-	-	-
39447 +	-	-	+	-	+	-	-	-	-
11675 +	+	-	-	-	-	-	-	-	-
11117 +	++	-	-	-	-	-	-	-	-

16107 +	+	-	-	-	-	-	-	-	-
38189 +	++	-	-	-	-	-	-	-	-
39448 +	++	-	-	-	-	-	-	-	-
17642 +	++	-	-	-	-	-	-	-	-
39201 +	-	–	+	++	+	+	–	-	-
39449 +	-	-	-	-	-	-	-	-	-
14399 +	++	-	-	-	-	-	-	-	-
18832 +	+	–+	+++	+++	+++	-	-	-	-
39450 +	+	–+	+++	+++	+++	+	–	-	+++
39451 +	+	–+	+++	+++	+++	+	–	-	-
17561 +	+	–+	+++	+++	+++	+	–	-	-
15994 +	++	-	-	-	-	-	-	-	-
39443 +	++	-	-	-	-	-	-	-	-
12097 +	-	-	-	-	-	-	-	-	-
17284 +	-	-	-	-	-	-	-	-	-
37836 +	++	-	-	-	-	-	-	-	-
39452 +	++	-	-	-	-	-	-	-	-
38417 +	++	-	-	-	-	-	-	-	-
39453 +	+	-	-	-	-	-	-	-	-
17629 +	+	-	-	-	-	-	-	-	-
39404 +	++	-	-	-	-	-	-	-	-
39454 +	+	–+	+++	+++	+++	+	–	-	-
14582 +	+	-	-	+	+	+	–	-	-
39455 +	++	-	-	-	-	-	-	-	-
38845 +	-	–+	-	-	-	-	-	-	-
39456 +	-	-	-	-	-	-	-	-	-
38346 +	++	-	-	-	-	-	-	-	-
13951 +	+	–+	+++	+++	+++	+	–	-	-
39457 +	++	-	-	-	-	-	-	-	-
39458 +	+	-	-	-	-	-	-	-	-
13858 +	++	-	-	-	-	-	-	-	-
39459 +	+	-	-	-	-	-	-	-	-
14861 +	++	-	-	-	-	-	-	-	-

38612 +	++	-	-	-	-	-	-	-	-
12014 +	-	-	-	-	-	-	-	-	-
39460 +	+	-	-	-	+	-	-	-	-
10960 +	+	-	-	-	-	-	-	-	-
38475 +	++	-	-	-	-	-	-	-	-
39461 +	-	–	-	-	-	-	-	-	-
39462 +	+	-	-	-	-	-	-	-	-
11601 +	+	-	-	-	-	-	-	-	-
39365 +	++	-	-	-	-	-	-	-	-
38741 +	-	-	-	-	-	-	-	-	-
38867 +	-	-	-	-	-	-	–	-	-
14355 +	+	-	-	-	-	-	–	-	-
11529 +	-	-	-	-	-	-	-	-	-
18773 +	-	-	-	-	-	-	-	-	-
19185 +	-	-	-	-	-	-	-	-	-
13804 +	++	-	-	-	-	-	-	-	-
39463 +	+	–+	+++	+++	+++	+	–	-	-
39184 +	++	-	-	-	-	-	-	-	-
38974 +	++	-	-	-	-	-	-	-	-
38548 +	++	-	-	-	-	+	–	-	-
18625 +	-	-	-	-	-	-	-	-	-
14384 +	++	-	-	-	-	-	-	-	-
13791 +	++	-	-	-	-	-	-	-	-
39464 +	+	–+	+++	+++	+++	-	-	-	-
39465 +	++	-	-	-	-	-	-	-	-
17646 +	-	-	-	-	-	-	-	-	-
14346 +	++	-	-	-	-	-	-	-	-
39466 +	++	–+	+++	+++	+++	+	–	-	-
39467 +	-	–+	+++	+++	+++	-	-	-	-
13659 +	+	-	-	-	-	-	-	-	-
39468 +	++	–+	+++	+++	+++	+	-	-	-
39469 +	+	-	-	-	-	-	-	-	-
39470 +	++	–+	+++	+++	+++	+	–	-	-

39471 +	-	-	-	-	-	-	-	-	-
39472 +	+	-	-	-	-	-	-	-	-
39473 +	+	-	-	-	-	-	-	-	-
13635 +	++	-	-	-	-	-	-	-	-
39474 +	++	-	-	-	-	-	-	-	-
39475 +	+	-	-	-	-	-	-	-	-
39476 +	+	---+	+++	+++	+++	-	-	-	-
14069 +	+	-	-	-	-	+	–	-	-
38673 +	++	-	-	-	-	-	-	-	-
13945 +	+	-	-	-	-	+	–	-	-
11447 +	-	-	-	-	-	-	-	-	-
14850 +	+	–	+	+	+	+	–	-	-
39226 +	++	-	-	-	-	-	-	-	-
38850 +	-	–	+	+	+	+	––	-	-
17602 +	-	–	-	-	-	-	–	-	-
38961 +	+	-	-	-	-	+	-	-	-
39477 +	++	---+	+++	+++	+++	+	–	-	-
38006 +	++	-	-	-	-	-	-	-	-
39478 +	++	---+	+++	+++	+++	-	-	-	-
39479 +	+	-	-	-	-	-	-	-	-
39480 +	+	---+	+++	+++	+++	-	-	-	-
39481 +	-	-	-	-	-	-	-	-	-
38133 +	-	-	-	+	+	+	–	-	-
38931 +	-	---+	++	++	+	+++	---	+++	+++
38564 +	++	-	-	-	-	-	-	-	-
18244 +	+	-	-	-	-	-	-	-	-
14527 +	++	-	-	-	-	-	-	-	-
17264 +	-	–	+	-	+	-	–	-	-
39482 +	-	-	-	-	-	-	-	-	-
14850 +	++	–	+	+	+	+	–	-	-
38809 +	+	-	-	-	-	-	-	-	-
39036 +	-	-	-	-	-	-	-	-	-
13815 +	++	–	+	+	+	++	––	+++	+++

39216 +	++	-	-	-	-	-	-	-	-
39483 +	-	-	-	-	-	-	-	-	-
39273 +	++	-	-	+	+	-	-	-	-
39484 +	+	-	-	-	-	-	-	-	-
39337 +	++	-	-	-	-	+	–	-	-
39313 +	-	-	-	-	-	-	-	-	-
39485 +	+	–+	+++	+++	+++	+	-	-	-
12134 +	-	-	-	-	-	-	-	-	-
13949 +	++	-	-	-	-	-	-	-	-
13902 +	++	-	-	-	-	-	-	-	-
39477 +	+	–+	+++	+++	+++	+	–	-	+++
39486 +	+	–+	+++	+++	+++	+	–	-	-
39072 +	-	–	+	-	-	-	-	-	-
38886 +	-	–	-	-	-	-	-	-	-
13812 +	++	-	-	-	-	-	-	-	-
16135 +	-	-	-	-	-	-	-	-	-
18032 +	-	-	-	-	-	+	–	-	-
11630 +	+	-	-	-	-	-	-	-	-
13520 +	++	-	-	-	-	+	–	-	-
38311 +	++	-	-	-	-	-	-	-	-
13992 +	++	-	-	-	-	-	-	-	-
38532 +	++	-	-	-	-	-	-	-	-
39487 +	++	-	-	-	-	-	-	-	-
14175 +	++	-	-	-	-	-	-	-	-
39488 +	++	–+	+++	+++	+++	-	-	-	-
39489 +	+	-	-	-	-	-	-	-	-
38790 +	++	-	-	-	-	-	-	-	-
39490 +	+	-	-	-	-	-	-	-	-
39491 +	+	-	-	-	-	-	-	-	-
39492 +	++	-	-	-	-	-	-	-	-
39159 +	++	-	-	-	-	-	-	-	-
39493 +	+	–+	+++	+++	+++	+	–	-	-
39465 +	++	-	-	-	-	-	-	-	-

14412 +	++	-	-	-	-	-	-	-	-
13933 +	+	-	-	-	-	-	-	-	-
13586 +	++	-	-	-	-	+	–	-	-
39156 +	++	-	-	-	-	-	-	-	-
38983 +	+	-	-	-	-	-	-	-	-
38224 +	-	-	-	-	-	-	-	-	-
39021 +	++	-	-	-	-	-	-	-	-
39494 +	++	–+	+++	+++	+++	+	–	-	-
39085 +	++	-	-	-	-	-	-	-	-
39495 +	++	–+	+++	+++	+++	+	–	-	-
17653 +	+	-	-	-	-	-	-	-	-
39496 +	-	-	-	-	-	-	-	-	-
13841 +	+	-	-	-	-	+	–	-	-
18708 +	+	-	-	-	-	-	-	-	-
39497 +	+	–+	+++	+++	+++	-	-	-	-
39498 +	+	–+	+++	+++	+++	-	-	-	-
39499 +	+	–+	+++	+++	+++	+	–	-	-
38391 +	-	–+	-	-	-	-	-	-	-
14326 +	+	-	-	-	-	-	-	-	-
38935 +	-	–	+	+	+	-	-	-	-
19982 +	-	-	-	-	-	-	-	-	-
39500 +	++	-	-	-	-	-	-	-	-
14267 +	++	-	-	-	-	-	-	-	-
12162 +	-	-	-	-	-	-	-	-	-
11206 +	+	-	-	-	-	-	-	-	-
39501 +	++	-	-	-	-	-	-	-	-
14495 +	++	-	-	-	-	-	-	-	-
13536 +	+	-	-	-	-	-	-	-	-
20371 +	-	-	+	-	-	-	-	-	-
39502 +	+	–+	+++	+++	+++	+	–	-	-
39503 +	+	–+	+++	+++	+++	+	–	+++	-
38388 +	++	-	-	-	-	-	-	-	-
39504 +	-	-	-	-	-	-	-	-	-

16604 +	-	-	-	-	-	-	-	-	-
38530 +	+	-	-	-	-	-	-	-	-
39505 +	+	--+	+++	+++	+++	+	-	-	-
11908 +	+	-	-	-	-	-	-	-	-
39481 +	-	-	-	-	-	-	-	-	-
11560 +	++	-	-	-	-	-	-	-	-
39506 +	+	--+	+++	+++	+++	-	–	-	-
14115 +	++	-	-	-	-	-	-	-	-
39507 +	+	--+	+++	+++	+++	-	–	-	-
11684 +	-	-	-	-	-	-	-	-	-
11180 +	+	-	-	-	-	-	-	-	-
11171 +	++	-	-	-	-	-	-	-	-
39508 +	+	-	-	-	-	-	-	-	-
13760 +	++	-	-	-	-	-	-	-	-
39509 +	+	--+	+++	-	-	-	-	++	++
39510 +	++	-	-	-	-	-	-	-	-
38725 +	+	-	-	-	-	+	-	-	-
17629 +	+	-	-	-	-	-	-	-	-
39455 +	++	-	-	-	-	-	-	-	-
39511 +	+	--+	+++	+++	+++	+	–	-	-
13726 +	++	-	-	-	-	+	–	-	-
39309 +	++	-	-	-	-	-	-	-	-
39416 +	++	-	-	-	-	-	-	-	-
38755 +	+	-	-	-	-	-	-	-	-
18973 +	+	--+	+++	+++	+++	+	-	-	-
17276 +	+	--+	+++	+++	+++	-	-	-	-
39088 +	+	–	+	+	-	-	-	-	-
39512 +	+	-	-	-	-	-	-	-	-
39513 +	++	-	-	-	-	-	-	-	-
38655 +	+	-	-	-	-	-	-	-	-
39514 +	-	-	-	-	-	-	-	-	-
39515 +	+	-	-	-	-	-	-	-	-
17901 +	++	-	-	-	-	-	-	-	-

39516 +	+	--+	+++	+++	+++	-	-	-	-
19005 +	-	-	-	-	-	-	-	-	-
39517 +	++	-	-	-	-	-	-	-	-
38897 +	++	-	-	-	-	-	-	-	-
39142 +	++	-	-	-	-	-	-	-	-
39518 +	+	-	-	-	-	-	-	-	-
39410 +	-	-	-	-	-	-	-	-	-
38788 +	++	-	-	-	-	-	-	-	-
19136 +	-	--	-	-	-	+	-	-	-
11565 +	+	-	-	-	-	-	-	-	-
14588 +	+	-	-	-	-	-	-	-	-
11438 +	-	-	-	-	-	-	-	-	-
39508 +	++	-	-	-	-	-	-	-	-
14298 +	++	-	-	-	-	-	-	-	-
13624 +	++	-	-	-	-	-	-	-	-
39298 +	-	-	-	-	-	-	-	-	-
39519 +	+	-	+	-	-	-	-	-	-
39520 +	+	-	-	-	-	-	-	-	-
39233 +	-	-	-	-	-	-	-	-	-
39521 +	-	-	-	-	-	-	-	-	-
13610 +	++	-	-	-	-	-	-	-	-
39041 +	+	-	-	-	-	-	-	-	-
39070 +	++	-	-	-	+	+	-	-	-
17911 +	++	-	-	-	-	-	-	-	-
39522 +	-	-	-	-	-	-	-	-	-
13553 +	++	-	-	-	-	+	-	-	-
39523 +	+	--+	+++	+++	+++	+	-	-	+++
39524 +	+	-	-	-	-	+	-	-	-
16111 +	++	-	+	+	+	-	-	-	-
14670 +	+	-	-	-	-	-	-	-	-
39525 +	+	-	-	-	-	-	-	-	-
38814 +	-	-	+	+	+	+++	---	-	-
39526 +	-	--	-	+	-	-	-	-	-

12185	+	-	-	-	-	-	-	-	-
17745	+	++	-	-	-	-	-	–	-
38433	+	++	-	-	-	-	-	-	-
39527	+	-	–	-	-	-	-	-	-
38938	+	++	-	-	-	-	-	-	-
39528	+	-	-	-	-	-	-	-	-
39529	+	++	–+	+++	+++	+++	-	–	-
38512	+	++	-	-	-	-	-	-	-
38784	+	++	-	-	-	-	-	-	-
13722	+	+	-	-	-	-	-	-	-
39530	+	+	-	-	-	-	-	-	-
39531	+	-	–	-	+	+	-	–	-
39532	+	+	-	-	-	-	-	-	-
13730	+	++	-	-	-	-	-	-	-
39296	+	++	-	-	-	-	-	-	-
39533	+	+	-	-	-	-	-	-	-
39534	+	+	-	-	-	-	-	-	-
39535	+	-	-	-	+	-	-	-	-
14447	+	++	-	-	-	-	-	-	-
39155	+	++	-	-	-	-	-	-	-
14225	+	++	-	-	-	-	-	-	-
39536	+	++	–+	+++	+++	+++	-	-	-
39309	+	++	-	-	-	-	-	-	-
39537	+	+	-	-	-	-	-	-	-
39538	+	+	–+	+++	+++	+++	+	-	-
39539	+	-	-	-	-	-	-	-	-
39540	+	+	-	-	-	-	+	–	-
17631	+	+	-	-	-	-	-	-	-
14542	+	++	-	-	-	-	-	-	-
38729	+	-	-	-	-	-	-	-	-
39541	+	-	-	-	-	-	-	-	-
39542	+	+	––	+	-	-	-	-	-
14282	+	++	-	-	-	-	-	-	-

11989 +	+	-	-	-	-	-	-	-	-
11792 +	+	-	-	-	-	-	-	-	-
39543 +	+	--+	+	+++	-	+	-	-	-
39544 +	-	-	+	-	+	++	--	-	-
13538 +	++	-	-	-	+	++	---	-	-
39017 +	++	-	-	-	-	-	-	-	-
38797 +	++	-	-	-	-	-	-	-	-
39191 +	+	-	-	-	-	+	-	-	-
37920 +	-	-	-	-	-	-	-	-	-
39545 +	-	-	-	-	-	-	-	-	-
39289 +	++	-	-	-	-	-	-	-	-
38984 +	+	--+	+++	+++	+++	+	-	-	-
38840 +	-	-	-	+	-	-	-	-	-
17545 +	-	-	-	-	-	-	-	-	-
39546 +	-	-	-	-	-	-	-	-	-
39547 +	-	-	-	-	-	-	-	-	-
17587 +	-	-	-	-	-	-	-	-	-
39548 +	-	--+	-	+	-	-	-	-	-
38941 +	++	-	-	-	-	-	-	-	-
38664 +	+	-	-	-	-	-	-	-	-
39549 +	+	-	-	-	-	-	-	-	-
13848 +	++	-	-	-	-	-	-	-	-
14158 +	+	-	-	-	-	-	-	-	-
19648 +	-	-	-	+	-	-	-	-	-
39550 +	++	-	-	-	-	-	-	-	-
13966 +	++	-	-	-	-	-	-	-	-
39402 +	+	-	-	-	+	-	-	-	-
19917 +	+	-	-	-	-	-	-	-	-
39541 +	-	-	-	-	-	-	-	-	-
38987 +	+	-	-	-	+	+	-	-	-
38526 +	-	-	-	-	-	-	-	-	-
38933 +	-	-	-	-	-	-	-	-	-
39551 +	+	--+	+	+++	++	+	-	-	-

39552 +	++	-	-	-	-	-	-	-	-
39553 +	++	-	-	-	-	+	–	-	-
38594 +	-	-	-	-	-	-	-	-	-
38967 +	+	-	-	-	-	+	–	-	-
39094 +	-	-	-	-	-	-	-	-	-
12227 +	+	-	-	-	-	-	-	-	-
39554 +	+	-	-	-	-	-	–	-	-
39555 +	+	–-+	+++	+++	+++	-	–	-	-
14231 +	++	-	-	-	-	-	-	-	-
39556 +	-	--	+	-	-	-	-	-	-
38886 +	-	-	+	-	-	-	-	-	-
11478 +	+	-	-	-	-	-	-	-	-
39530 +	+	-	-	-	-	-	-	-	-
39557 +	+	-	-	-	-	-	-	-	-
14077 +	+	-	-	-	-	-	-	-	-
39272 +	-	-	-	+	-	-	-	-	-
13824 +	++	-	-	-	-	-	-	-	-
38514 +	-	-	-	-	-	-	-	-	-
39406 +	-	-	-	-	-	-	-	-	-
13964 +	++	-	-	-	-	-	-	-	-
39423 +	+	-	-	-	-	-	-	-	-
39558 +	+	–-+	+++	+++	+++	+	–	-	-
39559 +	+	–-+	+++	+++	+++	+	–	-	-
14768 +	++	-	-	-	-	-	-	-	-
18531 +	-	-	-	-	-	-	-	-	-
39560 +	-	-	-	-	-	-	-	-	-
39561 +	++	-	-	-	-	-	-	-	-
12205 +	-	-	-	-	-	-	-	-	-
39562 +	+	-	-	-	-	-	–	-	-
38991 +	++	-	-	-	-	-	-	-	-
13776 +	++	-	-	-	-	-	-	-	-
11219 +	+	-	-	-	-	-	-	-	-
11082 +	+	-	-	-	-	-	-	-	-

10952 +	++	-	-	-	-	-	-	-	-
38797 +	++	-	-	-	-	-	-	-	-
39146 +	++	-	-	-	-	-	-	-	-
11893 +	++	-	-	-	-	-	-	-	-
17236 +	-	--+	+++	+++	+++	-	-	-	-
14468 +	+	-	-	-	-	-	-	-	-
16042 +	-	-	-	-	-	-	-	-	-
39563 +	+	--+	+++	+++	+++	-	–	-	-
16157 +	+	-	-	-	-	-	-	-	-
18428 +	+	-	-	-	-	-	-	-	-
39564 +	++	--+	+++	+++	+++	+	-	-	-
38515 +	-	-	-	-	-	-	-	-	-
39565 +	+	--+	+++	+++	+++	+	-	-	+++
39566 +	+	--+	+++	+++	+++	+	-	-	-
14776 +	++	-	-	-	-	-	-	-	-
39567 +	++	--+	+++	+++	+++	+	–	-	-
39568 +	-	-	-	-	-	-	-	-	-
38787 +	+	-	-	-	-	-	-	-	-
39569 +	-	-	-	-	+	-	-	-	-
38875 +	++	-	-	-	-	-	-	-	-
11024 +	+	-	-	-	-	+	–	-	-
13782 +	++	-	-	-	-	-	-	-	-
19027 +	++	--+	+++	+++	+++	-	–	-	-
14366 +	++	-	-	-	-	-	-	-	-
39097 +	+	--+	+++	+++	+++	-	-	-	-
14053 +	++	-	-	-	-	-	-	-	-
13543 +	++	-	-	-	-	-	–	-	-
39570 +	-	--+	+	+++	+	+	–	-	-
39571 +	+	--+	+++	+++	+++	+	–	-	-
39572 +	+	--+	+++	+++	+++	+	–	-	-
39448 +	++	-	-	-	-	-	-	-	-
38912 +	-	–	+	+++	-	+	-	-	-
39573 +	++	-	-	-	-	-	-	-	-

14218 +	++	-	-	-	-	-	-	-	-
39574 +	-	--+	+	++	-	-	-	-	-
39575 +	++	-	-	-	-	-	-	-	-
14020 +	+	-	-	-	-	-	-	-	-
39576 +	++	-	-	-	-	-	-	-	-
39577 +	-	-	-	-	-	-	-	-	-
13908 +	++	–	+	+	+	+++	---	-	-
14052 +	++	–	+	+	+	-	–	-	++
39578 +	-	-	-	-	-	-	-	-	-
39579 +	-	–	++	++	++	-	-	-	-
39580 +	+	--+	+++	+++	+++	+	–	-	-
17718 +	-	-	-	-	-	-	-	-	-
39522 +	-	-	-	-	-	-	-	-	-
17835 +	-	–	-	-	-	-	-	-	-
39174 +	-	-	-	-	-	-	-	-	-
14321 +	++	-	-	-	-	-	-	-	-
39581 +	+	--+	+++	+++	+++	-	–	-	-
39225 +	+	–	+	+	+	-	-	-	-
38964 +	-	–	-	-	-	-	-	-	-
11311 +	+	-	-	-	-	-	-	-	-
38870 +	-	-	+	+	-	-	–	-	-
39582 +	+	-	-	-	-	-	-	-	-
39189 +	++	–	+	+	+	-	-	-	-
37074 +	-	-	+	+	-	-	-	-	-
10952 +	++	-	-	-	-	-	-	-	-
11363 +	-	-	-	-	-	-	-	-	-
39583 +	+	–	++	+	++	+++	---	-	-
17250 +	+	--+	+++	+++	+++	-	-	-	-
39360 +	-	-	-	-	-	-	-	-	-
38802 +	-	-	-	-	-	-	-	-	-
11173 +	+	-	-	-	-	-	-	-	-
39364 +	-	-	-	-	-	-	-	-	-
39584 +	++	-	-	-	-	-	-	-	-

11020 +	++	-	-	-	-	-	-	-	-
17842 +	-	-	-	-	-	-	-	-	-
14105 +	++	-	-	-	-	-	-	-	-
13954 +	++	-	-	-	-	-	-	-	-
39174 +	-	-	-	-	-	-	-	-	-
13911 +	+	-	-	-	-	-	-	-	-
39585 +	+	-	-	-	-	++	−−	-	+
39586 +	-	−−+	+++	+++	+++	-	-	-	-
39587 +	+	−−+	+++	+++	+++	-	-	-	-
11214 +	-	-	-	-	-	-	-	-	-
39012 +	+	−	+	+	+	+	−−	-	-
12387 +	+	-	-	-	-	-	-	-	-
39474 +	+	-	-	-	-	-	−	-	-
38441 +	-	−	+	+	+	-	-	-	-
14069 +	+	-	-	-	-	+	−	-	-
38317 +	++	-	-	-	-	-	-	-	-
39588 +	++	-	-	-	-	-	-	-	-
12162 +	-	-	-	-	-	-	-	-	-
38881 +	-	-	-	-	-	-	-	-	-
39406 +	-	-	-	-	-	-	-	-	-
39589 +	++	-	-	-	-	-	-	-	-
39243 +	++	-	-	-	-	-	-	-	-
39138 +	+	−−+	+	+++	+++	+++	-	-	-
39590 +	+	-	-	-	-	-	−	-	-
39080 +	-	-	-	-	-	-	-	-	-
14211 +	++	-	-	-	-	-	-	-	-
20371 +	-	−	+	-	-	-	-	-	-
39591 +	+	−−+	+++	+++	+++	-	-	-	-
39592 +	-	−−+	+	+++	+	+	−	+++	++
39593 +	+	-	-	-	-	-	-	-	-
39326 +	+	-	-	-	-	-	-	-	-
39594 +	++	-	-	-	-	-	-	-	-
16068 +	+	-	-	-	-	-	-	-	-

39595 +	+	-	-	-	-	-	-	-	-
13862 +	++	-	-	-	-	-	-	-	-
13911 +	+	-	-	-	-	-	-	-	-
39079 +	+	--+	+++	+++	+++	+	-	-	-
13828 +	+	-	-	-	-	+	--	-	-
39323 +	++	-	-	-	-	-	-	-	-
39596 +	-	-	-	++	-	-	-	-	-
39357 +	++	-	-	-	-	+	-	-	-
39597 +	-	-	-	-	-	-	-	-	-
39343 +	+	-	-	-	-	-	-	-	-
38890 +	++	-	-	-	-	+	-	-	-
39510 +	++	-	-	-	-	-	-	-	-
14089 +	+	-	-	-	-	-	-	-	-
39598 +	+	-	-	-	-	-	-	-	-
16627 +	++	-	-	-	-	+	-	-	-
11120 +	++	-	-	-	-	-	-	-	-
16585 +	++	-	-	-	+	-	-	-	-
39599 +	+	-	-	-	-	-	-	-	-
39600 +	-	--+	+++	+++	+++	+	-	-	-
14479 +	++	-	-	-	-	-	-	-	-
13951 +	+	--+	+++	+++	+++	-	-	-	-
11450 +	-	-	-	-	-	-	-	-	-
39314 +	++	-	-	-	-	-	-	-	-
37305 +	+	--+	+++	+++	+++	-	-	-	-
39601 +	+	-	-	-	-	-	-	-	-
16659 +	+	-	-	-	-	-	-	-	-
39602 +	+	--+	+++	+++	+++	+	-	-	-
14298 +	++	-	-	-	-	-	-	-	-
11508 +	++	-	-	-	-	-	-	-	-
14088 +	+	-	-	-	-	-	-	-	-
14211 +	+	-	-	-	-	-	-	-	-
39171 +	++	-	-	-	-	-	-	-	-
39603 +	+	--+	+++	+++	+++	-	-	-	-

39604 +	++	-	-	-	-	-	-	-	-
38753 +	++	-	-	-	-	-	-	-	-
39321 +	++	--+	+++	+++	+++	+	-	-	-
39605 +	+	--+	+++	+++	+++	-	-	-	-
39606 +	-	-	-	-	-	-	-	-	-
19247 +	-	-	-	-	-	-	-	-	-
39306 +	++	-	-	-	-	-	-	-	-
39102 +	++	-	-	-	-	-	-	-	-
13612 +	+	-	+	+	+	+++	---	-	-
11333 +	+	-	-	-	-	-	-	-	-
12411 +	-	-	-	-	-	-	-	-	-
13739 +	++	-	-	-	-	-	-	-	-
11036 +	++	-	-	-	-	-	-	-	-
39607 +	-	-	-	-	-	-	-	-	-
37860 +	++	-	-	-	-	-	-	-	-
18050 +	-	-	-	-	-	-	-	-	-
38940 +	++	-	-	-	-	-	-	-	-
39121 +	-	-	-	-	-	-	-	-	-
39608 +	+	--+	+++	+++	+++	-	-	-	-
11776 +	-	-	-	-	-	-	-	-	-
14515 +	+	-	-	-	-	-	-	-	-
39609 +	-	--+	+	+++	-	-	-	+++	-
39610 +	-	-	+	-	+	-	-	-	-
38699 +	++	-	-	-	-	-	-	-	-
39611 +	+	--+	+++	+++	+++	+	-	-	-
39612 +	-	-	-	-	-	-	-	-	-
39613 +	+	--+	+++	+++	+++	-	-	-	-
12300 +	++	-	-	-	-	-	-	-	-
38270 +	++	-	-	-	-	-	-	-	-
39614 +	-	-	-	+	-	+	-	-	-
39107 +	+	--+	+++	-	-	-	-	+++	-
39615 +	+	-	-	-	-	-	-	-	-
38214 +	-	--	-	-	-	+	-	-	-

39616	+	++	-	-	-	-	+	–	-	-
38864	+	++	-	-	-	-	-	-	-	-
17902	+	+	-	-	-	-	-	-	-	-
16604	+	-	-	-	-	-	-	-	-	-
39617	+	-	--	+++	++	++	+++	---	-	-
38968	+	-	--	-	-	-	-	-	-	-
39618	+	+	-	-	-	-	-	-	-	-
39619	+	+	-	-	-	-	-	-	-	-
13774	+	+	-	-	-	-	+	–	-	-
16639	+	-	--+	+	+++	++	+++	--	-	-
39620	+	+	-	-	-	-	-	-	-	-
17363	+	+	--+	+++	+++	+++	-	-	-	-
39621	+	+	-	-	-	-	-	-	-	-
39527	+	-	-	-	-	-	-	-	-	-
17603	+	+	-	-	-	-	-	-	-	-
39622	+	+	--+	+	-	-	-	-	-	+
39432	+	+	–	+	+	-	++	--	-	-
38946	+	++	-	-	-	-	-	-	-	-
39623	+	-	-	-	-	-	-	-	-	-
11329	+	+	-	-	-	-	-	-	-	-
39624	+	+	-	-	-	-	-	-	-	-
39574	+	-	--+	+	++	-	-	-	-	-
13751	+	++	-	-	-	-	-	-	-	-
12501	+	-	-	-	-	-	-	-	-	-
39625	+	-	-	-	-	+	-	-	-	-
19681	+	+	-	-	-	-	-	-	-	-
14191	+	++	-	-	-	-	+	–	-	-
17982	+	+	--+	+++	+++	+++	-	–	-	-
14265	+	++	-	-	-	-	+	--	-	-
39626	+	+	-	-	-	-	-	–	-	-
39627	+	+	--+	+++	+++	+++	+	–	-	+++
18773	+	-	-	-	-	-	-	-	-	-
39032	+	+	--+	+++	+++	+++	+	–	-	-

38951 +	++	-	-	-	-	-	-	-	-
13580 +	++	-	-	-	-	-	-	-	-
12575 +	-	-	-	-	-	-	-	-	-
14282 +	++	-	-	-	-	-	-	-	-
39182 +	++	-	-	-	-	-	-	-	-
38797 +	++	-	-	-	-	-	-	-	-
17063 +	-	–	+	-	-	-	-	-	-
37508 +	++	–-+	+++	+++	+++	+	–	-	-
11989 +	+	-	-	-	-	-	-	-	-
38990 +	-	-	-	-	-	-	-	-	-
39628 +	++	-	+	-	-	-	-	-	-
39449 +	-	-	-	-	-	-	-	-	-
11638 +	++	-	-	-	-	-	-	-	-
39629 +	+	–-+	+++	+++	+++	+	–	-	-
38754 +	++	-	-	-	-	-	-	-	-
12370 +	+	-	-	-	-	-	-	-	-
13972 +	++	-	-	-	-	++	––	-	-
39108 +	+	-	-	-	-	-	-	-	-
39264 +	++	-	-	-	-	-	-	-	-
13783 +	+	-	-	-	-	-	-	-	-
39630 +	++	-	-	-	-	-	-	-	-
39631 +	-	–-+	+	+++	-	-	-	-	-
39632 +	+	–-+	+++	+++	+++	-	-	-	-
13959 +	++	–	+	+	+	+	–	+++	-
39633 +	-	-	-	-	-	-	-	-	-
14545 +	++	-	-	-	-	-	-	-	-
17155 +	++	-	-	-	-	-	-	-	-
16135 +	-	-	-	-	-	-	-	-	-
38660 +	+	––	+	+	+	+++	–––	-	-
39634 +	-	-	-	-	-	-	-	-	-
39635 +	+	–-+	+++	+++	+++	-	-	-	-
39636 +	+	-	-	-	-	-	-	-	-
39379 +	-	-	-	-	-	+	–	-	-

36983	+	-	-	-	-	-	-	-	-
39637	+	+	--+	+++	+++	+++	+	-	-
39557	+	-	-	-	-	-	-	-	-
11246	+	++	-	-	-	-	-	-	-
11776	+	-	-	-	-	-	-	-	-
39175	+	-	-	-	-	-	-	-	-
39638	+	++	-	-	-	-	-	-	-
37899	+	++	-	-	-	-	+	-	-
14376	+	+	-	-	-	-	-	-	-
12868	+	-	-	-	-	-	-	-	-
39639	+	+	-	-	-	-	-	-	-
13872	+	+	-	-	-	-	-	-	-
39640	+	-	–	-	-	-	-	-	-
13659	+	+	-	-	-	-	-	-	-
39641	+	+	--+	+++	+++	+++	+	–	-
38606	+	++	-	-	-	-	-	-	-
39642	+	+	-	-	-	-	-	-	-
12205	+	-	-	-	-	-	-	-	-
39643	+	++	-	-	-	-	-	-	-
39644	+	-	–	+	+	++	+++	---	-
38881	+	-	-	-	-	-	-	-	-
39645	+	++	-	-	-	-	+	–	-
38917	+	++	-	-	+	+	+	–	-
10966	+	++	--+	+++	+++	+++	+	–	-
16641	+	-	-	-	-	-	-	-	-
39646	+	++	-	-	-	-	-	-	-
39647	+	+	--+	+++	+++	+++	+	-	-
39406	+	-	-	-	-	-	-	-	-
39648	+	+	-	-	-	-	-	-	-
13898	+	++	-	-	-	-	-	-	-
39649	+	+	--+	+++	+++	+++	+	-	-
39650	+	++	-	-	-	-	-	-	-
39651	+	+	--+	+++	+++	+++	-	-	-

39652 +	+	−−	+++	+	++	-	-	-	-
36771 +	-	−−+	+	+++	-	+	−	-	-
17431 +	++	-	+	-	-	-	-	-	-
38399 +	++	-	-	-	-	-	-	-	-
18216 +	+	-	-	-	-	-	-	-	-
39304 +	-	−−	+	+++	+	+	−	-	-
39604 +	++	-	-	-	-	-	-	-	-
39119 +	+	−−+	+++	+++	+++	-	−	-	-
11890 +	+	-	-	-	-	-	-	-	-
13739 +	++	-	-	-	-	-	-	-	-
39653 +	++	-	-	-	-	-	-	-	-
39654 +	-	-	-	-	-	-	-	-	-
39655 +	+	-	-	-	-	-	-	-	-
17608 +	++	-	-	-	-	-	-	-	-
18789 +	-	-	-	-	-	-	-	-	-
39656 +	+	−−+	+++	+++	+++	+	-	-	-
17557 +	-	−−	-	++	-	-	-	-	-
39179 +	-	-	-	-	-	-	-	-	-
39203 +	-	-	-	-	-	-	-	-	-
39657 +	-	-	-	-	-	-	-	-	-
39319 +	+	−−+	+++	+++	+++	+	−	-	-
39402 +	+	-	-	-	-	-	-	-	-
13946 +	++	-	-	-	-	-	-	-	-
39062 +	+	−−+	+++	+++	+++	+	−	-	-
39639 +	++	-	-	-	-	-	-	-	-
12189 +	+	-	-	-	-	-	-	-	-
11594 +	-	-	-	-	-	-	-	-	-
39349 +	++	-	-	-	-	-	-	-	-
39658 +	+	−−+	+++	+++	+++	-	−	-	-
13802 +	++	-	-	-	-	-	-	-	-
12796 +	-	-	-	-	-	-	-	-	-
39659 +	+	-	-	-	-	-	-	-	-
13939 +	++	-	-	-	-	-	-	-	-

16611 +	+	-	-	-	-	-	-	-	-
39660 +	+	---+	+++	+++	+++	+	-	+++	-
39339 +	+	-	-	-	-	-	-	-	-
39661 +	+	---+	+++	+++	+++	+	-	-	-
38666 +	-	---+	++	+++	++	+	-	-	-
14183 +	+	-	-	-	-	-	-	-	-
16617 +	-	-	-	-	-	-	-	-	-
14265 +	++	-	-	-	-	+	-	-	-
39641 +	++	---+	+++	+++	+++	-	-	-	-
39662 +	++	---+	+++	+++	+++	+	-	-	-
39663 +	-	-	-	-	+	+	-	-	-
13789 +	+	-	-	-	-	+	-	-	-
17141 +	+	---+	+++	+++	+++	-	-	-	-
14695 +	+	-	-	-	-	-	-	-	-
14681 +	++	-	-	-	-	-	-	-	-
13517 +	++	-	-	-	-	-	-	-	-
39664 +	+	-	-	-	-	+	-	-	-
39550 +	++	-	-	-	-	-	-	-	-
39665 +	++	-	-	-	-	-	-	-	-
39263 +	++	-	-	-	-	-	-	-	-
38357 +	-	-	-	-	-	-	-	-	-
14034 +	++	-	-	-	-	++	--	-	-
11019 +	-	-	+	+	-	+	-	-	-
13946 +	++	-	-	-	-	-	-	-	-
39666 +	+	-	+	+	+	+++	---	-	-
38152 +	++	-	-	-	-	-	-	-	-
39667 +	+	---+	+++	+++	+++	+	-	-	-
13719 +	+	-	-	-	-	-	-	-	-
13982 +	++	-	-	-	-	-	-	-	-
39664 +	++	-	-	-	-	-	-	-	-
39668 +	+	---+	+++	+++	+++	-	-	-	-
13976 +	++	-	-	-	-	-	-	-	-
39120 +	+	---+	+++	+++	+++	+	-	-	-

39646 +	++	-	-	-	-	-	-	-	-
39163 +	-	-	-	-	-	-	-	-	-
13912 +	++	-	-	-	-	-	-	-	-
39669 +	-	-	-	-	-	-	-	-	-
14062 +	++	-	-	-	-	-	-	-	-
39082 +	+	-	-	-	-	-	-	-	-
39102 +	++	-	-	-	-	-	–	-	-
14074 +	++	-	-	-	-	-	-	-	-
39670 +	-	–	+	+	+	-	-	-	-
39671 +	+	–+	+++	+++	+++	-	–	-	-
12602 +	++	-	-	-	-	-	-	-	-
39672 +	+	–+	+++	+++	+++	+	-	-	-
39673 +	+	-	-	-	-	-	-	-	-
17247 +	-	–+	+	+++	+	++	––	-	-
39674 +	+	–+	+++	+++	+++	-	-	-	-
13640 +	++	-	-	-	+	++	–	-	-
38913 +	++	-	-	-	-	-	-	-	-
39675 +	+++	-	-	-	-	-	-	-	-
39676 +	-	-	-	-	-	-	-	-	-
38975 +	+	–+	+++	+++	+++	+	–	-	-
14373 +	+	-	-	-	-	-	-	-	-
16596 +	++	-	-	-	-	-	-	-	-
39585 +	+	-	-	-	-	++	––	-	-
39677 +	+	–+	+++	+++	+++	-	-	-	-
12032 +	-	-	-	-	-	-	-	-	-
38826 +	-	-	-	-	-	-	-	-	-
39678 +	+	–+	+++	+++	+++	+	–	-	-
38544 +	+	–	+	+	+	+++	–––	-	-
39679 +	-	–	-	+	-	-	-	-	-
39680 +	++	-	-	-	-	-	-	-	-
39681 +	+	-	-	-	-	-	-	-	-
38599 +	-	-	-	-	-	-	-	-	-
39265 +	++	-	-	-	-	-	-	-	-

39682 +	+	–	+	+	+	+++	---	.	.
39683 +	++	.	.	.	.	.	.	.	.
39625 +	.	.	.	+	.	.	.	.	.
39684 +	+	–	+	+	+	+++	---	++	.
39685 +	++	.	.	.	.	.	.	.	.
39686 +	++	.	.	.	.	.	.	.	.
16092 +	.	.	.	.	.	.	.	.	.
39687 +	.	.	.	.	.	.	.	.	.
39520 +	+	.	.	.	.	.	.	.	.
39153 +	++	.	.	.	.	.	.	.	.
39688 +	++	.	.	.	.	.	.	.	.
39689 +	+	--+	+++	+++	+++	.	–	.	.
39339 +	++	.	.	.	.	.	.	.	.
13598 +	.	.	.	.	.	.	.	.	.
11942 +	.	.	.	.	.	.	.	.	.
39690 +	+	--+	+++	+++	+++	.	–	.	.
39259 +	.	--+	.	+	.	.	.	.	.
39691 +	++	.	+	+	+	+	–	.	.
39308 +	+	.	.	.	.	.	.	.	.
38978 +	+	--+	+++	+++	+++	+	–	.	.
13774 +	+	.	.	.	.	+	–	.	.
17668 +	++	.	.	.	.	.	.	.	.
13726 +	+	.	.	.	.	+	–	.	.
38468 +	+	--	++	++	++	+++	---	.	.
39692 +	++	.	.	.	.	.	.	.	.
39693 +	+	.	.	.	.	.	.	.	.
16646 +	.	.	.	.	.	+	–	.	.
39694 +	+	.	.	.	.	.	.	.	.
38697 +	+	.	.	.	.	.	.	.	.
39695 +	+	.	.	.	.	.	.	.	.
39696 +	+	--+	+++	+++	+++	.	–	.	.
39697 +	.	--+	+++	+++	+++	.	–	.	.
39005 +	++	.	.	.	.	.	.	.	.

39698	+	+	−−+	+++	+++	+++	-	−	-	-
39699	+	-	-	-	-	-	-	-	-	-
39055	+	++	-	-	-	-	-	-	-	-
39700	+	+	-	-	-	-	-	-	-	-
11161	+	-	-	-	-	-	-	-	-	-
13848	+	++	-	-	-	-	-	-	-	-
14620	+	++	-	-	-	-	-	-	-	-
13696	+	++	-	-	-	-	-	-	-	-
15738	+	+	-	-	+	-	+++	−−−	-	-
38634	+	+	-	-	-	-	-	-	-	-
39692	+	++	-	-	-	-	-	-	-	-
39701	+	+	−−+	+++	+++	+++	+	−	-	-
39702	+	+	−−+	+++	+++	+++	+	−	-	-
13783	+	+	-	-	-	-	-	-	-	-
39373	+	+	−−+	+++	+++	+++	-	-	-	-
39703	+	-	−−	++	++	++	-	-	-	-
39704	+	++	-	-	-	-	-	-	-	-
39421	+	-	-	-	-	-	-	-	-	-
39705	+	+	-	-	-	-	-	-	-	-
39663	+	-	-	-	-	-	+	−	-	-
39706	+	+	-	-	-	-	+	−	-	-
39534	+	+	-	-	-	-	-	-	-	-
19320	+	+	−−+	+++	+++	+++	-	-	-	-
39707	+	-	-	-	++	-	-	-	-	-
39210	+	-	-	-	-	-	-	-	-	-
39537	+	+	-	-	-	-	-	-	-	-
14303	+	++	-	-	-	-	-	-	-	-
14338	+	+	-	-	-	-	-	-	-	-
13681	+	+	-	-	-	-	-	-	-	-
13690	+	+	-	-	-	-	-	-	-	-
13856	+	++	-	-	-	-	+	−−	-	-
39708	+	-	-	-	-	-	-	-	-	-
39709	+	+	−−+	+++	+++	+++	+	-	-	-

39710	+	-	-	-	-	-	-	-	-
38466	+	+	-	-	-	-	-	-	-
10984	+	+	–	+	+	+	+	–	-
39711	+	++	-	-	-	-	-	-	-
17962	+	+	-	-	-	-	-	-	-
14024	+	++	-	-	-	-	++	–	-
39143	+	+	-	-	-	-	-	-	-
11567	+	+	-	-	-	-	-	-	-
37513	+	++	-	-	-	+	-	-	-
39458	+	+	-	-	-	-	-	-	-
11481	+	+	-	-	-	-	-	-	-
39712	+	+	–+	+++	+++	+++	-	-	-
39713	+	-	-	-	-	-	-	-	-
39706	+	+	-	-	-	-	+	–	-
39176	+	++	-	-	-	-	-	-	-
16596	+	++	-	-	-	-	-	-	-
39643	+	++	-	-	-	-	-	-	-
38625	+	++	–	+	+	+	++	––	-
17429	+	++	-	-	-	-	-	-	-
14038	+	+	-	-	-	-	-	-	-
20439	+	+	-	-	-	-	-	-	-
14614	+	++	-	-	-	-	-	-	-
39714	+	-	-	-	++	-	-	-	-
39715	+	++	–+	+++	+++	+++	+	–	-
39716	+	++	-	-	-	-	-	-	-
12502	+	-	-	-	-	-	-	-	-
38185	+	+	–+	+++	+++	+++	-	–	-
38763	+	++	-	-	+	+	+	–	-
14088	+	+	-	-	-	-	-	-	-
39059	+	++	-	-	-	-	-	-	-
38476	+	-	-	-	-	-	-	-	-
39223	+	+	–	+	+	+	+++	–––	-
38156	+	-	––	-	+	+	-	-	-

38097 +	++	-	-	-	-	-	–	-	-
39717 +	+	-	-	-	-	-	-	-	-
39007 +	++	-	-	-	-	-	-	-	-
39718 +	++	–+	+++	+++	+++	++	-	-	-
39719 +	+	-	-	-	-	-	-	-	-
14670 +	+	-	-	-	-	-	-	-	-
39720 +	+	–+	+++	+++	+++	+	–	-	-
39721 +	+	-	-	-	-	+	–	-	-
39722 +	+	-	-	-	-	-	-	-	-
39723 +	+	-	-	-	-	-	-	-	-
39589 +	++	-	-	-	-	-	-	-	-
38769 +	++	–	+	+	+	++	––	-	-
39724 +	-	–+	+++	+++	+++	-	-	-	-
18238 +	-	–+	+++	+++	+++	-	-	-	-
39725 +	++	–+	+++	+++	+++	-	-	-	-
39489 +	+	-	-	-	-	-	-	-	-
39414 +	+	–+	+++	+++	+++	-	-	-	-
16031 +	+	-	-	-	-	-	-	-	-
38186 +	-	–+	+	++	+	-	-	-	-
11753 +	++	-	-	-	-	-	-	-	-
11251 +	++	-	-	-	-	-	-	-	-
39726 +	++	-	-	-	-	-	-	-	-
39727 +	-	-	-	-	-	+	–	-	-
39728 +	++	-	-	-	-	-	-	-	-
39729 +	+	-	-	-	-	-	-	-	-
39440 +	++	-	-	-	-	-	-	-	-
11323 +	+	-	-	-	-	-	-	-	-
13826 +	+	-	-	-	-	-	-	-	-
39730 +	+	-	-	-	-	-	-	-	-
39731 +	+	-	-	-	-	-	-	-	-
39732 +	+	–+	+++	+++	+++	+	–	-	+++
39620 +	+	-	-	-	-	-	-	-	-
39733 +	-	-	-	-	-	-	-	-	-

39734 +	+	--+	+++	+++	+++	+	-	.	.
39735 +	++	--+	+++	+++	+++	+	-	.	.
11611 +	++	.	.	.	.	.	.	.	.
38633 +	++	.	.	.	.	.	.	.	.
11964 +	.	.	.	.	.	.	.	.	.
39736 +	+	--+	+++	+++	+++	+	-	.	.
39737 +	.	-	.	+	.	+	-	.	.
14149 +	++	.	.	.	.	.	.	.	.
39134 +	.	-	+	+	.	+	-	.	.
17819 +	+	.	.	.	.	.	.	.	.
39136 +	++	.	.	+	+	++	--	.	.
13550 +	++	.	.	.	.	.	.	.	.
39738 +	.	--+	.	++	.	.	.	.	.
39739 +	+	.	.	.	.	.	.	.	.
39509 +	+	--+	+++	.	.	.	.	+++	.
39740 +	+	.	.	.	.	.	.	.	.
11337 +	+	.	.	.	.	.	.	.	.
39741 +	+	--+	+++	+++	+++	.	.	.	.
39570 +	.	--+	+	+++	+	+	-	.	.
39655 +	+	.	.	.	.	.	.	.	.
39456 +	.	.	.	.	.	.	.	.	.
39742 +	.	.	.	.	.	.	.	.	.
17050 +	+	.	.	.	.	.	.	.	.
37436 +	+	.	.	.	.	.	.	.	.
11788 +	+	.	.	.	.	.	.	.	.
17237 +	+	--+	+++	+++	+++	.	.	.	.
39183 +	+	.	.	.	.	.	.	.	.
39743 +	.	.	.	.	.	.	.	.	.
17276 +	+	--+	+++	+++	+++	+	.	.	.
16625 +	+	.	.	.	.	.	.	.	.
38441 +	.	.	.	.	.	.	.	.	.
39744 +	+	--+	+++	+++	+++	+++	---	.	.
12473 +	.	.	.	.	.	.	.	.	.

39542 +	+	−−	+	-	-	-	-	-	-
39654 +	-	-	-	-	-	-	-	-	-
37877 +	+	−−+	+++	+++	+++	+	-	-	-
39745 +	-	−	-	-	-	-	-	-	-
17403 +	+	−−+	+++	+++	+++	-	-	-	-
39746 +	-	−−+	+	++	-	-	-	-	-
39747 +	+	-	-	-	-	-	-	-	-
13923 +	++	-	-	-	-	-	-	-	-
39340 +	++	-	-	-	-	-	-	-	-
38846 +	-	-	-	-	-	-	-	-	-
38700 +	++	-	-	-	-	-	-	-	-
39455 +	++	-	-	-	-	-	-	-	-
15957 +	++	-	-	-	-	-	-	-	-
39748 +	-	-	-	-	-	-	-	-	-
39020 +	+	-	-	-	-	-	-	-	-
38775 +	-	−	-	-	-	-	-	-	-
39749 +	++	−−+	+++	+++	+++	-	-	-	-
12134 +	-	-	-	-	-	-	-	-	-
39750 +	+	-	-	-	-	-	-	-	-
38864 +	++	-	-	-	-	-	-	-	-
14444 +	+	-	-	-	-	-	-	-	-
11377 +	++	-	-	-	-	-	-	-	-
37970 +	++	-	-	-	-	-	-	-	-
39751 +	+	−	+	+	+	+++	−−−	-	-
17514 +	-	-	-	+	-	-	-	-	-
38448 +	++	-	-	-	-	-	-	-	-
39752 +	-	−−+	+++	+++	+++	+	-	-	-
39753 +	+	−	+	+	+	+++	−−−	+++	+++
11487 +	-	-	-	-	-	-	-	-	-
39754 +	+	−−+	+++	+++	+++	+	−	-	+++
13553 +	++	-	-	-	-	+	−	-	-
39755 +	+	-	-	-	-	++	−−	-	-
38889 +	++	-	-	-	-	-	−	-	-

39756 +	++	-	-	-	-	-	-	-	-
39757 +	+	-	-	-	-	-	-	-	-
13681 +	+	-	-	-	-	-	-	-	-
39758 +	+	--+	+++	+++	+++	+	-	-	-
20380 +	+	-	-	-	-	-	-	-	-
14405 +	++	-	-	-	-	-	-	-	-
14093 +	+	-	-	-	-	-	-	-	-
39156 +	++	-	-	-	-	-	-	-	-
14387 +	+	-	-	-	+	+	–	-	-
39759 +	+	--+	+++	+++	+++	-	-	-	-
39760 +	-	–	+	+++	+	-	-	-	-
11933 +	-	-	-	-	-	-	-	-	-
39761 +	+	--+	+++	+++	+++	-	-	-	-
17755 +	-	-	+	-	-	+	–	-	-
17835 +	-	–	-	-	-	-	-	-	-
39421 +	-	-	-	-	-	-	-	-	-
13964 +	+	-	-	-	-	-	-	-	-
39762 +	-	-	-	-	-	-	-	-	-
12023 +	++	-	-	-	-	-	-	-	-
39763 +	++	--+	+++	+++	+++	+	-	-	-
13844 +	++	-	-	-	-	-	-	-	-
12687 +	-	-	-	-	-	-	-	-	-
39764 +	+	--+	+++	+++	+++	+	–	-	-
39765 +	-	-	-	-	-	-	-	-	-
39714 +	-	–	-	++	-	-	-	-	-
39553 +	+	-	-	-	-	+	–	-	-
14443 +	++	-	-	-	-	-	-	-	-
39530 +	+	-	-	-	-	-	-	-	-
39766 +	+	-	-	-	-	-	-	-	-
39767 +	-	-	-	-	-	-	-	-	-
39768 +	+	-	-	-	-	-	–	-	-
16026 +	+	-	-	-	-	-	-	-	-
39769 +	++	-	-	-	-	+	–	-	-

39082 +	++	-	-	-	-	-	-	-	-
38173 +	++	--+	+++	+++	+++	-	-	-	-
39770 +	-	-	-	-	-	-	-	-	-
13181 +	++	-	-	-	-	-	-	-	-
38944 +	-	-	-	-	-	-	-	-	-
39662 +	+	--+	+++	+++	+++	+	-	-	-
39290 +	-	-	-	-	-	-	-	-	-
39417 +	+	-	-	-	-	-	-	-	-
39771 +	++	--+	+++	+++	+++	-	-	-	-
17941 +	-	-	-	-	-	-	-	-	-
14175 +	++	-	-	-	-	-	-	-	-
39397 +	++	-	-	-	-	-	-	-	-
39310 +	++	-	-	-	-	+	-	-	-
39733 +	-	-	-	-	-	-	-	-	-
39772 +	-	-	-	-	-	-	-	-	-
39773 +	+	-	-	-	-	+	-	-	-
39774 +	-	--+	+++	+++	+++	-	-	-	-
16574 +	+	-	+	+	-	-	-	-	-
38327 +	-	-	+	-	-	+	-	-	-
11607 +	-	-	-	-	-	-	-	-	-
39769 +	++	-	-	-	-	+	-	-	-
10998 +	+	-	-	-	-	-	-	-	-
14345 +	+	-	-	-	-	-	-	-	-
39775 +	++	-	-	-	-	-	-	-	-
13655 +	++	-	-	-	-	-	-	-	-
39776 +	+	--+	+++	+++	+++	+	-	-	-
14507 +	+	-	-	-	-	-	-	-	-
39777 +	+	-	+	+	+	-	-	-	-
39778 +	+	--+	+++	+++	+++	-	-	+++	-
12098 +	-	-	-	-	-	-	-	-	-
11577 +	++	-	+	-	+	-	-	-	-
37057 +	-	-	-	-	-	-	-	-	-
14813 +	+	-	-	-	-	-	-	-	-

38765	+	-	-	+	+	+	++	---	-	-
39463	+	+	--+	+++	+++	+++	+	-	-	-
11890	+	+	-	-	-	-	-	-	-	-
11339	+	+	-	-	-	-	-	-	-	-
17377	+	-	--+	+++	+++	+++	-	--	+	-
39469	+	++	-	-	-	-	-	-	-	-
39779	+	+	-	-	-	-	-	-	-	-
13746	+	++	-	-	-	-	-	-	-	-
13637	+	+	-	-	-	-	+	-	-	-
39780	+	+	--+	+++	+++	+++	-	-	-	-
17620	+	-	-	-	-	-	-	-	-	-
14006	+	+	-	-	-	-	-	-	-	-
38344	+	++	-	-	-	-	-	-	-	-
39700	+	++	-	-	-	-	-	-	-	-
39781	+	+	-	-	-	-	-	-	-	-
39358	+	-	-	-	-	-	-	-	-	-
39782	+	-	--+	+	++	+	-	-	-	-
39783	+	-	-	-	-	-	-	-	-	-
19961	+	-	-	-	-	-	-	-	-	-
18284	+	-	--+	-	+++	-	-	-	-	-
39784	+	+	-	-	-	-	-	-	-	-
11992	+	-	-	-	-	-	-	-	-	-
39785	+	+	-	-	-	-	-	-	-	-
39614	+	+	-	-	-	-	-	-	-	-
38092	+	-	-	+	-	-	-	-	-	-
11921	+	-	-	-	-	-	-	-	-	-
17491	+	+	--+	+++	+++	+++	-	-	-	-
39552	+	++	-	-	-	-	-	-	-	-
18014	+	++	-	-	-	-	-	-	-	-
11933	+	-	-	-	-	-	-	-	-	-
39475	+	+	-	-	-	-	-	-	-	-
39786	+	-	-	-	+	-	-	-	-	-
39787	+	+	--+	+++	+++	+++	-	-	-	-

39788	+	-	-	-	-	-	-	-	-
11354	+	-	-	-	-	-	-	-	-
39789	+	-	-	-	-	-	-	-	-
39790	+	+++	+++	+++	+++	-	-	-	-
39791	+	-	-	-	-	-	-	-	-
39792	++	-	-	-	-	-	-	-	-
39793	+	+++	+++	+++	+++	-	-	-	-
38947	+	-	-	-	-	-	-	-	-
39794	+	+++	+++	+++	+++	+	-	-	-
39795	+	-	-	-	-	-	-	-	-
11060	+	-	-	-	-	-	-	-	-
39796	+	-	+	-	-	+	-	-	-
37661	+	-	-	-	-	-	-	-	-
39078	++	-	-	+	+	-	-	-	-
39797	++	-	-	-	-	-	-	-	-
18093	++	-	-	-	-	-	-	-	-
11946	+	-	-	-	-	-	-	-	-
14330	++	-	-	-	-	-	-	-	-
11307	+	-	-	-	-	-	-	-	-
39798	+	-	-	-	-	+	-	-	-
39767	+	-	-	-	-	-	-	-	-
39544	+	-	-	-	-	++	--	++	-
13817	+	-	-	-	-	-	-	-	-
17870	+	-	-	-	-	-	-	-	-
13967	++	-	-	-	-	-	-	-	-
39799	+	+++	+++	+++	+++	-	-	-	-
13743	+	-	-	-	+	++	--	-	-
39800	+	-	-	-	+	-	-	-	-
39801	+	-	-	-	-	-	-	-	-
39802	+	-	-	-	-	-	-	-	-
39567	++	+++	+++	+++	+++	+	-	-	-
17690	+	-	-	-	-	-	-	-	-
18726	++	-	-	-	-	-	-	-	-

13875 +	+	-	-	-	-	-	-	-	-
39803 +	+	-	-	-	-	-	-	-	-
17882 +	-	–	-	+	-	-	-	-	-
39804 +	+	-	-	-	-	-	-	-	-
14681 +	++	-	-	-	-	-	-	-	-
39805 +	+	-	-	-	-	-	-	-	-
17795 +	-	-	-	-	-	-	-	-	-
12273 +	-	-	-	-	-	-	-	-	-
39806 +	++	-	-	-	-	-	-	-	-
39807 +	+	-	-	-	-	-	-	-	-
39808 +	-	-	-	-	-	-	-	-	-
14149 +	++	-	-	-	-	-	-	-	-
39809 +	+	–+	+++	+++	+++	+	–	-	-
39553 +	++	-	-	-	-	+	–	-	-
39642 +	+	-	-	-	-	-	-	-	-
18844 +	-	-	-	-	-	-	-	-	-
11948 +	+	-	-	-	-	-	-	-	-
39810 +	++	-	-	-	-	-	-	-	-
39811 +	-	-	-	-	-	+	–	-	-
14301 +	++	-	-	-	-	-	-	-	-
39812 +	-	-	-	-	-	-	-	-	-
39813 +	+	-	-	-	-	-	-	-	-
39814 +	+	–+	+++	+++	+++	-	-	-	-
39815 +	+	–+	+++	+++	+++	+	–	-	-
16606 +	-	-	-	+	-	-	-	-	-
12667 +	++	-	-	-	-	-	-	-	-
39816 +	++	-	-	-	-	-	-	-	-
11344 +	+	-	-	-	-	-	-	-	-
11698 +	-	-	-	-	-	-	-	-	-
39817 +	++	-	-	-	+	-	-	-	-
38596 +	+	–+	+++	+++	+++	+	–	-	-
14354 +	++	-	+	-	+	-	-	-	-
11235 +	-	-	-	-	-	-	-	-	-

39818 +	-	-	-	-	-	-	-	-	-
39819 +	+	---+	+++	+++	+++	-	-	-	-
39820 +	-	---+	+++	+++	+++	-	-	-	-
17823 +	-	-	-	-	-	-	-	-	-
39027 +	++	-	-	-	-	-	-	-	-
13897 +	++	-	-	-	-	-	-	-	-
18152 +	-	-	-	-	-	-	-	-	-
19192 +	+	---+	+++	+++	+++	-	-	-	-
39821 +	+	-	-	-	-	+	–	-	-
39822 +	++	-	-	-	-	-	-	-	-
39823 +	+	-	-	-	-	-	-	-	-
11165 +	++	-	-	-	-	-	-	-	-
14052 +	++	–	+	+	+	-	-	++	-
39824 +	++	-	-	-	-	-	-	-	-
14295 +	++	-	-	-	-	-	-	-	-
38205 +	-	---+	+	-	+	-	-	-	-
39825 +	+	--	++	++	++	-	-	-	-
39826 +	-	---+	+++	+++	+++	-	-	-	-
39827 +	+	-	-	-	-	-	-	-	-
39828 +	+	-	-	-	-	-	-	-	-
39038 +	++	-	-	-	-	-	-	-	-
14077 +	++	-	-	+	+	-	-	-	-
15964 +	++	-	-	-	-	-	-	-	-
39829 +	+	---+	+++	+++	+++	+	-	-	-
19080 +	+	---+	+++	+++	+++	-	-	-	-
39369 +	-	-	-	-	-	-	-	-	-
39830 +	+	---+	+++	+++	+++	+	-	-	-
39831 +	++	-	-	-	-	-	-	-	-
13555 +	+	-	-	-	-	+	–	-	-
39832 +	+	-	-	-	-	-	-	-	-
13775 +	+	-	-	+	+	++	--	-	-
14065 +	+	-	-	-	-	-	-	-	-
13816 +	++	-	-	-	-	-	-	-	-

39833	+	+	−−+	+++	+++	+++	+	−	-	-
38514	+	-	-	-	-	-	-	-	-	-
37779	+	++	-	+	-	-	-	−	-	-
39834	+	-	-	-	-	-	-	-	-	-
19163	+	+	−−+	+++	+++	+++	-	−	-	-
12025	+	-	-	-	-	-	-	-	-	-
14607	+	++	-	-	-	-	-	-	-	-
39551	+	-	−−+	+	+++	++	+	−	-	-
13830	+	++	-	-	-	-	++	−−	-	-
14515	+	+	-	-	-	-	-	-	-	-
39835	+	+	-	-	-	-	-	-	-	-
14374	+	+	-	-	-	-	-	-	-	-
39836	+	+	-	-	-	-	-	-	-	-
14585	+	+	-	-	-	-	-	-	-	-
16056	+	-	-	-	-	-	-	-	-	-
13769	+	++	-	-	-	-	-	-	-	-
39837	+	+	-	-	-	+	-	−	-	-
17538	+	-	-	-	+	+	-	-	-	-
14141	+	+	-	-	-	-	-	-	-	-
39838	+	+	-	-	-	-	+	−	-	-
10998	+	+	-	+	-	-	-	-	-	-
39380	+	++	-	-	-	-	-	-	-	-
39022	+	++	-	-	-	+	-	-	-	-
38302	+	+	-	-	-	-	-	-	-	-
19655	+	-	-	-	-	-	-	-	-	-
39342	+	+	-	+	-	-	-	-	-	-
14478	+	+	-	-	-	-	-	-	-	-
39839	+	+	−−+	+++	+++	+++	+	−	-	-
39840	+	+	−−+	+++	+++	+++	+	-	-	-
39638	+	++	-	-	-	-	-	-	-	-
39841	+	-	-	-	-	-	-	-	-	-
17196	+	+	−−+	+++	+++	+++	+	-	-	-
39513	+	+	-	-	-	-	-	-	-	-

19269 +	-	-	-	-	-	-	-	-	-
38603 +	-	-	-	-	-	-	-	-	-
39500 +	+	-	-	-	-	-	-	-	-
39782 +	-	--+	+	++	-	-	-	-	-
38317 +	++	-	-	-	-	+	–	-	-
11986 +	-	-	-	-	-	-	-	-	-
39684 +	+	–	+	+	+	+++	---	+++	-
39842 +	+	-	-	-	-	-	-	-	-
38326 +	+	--+	+++	+++	+++	+	-	-	-
14588 +	+	-	-	-	-	-	-	-	-
39843 +	++	--+	+++	+++	+++	-	-	-	-
14206 +	+	-	-	-	-	-	-	-	-
13310 +	++	-	-	-	-	-	-	-	-
39844 +	++	-	-	-	-	-	-	-	-
39845 +	-	-	-	-	-	-	-	-	-
13558 +	+	--+	+++	+++	+++	+	-	-	-
39846 +	-	--+	+++	+++	+++	-	-	+	-
11435 +	+	-	-	-	-	-	-	-	-
39573 +	+	-	-	-	-	-	-	-	-
16079 +	-	-	-	-	-	-	-	-	-
19561 +	-	-	-	-	-	-	-	-	-
38962 +	+	-	-	-	-	-	-	-	-
11804 +	-	-	-	-	-	-	-	-	-
13730 +	++	-	-	-	-	-	-	-	-
17442 +	+	-	+	+	+	++	–	-	-
39847 +	+	--+	+++	+++	+++	+	–	-	-
39576 +	+	-	-	-	-	-	-	-	-
13666 +	+	-	-	-	-	+++	--	-	-
39177 +	++	-	-	-	-	-	-	-	-
39848 +	-	-	-	-	-	-	-	-	-
39691 +	++	-	+	+	+	+	–	-	-
39216 +	++	-	-	-	-	-	-	-	-
39849 +	+	-	-	-	-	-	-	-	-

39850 +	+	-	-	-	-	-	-	-	-
20380 +	+	-	-	-	-	-	-	-	-
16671 +	++	-	-	-	-	-	-	-	-
39333 +	+	-	-	-	-	-	-	-	-
39630 +	++	-	-	-	-	-	-	-	-
39179 +	-	-	-	-	-	-	-	-	-
13844 +	++	-	-	-	-	-	-	-	-
13543 +	+	-	-	-	-	-	-	-	-
19441 +	+	-	-	-	-	-	-	-	-
39262 +	-	-	-	-	-	-	-	-	-
39851 +	+	-	-	-	-	-	-	-	-
39852 +	+	-	-	-	-	-	-	-	-
39642 +	+	-	-	-	-	-	-	-	-
13970 +	+	-	-	-	-	-	-	-	-
39729 +	+	-	-	-	-	-	-	-	-
14001 +	+	-	-	-	-	-	-	-	-
38538 +	++	-	-	-	-	-	-	-	-
39853 +	+	--+	+++	+++	+++	-	-	-	-
13742 +	+	-	-	-	-	-	-	-	-
39854 +	+	-	-	-	-	-	-	-	-
39785 +	+	-	-	-	-	-	-	-	-
12094 +	++	-	-	-	-	-	-	-	-
39855 +	-	-	-	-	-	-	-	-	-
11109 +	++	-	-	-	-	-	-	-	-
39824 +	++	-	-	-	-	-	-	-	-
39518 +	+	-	-	-	-	-	-	-	-
13638 +	++	-	-	-	-	+	-	-	-
39338 +	+	-	-	-	-	-	-	-	-
16035 +	+	-	-	-	-	-	-	-	-
12626 +	-	-	-	-	-	-	-	-	-
17247 +	-	--+	+	+++	+	++	--	-	-
39856 +	+	--+	+++	+++	+++	+	-	-	-
39857 +	-	--+	+++	+++	+++	-	-	-	-

38904 +	++	-	-	+	-	-	-	-	-
39053 +	+	--+	+++	+++	+++	-	-	-	-
39439 +	++	-	+	-	-	+	-	-	-
13645 +	+	-	-	-	-	-	-	-	-
39858 +	+	--+	+++	+++	+++	+	-	-	-
39204 +	+	-	+	+	+	+	-	-	-
39859 +	-	-	-	-	-	-	-	-	-
39282 +	+	-	-	-	-	-	-	-	-
17817 +	+	-	-	-	-	-	-	-	-
13761 +	+	-	-	-	-	-	-	-	-
39860 +	+	-	+	-	-	-	-	-	-
13789 +	+	-	-	-	-	+	-	-	-
39861 +	-	-	-	+	-	-	-	-	-
12473 +	-	-	-	-	-	-	-	-	-
39757 +	++	-	-	-	-	-	-	-	-
11729 +	-	-	-	-	-	-	-	-	-
17594 +	-	-	-	-	-	-	-	-	-
39085 +	++	-	-	-	-	-	-	-	-
14034 +	+	-	-	-	-	++	--	-	-
39556 +	-	--	-	-	-	-	-	-	-
17173 +	++	--+	+++	+++	+++	-	-	-	-
39862 +	+	-	-	-	-	-	-	-	-
39834 +	-	-	-	-	-	-	-	-	-
12070 +	-	-	-	-	-	-	-	-	-
18172 +	-	-	-	-	-	-	-	-	-
39810 +	++	-	-	-	-	-	-	-	-
39863 +	++	--+	+++	+++	+++	+	-	-	-
39864 +	-	-	-	-	-	-	-	-	-
39865 +	+	--+	+++	+++	+++	+	-	-	-
17485 +	-	-	-	-	-	-	-	-	-
39546 +	-	-	-	-	-	-	-	-	-
39866 +	+	--+	+++	+++	+++	+	-	-	-
39867 +	+	--+	+++	+++	+++	-	-	-	-

39805 +	++	-	-	-	-	-	-	-	-
39868 +	+	-	-	-	-	-	-	-	-
39449 +	-	-	-	-	-	-	-	-	-
39869 +	-	-	-	-	-	-	-	-	-
39870 +	+	-	-	-	-	-	-	-	-
17778 +	+	-	-	-	-	-	-	-	-
13923 +	+	-	-	-	-	-	–	-	-
39871 +	+	–+	+++	+++	+++	+	–	-	-
39535 +	-	-	-	+	-	-	-	-	-
39872 +	-	-	-	-	-	-	–	-	-
13531 +	+	-	-	-	-	-	-	-	-
39730 +	+	-	-	-	-	-	-	-	-
14243 +	+	-	-	-	-	-	-	-	-
39251 +	-	–	-	-	-	-	–	-	-
39873 +	-	–	+	-	+	-	-	-	-
39813 +	+	-	-	-	-	-	-	-	-
39874 +	+	–+	+++	+++	+++	-	-	-	-
39875 +	+	-	-	-	-	+	–	-	-
12110 +	+	-	-	-	-	-	-	-	-
39876 +	+	–+	+++	+++	+++	-	-	-	-
39877 +	-	-	-	-	-	-	-	-	-
38885 +	+	-	-	-	-	-	-	-	-
39704 +	++	-	-	-	-	-	-	-	-
39844 +	++	-	-	-	-	-	-	-	-
39878 +	+	–+	+++	+++	+++	+	-	-	-
13857 +	++	-	-	-	-	-	-	-	-
38697 +	+	-	-	-	-	-	-	-	-
14007 +	++	–+	+++	+++	+++	-	–	-	-
39879 +	+	-	-	-	-	-	-	-	-
39245 +	+	–+	+++	+++	+++	+	–	-	-
13804 +	+	-	-	-	-	-	-	-	-
39066 +	+	-	-	-	-	-	-	-	-
14240 +	+	–+	+++	+++	+++	+	-	-	-

39274 +	++	-	-	-	-	-	-	-	-
11020 +	++	-	-	-	-	-	-	-	-
13887 +	++	-	-	-	-	-	-	-	-
39880 +	+	-	-	-	-	-	-	-	-
17942 +	-	-	-	-	-	-	-	-	-
38598 +	++	-	-	-	-	-	-	-	-
11946 +	-	-	-	-	-	-	-	-	-
38961 +	+	-	-	-	-	-	-	-	-
39881 +	+	–	++	++	++	-	-	-	-
39753 +	+	–	+	+	+	+++	---	+++	-
19081 +	+	-	-	-	-	-	-	-	-
11075 +	-	-	+	-	-	-	-	-	-
39882 +	+	-	-	-	-	-	-	-	-
38257 +	++	-	-	-	-	-	-	-	-
39883 +	+	--+	+++	+++	+++	+	-	+++	-
13851 +	+	-	-	-	-	-	-	-	-
39884 +	-	-	-	-	-	-	-	-	-
39885 +	+	–	+	+	+	-	-	-	-
39886 +	++	--+	+++	+++	+++	+	–	-	-
39887 +	+	--+	+++	+++	+++	+	–	-	-
39888 +	+	-	-	-	-	-	-	-	-
39889 +	-	--+	+	+++	+	-	-	+++	-
39890 +	+	-	-	-	-	-	-	-	-
39891 +	+	-	-	-	-	-	-	-	-
39007 +	+	-	-	-	-	-	-	-	-
39738 +	-	--+	-	++	-	-	-	++	-
11449 +	+	-	-	-	-	-	-	-	-
39191 +	+	-	-	-	-	+	–	-	-
13606 +	+	-	-	-	-	-	-	-	-
39713 +	-	-	+	-	-	-	-	-	-
19575 +	-	--+	-	+	-	-	-	-	-
18140 +	-	-	-	+	-	+	–	-	-
13638 +	+	-	-	-	-	+	–	-	-

39892 +	+	-	-	-	-	-	-	-	-
39893 +	-	-	-	-	-	-	-	-	-
39453 +	++	-	-	-	-	-	-	-	-
39894 +	+	-	-	-	-	-	-	-	-
39211 +	-	–	-	-	-	-	–	-	-
38726 +	-	–	+	+	+	++	––	-	-
17070 +	+	-	-	-	-	-	-	-	-
14065 +	+	-	-	-	-	-	-	-	-
11581 +	++	-	-	-	-	-	-	-	-
39895 +	+	–+	+++	+++	+++	+	-	-	-
39422 +	+	–+	+++	+++	+++	+	–	-	-
39896 +	+	–+	+++	+++	+++	-	–	-	-
39257 +	+	-	-	-	-	-	-	-	-
39514 +	-	-	-	-	-	-	-	-	-
14358 +	+	-	-	-	-	-	-	-	-
38693 +	-	-	-	-	-	-	-	-	-
13872 +	+	-	-	-	-	-	-	-	-
39897 +	+	–	+	-	-	-	-	-	-
39482 +	-	-	-	-	-	-	-	-	-
39019 +	+	-	-	-	-	-	-	-	-
39898 +	+	–+	+++	+++	+++	+	–	-	-
39899 +	-	-	-	-	-	-	-	-	-
14011 +	+	-	+	+	-	-	-	-	-
39060 +	-	-	-	-	-	-	-	-	-
39900 +	+	–	-	-	-	+	–	-	-
12070 +	-	-	-	-	-	-	-	-	-
39901 +	+	–+	+++	+++	+++	+	-	-	-
14635 +	++	-	-	-	-	-	-	-	-
39902 +	+	-	-	-	-	-	-	-	-
38548 +	++	-	-	-	-	+	–	-	-
14126 +	++	-	-	-	-	+	–	-	-
15971 +	+	-	-	-	-	+	-	-	-
39615 +	+	-	-	-	-	-	-	-	-

13984 +	++	-	-	-	-	-	-	-	-
16149 +	+	-	-	-	-	-	-	-	-
39903 +	-	--+	+++	+++	+++	-	-	-	-
39904 +	-	-	-	+	-	-	-	-	-
18610 +	+	-	-	-	-	-	-	-	-
11986 +	-	-	-	-	-	-	-	-	-
39311 +	+	--+	+++	+++	+++	+	–	-	-
39905 +	++	--+	+++	+++	+++	-	–	-	-
39322 +	+	–	+	+	+	-	-	-	-
39081 +	-	-	-	-	-	-	-	-	-
11445 +	+	-	-	-	-	+	–	-	-
39906 +	+	--+	+++	+++	+++	+	–	-	-
11638 +	++	-	-	-	-	-	-	-	-
39907 +	+	--+	+++	+++	+++	+	-	-	-
38655 +	+	-	+	-	+	-	–	-	-
39908 +	++	--+	+++	+++	+++	-	–	-	-
17962 +	+	-	-	-	-	-	-	-	-
39909 +	+	--+	+++	+++	+++	+	–	-	-
39271 +	++	-	-	-	-	-	-	-	-
14106 +	+	-	-	-	-	-	-	-	-
18353 +	+	--+	+++	+++	+++	+	–	-	-
39023 +	+	-	-	-	-	-	-	-	-
39889 +	-	--+	+	+++	+	-	-	-	-
18428 +	+	-	-	-	-	-	-	-	-
36749 +	+	--+	+++	+++	+++	-	-	-	-
39421 +	-	-	-	-	-	-	-	-	-
39496 +	-	-	-	-	-	-	-	-	-
38749 +	++	--+	+++	+++	+++	-	-	-	-
39910 +	+	--+	+++	+++	+++	-	–	-	-
38918 +	++	--+	+++	+++	+++	+	–	-	-
39911 +	+	--+	+++	+++	+++	-	–	-	-
39406 +	-	-	-	-	-	-	-	-	-
39912 +	-	-	-	-	-	-	-	-	-

39796 +	++	–	-	-	-	-	-	-	-
39913 +	+	–+	+++	+++	+++	+	-	-	-
38460 +	++	–+	+++	+++	+++	+	–	-	-
39914 +	-	–+	+	+++	+	+++	–	-	-
39406 +	-	-	-	-	-	-	-	-	-
39915 +	+	-	-	-	-	-	-	-	-
39916 +	+	-	-	-	-	-	-	-	-
14350 +	++	-	-	-	-	-	-	-	-
18115 +	-	-	-	-	-	-	-	-	-
39917 +	+	–+	+++	+++	+++	-	-	-	-
38856 +	+	-	-	-	-	-	-	-	-
16640 +	+	-	-	-	-	+	–	-	-
39918 +	+	–+	+++	+++	+++	-	-	-	-
39501 +	+	-	-	-	-	-	-	-	-
39919 +	+	-	-	-	-	-	-	-	-
39920 +	-	-	-	-	-	++	–	-	-
13772 +	++	-	-	-	-	-	-	-	-
11890 +	++	-	-	-	-	-	-	-	-
39921 +	+	–+	+++	+++	+++	-	–	-	-
39037 +	++	-	-	-	-	-	-	-	-
39922 +	++	-	+	-	-	-	-	-	-
39923 +	-	–+	+++	+++	+++	+	–	-	-
13792 +	+	-	-	-	-	+	–	-	-
17702 +	+	-	-	-	+	+	–	-	-
18739 +	-	-	-	-	-	-	-	-	-
18765 +	-	-	-	-	-	-	-	-	-
39821 +	+	-	-	-	-	+	–	-	-
39924 +	++	-	+	-	+	-	-	-	-
39925 +	+	–	+++	+++	+++	+	-	-	-
39926 +	+	–+	+++	+++	+++	-	–	-	-
38738 +	+	–+	+++	+++	+++	+	-	-	-
39927 +	+	-	-	-	-	-	-	-	-
11672 +	+	-	-	-	-	-	–	-	-

39860 +	+	–	+	-	-	-	-	-	-
39561 +	++	-	-	-	-	-	-	-	-
39928 +	++	-	-	-	-	-	-	-	-
39178 +	++	-	-	-	-	-	-	-	-
39929 +	+	––+	+++	+++	+++	-	–	+++	-
39152 +	++	-	-	-	-	-	-	-	-
39882 +	+	-	-	+	-	-	-	-	-
11073 +	++	-	-	-	-	-	-	-	-
14170 +	+	-	-	-	-	-	-	-	-
39695 +	++	-	-	-	-	-	-	-	-
39930 +	+	––+	+++	+++	+++	+	-	-	-
18124 +	+	-	-	-	-	-	-	-	-
39931 +	+	––+	+++	+++	+++	-	-	-	-
39352 +	++	-	-	-	-	-	-	-	-
38598 +	++	-	-	-	-	-	-	-	-
14107 +	+	-	-	-	-	-	-	-	-
39932 +	+	-	-	-	-	-	-	-	-
39531 +	-	–	+	+	-	-	–	-	-
39525 +	+	-	-	-	-	-	-	-	-
11277 +	-	-	-	-	-	-	-	-	-
39933 +	+	-	-	-	-	-	-	-	-
13599 +	+	-	-	-	-	+	––	-	-
13931 +	+	–	+	+	+	+++	–––	+++	-
39934 +	+	––	+	-	+	+++	––	-	-
39935 +	+	––+	+++	+++	+++	+	-	-	-
39598 +	+	-	-	-	-	-	-	-	-
39936 +	+	-	-	-	-	-	-	-	-
39937 +	+	-	-	-	-	-	-	-	-
12088 +	-	-	-	-	-	-	-	-	-
39938 +	+	-	-	-	-	-	-	-	-
39939 +	+	-	-	-	-	-	-	-	-
13592 +	+	-	-	-	-	-	-	-	-
39940 +	+	––+	+++	+++	+++	-	-	-	-

17492 +	+	-	-	-	-	-	-	-	-
17066 +	+	-	-	-	-	-	-	-	-
39941 +	-	-	-	-	-	-	-	-	-
39942 +	+	-	+	-	-	-	-	-	-
38632 +	+	–	++	++	++	+++	---	+++	+++
39943 +	+	--+	+++	+++	+++	-	–	-	-
13809 +	+	-	-	-	-	-	-	-	-
39590 +	+	-	-	-	-	-	-	-	-
39944 +	+	-	-	-	-	-	-	-	-
12327 +	++	--+	+++	+++	+++	-	-	-	-
11799 +	++	-	-	-	-	-	-	-	-
39152 +	+	-	-	-	-	-	-	-	-
39945 +	+	-	-	-	-	-	–	-	-
37513 +	+	-	-	-	-	-	-	-	-
17536 +	++	--+	+++	+++	+++	-	-	-	-
17312 +	+	--+	+++	+++	+++	-	-	-	-
39946 +	+	--+	+++	+++	+++	-	-	-	-
39947 +	+	-	-	-	-	-	-	-	-
39014 +	++	-	-	-	-	-	-	-	-
39619 +	++	-	-	-	-	-	-	-	-
14147 +	+	-	-	-	-	-	-	-	-
11889 +	-	-	-	-	-	-	-	-	-
18220 +	+	--+	+++	+++	+++	+	–	-	-
39063 +	++	-	-	-	-	-	-	-	-
18536 +	-	-	++	-	-	-	-	-	-
38971 +	++	--+	+++	+++	+++	+	-	-	-
39339 +	+	-	-	-	-	-	-	-	-
39948 +	+	-	-	-	-	-	-	-	-
11601 +	+	-	-	-	-	-	-	-	-
39949 +	++	-	-	-	-	-	-	-	-
39375 +	++	-	-	-	-	-	-	-	-
39950 +	+	-	-	-	-	-	-	-	-
39951 +	-	–	-	-	-	-	-	-	-

39547 +	-	–	-	-	-	-	-	-	-
39528 +	-	–	+	-	-	-	-	-	-
11499 +	+	-	-	-	-	-	-	-	-
39657 +	-	-	-	-	-	-	-	-	-
39952 +	+	-	-	-	-	-	-	-	-
17916 +	-	-	-	-	-	-	-	-	-
39915 +	+	-	-	-	-	-	-	-	-
13887 +	++	-	-	-	-	-	-	-	-
39953 +	+	–+	+++	+++	+++	+	–	-	-
14132 +	+	-	-	-	-	-	-	-	-
39954 +	-	–+	+	++	-	-	-	-	-
39461 +	-	–	-	-	-	-	-	-	-
39955 +	+	–+	+++	+++	+++	+	-	-	-
14090 +	+	-	-	-	-	-	-	-	-
17431 +	+	-	-	+	-	-	-	-	-
39956 +	+	–+	+++	+++	+++	-	-	-	-
12195 +	+	-	-	-	-	-	-	-	-
39957 +	++	-	-	-	-	-	-	-	-
11628 +	-	-	-	-	-	-	-	-	-
11027 +	+	-	-	-	-	-	-	-	-
17568 +	-	-	-	-	-	-	-	-	-
13962 +	++	-	-	-	-	+	––	-	-
39958 +	+	–+	+++	+++	+++	+	-	-	-
14531 +	++	-	-	-	-	-	-	-	-
39371 +	++	–+	+++	+++	+++	+	–	-	-
17330 +	+	–+	+++	+++	+++	-	–	-	-
39959 +	+	–+	+++	+++	+++	-	-	-	-
38746 +	++	–+	+++	+++	+++	-	–	-	-
17733 +	+	–+	+++	+++	+++	-	–	-	-
39960 +	+	–	+	+	+	-	-	-	-
16616 +	++	–+	+++	+++	+++	-	-	-	-
13818 +	++	-	-	-	-	-	-	-	-
18682 +	-	-	-	-	-	-	-	-	-

39961 +	+	--+	+++	+++	+++	-	-	-	-
39681 +	+	-	-	-	-	-	-	-	-
13970 +	+	-	-	-	-	-	-	-	-
39962 +	+	-	-	-	-	-	-	-	-
39597 +	-	-	-	-	-	-	-	-	-
11047 +	+	-	-	-	-	-	-	-	-
39071 +	+	--+	+++	+++	+++	+	-	-	-
39583 +	+	-	++	+	+	+++	---	-	-
16601 +	-	-	-	-	-	-	-	-	-
14168 +	++	-	-	-	-	-	-	-	-
18847 +	+	-	-	-	-	-	-	-	-
39963 +	+	-	-	-	-	-	-	-	-
39639 +	+	-	-	-	-	-	-	-	-
39964 +	+	-	-	-	-	-	-	-	-
39719 +	+	-	-	-	-	-	-	-	-
12385 +	+	-	-	-	-	-	-	-	-
39892 +	+	-	-	-	-	-	-	-	-
39965 +	++	-	-	+	+	-	-	-	-
19193 +	-	--+	+++	+++	+++	-	-	-	-
39966 +	++	-	+	-	-	-	-	-	-
39967 +	+	--+	+++	+++	+++	-	-	-	-
39968 +	++	-	-	-	-	-	-	-	-
39464 +	+	--+	+++	+++	+++	-	-	-	-
17264 +	-	-	-	-	-	+	-	-	-
14410 +	+	-	-	-	-	-	-	-	-
39875 +	+	-	-	-	-	+	-	-	-
39354 +	++	-	-	-	-	-	-	-	-
39969 +	+	--+	+++	+++	+++	-	-	-	-
36492 +	++	--+	+++	+++	+++	+	-	-	-
39633 +	-	-	-	-	-	-	-	-	-
39970 +	+	--+	+++	+++	+++	+	-	-	-
39114 +	++	-	-	-	-	-	-	-	-
39775 +	+	-	-	-	-	-	-	-	-

39539 +	-	-	-	-	-	-	-	-	-
39576 +	+	-	-	-	-	-	-	-	-
39971 +	++	--+	+++	+++	+++	-	-	-	-
39607 +	-	-	-	-	-	-	-	-	-
39972 +	+	-	-	-	-	-	-	-	-
39973 +	-	--+	+++	+++	+++	+	-	-	-
39974 +	+	--+	+++	+++	+++	+	-	-	-
11698 +	-	-	-	-	-	-	-	-	-
39131 +	++	--+	+++	+++	+++	+	-	-	-
39683 +	+	-	-	-	-	-	-	-	-
39975 +	+	--+	+++	+++	+++	-	–	-	-
37740 +	+	-	+	-	-	-	-	-	-
39976 +	-	-	-	-	-	-	-	-	-
39977 +	+	-	-	-	-	-	-	-	-
39593 +	+	-	-	-	-	-	-	-	-
13662 +	+	-	-	-	-	-	-	-	-
39691 +	++	-	+	+	+	+	–	-	-
39225 +	+	–	+	+	+	-	-	-	-
18536 +	+	–	+	-	-	-	-	-	-
39978 +	-	-	-	-	-	-	-	-	-
39979 +	+	-	-	-	-	-	-	-	-
11025 +	+	-	+	-	-	-	-	-	-
38558 +	+	–	+	+++	+	+++	--	-	-
39276 +	+	-	-	-	-	-	-	-	-
39980 +	-	-	-	-	-	-	-	-	-
39405 +	+	-	-	-	-	-	-	-	-
13975 +	++	-	-	-	-	-	-	-	-
39625 +	-	-	-	-	-	-	-	-	-
39981 +	-	--+	+	+++	+	-	-	-	-
13919 +	+	-	-	-	-	-	-	-	-
18562 +	++	--+	+++	+++	+++	+	–	-	-
39750 +	++	-	-	-	-	-	-	-	-
18078 +	-	-	-	-	-	-	-	-	-

39982	+	+	−−+	+++	+++	+++	+	−	-	-
18157	+	-	-	-	-	-	-	-	-	-
13775	+	+	-	-	-	+	++	−−	-	-
14203	+	+	-	-	-	-	-	-	-	-
18068	+	++	-	-	-	-	-	-	-	-
39983	+	+	-	-	-	-	-	-	-	-
19282	+	+	−−+	+++	+++	+++	-	-	-	-
39352	+	+	-	-	-	-	-	-	-	-
38339	+	-	-	+	+	+	+	−	-	-
39984	+	+	−−+	+++	+++	+++	+	-	-	-
39985	+	+	-	-	-	-	-	-	-	-
39986	+	-	-	-	-	-	-	-	-	-
12278	+	+	-	-	-	-	-	-	-	-
38635	+	++	-	-	-	-	-	-	-	-
39987	+	+	−−+	+++	+++	+++	-	-	-	-
39988	+	-	-	-	-	-	-	-	-	-
12796	+	-	-	-	-	-	-	-	-	-
38797	+	++	-	-	-	-	-	-	-	-
39989	+	+	-	-	-	-	-	-	-	-
39965	+	++	-	-	-	-	-	-	-	-
39990	+	+	−−+	+++	+++	+++	-	-	-	-
39707	+	-	−	-	++	+	-	-	-	-
39991	+	+	−−+	+++	+++	+++	-	-	-	-
39992	+	+	-	-	-	-	-	−	-	-
39993	+	+	-	-	-	-	-	-	-	-
14862	+	+	-	-	+	-	+	-	-	-
39328	+	++	-	-	-	-	-	-	-	-
39919	+	+	-	-	-	-	-	-	-	-
39994	+	+	-	-	-	-	-	-	-	-
39995	+	+	−−+	+++	+++	+++	-	−	-	-
18042	+	+	-	-	-	-	-	-	-	-
11028	+	+	-	-	-	+	-	-	-	-
12512	+	-	-	-	-	-	-	-	-	-

12570 +	+	-	-	-	-	-	-	-	-
39089 +	+	-	-	-	-	-	–	-	-
17839 +	+	-	-	-	-	-	-	-	-
39996 +	+	-	-	-	-	-	-	-	-
18119 +	+	-	-	-	-	-	-	-	-
39745 +	-	–	-	-	-	-	-	-	-
39172 +	+	-	-	-	-	-	-	-	-
11246 +	+	-	-	-	-	-	-	-	-
39156 +	++	-	-	-	-	-	-	-	-
39596 +	-	–	+	+	-	+	–	-	-
39358 +	-	-	-	-	-	-	-	-	-
39449 +	-	-	-	-	-	-	-	-	-
39291 +	++	-	-	-	-	-	-	-	-
39185 +	++	-	-	-	-	-	–	-	-
39997 +	-	-	-	-	-	-	-	-	-
14347 +	+	-	-	-	-	-	-	-	-
17190 +	+	–+	+++	+++	+++	+	–	-	-
13535 +	+	-	-	-	-	-	-	-	-
39998 +	+	–+	+++	+++	+++	-	-	-	-
38484 +	-	-	-	-	-	-	-	-	-
39999 +	+	-	-	-	-	-	-	-	-
40000 +	+	–+	+++	+++	+++	+	–	-	-
40001 +	+	–+	+++	+++	+++	+	–	-	+++
40002 +	-	–+	-	+	-	-	-	-	-
38486 +	+	-	-	-	-	-	-	-	-
39247 +	+	–+	+++	+++	+++	+	–	-	-
39255 +	++	-	-	-	-	-	-	-	-
14924 +	++	–	+	+	+	+++	–––	-	-
18093 +	++	-	-	-	-	-	-	-	-
12501 +	-	-	-	-	-	-	-	-	-
38242 +	+	-	-	-	-	-	-	-	-
39790 +	++	–+	+++	+++	+++	+	–	-	-
39459 +	+	-	-	-	-	-	-	-	-

14288 +	+	-	-	-	-	-	-	-	-
40003 +	-	-	+	+	-	-	-	-	-
17695 +	-	-	-	-	-	-	-	-	-
14614 +	++	-	-	-	-	-	-	-	-
40004 +	+	-	-	-	-	-	-	-	-
40005 +	+	-	-	-	-	-	-	-	-
12387 +	+	-	-	-	-	-	-	-	-
40006 +	+	-	-	-	-	-	-	-	-
39740 +	+	-	-	-	-	-	-	-	-
39681 +	+	-	-	-	-	-	-	-	-
40007 +	+	-	-	-	-	+	-	-	-
39952 +	+	-	-	-	-	-	-	-	-
40008 +	-	-	-	-	-	-	-	-	-
40009 +	+	--+	-	+++	-	+++	-	-	-
17999 +	-	-	-	-	-	-	-	-	-
40010 +	+	-	+	++	++	-	-	-	-
40011 +	+	-	-	-	-	+	-	-	-
39350 +	-	-	-	-	-	-	-	-	-
40012 +	+	--+	+++	+++	+++	+	-	-	-
40013 +	+	--+	+++	+++	+++	-	-	-	-
39352 +	++	-	-	-	-	-	-	-	-
11592 +	-	-	-	-	-	-	-	-	-
39879 +	+	-	-	-	-	-	-	-	-
39124 +	-	-	-	-	-	+	-	-	-
40014 +	+	--+	+++	+++	+++	+	-	+++	-
17611 +	+	--+	+++	+++	+++	-	-	-	-
39670 +	-	-	+	+	+	-	-	-	-
17689 +	-	-	-	-	-	-	-	-	-
40015 +	-	--+	+++	++	+++	-	-	-	-
40016 +	+	--+	+++	+++	+++	-	-	-	-
40017 +	+	-	-	-	-	-	-	-	-
39716 +	+	-	-	-	-	-	-	-	-
40018 +	-	--+	+	+++	+	+++	---	-	-

40019 +	-	--+	+	+++	+	+	-	+++	-
39663 +	-	-	-	-	-	+	-	-	-
40020 +	+	--+	+++	+++	+++	+	-	-	-
17355 +	-	--+	+++	+++	+++	+	-	-	-
40021 +	+	--+	+++	+++	+++	+	-	-	-
39050 +	++	-	-	-	-	-	-	-	-
17097 +	-	-	-	-	-	-	-	-	-
40022 +	+	--+	+++	+++	+++	+	-	-	-
18240 +	-	-	-	-	-	-	-	-	-
37693 +	+	-	++	++	+	-	-	-	-
11741 +	++	-	-	-	-	-	-	-	-
14170 +	+	-	-	-	-	-	-	-	-
40023 +	+	--+	+++	+++	+++	+	-	+++	-
40024 +	+	--+	+++	+++	+++	-	-	-	-
40025 +	-	-	-	-	-	-	-	-	-
40026 +	+	-	-	-	-	-	-	-	-
38306 +	+	--+	+++	+++	+++	+	-	-	-
19739 +	+	-	-	-	-	-	-	-	-
40027 +	+	--+	+++	+++	+++	-	-	-	-
14301 +	++	-	-	-	-	-	-	-	-
14376 +	+	-	-	-	-	-	-	-	-
38626 +	-	-	+	-	+	-	-	-	-
37189 +	+	-	-	-	+	-	-	-	-
39440 +	++	-	-	-	-	-	-	-	-
39473 +	+	-	-	-	-	-	-	-	-
40028 +	+	-	-	-	-	-	-	-	-
40029 +	+	-	-	-	-	-	-	-	-
14178 +	++	-	-	-	-	-	-	-	-
11025 +	+	-	-	-	-	-	-	-	-
39086 +	++	-	-	-	-	-	-	-	-
13519 +	+	-	+	-	+	+++	---	-	-
15940 +	+	-	+	-	+	-	-	-	-
40030 +	++	--+	+++	+++	+++	+	-	-	-

37002	+	-	--+	+	+	+	+	-	-	-
39743	+	-	-	-	-	-	-	-	-	-
40031	+	-	--+	+++	+++	+++	-	-	-	-
38418	+	++	-	-	-	-	-	-	-	-
39850	+	++	-	-	-	-	-	-	-	-
40032	+	+	-	+	-	-	+	-	-	-
40033	+	+	-	-	-	-	-	-	-	-
40016	+	+	--+	+++	+++	+++	+	–	-	-
39524	+	+	-	+	-	-	-	-	-	-
13772	+	++	-	-	-	-	-	-	-	-
40034	+	+	-	-	-	-	-	-	-	-
39329	+	++	-	-	-	-	-	-	-	-
40035	+	+	--+	+++	+++	+++	+	–	-	-
11063	+	-	-	-	-	-	-	-	-	-
39288	+	-	-	-	-	-	-	-	-	-
40036	+	-	-	-	-	-	-	-	-	-
39693	+	++	-	-	-	-	-	-	-	-
40037	+	-	-	+	-	-	-	-	-	-
38626	+	-	-	-	-	+	-	-	-	-
40038	+	+	--+	+++	+++	+++	+	–	-	-
40039	+	-	-	-	-	-	-	-	-	-
39680	+	++	-	-	-	-	-	-	-	-
11264	+	+	-	-	-	-	-	-	-	-
40040	+	+	--+	+++	+++	+++	+	–	-	-
39492	+	++	-	-	-	-	-	-	-	-
40041	+	-	-	-	-	-	+	–	-	-
40042	+	+	--+	+++	+++	+++	+	-	-	-
40043	+	++	-	-	-	-	-	–	-	-
39622	+	+	--+	+	-	-	-	-	++	-
17832	+	+	-	-	-	-	-	-	-	-
14409	+	+	-	-	-	-	-	–	-	-
18132	+	+	-	-	-	-	-	-	-	-
40044	+	+	--+	+++	+++	+++	+	-	-	-

39832 +	+	-	-	-	-	-	-	-	-
16077 +	+	-	-	-	-	-	-	-	-
40045 +	++	-	-	-	-	-	-	-	-
40030 +	+	---+	+++	+++	+++	+	–	-	-
40046 +	-	---+	+	-	-	+	–	-	-
40047 +	-	-	-	-	-	-	-	-	-
11047 +	+	-	-	-	-	-	-	-	-
12539 +	-	-	-	-	-	-	-	-	-
11432 +	+	-	-	-	-	-	-	-	-
11989 +	+	-	-	-	-	-	-	-	-
40048 +	+	-	-	-	-	-	-	-	-
39393 +	+	---+	+++	+++	+++	+	–	-	-
40049 +	+	---+	+++	+++	+++	-	-	-	-
40050 +	+	–	+	+	+	-	-	-	-
17046 +	+	-	-	-	-	-	-	-	-
40051 +	+	--	++	++	+	+++	---	-	-
40052 +	+	-	-	-	-	-	-	-	-
39653 +	++	-	-	-	-	-	-	-	-
40053 +	+	-	-	-	-	-	-	-	-
18712 +	-	-	-	-	-	-	-	-	-
40054 +	+	-	-	-	-	+	–	-	-
17294 +	+	---+	+++	+++	+++	-	–	-	-
40055 +	-	-	-	-	-	-	-	-	-
17033 +	++	-	-	-	-	-	-	-	-
39320 +	+	-	-	-	-	-	-	-	-
39475 +	+	-	-	-	-	-	-	-	-
18525 +	-	-	-	-	-	-	-	-	-
39775 +	+	-	-	-	-	-	-	-	-
40056 +	+	---+	+++	+++	+++	+	-	-	-
14243 +	+	-	-	-	-	-	-	-	-
11354 +	-	-	-	-	-	-	-	-	-
17893 +	+	-	-	-	-	-	-	-	-
40038 +	+	---+	+++	+++	+++	+	-	-	-

39800 +	+	-	-	+	-	-	-	-	-
40057 +	+	--+	+++	+++	+++	-	-	-	-
39584 +	+	-	-	-	-	-	-	-	-
15491 +	+	–	+	+	+	+++	---	-	-
38563 +	+	–	+	-	-	-	-	-	-
40058 +	++	--+	+++	+++	+++	+	-	-	-
40045 +	++	-	-	-	-	-	-	-	-
39886 +	+	--+	+++	+++	+++	+	-	-	-
40059 +	+	-	-	-	-	-	-	-	-
39717 +	+	-	-	-	-	-	-	-	-
39948 +	+	-	-	-	-	-	-	-	-
40060 +	+	--+	+++	+++	+++	-	-	-	-
39906 +	+	--+	+++	+++	+++	+	–	-	-
40061 +	-	--	+	++	++	-	-	-	-
40062 +	-	-	++	+	-	-	-	-	-
11587 +	+	-	-	-	-	-	-	-	-
39636 +	+	-	-	-	-	-	-	-	-
40063 +	+	-	-	-	-	-	-	-	-
14501 +	+	-	-	-	-	-	-	-	-
40048 +	++	-	-	-	-	-	-	-	-
39807 +	++	-	-	-	+	-	-	-	-
11274 +	++	-	-	-	-	-	-	-	-
40064 +	-	-	-	-	-	-	-	-	-
40065 +	+	--+	+++	+++	+++	-	-	-	-
39964 +	+	-	+	-	-	-	-	-	-
11063 +	-	-	-	-	-	-	-	-	-
40066 +	+	-	-	-	-	-	-	-	-
39048 +	+	--+	+++	+++	+++	+	–	-	-
13792 +	+	-	-	-	-	-	–	-	-
11462 +	-	-	-	-	-	-	-	-	-
11416 +	-	-	-	-	-	-	-	-	-
39206 +	+	--+	+++	+++	+++	-	–	-	-
40067 +	+	-	-	-	-	-	-	-	-

39181 +	-	-	-	-	-	-	-	-	-
40068 +	+	-	-	-	-	-	-	-	-
39862 +	+	-	-	-	-	-	-	-	-
14374 +	++	-	-	-	-	-	-	-	-
14324 +	+	-	-	-	-	-	-	-	-
14197 +	++	-	-	-	-	+	–	-	-
38309 +	++	–+	+++	+++	+++	+	–	-	-
40069 +	+	-	-	-	-	-	-	-	-
18070 +	-	-	-	-	-	-	-	-	-
40070 +	+	-	-	-	-	-	-	-	-
13847 +	+	-	-	-	-	-	-	-	-
39719 +	+	-	-	-	-	-	-	-	-
40071 +	-	-	-	-	-	-	-	-	-
39051 +	++	-	-	-	-	-	-	-	-
40072 +	-	-	+	-	-	+++	–––	-	-
39608 +	++	–+	+++	+++	+++	-	-	-	-
40073 +	-	–+	+++	+++	+++	-	-	-	-
40074 +	-	-	-	-	-	-	-	-	-
40075 +	++	–+	+++	+++	+++	+	-	-	-
40076 +	+	–+	+++	+++	+++	+	–	-	-
12273 +	-	-	-	-	-	-	-	-	-
40077 +	+	-	-	-	-	-	-	-	-
11755 +	+	-	-	-	-	-	-	-	-
40078 +	-	-	-	-	-	-	-	-	-
37485 +	+	–+	+++	+++	+++	-	-	-	-
39634 +	-	-	-	-	-	-	-	-	-
39747 +	+	-	-	-	-	-	-	-	-
38497 +	+	–+	+++	+++	+++	+	–	-	-
38575 +	-	–	-	-	-	-	-	-	-
40077 +	+	-	-	-	-	-	-	-	-
13918 +	++	-	-	-	-	-	-	-	-
12521 +	-	-	-	-	-	-	-	-	-
39250 +	++	-	-	-	-	-	-	-	-

40079	+	+	–+	+++	+++	+++	-	–	-	-
40080	+	+	–+	+++	+++	+++	-	-	-	-
39841	+	-	-	-	-	-	-	-	-	-
11741	+	+	-	-	-	-	-	-	-	-
39255	+	++	-	-	-	-	-	-	-	-
40081	+	++	–+	+++	+++	+++	+	–	-	-
40078	+	-	-	-	-	-	-	-	-	-
37320	+	-	-	-	-	-	-	-	-	-
39942	+	+	-	-	-	-	-	-	-	-
16106	+	+	-	-	-	+	++	––	-	-
18324	+	+	–+	+++	+++	+++	+	-	-	-
11270	+	+	-	-	-	-	-	-	-	-
14089	+	+	-	-	-	-	+	–	-	-
40082	+	+	-	-	-	-	-	-	-	-
39431	+	-	-	-	-	-	-	-	-	-
39460	+	+	-	-	-	-	-	-	-	-
17475	+	-	-	-	-	+	+	–	-	-
11946	+	-	-	-	-	-	-	-	-	-
14635	+	++	-	-	-	-	-	-	-	-
38415	+	+	-	-	-	-	-	-	-	-
18883	+	+	–+	+++	+++	+++	-	–	-	-
40083	+	-	––	+	-	+	-	-	-	-
40084	+	+	-	-	-	-	-	-	-	-
39455	+	+	-	-	-	-	-	-	-	-
39791	+	+	-	-	-	-	-	-	-	-
40085	+	+	-	-	-	-	-	-	-	-
14261	+	+	-	-	-	-	-	-	-	-
37847	+	++	-	-	-	-	-	-	-	-
40086	+	-	-	-	-	-	-	-	-	-
40087	+	+	–+	+++	+++	+++	+++	–––	-	-
18904	+	+	–+	+++	+++	+++	+	-	-	-
40088	+	+	–+	+++	+++	+++	+	–	-	-
39616	+	++	-	-	-	-	+	–	-	-

40089 +	+	-	-	-	-	-	-	-	-
40090 +	+	--+	+++	+++	+++	+	-	-	-
11104 +	+	-	-	-	-	-	-	-	-
40089 +	+	-	-	-	-	-	-	-	-
19268 +	+	--+	+++	+++	+++	+	-	-	-
14033 +	+	-	-	-	-	-	-	-	-
14514 +	+	-	-	-	-	-	-	-	-
18391 +	-	--+	+++	+++	+++	-	-	-	-
13559 +	+	-	+	-	-	-	-	-	-
39872 +	-	-	-	-	-	-	-	-	-
40091 +	+	--+	+++	+++	+++	-	--	-	-
13719 +	++	-	-	-	-	-	-	-	-
38776 +	+	--+	+++	+++	+++	-	-	-	-
11467 +	-	-	-	-	-	-	-	-	-
40092 +	+	-	-	-	-	-	-	-	-
39462 +	+	-	-	-	-	-	-	-	-
40093 +	-	-	-	-	-	-	-	-	-
39999 +	+	-	-	-	-	-	-	-	-
14046 +	++	-	-	-	-	-	-	-	-
36761 +	-	--+	-	++	+	-	-	-	-
14288 +	+	-	-	-	-	-	-	-	-
13536 +	+	-	-	-	-	-	-	-	-
40094 +	++	--+	+++	+++	+++	-	-	-	-
40095 +	++	-	-	-	-	-	-	-	-
17490 +	+	--+	+++	+++	+++	+	-	-	-
39612 +	-	-	-	-	-	-	-	-	-
39004 +	+	-	-	-	-	-	-	-	-
39588 +	++	-	-	-	-	-	-	-	-
12050 +	-	-	-	-	-	-	-	-	-
14261 +	+	-	-	-	-	-	-	-	-
39438 +	++	-	-	-	-	-	-	-	-
40003 +	-	-	+	-	-	-	-	-	-
40096 +	-	-	-	-	-	-	-	-	-

40097 +	+	--+	+++	+++	+++	+	-	-	-
40098 +	+	-	-	-	-	-	-	-	-
40099 +	+	-	-	-	-	-	-	-	-
20363 +	+	-	-	-	-	-	-	-	-
17702 +	+	-	-	-	-	+	–	-	-
40100 +	-	-	-	-	-	-	-	-	-
17208 +	+	-	-	-	-	-	-	-	-
11481 +	+	-	-	-	+	-	-	-	-
40101 +	++	--+	+++	+++	+++	-	-	-	-
13615 +	+	-	-	-	-	-	-	-	-
40102 +	-	-	-	-	-	-	-	-	-
40063 +	+	-	-	-	-	-	-	-	-
40103 +	+	-	-	-	-	-	-	-	-
17911 +	+	-	-	-	-	-	-	-	-
40104 +	+	--+	+++	+++	+++	+	–	-	-
40105 +	+	-	-	-	-	-	-	-	-
39729 +	+	-	-	-	-	-	-	-	-
40106 +	-	-	-	-	-	-	-	-	-
12269 +	-	-	-	-	-	-	-	-	-
40107 +	++	--+	+++	+++	+++	-	-	-	-
15051 +	+	--+	+++	+++	+++	+	-	-	-
39252 +	++	-	-	-	-	-	-	-	-
12512 +	-	-	-	-	-	-	-	-	-
13722 +	+	-	-	-	-	-	-	-	-
39526 +	-	--	+	+	-	-	-	-	-
39823 +	+	-	-	-	-	-	-	-	-
40108 +	+	--+	+++	+++	+++	+	–	-	-
38856 +	+	-	-	-	-	-	-	-	-
13976 +	+	-	-	-	-	-	-	-	-
11771 +	-	-	-	-	-	-	-	-	-
40109 +	+	--+	+++	+++	+++	+	–	-	-
14130 +	+	-	-	-	-	-	-	-	-
12195 +	+	-	-	-	-	-	-	-	-

40110 +	+	-	-	-	-	+	-	-	-
39812 +	-	-	-	-	-	-	-	-	-
13709 +	+	-	-	-	-	++	−−	-	-
40111 +	+	−−+	+++	+++	+++	-	−	-	-
11035 +	+	-	-	-	-	-	-	-	-
16642 +	+	-	+	+	+	+	−	-	-
12796 +	-	-	-	-	-	-	-	-	-
14158 +	+	-	-	-	-	-	-	-	-
38651 +	+	-	-	-	-	-	-	-	-
16137 +	++	-	-	-	-	-	-	-	-
18048 +	++	-	-	-	-	-	-	-	-
13741 +	+	-	+	-	-	++	−−	-	-
39398 +	++	-	-	-	-	-	-	-	-
39854 +	++	-	-	-	-	-	-	-	-
11082 +	+	-	-	-	-	-	-	-	-
18763 +	+	-	-	-	-	-	-	-	-
40112 +	+	−−+	+++	+++	+++	-	−	-	-
39169 +	+	−−+	+++	+++	+++	-	-	-	-
13980 +	+	-	-	-	-	-	-	-	-
39717 +	++	-	-	-	-	-	-	-	-
40113 +	+	−−+	+++	+++	+++	-	−	-	-
11462 +	-	-	-	-	-	-	-	-	-
40114 +	+	−−+	+++	+++	+++	+	−	-	-
40115 +	+	−−+	+++	+++	+++	-	-	-	-
14249 +	+	-	-	-	-	-	-	-	-
13782 +	+	-	-	-	-	-	-	-	-
13670 +	+	-	-	-	-	-	-	-	-
39336 +	+	-	-	-	-	-	-	-	-
40116 +	+	−−+	+++	+++	+++	-	−	-	-
39996 +	+	-	-	-	-	-	-	-	-
13550 +	+	-	-	-	-	-	-	-	-
40117 +	+	−−+	+++	+++	+++	+	-	-	-
11452 +	-	-	-	-	-	-	-	-	-

40118 +	++	--+	+++	+++	+++	+	-	-	-
40119 +	-	-	-	+++	+	-	-	-	-
40120 +	-	--+	+++	+++	+++	-	-	-	-
40121 +	+	--+	+++	+++	+++	-	-	-	-
39251 +	-	-	-	-	-	-	-	-	-
40122 +	-	-	+	+	++	+++	---	-	-
16031 +	+	-	-	-	-	-	-	-	-
40123 +	+	--+	+++	+++	+++	-	-	-	-
39954 +	-	--+	+	++	-	-	-	+++	-
39831 +	+	-	-	-	-	-	-	-	-
13997 +	+	-	-	-	-	-	-	-	-
39231 +	+	--+	+++	+++	+++	-	-	-	-
16639 +	+	--+	+	+++	++	+++	--	-	-
40124 +	+	--+	+++	+++	+++	+	-	-	-
39694 +	+	-	-	-	-	-	-	-	-
40125 +	++	-	+	+	+	-	-	-	-
40126 +	+	--+	+++	+++	+++	-	-	-	-
40127 +	+	--+	+++	+++	+++	+	-	-	-
40128 +	+	--+	+++	+++	+++	-	-	-	-
12122 +	-	-	-	-	-	-	-	-	-
40129 +	-	-	-	-	-	-	-	-	-
11274 +	+	-	-	-	-	-	-	-	-
39618 +	+	-	-	-	-	-	-	-	-
40069 +	+	-	-	-	-	-	-	-	-
13933 +	++	-	-	-	-	-	-	-	-
40130 +	-	-	-	-	-	-	-	-	-
39627 +	+	--+	+++	+++	+++	+	-	-	-
40131 +	+	-	-	-	-	-	-	-	-
16621 +	+	-	-	-	-	-	-	-	-
40132 +	-	-	-	-	-	-	-	-	-
13909 +	+	-	+	-	-	-	-	-	-
13997 +	++	-	-	-	-	-	-	-	-
39430 +	++	-	-	-	-	-	-	-	-

40133	+	+	−−+	+++	+++	+++	-	-	-	-
38563	+	-	−	+	-	+	-	-	-	-
39919	+	+	-	-	-	-	-	-	-	-
40134	+	+	-	-	-	-	-	-	-	-
15971	+	+	-	-	-	-	-	-	-	-
39728	+	++	-	-	-	-	-	-	-	-
18567	+	-	-	-	-	-	-	−	-	-
19932	+	+	−−+	+++	+++	+++	-	-	-	-
40085	+	+	-	-	-	-	-	-	-	-
14400	+	++	-	+	-	+	+	−	-	-
39766	+	+	-	-	-	-	-	-	-	-
40032	+	+	-	-	-	-	+	−	-	-
40135	+	+	-	-	-	-	-	-	-	-
40136	+	+	−−+	+++	+++	+++	+	-	-	-
40137	+	+	−−+	+++	+++	+++	-	-	-	-
40138	+	++	−−+	+++	+++	+++	+	-	-	-
14041	+	+	-	-	-	-	-	-	-	-
17668	+	++	-	-	-	-	-	-	-	-
14263	+	+	-	-	-	-	-	-	-	-
40139	+	+	-	-	-	-	-	-	-	-
37413	+	-	−−	-	+	-	-	-	-	-
40140	+	+	−−+	+++	+++	+++	+	-	-	-
12596	+	-	-	-	-	-	-	-	-	-
15964	+	++	-	-	-	-	-	-	-	-
39645	+	+	-	-	-	-	+	−	-	-
40141	+	+	-	-	-	-	-	-	-	-
40142	+	-	-	-	-	-	-	-	-	-
39891	+	+	-	-	-	-	-	-	-	-
40143	+	+	-	-	-	-	-	-	-	-
38901	+	++	-	-	-	-	-	-	-	-
13535	+	+	-	-	-	-	-	-	-	-
40144	+	+	-	-	-	-	-	-	-	-
38985	+	+	-	-	-	-	-	-	-	-

40145 +	-	---+	+++	+++	+++	-	-	-	-
14468 +	++	-	-	-	-	-	-	-	-
38132 +	-	-	-	-	-	-	-	-	-
18312 +	+	---+	+++	+++	+++	-	-	-	-
38774 +	+	---+	+++	+++	+++	+	-	-	-
39755 +	++	-	-	-	+	++	--	-	-
19957 +	+	-	-	-	-	-	-	-	-
19239 +	++	---+	+++	+++	+++	+	-	-	-
39598 +	+	-	-	-	-	-	-	-	-
11415 +	-	-	-	-	-	-	-	-	-
14020 +	+	-	-	-	-	-	-	-	-
40146 +	-	-	+	+	+	-	-	-	-
40147 +	+	---+	+++	+++	+++	+	–	-	-
40148 +	-	-	-	-	-	-	-	-	-
39879 +	+	-	-	-	-	-	-	-	-
11527 +	-	-	-	-	-	-	-	-	-
14345 +	+	-	-	-	-	-	-	-	-
40149 +	+	---+	+++	+++	+++	-	-	-	+++
40150 +	+	---+	+++	+++	+++	-	–	-	-
14183 +	+	-	-	-	-	-	-	-	-
13743 +	+	-	-	-	+	++	--	-	-
13690 +	++	-	-	-	-	-	-	-	-
13507 +	+	-	-	-	-	+	–	-	-
40151 +	-	-	-	-	-	-	-	-	-
38867 +	-	-	-	+	-	-	-	-	-
39768 +	+	-	-	-	-	-	–	-	-
39683 +	+	-	-	-	-	-	-	-	-
40152 +	+	---+	+++	+++	+++	-	-	-	-
39590 +	+	-	-	-	-	+	-	-	-
17414 +	+	-	-	-	-	-	-	-	-
38831 +	+	---+	++	+++	++	+++	---	-	-
39511 +	+	---+	+++	+++	+++	+	–	-	-
39068 +	++	---+	+++	+++	+++	+	-	-	-

40153 +	++	-	-	-	-	-	-	-	-
40106 +	-	-	-	-	-	-	-	-	-
17711 +	-	--+	+	+++	-	-	-	-	-
11109 +	+	-	-	-	-	-	-	-	-
20462 +	+	-	-	-	-	-	-	-	-
40025 +	+	-	-	-	-	-	-	-	-
14001 +	+	-	-	-	-	-	-	-	-
39869 +	-	-	-	-	-	-	-	-	-
12278 +	+	-	-	-	-	-	-	-	-
17544 +	-	--+	+++	+++	+++	-	-	-	-
39381 +	+	-	-	-	-	-	-	-	-
37466 +	++	-	-	-	-	-	-	-	-
40154 +	++	--+	+++	+++	+++	-	–	-	-
13937 +	+	-	-	-	-	-	-	-	-
40155 +	+	--+	+++	+++	+++	+	–	-	-
14432 +	+	-	-	-	-	-	-	-	-
14316 +	+	-	-	-	-	+	–	-	-
40156 +	-	-	-	-	-	-	-	-	-
40157 +	+	--+	+++	+++	+++	+	-	-	-
39708 +	-	-	-	-	-	-	-	-	-
40158 +	+	--+	+++	+++	+++	+	–	-	-
14196 +	++	-	-	-	-	-	-	-	-
40159 +	+	--+	+++	+++	+++	-	-	-	-
40160 +	-	-	-	-	-	-	-	-	-
40161 +	+	-	-	-	-	-	-	-	-
40162 +	+	-	-	-	-	-	-	-	-
40163 +	+	-	-	-	-	-	-	-	-
40164 +	+	--+	+++	+++	+++	+	–	-	-
40165 +	+	--+	+++	+++	+++	+	–	-	-
38812 +	-	-	-	-	-	-	–	-	-
11374 +	-	-	-	-	-	-	-	-	-
11753 +	+	-	-	-	-	-	-	-	-
11190 +	-	-	-	-	-	-	-	-	-

40166 +	+	-	-	-	-	+	-	-	-
39517 +	++	-	-	-	-	-	-	-	-
40167 +	-	-	-	-	-	-	–	-	-
14099 +	+	-	-	-	-	-	-	-	-
40168 +	+	–-+	+++	+++	+++	-	-	-	-
39319 +	++	–-+	+++	+++	+++	-	–	-	-
40169 +	-	-	-	-	-	-	-	-	-
40053 +	+	-	-	-	-	-	-	-	-
40170 +	+	-	-	-	-	-	-	-	-
13516 +	+	-	-	-	-	+	–	-	-
39765 +	-	-	-	-	-	-	-	-	-
20363 +	+	-	-	-	-	-	-	-	-
18705 +	-	–	+	-	-	-	-	-	-
11587 +	+	-	-	-	-	-	-	-	-
11758 +	+	-	-	-	-	-	-	-	-
40171 +	+	–-+	+++	+++	+++	-	-	-	-
39924 +	++	-	-	-	-	-	-	-	-
40172 +	-	-	-	-	-	+	-	-	-
13954 +	+	-	-	-	-	-	-	-	-
11067 +	+	-	-	-	-	-	-	-	-
12502 +	-	-	-	-	-	-	-	-	-
39141 +	++	-	-	-	-	-	-	-	-
17013 +	+	-	-	-	-	-	-	-	-
39576 +	++	-	-	-	-	-	-	-	-
40173 +	+	–-+	+	-	+	-	-	-	-
39765 +	-	-	-	-	-	-	-	-	-
40174 +	-	–	-	-	-	+	-	-	-
13793 +	+	-	+	-	+	+++	---	-	-
39444 +	++	–-+	+++	+++	+++	-	–	-	-
40098 +	++	-	-	-	-	-	-	-	-
40175 +	++	–-+	+++	+++	+++	+	–	-	-
40176 +	+	–-+	+++	+++	+++	-	-	-	-
17672 +	-	––	-	+	-	+	-	-	-

14073 +	+	-	-	-	-	-	-	-	-
38702 +	-	-	-	-	-	-	-	-	-
40177 +	+	--+	+++	+++	+++	-	-	-	-
18608 +	-	-	-	-	-	-	-	-	-
39994 +	+	-	-	-	-	-	-	-	-
40178 +	+	-	-	-	-	-	-	-	-
40179 +	-	-	-	-	-	-	-	-	-
40180 +	+	--+	+++	+++	+++	+	-	-	-
39784 +	+	-	-	-	-	-	-	-	-
40125 +	+	-	-	+	+	-	-	-	-
40181 +	+	--+	+++	+++	+++	+	-	-	-
14217 +	+	-	-	-	-	++	--	-	-
39873 +	-	-	+	-	-	-	-	-	-
39137 +	-	--+	+	++	-	-	-	-	-
17723 +	+	-	-	-	-	-	-	-	-
40182 +	-	-	-	-	-	+	-	-	-
39657 +	-	-	-	-	-	-	-	-	-
39315 +	+	--+	+++	+++	+++	+	-	-	-
40183 +	++	-	-	-	-	-	-	-	-
17587 +	-	-	-	-	-	-	-	-	-
39326 +	+	-	-	-	-	-	-	-	-
40038 +	+	--+	+++	+++	+++	+	-	-	-
40184 +	+	--+	+++	+++	+++	-	-	-	-
17795 +	-	-	-	-	-	-	-	-	-
39236 +	+	--+	+++	+++	+++	+	-	-	+++
40185 +	++	--	++	++	++	+	-	-	+++
40186 +	+	--+	+++	+++	+++	+	-	-	-
39382 +	+	--+	+++	+++	+++	+	-	-	-
12110 +	+	-	-	-	-	-	-	-	-
16576 +	+	-	-	-	-	-	-	-	-
39847 +	+	--+	+++	+++	+++	-	-	-	-
40187 +	+	--+	+++	+++	+++	-	-	-	-
40188 +	+	-	-	-	-	-	-	-	-

39841 +	+	-	-	-	-	+	-	-	-
40189 +	+	-	-	-	-	-	-	-	-
18008 +	-	-	-	-	-	-	-	-	-
14196 +	+	-	-	-	-	-	-	-	-
13956 +	+	-	-	-	-	-	-	-	-
40190 +	-	--	++	+	++	-	-	-	-
14000 +	+	-	-	-	-	-	-	-	-
40191 +	+	--+	+++	+++	+++	-	-	-	+
40192 +	-	–	-	-	-	-	-	-	-
12539 +	-	-	-	-	-	-	-	-	-
40193 +	+	--+	+++	+++	+++	-	–	-	-
40194 +	+	--+	+++	+++	+++	+	–	-	-
40195 +	+	--+	+++	+++	+++	-	-	-	-
40196 +	+	-	-	-	-	-	-	-	-
39913 +	+	--+	+++	+++	+++	-	–	-	-
37944 +	-	-	-	-	-	-	-	-	-
40197 +	++	--+	+++	+++	+++	-	–	-	-
13959 +	++	–	+	+	+	+	–	-	-
16047 +	+	-	-	-	-	-	-	-	-
39539 +	-	-	-	-	-	-	-	-	-
40198 +	+	--+	+++	+++	+++	+	-	-	-
11270 +	+	-	-	-	-	-	-	-	-
13862 +	+	-	-	-	-	-	-	-	-
16636 +	+	-	-	-	-	+	–	-	-
12087 +	-	-	-	-	-	-	-	-	-
39806 +	+	-	-	-	-	-	-	-	-
17546 +	-	--+	+++	+++	+++	-	–	-	-
18847 +	++	-	-	-	-	-	-	-	-
12023 +	+	-	-	-	-	-	-	-	-
18216 +	+	-	-	-	-	-	-	-	-
13912 +	+	-	-	-	-	-	-	-	-
40199 +	+	--+	+++	+++	+++	-	-	-	-
40200 +	+	--+	+++	+++	+++	+	–	-	-

15491 +	++	–	+	+	+	+++	---	-	-
17060 +	-	--+	+	++	+	-	-	-	-
40201 +	+	--+	+++	+++	+++	+	-	-	-
40202 +	+	--+	+++	+++	+++	+	-	-	-
20380 +	+	-	-	-	-	-	-	-	-
39939 +	+	-	-	-	-	-	-	-	-
40041 +	-	-	-	-	-	+	–	-	-
40203 +	+	--+	+++	+++	+++	-	–	-	-
14028 +	-	-	-	-	-	-	-	-	-
40204 +	+	-	-	-	-	-	-	-	-
40205 +	+	-	-	-	-	-	-	-	-
20432 +	+	--+	+++	+++	+++	-	-	-	-
11882 +	-	-	-	-	-	-	-	-	-
40206 +	-	-	-	-	-	-	-	-	-
40034 +	+	-	-	-	-	-	-	-	-
14585 +	++	-	-	-	-	-	-	-	-
40207 +	+	--+	+++	+++	+++	-	–	-	-
39519 +	+	–	-	-	-	-	-	-	-
40208 +	+	-	-	-	-	-	-	-	-
39074 +	-	--+	+	+++	-	-	-	-	-
40209 +	+	--+	+++	+++	+++	+	-	-	-
39270 +	+	-	+	-	-	-	-	-	-
40210 +	+	-	-	-	-	-	-	-	-
17996 +	+	-	-	-	-	+	–	-	-
17622 +	+	-	-	-	-	-	-	-	-
40037 +	-	-	-	-	-	-	-	-	-
38688 +	+	--+	+++	+++	+++	+	-	-	-
40211 +	+	-	-	-	-	-	-	-	-
40212 +	++	--+	+++	+++	+++	-	-	+	-
14147 +	+	-	-	-	-	-	-	-	-
13655 +	+	-	-	-	-	-	-	-	-
39682 +	+	–	+	+	+	+++	---	-	-
14206 +	+	-	-	-	-	-	-	-	-

39007 +	+	-	-	-	-	-	-	-	-
38654 +	++	-	-	-	-	-	-	-	-
40213 +	+	--+	+++	+++	+++	-	-	-	-
40214 +	+	--+	+++	+++	+++	+	–	-	-
40215 +	+	-	-	-	-	-	-	-	-
14588 +	+	-	-	-	-	-	-	-	-
40216 +	+	-	-	-	-	-	-	-	-
16640 +	+	-	-	-	-	+	–	-	-
40217 +	+	-	-	-	-	-	-	-	-
40218 +	+	--+	+++	+++	+++	-	-	-	-
39978 +	-	-	-	-	-	-	-	-	-
14491 +	+	-	-	-	-	-	-	-	-
14588 +	+	-	-	-	-	-	-	-	-
38579 +	-	-	-	-	-	-	-	-	-
39650 +	++	-	-	-	-	-	-	-	-
40215 +	+	-	-	-	-	-	-	-	-
39327 +	+	--+	+++	+++	+++	+	-	-	-
40219 +	+	-	-	-	-	-	-	-	-
39179 +	-	-	-	-	-	-	-	-	-
14496 +	+	-	-	-	-	-	-	-	-
39543 +	-	--+	+	+++	+	+	–	-	-
40220 +	++	-	-	-	-	+	-	-	-
40221 +	++	--+	+++	+++	+++	-	–	-	-
14061 +	+	-	-	-	-	++	--	-	-
40222 +	+	-	+	-	-	+	–	-	-
40223 +	+	-	-	-	-	-	-	-	-
40224 +	+	--+	+++	+++	+++	+	–	-	-
40225 +	+	--+	+++	+++	+++	-	–	-	-
40226 +	+	--+	+++	+++	+++	-	-	-	-
40227 +	-	--+	+++	+++	+++	+	-	-	-
39640 +	-	–	-	-	-	-	-	-	-
17812 +	-	-	-	-	-	-	-	-	-
39665 +	+	-	-	-	-	-	-	-	-

39870 +	+	-	-	-	-	-	-	-	-
18396 +	-	-	-	-	-	+	-	-	-
40228 +	+	--+	+++	+++	+++	+	-	-	-
14192 +	++	-	-	-	-	-	-	-	-
40229 +	+	--+	+++	+++	+++	+	-	-	-
13767 +	++	-	-	-	-	-	-	-	-
13973 +	+	-	-	-	-	-	-	-	-
39139 +	-	-	-	-	-	-	-	-	-
40230 +	+	-	-	-	-	-	-	-	-
13787 +	+	-	-	-	-	+	-	-	-
40231 +	-	--+	-	+++	+	++	-	-	-
39863 +	+	--+	+++	+++	+++	-	-	-	-
40052 +	+	-	-	-	-	-	-	-	-
40232 +	+	--+	+++	+++	+++	+	-	-	-
40233 +	-	-	-	-	-	-	-	-	-
18800 +	-	-	-	-	-	-	-	-	-
40067 +	++	-	-	-	-	-	-	-	-
18765 +	-	-	-	-	-	-	-	-	-
13856 +	+	-	-	-	-	+	--	-	-
39345 +	+	-	-	-	-	-	-	-	-
40234 +	+	-	-	-	-	-	-	-	-
39186 +	-	-	-	-	-	-	-	-	-
12189 +	+	-	-	-	-	-	-	-	-
13850 +	+	-	-	-	-	-	-	-	-
19492 +	+	--+	+++	+++	+++	-	-	-	-
40235 +	-	-	-	-	-	+	-	-	-
40029 +	+	-	-	-	-	-	-	-	-
40236 +	+	--+	+++	+++	+++	+	-	-	-
13992 +	+	-	-	-	-	-	-	-	-
40237 +	+	-	-	-	-	-	-	-	-
40238 +	+	-	-	-	-	-	-	-	-
17277 +	+	--+	+++	+++	+++	-	-	-	-
40239 +	+	--+	+++	+++	+++	+	-	-	-

13670 +	+	-	-	-	-	-	-	-	-
40240 +	+	--+	+++	+++	+++	-	-	-	-
40241 +	-	-	+	+	++	-	-	-	-
40242 +	-	-	-	-	-	-	-	-	-
39808 +	-	-	-	-	-	-	-	-	-
40243 +	+	--+	+++	+++	+++	+	-	-	-
13888 +	+	-	-	-	-	-	-	-	-
39595 +	+	-	-	-	-	-	-	-	-
14685 +	+	-	-	-	-	++	--	-	-
40244 +	+	-	-	-	-	-	-	-	-
40245 +	+	-	-	-	-	-	-	-	-
17737 +	++	-	-	-	-	-	-	-	-
40246 +	+	-	-	-	-	-	-	-	-
40247 +	+	--+	+++	+++	+++	-	-	-	-
40248 +	-	-	-	-	-	-	-	-	-
40249 +	+	--+	+++	+++	+++	+	-	-	-
40250 +	-	-	+	+	+	+++	---	-	-
40251 +	+	--+	+++	+++	+++	+	-	+++	-
11556 +	-	-	-	-	-	-	-	-	-
40252 +	+	--+	+++	+++	+++	-	-	-	-
11200 +	-	-	-	-	-	-	-	-	-
14360 +	+	-	-	-	-	-	-	-	-
39993 +	+	-	-	-	-	-	-	-	-
12380 +	-	-	-	-	-	-	-	-	-
11307 +	+	-	-	-	-	-	-	-	-
39043 +	+	-	-	-	-	-	-	-	-
14360 +	+	-	-	-	-	-	-	-	-
13984 +	+	-	-	-	-	-	-	-	-
11035 +	+	-	-	-	-	-	-	-	-
40253 +	+	--+	+++	+++	+++	-	-	-	-
40254 +	+	-	-	-	-	-	-	-	-
39267 +	+	-	-	-	-	-	-	-	-
40255 +	+	--+	+++	+++	+++	+	-	-	-

40073	+	-	--+	+++	+++	+++	-	-	-	-
40256	+	++	--+	+++	+++	+++	+	-	-	-
14373	+	+	-	-	-	-	-	-	-	-
39742	+	-	-	-	-	-	-	-	-	-
39927	+	+	-	-	-	-	-	-	-	-
14169	+	+	-	-	-	-	-	-	-	-
13600	+	+	-	-	-	+	++	--	-	-
40257	+	+	--+	+++	+++	+++	+	-	-	-
40258	+	++	-	-	-	-	+	-	-	-
40259	+	+	--+	+++	+++	+++	-	-	-	-
40148	+	-	-	-	-	-	-	-	-	-
18789	+	-	-	-	-	-	-	-	-	-
40223	+	+	-	-	-	-	-	-	-	-
39487	+	++	-	-	-	-	-	-	-	-
38544	+	+	-	+	+	+	+++	---	-	-
40260	+	-	-	-	-	-	-	-	-	-
40261	+	-	-	-	+	-	-	-	-	-
40262	+	+	-	+	-	-	-	-	-	-
13937	+	+	-	-	-	-	-	-	-	-
40083	+	-	--	-	+	-	-	-	-	-
40054	+	++	-	-	-	-	+	-	-	-
11343	+	-	-	-	-	-	-	-	-	-
14116	+	+	-	-	-	-	-	-	-	-
14514	+	+	-	-	-	-	-	-	-	-
14479	+	+	-	-	-	-	-	-	-	-
18676	+	+	-	-	-	-	-	-	-	-
40263	+	++	--+	+++	+++	+++	+	-	-	-
12575	+	-	-	-	-	-	-	-	-	-
13862	+	+	-	-	-	-	-	-	-	-
11120	+	+	-	-	-	-	-	-	-	-
13694	+	+	-	-	-	-	-	-	-	-
13758	+	+	-	-	-	-	-	-	-	-
11291	+	+	-	-	-	-	-	-	-	-

40264	+	-	--+	+++	+++	+++	+	-	-	-
40265	+	-	--+	+++	+++	+++	+++	---	-	-
11445	+	+	-	-	-	-	-	-	-	-
13885	+	+	-	-	-	-	-	-	-	-
39446	+	+	-	-	-	-	-	-	-	-
13854	+	+	-	-	-	-	-	-	-	-
14969	+	++	-	+	-	-	+++	---	-	-
40266	+	+	--+	+++	+++	+++	-	-	-	-
39717	+	+	-	-	-	-	-	-	-	-
13878	+	+	-	-	-	-	+	-	-	-
17556	+	+	-	-	-	-	-	-	-	-
12411	+	-	-	-	-	-	-	-	-	-
14410	+	+	-	-	-	-	-	-	-	-
40267	+	++	--+	+++	+++	+++	+	-	-	-
39512	+	+	-	-	-	-	-	-	-	-
13640	+	+	-	-	-	-	+	--	-	-
40268	+	+	-	-	-	-	-	-	-	-
40269	+	+	--+	+++	+++	+++	-	-	-	-
40211	+	+	-	-	-	-	-	-	-	-
40270	+	+	--+	+++	+++	+++	+	-	-	-
40271	+	+	--+	+++	+++	+++	-	-	-	-
13684	+	+	-	-	-	-	-	-	-	-
40178	+	+	-	-	-	-	-	-	-	-
40272	+	+	-	-	-	+	+++	---	+++	-
40273	+	+	-	-	-	-	-	-	-	-
40137	+	+	--+	+++	+++	+++	-	-	-	-
11250	+	-	-	-	-	-	-	-	-	-
38302	+	-	-	-	-	-	-	-	-	-
14423	+	+	-	-	-	-	-	-	-	-
14429	+	+	-	-	-	-	-	-	-	-
38914	+	+	-	-	-	-	+	-	-	-
12052	+	-	-	-	-	-	-	-	-	-
40274	+	+	-	-	-	-	+	-	-	-

40275 +	+	-	-	-	-	-	-	-	-
11623 +	+	-	-	-	-	-	-	-	-
40276 +	+	---+	+++	+++	+++	-	-	-	-
17193 +	+	---+	+++	+++	+++	-	–	-	-
39472 +	+	-	-	-	-	-	-	-	-
40277 +	-	-	-	-	-	-	-	-	-
39859 +	-	-	-	-	-	-	-	-	-
40278 +	++	-	-	+	+	+++	----	-	-
40279 +	+	---+	+++	+++	+++	-	–	-	-
40006 +	+	-	-	-	-	-	-	-	-
40280 +	+	---+	+++	+++	+++	-	–	-	-
12273 +	-	-	-	-	-	-	-	-	-
39225 +	+	–	+	+	++	-	-	-	-
37759 +	++	---+	+++	+++	+++	+	-	-	-
40281 +	+	---+	+++	+++	+++	+	-	-	-
38858 +	-	-	-	-	-	-	-	-	-
40282 +	+	-	+	-	+	++	--	-	-
19275 +	+	---+	+++	+++	+++	-	–	-	-
40283 +	+	---+	+++	-	+	-	-	-	-
38697 +	+	-	-	-	-	-	-	-	-
40284 +	+	-	-	-	-	-	-	-	-
40285 +	-	---+	-	+	-	-	-	-	-
39989 +	+	-	-	-	-	-	–	-	-
11745 +	+	-	-	-	-	+	–	-	-
13690 +	+	-	-	-	-	-	-	-	-
39853 +	+	---+	+++	+++	+++	-	-	-	-
40286 +	+	---+	+++	+++	+++	+	–	-	-
12868 +	-	-	-	-	-	-	-	-	-
40287 +	+	-	-	-	-	-	-	-	-
11452 +	-	-	-	-	-	-	-	-	-
39705 +	+	-	-	-	-	-	-	-	-
13757 +	+	-	-	-	-	-	-	-	-
10964 +	-	-	-	-	-	-	-	-	-

40288 +	+	-	-	-	-	-	-	-	-
17912 +	+	–	++	-	+	-	-	-	-
39495 +	+	–+	+++	+++	+++	+	–	-	-
39147 +	+	-	-	-	-	-	-	-	-
40289 +	+	–+	+++	+++	+++	-	-	-	-
39197 +	-	-	-	-	-	-	-	-	-
39914 +	-	–+	+	+++	+	+++	–––	+++	-
40290 +	+	–+	+++	+++	+++	+	–	-	-
40291 +	++	–+	+++	+++	+++	+	-	-	-
13975 +	+	-	-	-	-	-	-	-	-
39723 +	++	-	-	-	-	-	-	-	-
39332 +	+	–	+	+	+	-	–	-	-
38921 +	+	–+	+++	+++	+++	+	-	-	-
17313 +	+	-	-	-	-	+	–	-	-
11635 +	-	-	-	-	-	-	-	-	-
16035 +	+	-	-	-	-	-	-	-	-
40292 +	+	-	-	-	-	-	-	-	-
11088 +	-	-	-	-	-	-	-	-	-
13900 +	+	-	-	-	-	-	-	-	-
13601 +	+	-	-	-	-	-	-	-	-
39025 +	+	–+	+++	+++	+++	-	-	-	-
13549 +	+	-	-	-	-	+	–	-	-
13741 +	+	-	-	-	-	++	––	-	-
39546 +	-	-	-	-	-	-	-	-	-
13534 +	+	-	-	-	-	-	-	-	-
40293 +	-	-	-	-	-	-	-	-	-
19796 +	+	–+	+++	+++	+++	-	–	-	-
11180 +	+	-	-	-	-	-	-	-	-
39786 +	-	-	-	+	-	-	-	-	-
40294 +	+	–+	+++	+++	+++	+	–	-	-
39548 +	-	–+	-	+	-	-	-	+++	-
40295 +	+	-	-	-	-	-	-	-	-
39639 +	+	-	-	-	-	-	-	-	-

40296 +	+	-	-	-	-	-	-	-	-
40297 +	+	-	-	-	-	-	-	-	-
18749 +	-	-	-	-	-	-	-	-	-
17843 +	-	-	-	-	-	-	-	-	-
40298 +	+	--+	+++	+++	+++	+	-	-	-
40018 +	-	--+	++	+++	+	+++	---	-	-
40036 +	-	-	-	-	-	-	-	-	-
40299 +	-	-	-	-	-	-	-	-	-
40300 +	+	-	-	-	-	-	-	-	-
40301 +	+	--+	+++	+++	+++	++	-	-	-
14873 +	++	-	+	+	++	+++	---	-	-
15963 +	+	-	-	-	-	-	-	-	-
40302 +	+	--+	+++	+++	+++	+	-	-	-
40303 +	+	-	-	-	-	-	-	-	-
11339 +	+	-	-	-	-	-	-	-	-
18365 +	+	-	-	-	-	-	-	-	-
14107 +	+	-	-	-	-	-	-	-	-
40304 +	+	-	-	-	-	-	-	-	-
39359 +	+	-	-	-	-	-	-	-	-
39784 +	+	-	-	-	-	-	-	-	-
40305 +	-	-	-	-	-	-	-	-	-
14588 +	+	-	-	-	-	-	-	-	-
40306 +	+	-	-	-	-	-	-	-	-
40307 +	+	-	-	-	-	-	-	-	-
40308 +	+	--+	+++	+++	+++	+	-	-	-
18730 +	-	-	-	-	-	-	-	-	-
14316 +	+	-	-	-	-	+	-	-	-
40309 +	+	--+	+++	+++	+++	+	-	-	-
14440 +	+	-	-	-	-	-	-	-	-
40310 +	+	--+	+++	+++	+++	-	-	-	-
11992 +	-	-	-	-	-	-	-	-	-
39225 +	+	-	+	+	+	-	-	-	-
14029 +	+	-	-	-	-	-	-	-	-

40311 +	+	-	-	-	-	+	–	-	-
13758 +	+	-	-	-	-	-	-	-	-
11040 +	+	–	++	++	++	+++	---	-	-
40312 +	+	--+	+++	+++	+++	-	-	-	-
40313 +	+	--+	+++	+++	+++	+	-	-	-
40314 +	+	-	-	-	-	-	-	-	-
40240 +	+	--+	+++	+++	+++	-	-	-	-
40144 +	+	-	-	-	-	-	-	-	-
40315 +	+	-	-	-	-	+	–	-	-
11329 +	-	-	-	-	-	-	-	-	-
40316 +	+	-	-	-	-	-	-	-	-
14103 +	+	-	-	-	-	-	-	-	-
40317 +	+	--+	+++	+++	+++	-	–	-	-
11515 +	+	-	-	-	-	-	-	-	-
40318 +	+	-	-	-	-	-	-	-	-
40319 +	-	-	-	-	-	+++	---	-	-
39494 +	+	--+	+++	+++	+++	+	-	-	-
40320 +	+	-	-	-	-	-	-	-	-
40321 +	+	--+	+++	+++	+++	-	–	-	-
36417 +	+	--+	+++	+++	+++	-	–	-	-
39665 +	+	-	-	-	-	-	-	-	-
40322 +	+	--+	+++	+++	+++	-	-	-	-
40323 +	+	–	+	-	-	-	-	-	-
39950 +	++	-	-	-	-	-	-	-	-
14137 +	++	-	-	-	-	-	-	-	-
11916 +	-	-	-	-	-	-	-	-	-
40324 +	-	-	-	-	-	-	-	-	-
39381 +	++	-	-	-	-	-	-	-	-
40325 +	+	-	-	-	-	-	-	-	-
40326 +	+	-	-	-	-	-	-	-	-
40327 +	+	-	-	-	-	-	-	-	-
40314 +	+	-	-	-	-	-	-	-	-
40323 +	+	–	+	-	-	-	-	-	-

14496 +	+	-	-	-	-	-	-	-	-
38994 +	++	-	-	-	-	-	-	-	-
11965 +	+	-	-	-	-	-	-	-	-
39248 +	++	-	-	-	-	-	-	-	-
13903 +	+	-	-	-	-	-	–	-	-
39936 +	+	-	-	-	-	-	-	-	-
14433 +	+	-	-	-	-	-	-	-	-
18800 +	-	-	-	-	-	-	-	-	-
39288 +	-	-	-	-	-	-	-	-	-
13510 +	+	-	-	-	+	+	–	-	-
40328 +	-	-	-	-	-	-	-	-	-
40329 +	+	-	-	-	-	-	-	-	-
17325 +	-	–+	+++	+++	+++	+	-	-	-
40330 +	+	–+	+++	+++	+++	+	-	-	-
40331 +	+	-	-	-	-	-	-	-	-
12143 +	+	-	-	-	-	-	-	-	-
40332 +	+	-	-	+	-	-	-	-	-
11792 +	+	-	-	-	-	-	-	-	-
13973 +	+	-	-	-	-	-	-	-	-
39190 +	+	-	-	-	-	-	-	-	-
40333 +	+	-	-	-	-	-	-	-	-
17203 +	++	–+	+++	+++	+++	-	-	-	-
40334 +	-	–	+	-	-	-	-	-	-
11529 +	-	-	-	-	-	-	-	-	-
13945 +	+	-	-	-	-	+	–	-	-
37020 +	+	-	-	-	-	-	-	-	-
13549 +	+	-	-	-	-	+	–	-	-
40335 +	+	–+	+++	+++	+++	-	-	-	-
40204 +	+	-	-	-	-	-	-	-	-
40305 +	-	-	-	-	-	-	-	-	-
12295 +	-	-	-	-	-	-	-	-	-
18971 +	+	-	-	-	-	-	-	-	-
14558 +	+	-	-	-	-	-	–	-	-

17645 +	-	-	-	-	-	-	-	-	-
11158 +	+	-	-	-	-	-	-	-	-
40336 +	-	-	-	-	-	-	-	-	-
39504 +	-	-	-	-	-	-	-	-	-
40337 +	++	--+	+++	+++	+++	+	-	-	-
39631 +	-	--+	+	+++	-	-	-	-	-
40338 +	++	--+	+++	+++	+++	+	-	-	-
40339 +	+	--+	+++	+++	+++	+	-	-	-
39096 +	+	-	-	-	-	-	-	-	-
18787 +	+	-	-	-	-	-	-	-	-
17429 +	+	-	-	-	-	-	-	-	-
39902 +	+	-	-	-	-	-	-	-	-
39683 +	+	-	-	-	-	-	-	-	-
11855 +	-	-	-	-	-	-	-	-	-
40340 +	+	-	-	-	-	-	-	-	-
13830 +	++	-	-	-	-	++	--	-	-
18224 +	+	-	-	-	-	-	-	-	-
40341 +	+	--+	+++	+++	+++	-	-	-	-
40342 +	+	-	-	-	-	-	-	-	-
39783 +	-	-	-	-	-	-	-	-	-
40108 +	+	--+	+++	+++	+++	+	-	-	-
40343 +	-	--	-	+++	-	-	-	-	-
40344 +	-	-	+	++	+	+	-	++	-
40345 +	+	--+	+++	+++	+++	-	-	-	-
17769 +	+	-	-	-	-	-	-	-	-
40346 +	+	--+	+++	+++	+++	+	-	-	-
39807 +	+	-	-	-	-	-	-	-	-
40347 +	+	--+	+++	+++	+++	+	-	-	-
39441 +	+	-	+	+	+	-	-	-	-
11381 +	+	-	-	-	-	-	-	-	-
14057 +	-	-	+	-	+	-	-	-	-
17635 +	+	--+	+++	+++	+++	-	-	-	-
38756 +	+	--+	++	+++	+++	+++	--	-	-

40348 +	++	−−+	+++	+++	+++	-	-	-	-
40349 +	-	-	-	-	-	+	−	-	-
40350 +	+	−−+	+++	+++	+++	+	-	-	-
40351 +	+	−−+	+++	+++	+++	-	−	-	-
20362 +	-	-	-	-	-	-	-	-	-
40352 +	+	−−+	+++	+++	+++	-	−	-	-
40353 +	+	−−+	+++	+++	+++	+	−	-	-
40146 +	-	−	+	++	+	-	-	-	-
13728 +	+	-	-	-	-	-	-	-	-
13905 +	+	-	-	-	-	-	-	-	-
39326 +	+	−	-	-	-	-	-	-	-
39842 +	+	-	-	-	-	-	-	-	-
40354 +	+	−−+	+++	+++	+++	+	−	-	-
38755 +	+	-	-	-	-	-	−	-	-
13905 +	+	-	-	-	-	-	-	-	-
11436 +	+	-	-	-	-	-	-	-	-
14400 +	++	-	-	+	+	+	−	-	-
18285 +	+	−−+	+++	+++	+++	-	-	-	-
40355 +	+	−−+	+++	+++	+++	-	-	-	-
40356 +	+	−−+	+++	+++	+++	+	-	-	-
39594 +	++	-	-	-	-	-	-	-	-
40352 +	+	−−+	+++	+++	+++	-	-	-	-
37318 +	+	−−+	++	+++	++	++	-	-	-
40357 +	+	-	+	+	+	+++	−−−	-	-
17710 +	-	-	-	-	-	-	-	-	-
11602 +	+	-	-	-	-	-	-	-	-
14090 +	+	-	-	-	-	-	-	-	-
17773 +	++	-	-	-	-	-	-	-	-
40296 +	+	-	-	-	-	-	-	-	-
39756 +	++	-	-	-	-	-	-	-	-
39952 +	+	-	-	-	-	-	-	-	-
40358 +	++	−−+	+++	+++	+++	-	-	-	-
40359 +	+	−−+	+++	+++	+++	-	-	-	-

18712	+	-	-	-	-	-	-	-	-
40360	+	+	--+	+++	+++	+++	+	-	-	-
39818	+	-	-	-	-	-	-	-	-	-
40106	+	-	-	-	-	-	-	-	-	-
39939	+	+	-	-	-	-	-	-	-	-
40361	+	+	--+	+++	+++	+++	+	-	-	-
40362	+	-	-	-	-	-	-	-	-	-
40363	+	+	--+	+++	+++	+++	-	-	-	-
39376	+	+	--+	+++	+++	+++	+	-	-	-
40364	+	+	--+	+++	+++	+++	-	-	-	-
40365	+	+	--+	+++	+++	+++	+	-	-	-
40366	+	+	--+	+++	+++	+++	+	-	-	-
14011	+	+	-	-	-	-	-	-	-	-
40183	+	+	-	-	-	-	-	-	-	-
13507	+	+	-	-	+	+	+	-	-	-
12370	+	+	-	-	-	-	-	-	-	-
39642	+	++	-	-	-	-	-	-	-	-
37949	+	+	--+	+++	+++	+++	+	-	-	-
13556	+	+	-	-	-	+	++	--	-	-
11941	+	-	-	-	-	-	-	-	-	-
40017	+	+	-	-	-	-	-	-	-	-
40367	+	+	--+	+++	+++	+++	+	-	-	-
40368	+	+	-	-	-	-	-	-	-	-
40369	+	+	-	-	-	-	-	-	-	-
40135	+	+	-	-	-	-	-	-	-	-
40370	+	+	-	-	-	-	+	-	-	-
40371	+	-	--+	+++	+++	+++	-	-	-	+++
10993	+	+	-	-	-	-	-	-	-	-
40372	+	+	-	-	-	-	-	-	-	-
13935	+	+	-	-	-	-	-	-	-	-
11152	+	++	-	-	-	-	-	-	-	-
40373	+	-	--+	+++	+++	+++	-	-	-	-
40374	+	+	--+	+++	+++	+++	-	-	-	-

14584	+	-	-	-	-	-	-	-	-
40375	+	++	--+	+++	+++	+++	+	-	-	-
40170	+	+	-	-	-	-	-	-	-	-
39475	+	+	-	-	-	-	-	-	-	-
13853	+	+	-	-	-	-	-	-	-	-
39977	+	+	-	-	-	-	-	-	-	-
15055	+	+	-	-	-	-	+	-	-	-
40376	+	++	--+	+++	+++	+++	-	-	-	-
17633	+	-	-	-	-	-	-	-	-	-
40377	+	+	--+	+++	+++	+++	+	-	-	-
40304	+	+	-	-	-	-	-	-	-	-
40378	+	+	-	-	-	-	-	-	-	-
39792	+	+	-	-	-	-	-	-	-	-
40329	+	+	-	-	-	-	-	-	-	-
40379	+	-	-	-	-	-	-	-	-	-
40380	+	-	-	++	++	+	-	-	-	-
13573	+	+	-	-	-	-	++	--	-	-
40381	+	-	-	-	-	-	-	-	-	-
40382	+	-	--+	+++	+++	+++	-	-	-	-
38963	+	-	-	-	-	-	-	-	-	-
40383	+	+	--+	+++	+++	+++	+	-	-	-
38348	+	-	-	-	-	-	-	-	-	-
40384	+	+	--+	+++	+++	+++	-	-	-	-
39623	+	-	-	-	-	-	-	-	-	-
39203	+	-	-	-	-	-	-	-	-	-
40385	+	-	-	-	-	-	-	-	-	-
16658	+	-	-	-	-	+	++	--	-	-
39502	+	+	--+	+++	+++	+++	-	-	-	-
39396	+	++	-	-	-	-	-	-	-	-
40386	+	+	--+	+++	+++	+++	+	-	-	-
40387	+	+	-	-	-	-	-	-	-	-
40388	+	-	-	-	-	-	-	-	-	-
39724	+	++	--+	+++	+++	+++	-	-	-	-

19076	+	-	--+	+++	+++	+++	-	-	-	-
18752	+	+	--+	+++	+++	+++	-	-	-	-
40098	+	+	-	-	-	-	-	-	-	-
40389	+	+	--+	+++	+++	+++	+	-	-	-
39388	+	-	-	-	-	+	+	-	-	-
40390	+	-	--+	+++	+++	+++	-	-	-	-
12577	+	-	-	-	-	-	-	-	-	-
40391	+	+	-	-	-	-	-	-	-	-
40392	+	+	-	-	-	-	-	-	-	-
39685	+	+	-	-	-	-	-	-	-	-
13883	+	+	-	+	+	+	+++	---	-	-
40393	+	+	--+	+++	+++	+++	+++	---	-	-
40394	+	+	-	-	-	-	-	-	-	-
39665	+	++	-	-	-	-	-	-	-	-
40395	+	-	-	-	-	-	-	-	-	-
38493	+	++	-	-	-	-	-	-	-	-
13791	+	+	-	-	-	-	-	-	-	-
39607	+	-	-	-	-	-	-	-	-	-
17604	+	+	-	-	-	-	-	-	-	-
11941	+	-	-	-	-	-	-	-	-	-
39269	+	+	--+	+++	+++	+++	+	-	-	-
38733	+	+	--+	+++	+++	+++	+	-	-	-
40396	+	+	-	-	-	-	-	-	-	-
16621	+	+	-	-	-	-	-	-	-	-
17038	+	-	--+	+	+++	-	-	-	-	-
39255	+	+	-	-	-	-	-	-	-	-
17749	+	-	-	-	-	-	-	-	-	-
13674	+	+	-	-	-	-	+	-	-	-
40219	+	+	-	-	-	-	-	-	-	-
39939	+	+	-	-	-	-	-	-	-	-
40397	+	-	-	-	-	-	-	-	-	-
40398	+	+	--+	+++	+++	+++	+	-	-	-
14286	+	+	-	-	-	-	-	-	-	-

39893 +	-	-	-	-	-	-	-	-	-
40399 +	-	-	-	-	-	-	-	-	-
17770 +	+	-	-	-	-	-	-	-	-
11952 +	-	-	-	-	-	-	-	-	-
40357 +	-	–	+	-	+	+++	---	-	-
38842 +	+	--+	+++	+++	+++	-	–	-	-
39802 +	+	-	-	-	-	-	-	-	-
11461 +	-	-	-	-	-	-	-	-	-
40283 +	+	--+	+++	-	-	-	-	+++	-
12286 +	+	-	-	-	-	-	-	-	-
12570 +	-	-	-	-	-	-	-	-	-
37339 +	-	–	-	-	-	-	-	-	-
12070 +	-	-	-	-	-	-	-	-	-
38383 +	-	-	-	-	+	-	-	-	-
11108 +	+	-	-	-	-	-	-	-	-
40400 +	+	--+	+++	+++	+++	-	–	-	-
39777 +	+	-	-	+	+	-	-	-	-
11777 +	-	-	-	-	-	-	-	-	-
40401 +	+	--+	+++	+++	+++	+	–	-	-
37797 +	+	--+	+++	+++	+++	+	–	-	-
40402 +	+	--+	+++	+++	+++	+	-	-	-
13597 +	+	-	-	-	-	-	–	-	-
40403 +	+	--+	+++	+++	+++	+	–	-	-
40044 +	+	--+	+++	+++	+++	+	–	-	-
14371 +	+	-	-	-	-	-	-	-	-
40404 +	-	--+	+++	+++	+++	-	–	-	-
40405 +	+	--+	+++	+++	+++	+	–	-	-
40406 +	-	-	-	-	-	-	-	-	-
11388 +	+	-	-	-	-	-	-	-	-
39736 +	+	--+	+++	+++	+++	+	–	-	-
37317 +	++	--+	+++	+++	+++	-	-	-	-
39306 +	+	-	-	-	-	-	-	-	-
40203 +	+	--+	+++	+++	+++	+	–	-	-

40407 +	++	--+	+++	+++	+++	+	-	-	-
40268 +	+	-	-	-	-	-	-	-	-
14387 +	+	-	-	-	-	+	-	-	-
17046 +	+	-	-	-	-	-	-	-	-
40395 +	-	-	-	-	-	-	-	-	-
40408 +	+	-	-	-	-	-	-	-	-
40409 +	-	-	-	-	-	-	-	-	-
11264 +	+	-	-	-	-	-	-	-	-
13885 +	+	-	-	-	-	-	-	-	-
12246 +	-	-	-	-	-	-	-	-	-
12000 +	+	-	-	-	-	-	-	-	-
13554 +	+	-	-	-	-	-	-	-	-
40410 +	-	--+	+++	+++	+++	+	-	-	-
13633 +	+	-	-	-	-	-	-	-	-
39681 +	+	-	-	-	-	-	-	-	-
39575 +	++	-	-	-	-	-	-	-	-
13597 +	+	-	-	-	-	-	-	-	-
18384 +	-	-	-	-	-	+	-	-	-
14130 +	+	-	-	-	-	-	-	-	-
11823 +	+	-	+	-	+	-	-	-	-
13878 +	++	-	-	-	-	+	-	-	-
40411 +	+	-	-	-	-	-	-	-	-
40412 +	+	--+	+++	+++	+++	+	-	-	-
40413 +	-	--+	+++	+++	+++	-	-	-	-
18062 +	-	-	-	-	-	-	-	-	-
40414 +	+	-	-	-	-	-	-	-	-
15041 +	+	-	-	-	-	++	--	-	-
40415 +	+	-	-	-	-	-	-	-	-
40189 +	+	-	-	-	-	-	-	-	-
40234 +	+	-	-	-	-	-	-	-	-
40416 +	-	-	+	-	+	-	-	-	-
39890 +	+	-	-	-	-	-	-	-	-
40369 +	+	-	-	-	-	-	-	-	-

40417 +	+	−+	+++	+++	+++	+	-	-	-
40418 +	+	−+	+++	+++	+++	+	-	-	-
38956 +	-	−−	+	+	+	+	−−	-	-
40419 +	+	-	-	+	+	-	-	-	-
39679 +	-	−	-	+	-	-	-	-	-
40420 +	+	-	-	-	-	-	-	-	-
11088 +	-	-	-	-	-	-	-	-	-
40421 +	+	−+	+++	+++	+++	-	−	-	-
13962 +	+	-	-	-	-	+	−	-	-
40422 +	+	−+	+++	+++	+++	-	-	+++	-
17427 +	++	-	-	-	-	-	-	-	-
40423 +	-	-	-	+	+	+++	−−−	-	-
12380 +	-	-	-	-	-	-	-	-	-
39797 +	++	-	+	-	-	-	−	-	-
39993 +	+	-	-	-	-	-	-	-	-
12227 +	+	-	-	-	-	-	-	-	-
39558 +	+	−+	+++	+++	+++	-	-	-	-
14691 +	+	-	-	-	-	-	-	-	-
14582 +	+	-	-	-	-	+	−	-	-
11351 +	++	-	-	-	-	-	-	-	-
38680 +	+	-	-	-	-	-	-	-	-
39592 +	-	−+	+	+++	+	+	−	-	-
18562 +	+	−+	+++	+++	+++	+	-	-	-
40424 +	+	−+	+++	+++	+++	-	−	-	-
40154 +	++	−+	+++	+++	+++	-	−	-	-
40425 +	-	−+	+++	+++	+++	+	-	-	-
39897 +	+	−	+	-	-	-	-	-	-
13560 +	+	-	-	-	-	+	−	-	-
14426 +	+	-	-	-	-	+	−	-	-
40426 +	+	−+	+++	+++	+++	+	−	-	-
40427 +	+	-	-	-	-	-	-	-	-
14307 +	+	-	-	-	-	-	-	-	-
40428 +	-	-	-	-	-	-	-	-	-

13822	+	+	-	-	-	-	+	–	-	-
18335	+	+	-	-	-	-	-	-	-	-
40429	+	+	-	-	-	-	-	-	-	-
39740	+	+	-	-	-	-	-	-	-	-
40430	+	+	-	-	-	-	-	-	-	-
39839	+	+	---+	+++	+++	+++	+	–	-	+++
16642	+	++	-	+	+	+	+	--	-	-
39719	+	+	-	-	-	-	-	-	-	-
38395	+	-	-	-	-	-	-	-	-	-
40431	+	+	-	-	-	-	-	-	-	-
10978	+	+	-	-	+	+	-	-	-	-
14501	+	++	-	-	-	-	-	-	-	-
15950	+	+	–	+	+	+	+++	---	-	-
16047	+	+	-	-	-	-	-	-	-	-
13980	+	+	-	-	-	-	-	-	-	-
40432	+	+	-	+	-	-	-	-	-	-
40433	+	++	-	-	-	-	-	-	-	-
40434	+	+	---+	+++	+++	+++	+	-	-	-
38954	+	++	-	-	-	-	-	-	-	-
40435	+	+	-	-	-	-	-	-	-	-
40297	+	+	-	-	-	-	-	-	-	-
17064	+	-	-	-	-	-	-	-	-	-
40436	+	-	–	+	-	-	-	-	-	-
14168	+	++	-	-	-	-	-	-	-	-
13654	+	+	-	-	-	-	-	-	-	-
40437	+	-	-	-	-	-	-	-	-	-
11353	+	-	-	-	-	-	-	-	-	-
39515	+	+	-	-	-	-	-	-	-	-
40438	+	+	-	-	-	-	-	-	-	-
17905	+	+	-	-	-	-	-	-	-	-
40439	+	+	---+	+++	+++	+++	-	-	-	-
14692	+	+	–	+	-	-	++	--	-	-
39424	+	++	-	-	-	-	-	-	-	-

39626 +	+	-	-	-	-	-	-	-	-
40440 +	+	-	-	-	-	-	-	-	-
40441 +	+	-	-	-	-	-	-	-	-
12291 +	-	-	-	-	-	-	-	-	-
40411 +	+	-	-	-	-	-	-	-	-
20365 +	-	-	-	-	-	-	-	-	-
40442 +	+	-	-	-	-	-	-	-	-
11294 +	+	-	-	-	-	-	-	-	-
39669 +	-	-	-	-	-	-	-	-	-
39938 +	+	-	-	-	-	-	-	-	-
19124 +	-	-	+	++	-	+	–	-	-
40019 +	-	–+	+	+++	+	+	–	-	-
40443 +	+	–+	+++	+++	+++	+	-	-	-
13586 +	++	-	+	-	-	++	–	-	-
40444 +	+	-	-	-	-	-	-	-	-
40445 +	+	–+	+++	+++	+++	-	-	-	-
40437 +	-	-	-	-	-	-	-	-	-
14432 +	+	-	-	-	-	-	-	-	-
40446 +	+	-	-	-	-	-	-	-	-
17556 +	+	-	-	-	-	-	-	-	-
12406 +	+	-	-	-	-	-	-	-	-
40447 +	+	-	-	-	-	-	-	-	-
40250 +	-	-	+	+	+	+++	–––	-	-
19305 +	+	–+	+++	+++	+++	+	–	-	-
40448 +	+	–+	+++	+++	+++	-	-	-	-
12142 +	+	-	-	-	-	-	-	-	-
39275 +	+	-	+	+	+	+	–	-	-
40449 +	+	–+	+++	+++	+++	-	–	-	-
38557 +	-	–	+	-	-	-	-	-	-
40450 +	+	-	-	-	-	-	-	-	-
14133 +	+	-	-	-	-	-	-	-	-
14490 +	+	-	-	-	-	-	-	-	-
40451 +	+	-	-	-	-	-	-	-	-

40452 +	++	-	-	-	-	-	-	-	-
40453 +	+	-	-	-	-	-	-	-	-
13723 +	+	-	-	-	-	-	-	-	-
40311 +	+	-	-	-	-	+	–	-	-
39207 +	+	-	-	-	-	-	-	-	-
40454 +	+	–	+	+	+	+++	–––	-	-
40455 +	-	––	++	++	++	+++	–––	-	-
38664 +	++	-	-	-	-	-	-	-	-
13555 +	+	-	-	-	-	+	–	-	-
14664 +	+	-	-	-	-	+	–	-	-
40248 +	-	–	-	-	-	-	-	-	-
40456 +	+	––+	+++	+++	+++	-	-	-	-
39456 +	-	-	-	-	-	-	-	-	-
39408 +	+	-	-	-	-	-	-	-	-
40457 +	-	-	-	-	-	-	-	-	-
11245 +	+	-	-	-	-	-	-	-	-
14481 +	-	-	-	-	-	-	-	-	-
13875 +	+	-	-	-	-	-	-	-	-
20402 +	+	––+	+++	+++	+++	-	–	-	-
40458 +	+	-	-	-	-	-	-	-	-
40459 +	+	-	-	-	-	-	-	-	-
39491 +	+	-	-	-	-	-	-	-	-
11449 +	+	-	-	-	-	-	-	-	-
14217 +	+	-	-	-	-	++	––	-	-
18809 +	-	-	-	-	-	+	-	-	-
11389 +	+	-	-	-	-	-	-	-	-
40460 +	+	-	-	-	-	-	–	-	-
13575 +	+	-	-	-	-	-	-	-	-
11497 +	-	–	+	+	+	+++	–––	-	-
40461 +	+	-	-	-	-	-	-	-	-
40462 +	-	–	-	-	-	-	-	-	-
40463 +	+	-	-	-	-	-	-	-	-
40464 +	-	-	-	-	-	-	-	-	-

12033 +	+	-	-	-	-	-	-	-	-
40336 +	-	-	-	-	-	-	-	-	-
40465 +	+	-	-	-	-	-	-	-	-
40466 +	+	---+	+++	+++	+++	++	-	-	-
40467 +	+	---+	+++	+++	+++	+	–	-	-
18492 +	+	---+	+++	+++	+++	+	–	+++	-
17499 +	-	---+	+	+	+	-	–	-	-
11002 +	-	-	-	-	-	-	-	-	-
40214 +	+	---+	+++	+++	+++	+	-	-	-
18513 +	++	-	-	-	-	-	-	-	-
40468 +	-	---+	+	+++	+	-	-	+++	-
40336 +	-	-	-	-	-	-	-	-	-
11143 +	-	-	-	-	-	-	-	-	-
40469 +	+	-	-	-	-	-	-	-	-
40470 +	-	-	+	-	+	+++	---	-	-
13666 +	+	-	-	-	+	+++	---	-	-
17009 +	+	–	+	+	++	+++	---	-	+++
40471 +	-	–	+	+++	++	+++	---	-	-
40472 +	-	-	-	-	-	-	-	-	-
11548 +	+	-	-	-	-	-	-	-	-
12000 +	+	-	-	-	-	-	-	-	-
14178 +	+	-	-	-	-	-	-	-	-
38386 +	++	-	-	-	-	-	–	-	-
13692 +	+	-	-	-	-	-	-	-	-
40273 +	+	-	-	-	-	-	-	-	-
40320 +	+	-	-	-	-	-	-	-	-
40306 +	+	-	-	-	-	-	-	-	-
18126 +	-	-	-	-	-	-	-	-	-
39587 +	+	---+	+++	+++	+++	+	–	-	-
38314 +	+	-	-	-	-	-	-	-	-
40473 +	+	–	+	-	-	-	-	-	-
40474 +	+	---+	+++	+++	+++	+	–	-	-
17101 +	+	---+	+++	+++	+++	-	-	-	-

11281 +	+	-	-	-	-	-	-	-	-
40475 +	-	–	-	+	-	-	-	-	-
40476 +	+	-	-	-	-	-	-	-	-
18885 +	+	–+	+++	+++	+++	+	–	-	-
40430 +	+	-	-	-	-	-	-	-	-
40477 +	+	-	-	-	-	-	-	-	-
40153 +	+	-	-	-	-	-	-	-	-
40478 +	+	–+	+++	+++	+++	+	–	-	-
40479 +	+	–+	+++	+++	+++	+	–	-	-
40480 +	+	–+	+++	+++	+++	-	–	-	-
11028 +	+	-	-	-	-	-	-	-	-
16128 +	+	-	-	-	-	-	-	-	-
17778 +	+	-	-	-	-	-	-	-	-
40481 +	+	–+	+++	+++	+++	+	-	-	-
14340 +	+	-	-	-	-	+	–	-	-
40482 +	+	–+	+++	+++	+++	+	-	-	-
39944 +	+	-	-	-	-	-	-	-	-
40483 +	+	-	-	-	-	-	-	-	-
16565 +	+	–	-	+	-	-	-	-	-
13888 +	+	-	-	-	-	-	-	-	-
40238 +	+	-	-	-	-	-	-	-	-
40484 +	+	-	-	-	-	-	-	-	-
40311 +	++	-	-	-	+	+	–	-	-
40485 +	+	–+	+++	+++	+++	+	–	-	-
12246 +	-	-	-	-	-	-	-	-	-
39747 +	+	-	-	-	-	-	–	-	-
40486 +	+	-	-	-	-	-	-	-	-
38766 +	+	-	-	-	-	-	-	-	-
40487 +	-	-	-	-	+	+	–	-	-
13898 +	+	-	-	-	-	-	-	-	-
14347 +	+	-	-	-	-	-	-	-	-
40488 +	+	-	-	-	-	-	-	-	-
17697 +	-	–	-	-	-	-	–	-	-

40489 +	+	-	-	-	-	-	-	-	-
40490 +	-	-	-	-	-	-	-	-	-
40491 +	+	---+	+++	+++	+++	-	-	-	-
38839 +	++	-	-	-	-	-	-	-	-
40492 +	-	-	+	+	+	+++	---	-	-
40493 +	-	---+	-	+	-	-	-	-	-
40429 +	+	-	-	-	-	-	-	-	-
14141 +	+	-	-	-	-	-	-	-	-
39103 +	+	–	+	+	++	-	-	-	-
40494 +	+	---+	+++	+++	+++	+++	---	-	-
40495 +	++	---+	+++	+++	+++	-	-	-	-
39996 +	+	-	-	-	-	-	-	-	-
13539 +	+	-	-	-	-	-	-	-	-
11223 +	+	-	-	-	-	-	-	-	-
40496 +	+	-	-	-	-	-	-	-	-
40497 +	+	---+	+++	+++	+++	-	-	-	-
40245 +	+	-	-	-	-	-	-	-	-
13545 +	+	-	-	-	-	+	-	-	-
40432 +	+	-	-	-	-	-	-	-	-
13719 +	+	-	-	-	-	-	-	-	-
40414 +	+	-	-	-	-	-	-	-	-
40498 +	-	-	-	-	-	-	-	-	-
40206 +	-	-	-	-	-	-	-	-	-
40499 +	+	-	-	-	-	-	-	-	-
40500 +	+	---+	+++	+++	+++	+	–	-	-
40501 +	+	---+	+++	+++	+++	-	–	-	-
39240 +	+	-	-	-	-	-	-	-	-
17557 +	-	--	-	++	-	-	-	-	-
40502 +	+	---+	+++	+++	+++	-	–	-	-
40489 +	+	-	-	-	-	-	-	-	-
10994 +	+	---+	+++	+++	+++	-	-	-	-
40503 +	-	-	+	-	+	+++	---	-	-
14032 +	+	-	-	-	-	+	–	-	-

40504 +	++	−−+	+++	+++	+++	+	-	-	-
17663 +	-	−−	-	++	-	-	-	-	-
40505 +	-	−−+	+++	+++	+++	-	-	-	-
40506 +	-	−−+	+++	+++	+++	-	-	-	-
17475 +	-	-	-	-	-	+	−	-	-
40507 +	+	−−+	+++	+++	+++	+	−	-	-
39748 +	-	-	-	-	-	-	-	-	-
40095 +	+	-	-	-	-	-	-	-	-
39105 +	+	-	-	-	-	-	-	-	-
40481 +	+	−−+	+++	+++	+++	+	−	-	-
40079 +	+	−−+	+++	+++	+++	+	−	-	-
39540 +	++	-	-	-	-	+	−	-	-
37503 +	-	-	-	-	-	-	-	-	-
40508 +	+	−−+	+++	+++	+++	-	-	-	-
40509 +	+	-	-	-	-	-	-	-	-
13896 +	+	-	-	-	-	-	-	-	-
40510 +	++	−−+	+++	+++	+++	+	-	-	-
40511 +	+	-	-	-	-	-	−	-	-
13803 +	+	-	-	-	-	-	-	-	-
40512 +	+	−−+	+++	+++	+++	-	-	-	-
17600 +	-	-	-	-	-	-	-	-	-
40513 +	+	−−+	+++	+++	+++	+	-	-	-
39855 +	-	-	-	-	-	-	-	-	-
17524 +	-	-	-	-	-	-	-	-	-
17313 +	+	-	-	-	-	+	−	-	-
39283 +	++	-	-	-	-	-	-	-	-
20367 +	-	-	-	-	-	-	-	-	-
12170 +	+	-	-	-	-	-	-	-	-
40514 +	+	−−+	+++	+++	+++	+	-	-	-
39599 +	++	-	-	-	-	-	-	-	-
40515 +	+	−−+	+++	+++	+++	+	-	-	-
40516 +	+	−−+	+++	+++	+++	-	-	-	-
13822 +	+	-	-	-	-	+	−	-	-

40517	+	+	−−+	+++	+++	+++	+	-	-	-
40518	+	+	−−+	+++	+++	+++	-	-	-	-
38707	+	-	−	+	+	+	-	-	-	-
40519	+	+	−−+	+++	+++	+++	+	-	-	-
40074	+	-	-	-	-	-	-	-	-	-
40246	+	+	-	-	-	-	-	-	-	-
40520	+	-	-	-	-	-	-	-	-	-
38412	+	-	−−+	+++	+++	+++	-	-	-	-
39995	+	+	−−+	+++	+++	+++	-	−	-	-
19213	+	-	-	-	-	-	-	-	-	-
17622	+	+	-	-	-	-	-	-	-	-
40521	+	-	-	-	+	-	-	-	-	-
40475	+	-	−	+	+	-	-	-	-	-
40522	+	+	−−+	+++	+++	+++	+	-	-	-
40523	+	+	-	-	-	-	-	-	-	-
40524	+	-	-	-	-	-	-	-	-	-
40525	+	+	−−+	+++	+++	+++	+++	−−−	-	-
40202	+	+	−−+	+++	+++	+++	-	−	-	-
40526	+	+	−−+	+++	+++	+++	+	−	-	-
40527	+	+	-	-	-	-	-	-	-	-
40230	+	+	-	-	+	+	-	-	-	-
40528	+	-	-	-	-	-	-	-	-	-
11388	+	+	-	-	-	-	-	-	-	-
39726	+	++	-	-	-	-	-	-	-	-
11002	+	-	-	-	-	-	-	-	-	-
40523	+	+	-	-	-	-	-	-	-	-
39852	+	+	-	-	-	+	-	-	-	-
17603	+	+	-	-	-	-	-	−	-	-
13753	+	+	-	-	-	-	-	−	-	-
40529	+	+	−−+	+++	+++	+++	-	−	-	-
40530	+	+	-	-	-	-	-	-	-	-
40493	+	-	−−+	-	+	-	-	-	-	-
39957	+	+	-	-	-	-	-	-	-	-

40531	+	+	−−+	+++	+++	+++	+	−	-	-
17064	+	-	-	-	-	-	-	-	-	-
40532	+	++	-	+	++	++	+	−	-	-
40533	+	+	−−+	+++	+++	+++	+	−	-	+++
40299	+	-	-	+	-	-	-	-	-	-
37753	+	+	-	+	-	-	+	-	-	-
14047	+	+	-	-	-	-	-	-	-	-
18245	+	+	-	-	-	-	-	-	-	-
40534	+	+	−−+	+++	+++	+++	+	−	-	-
20425	+	+	-	-	-	-	-	-	-	-
40151	+	-	-	-	-	-	-	-	-	-
13615	+	++	-	-	-	-	-	-	-	-
40535	+	+	−−+	+++	+++	+++	-	-	-	-
18253	+	+	-	-	-	-	-	-	-	-
13768	+	+	-	-	-	-	++	−−	-	-
40536	+	-	−−+	+++	+++	+++	-	-	-	-
40316	+	+	-	-	-	-	-	-	-	-
16041	+	+	-	-	-	-	-	-	-	-
17832	+	+	-	-	-	-	-	-	-	-
17178	+	+	−−+	+++	+++	+++	-	−	-	-
40327	+	+	-	-	-	-	-	-	-	-
11381	+	+	-	-	-	-	-	-	-	-
18864	+	+	−−+	+++	+++	+++	+	-	-	-
14286	+	+	-	-	-	-	-	-	-	-
18457	+	+	-	-	-	-	-	-	-	-
39285	+	+	-	-	-	-	-	-	-	-
11260	+	+	-	-	-	-	-	-	-	-
40537	+	+	-	-	-	-	-	-	-	-
40179	+	-	-	-	-	-	-	-	-	-
11340	+	-	-	-	-	-	-	-	-	-
17492	+	+	-	-	-	-	-	-	-	-
40498	+	-	-	-	-	-	-	-	-	-
39768	+	+	-	-	-	-	+	−	-	-

13900 +	+	-	-	-	-	-	-	-	-
15986 +	+	-	-	-	-	-	-	-	-
39562 +	+	-	-	-	-	+	–	-	-
17064 +	-	-	-	-	-	-	-	-	-
40059 +	+	-	-	-	-	-	-	-	-
40406 +	-	-	-	-	-	-	-	-	-
40538 +	+	-	-	-	-	-	-	-	-
40539 +	+	–+	+++	+++	+++	+	–	-	-
40540 +	+	–+	+++	+++	+++	+	-	-	-
40541 +	-	-	-	-	-	-	-	-	-
14293 +	+	-	-	-	-	-	-	-	-
39624 +	+	-	-	-	-	-	-	-	-
40525 +	+	–+	+++	+++	+++	+++	–––	-	-
17103 +	+	–+	+++	+++	+++	-	-	-	-
40542 +	+	-	-	-	-	-	-	-	-
40462 +	-	––	-	-	-	-	-	-	-
11452 +	-	-	-	-	-	-	-	-	-
40423 +	+	-	+	+	+	+++	–––	-	-
40543 +	+	–+	+++	+++	+++	-	––	-	-
40544 +	-	–+	+++	+++	+++	-	-	-	-
40545 +	+	–+	+++	+++	+++	-	–	-	-
40274 +	++	-	-	-	-	+	–	-	-
14328 +	+	-	-	-	-	-	-	-	-
11178 +	+	–	-	-	-	-	-	-	-
40546 +	-	–+	+++	+++	+++	-	-	-	-
14719 +	+	-	-	-	-	+	–	-	-
40547 +	-	-	-	-	-	-	-	-	-
39877 +	-	-	-	-	-	-	-	-	-
17313 +	+	-	-	-	-	+	–	-	-
40548 +	+	-	-	-	-	-	-	-	-
40549 +	+	–+	+++	+++	+++	+	–	-	-
17926 +	-	–	-	-	-	-	-	-	-
19339 +	-	-	-	-	-	-	-	-	-

14355 +	+	-	-	-	-	-	-	-	-
40550 +	-	-	-	-	+	-	-	-	-
40551 +	+	--+	+++	+++	+++	-	-	-	-
39415 +	+	-	-	-	-	-	-	-	-
39546 +	-	-	-	-	-	-	-	-	-
40552 +	-	-	-	-	-	-	-	-	-
39224 +	+	--+	+++	+++	+++	+	–	-	-
40553 +	+	--+	+++	+++	+++	-	-	-	-
38998 +	++	-	-	-	+	-	-	-	-
40554 +	-	-	-	-	-	-	-	-	-
40555 +	+	--+	+++	+++	+++	-	-	-	-
13556 +	+	-	-	-	-	++	--	-	-
14590 +	+	-	-	-	-	-	-	-	-
39827 +	++	-	-	-	+	-	-	-	-
40556 +	+	--+	+++	+++	+++	+	–	-	-
17941 +	-	-	-	-	-	-	-	-	-
40557 +	+	--+	+++	+++	+++	+	–	-	-
18693 +	++	-	-	-	-	+	-	-	-
40185 +	++	–	++	++	++	+	–	-	-
40472 +	-	-	-	-	-	-	-	-	-
40558 +	+	--+	+++	+++	+++	-	-	-	-
39484 +	+	-	-	-	-	-	-	-	-
14101 +	+	-	-	-	-	-	-	-	-
40383 +	+	--+	+++	+++	+++	+	–	-	-
40542 +	+	-	-	-	-	-	-	-	-
39187 +	++	--+	+++	+++	+++	+	-	-	-
37928 +	++	-	-	-	-	-	-	-	-
40559 +	-	-	-	-	-	-	-	-	-
38811 +	+	--+	+++	+++	+++	+	–	-	-
39888 +	+	-	-	-	-	-	-	-	-
38038 +	++	-	-	-	-	-	-	-	-
13573 +	+	-	-	-	-	++	--	-	-
13920 +	+	-	-	-	-	-	-	-	-

40560	+	+	−+	+++	+++	+++	+	−	-	-
40140	+	+	−+	+++	+++	+++	+	-	-	-
40541	+	-	-	-	-	-	-	-	-	-
39324	+	-	-	+	-	-	+	−	-	-
40561	+	+	−+	+++	+++	+++	+	−	-	-
39621	+	+	-	-	-	-	-	-	-	-
13914	+	+	-	-	-	-	-	-	-	-
40175	+	+	−+	+++	+++	+++	+	−	-	-
17349	+	+	−+	+++	+++	+++	-	-	-	-
40562	+	+	−+	+++	+++	+++	-	-	-	-
40452	+	+	-	-	-	-	-	-	-	-
40563	+	+	-	-	-	-	-	-	-	-
16636	+	+	-	-	-	-	+	−	-	-
40564	+	+	−+	+++	+++	+++	-	−	-	-
40565	+	-	-	-	-	-	-	-	-	-
40566	+	+	−+	+++	+++	+++	-	−	-	-
13759	+	+	-	-	-	-	-	-	-	-
39879	+	+	-	-	-	-	-	-	-	-
36946	+	+++	−+	+++	+++	+++	-	−	-	-
40567	+	++	-	-	-	-	+	−	-	-
14532	+	+	-	-	-	-	+	−	-	-
40237	+	+	-	-	-	-	-	-	-	-
13691	+	+	-	-	-	-	++	−−−	-	-
39381	+	+	-	-	-	-	-	-	-	-
40047	+	-	-	-	-	-	-	-	-	-
13909	+	+	-	-	-	-	-	-	-	-
39222	+	++	-	-	-	-	-	-	-	-
39087	+	+	-	-	-	-	-	-	-	-
40469	+	+	-	-	-	-	-	-	-	-
40438	+	+	-	-	-	-	-	-	-	-
39880	+	+	-	-	-	-	-	-	-	-
40568	+	-	−+	+++	+++	+++	-	-	-	-
40464	+	-	-	-	-	-	-	-	-	-

14033 +	+	-	-	-	-	-	-	-	-
18676 +	+	-	-	-	-	-	-	-	-
11333 +	+	-	-	-	-	-	-	-	-
18140 +	-	-	-	+	-	+	-	-	-
16157 +	+	-	-	-	-	-	-	-	-
40569 +	+	-	-	-	-	-	-	-	-
39864 +	-	-	-	-	-	-	-	-	-
39545 +	-	-	-	-	-	-	-	-	-
39933 +	+	-	-	-	-	-	-	-	-
40570 +	-	-	-	-	-	+	-	-	-
40571 +	++	--+	+++	+++	+++	+	-	-	-
40572 +	-	-	-	-	-	-	-	-	-
40573 +	+	-	-	-	-	-	-	-	-
40550 +	+	-	-	-	+	-	-	-	-
14308 +	+	-	-	-	-	-	-	-	-
40574 +	+	-	-	-	-	-	-	-	-
13715 +	+	-	-	-	-	++	--	+	+
39490 +	+	-	-	-	-	-	-	-	-
40575 +	+	-	-	-	-	-	-	-	-
39768 +	+	-	-	-	-	-	-	-	-
40300 +	+	-	-	-	-	-	-	-	-
13853 +	+	-	-	-	-	-	-	-	-
39663 +	-	-	-	-	-	+	–	-	-
40576 +	+	--+	+++	+++	+++	+	-	-	-
40102 +	-	-	-	-	-	-	-	-	-
39920 +	+	-	-	-	-	++	--	-	-
40577 +	+	--+	+++	+++	+++	-	-	-	-
18261 +	+	-	-	-	-	-	-	-	-
14106 +	+	-	-	-	-	-	-	-	-
39335 +	+	-	-	-	-	-	-	-	-
40578 +	+	--+	+++	+++	+++	+	–	-	-
39674 +	-	--+	+++	+++	+++	+	--	-	-
39249 +	++	–	-	+	-	+	-	-	-

40579 +	+	–	-	-	-	-	-	-	-
40580 +	+	-	-	-	-	-	-	-	-
39457 +	++	-	-	-	-	-	–	-	-
12345 +	-	-	-	-	-	-	-	-	-
40574 +	+	-	-	-	-	-	-	-	-
40581 +	+	-	-	-	-	-	-	-	-
40582 +	+	-	-	-	-	-	-	-	-
20377 +	-	–	-	-	-	-	-	-	-
18166 +	-	-	-	-	-	-	-	-	-
40583 +	+	–	+	+	+	+++	---	-	-
40150 +	+	--+	+++	+++	+++	+	-	-	-
14307 +	+	-	-	-	-	-	-	-	-
13512 +	+	-	-	+	-	++	--	-	-
16026 +	+	-	-	-	-	-	-	-	-
40584 +	++	--+	+++	+++	+++	+	-	-	-
40585 +	+	-	-	-	-	-	-	-	-
39084 +	+	-	-	-	-	+	-	-	-
17723 +	+	-	-	-	-	-	-	-	-
17821 +	-	-	-	-	-	-	-	-	-
11703 +	+	-	-	-	-	-	-	-	-
39836 +	+	-	-	-	-	-	-	-	-
40586 +	+	--+	+++	+++	+++	-	-	-	-
40587 +	+	--+	+++	+++	+++	+++	---	-	-
13909 +	+	-	-	+	-	+	–	-	-
40160 +	-	-	-	-	-	-	-	-	-
40588 +	+	-	-	-	-	-	-	-	-
40589 +	++	--+	+++	+++	+++	-	–	-	-
40590 +	++	--+	+++	+++	+++	+	–	-	-
13889 +	+	-	-	-	-	+	–	-	-
40591 +	+	-	-	-	-	-	-	-	-
40592 +	+	--+	+++	+++	+++	+	-	-	-
37746 +	++	-	-	-	-	-	-	-	-
40496 +	+	-	-	-	-	-	-	-	-

40520 +	-	-	-	-	-	-	-	-	-
11623 +	+	-	-	-	-	-	-	-	-
40593 +	+	-	+	-	+	-	-	-	-
40594 +	+	---+	+++	+++	+++	+	-	-	-
40340 +	+	-	-	-	-	-	-	-	-
13728 +	+	-	-	-	-	-	-	-	-
38087 +	+	---+	+++	+++	+++	-	-	-	-
12291 +	-	-	-	-	-	-	-	-	-
40595 +	-	-	+	-	+	+++	---	-	-
13757 +	+	-	-	-	-	-	-	-	-
14478 +	+	-	-	-	-	-	-	-	-
40234 +	+	-	-	-	-	-	-	-	-
40596 +	+	-	-	-	-	-	-	-	-
40597 +	+	-	-	-	-	-	-	-	-
40598 +	+	---+	+++	+++	+++	-	-	-	-
40599 +	-	-	-	-	-	-	-	-	-
11343 +	-	-	-	-	-	-	-	-	-
11823 +	+	-	+	-	-	-	-	-	-
40600 +	+	---+	+++	+++	+++	+	-	-	-
40601 +	++	-	-	-	-	-	-	-	-
10993 +	+	-	-	-	-	-	-	-	-
12142 +	+	-	-	-	-	-	-	-	-
40602 +	+	---+	+++	+++	+++	-	-	-	-
11254 +	+	-	-	-	-	-	-	-	-
40397 +	-	-	-	-	-	-	-	-	-
40603 +	-	-	+	+	+	++	--	-	-
38668 +	-	-	+	-	-	-	-	-	-
40604 +	+	---+	+++	+++	+++	+	-	-	-
40605 +	+	-	-	-	-	-	-	-	-
39450 +	+	---+	+++	+++	+++	+	-	-	-
12087 +	-	-	-	-	-	-	-	-	-
38374 +	++	---+	+++	+++	+++	-	-	-	-
12539 +	-	-	-	-	-	-	-	-	-

38823	+	+	−−+	+++	+++	+++	+	−	-	-
40606	+	+	−−+	+++	+++	+++	+	−	-	-
18677	+	+	-	-	-	-	-	-	-	-
40607	+	-	-	-	-	-	-	-	-	-
40608	+	+	-	-	-	-	-	-	-	-
13909	+	+	-	-	-	+	-	-	-	-
40609	+	-	−	-	-	-	-	-	-	-
40610	+	+	-	-	-	-	-	-	-	-
39572	+	+	−−+	+++	+++	+++	-	-	-	-
13610	+	+	-	-	-	-	-	-	-	-
40444	+	+	-	-	-	-	-	-	-	-
40611	+	+	-	-	-	-	-	-	-	-
11361	+	-	-	-	-	-	-	-	-	-
11607	+	-	-	-	-	-	-	-	-	-
19632	+	+	−−	++	++	-	-	-	-	-
16625	+	+	-	-	-	-	-	-	-	-
38104	+	-	-	-	-	-	+	−	-	-
40612	+	+	−−+	+++	+++	+++	+	−	-	-
14397	+	+	-	+	+	+	+++	−−−	-	-
40613	+	+	−−+	+++	+++	+++	-	−	-	-
14655	+	+	-	-	-	-	-	-	-	-
40614	+	+	-	-	-	-	-	-	-	-
38229	+	+	−	+	+	+	+++	−−−	-	-
39471	+	-	-	-	-	-	-	-	-	-
40306	+	+	-	-	-	-	-	-	-	-
39883	+	+	−−+	+++	+++	+++	+	−	-	-
40325	+	+	-	-	-	-	-	-	-	-
40615	+	+	−−+	+++	+++	+++	+	-	+++	-
39731	+	-	-	-	-	-	-	-	-	-
40616	+	+	−−+	+++	+++	+++	+	-	-	-
11110	+	+	-	-	-	-	-	-	-	-
11060	+	+	-	-	-	-	-	-	-	-
13942	+	+	-	-	-	-	-	-	-	-

19830 +	+	-	-	-	-	-	-	-	-
38804 +	++	--+	+++	+++	+++	+	-	-	-
19608 +	+	-	-	-	-	-	-	-	-
40617 +	+	--+	+++	+++	+++	+	-	-	-
13718 +	+	-	-	-	-	-	-	-	-
16590 +	+	-	-	-	-	-	-	-	-
40618 +	+	--+	+++	+++	+++	-	-	-	-
39192 +	+	-	-	-	-	-	-	-	-
20474 +	-	-	-	-	-	-	-	-	-
39307 +	+	-	+	-	+	-	-	-	-
11630 +	+	-	-	-	-	-	-	-	-
40619 +	-	-	-	-	-	++	---	-	-
38534 +	-	--+	+	+	-	-	-	-	-
40620 +	+	-	-	-	-	+	-	-	-
40621 +	+	--+	+++	+++	+++	+	-	-	-
40622 +	-	-	-	-	-	-	-	-	-
39401 +	+	-	-	-	-	-	-	-	-
39034 +	+	--+	+++	+++	+++	-	-	-	-
40454 +	+	-	+	+	+	+++	---	-	+++
40026 +	+	-	-	-	-	-	-	-	-
39569 +	-	-	-	-	-	-	-	-	-
40623 +	++	-	+	-	-	+	-	-	-
40624 +	+	--+	+++	+++	+++	-	-	-	-
13810 +	+	-	-	-	-	+	-	-	-
13812 +	+	-	-	-	-	-	-	-	-
40625 +	+	-	-	-	-	-	-	-	-
40242 +	-	-	-	-	-	-	-	-	-
40626 +	+	--	++	++	++	+++	---	-	-
14389 +	+	-	-	-	-	-	-	-	-
40414 +	+	-	-	-	-	-	-	-	-
40627 +	+	-	-	-	-	-	-	-	-
40628 +	+	-	-	-	-	+	-	-	-
40629 +	-	-	-	-	-	-	-	-	-

40630 +	+	-	-	-	+	+++	---	-	-
39849 +	+	-	-	-	-	-	-	-	-
40403 +	++	--+	+++	+++	+++	+	–	-	-
12041 +	+	-	-	-	-	-	-	-	-
39251 +	-	-	-	-	-	-	-	-	-
40631 +	+	--+	+++	+++	+++	-	-	-	-
40632 +	+	-	-	-	-	-	-	-	-
39549 +	+	-	-	-	-	-	-	-	-
39841 +	-	-	-	-	-	-	-	-	-
17991 +	-	-	-	-	-	-	-	-	-
39813 +	+	-	-	-	-	-	-	-	-
17579 +	+	--+	+++	+++	+++	-	-	-	-
14142 +	+	-	-	-	-	-	-	-	-
40633 +	-	-	-	-	-	-	-	-	-
12233 +	-	-	-	-	-	-	-	-	-
13684 +	++	-	-	-	-	-	–	-	-
40634 +	+	-	-	-	-	-	-	-	-
13723 +	+	-	-	-	-	-	-	-	-
40216 +	+	-	-	-	-	-	-	-	-
12513 +	-	-	-	-	-	-	-	-	-
39765 +	-	-	-	-	-	-	-	-	-
40635 +	-	-	-	-	-	-	-	-	-
40636 +	+	-	-	-	+	++	--	-	-
39688 +	+	-	-	-	-	-	-	-	-
39868 +	+	-	-	-	-	-	-	-	-
17414 +	+	-	-	-	-	-	-	-	-
40637 +	+	--+	+++	+++	+++	++	–	-	-
19069 +	-	-	-	-	-	-	-	-	-
13643 +	+	-	-	-	-	-	–	-	-
38924 +	-	-	-	-	-	-	-	-	-
39568 +	-	-	-	-	-	-	-	-	-
18261 +	+	-	-	-	-	-	-	-	-
40638 +	-	–	+	+	+	+++	---	+++	-

13583 +	+	-	-	-	-	-	-	-	-
40639 +	-	-	-	-	-	-	-	-	-
40640 +	-	---+	+++	+++	+++	-	-	-	-
40641 +	+	---+	+++	+++	+++	+	–	-	-
39729 +	+	-	-	-	-	-	-	-	-
40642 +	-	-	-	-	-	-	-	-	-
40643 +	+	-	-	-	-	-	-	-	-
40644 +	+	---+	+++	+++	+++	-	-	-	-
20365 +	-	-	-	-	-	-	-	-	-
40370 +	+	-	-	-	-	+	–	-	-
40188 +	+	-	-	-	-	-	-	-	-
38942 +	+	---+	+++	+++	+++	-	–	-	-
40593 +	+	-	+	-	-	-	-	-	-
40645 +	+	---+	+++	+++	+++	+++	---	+++	-
40646 +	+	---+	+++	+++	+++	+	–	-	-
40647 +	+	–	+	+	++	-	-	-	-
40446 +	-	-	-	-	-	-	-	-	-
40648 +	++	---+	+++	+++	+++	+	-	-	-
40649 +	+	---+	+++	+++	+++	+	-	-	-
39723 +	+	-	-	-	-	-	-	-	-
40650 +	-	-	-	-	-	-	-	-	-
13920 +	+	-	-	-	-	-	-	-	-
11758 +	+	-	-	-	-	-	-	-	-
40435 +	+	-	-	-	-	-	-	-	-
40651 +	+	---+	+++	+++	+++	+	-	-	-
40652 +	++	---+	+++	+++	+++	+	-	-	-
40453 +	+	-	-	-	-	-	-	-	-
13534 +	+	-	-	-	-	-	-	-	-
40653 +	+	---+	+++	+++	+++	-	–	-	-
39740 +	+	-	-	-	-	-	-	-	-
13575 +	+	-	-	-	-	-	-	-	-
40654 +	+	-	-	-	-	-	-	-	-
40655 +	+	-	-	-	-	-	-	-	-

13793 +	++	-	+	-	-	+++	---	-	-
11024 +	+	-	-	-	-	-	-	-	-
40656 +	+	--+	+++	+++	+++	-	-	-	-
14193 +	+	-	-	-	-	-	-	-	-
40203 +	+	--+	+++	+++	+++	-	-	-	-
40657 +	++	--+	+++	+++	+++	-	-	-	-
40658 +	-	--+	+++	+++	+++	-	-	-	-
13577 +	+	-	-	-	-	+	-	-	-
11178 +	+	-	+	+	+	-	-	-	-
40659 +	+	--+	+++	+++	+++	-	-	-	-
40099 +	+	-	-	-	-	-	-	-	-
40114 +	+	--+	+++	+++	+++	+	-	-	-
39962 +	++	-	-	-	-	-	-	-	-
39801 +	+	-	-	-	-	-	-	-	-
40660 +	+	-	-	-	-	-	-	-	-
40661 +	+	-	-	-	-	-	-	-	-
14160 +	+	-	-	-	-	-	-	-	-
40551 +	++	--+	+++	+++	+++	+	-	-	-
38212 +	++	--+	+++	+++	+++	-	-	-	+++
39784 +	+	-	-	-	-	-	-	-	-
39045 +	++	-	-	-	-	-	-	-	-
40426 +	+	--+	+++	+++	+++	+	-	-	-
11949 +	+	-	-	-	-	-	-	-	-
39979 +	+	-	-	-	-	-	-	-	-
40662 +	-	--+	+++	+++	+++	-	-	-	-
40663 +	-	-	+	+	+	-	-	-	-
40664 +	+	--+	+++	+++	+++	-	-	-	-
40665 +	+	--+	+++	+++	+++	+	-	-	-
38298 +	+	-	-	-	-	-	-	-	-
12108 +	+	-	-	-	-	-	-	-	-
13944 +	+	-	-	-	-	++	--	-	+
11436 +	+	-	-	-	-	-	-	-	-
40666 +	+	--+	+++	+++	+++	+	-	-	-

40667	+	-	-	-	-	-	-	-	-
39577	+	-	-	-	-	+	-	-	-
40668	+	+-	+++	+++	+++	+	-	+++	-
14011	+	-	-	-	+	-	-	-	-
39254	+	-	-	-	-	-	-	-	-
11671	+	-	-	-	-	-	-	-	-
40427	+	-	-	-	-	-	-	-	-
13771	+	-	-	-	-	-	-	-	-
17991	+	-	-	-	-	-	-	-	-
40669	+	+-	+++	+++	+++	+	-	-	-
40670	+	-	-	-	-	-	-	-	-
40671	+	++	+-	+++	+++	+++	+	-	-
40672	+	-	-	-	-	-	-	-	-
38302	+	-	-	-	-	-	-	-	-
38750	+	-	-	-	-	-	-	-	-
40673	+	+	+-	+++	+++	+++	+	-	-
18610	+	-	-	-	-	-	-	-	-
40331	+	-	-	-	-	-	-	-	-
20377	+	-	-	-	+	-	-	-	-
18156	+	-	-	-	-	-	-	-	-
40674	+	+	+-	+++	+++	+++	-	-	-
14404	+	+	-	-	-	-	-	-	-
40675	+	+	-	-	-	-	-	-	-
17420	+	+	-	-	-	-	-	-	-
40676	+	+	+-	+++	+++	+++	+	-	+++
40677	+	-	-	+	+	+	-	-	-
40678	+	+	+-	+++	+++	+++	-	-	-
40292	+	+	-	-	-	-	-	-	-
39816	+	+	-	-	-	-	-	-	-
11764	+	+	-	-	-	-	-	-	-
40679	+	+	+-	+++	+++	+++	-	-	-
18629	+	-	-	-	-	-	+	-	-
40680	+	+	+-	+++	+++	+++	-	-	-

40092 +	+	-	-	-	-	-	-	-	-
40681 +	+	–	+	++	++	-	-	-	-
40682 +	-	-	-	-	-	+	–	-	-
40683 +	+	–-+	+++	+++	+++	+	–	-	-
13987 +	+	-	-	-	-	-	-	-	-
40326 +	+	-	-	-	-	-	-	-	-
38735 +	++	–-+	+++	+++	+++	+	–	-	-
40684 +	+	-	-	-	-	-	-	-	-
40685 +	+	–-+	+++	+++	+++	+	-	-	-
11558 +	+	-	-	-	-	-	-	-	-
11235 +	-	-	-	-	-	-	-	-	-
39128 +	+	–-+	+++	+++	+++	+	-	-	-
40686 +	+	-	-	-	-	-	-	-	-
40687 +	-	-	-	-	-	-	-	-	-
40254 +	+	-	-	-	-	-	-	-	-
40688 +	+	–-+	+++	+++	+++	-	-	-	-
11073 +	+	-	-	-	-	-	-	-	-
13765 +	+	-	-	-	-	+	––	-	-
15966 +	+	-	-	-	-	-	-	-	-
11359 +	+	-	-	-	-	-	-	-	-
40689 +	+	–-+	+++	+++	+++	+	-	-	-
11918 +	+	-	-	-	-	-	-	-	-
40690 +	+	–-+	+++	+++	+++	-	-	-	-
38969 +	-	––	++	+	-	+++	–––	-	-
40691 +	+	-	-	-	-	-	-	-	-
13768 +	+	-	-	-	-	+++	–––	-	-
39737 +	-	–	+	+	-	+	–	-	-
15986 +	+	-	-	-	-	-	-	-	-
14312 +	+	-	-	-	-	-	-	-	-
39949 +	+	-	-	-	-	+	-	-	-
11110 +	+	-	-	-	-	-	-	-	-
40692 +	-	-	-	-	-	-	-	-	-
13702 +	-	-	-	-	-	-	-	-	-

11254 +	+	-	-	-	-	-	-	-	-
18286 +	-	-	-	-	-	+	–	-	-
40528 +	-	-	-	-	-	-	-	-	-
14279 +	+	-	-	-	-	-	-	-	-
17905 +	+	-	-	-	-	-	-	-	-
40050 +	+	–	+	+	+	-	-	-	-
38655 +	-	-	-	-	-	-	-	-	-
13874 +	+	-	-	-	+	-	-	-	-
40039 +	-	-	-	-	-	-	-	-	-
40260 +	-	-	-	-	-	-	-	-	-
40693 +	+	–+	+++	+++	+++	-	-	-	-
40694 +	+	–+	+++	+++	+++	-	–	-	-
40225 +	+	–+	+++	+++	+++	+	-	-	-
40695 +	-	-	-	-	-	-	-	-	-
40567 +	++	-	-	-	-	-	-	-	-
40696 +	+	–+	+++	+++	+++	+	-	-	-
40697 +	-	–+	-	+	-	-	-	-	-
40698 +	-	–+	+++	+++	+++	-	–	-	-
39286 +	-	-	-	-	-	-	-	-	-
38999 +	++	-	-	-	-	-	-	-	-
11305 +	+	-	-	-	-	-	-	-	-
40699 +	+	–+	+++	+++	+++	-	-	-	-
14969 +	+	-	-	-	+	+++	---	-	+++
38400 +	+	–+	+++	+++	+++	+	–	-	-
40700 +	-	-	+	-	+	+++	---	-	-
17902 +	++	-	-	-	-	-	-	-	-
40701 +	+	–+	+++	+++	+++	+++	---	-	-
14237 +	+	-	-	-	-	-	-	-	-
40702 +	-	–	+	+	+	+++	---	++	++
13809 +	+	-	-	-	-	-	-	-	-
40168 +	++	–+	+++	+++	+++	-	-	-	-
20058 +	++	–+	+++	+++	+++	-	-	-	-
39625 +	-	-	-	-	-	-	-	-	-

38176	+	+	−+	+++	+++	+++	-	−	-	-
40521	+	-	-	-	+	-	-	-	-	-
39813	+	+	-	-	-	-	-	-	-	-
40703	+	+	−	+	+	-	-	-	-	-
18812	+	-	-	-	-	-	-	-	-	-
11340	+	-	-	-	-	-	-	-	-	-
15041	+	+	-	-	-	-	++	−−	++	-
40704	+	+	−+	+++	+++	+++	+	-	-	-
40705	+	-	-	-	-	-	-	-	-	-
19663	+	+	-	-	-	-	-	-	-	-
40217	+	+	-	-	-	-	-	-	-	-
40706	+	+	-	-	-	-	-	-	-	-
11555	+	+	-	-	-	-	-	-	-	-
40707	+	+	-	-	-	-	-	-	-	-
40708	+	+	−+	+++	+++	+++	+	−	-	-
39842	+	+	-	-	-	-	-	-	-	-
18682	+	-	-	-	-	-	-	-	-	-
17246	+	+	−+	+++	+++	+++	-	-	-	-
40709	+	+	-	+	-	-	-	-	-	-
40710	+	+	-	-	-	-	+	−	-	-
40711	+	+	−+	+++	+++	+++	+	−	-	-
40488	+	+	-	-	-	-	-	-	-	-
12485	+	-	-	-	-	-	-	-	-	-
14584	+	-	-	-	-	-	-	-	-	-
40712	+	+	−+	+++	+++	+++	-	-	-	-
40713	+	+	-	-	-	-	+	-	-	-
13865	+	+	-	-	-	-	-	-	-	-
40714	+	+	-	-	-	-	-	-	-	-
39881	+	+	−	++	+	++	-	−	-	-
40715	+	+	−+	+++	+++	+++	+	-	-	-
12577	+	-	-	-	-	-	-	-	-	-
39399	+	+	-	-	-	-	-	-	-	-
40449	+	+	−+	+++	+++	+++	-	−	-	-

40716 +	+	−+	+++	+++	+++	+	−	-	-
40384 +	+	−+	+++	+++	+++	-	−	-	-
40215 +	++	-	-	-	-	-	-	-	-
40717 +	-	-	-	-	-	-	-	-	-
14590 +	+	-	-	-	-	-	-	-	-
40718 +	+	-	-	-	-	-	-	-	-
17871 +	-	−	-	-	-	-	-	-	-
40406 +	-	-	-	-	-	-	-	-	-
40675 +	+	-	-	-	-	-	-	-	-
20380 +	+	-	-	-	-	-	-	-	-
40451 +	+	-	-	-	-	-	-	-	-
40719 +	+	−+	+++	+++	+++	+	-	-	-
16007 +	+	-	-	-	-	-	-	-	-
40660 +	++	-	-	-	-	-	-	-	-
13506 +	+	-	-	-	-	+	−	-	-
40720 +	+	−+	+++	+++	+++	+	-	-	-
40721 +	+	−+	+++	+++	+++	-	−	-	-
14011 +	+	-	-	-	-	-	-	-	-
39554 +	+	-	-	-	-	-	-	-	-
40722 +	-	−+	+++	+++	+++	-	-	-	-
14500 +	+	−	+	+	+	+++	−−−	-	-
40296 +	+	-	-	-	-	-	-	-	-
12626 +	-	-	-	-	-	-	-	-	-
40068 +	+	-	-	-	-	-	-	-	-
14308 +	+	-	-	-	-	-	-	-	-
18284 +	-	−+	+	+++	+	-	-	-	-
38400 +	+	−+	+++	+++	+++	+	−	-	-
14157 +	+	-	-	-	-	-	-	-	-
13766 +	+	-	+	+	+	+++	−−−	-	-
16128 +	+	-	-	-	-	-	-	-	-
14494 +	-	-	-	-	-	-	-	-	-
37020 +	++	-	-	-	-	-	-	-	-
12295 +	-	-	-	-	-	-	-	-	-

40723	+	+	–+	+++	+++	+++	+	-	-	-
40196	+	+	-	-	-	-	-	-	-	-
40724	+	+	–+	+++	+++	+++	+	-	-	-
40335	+	+	–+	+++	+++	+++	+	-	-	-
13854	+	+	-	-	-	-	-	-	-	-
40336	+	-	-	-	-	-	-	-	-	-
17313	+	+	-	-	-	-	+	–	-	-
40725	+	+	–+	+++	+++	+++	-	-	-	-
40726	+	-	-	-	-	-	+	-	-	-
40727	+	+	-	-	-	-	+	–	-	-
40728	+	+	-	-	-	-	-	-	-	-
16079	+	-	-	-	-	-	-	-	-	-
40729	+	+	–+	+++	+++	+++	-	-	-	-
40283	+	+	–+	+++	-	-	-	-	-	-
40333	+	+	-	-	-	-	-	-	-	-
11576	+	-	-	-	-	-	-	-	-	-
12539	+	-	-	-	-	-	-	-	-	-
14481	+	-	-	-	-	-	-	-	-	-
40392	+	+	-	-	-	-	-	-	-	-
40730	+	+	–+	+++	+++	+++	+	–	-	-
16086	+	+	-	-	-	-	-	-	-	-
17567	+	-	–	-	-	-	-	-	-	-
13721	+	+	-	-	-	-	-	-	-	-
40731	+	+	–+	+++	+++	+++	-	-	-	-
40578	+	+	–+	+++	+++	+++	+	–	-	-
40732	+	+	–+	+++	+++	+++	-	-	-	-
40733	+	+	–	+	+	+	+++	–––	-	-
39539	+	-	-	-	-	-	-	-	-	-
10986	+	+	-	-	-	-	-	-	-	-
40734	+	+	–+	+++	+++	+++	+	–	-	-
40735	+	+	-	-	-	-	-	-	-	-
38113	+	+	-	-	-	+	+	-	-	-
40619	+	-	–	+	-	+	++	–––	-	-

13771	+	+	-	-	-	-	+	-	-	-
40258	+	+	-	-	-	-	+	-	-	-
40736	+	+	--+	+++	+++	+++	-	–	-	-
40605	+	+	-	+	-	+	-	-	-	-
11165	+	+	-	-	-	-	-	-	-	-
39564	+	++	--+	+++	+++	+++	-	-	-	+++
14780	+	+	--+	+++	+++	+++	+	-	-	-
40014	+	+	--+	+++	+++	+++	+	-	-	-
40737	+	+	-	-	-	-	-	-	-	-
40738	+	+	--+	+++	+++	+++	-	–	-	-
40739	+	+	-	-	-	-	-	-	-	-
40740	+	+	-	-	-	-	-	-	-	-
13633	+	+	-	-	-	-	-	-	-	-
39762	+	-	-	-	-	-	-	-	-	-
40741	+	+	--+	+++	+++	+++	-	-	-	-
36737	+	+	--+	+++	+++	+++	+	–	-	-
13693	+	+	-	-	-	-	++	--	-	-
40742	+	+	--+	+++	+++	+++	-	-	-	-
39572	+	+	--+	+++	+++	+++	+	–	-	-
13849	+	+	-	-	-	-	++	--	-	-
40743	+	+	-	-	-	-	+	-	-	-
40744	+	+	--+	+++	+++	+++	+	-	-	-
17338	+	+	--+	+++	+++	+++	-	-	-	-
17521	+	+	-	-	-	+	-	-	-	-
19457	+	+	--+	+++	+++	+++	-	-	-	-
40745	+	-	–	+	+	++	+	–	-	-
40746	+	+	--+	+++	+++	+++	-	-	-	-
40234	+	+	-	-	-	-	-	-	-	-
40687	+	-	-	-	-	-	-	-	-	-
40283	+	+	--+	+++	-	-	-	-	+++	-
40747	+	-	-	-	-	-	-	-	-	-
13632	+	+	-	-	-	+	++	--	-	-
39956	+	+	--+	+++	+++	+++	+	–	-	-

11604 +	+	-	-	-	-	-	-	-	-
13873 +	+	-	-	-	-	-	-	-	-
40748 +	+	-	-	-	+	-	–	-	-
40749 +	+	–+	+++	+++	+++	-	–	-	-
14547 +	+	-	-	-	-	-	-	-	-
14142 +	+	-	-	-	-	-	-	-	-
38747 +	+	–	++	++	+++	+++	–––	-	-
40573 +	+	-	-	-	-	-	-	-	-
40750 +	+	–+	+++	+++	+++	+	–	-	-
13588 +	+	-	-	-	-	+	–	-	-
13817 +	+	-	-	-	-	-	-	-	-
11200 +	-	-	-	-	-	-	-	-	-
40751 +	+	–+	+++	+++	+++	+	-	-	-
40487 +	-	–	+	-	+	-	-	-	-
13690 +	+	-	-	-	-	-	-	-	-
40752 +	+	–+	+++	+++	+++	-	-	-	-
40086 +	-	-	-	-	-	-	-	-	-
17824 +	-	-	-	-	-	-	-	-	-
40753 +	+	–+	+++	+++	+++	+	-	-	-
16138 +	+	-	-	-	-	-	-	-	-
14433 +	+	-	-	-	-	-	-	-	-
40754 +	-	-	-	-	-	-	-	-	-
40581 +	+	-	-	-	-	-	-	-	-
39009 +	+	-	-	-	-	-	-	-	-
14494 +	-	-	-	-	-	-	-	-	-
40755 +	+	–+	+++	+++	+++	+	-	-	-
14061 +	+	-	-	-	-	++	––	-	-
11643 +	+	-	-	-	-	-	-	-	-
40756 +	+	–+	+++	+++	+++	-	-	-	-
14032 +	+	-	-	-	-	+	–	-	-
10984 +	+	-	+	+	+	+	–	-	-
40757 +	+	–+	+++	+++	+++	+	–	-	-
17263 +	++	–+	+++	+++	+++	-	-	-	-

16047 +	+	-	-	-	-	-	-	-	-
40758 +	+	--+	+++	+++	+++	++	-	-	-
13541 +	+	-	-	-	-	+++	---	-	-
40319 +	-	-	+	-	-	+++	---	-	-
12017 +	+	-	-	-	-	-	-	-	-
40759 +	+	-	-	-	-	-	-	-	-
40760 +	+	-	-	-	-	-	-	-	-
39899 +	-	-	-	-	-	-	-	-	-
11900 +	+	-	-	-	-	++	--	-	-
14203 +	+	-	-	-	-	-	-	-	-
40761 +	++	--+	+++	+++	+++	-	-	-	-
39598 +	+	-	-	-	-	-	-	-	-
40001 +	++	--+	+++	+++	+++	+	-	-	-
17364 +	+	--+	+++	+++	+++	-	-	-	-
40762 +	+	-	-	-	-	-	-	-	-
40763 +	+	--+	+++	++	+++	+++	---	-	-
17853 +	+	--+	+++	+++	+++	-	-	-	-
39783 +	-	-	-	-	-	-	-	-	-
14056 +	+	-	-	-	-	-	-	-	-
14577 +	+	-	-	-	-	-	-	-	-
40764 +	+	--+	+++	+++	+++	+	-	-	-
17951 +	+	-	-	-	-	-	-	-	-
40765 +	+	-	-	-	-	-	-	-	-
40632 +	+	-	-	-	-	-	-	-	-
13567 +	+	-	-	-	-	+	-	-	-
40766 +	+	--+	+++	+++	+++	+	-	+++	-
40767 +	-	-	+	-	+	-	-	-	-
40768 +	-	--	-	-	-	-	-	-	-
13988 +	+	-	-	+	+	+	-	-	-
40769 +	-	-	+	+	++	-	-	-	-
40770 +	++	--+	+++	+++	+++	+	-	-	-
39751 +	+	-	+	+	+	+++	---	-	-
40771 +	+	--+	+++	+++	+++	+	-	-	-

40772 +	+	-	-	-	-	-	-	-	-
11412 +	+	-	-	-	-	-	-	-	-
40773 +	+	---+	+++	+++	+++	+	-	-	-
14719 +	+	-	-	-	-	+	-	-	-
16653 +	+	-	-	-	-	++	--	-	-
18336 +	-	-	-	-	-	-	-	-	-
11108 +	+	-	-	-	-	-	-	-	-
40774 +	+	-	-	-	-	-	-	-	-
11671 +	-	-	-	-	-	-	-	-	-
14340 +	+	-	-	-	-	+	-	-	-
40775 +	++	---+	+++	+++	+++	-	-	-	-
17354 +	+	-	-	-	+	++	--	-	-
12539 +	-	-	-	-	-	-	-	-	-
39783 +	-	-	-	-	-	-	-	-	-
40776 +	-	-	-	-	-	-	-	-	-
40777 +	+	-	-	-	-	-	-	-	-
14008 +	+	-	-	-	-	-	-	-	-
14324 +	+	-	-	-	-	-	-	-	-
40778 +	-	-	-	-	-	-	-	-	-
40779 +	+	-	-	-	-	-	-	-	-
40780 +	-	-	-	-	-	-	-	-	-
11882 +	-	-	-	-	-	-	-	-	-
40781 +	++	-	-	-	-	-	-	-	-
12277 +	+	-	-	-	-	-	-	-	-
40782 +	+	-	-	-	-	-	-	-	-
40783 +	+	---+	+++	+++	+++	+	-	-	-
40784 +	-	-	-	-	-	+	-	-	-
17643 +	+	---+	+++	+++	+++	-	-	-	-
40442 +	+	-	-	-	-	-	-	-	-
18864 +	+	---+	+++	+++	+++	+	-	-	-
40785 +	-	-	-	-	-	-	-	-	-
40786 +	-	---+	+++	+++	+++	-	-	-	-
40746 +	+	---+	+++	+++	+++	-	-	-	-

40787	+	+	−−+	+++	+++	+++	+	−	-	-
40524	+	-	-	-	-	-	-	-	-	-
40788	+	+	−−+	+++	+++	+++	-	-	-	-
40477	+	+	-	-	-	-	-	-	-	-
40789	+	+	-	-	-	+	+	-	-	-
40790	+	+	-	-	-	-	-	-	-	-
17423	+	+	-	-	-	-	-	-	-	-
12170	+	+	-	-	-	-	-	-	-	-
40791	+	+	−−+	+++	+++	+++	-	−	-	-
40792	+	+	−−+	+++	+++	+++	-	-	-	-
40793	+	+	−−+	+++	+++	+++	+	−	-	-
40726	+	-	-	-	-	-	-	−	-	-
40794	+	-	-	-	-	-	-	-	-	-
18065	+	-	−	+	+	-	-	-	-	-
19432	+	+	−−+	+++	+++	+++	-	-	-	-
40795	+	-	-	+	-	+	-	-	-	-
39068	+	+	−−+	+++	+++	+++	-	-	-	-
18238	+	+	−−+	+++	+++	+++	-	-	-	-
40796	+	+	−−+	+++	+++	+++	+	-	-	-
13671	+	+	-	-	-	-	-	-	-	-
19282	+	+	−−+	+++	+++	+++	-	-	-	-
40797	+	+	-	-	-	-	-	-	-	-
14530	+	+	-	-	+	+	++	−−	-	-
14063	+	+	-	-	-	-	-	-	-	-
11997	+	+	-	-	-	-	-	-	-	-
40798	+	+	−−+	+++	+++	+++	-	−	-	-
40131	+	+	-	-	-	-	-	-	-	-
39773	+	+	-	-	-	-	+	-	-	-
13572	+	+	-	-	-	-	-	-	-	-
17994	+	-	-	-	-	-	-	-	-	-
40799	+	-	-	-	-	-	-	-	-	-
12393	+	+	-	-	-	-	-	-	-	-
40800	+	-	-	-	-	-	-	-	-	-

39774	+	+	−+	+++	+++	+++	+	−	-	-
40801	+	+	−+	+++	+++	+++	-	-	-	-
40802	+	-	-	-	-	-	-	-	-	-
39711	+	+	-	-	-	-	-	-	-	-
40803	+	+	-	-	-	-	-	-	-	-
11744	+	+	-	-	-	-	-	-	-	-
40091	+	++	−+	+++	+++	+++	-	−	-	-
40804	+	-	−+	+++	+++	+++	-	−	-	-
39746	+	-	−+	+	++	-	-	-	-	-
14279	+	+	-	-	-	-	-	-	-	-
40096	+	-	-	-	-	-	-	-	-	-
40805	+	+	−+	+++	+++	+++	+	−	-	-
40806	+	+	−+	+++	+++	+++	-	-	+	-
40807	+	+	-	+	+	+	+++	−−−	-	-
40808	+	+	−+	+++	+++	+++	-	-	-	-
40809	+	+	-	-	-	-	-	-	-	-
40810	+	++	−+	+++	+++	+++	+	-	-	-
40533	+	++	−+	+++	+++	+++	+	−	-	-
20474	+	-	-	-	-	-	-	-	-	-
40811	+	+	-	-	-	-	-	−	-	-
40000	+	+	−+	+++	+++	+++	+	−	-	-
40601	+	+	-	-	-	-	-	-	-	-
40812	+	+	−	++	++	++	+++	−−−	-	-
40813	+	+	−+	+++	+++	+++	+	-	-	-
38736	+	++	-	-	-	-	-	-	-	-
40066	+	+	-	-	-	-	-	-	-	-
18473	+	+	-	-	-	-	-	-	-	-
17465	+	+	-	-	-	-	+	−	-	-
13922	+	+	-	-	-	-	-	-	-	-
39440	+	++	-	-	-	-	-	-	-	-
39919	+	+	-	-	-	-	-	-	-	-
40814	+	+	-	-	-	-	-	-	-	-
14504	+	+	-	-	-	-	-	-	-	-

13759	+	+	-	-	-	-	+	–	-	-
13740	+	+	-	-	-	-	+	–	-	-
40815	+	+	-	-	-	-	-	-	-	-
13828	+	+	-	-	-	-	+	–	-	-
39916	+	+	-	-	-	-	-	-	-	-
40385	+	-	-	-	-	-	-	-	-	-
39760	+	-	–	+	+++	++	-	-	-	-
40816	+	-	-	-	-	-	-	-	-	-
40042	+	+	–+	+++	+++	+++	+	–	-	-
40817	+	++	–+	+++	+++	+++	+	–	-	-
40818	+	+	–+	+++	+++	+++	-	-	-	-
40669	+	+	–+	+++	+++	+++	-	-	-	-
40819	+	+	–+	+++	+++	+++	-	-	-	-
40707	+	+	-	-	-	-	-	-	-	-
39534	+	+	-	-	-	-	-	-	-	-
40538	+	+	-	-	-	-	-	-	-	-
17931	+	-	-	-	-	-	-	-	-	-
40243	+	+	–+	+++	+++	+++	+	–	-	-
11201	+	-	-	-	-	-	-	-	-	-
40820	+	-	–+	+++	+++	+++	+	-	-	-
13873	+	+	-	-	-	-	-	-	-	-
40821	+	+	–+	+++	+++	+++	-	-	-	-
18890	+	-	-	-	-	-	-	-	-	-
40166	+	-	-	-	-	-	+	-	-	-
40822	+	++	–+	+++	+++	+++	+	–	-	-
40823	+	-	-	-	-	-	-	-	-	-
19638	+	-	-	-	-	-	-	-	-	-
39945	+	+	-	-	-	-	+	–	-	-
11223	+	+	-	-	-	-	-	-	-	-
12277	+	+	-	-	-	-	-	-	-	-
40824	+	+	–+	+++	+++	+++	+	–	-	+++
40472	+	-	-	-	-	-	-	-	-	-
40599	+	-	-	-	-	-	-	-	-	-

40290	+	+	−−+	+++	+++	+++	+	-	-	-
39403	+	-	-	-	-	-	-	-	-	-
40825	+	+	−−+	+++	+++	+++	-	-	-	-
39691	+	+	-	+	+	+	+	−	-	-
19441	+	+	-	-	-	-	-	-	-	-
40420	+	+	-	-	-	-	-	-	-	-
11668	+	++	-	-	-	-	-	-	-	-
40588	+	+	-	-	-	-	-	-	-	-
40826	+	-	−	-	-	-	-	-	-	-
40827	+	+	-	-	-	-	-	-	-	-
19175	+	+	-	-	-	-	-	-	-	-
40828	+	++	-	+	-	-	-	-	-	-
11396	+	-	-	-	-	-	-	-	-	-
40829	+	+	-	-	-	-	-	-	-	-
40830	+	+	−−+	+++	+++	+++	-	-	-	-
40831	+	+	-	+	+	-	+++	−−−	-	-
40832	+	+	-	-	-	-	-	-	-	-
37551	+	+	−−+	+++	+++	+++	+	-	-	-
40833	+	-	−−+	+	+++	+	-	-	-	-
17013	+	+	-	-	-	-	-	-	-	-
40834	+	+	−−+	+++	+++	+++	+	-	-	-
40043	+	++	-	-	-	-	+	-	-	-
40835	+	+	-	-	-	-	-	-	-	-
40836	+	-	-	-	-	-	-	-	-	-
13935	+	+	-	-	-	-	-	-	-	-
40531	+	++	−−+	+++	+++	+++	+	−	-	-
40575	+	+	-	-	-	-	-	-	-	-
40837	+	-	-	-	-	-	-	-	-	-
40365	+	+	−−+	+++	+++	+++	+	−	-	-
40315	+	+	-	-	-	-	+	−	-	-
40797	+	+	-	-	-	-	-	-	-	-
13803	+	+	-	-	-	-	-	-	-	-
12247	+	-	-	-	-	-	-	-	-	-

40838	+	-	--+	+++	+++	+++	-	-	-	-
40839	+	+	--+	+++	+++	+++	-	-	-	-
38916	+	+	--+	+++	+++	+++	-	-	-	-
16086	+	+	-	-	-	-	-	-	-	-
14008	+	+	-	-	-	-	-	-	-	-
40840	+	+	-	-	-	-	-	-	-	-
40169	+	-	-	-	-	-	-	-	-	-
38262	+	+	--+	+++	+++	+++	-	-	-	-
40415	+	+	-	-	-	-	-	-	-	-
11279	+	-	-	-	-	-	-	-	-	-
40759	+	+	-	-	-	-	-	-	-	-
11244	+	-	-	-	-	-	-	-	-	-
17550	+	-	-	+	-	-	-	-	-	-
40355	+	+	--+	+++	+++	+++	+	-	-	-
40841	+	+	-	-	-	-	-	-	-	-
12017	+	+	-	-	-	-	-	-	-	-
40842	+	-	-	-	-	-	-	-	-	-
40222	+	-	-	-	-	-	+	-	-	-
17514	+	-	-	-	+	-	-	-	-	-
19754	+	-	-	-	-	-	-	-	-	-
40306	+	+	-	-	-	-	-	-	-	-
40843	+	-	-	-	-	-	-	-	-	-
40844	+	+	--+	+++	+++	+++	+	-	-	-
40325	+	+	-	-	-	-	-	-	-	-
11187	+	+	-	-	-	-	-	-	-	-
39775	+	++	-	-	-	-	-	-	-	-
14249	+	+	-	-	-	-	-	-	-	-
13588	+	+	-	-	-	-	+	-	-	-
40845	+	+	--+	+++	+++	+++	-	-	-	-
19094	+	+	-	-	-	-	-	-	-	-
40229	+	-	--+	+++	+++	+++	+	-	-	-
40586	+	-	--+	+++	+++	+++	-	-	-	-
39549	+	+	-	-	-	-	-	-	-	-

14371 +	+	-	-	-	-	-	-	-	-
40846 +	-	-	-	-	-	+	-	-	-
11764 +	+	-	-	-	-	-	-	-	-
11750 +	-	-	-	-	-	-	-	-	-
17414 +	+	-	-	-	-	-	-	-	-
39779 +	+	-	-	-	-	-	-	-	-
40072 +	-	–	+	++	-	+++	---	-	-
39789 +	-	-	-	-	-	-	-	-	-
40847 +	+	--+	+++	+++	+++	-	-	-	-
40848 +	+	--+	+++	+++	+++	+	-	-	-
40450 +	+	-	-	-	-	-	-	-	-
12639 +	-	-	-	-	-	-	-	-	-
13694 +	+	-	-	-	-	-	-	-	-
40849 +	+	--+	+++	+++	+++	-	-	-	-
39747 +	+	-	-	-	-	-	-	-	-
40767 +	-	-	-	-	-	-	-	-	-
40790 +	+	-	-	-	-	-	-	-	-
18365 +	+	-	-	-	-	-	-	-	-
13742 +	+	-	-	-	-	-	-	-	-
17862 +	-	–	+	-	-	-	-	-	-
40850 +	-	-	-	+	-	+++	--	-	-
40851 +	+	--+	+++	+++	+++	+	–	+++	-
18156 +	-	-	-	-	-	-	-	-	-
11369 +	+	-	-	-	-	-	-	-	-
13676 +	+	-	-	-	-	-	-	-	-
13662 +	+	-	-	-	-	-	-	-	-
40852 +	+	-	-	-	+	+	-	-	-
40853 +	-	-	-	-	-	-	-	-	-
40573 +	+	-	-	-	-	-	-	-	-
13799 +	++	-	-	-	-	-	-	-	-
40854 +	+	-	-	-	-	-	-	-	-
39648 +	+	-	-	-	-	-	-	-	-
40840 +	+	-	-	-	-	-	-	-	-

13779 +	+	-	-	-	-	-	-	-	-
40855 +	+	--+	+++	+++	+++	+	-	-	-
40856 +	+	-	-	-	-	-	-	-	-
14429 +	+	-	-	-	-	-	-	-	-
40857 +	+	--+	+++	+++	+++	+++	---	-	+++
40858 +	++	--+	+++	+++	+++	+	-	-	-
40417 +	+	--+	+++	+++	+++	+	-	-	-
16068 +	+	-	-	-	-	-	-	-	-
39230 +	++	-	-	-	-	-	-	-	-
40859 +	+	--+	+++	+++	+++	+	-	+++	-
40860 +	+	-	-	-	-	-	-	-	-
19088 +	-	-	-	-	-	-	-	-	-
11997 +	+	-	-	-	-	-	-	-	-
40861 +	-	-	-	-	-	-	-	-	-
16642 +	+	-	-	+	+	+	-	+	-
11291 +	++	-	-	-	-	-	-	-	-
40862 +	+	-	-	-	-	-	-	-	-
40863 +	-	--+	+++	+++	+++	-	-	-	-
40864 +	-	-	-	-	-	-	-	-	-
19444 +	+	--+	+++	+++	+++	+	-	-	-
14423 +	+	-	-	-	-	-	-	-	-
40325 +	+	-	-	-	-	-	-	-	-
40865 +	+	-	-	-	-	-	-	-	-
40866 +	+	--+	+++	+++	+++	-	-	-	-
40867 +	+	--+	+++	+++	+++	+	-	-	-
39982 +	+	--+	+++	+++	+++	+	-	-	-
40868 +	-	-	-	-	-	-	-	-	-
13645 +	+	-	-	-	-	-	-	-	-
40869 +	-	-	-	-	-	-	-	-	-
18969 +	-	-	+	++	-	+	-	-	-
11562 +	-	-	-	-	-	-	-	-	-
13562 +	+	-	-	-	-	-	-	-	-
39470 +	+	--+	+++	+++	+++	-	-	-	-

38563	+	-	-	+	-	-	-	-	-	-
40870	+	-	--+	+++	+++	+++	-	-	-	-
12286	+	+	-	-	-	-	-	-	-	-
40779	+	+	-	-	-	-	-	-	-	-
16598	+	+	-	-	-	-	-	-	-	-
40628	+	+	-	-	-	-	+	-	-	-
17950	+	+	--+	+++	+++	+++	-	-	-	-
39628	+	+	-	-	-	-	-	-	-	-
38447	+	+	--+	+++	+++	+++	+	-	-	-
39835	+	+	-	-	-	-	-	-	-	-
39892	+	+	-	-	-	-	-	-	-	-
40871	+	-	-	-	-	-	-	-	-	-
40010	+	+	-	+	+	++	-	-	-	-
38045	+	-	-	-	-	-	-	-	-	-
39715	+	+	--+	+++	+++	+++	+	-	-	-
40441	+	+	-	-	-	-	-	-	-	-
40872	+	+	-	-	-	-	-	-	-	-
39980	+	-	-	-	-	-	-	-	-	-
40597	+	+	-	-	-	-	-	-	-	-
18890	+	-	-	-	-	-	-	-	-	-
15026	+	+	-	-	-	-	++	--	-	-
11162	+	-	-	-	-	-	-	-	-	-
40873	+	+	--+	+++	+++	+++	-	-	-	-
40874	+	+	--+	+++	+++	+++	+	-	-	-
17511	+	+	--+	+++	+++	+++	+	-	-	-
12385	+	+	-	-	-	-	-	-	-	-
39667	+	+	--+	+++	+++	+++	+	-	-	-
14101	+	+	-	-	-	-	-	-	-	-
40875	+	+	--+	+++	+++	+++	+	-	-	-
19696	+	+	--+	+++	+++	+++	-	-	-	-
40463	+	+	-	-	-	-	-	-	-	-
40876	+	+	--+	+++	+++	+++	-	-	-	-
17208	+	+	-	-	-	-	-	-	-	-

39358 +	-	-	-	-	-	-	-	-	-
40706 +	+	-	-	-	-	-	-	-	-
13955 +	+	-	-	-	-	-	-	-	-
11576 +	-	-	-	-	-	-	-	-	-
39792 +	+	-	-	-	+	-	-	-	-
11515 +	+	-	-	-	-	-	-	-	-
39790 +	+	--+	+++	+++	+++	+	-	-	-
40877 +	-	-	-	-	-	-	-	-	-
40878 +	++	--+	+++	+++	+++	+	-	-	-
40760 +	+	-	-	-	-	-	-	-	-
40004 +	-	-	-	-	-	-	-	-	-
40309 +	++	--+	+++	+++	+++	+	-	-	-
13765 +	+	-	-	-	-	+	-	+++	-
12184 +	+	-	-	-	-	-	-	-	-
40879 +	-	--+	+++	+++	+++	-	-	-	+
13847 +	+	-	-	-	-	-	-	-	-
13699 +	+	-	-	-	-	-	-	-	-
18332 +	-	-	-	-	-	-	-	-	-
40598 +	++	--+	+++	+++	+++	+	-	-	-
40880 +	+	-	-	-	-	-	-	-	-
40292 +	+	-	-	-	-	-	-	-	-
40361 +	+	--+	+++	+++	+++	+	-	-	-
13609 +	+	-	-	-	-	-	-	-	-
40536 +	+	--+	+++	+++	+++	-	-	-	-
40881 +	-	-	+	+	-	+++	---	-	-
40344 +	-	-	+	++	+	+	-	-	-
40882 +	-	--+	+++	+++	+++	-	-	-	-
16623 +	+	-	-	-	-	-	-	-	-
40553 +	+	--+	+++	+++	+++	+	-	-	+++
12244 +	+	-	-	-	-	-	-	-	-
11413 +	-	-	-	-	-	-	-	-	-
11434 +	-	-	-	-	-	-	-	-	-
40883 +	+	--+	+++	+++	+++	-	-	-	+++

40884 +	+	-	+	-	-	-	-	-	-
40885 +	-	-	-	-	-	-	-	-	-
40886 +	+	--+	+++	+++	+++	+	-	-	-
40887 +	+	-	-	-	-	-	-	-	-
40888 +	+	-	-	-	-	-	-	-	-
40889 +	-	--+	+++	+++	+++	+	-	-	-
40890 +	+	--+	+++	+++	+++	-	–	-	-
40891 +	+	-	-	-	-	-	-	-	-
39772 +	-	-	-	-	-	-	-	-	-
39798 +	-	-	-	-	-	-	–	-	-
40892 +	+	--+	+++	+++	+++	+++	---	+++	-
40893 +	-	-	-	-	-	-	-	-	-
40894 +	-	-	-	-	-	-	-	-	-
17849 +	-	-	-	-	-	-	-	-	-
40895 +	+	--+	+++	+++	+++	+	-	-	-
40807 +	-	–	+	+	+	+++	---	-	-
17813 +	+	-	-	-	-	+	–	-	-
40176 +	+	--+	+++	+++	+++	+	–	-	-
40896 +	+	--+	+++	+++	+++	+	-	-	-
19339 +	-	-	-	-	-	-	-	-	-
40897 +	+	--+	+++	+++	+++	+	-	-	-
38045 +	-	-	-	-	-	-	-	-	-
40737 +	+	-	-	-	-	-	-	-	-
19805 +	+	-	-	-	-	-	-	-	-
39935 +	+	--+	+++	+++	+++	-	–	-	-
40898 +	+	--+	+++	+++	+++	-	-	-	-
17096 +	+	-	-	-	-	-	-	-	-
12580 +	-	-	-	-	-	-	-	-	-
40899 +	-	-	-	-	-	-	-	-	-
13528 +	+	-	-	-	-	+	–	-	-
40114 +	+	--+	+++	+++	+++	+	–	-	-
13632 +	+	-	-	-	+	++	--	-	-
13649 +	+	-	-	-	-	+	–	-	-

15966 +	+	-	-	-	-	-	-	-	-
40648 +	+	---+	+++	+++	+++	+	-	-	-
40900 +	+	---+	+++	+++	+++	+	-	-	-
40901 +	+	---+	+++	+++	+++	+	-	-	-
39686 +	+	-	-	-	-	-	-	-	-
40902 +	-	-	-	-	-	-	-	-	-
40706 +	+	-	-	-	-	-	-	-	-
17602 +	-	-	-	-	-	-	-	-	-
14041 +	+	-	-	-	-	-	-	-	-
40903 +	+	-	-	-	-	-	-	-	-
40904 +	+	-	+	+	+	-	-	-	-
40905 +	+	---+	+++	+++	+++	+	-	-	-
39407 +	+	-	-	-	-	-	-	-	-
38975 +	+	---+	+++	+++	+++	+	-	-	-
40906 +	-	---+	+++	+++	+++	-	-	-	-
40907 +	-	---+	+++	+++	+++	+	-	-	-
37986 +	+	-	+	-	-	-	-	-	-
40908 +	-	---+	+	+++	+	++	--	+++	-
40909 +	+	-	-	-	-	-	-	-	-
12041 +	+	-	-	-	-	-	-	-	-
40566 +	+	---+	+++	+++	+++	+	-	-	-
40910 +	-	--	-	+	-	-	-	-	-
11677 +	+	-	-	-	-	-	-	-	-
40911 +	+	---+	+++	+++	+++	-	-	-	-
40912 +	-	-	-	-	-	-	-	-	-
15177 +	-	-	+	++	++	+++	--	-	-
40913 +	+	---+	+++	+++	+++	-	-	-	-
40914 +	+	-	-	-	-	-	-	-	-
11672 +	+	-	-	-	-	+	-	-	-
38822 +	+	-	-	-	-	-	-	-	-
10977 +	+	-	-	-	-	-	-	-	-
40915 +	+	---+	+++	+++	+++	+	-	-	-
39807 +	+	-	-	-	-	-	-	-	-

40582 +	+	-	-	-	-	-	-	-	-
11937 +	+	-	-	-	-	-	-	-	-
39687 +	-	-	-	-	-	-	-	-	-
40916 +	-	-	-	-	-	-	-	-	-
40875 +	++	--+	+++	+++	+++	+	-	-	-
39437 +	+	--+	+++	+++	+++	+	-	-	-
40917 +	+	--+	+++	+++	+++	-	–	-	-
13577 +	+	-	-	-	-	+	–	-	-
13918 +	+	-	-	-	-	-	-	-	-
11179 +	+	-	-	-	-	-	-	-	-
40918 +	+	--+	+++	+++	+++	+	–	-	-
40919 +	-	-	-	-	-	-	-	-	-
40920 +	+	--+	+++	+++	+++	+	-	-	-
40290 +	+	--+	+++	+++	+++	+	–	-	-
19213 +	-	-	-	-	-	-	-	-	-
16070 +	-	-	-	-	-	-	-	-	-
40921 +	-	–	+++	++	-	-	–	-	-
39910 +	+	--+	+++	+++	+++	-	-	-	-
40922 +	+	-	-	-	-	-	-	-	-
39629 +	+	--+	+++	+++	+++	+	–	-	-
14440 +	+	-	-	-	-	-	-	-	-
40603 +	-	–	+	+	+	+	--	-	-
40573 +	+	-	-	-	-	-	-	-	-
40451 +	+	-	-	-	-	-	-	-	-
40923 +	-	-	-	-	-	-	-	-	-
19238 +	+	--+	+++	+++	+++	-	–	-	-
39534 +	+	-	-	-	-	-	-	-	-
40924 +	+	--+	+++	+++	+++	+	–	-	-
11755 +	+	-	-	-	-	-	-	-	-
40872 +	+	-	-	-	-	-	-	-	-
12021 +	-	-	-	-	-	-	-	-	-
39721 +	+	-	+	-	+	-	-	-	-
13760 +	+	-	-	-	-	-	-	-	-

15981 +	+	-	-	-	-	-	-	-	-
18192 +	+	--+	+++	+++	+++	-	-	-	-
40925 +	-	-	+	++	-	-	-	-	-
40926 +	+	-	-	-	-	+	–	-	-
40378 +	+	-	-	-	-	-	-	-	-
40927 +	+	--+	+++	+++	+++	-	–	-	-
17614 +	+	-	-	-	-	-	-	-	-
39864 +	-	-	-	-	-	-	-	-	-
40928 +	+	--+	+++	+++	+++	-	-	-	-
40661 +	+	-	-	-	-	-	-	-	-
39960 +	-	–	+	+	+	-	-	-	-
40929 +	+	-	-	-	-	-	-	-	-
14451 +	+	-	-	-	-	+	–	-	-
40930 +	+	-	-	-	-	-	-	-	-
11260 +	+	-	-	-	-	-	-	-	-
18409 +	-	-	-	-	-	-	-	-	-
12654 +	+	-	-	-	-	-	-	-	-
40931 +	+	-	-	-	-	-	–	-	-
40932 +	+	--+	+++	+++	+++	+	–	-	-
40933 +	+	-	-	-	-	-	-	-	-
18253 +	+	-	-	-	-	-	-	-	-
11703 +	+	-	-	-	-	-	-	-	-
13582 +	+	-	-	-	-	-	-	-	-
40829 +	+	-	-	-	-	-	-	-	-
12173 +	-	-	-	-	-	-	-	-	-
40934 +	+	--+	+++	+++	+++	-	–	-	-
39325 +	-	-	-	-	-	-	-	-	-
13754 +	+	-	-	-	-	-	-	-	-
39985 +	+	-	-	-	-	-	-	-	-
13538 +	+	-	-	+	-	++	--	-	-
17074 +	-	-	-	-	-	-	-	-	-
40935 +	+	--+	+++	+++	+++	-	-	-	-
39864 +	-	-	-	-	-	-	-	-	-

14328 +	+	-	-	-	-	-	-	-	-
40936 +	-	–	-	++	-	-	-	-	-
39399 +	+	-	-	-	-	-	-	-	-
40192 +	-	–	-	-	-	-	-	-	-
40937 +	+	-	-	-	-	-	-	-	-
14862 +	+	-	-	-	-	-	-	-	-
40938 +	+	–+	+++	+++	+++	+	-	-	-
39937 +	+	-	-	-	-	-	-	-	-
40459 +	+	-	-	-	-	-	-	-	-
40939 +	-	-	-	-	-	-	-	-	-
40940 +	+	–+	+++	+++	+++	-	-	-	-
11332 +	+	-	-	-	-	-	-	-	-
14500 +	+	–	+	+	+	+++	---	-	-
40552 +	-	-	-	-	-	-	-	-	-
19612 +	-	–+	+++	+++	+++	-	-	-	-
40941 +	+	–+	+++	+++	+++	-	–	-	-
40942 +	+	-	-	-	-	+	-	-	-
40126 +	++	–+	+++	+++	+++	+	-	-	-
40569 +	+	-	-	-	-	-	-	-	-
11281 +	+	-	-	-	-	-	-	-	-
14428 +	+	-	-	-	-	-	-	-	-
39996 +	+	-	-	-	-	-	-	-	-
13957 +	-	-	-	-	-	-	-	-	-
40278 +	+	-	-	-	+	+++	---	-	-
39447 +	+	-	-	-	-	+	-	-	-
17051 +	-	-	-	-	-	-	-	-	-
11247 +	+	-	-	-	-	-	-	-	-
40943 +	+	–	++	+	++	-	-	-	-
38876 +	-	-	-	-	-	-	-	-	-
40944 +	+	–+	+++	+++	+++	+	-	-	-
13609 +	+	-	-	-	-	-	-	-	-
40945 +	+	-	-	-	-	-	-	-	-
40946 +	+	–	+	++	++	-	-	-	-

40563 +	+	-	-	-	-	-	-	-	-
39928 +	+	-	-	-	+	-	-	-	-
40947 +	-	--+	+++	+++	+++	-	-	-	-
39152 +	+	-	-	-	-	-	-	-	-
40948 +	-	-	-	-	-	-	-	-	-
40949 +	+	--+	+++	+++	+++	+	-	-	-
40950 +	+	-	-	-	-	-	-	-	-
40951 +	+	-	+	+	+	+++	---	+++	+++
40952 +	+	-	-	-	-	-	-	-	-
19094 +	+	-	-	-	-	-	-	-	-
38523 +	++	-	+	+	-	-	-	-	-
13508 +	+	-	-	-	-	++	---	-	-
40953 +	-	-	-	-	-	-	-	-	-
40713 +	+	-	+	-	-	-	-	-	-
40954 +	-	--+	+	++	-	-	-	-	-
40295 +	+	-	-	-	-	-	-	-	-
13606 +	+	-	-	-	-	-	-	-	-
40955 +	+	--+	+++	+++	+++	+	-	-	-
40956 +	+	--+	+++	+++	+++	+	-	-	-
18237 +	+	-	-	-	-	-	-	-	-
12094 +	+	-	-	-	-	-	-	-	-
16103 +	+	-	-	-	-	-	-	-	-
40957 +	+	-	-	-	-	-	-	-	-
11513 +	-	-	-	++	-	-	-	-	-
40958 +	+	--+	+++	+++	+++	+	-	-	-
40959 +	+	--+	+++	+++	+++	-	-	-	-
40960 +	-	-	-	-	-	-	-	-	-
40961 +	+	--+	+++	+++	+++	+	-	-	-
40962 +	+	--+	+++	+++	+++	-	-	-	-
40963 +	+	--+	+++	+++	+++	-	-	-	-
39803 +	++	-	-	-	-	-	-	-	-
40581 +	+	-	-	-	-	-	-	-	-
39281 +	+	--+	+++	+++	+++	-	-	-	-

13560 +	+	-	-	-	-	+	–	-	-
40158 +	+	–+	+++	+++	+++	+	–	-	-
40964 +	+	-	-	-	-	-	-	-	-
18579 +	+	-	-	-	-	-	-	-	-
14078 +	+	-	-	-	-	-	-	-	-
40965 +	+	–+	+++	+++	+++	+	–	-	-
40680 +	+	–+	+++	+++	+++	+	-	-	-
40966 +	+	-	-	-	-	-	-	-	-
40967 +	+	–+	+++	+++	+++	-	-	-	-
40968 +	+	–	+++	++	++	+++	–	-	-
40969 +	+	-	-	-	-	-	-	-	-
40970 +	-	-	-	-	-	-	-	-	-
40971 +	+	-	-	-	-	-	-	-	-
19350 +	++	-	-	-	-	-	-	-	-
40972 +	+	-	-	-	-	-	-	-	-
40973 +	+	–+	+++	+++	+++	-	–	+++	-
20402 +	+	–+	+++	+++	+++	-	-	-	-
39799 +	+	–+	+++	+++	+++	-	-	-	-
13716 +	+	-	-	-	-	++	–	-	-
40324 +	-	-	-	-	-	-	-	-	-
39507 +	+	–+	+++	+++	+++	+	-	-	-
11244 +	-	-	-	-	-	-	-	-	-
12549 +	-	-	-	-	-	-	-	-	-
39848 +	-	-	-	-	-	-	-	-	-
39772 +	-	-	-	-	-	-	-	-	-
40974 +	+	-	-	-	-	-	-	-	-
40975 +	+	-	-	-	-	-	-	-	-
40908 +	-	–+	+	+++	+	++	–	-	-
40976 +	+	-	-	-	-	-	-	-	-
40977 +	+	–+	+++	+++	+++	-	-	+++	-
10986 +	+	-	-	-	-	-	-	-	-
40028 +	+	-	-	-	-	-	-	-	-
40978 +	+	-	-	-	-	-	–	-	-

40130 +	-	-	-	-	-	-	-	-	-
40162 +	+	-	-	-	-	-	-	-	-
17674 +	+	-	-	-	-	-	-	-	-
18142 +	+	-	-	-	-	-	-	-	-
40979 +	+	---+	+++	+++	+++	+	-	-	-
17248 +	+	-	-	-	-	+	–	-	-
12098 +	-	-	-	-	-	-	-	-	-
40980 +	+	---+	+++	+++	+++	-	–	-	-
12343 +	-	-	-	++	-	-	-	-	-
40349 +	-	-	-	-	-	+	–	-	-
40448 +	+	---+	+++	+++	+++	+	-	-	-
40981 +	+	---+	+++	+++	+++	-	-	-	-
40134 +	+	-	-	-	-	-	-	-	-
40982 +	+	-	-	-	-	-	-	-	-
40737 +	+	-	-	-	-	-	-	-	-
11949 +	+	-	-	-	-	-	-	-	-
40983 +	+	---+	+++	+++	+++	-	-	-	-
39881 +	+	–	+	+	+	-	-	-	-
39578 +	-	-	-	-	-	-	-	-	-
17409 +	-	-	-	-	-	+	-	-	-
15978 +	-	-	-	-	-	-	-	-	-
40702 +	-	–	+	+	+	+++	---	-	++
17284 +	+	-	-	-	-	-	-	-	-
18971 +	+	-	-	-	-	-	-	-	-
40984 +	-	-	-	-	-	-	-	-	-
14647 +	+	-	-	-	-	-	-	-	-
40985 +	+	-	-	-	-	-	-	-	-
40986 +	+	-	-	-	-	-	-	-	-
40611 +	+	-	-	-	-	-	-	-	-
40658 +	+	---+	+++	+++	+++	+	-	-	-
14386 +	+	-	-	-	-	-	-	-	-
14658 +	-	-	-	-	-	-	-	-	-
39118 +	+	---+	+++	+++	+++	-	-	-	-

11359 +	+	-	-	-	-	-	-	-	-
40987 +	-	-	-	-	-	-	-	-	-
40127 +	+	--+	+++	+++	+++	-	-	-	-
40988 +	-	-	-	-	-	-	-	-	-
40989 +	-	--+	+++	+++	+++	+	-	-	-
40990 +	+	-	-	-	-	-	-	-	-
40991 +	+	-	-	-	-	-	-	-	-
40992 +	-	-	-	-	-	-	-	-	-
17490 +	-	--+	+++	+++	+++	-	-	-	-
13676 +	+	-	-	-	-	-	-	-	-
40993 +	+	--+	+++	+++	+++	+++	---	+++	+++
40642 +	-	-	-	-	-	-	-	-	-
40736 +	++	--+	+++	+++	+++	+	-	-	-
19421 +	+	-	-	-	-	-	-	-	-
40994 +	-	-	+	+	-	-	-	-	-
40995 +	-	--+	+++	+++	+++	+++	---	-	-
40996 +	++	--+	+++	+++	+++	+	-	-	-
39607 +	-	-	-	-	-	-	-	-	-
40525 +	+	--+	+++	+++	+++	+++	---	-	-
40997 +	-	--+	+++	+++	+++	+	-	-	-
40440 +	++	-	-	-	-	-	-	-	-
40071 +	-	-	-	-	-	-	-	-	-
13800 +	++	--+	+++	+++	+++	-	-	-	-
40998 +	+	--+	+++	+++	+++	-	-	-	-
13712 +	+	-	-	-	-	-	-	-	-
11811 +	+	-	-	-	-	-	-	-	-
40999 +	-	-	-	-	-	-	-	-	-
40406 +	-	-	-	-	-	-	-	-	-
13712 +	+	-	-	-	-	-	-	-	-
40342 +	+	-	-	-	-	-	-	-	-
13821 +	+	-	-	-	-	-	-	-	-
39851 +	+	-	-	-	-	-	-	-	-
13654 +	+	-	-	-	-	-	-	-	-

41000 +	++	−+	+++	+++	+++	+	-	-	-
17410 +	+	-	-	-	-	-	-	-	-
36748 +	++	−+	+++	+++	+++	+	−	-	-
41001 +	-	-	-	-	-	-	-	-	-
39610 +	-	-	-	-	-	-	-	-	-
11569 +	+	-	-	-	-	-	-	-	-
41002 +	-	-	-	-	-	-	-	-	-
40040 +	+	−+	+++	+++	+++	+	−	-	-
14237 +	+	-	-	-	-	-	-	-	-
41003 +	+	−+	+++	+++	+++	+	-	-	-
41004 +	-	−+	+++	+++	+++	-	−	-	-
40861 +	-	−	-	-	-	-	-	-	-
41005 +	+	−+	+++	+++	+++	+	−	-	-
41006 +	+	−	+	+	+	+++	−−−	+++	-
40530 +	+	-	-	-	-	-	-	-	-
18064 +	-	−−	+	+	-	+	-	-	-
40357 +	-	−	+	+	+	+++	−−−	-	-
41007 +	+	−+	+++	+++	+++	+	-	-	-
40765 +	+	-	-	-	-	-	-	-	-
12639 +	-	-	-	-	-	-	-	-	-
12345 +	-	-	-	-	-	-	-	-	-
41008 +	-	−	-	-	+	-	-	-	-
40156 +	-	-	-	-	-	-	-	-	-
41009 +	+	−	+	+	+	+++	−−−	+++	+++
41010 +	+	-	-	-	-	-	-	-	-
40480 +	+	−+	+++	+++	+++	-	-	-	-
18335 +	+	-	-	-	-	-	-	-	-
39937 +	+	-	-	-	-	-	-	-	-
11567 +	+	-	-	-	-	-	-	-	-
41011 +	+	-	-	-	-	-	-	-	-
14580 +	+	-	-	-	-	++	−−	-	-
18178 +	+	-	-	-	-	-	-	-	-
40471 +	-	−	+	+++	++	+++	−−−	+++	-

41012	+	-	--+	+++	+++	+++	+	-	-	-
41013	+	+	--+	+++	+++	+++	+++	---	-	+++
41014	+	+	--+	+++	+++	+++	-	-	-	-
40960	+	-	-	-	-	-	-	-	-	-
15935	+	+	-	-	-	-	+++	---	-	-
41015	+	+	-	-	-	-	-	-	-	-
39590	+	+	-	-	-	-	-	-	-	-
41016	+	+	--+	+++	+++	+++	+++	---	-	-
41017	+	+	--+	+++	+++	+++	-	-	-	-
40011	+	+	-	-	-	+	+	-	-	-
40958	+	+	--+	+++	+++	+++	+	-	-	+++
41018	+	+	-	-	-	-	-	-	-	-
41019	+	+	--+	+++	+++	+++	-	-	-	-
41020	+	+	--+	+++	+++	+++	+	-	-	-
41021	+	+	-	-	-	-	-	-	-	-
41022	+	+	-	-	-	-	-	-	-	-
41023	+	+	-	-	-	-	-	-	-	-
40244	+	+	-	-	-	-	-	-	-	-
40581	+	+	-	-	-	-	-	-	-	-
11604	+	+	-	-	-	-	-	-	-	-
40595	+	-	-	+	-	+	+++	---	-	-
41024	+	+	--+	+++	+++	+++	-	-	-	+
13567	+	+	-	-	-	-	+	-	-	-
40035	+	+	--+	+++	+++	+++	+	-	-	-
41025	+	+	-	-	-	-	-	-	-	-
41026	+	+	--+	+++	+++	+++	+	-	-	-
14260	+	+	-	-	-	-	-	-	-	-
11779	+	+	-	-	-	-	-	-	-	-
39571	+	+	--+	+++	+++	+++	+	-	-	-
41027	+	++	--+	+++	+++	+++	-	-	-	-
41028	+	+	-	-	-	-	-	-	-	-
39198	+	+	-	-	-	-	-	-	-	-
41029	+	+	-	-	-	-	-	-	-	-

38651 +	+	-	-	-	-	-	-	-	-
41030 +	-	--+	+++	+++	+++	-	-	-	-
41031 +	+	--+	+++	+++	+++	-	-	-	+
41032 +	-	-	-	-	-	-	-	-	-
11777 +	-	-	-	-	-	-	-	-	-
40910 +	-	--	-	+	-	-	-	-	-
41033 +	+	-	-	-	-	-	-	-	-
41034 +	+	--+	+++	+++	+++	+	-	-	-
41035 +	+	--+	+++	+++	+++	+	-	-	-
41036 +	+	--+	+++	+++	+++	+	-	-	-
41037 +	+	--+	+++	+++	+++	+	-	-	-
41038 +	-	-	-	-	-	-	-	-	-
12188 +	-	-	-	-	-	-	-	-	-
40860 +	+	-	-	-	-	-	-	-	-
41039 +	-	--+	+++	+++	+++	-	-	-	-
41040 +	+	--+	+++	+++	+++	+	-	-	-
41041 +	-	-	-	-	-	-	-	-	-
41042 +	+	--+	+++	+++	+++	+	-	-	-
41043 +	-	--+	+++	+++	+++	-	-	-	-
40490 +	-	-	-	-	-	-	-	-	-
40836 +	-	-	-	-	-	-	-	-	-
12687 +	-	-	-	-	-	-	-	-	-
41044 +	+	--+	+++	+++	+++	+	-	-	-
12232 +	-	-	-	-	-	-	-	-	-
40638 +	-	-	+	+	+	+++	---	+++	-
13956 +	+	-	-	-	-	-	-	-	-
40106 +	-	-	-	-	-	-	-	-	-
41045 +	+	-	-	-	-	-	-	-	-
40470 +	+	-	+	-	+	+++	---	-	-
40198 +	+	--+	+++	+++	+++	-	-	-	-
11471 +	+	-	-	-	-	-	-	-	-
40391 +	+	-	-	-	-	-	-	-	-
40785 +	-	-	-	-	-	-	-	-	-

40587 +	+	−−+	+++	+++	+++	+++	−−−	-	-
41046 +	-	−−+	+++	+++	+++	-	-	-	-
40969 +	+	-	-	-	-	-	-	-	-
40686 +	+	-	-	-	-	-	-	-	-
16047 +	+	-	-	-	-	-	-	-	-
41047 +	+	−−+	+++	+++	+++	+	−	-	+++
39425 +	+	-	-	-	-	-	-	-	-
18540 +	+	−−+	+++	+++	+++	+	−	-	-
17812 +	-	-	-	-	-	-	-	-	-
41048 +	+	−−+	+++	+++	+++	+	-	-	-
16633 +	+	-	-	-	-	-	-	-	-
39335 +	++	-	-	-	-	-	-	-	-
41049 +	+	-	-	-	-	-	-	-	-
11214 +	-	-	-	-	-	-	-	-	-
41050 +	+	−−+	+++	+++	+++	-	-	-	-
41051 +	-	-	-	-	+	-	-	-	-
40262 +	+	-	-	-	-	-	-	-	-
41052 +	-	-	-	-	-	-	-	-	-
13749 +	+	-	-	-	-	-	-	-	-
41053 +	+	−−+	+++	+++	+++	+	−	-	-
13528 +	+	-	-	-	-	+	−	-	-
17595 +	-	-	-	-	-	-	-	-	-
39657 +	-	-	-	-	-	-	-	-	-
41054 +	+	−−+	+++	+++	+++	-	−	-	-
13652 +	+	-	-	-	-	-	-	-	-
18175 +	+	−−+	+++	+++	+++	+	-	-	-
40974 +	+	-	-	-	-	-	-	-	-
40924 +	+	−−+	+++	+++	+++	-	-	-	-
41055 +	+	−−+	+++	+++	+++	+	−	-	-
15957 +	+	-	-	-	-	-	-	-	-
41056 +	+	-	+	-	+	-	-	-	-
19433 +	+	−−+	+++	+++	+++	-	-	-	-
41057 +	+	-	-	-	-	-	-	-	-

41058 +	+	-	-	-	-	-	-	-	-
41059 +	+	---+	+++	+++	+++	-	-	-	-
41060 +	+	---+	+++	+++	+++	-	-	-	-
14417 +	+	-	-	-	+	+	--	-	-
41061 +	+	---+	+++	+++	+++	-	-	-	-
41062 +	+	-	-	-	-	-	-	-	-
40945 +	+	-	-	-	-	-	-	-	-
41063 +	-	-	-	-	-	-	-	-	-
40285 +	-	---+	-	+	-	-	-	-	-
40451 +	+	-	-	-	-	-	-	-	-
39877 +	-	-	-	-	-	-	-	-	-
19371 +	-	-	-	-	-	-	-	-	-
40809 +	+	-	-	-	-	-	-	-	-
41064 +	+	-	-	-	-	-	-	-	-
17562 +	-	-	-	-	-	-	-	-	-
41065 +	-	-	-	-	-	-	-	-	-
18760 +	+	---+	+++	+++	+++	-	-	-	-
11137 +	+	-	-	-	-	-	-	-	-
41066 +	+	-	-	-	-	-	-	-	-
40110 +	+	-	-	-	-	-	-	-	-
39702 +	+	---+	+++	+++	+++	-	-	-	-
40672 +	+	-	-	-	-	-	-	-	-
41067 +	+	---+	+++	+++	+++	+	-	-	-
41068 +	+	-	-	-	-	-	-	-	-
13709 +	+	-	-	-	+	++	--	-	-
40806 +	-	---+	+++	+++	+++	+	-	-	-
41069 +	++	---+	+++	+++	+++	+	-	-	-
41070 +	+	-	-	-	-	+	-	-	-
41071 +	+	-	-	-	-	-	-	-	-
41072 +	+	-	-	-	-	+	-	-	-
39976 +	-	-	-	-	-	-	-	-	-
41073 +	+	---+	+++	+++	+++	+	-	-	+++
40554 +	-	-	-	-	-	-	-	-	-

41074 +	-	–	+	+	++	-	–	-	-
11627 +	+	-	-	-	-	-	-	-	-
41075 +	+	–+	+++	+++	+++	-	-	-	-
41038 +	-	-	-	-	-	-	-	-	-
11258 +	+	-	-	-	-	-	-	-	-
11548 +	+	-	-	-	-	-	-	-	-
41076 +	-	-	-	-	-	-	-	-	-
41077 +	+	-	-	-	-	-	-	-	-
11369 +	+	-	-	-	-	-	-	-	-
11556 +	-	-	-	-	-	-	-	-	-
13782 +	+	-	-	-	-	-	-	-	-
11897 +	-	-	-	-	-	-	-	-	-
41078 +	+	–+	+++	+++	+++	-	-	-	-
40727 +	+	-	-	-	-	+	–	-	-
40964 +	+	-	-	-	-	-	-	-	-
41079 +	+	–+	+++	+++	+++	-	-	-	-
18677 +	+	-	-	-	-	-	-	-	-
41080 +	+	-	-	-	-	-	-	-	-
41081 +	-	–	+	-	-	-	–	-	-
41034 +	++	–+	+++	+++	+++	+	–	-	-
16598 +	+	-	-	-	-	-	-	-	-
41082 +	+	-	-	-	-	-	-	-	-
41083 +	+	–+	+++	+++	+++	-	-	-	-
40815 +	+	-	-	-	-	-	-	-	-
15026 +	+	-	-	-	+	++	––	-	-
39943 +	+	–+	+++	+++	+++	+	-	-	-
41084 +	+	–+	+++	+++	+++	-	–	-	-
41085 +	+	-	-	-	-	-	-	-	-
11104 +	+	-	-	-	-	-	-	-	-
20032 +	+	–+	+++	+++	+++	-	–	-	-
40718 +	+	-	-	-	-	-	-	-	-
19602 +	+	-	-	-	-	-	-	-	-
17971 +	+	-	-	-	-	-	-	-	-

41086 +	+	--+	+++	+++	+++	-	-	+++	-
12014 +	-	-	-	-	-	-	-	-	-
40802 +	-	-	-	-	-	-	-	-	-
19917 +	+	-	-	-	-	-	-	-	-
18308 +	-	-	-	-	-	-	-	-	-
40894 +	-	-	-	-	-	-	-	-	-
13754 +	+	-	-	-	-	-	-	-	-
41087 +	+	-	-	-	-	-	-	-	-
38870 +	-	-	-	+	+	-	-	-	-
14505 +	+	-	-	-	-	-	-	-	-
16082 +	-	-	-	-	-	-	-	-	-
38973 +	+	--+	+++	+++	+++	-	-	-	-
17855 +	+	-	-	-	-	-	-	-	-
13594 +	+	-	-	-	-	++	---	-	-
13749 +	+	-	-	-	-	-	-	-	-
41001 +	-	-	-	-	-	-	-	-	-
41088 +	+	-	-	-	-	-	-	-	-
13955 +	+	-	-	-	-	-	-	-	-
40186 +	+	--+	+++	+++	+++	-	-	-	-
11471 +	+	-	-	-	-	-	-	-	-
41089 +	-	--+	+++	+++	+++	+	-	-	-
19310 +	+	-	-	-	-	-	-	-	-
41090 +	+	--+	+++	+++	+++	-	-	-	-
40849 +	+	--+	+++	+++	+++	-	-	-	-
40621 +	+	--+	+++	+++	+++	+	-	-	-
41091 +	+	--+	+++	+++	+++	+	-	-	-
41092 +	+	-	-	-	-	+	-	-	-
11245 +	+	-	-	-	-	-	-	-	-
41093 +	-	-	-	-	-	-	-	-	-
16622 +	-	-	+	-	-	-	-	-	-
41094 +	+	--+	+++	+++	+++	-	-	-	-
41092 +	+	-	-	-	-	+	-	-	-
40072 +	+	-	+	+	+	+++	---	-	-

40609 +	-	-	-	-	-	-	-	-	-
16638 +	++	-	-	-	-	-	-	-	-
40472 +	-	-	-	-	-	-	-	-	-
41095 +	+	---+	+++	+++	+++	-	-	-	-
41096 +	+	---+	+++	+++	+++	+	–	-	-
39280 +	-	-	-	-	-	-	-	-	-
40104 +	+	---+	+++	+++	+++	+	–	-	-
40916 +	-	-	-	-	-	-	-	-	-
41097 +	-	---+	+++	+++	+++	+	-	-	-
38022 +	+	---+	+++	+++	+++	+	-	-	-
41098 +	+	---+	+++	+++	+++	-	-	-	-
17821 +	-	-	-	-	-	-	-	-	-
41099 +	+	---+	+++	+++	+++	-	-	-	-
41100 +	+	-	-	-	-	-	-	-	-
14658 +	-	-	-	-	-	-	-	-	-
12343 +	-	-	-	++	-	-	-	-	-
13671 +	+	-	-	-	-	-	-	-	-
41101 +	+	-	-	-	-	+	-	-	-
41102 +	+	---+	+++	+++	+++	-	-	-	-
40357 +	-	–	+	+	+	+++	---	-	-
41103 +	-	-	-	-	-	-	-	-	-
41104 +	+	-	-	-	-	-	-	-	-
14580 +	+	-	-	-	-	++	--	-	-
14148 +	+	-	-	-	-	-	-	-	-
41105 +	-	-	-	-	-	-	-	-	-
40614 +	+	-	-	-	-	-	-	-	-
41106 +	-	-	-	-	-	-	-	-	-
41107 +	-	-	-	-	-	-	-	-	-
41108 +	+	-	-	-	-	-	-	-	-
11150 +	-	-	-	-	-	-	-	-	-
10989 +	+	-	+	+	-	+++	---	-	-
13516 +	+	-	-	-	-	+	–	-	-
16653 +	+	-	-	+	+	++	--	-	-

41109	+	+	−−+	+++	+++	+++	-	-	-	-
41110	+	-	−−+	+	+++	+	++	−−	-	-
38767	+	-	-	-	+	-	-	-	-	-
13721	+	+	-	-	-	-	-	-	-	-
40321	+	+	−−+	+++	+++	+++	+	−	-	-
13805	+	+	-	-	-	-	-	-	-	-
41111	+	-	-	-	-	-	-	-	-	-
11305	+	+	-	-	-	-	-	-	-	-
41112	+	-	−−+	+++	+++	+++	-	−	-	-
18863	+	+	-	-	-	-	-	-	-	-
39001	+	++	-	-	-	-	-	-	-	-
41113	+	-	-	-	-	-	-	-	-	-
41114	+	+	-	-	-	-	-	-	-	-
41115	+	-	-	-	-	-	-	-	-	-
40391	+	+	-	-	-	-	-	-	-	-
18073	+	+	-	-	-	-	-	-	-	-
17803	+	+	-	-	-	-	-	-	-	-
17644	+	-	-	-	+	-	-	-	-	-
41053	+	+	−−+	+++	+++	+++	-	-	-	-
41116	+	+	−−+	+++	+++	+++	+	-	-	-
41117	+	+	-	-	-	-	-	−	-	-
40738	+	+	−−+	+++	+++	+++	-	−	-	-
40860	+	+	-	-	-	-	-	-	-	-
13996	+	-	-	-	-	-	-	-	-	-
12485	+	-	-	-	-	-	-	-	-	-
13692	+	+	-	-	-	-	-	-	-	-
41118	+	+	-	-	-	-	-	-	-	-
17921	+	+	-	-	-	-	-	-	-	-
41119	+	+	−−+	+++	+++	+++	-	-	-	-
41120	+	+	−−+	+++	+++	+++	-	-	-	-
41121	+	-	-	-	-	-	-	-	-	-
37837	+	+	-	-	-	-	-	-	-	-
15000	+	+	-	-	+	+	-	-	-	-

17325	+	+	–+	+++	+++	+++	-	–	-	-
41122	+	+	–+	+++	+++	+++	-	–	-	-
14765	+	+	-	-	-	-	+	–	-	-
41123	+	+	–+	+++	+++	+++	+	–	-	-
13667	+	+	-	-	-	-	++	––	-	-
41124	+	+	–+	+++	+++	+++	+	–	-	-
13674	+	+	-	-	-	-	-	–	-	-
11779	+	+	-	-	-	-	-	-	-	-
11890	+	+	-	-	-	-	-	-	-	-
41125	+	+	-	-	-	-	-	-	-	-
40296	+	+	-	-	-	-	-	-	-	-
41126	+	+	–+	+++	+++	+++	+	–	-	-
40476	+	+	-	-	-	-	-	-	-	-
40864	+	-	–	-	-	-	-	-	-	-
40608	+	+	-	-	-	-	-	-	-	-
40620	+	+	-	-	-	-	+	–	-	-
40853	+	-	-	-	-	-	-	-	-	-
39788	+	+	-	-	-	-	-	-	-	-
17620	+	-	-	-	-	-	-	-	-	-
41127	+	-	–+	+++	+++	+++	-	-	-	-
14300	+	+	-	-	-	-	+	–	-	-
14404	+	+	-	-	-	-	-	-	-	-
41128	+	+	–+	+++	+++	+++	+	–	-	-
18642	+	+	-	-	+	-	-	-	-	-
11818	+	+	-	-	-	-	-	-	-	-
14426	+	+	-	-	-	-	+	–	-	-
41129	+	+	–+	+++	+++	+++	+	–	-	-
40810	+	+	–+	+++	+++	+++	-	–	-	-
39937	+	+	-	-	-	-	-	-	-	-
41130	+	-	-	-	-	-	-	-	-	-
41131	+	+	–+	+++	+++	+++	-	-	-	-
18245	+	+	-	-	-	-	-	-	-	-
39871	+	+	–+	+++	+++	+++	+	–	-	-

39912 +	-	-	-	-	-	-	-	-	-
39601 +	+	-	-	-	-	-	-	-	-
41132 +	+	-	+	-	-	-	-	-	-
40977 +	+	--+	+++	+++	+++	+	-	-	-
41133 +	+	-	-	-	-	-	-	-	-
38045 +	-	-	-	-	-	-	-	-	-
12251 +	+	-	-	-	-	-	-	-	-
41134 +	-	--+	+++	+++	+++	-	-	-	-
41135 +	+	--+	+++	+++	+++	-	-	-	-
41136 +	+	--+	+++	+++	+++	-	–	-	-
12571 +	+	-	-	-	-	-	-	-	-
39220 +	-	-	+	-	-	-	–	-	-
14547 +	+	-	-	-	-	-	-	-	-
40591 +	+	-	-	-	-	-	-	-	-
17053 +	-	-	-	-	-	-	-	-	-
17677 +	+	-	-	-	-	-	-	-	-
41137 +	+	-	-	-	-	-	-	-	-
38888 +	++	-	-	-	-	+	–	-	-
40260 +	-	-	-	-	-	-	-	-	-
41138 +	-	-	-	-	-	-	-	-	-
41139 +	+	-	+	-	+	-	-	-	-
41140 +	+	--+	+++	+++	+++	+	-	-	-
39549 +	+	-	-	-	-	-	-	-	-
13559 +	+	-	+	-	+	-	-	-	-
14127 +	+	-	-	-	+	+	-	-	-
19128 +	+	-	-	-	-	-	-	-	-
41141 +	-	--+	+++	+++	+++	-	-	-	-
11234 +	+	--+	+++	+++	+++	+	-	-	-
41142 +	+	--+	+++	+++	+++	+	–	-	-
41143 +	-	-	-	-	-	-	-	-	-
40588 +	+	-	-	-	-	-	-	-	-
40777 +	+	-	-	-	-	-	-	-	-
41144 +	+	--+	+++	+++	+++	+	-	-	-

39828 +	+	-	-	-	-	-	-	-	-
40307 +	+	-	-	-	-	-	-	-	-
40527 +	+	-	-	-	-	-	-	-	-
41145 +	+	–	+	+	+	+++	---	-	-
14000 +	+	-	-	-	-	-	-	-	-
38400 +	+	--+	+++	+++	+++	-	-	-	-
41146 +	+	–	+	+	+	+++	---	-	-
17505 +	-	-	-	-	-	-	-	-	-
41147 +	+	--+	+++	+++	+++	+	–	-	-
41148 +	+	-	-	-	-	-	-	-	-
41149 +	-	-	-	-	-	-	-	-	-
12287 +	+	-	-	-	-	-	-	-	-
40843 +	-	-	-	-	-	-	-	-	-
40905 +	+	--+	+++	+++	+++	+	–	-	-
40778 +	-	-	-	-	-	-	-	-	-
40856 +	+	-	-	-	-	-	-	-	-
41150 +	-	-	-	-	-	-	-	-	-
41151 +	+	--+	+++	+++	+++	++	---	-	-
41152 +	+	--	++	+	+++	-	-	-	-
41153 +	+	--+	+++	+++	+++	+++	---	-	-
41154 +	+	--+	+++	+++	+++	+	–	-	-
41009 +	+	–	+	+	+	+++	---	-	-
11435 +	+	-	-	-	-	-	-	-	-
41155 +	+	--+	+++	+++	+++	-	-	-	-
18222 +	+	-	-	-	-	-	-	-	-
41156 +	+	-	-	-	-	-	-	-	-
40585 +	+	-	-	-	-	-	-	-	-
19770 +	-	-	-	-	-	-	-	-	-
19447 +	-	-	-	-	-	-	-	-	-
17793 +	-	-	-	-	-	-	-	-	-
40795 +	-	–	+	-	-	+	-	-	-
41157 +	+	--+	+++	+++	+++	-	–	-	-
40275 +	+	-	-	-	-	-	-	-	-

41158	+	+	-	-	-	-	-	-	-	-
18005	+	+	--+	+++	+++	+++	+	-	-	-
41159	+	+	-	-	-	-	-	-	-	-
13600	+	+	-	-	-	-	++	--	-	-
41160	+	+	-	-	-	-	-	-	-	-
13755	+	+	-	-	-	-	-	-	-	-
19444	+	+	--+	+++	+++	+++	-	-	-	-
40405	+	+	--+	+++	+++	+++	-	-	-	-
40991	+	+	-	-	-	-	-	-	-	-
41161	+	+	-	-	-	-	+	-	-	-
12536	+	+	-	-	-	-	-	-	-	-
17904	+	-	-	-	-	-	-	-	-	-
40992	+	-	-	-	-	-	-	-	-	-
40547	+	-	-	-	+	-	-	-	-	-
18652	+	+	--+	+++	+++	+++	-	-	-	-
41162	+	+	--+	+++	+++	+++	-	-	-	-
12454	+	+	-	-	-	-	-	-	-	-
41163	+	-	-	+	+	++	+++	---	-	-
39209	+	+	-	-	-	-	-	-	-	-
40290	+	+	--+	+++	+++	+++	+	-	-	-
19371	+	-	-	-	-	-	-	-	-	-
11590	+	+	-	-	-	-	-	-	-	-
41164	+	+	--+	+++	+++	+++	-	-	-	-
41165	+	+	--+	+++	+++	+++	-	-	-	-
40984	+	-	-	-	-	-	-	-	-	-
16138	+	+	-	-	-	-	-	-	-	-
39988	+	-	-	-	-	-	-	-	-	-
41166	+	+	--+	+++	+++	+++	-	-	-	-
38045	+	-	-	-	-	-	-	-	-	-
41167	+	+	-	-	-	-	-	-	-	-
41155	+	+	--+	+++	+++	+++	+	-	-	-
41168	+	+	--+	+++	+++	+++	+	-	-	-
16020	+	+	-	-	-	-	-	-	-	-

38185	+	+	–+	+++	+++	+++	+	–	-	-
40911	+	+	–+	+++	+++	+++	-	-	-	-
41169	+	+	–+	+++	+++	+++	+	–	-	-
17072	+	+	-	-	-	-	-	-	-	-
13927	+	+	-	-	-	-	-	-	-	-
40484	+	+	-	-	-	-	-	-	-	-
39150	+	-	-	-	-	-	-	-	-	-
17639	+	+	-	-	-	-	-	-	-	-
41170	+	+	-	-	-	-	-	-	-	-
41171	+	+	–+	+++	+++	+++	+	-	-	-
13936	+	+	-	-	-	-	-	-	-	-
40468	+	-	–+	+	+++	+	-	-	-	-
40639	+	-	-	-	-	-	-	-	-	-
41172	+	+	–+	+++	+++	+++	+	-	-	-
41021	+	+	-	-	-	-	-	-	-	-
19207	+	+	-	-	-	-	-	-	-	-
41173	+	+	-	+	+	+	+++	––	-	-
41174	+	+	–	+	+	+	-	-	-	-
40084	+	+	-	-	-	-	-	-	-	-
14043	+	+	-	-	-	-	++	––	-	-
41175	+	+	–+	+++	+++	+++	+	–	-	-
40789	+	+	-	+	+	-	+	–	-	-
41176	+	+	-	-	-	-	-	-	-	-
38509	+	+	–+	+++	+++	+++	-	-	-	-
16659	+	++	-	-	-	-	-	-	-	-
19805	+	+	-	-	-	-	-	-	-	-
17063	+	-	-	-	-	-	-	-	-	-
17689	+	-	-	+	-	-	+	–	-	-
14545	+	+	-	-	-	-	-	-	-	-
39792	+	+	-	-	-	-	-	-	-	-
41177	+	+	–+	+++	+++	+++	-	-	-	-
40354	+	+	–+	+++	+++	+++	-	–	-	-
16633	+	+	-	-	-	-	-	-	-	-

40284 +	+	-	-	-	-	-	-	-	-
14504 +	+	-	-	-	-	-	-	-	-
41178 +	+	-	-	-	-	-	-	-	-
39727 +	-	–	+	-	-	+	-	-	-
40968 +	+	––	+++	++	+++	+++	–––	-	-
13036 +	+	-	-	-	-	++	––	-	-
39815 +	+	––+	+++	+++	+++	+	-	-	-
41179 +	+	––+	+++	+++	+++	+	–	-	-
40970 +	-	-	-	-	-	-	-	-	-
13896 +	+	-	-	-	-	-	-	-	-
14417 +	+	-	-	+	-	+	–	-	-
41180 +	-	–	-	-	-	-	-	-	-
17770 +	+	-	-	-	-	-	-	-	-
41181 +	+	––+	+++	+++	+++	-	–	-	-
41182 +	+	-	-	-	-	-	-	-	-
40852 +	+	-	-	-	-	+	-	-	-
41183 +	+	––+	+++	+++	+++	+	-	-	-
13693 +	+	-	-	-	-	++	––	-	-
41184 +	-	-	-	-	-	-	-	-	-
41185 +	-	-	-	-	+	++	–––	++	-
41186 +	+	––+	+++	+++	+++	-	–	-	-
41187 +	+	-	-	-	-	-	-	-	-
11937 +	+	-	-	-	-	+	-	-	-
18717 +	-	-	-	-	-	-	-	-	-
40548 +	+	-	-	-	-	-	-	-	-
41128 +	+	––+	+++	+++	+++	+	–	-	-
12108 +	+	-	-	-	-	-	-	-	-
13942 +	+	-	-	-	-	-	-	-	-
14056 +	+	-	-	-	-	-	-	-	-
17064 +	-	-	-	-	-	-	-	-	-
41188 +	+	––+	+++	+++	+++	-	-	-	-
39878 +	+	––+	+++	+++	+++	-	–	-	-
14867 +	+	-	-	+	+	++	–––	-	-

13879 +	+	-	-	-	-	-	-	-	-
41158 +	+	-	-	-	-	-	-	-	-
13835 +	+	-	-	-	-	-	-	-	-
11353 +	-	-	-	-	-	-	-	-	-
41189 +	-	-	-	-	-	-	-	-	-
39842 +	+	-	-	-	-	-	-	-	-
39602 +	+	--+	+++	+++	+++	-	-	-	-
14621 +	+	-	-	-	-	+	–	-	-
41190 +	++	-	+	-	-	+	–	-	-
17811 +	-	-	-	-	-	-	-	-	-
41191 +	+	--+	+++	+++	+++	-	–	-	-
17689 +	-	-	+	+	-	+	-	-	-
11744 +	+	-	-	-	-	-	-	-	-
17677 +	+	-	-	-	-	-	-	-	-
39529 +	+	--+	+++	+++	+++	-	–	-	-
18320 +	+	-	-	-	-	-	-	-	-
41192 +	+	--+	+++	+++	+++	+	–	-	-
41193 +	+	-	-	-	-	-	-	-	-
11830 +	-	-	-	-	-	-	-	-	-
41194 +	+	--+	+++	+++	+++	+	–	-	-
39368 +	+	-	-	-	-	-	-	-	-
41195 +	+	–	+	+	++	+++	---	+++	+++
15147 +	+	-	+	-	+	++	--	-	-
39968 +	+	-	-	-	-	-	-	-	-
40684 +	+	-	-	-	-	-	-	-	-
41196 +	-	-	-	-	-	-	-	-	-
41010 +	+	-	-	-	-	-	-	-	-
39795 +	+	-	-	-	-	-	-	-	-
40730 +	+	--+	+++	+++	+++	+	–	-	+++
40627 +	+	-	-	-	-	-	-	-	-
13957 +	-	-	-	-	-	-	-	-	-
41197 +	-	-	-	-	-	-	-	-	-
14157 +	+	-	-	-	-	-	-	-	-

41198 +	+	-	-	-	-	-	-	-	-
40205 +	++	-	-	+	-	-	-	-	-
41199 +	-	-	-	-	-	-	-	-	-
41200 +	-	–	-	-	-	-	-	-	-
11194 +	+	-	-	-	-	-	-	-	-
39503 +	+	–+	+++	+++	+++	+	–	-	-
41137 +	+	-	-	-	-	-	-	-	-
41201 +	-	-	-	+	-	-	-	-	-
41202 +	-	-	-	-	-	-	-	-	-
41060 +	+	–+	+++	+++	+++	+	-	-	-
40923 +	-	-	-	-	-	-	-	-	-
41203 +	+	-	-	-	-	-	-	-	-
18457 +	+	-	-	-	-	-	-	-	-
40305 +	-	-	-	+	-	-	–	-	-
41204 +	+	-	-	-	-	-	-	-	-
41205 +	-	-	+	+	+	+++	---	++	-
41206 +	+	–+	+++	+++	+++	+	–	-	-
40572 +	-	-	-	-	-	-	-	-	-
41207 +	+	–+	+++	+++	+++	-	-	-	-
18237 +	+	-	-	-	-	-	-	-	-
39789 +	-	-	-	-	-	-	-	-	-
11775 +	-	-	-	-	-	-	-	-	-
11045 +	+	-	-	-	-	-	-	-	-
40503 +	-	-	+	+	+	+++	---	-	-
17617 +	++	–+	+++	+++	+++	+	–	-	-
40215 +	+	-	-	-	-	-	-	-	-
41208 +	+	–+	+++	+++	+++	+	-	-	-
40245 +	+	-	-	-	-	-	-	-	-
41114 +	+	-	-	-	-	-	-	-	-
40714 +	+	-	-	-	-	-	-	-	-
41209 +	-	–+	+++	+++	+++	-	-	-	-
41210 +	+	-	-	-	-	-	-	-	-
41211 +	+	-	-	-	-	-	-	-	-

41212 +	-	-	-	-	-	-	-	-	-
39523 +	+	--+	+++	+++	+++	+	-	+++	-
39861 +	-	-	-	+	-	-	-	-	-
14019 +	+	-	-	-	-	-	-	-	-
13719 +	+	-	-	-	-	-	-	-	-
41213 +	+	--+	+++	+++	+++	+	-	-	-
41214 +	+	--+	+++	+++	+++	+	-	-	-
19627 +	-	--	-	+	-	-	-	-	-
39194 +	++	-	-	-	-	-	-	-	-
41215 +	+	--+	+++	+++	+++	+	-	-	-
41216 +	+	-	-	-	-	-	-	-	-
11541 +	-	-	-	-	-	-	-	-	-
40087 +	+	--+	+++	+++	+++	+++	---	-	-
40007 +	+	-	-	-	-	-	-	-	-
40803 +	+	-	-	-	-	-	-	-	-
41217 +	+	--+	+++	+++	+++	-	-	-	-
41190 +	+	-	-	-	-	-	-	-	-
41218 +	+	--+	+++	+++	+++	+	-	-	-
41219 +	+	--+	+++	+++	+++	+	-	-	-
41047 +	+	--+	+++	+++	+++	+	-	-	-
40848 +	+	--+	+++	+++	+++	+	-	-	-
16055 +	+	-	-	-	-	-	-	-	-
40973 +	+	--+	+++	+++	+++	-	-	-	-
41220 +	+	--+	+++	+++	+++	+	-	-	-
18717 +	-	-	-	-	-	-	-	-	-
41221 +	+	--+	+++	+++	+++	+	-	-	-
41222 +	+	--+	+++	+++	+++	+	-	+++	-
38377 +	+	-	+	-	++	-	-	-	-
40788 +	-	--+	+++	+++	+++	-	-	-	-
18100 +	+	--+	+++	+++	+++	-	-	-	-
41223 +	+	-	-	-	-	-	-	-	-
41224 +	+	--+	+++	+++	+++	-	-	-	-
40163 +	+	-	-	-	-	-	-	-	-

41132	+	+	-	+	-	-	-	-	-	-
41225	+	+	--+	+++	+++	+++	-	-	-	-
40428	+	-	-	-	-	-	-	-	-	-
41226	+	-	--+	+++	+++	+++	+	-	-	-
41227	+	+	--+	+++	+++	+++	+	–	-	-
12273	+	-	-	-	-	-	-	-	-	-
41228	+	-	-	-	-	-	-	–	-	-
41229	+	+	--+	+++	+++	+++	-	-	-	-
40696	+	+	--+	+++	+++	+++	+	–	-	-
39113	+	++	--+	+++	+++	+++	-	–	-	-
17136	+	+	--+	+++	+++	+++	+	–	-	-
12406	+	+	-	-	-	-	-	-	-	-
39387	+	+	-	-	-	-	-	-	-	-
41230	+	-	-	-	-	-	-	-	-	-
39770	+	-	-	-	-	-	-	-	-	-
18073	+	+	-	-	-	-	-	-	-	-
11643	+	+	-	-	-	-	-	-	-	-
41231	+	+	--+	+++	+++	+++	+	-	-	-
41232	+	+	--+	+++	+++	+++	+	-	-	-
41233	+	+	--+	+++	+++	+++	+	–	-	-
40659	+	++	--+	+++	+++	+++	+	-	-	-
41234	+	+	-	-	-	+	-	-	-	-
41235	+	++	--+	+++	+++	+++	+	–	-	-
40303	+	+	-	-	-	-	-	-	-	-
38859	+	+	--+	+++	+++	+++	-	-	-	-
41236	+	++	--+	+++	+++	+++	-	-	-	-
40038	+	+	--+	+++	+++	+++	-	–	-	-
13849	+	+	-	-	-	-	+	–	-	-
40909	+	+	-	-	-	-	-	-	-	-
12184	+	+	-	-	-	-	-	-	-	-
12244	+	+	-	-	-	-	-	-	-	-
41237	+	+	--+	+++	+++	+++	+	–	-	-
18779	+	-	-	-	+	-	-	-	-	-

40937 +	+	-	-	-	-	-	-	-	-
40854 +	+	-	-	-	-	-	-	-	-
40338 +	+	---+	+++	+++	+++	+	-	-	-
41238 +	+	---+	+++	+++	+++	-	-	-	-
41239 +	+	---+	+++	+++	+++	-	-	-	-
41022 +	+	-	-	-	-	-	-	-	-
41240 +	+	-	-	-	-	-	-	-	-
40793 +	+	---+	+++	+++	+++	-	-	+++	-
17476 +	-	-	-	-	-	++	--	-	-
41028 +	+	-	-	-	-	-	-	-	-
19296 +	+	---+	+++	+++	+++	-	-	-	-
41241 +	-	-	-	-	-	-	-	-	-
13879 +	+	-	-	-	-	-	-	-	-
39133 +	-	--	+	+	-	-	-	-	-
19074 +	-	-	-	-	-	-	-	-	-
41242 +	+	---+	+++	+++	+++	-	-	-	-
16070 +	-	-	-	-	-	-	-	-	-
41243 +	+	---+	+++	+++	+++	+	-	-	-
41244 +	+	-	-	-	-	-	-	-	-
39778 +	+	---+	+++	+++	+++	+	-	-	-
41245 +	+	---+	+++	+++	+++	-	-	-	-
15981 +	+	-	-	-	-	-	-	-	-
41246 +	-	-	-	-	-	-	-	-	-
14799 +	+	---+	+++	+++	+++	+	-	-	-
41247 +	+	---+	+++	+++	+++	-	-	-	-
40940 +	+	---+	+++	+++	+++	+	-	-	-
41248 +	+	---+	+++	+++	+++	+	-	-	-
41249 +	+	---+	+++	+++	+++	-	-	-	-
41250 +	+	---+	+++	+++	+++	-	-	-	-
41251 +	+	---+	+++	+++	+++	+	-	-	-
17051 +	-	-	-	-	-	-	-	-	-
41252 +	+	---+	+++	+++	+++	-	-	-	-
41199 +	-	-	-	-	-	-	-	-	-

40728 +	+	-	-	-	-	-	-	-	-
13672 +	+	-	-	-	-	-	-	-	-
40971 +	+	-	-	-	-	-	-	-	-
41253 +	+	---+	+++	+++	+++	+	-	-	-
11504 +	+	-	-	-	-	-	-	-	-
15997 +	+	-	-	-	-	-	-	-	-
39966 +	+	-	-	-	-	-	-	-	-
18567 +	-	-	-	-	-	-	-	-	-
11416 +	-	-	-	-	-	-	-	-	-
41254 +	+	-	-	-	-	-	-	-	-
14193 +	+	-	-	-	-	-	-	-	-
41255 +	++	---+	+++	+++	+++	+	-	-	+++
18134 +	+	-	-	-	-	-	-	-	-
41212 +	-	-	-	-	-	-	-	-	-
14740 +	+	-	+	+	+	+++	---	-	-
39883 +	+	---+	+++	+++	+++	+	-	+++	-
12571 +	+	-	-	-	-	-	-	-	-
41256 +	-	--	+	+	+	-	-	-	-
11811 +	+	-	-	-	-	-	-	-	-
41257 +	+	---+	+++	+++	+++	+	-	-	-
41258 +	+	-	-	-	-	-	-	-	-
41259 +	-	-	-	-	-	-	-	-	-
41260 +	+	---+	+++	+++	+++	-	-	-	-
38833 +	+	-	+	-	-	+	-	-	-
18726 +	+	-	-	-	-	-	-	-	-
41261 +	-	---+	+++	+++	+++	-	-	-	-
40913 +	+	---+	+++	+++	+++	+	-	-	-
41262 +	-	-	-	-	-	-	-	-	-
14647 +	+	-	-	-	-	-	-	-	-
40670 +	+	-	-	-	-	-	-	-	-
11146 +	+	-	-	-	-	-	-	-	-
41263 +	-	-	-	-	-	-	-	-	-
13679 +	+	-	+	+	+	+++	---	-	+++

41199 +	-	-	-	-	-	-	-	-	-
39436 +	-	-	-	-	-	-	-	-	-
41264 +	+	-	-	-	-	-	-	-	-
40902 +	-	-	-	-	-	-	-	-	-
13667 +	+	-	-	-	-	+	--	-	-
11680 +	-	-	-	-	-	-	-	-	-
41265 +	+	--+	+++	+++	+++	-	-	-	-
40366 +	+	--+	+++	+++	+++	+	-	-	+++
41266 +	+	--+	+++	+++	+++	-	-	-	-
38828 +	++	-	-	-	-	-	-	-	-
41267 +	+	--+	+++	+++	+++	+	-	-	-
41268 +	+	--+	+++	+++	+++	+	-	-	-
41269 +	+	--+	+++	+++	+++	+	-	-	-
41270 +	++	--+	+++	+++	+++	+	-	-	-
40407 +	+	--+	+++	+++	+++	+	-	-	-
39710 +	+	-	-	-	-	-	-	-	-
40051 +	+	--	++	++	++	+++	---	-	-
40117 +	+	--+	+++	+++	+++	-	-	-	-
12472 +	-	-	-	-	-	-	-	-	-
41211 +	+	-	-	-	-	-	-	-	-
41271 +	+	--+	+++	+++	+++	+	-	-	-
39915 +	+	-	-	-	-	-	-	-	-
41272 +	+	-	-	-	-	-	-	-	-
17917 +	+	-	-	-	-	-	-	-	-
17549 +	-	-	-	-	-	-	-	-	-
39132 +	+	-	-	-	-	-	-	-	-
12104 +	-	-	-	-	-	-	-	-	-
41273 +	+	--+	+++	+++	+++	+	-	-	-
41274 +	+	-	-	-	-	+	-	-	-
41275 +	+	-	-	-	-	-	-	-	-
40424 +	+	--+	+++	+++	+++	-	-	-	-
16042 +	-	-	-	-	-	-	-	-	-
17355 +	+	--+	+++	+++	+++	-	-	-	-

41276	+	+	−−+	+++	+++	+++	-	-	-	-
13893	+	+	-	-	-	-	-	-	-	-
16022	+	+	-	-	-	-	-	-	-	-
41277	+	-	−	++	+	++	+	-	-	-
40275	+	+	-	-	-	-	-	-	-	-
41018	+	+	-	-	-	-	-	-	-	-
14662	+	-	-	-	-	-	-	-	-	-
40291	+	+	−−+	+++	+++	+++	+	−	-	-
11440	+	-	-	-	-	-	-	-	-	-
41278	+	+	-	-	-	-	-	-	-	-
41279	+	+	−−	++	++	++	+++	−−−	-	-
39389	+	+	-	-	-	-	-	-	-	-
41005	+	+	−−+	+++	+++	+++	-	−	-	-
40991	+	+	-	-	-	-	-	-	-	-
41280	+	+	−−+	+++	+++	+++	-	−	-	-
41281	+	+	-	-	-	-	-	-	-	-
14386	+	+	-	-	-	-	-	-	-	-
40511	+	+	-	-	-	-	-	-	-	-
41147	+	+	−−+	+++	+++	+++	-	−	-	-
41282	+	+	−−+	+++	+++	+++	+	−	-	-
41283	+	+	−−+	+++	+++	+++	-	-	-	-
14419	+	+	-	-	-	-	-	-	-	-
41241	+	-	-	-	-	-	+	-	-	-
11775	+	-	-	-	-	-	-	-	-	-
41284	+	+	-	-	-	-	+	−	-	-
16103	+	+	-	-	-	-	-	-	-	-
41285	+	+	−−+	+++	+++	+++	-	-	-	-
14078	+	+	-	-	-	-	-	-	-	-
38870	+	-	-	-	-	-	-	-	-	-
12202	+	-	-	-	-	-	-	-	-	-
40588	+	+	-	-	-	-	-	-	-	-
40747	+	-	-	-	-	-	-	-	-	-
41286	+	+	-	+	-	-	+	−	-	-

18776 +	+	-	-	-	-	-	-	-	-
41287 +	+	-	-	-	-	-	-	-	-
41288 +	+	-	-	-	-	-	-	-	-
14505 +	+	-	-	-	-	-	-	-	-
41244 +	+	-	-	-	-	-	-	-	-
40623 +	++	-	-	-	-	-	-	-	-
41289 +	+	--+	+++	+++	+++	+	-	-	-
41290 +	-	-	-	-	-	-	-	-	-
12325 +	-	-	-	-	-	-	-	-	-
18114 +	-	-	-	-	-	-	-	-	-
13716 +	+	-	-	-	-	+++	---	-	-
41291 +	+	-	-	-	-	-	-	-	-
40461 +	+	-	-	-	-	-	-	-	-
11731 +	+	-	-	-	-	-	-	-	-
40033 +	+	-	+	-	-	-	-	-	-
41292 +	-	-	-	-	-	-	-	-	-
41293 +	+	--+	+++	+++	+++	+	-	-	-
11918 +	+	-	-	-	-	-	-	-	-
17828 +	+	-	-	-	-	-	-	-	-
17963 +	+	-	-	-	-	-	-	-	-
14276 +	+	-	-	-	-	-	-	-	-
41251 +	+	--+	+++	+++	+++	-	-	-	-
41294 +	-	-	-	-	-	-	-	-	-
39985 +	+	-	-	-	-	-	-	-	-
41295 +	-	-	+	-	-	+	-	-	-
20425 +	+	-	-	-	-	-	-	-	-
17916 +	-	-	-	-	-	-	-	-	-
40922 +	+	-	-	-	-	-	-	-	-
41296 +	+	--+	+++	+++	+++	+	-	-	-
39395 +	+	-	-	-	-	-	-	-	-
41297 +	-	-	-	-	+	-	-	-	-
41199 +	-	-	-	-	-	-	-	-	-
40655 +	+	-	-	-	-	-	-	-	-

41298	+	+	−−+	+++	+++	+++	-	−	-	-
40465	+	+	-	-	-	-	-	-	-	-
17254	+	+	−−+	+++	+++	+++	+	−	-	-
40706	+	+	-	-	-	-	-	-	-	-
41299	+	+	-	-	-	-	-	-	-	-
18052	+	+	-	-	-	-	-	-	-	-
41300	+	+	−−+	+++	+++	+++	+	-	-	-
41301	+	+	-	-	-	-	-	-	-	-
13675	+	+	-	-	-	-	-	-	-	-
41302	+	+	-	-	-	-	-	-	-	-
14162	+	+	-	-	-	-	-	-	-	-
17639	+	+	-	-	-	-	-	-	-	-
40164	+	+	−−+	+++	+++	+++	-	−	-	-
41303	+	+	−−+	+++	+++	+++	-	−	-	-
41160	+	+	-	-	-	-	-	-	-	-
37857	+	+	-	-	-	-	-	-	-	-
13870	+	+	-	-	-	-	-	-	-	-
40159	+	+	−−+	+++	+++	+++	-	-	-	-
18492	+	+	−−+	+++	+++	+++	+	−	-	+++
40998	+	+	−−+	+++	+++	+++	+	−	-	-
41304	+	+	−−+	+++	+++	+++	+	-	-	+++
40918	+	+	−−+	+++	+++	+++	+	-	-	-
40389	+	+	−−+	+++	+++	+++	+	−	-	-
40132	+	-	-	-	-	-	-	-	-	-
41305	+	-	-	-	-	-	-	-	-	-
39497	+	+	−−+	+++	+++	+++	+	−	-	-
41306	+	-	-	-	-	-	-	-	-	-
13529	+	+	-	-	-	-	++	−−	-	-
41307	+	++	−	+	+	++	++	−−	-	-
40228	+	+	−−+	+++	+++	+++	+	−	-	+++
40695	+	-	-	-	-	-	-	-	-	-
18165	+	-	-	-	-	-	-	-	-	-
41062	+	+	-	-	-	-	-	-	-	-

41308 +	-	--+	-	+++	+	+	-	-	-
40483 +	+	-	-	-	-	-	-	-	-
41309 +	+	--+	+++	+++	+++	-	-	-	-
41310 +	+	-	-	-	-	-	-	-	-
11052 +	-	-	-	-	-	-	-	-	-
37616 +	-	-	-	-	-	-	-	-	-
13539 +	+	-	-	-	-	-	-	-	-
16007 +	+	-	-	-	-	-	-	-	-
41311 +	-	-	-	-	-	-	-	-	-
11801 +	-	-	-	-	-	-	-	-	-
41312 +	-	-	-	-	-	-	-	-	-
40322 +	+	--+	+++	+++	+++	-	-	+++	-
41313 +	+	-	-	-	-	-	-	-	-
40387 +	+	-	-	-	-	-	-	-	-
41174 +	+	–	+	+	+	-	-	-	-
41314 +	+	--+	+++	+++	+++	+	–	-	-
41315 +	-	-	-	-	+	-	-	-	-
12325 +	-	-	-	-	-	-	-	-	-
41007 +	+	--+	+++	+++	+++	+	-	-	-
13865 +	+	-	-	-	-	-	-	-	-
41316 +	+	-	-	-	-	+	-	-	-
40056 +	+	--+	+++	+++	+++	+	–	-	-
38955 +	-	-	+	-	+	-	–	-	-
14451 +	+	-	-	-	-	+	–	-	-
41317 +	-	-	-	-	-	-	-	-	-
40272 +	+	-	-	-	+	+++	---	-	-
41318 +	+	-	-	-	-	-	-	-	-
18179 +	+	-	-	-	-	-	-	-	-
41319 +	-	-	+	-	+	-	-	-	-
18176 +	-	-	-	-	-	-	-	-	-
40098 +	+	-	-	-	-	-	-	-	-
41320 +	+	-	-	-	-	+	-	-	-
41321 +	+	--+	+++	+++	+++	+	-	-	-

41322	+	-	-	-	-	-	+	-	-	-
41323	+	+	-	-	-	-	-	-	-	-
41324	+	+	--+	+++	+++	+++	+	-	-	-
41325	+	-	-	+	-	+	-	-	-	-
41326	+	+	--+	+++	+++	+++	+	-	-	+++
41327	+	+	--+	+++	+++	+++	+	-	-	-
41328	+	+	--+	+++	+++	+++	+	-	-	+++
11075	+	-	-	+	-	+	-	-	-	-
41329	+	-	--+	+++	+++	+++	+	-	-	-
41330	+	-	-	-	-	-	-	-	-	-
41331	+	+	--+	+++	+++	+++	+	-	-	-
41332	+	-	-	-	-	-	-	-	-	-
41102	+	++	--+	+++	+++	+++	+	-	-	-
41333	+	+	-	-	-	-	-	-	-	-
41334	+	+	--+	+++	+++	+++	-	-	-	-
41335	+	+	-	-	+	-	+	-	-	-
41336	+	+	--+	+++	+++	+++	+	-	-	-
18757	+	-	-	-	-	-	-	-	-	-
41337	+	+	-	-	-	-	-	-	-	-
41338	+	+	--+	+++	+++	+++	+	-	-	-
41339	+	+	--+	+++	+++	+++	-	-	-	-
40271	+	-	--+	+++	+++	+++	-	-	-	-
41323	+	+	-	-	-	-	-	-	-	-
41340	+	+	-	+	-	-	-	-	-	-
41313	+	+	-	-	-	-	-	-	-	-
12202	+	-	-	-	-	-	-	-	-	-
39907	+	+	--+	+++	+++	+++	+	-	-	-
41234	+	+	-	-	-	-	-	-	-	-
41341	+	-	--+	+++	+++	+++	-	-	-	-
41342	+	+	-	-	-	-	-	-	-	-
13779	+	+	-	-	-	-	-	-	-	-
40750	+	+	--+	+++	+++	+++	+	-	-	-
41343	+	+	--+	+++	+++	+++	+	-	-	-

41344 +	+	–	+	++	-	+++	---	-	-
41345 +	+	--+	+++	+++	+++	-	–	-	-
18050 +	-	-	-	-	-	-	-	-	-
41191 +	-	--+	+++	+++	+++	-	–	-	-
19027 +	+	--+	+++	+++	+++	+	-	-	-
17617 +	+	--+	+++	+++	+++	-	–	-	-
41346 +	+	--+	+++	+++	+++	+	-	-	-
41347 +	+	–	+	+	+	+	-	-	-
41348 +	+	--+	+++	+++	+++	+	–	-	-
17317 +	+	--+	+++	+++	+++	-	-	-	-
41349 +	+	-	-	-	-	-	-	-	-
39363 +	+	--+	+++	+++	+++	+	-	-	-
14210 +	+	–	+	+	+	++	--	-	-
40832 +	+	-	-	-	-	-	-	-	-
11537 +	-	-	-	-	-	-	-	-	-
40379 +	-	–	-	-	-	-	-	-	-
40457 +	-	-	-	-	-	-	-	-	-
40404 +	+	--+	+++	+++	+++	-	-	-	-
41350 +	-	-	-	-	-	-	-	-	-
41351 +	+	--+	+++	+++	+++	+	–	-	-
41352 +	+	--+	+++	+++	+++	-	–	-	-
17720 +	-	-	-	-	-	-	-	-	-
41353 +	+	--+	+++	+++	+++	+	-	-	-
41354 +	++	--+	+++	+++	+++	-	-	-	-
41326 +	+	--+	+++	+++	+++	-	–	-	-
12085 +	+	-	-	-	-	-	-	-	-
12340 +	-	-	-	-	-	-	-	-	-
41355 +	+	--+	+++	+++	+++	-	-	-	-
41356 +	-	–	+	+	-	+++	---	-	-
38145 +	+	--+	+++	+++	+++	-	-	-	-
41357 +	+	--+	+++	+++	+++	-	-	-	-
41358 +	+	--+	+++	+++	+++	-	-	-	-
41359 +	+	--+	+++	+++	+++	+	–	-	-

10978 +	+	-	-	-	+	-	-	-	-
41360 +	-	-	-	-	-	-	-	-	-
41361 +	+	--+	+++	+++	+++	+	-	-	-
41362 +	+	--+	+++	+++	+++	-	-	-	-
39239 +	+	-	-	-	-	-	-	-	-
17825 +	-	-	-	-	-	-	-	-	-
11145 +	+	-	-	-	-	-	-	-	-
41363 +	+	--+	+++	+++	+++	-	-	-	-
41364 +	+	--+	+++	+++	+++	-	-	-	-
41298 +	+	--+	+++	+++	+++	-	-	+++	-
40800 +	-	-	-	-	-	-	-	-	-
41365 +	-	--+	+++	++	+++	-	-	-	-
41366 +	+	--+	+++	+++	+++	+++	---	-	-
41367 +	-	-	-	-	-	-	-	-	-
41368 +	+	--+	+++	+++	+++	-	-	-	-
41369 +	+	--+	+++	+++	+++	+	-	+++	-
40774 +	+	-	-	-	-	-	-	-	-
41370 +	+	--+	+++	+++	+++	+	-	-	-
18177 +	+	-	-	-	-	-	-	-	-
11975 +	+	-	-	-	-	-	-	-	-
40962 +	+	--+	+++	+++	+++	-	-	-	-
41371 +	+	--+	+++	+++	+++	+	-	-	-
41372 +	+	--+	+++	+++	+++	+	-	-	-
41373 +	+	--+	+++	+++	+++	-	-	-	-
18579 +	+	-	-	-	-	-	-	-	-
40224 +	+	--+	+++	+++	+++	+	-	-	-
41240 +	+	-	-	-	-	-	-	-	-
38280 +	+	-	-	-	-	-	-	-	-
41374 +	+	--+	+++	+++	+++	+	-	+++	-
38489 +	+	--+	+++	+++	+++	-	-	-	-
38382 +	-	-	-	-	-	-	-	-	-
17053 +	-	-	-	-	-	-	-	-	-
19341 +	+	-	-	-	-	-	-	-	-

39985 +	+	-	-	-	-	-	-	-	-
18576 +	-	-	-	-	-	-	-	-	-
18119 +	+	-	-	-	-	-	-	-	-
41198 +	+	-	-	-	-	-	-	-	-
40855 +	+	--+	+++	+++	+++	-	-	-	-
17600 +	-	-	-	-	-	-	-	-	-
41375 +	+	--+	+++	+++	+++	+	-	-	-
41376 +	+	--+	+++	+++	+++	-	-	-	-
17904 +	-	-	-	-	-	-	-	-	-
41377 +	+	--+	+++	+++	+++	+	-	-	-
41378 +	+	-	-	-	-	-	-	-	-
41379 +	+	--+	+++	+++	+++	+	-	-	-
11168 +	+	-	-	-	-	-	-	-	-
41380 +	+	--+	+++	+++	+++	+	-	-	-
11885 +	-	-	-	-	-	-	-	-	-
41381 +	+	--+	+++	+++	+++	-	-	-	-
41382 +	+	-	-	-	-	-	-	-	-
41383 +	+	--+	+++	+++	+++	-	-	-	-
41384 +	-	-	-	-	-	-	-	-	-
13820 +	+	-	-	-	-	++	--	-	-
38097 +	+	-	-	-	-	-	-	-	-
41291 +	+	-	-	-	-	-	-	-	-
13607 +	+	-	-	-	-	-	-	-	-
18973 +	+	--+	+++	+++	+++	+	-	-	-
41385 +	-	--+	+++	+++	+++	+++	---	-	-
11153 +	+	-	-	-	-	-	-	-	-
39162 +	+	-	-	-	-	-	-	-	-
39983 +	+	-	-	-	-	-	-	-	-
41386 +	+	-	-	-	-	-	-	-	-
41387 +	+	-	-	-	-	-	-	-	-
11021 +	+	-	-	-	-	-	-	-	-
41388 +	+	--+	+++	+++	+++	-	-	-	-
11852 +	-	-	-	-	-	-	-	-	-

17067	+	+	−	+	+	+	-	-	-	-
40072	+	-	-	-	-	-	+++	−−−	-	-
39530	+	+	-	-	-	-	-	-	-	-
41389	+	-	-	-	-	-	-	-	-	-
41390	+	+	−−+	+++	+++	+++	+	-	-	-
39722	+	+	-	-	-	-	-	-	-	-
41347	+	+	−	+	+	+	-	-	-	-
40298	+	+	−−+	+++	+++	+++	-	−	-	-
40252	+	++	−−+	+++	+++	+++	-	−−	-	-
41391	+	-	−	+	-	-	-	−	-	-
41392	+	+	−−+	+++	+++	+++	+	-	-	-
41393	+	+	-	-	-	-	-	-	-	-
19060	+	+	−−+	+++	+++	+++	+	-	-	-
41394	+	+	−−+	+++	+++	+++	+	-	-	-
40737	+	+	-	-	-	-	-	-	-	-
39789	+	-	-	-	-	-	-	-	-	-
12360	+	-	-	-	-	+	-	-	-	-
38710	+	-	−	+	+	+	-	-	-	-
41395	+	+	-	-	-	-	-	-	-	-
39922	+	+	-	-	+	-	-	-	-	-
13571	+	+	-	-	-	+	++	−−	-	-
41396	+	+	−−+	+++	+++	+++	+	-	-	-
13821	+	+	-	-	-	-	-	-	-	-
13740	+	+	-	-	-	-	+	−	-	-
41397	+	-	−−+	+++	+++	+++	-	−	-	-
41398	+	-	−−+	+++	+++	+++	-	−	-	-
39302	+	+	-	-	-	-	-	-	-	-
11781	+	+	-	-	-	-	-	-	-	-
40364	+	+	−−+	+++	+++	+++	-	-	-	-
41399	+	-	-	-	-	-	-	-	-	-
39915	+	+	-	-	-	-	-	-	-	-
41400	+	-	-	-	+	-	-	-	-	-
40311	+	+	-	-	-	-	+	−	-	-

39553	+	++	-	-	-	-	+	–	-	-
41126	+	+	–+	+++	+++	+++	+	–	-	-
41401	+	-	-	-	-	-	++	––	-	-
11251	+	+	-	-	-	-	-	-	-	-
11534	+	-	-	-	-	-	-	-	-	-
11114	+	+	-	-	-	-	-	-	-	-
41245	+	+	–+	+++	+++	+++	+	-	-	-
41402	+	-	-	-	-	-	-	-	-	-
13506	+	+	-	-	-	-	+	–	-	-
41403	+	-	––	++	++	++	+++	–––	-	-
41026	+	+	–+	+++	+++	+++	+	–	-	-
41404	+	+	–+	+++	+++	+++	-	–	-	-
41405	+	+	–+	+++	+++	+++	-	-	-	-
19337	+	-	-	-	-	-	-	-	-	-
20362	+	-	-	-	-	-	-	-	-	-
41406	+	+	–+	+++	+++	+++	+++	–––	-	-
41407	+	+	-	-	-	-	+	-	-	-
16055	+	+	-	-	-	-	+	-	-	-
13927	+	+	-	-	-	-	-	-	-	-
41408	+	+	–+	+++	+++	+++	+	–	-	-
41409	+	-	-	-	-	-	-	-	-	-
12222	+	-	-	-	-	-	-	-	-	-
40458	+	+	-	-	-	-	-	-	-	-
40776	+	-	-	-	-	-	-	-	-	-
17928	+	++	-	+	-	-	-	-	-	-
19957	+	+	-	-	-	-	-	-	-	-
13729	+	+	-	-	-	-	+	––	-	-
41410	+	-	-	-	-	+	-	-	-	-
40948	+	-	-	-	-	-	-	-	-	-
41411	+	+	–+	+++	+++	+++	+	-	-	-
41145	+	+	–	+	+	+	+++	–––	-	-
40845	+	+	–+	+++	+++	+++	+	–	-	-
13755	+	+	-	-	-	-	-	-	-	-

40408 +	+	-	-	-	-	-	-	-	-
18096 +	-	-	-	-	-	-	-	-	-
38771 +	-	---+	+++	+++	+++	-	-	-	-
17097 +	-	-	-	-	-	-	-	-	-
41412 +	++	---+	+++	+++	+++	-	-	-	-
41413 +	+	---+	+++	+++	+++	-	-	-	-
17451 +	+	---+	+++	+++	+++	-	-	-	-
40292 +	+	-	-	-	-	-	-	-	-
40622 +	-	-	-	-	-	-	-	-	-
13729 +	+	-	-	-	-	+	--	-	-
41414 +	+	-	-	-	-	-	-	-	-
40008 +	-	-	-	-	-	-	-	-	-
41415 +	+	---+	++	++	++	+++	---	-	-
40692 +	-	-	-	-	-	-	-	-	-
40873 +	+	---+	+++	+++	+++	-	-	-	-
40610 +	+	-	-	-	-	-	-	-	-
41416 +	+	---+	+++	+++	+++	+	-	-	-
18749 +	-	-	-	-	-	-	-	-	-
40650 +	-	-	-	-	-	-	-	-	-
41417 +	++	---+	+++	+++	+++	+	-	-	-
41418 +	+	-	-	-	-	-	-	-	-
40784 +	-	-	-	-	-	-	-	-	-
17427 +	+	-	-	-	-	-	-	-	-
17921 +	+	-	-	-	-	-	-	-	-
14332 +	+	-	-	-	-	-	-	-	-
39613 +	+	---+	+++	+++	+++	++	-	-	-
41419 +	+	-	+	+	+	+++	---	-	-
14695 +	+	-	-	-	+	-	-	-	-
19335 +	+	---+	+++	+++	+++	-	-	-	-
39030 +	-	-	-	-	-	-	-	-	-
13545 +	+	-	-	-	-	-	-	-	-
12357 +	-	-	-	-	-	-	-	-	-
39666 +	+	-	+	+	+	+++	---	-	-

14394 +	+	-	-	-	-	-	-	-	-
41420 +	+	--+	+++	+++	+++	-	-	-	-
40414 +	+	-	-	-	-	-	-	-	-
40966 +	+	-	-	-	-	-	-	-	-
17882 +	-	-	-	+	-	-	-	-	-
41421 +	+	--+	+++	+++	+++	+	-	-	-
41081 +	-	-	-	-	-	-	-	-	-
38651 +	+	-	-	-	-	-	-	-	-
41422 +	+	-	-	-	-	-	-	-	-
41006 +	-	-	+	+	+	+++	---	-	-
40630 +	+	-	-	-	+	+++	---	-	-
41423 +	+	--+	+++	+++	+++	-	-	-	-
40733 +	+	-	-	-	+	+++	---	-	-
40762 +	+	-	-	-	-	-	-	-	-
13944 +	+	-	-	-	-	++	--	-	-
41424 +	-	--+	+++	+++	+++	+	-	-	-
40827 +	+	-	-	-	-	-	-	-	-
13579 +	+	-	-	-	+	++	--	-	-
14763 +	+	-	-	-	-	-	-	-	-
40528 +	-	-	-	-	-	-	-	-	-
41425 +	+	--+	+++	+++	+++	+	-	-	-
41426 +	-	-	-	-	-	-	-	-	-
39331 +	-	-	+	+	+	+++	---	-	-
11462 +	-	-	-	-	-	-	-	-	-
19648 +	-	-	-	-	-	-	-	-	-
38932 +	+	--+	+++	+++	+++	+	-	-	-
41427 +	+	-	-	-	-	-	-	-	-
17117 +	+	-	-	-	-	-	-	-	-
11040 +	+	-	++	++	-	+++	---	-	-
39822 +	++	-	-	-	-	-	-	-	-
13753 +	+	-	-	-	-	+	-	-	-
40396 +	+	-	-	-	-	-	-	-	-
41161 +	+	-	-	-	-	+	-	-	-

17803 +	+	-	-	-	-	-	-	-	-
11635 +	-	-	-	-	-	-	-	-	-
41428 +	+	-	-	-	-	-	-	-	-
41429 +	-	–	++	++	+	-	-	-	-
13679 +	+	–	+	+	+	+++	---	-	-
13825 +	+	-	-	-	-	-	-	-	-
41430 +	++	--+	+++	+++	+++	-	–	-	+
11818 +	+	-	-	-	-	-	-	-	-
40823 +	-	-	-	-	-	-	-	-	-
41431 +	+	--+	+++	+++	+++	-	–	-	-
41432 +	-	--+	+++	+++	+++	-	–	-	-
41189 +	-	-	-	-	-	-	-	-	-
17763 +	-	-	-	-	-	-	-	-	-
39689 +	+	--+	+++	+++	+++	+	–	-	-
39723 +	+	-	-	-	-	-	-	-	-
17773 +	++	-	-	-	-	-	-	-	-
17589 +	+	-	-	-	-	-	-	-	-
18710 +	-	–	-	-	-	-	-	-	-
41288 +	+	-	-	-	-	-	-	-	-
13867 +	+	-	-	-	-	-	-	-	-
18123 +	+	-	-	-	-	-	–	-	-
18763 +	+	-	-	-	-	-	-	-	-
41143 +	-	-	-	-	-	-	-	-	-
13820 +	+	-	-	-	-	++	--	-	-
17576 +	-	--	+	+++	-	-	-	-	-
40781 +	+	-	-	-	-	-	-	-	-
18696 +	-	–	-	-	-	-	-	-	-
41433 +	+	--+	+++	+++	+++	-	-	-	-
41434 +	-	-	-	-	-	-	-	-	-
12222 +	-	-	-	-	-	-	-	-	-
14397 +	+	-	-	+	+	+++	---	-	-
40514 +	+	--+	+++	+++	+++	-	-	-	-
11084 +	+	-	-	-	-	-	-	-	-

40714 +	+	-	-	-	-	-	-	-	-
19914 +	-	-	-	-	-	-	-	-	-
39361 +	+	-	-	-	-	-	-	-	-
19247 +	-	-	-	-	-	-	-	-	-
14260 +	+	-	-	-	-	-	-	-	-
40492 +	-	–	+	+	+	+++	---	-	-
41435 +	-	-	-	-	-	-	-	-	-
40982 +	+	-	-	-	-	-	-	-	-
41178 +	+	-	-	-	-	-	-	-	-
11812 +	++	-	-	-	-	-	-	-	-
41436 +	+	-	-	-	-	-	-	-	-
41437 +	+	--	+++	++	+++	+++	---	-	-
41438 +	+	-	-	-	-	-	-	-	-
12050 +	-	-	-	-	-	-	-	-	-
41439 +	-	-	-	-	-	-	-	-	-
39572 +	++	--+	+++	+++	+++	+	-	-	-
17358 +	+	--+	+++	+++	+++	+	–	-	-
41015 +	+	-	-	-	-	-	-	-	-
13883 +	+	–	+	+	+	+++	---	-	-
11010 +	+	-	-	-	+	-	-	-	-
41440 +	+	-	-	-	-	+	-	-	-
41441 +	+	--+	+++	+++	+++	-	-	-	-
41318 +	+	-	-	-	-	-	-	-	-
14638 +	+	-	-	-	-	+	–	-	-
39754 +	+	--+	+++	+++	+++	-	–	-	-
41184 +	-	-	-	-	-	-	-	-	-
41442 +	-	-	-	-	-	-	-	-	-
41443 +	-	-	-	-	-	-	-	-	-
13825 +	+	-	-	-	-	-	-	-	-
41222 +	+	--+	+++	+++	+++	-	–	-	-
12680 +	-	-	-	-	-	-	-	-	-
41306 +	-	-	-	-	-	-	-	-	-
37657 +	-	-	-	-	-	-	-	-	-

17423 +	+	-	-	-	-	-	-	-	-
11045 +	+	-	-	-	-	-	-	-	-
40745 +	+	–	+	+	+	+	–	-	-
41444 +	+	---+	+++	+++	+++	-	-	-	-
40590 +	+	---+	+++	+++	+++	+	-	-	-
41445 +	+	---+	+++	+++	+++	-	-	-	-
41446 +	+	-	-	-	-	-	-	-	-
41041 +	-	-	-	-	-	-	-	-	-
12472 +	-	-	-	-	-	-	-	-	-
14312 +	+	-	-	-	-	-	-	-	-
14409 +	+	-	-	-	-	-	–	-	-
41447 +	++	---+	+++	+++	+++	+	-	-	-
13903 +	+	-	-	-	-	+	-	-	-
11934 +	+	-	-	-	-	-	-	-	-
41448 +	+	-	-	-	-	+	–	-	-
41449 +	+	-	-	-	-	+	–	-	-
38212 +	++	---+	+++	+++	+++	-	-	-	-
11946 +	-	-	-	-	-	-	-	-	-
41434 +	-	-	-	-	-	-	-	-	-
40827 +	+	-	-	-	-	-	-	-	-
14194 +	+	-	+	-	+	++	--	-	-
41443 +	-	-	+	-	+	-	-	-	-
40634 +	+	-	-	-	-	-	-	-	-
41317 +	-	-	-	-	-	-	-	-	-
41449 +	+	-	-	-	-	+	–	-	-
41450 +	-	-	-	-	-	-	-	-	-
41451 +	-	-	-	+	-	-	-	-	-
40951 +	+	–	+	+	+	+++	---	-	-
14662 +	-	-	-	-	-	-	-	-	-
12233 +	-	-	-	-	-	-	-	-	-
17942 +	-	-	-	-	-	-	-	-	-
41452 +	+	---+	+++	+++	+++	+	-	-	-
40333 +	+	-	-	-	-	-	-	-	-

39678 +	+	--+	+++	+++	+++	+	-	+++	-
41453 +	-	-	-	-	-	+++	---	-	-
41009 +	-	-	+	+	+	+++	---	-	-
11442 +	-	-	-	-	-	-	-	-	-
11084 +	+	-	-	-	-	+	-	-	-
14763 +	+	-	-	-	-	-	-	-	-
13917 +	+	-	-	-	-	-	-	-	-
40841 +	+	-	-	-	-	-	-	-	-
13541 +	+	-	-	-	-	+++	---	-	-
41002 +	-	-	-	-	-	-	-	-	-
14419 +	+	-	-	-	-	-	-	-	-
12580 +	-	-	-	-	-	-	-	-	-
40212 +	+	--+	+++	+++	+++	-	-	-	-
41205 +	-	-	+	+	+	+++	---	-	-
41454 +	-	-	-	-	-	-	-	-	-
18820 +	-	-	-	-	-	-	-	-	-
18052 +	+	-	-	-	-	-	-	-	-
40447 +	+	-	-	-	-	-	-	-	-
40328 +	-	-	-	-	-	-	-	-	-
41455 +	-	-	-	-	-	-	-	-	-
19144 +	-	-	-	-	-	-	-	-	-
41422 +	+	-	-	-	-	-	-	-	-
15950 +	+	-	-	-	+	+++	---	-	-
11627 +	+	-	-	-	-	-	-	-	-
12251 +	+	-	-	-	-	-	-	-	-
17893 +	+	-	-	-	-	-	-	-	-
40842 +	-	-	-	-	-	-	-	-	-
40394 +	+	-	-	-	-	-	-	-	-
40650 +	-	-	-	-	-	-	-	-	-
41399 +	-	-	-	-	-	-	-	-	-
40794 +	-	-	-	-	-	-	-	-	-
16562 +	++	-	-	-	-	-	-	-	-
41456 +	+	-	-	+	-	+	--	-	-

12680 +	-	-	-	-	-	-	-	-	-
41457 +	+	---+	+++	+++	+++	-	-	-	-
41458 +	-	-	-	-	-	-	-	-	-
11032 +	+	---+	+++	+++	+++	+	-	-	-
13572 +	+	-	-	-	-	-	-	-	-
12215 +	-	-	-	-	-	-	-	-	-
20383 +	-	-	-	-	-	-	-	-	-
17855 +	+	-	-	-	-	-	-	-	-
13987 +	+	-	-	-	-	-	-	-	-
40860 +	+	-	-	-	-	-	-	-	-
11150 +	-	-	-	-	-	-	-	-	-
11624 +	+	-	-	-	-	-	-	-	-
41459 +	+	---+	+++	+++	+++	-	–	-	-
13513 +	+	-	-	-	-	++	--	-	-
39290 +	-	-	-	-	-	-	-	-	-
41460 +	+	-	-	-	-	-	-	-	-
37409 +	+	–	+	-	-	-	-	-	-
41461 +	+	-	-	-	-	-	-	-	-
41462 +	+	---+	+++	+++	+++	-	-	-	-
41463 +	+	-	-	-	-	-	-	-	-
41464 +	-	---+	+++	+++	+++	+	-	-	-
39167 +	-	-	-	-	-	-	-	-	-
41465 +	-	-	-	-	-	-	-	-	-
12498 +	-	-	-	-	-	-	-	-	-
41466 +	-	-	-	-	-	+	–	-	-
41467 +	+	–	+	+	++	-	-	-	-
41468 +	+	---+	+++	+++	+++	+	–	-	-
41461 +	+	-	-	-	-	-	-	-	-
17813 +	+	-	-	-	-	-	–	-	-
17568 +	-	-	-	-	-	-	-	-	-
14691 +	+	-	-	-	-	-	-	-	-
38835 +	-	-	-	-	-	-	-	-	-
13699 +	+	-	-	-	-	-	-	-	-

41469	+	-	–	++	++	++	+++	---	-	-
16643	+	+	-	-	-	-	-	-	-	-
41057	+	+	-	-	-	-	-	-	-	-
41470	+	+	-	-	+	+	++	--	-	-
40946	+	+	--	++	++	++	+	–	-	-
40362	+	-	-	-	-	-	-	-	-	-
41471	+	+	--+	+++	+++	+++	-	–	-	-
41472	+	+	–	+	+	+	+++	---	+++	+++
39533	+	-	-	-	-	-	-	-	-	-
38899	+	-	-	-	-	-	-	-	-	-
14148	+	+	-	-	-	-	-	-	-	-
41473	+	-	-	-	-	-	-	-	-	-
41474	+	+	-	-	-	-	-	-	-	-
17966	+	+	--	-	-	-	-	-	-	-
40064	+	-	-	-	-	-	-	-	-	-
41455	+	-	-	-	-	-	-	-	-	-
19337	+	+	-	-	-	-	-	-	-	-
41077	+	+	-	-	-	-	-	-	-	-
39008	+	+	-	-	-	-	-	-	-	-
41105	+	-	-	-	-	-	-	-	-	-
38857	+	-	-	-	-	+	-	-	-	-
40636	+	+	-	+	-	-	++	--	-	-
41277	+	+	--	++	++	++	-	-	-	-
40260	+	-	-	-	-	-	-	-	-	-
13582	+	+	-	-	-	-	-	-	-	-
40070	+	+	-	-	-	-	-	-	-	-
41475	+	+	--+	+++	+++	+++	+	–	-	-
41196	+	-	-	-	-	-	-	-	-	-
40588	+	+	-	-	-	-	-	-	-	-
17302	+	+	–	+	+	+	++	--	-	-
13829	+	+	-	-	+	+	+	--	-	-
41476	+	+	-	-	-	-	-	-	-	-
39659	+	+	-	-	-	-	-	-	-	-

41477	+	-	--+	+++	+++	+++	+	–	-	-
41478	+	-	-	-	-	+	-	-	-	-
18502	+	-	-	-	-	-	-	-	-	-
13643	+	+	-	-	-	+	+	-	-	-
17358	+	+	--+	+++	+++	+++	+	–	-	-
39303	+	+	-	-	-	-	-	-	-	-
13668	+	+	-	-	-	-	+	–	-	-
14210	+	+	–	+	+	+	++	--	-	-
39144	+	+	-	+	-	+	+	–	-	-
12539	+	-	-	-	-	-	-	-	-	-
40580	+	+	-	-	-	-	-	-	-	-
41009	+	+	–	+	+	+	+++	---	+++	+++
41479	+	-	-	-	-	-	-	-	-	-
38520	+	-	-	-	-	-	+	-	-	-
39261	+	-	-	-	-	-	-	-	-	-
40903	+	+	-	-	-	-	-	-	-	-
41480	+	-	--+	+++	+++	+++	-	-	-	-
13513	+	+	-	-	-	-	+	--	-	-
13786	+	+	-	-	-	+	+	–	-	-
18123	+	+	-	-	-	+	-	-	-	-
40559	+	-	-	-	-	-	-	-	-	-
39092	+	-	-	-	-	-	-	-	-	-
41258	+	+	-	-	-	-	-	-	-	-
39884	+	-	-	-	-	-	-	-	-	-
14127	+	+	-	-	-	+	+	-	-	-
41481	+	+	-	-	-	-	-	-	-	-
16658	+	-	-	-	-	+	++	--	-	-
13675	+	+	-	-	-	-	-	-	-	-
41482	+	-	-	-	-	-	-	-	-	-
39335	+	+	-	-	-	-	-	-	-	-
41483	+	+	--+	+++	+++	+++	-	-	-	-
18001	+	+	-	-	-	-	-	-	-	-
40667	+	-	-	-	-	-	-	-	-	-

41484	+	-	-	-	-	-	-	-	-
41414	+	+	-	-	-	-	-	-	-
41485	+	-	-	-	-	-	-	-	-
41472	+	+	–	+	+	+	+++	---	+++	+++
41486	+	-	-	-	-	-	-	-	-
17572	+	-	-	-	-	+	-	-	-
41072	+	+	-	-	-	-	+	–	-	-
41487	+	+	-	-	-	-	-	-	-	-
41488	+	+	-	-	-	-	-	-	-	-
40416	+	-	–	+	+	+	-	-	-	-
41489	+	-	-	-	-	-	+	–	-	-
41490	+	-	-	-	-	-	-	-	-	-
41491	+	+	--+	+++	+++	+++	+	–	-	-
41492	+	+	-	-	-	-	+	–	-	-
40368	+	+	-	-	-	-	-	-	-	-
41493	+	+	–	+	+	+	+++	---	-	-
41494	+	+	-	-	-	-	-	-	-	-
41495	+	+	-	-	-	-	-	-	-	-
41458	+	-	-	-	-	-	-	-	-	-
41496	+	-	–	+	+	+	-	-	-	-
17731	+	+	-	-	-	-	-	-	-	-
40372	+	+	-	+	-	-	-	-	-	-
41189	+	-	-	-	-	-	-	-	-	-
41393	+	+	-	-	-	-	-	-	-	-
41121	+	-	-	-	-	-	-	-	-	-
39917	+	++	--+	+++	+++	+++	-	-	-	-
41025	+	+	-	-	-	-	-	-	-	-
40984	+	-	-	-	-	-	-	-	-	-
14113	+	+	-	-	-	+	+	–	-	-
13839	+	+	-	-	-	-	++	--	-	-
41170	+	+	-	-	-	-	-	-	-	-
41497	+	-	–	+	+	+	+++	---	-	-
41485	+	-	–	+	-	-	-	-	-	-

41498 +	+	-	-	-	-	-	-	-	-
40952 +	+	-	-	-	-	-	-	-	-
13627 +	+	-	-	-	-	++	---	-	-
40341 +	++	--+	+++	+++	+++	+	–	-	-
39900 +	+	-	-	-	-	-	–	-	-
14659 +	+	-	-	-	-	+	–	-	-
41435 +	-	-	-	-	-	-	-	-	-
18705 +	-	–	-	+	-	+	-	-	-
40717 +	-	-	-	-	-	-	-	-	-
40184 +	+	--+	+++	+++	+++	+	-	-	-
39840 +	+	--+	+++	+++	+++	+	-	-	-
18212 +	-	-	-	-	-	-	-	-	-
40881 +	-	–	+	+	+	+++	---	-	-
18272 +	+	-	-	-	-	-	-	-	-
39218 +	+	-	-	-	-	-	-	-	-
41499 +	+	-	-	-	-	+	–	-	-
17769 +	+	-	-	-	-	-	-	-	-
40174 +	-	-	-	-	-	+	–	-	-
41500 +	-	-	-	-	-	-	-	-	-
13766 +	+	-	+	+	+	+++	---	-	-
41205 +	-	-	+	+	+	+++	---	-	-
40324 +	-	-	-	+	+	-	-	-	-
38372 +	+	--+	+++	+++	+++	+	-	-	-
17895 +	+	-	-	-	-	-	-	-	-
13936 +	+	-	-	-	-	-	-	-	-
41401 +	-	-	-	-	-	++	--	-	-
40827 +	+	-	-	-	-	-	-	-	-
41401 +	-	-	-	-	-	++	--	-	-
41308 +	-	--+	-	+++	+	+	-	-	-
41501 +	+	-	-	-	-	-	-	-	-
18212 +	-	-	-	-	-	-	-	-	-
41490 +	-	-	-	-	-	-	-	-	-
17248 +	+	-	-	-	-	++	–	-	-

41420	+	+	−−+	+++	+++	+++	+	-	-	-
41502	+	+	−	+	+	+	+++	−−−	-	-
41247	+	+	−−+	+++	+++	+++	+	−	-	-
17785	+	+	-	-	-	-	-	-	-	-
14784	+	+	-	-	-	-	+	−−	-	-
41503	+	+	-	-	-	-	-	-	-	-
17555	+	++	-	-	-	-	-	-	-	-
17983	+	-	-	-	-	-	-	-	-	-
11602	+	+	-	-	-	-	-	-	-	-
41110	+	-	−−+	+	+++	+	++	−−	-	-
13668	+	+	-	-	-	-	+	−	-	-
40292	+	+	-	-	-	-	-	-	-	-
18142	+	+	-	-	-	-	-	-	-	-
13639	+	+	-	-	-	-	-	-	-	-
17804	+	-	-	-	++	-	-	-	-	-
40835	+	+	-	-	-	-	-	-	-	-
40363	+	+	−−+	+++	+++	+++	-	−	-	-
41275	+	+	-	-	-	-	-	-	-	-
41504	+	+	−−+	+++	+++	+++	+	-	-	-
18108	+	-	-	-	-	-	-	-	-	-
41045	+	+	-	-	-	-	-	-	-	-
41319	+	-	-	-	-	-	-	-	-	-
13988	+	+	-	+	-	+	+	−	-	-
18787	+	+	-	-	-	-	-	-	-	-
17465	+	+	-	-	-	-	+	−	-	-
41104	+	+	-	-	-	-	-	-	-	-
41505	+	-	-	-	-	-	-	-	-	-
41205	+	-	-	+	+	+	+++	−−−	-	-
40807	+	-	-	+	+	+	+++	−−−	-	-
39312	+	-	-	-	-	-	-	-	-	-
40714	+	+	-	-	-	-	-	-	-	-
18513	+	+	-	-	-	-	-	-	-	-
40141	+	+	-	+	+	-	-	-	-	-

18157 +	+	-	-	-	-	-	-	-	-
18332 +	-	-	-	-	-	-	-	-	-
40893 +	-	-	-	-	-	-	-	-	-
17836 +	-	-	-	-	-	-	-	-	-
18028 +	-	-	-	-	-	-	-	-	-
12549 +	-	-	-	-	-	-	-	-	-
41506 +	-	-	-	-	-	-	-	-	-
41507 +	-	-	-	-	-	-	-	-	-
41508 +	-	-	-	-	-	-	-	-	-
16642 +	+	-	+	+	+	++	–	-	-
13591 +	+	-	+	-	+	++	––	-	-
41509 +	-	-	-	-	-	-	-	-	-
18776 +	+	-	-	-	-	-	-	-	-
41473 +	-	-	-	-	-	-	-	-	-
41510 +	+	-	-	-	-	-	–	-	-
41056 +	+	-	-	-	-	-	-	-	-
18114 +	-	-	-	-	-	-	-	-	-
13649 +	+	-	-	-	-	+	–	-	-
39582 +	+	-	-	-	-	-	-	-	-
37976 +	+	–+	+++	+++	+++	+	-	-	-
12202 +	-	-	-	-	-	-	-	-	-
41511 +	+	-	-	-	-	+	–	-	-
18863 +	+	-	-	-	-	-	-	-	-
14019 +	+	-	-	-	-	-	-	-	-
40650 +	-	-	-	-	-	-	-	-	-
20383 +	-	-	-	-	-	-	-	-	-
14526 +	+	-	-	-	-	-	-	-	-
16082 +	-	-	-	-	-	-	-	-	-
14428 +	+	-	-	-	-	-	-	-	-
14029 +	+	-	-	-	-	-	-	-	-
41512 +	-	-	-	-	-	-	-	-	-
37266 +	+	-	-	-	-	-	-	-	-
41513 +	-	-	-	-	-	-	-	-	-

18145 +	-	-	-	-	-	-	-	-	-
11534 +	-	-	-	-	-	-	-	-	-
13512 +	+	-	-	-	+	+++	--	-	-
18320 +	+	-	-	-	-	-	-	-	-
39952 +	+	-	-	-	-	-	-	-	-
41514 +	-	-	-	-	-	-	-	-	-
41515 +	+	-	-	-	-	-	-	-	-
13931 +	+	–	+	+	+	+++	---	-	+++
41516 +	+	--+	+++	+++	+++	+	–	-	-
41517 +	+	-	-	-	-	-	-	-	-
14252 +	+	-	-	+	+	+	–	-	-
16671 +	+	-	-	-	-	-	-	-	-
17256 +	+	-	-	-	-	+	–	-	-
14765 +	+	-	-	-	-	+	–	-	-
41518 +	-	–	+	-	+	+	–	-	-
41519 +	+	-	-	-	-	-	-	-	-
40399 +	-	-	-	-	-	-	-	-	-
17713 +	+	-	-	-	-	-	-	-	-
41312 +	-	-	-	-	-	-	-	-	-
41520 +	+	-	-	-	-	-	-	-	-
40447 +	+	-	-	-	-	-	-	-	-
41495 +	+	-	-	-	-	-	-	-	-
41521 +	-	–	+	+	+	+++	---	-	-
41512 +	-	-	-	-	-	-	-	-	-
41508 +	-	-	-	-	-	-	-	-	-
41088 +	+	-	-	-	-	-	-	-	-
40969 +	+	-	-	-	-	-	-	-	-
11412 +	+	-	-	-	-	-	-	-	-
17767 +	-	--+	+	+	-	-	-	-	-
41522 +	-	-	-	-	-	-	-	-	-
41523 +	-	-	-	-	-	-	-	-	-
41450 +	-	-	-	-	-	-	-	-	-
41524 +	-	-	-	-	-	-	-	-	-

11900	+	+	-	-	-	-	++	--	-	-
41502	+	+	–	+	+	+	+++	---	-	-
41525	+	+	-	-	-	-	+	–	-	-
39941	+	-	-	-	-	-	-	-	-	-
13585	+	+	-	-	-	-	-	-	-	-
11313	+	+	-	-	-	+	++	--	-	-
18062	+	-	-	-	-	-	-	-	-	-
17697	+	-	-	+	+	+	+	-	-	-
11248	+	-	-	-	-	-	-	-	-	-
41520	+	+	-	-	-	-	-	-	-	-
41526	+	+	-	+	-	+	-	-	-	-
17983	+	-	-	-	-	-	-	-	-	-
12521	+	-	-	-	-	-	-	-	-	-
41527	+	-	-	-	-	-	-	-	-	-
17633	+	-	-	-	-	-	-	-	-	-
41528	+	-	-	-	-	-	-	-	-	-
41529	+	-	-	-	-	-	-	-	-	-
14842	+	+	-	-	-	-	-	-	-	-
13922	+	+	-	-	-	-	-	-	-	-
13846	+	+	-	-	-	-	-	-	-	-
41466	+	-	-	-	-	-	+	–	-	-
41530	+	+	–+	+++	+++	+++	-	–	-	-
39609	+	-	–+	-	+++	-	-	-	-	-
38364	+	++	–	-	+	+	-	-	-	-
41520	+	+	-	-	-	-	-	-	-	-
41525	+	+	-	-	-	-	++	--	-	-
40904	+	+	-	+	-	+	+	–	-	-
41531	+	+	-	-	-	-	-	-	-	-
41532	+	+	–+	+++	+++	+++	+	–	-	-
11434	+	-	-	-	-	-	-	-	-	-
41533	+	-	-	-	-	-	-	–	-	-
41302	+	+	-	-	-	-	-	-	-	-
11781	+	+	-	-	-	-	-	-	-	-

12498 +	-	-	-	-	-	-	-	-	-
41494 +	+	-	-	-	-	-	-	-	-
17804 +	-	-	-	++	-	-	–	-	-
16011 +	-	-	-	-	-	-	-	-	-
40815 +	+	-	-	-	-	-	-	-	-
39565 +	+	–+	+++	+++	+++	+	-	-	-
14638 +	+	-	-	-	-	+	–	-	-
41534 +	-	–+	+	+++	+	+++	–––	-	-
41310 +	+	-	-	-	-	-	-	-	-
11137 +	+	-	-	-	-	-	-	-	-
17828 +	+	-	-	-	-	-	-	-	-
41330 +	-	–	-	-	-	-	-	-	-
11426 +	++	-	-	-	-	-	-	-	-
41535 +	+	-	-	-	-	-	-	-	-
12173 +	-	-	-	-	-	-	-	-	-
17420 +	+	-	-	-	-	-	–	-	-
41107 +	-	-	-	-	-	-	-	-	-
41536 +	-	-	-	-	-	+	–	-	-
13968 +	+	-	-	-	-	-	-	-	-
18000 +	-	-	-	-	-	-	-	-	-
41076 +	-	-	-	-	-	-	-	-	-
13508 +	+	-	-	-	-	++	––	-	-
41470 +	+	-	+	+	+	+++	–––	-	-
41537 +	-	-	-	-	-	-	-	-	-
41460 +	+	-	-	-	-	-	-	-	-
40735 +	+	-	-	-	-	-	-	-	-
17744 +	+	-	-	-	-	-	-	-	-
19272 +	+	-	-	-	-	-	-	-	-
16020 +	+	-	-	-	-	-	-	-	-
17050 +	+	–	-	-	+	-	-	-	-
40607 +	-	-	-	-	-	-	-	-	-
41538 +	+	–+	+++	+++	+++	+	–	-	+++
18065 +	-	–	+	-	-	-	-	-	-

18004 +	-	-	-	-	-	-	-	-	-
39317 +	+	-	-	-	-	-	-	-	-
19512 +	-	-	-	-	-	-	-	-	-
17917 +	+	-	-	-	-	-	-	-	-
41533 +	-	-	-	-	-	-	-	-	-
17834 +	-	-	-	-	-	-	-	-	-
14014 +	-	-	-	-	-	-	-	-	-
19512 +	-	-	-	-	-	-	-	-	-
14113 +	+	-	-	-	-	+	–	-	-
16116 +	++	-	-	-	-	-	-	-	-
41201 +	-	-	-	+	-	-	–	-	-
14144 +	+	-	-	-	-	++	––	-	-
40735 +	+	-	-	-	-	-	-	-	-
40380 +	-	–	+	+	-	+	-	-	-
41539 +	+	-	+	-	-	-	-	-	-
39067 +	++	-	-	-	-	-	-	-	-
17640 +	+	–	+	+	+	-	-	-	-
15147 +	+	-	-	-	-	++	––	-	-
18812 +	-	-	-	-	-	-	-	-	-
11742 +	+	-	-	-	-	-	-	-	-
41482 +	-	-	-	-	-	+	-	-	-
41093 +	-	-	-	-	-	-	-	-	-
12215 +	-	-	-	-	-	-	-	-	-
41029 +	+	-	-	-	-	-	-	-	-
41202 +	-	-	-	-	-	-	-	-	-
41493 +	+	-	+	+	+	+++	–––	-	-
41540 +	-	-	-	-	-	-	-	-	-
14491 +	+	-	-	-	-	-	-	-	-
13601 +	+	-	-	-	-	-	-	-	-
41541 +	-	-	-	-	-	-	-	-	-
41542 +	-	-	-	-	-	-	-	-	-
41463 +	+	-	-	-	-	-	-	-	-
41476 +	-	-	-	-	-	-	-	-	-

18592 +	+	-	-	-	-	-	-	-	-
41543 +	-	-	-	-	-	-	-	-	-
41527 +	-	-	-	-	-	-	-	-	-
13652 +	+	-	-	-	-	-	-	-	-
41544 +	-	-	-	-	-	-	-	-	-
39606 +	-	-	-	-	-	-	-	-	-
14071 +	+	-	-	+	+	+++	---	-	-
19298 +	-	-	-	+	-	-	-	-	-
41114 +	+	-	-	-	-	-	-	-	-
41453 +	-	-	-	-	-	+++	---	-	-
40956 +	+	--+	+++	+++	+++	-	-	-	-
40332 +	+	-	-	-	-	-	-	-	-
18678 +	-	-	-	-	-	-	-	-	-
41525 +	+	-	-	-	-	++	--	-	-
17774 +	-	-	-	-	-	-	-	-	-
41290 +	-	-	-	-	-	-	-	-	-
41203 +	+	-	-	-	-	-	-	-	-
11952 +	-	-	-	-	-	-	-	-	-
13525 +	++	-	-	-	-	+	-	-	-
39699 +	-	-	-	-	-	-	-	-	-
41545 +	-	-	-	-	-	-	-	-	-
39673 +	+	-	-	-	-	-	-	-	-
41546 +	+	--+	+++	+++	+++	-	-	-	-
13786 +	+	-	-	-	-	+	-	-	-
41117 +	+	-	-	-	-	-	-	-	-
41254 +	+	-	-	-	-	-	-	-	-
17302 +	+	-	+	-	+	++	---	-	-
41538 +	+	--+	+++	+++	+++	+	-	-	-
41547 +	-	-	-	-	-	-	-	-	-
40182 +	-	-	+	+	-	-	-	-	-
14407 +	+	-	-	-	-	-	-	-	-
41130 +	-	-	-	-	-	-	-	-	-
41176 +	+	-	-	-	-	-	-	-	-

40739 +	+	-	-	-	-	-	-	-	-
41548 +	+	-	-	-	-	-	-	-	-
17505 +	-	-	-	-	-	+	-	-	-
40328 +	-	-	-	-	-	-	-	-	-
41549 +	+	---+	+++	+++	+++	+	-	-	-
13870 +	+	-	-	-	-	-	-	-	-
41550 +	-	-	-	-	-	-	–	-	-
16643 +	+	-	-	-	-	-	-	-	-
40565 +	-	-	-	-	-	-	–	-	-
19655 +	-	-	-	-	-	-	-	-	-
41551 +	-	-	-	-	-	-	-	-	-
41552 +	-	–	-	-	-	+	-	-	-
40528 +	-	-	-	-	-	-	-	-	-
40950 +	+	-	-	-	-	-	-	-	-
39667 +	+	---+	+++	+++	+++	-	-	-	-
39885 +	+	–	+	+	+	-	-	-	-
41259 +	-	-	-	-	-	-	-	-	-
41543 +	-	-	-	-	-	-	-	-	-
41484 +	-	-	-	-	-	-	-	-	-
41419 +	+	–	+	+	+	+++	---	-	-
41230 +	-	–	-	-	-	-	-	-	-
41553 +	-	-	-	-	-	-	-	-	-
18183 +	-	-	-	-	-	-	-	-	-
41554 +	-	-	-	-	-	-	-	-	-
13518 +	+	-	-	-	-	+	–	-	-
17698 +	-	-	-	-	-	-	-	-	-
17767 +	-	---+	+	+	-	-	-	-	-
41401 +	-	-	-	-	-	++	---	-	-
41279 +	+	–	++	++	++	+++	---	-	-
39347 +	++	-	-	-	+	-	--	-	-
40419 +	+	-	+	-	+	-	–	-	-
40829 +	+	-	-	-	-	-	-	-	-
41555 +	-	-	-	-	-	-	-	-	-

19961 +	-	-	-	-	-	-	-	-	-
41106 +	-	-	-	-	-	-	-	-	-
11541 +	-	-	-	-	-	-	-	-	-
41556 +	+	-	-	-	-	-	–	-	-
13518 +	+	-	-	-	-	+	–	-	-
41535 +	+	-	-	-	-	-	-	-	-
41557 +	-	-	-	-	-	-	-	-	-
41558 +	+	-	-	-	-	-	-	-	-
11729 +	-	-	-	-	-	-	-	-	-
40165 +	-	–+	+++	+++	+++	+	–	-	-
41559 +	+	–+	+++	+++	+++	+	–	-	-
39739 +	+	-	-	-	-	-	-	-	-
18409 +	-	-	-	-	-	-	-	-	-
41472 +	+	–	+	+	+	+++	–––	-	-
40957 +	+	-	-	-	+	-	-	-	-
11402 +	-	-	-	-	-	-	-	-	-
41560 +	-	-	-	-	-	-	-	-	-
13701 +	+	-	-	-	+	++	––	-	-
18757 +	+	-	-	-	-	-	-	-	-
17183 +	+	–+	+++	+++	+++	-	-	-	-
41561 +	+	-	-	-	-	-	-	-	-
41543 +	-	-	-	-	-	-	-	-	-
41562 +	-	–	-	+	+	+	–	-	-
41563 +	-	-	-	-	-	-	-	-	-
41564 +	-	-	-	-	-	-	-	-	-
41436 +	+	-	-	-	-	-	-	-	-
41565 +	-	-	-	-	-	-	-	-	-
40919 +	-	-	-	-	-	-	-	-	-
41358 +	+	–+	+++	+++	+++	+	–	-	-
11396 +	-	-	-	-	-	-	-	-	-
16574 +	+	-	-	-	-	-	-	-	-
39817 +	+	-	-	-	-	-	-	-	-
41566 +	+	––	++	++	++	+	-	-	-

41150 +	-	-	-	-	-	-	-	-	-
18961 +	++	-	-	-	-	-	-	-	-
41566 +	+	–	++	++	+++	+	–	-	-
41567 +	+	–	+	+	+	+++	---	+++	+++
14099 +	+	-	-	-	-	-	-	-	-
40492 +	+	-	+	+	+	+++	---	-	-
12388 +	+	-	-	-	-	-	-	-	-
41568 +	+	-	-	-	-	-	-	-	-
18420 +	+	-	-	-	-	-	-	-	-
38829 +	++	-	-	-	-	-	-	-	-
17774 +	-	-	-	-	-	-	-	-	-
11892 +	-	-	-	-	-	-	-	-	-
41108 +	+	-	-	-	-	-	-	-	-
41427 +	+	-	-	-	-	-	-	-	-
41270 +	++	--+	+++	+++	+++	+	–	-	-
12122 +	-	-	-	-	-	-	-	-	-
41569 +	-	-	-	-	-	-	-	-	-
40833 +	-	--+	+	+++	+	-	-	-	-
41570 +	-	-	-	-	-	-	–	-	-
39419 +	+	-	-	-	-	-	-	-	-
41571 +	-	-	+	-	-	-	-	-	-
10989 +	+	-	+	-	+	+++	---	-	-
41541 +	-	-	-	-	-	-	-	-	-
14784 +	-	-	-	-	+	+	–	-	-
12710 +	-	-	-	-	-	-	-	-	-
41564 +	-	-	-	-	-	-	-	-	-
41572 +	+	-	-	-	-	-	-	-	-
14194 +	+	-	-	+	-	++	--	-	+++
41518 +	-	–	+	+	+	+	–	-	-
38313 +	+	–	++	+	++	+++	--	-	-
11830 +	-	-	-	-	-	-	-	-	-
40381 +	-	-	-	-	-	-	-	-	-
41103 +	-	-	-	-	-	-	-	-	-

41507 +	-	-	-	-	-	-	-	-	-
41446 +	+	-	-	-	-	-	-	-	-
41456 +	+	-	-	-	-	++	−−	-	-
41573 +	++	−−+	+++	+++	+++	-	-	-	-
41513 +	-	-	-	-	-	-	-	-	-
41400 +	-	-	-	-	-	+	-	-	-
13591 +	+	-	-	-	+	++	−−	-	-
41574 +	-	-	-	-	-	-	-	-	-
41182 +	+	-	-	-	-	-	-	-	-
41575 +	+	−−+	+++	+++	+++	+	−	-	-
41576 +	+	-	-	-	-	+	−	-	-
41577 +	-	-	-	-	-	-	-	-	-
40129 +	-	-	-	-	-	-	-	-	-
13519 +	+	-	+	-	+	+++	−−−	-	-
14518 +	+	-	-	+	+	+++	−−−	-	-
37920 +	-	-	-	-	-	-	-	-	-
41578 +	-	-	-	-	-	-	-	-	-
40525 +	+	−−+	+++	+++	+++	+++	−−−	-	-
11540 +	-	-	-	-	-	-	-	-	-
17799 +	-	-	-	-	-	-	-	-	-
40221 +	+	−−+	+++	+++	+++	++	−	-	-
13571 +	+	-	-	-	-	+++	−−	-	-
40282 +	+	-	-	+	+	++	−	-	-
12943 +	-	-	-	-	-	-	-	-	-
18799 +	+	−−	++	++	+	-	-	-	-
41579 +	-	−	-	-	-	-	-	-	-
14358 +	+	-	-	-	-	-	-	-	-
40925 +	-	-	-	++	-	-	-	-	-
18047 +	++	-	-	-	-	-	-	-	-
39236 +	+	−−+	+++	+++	+++	-	-	-	-
41537 +	-	-	-	-	-	-	-	-	-
38082 +	+	−−+	+++	+++	+++	+	−	-	-
41580 +	+	-	-	-	+	++	−−	-	-

41552 +	-	-	-	-	-	-	-	-	-
40328 +	-	-	-	-	-	-	-	-	-
11442 +	-	-	-	-	-	-	-	-	-
41581 +	-	–	+	+++	-	-	-	-	-
41524 +	-	-	-	-	-	-	-	-	-
41582 +	+	-	-	-	-	-	-	-	-
12210 +	-	-	-	-	-	-	-	-	-
41583 +	-	-	-	-	-	-	-	-	-
41584 +	-	–	-	+++	+	+	-	-	-
41585 +	-	-	-	-	-	-	-	-	-
41586 +	+	-	-	-	-	+	-	-	-
11597 +	-	-	-	-	-	-	-	-	-
12297 +	-	-	-	-	-	-	-	-	-
41587 +	-	-	-	-	-	-	-	-	-
13036 +	+	-	-	-	-	++	––	-	-
19139 +	+	–-+	+++	+++	+++	-	-	-	-
41588 +	+	-	-	-	-	-	-	-	-
40423 +	+	-	-	+	+	+++	–––	-	-
41589 +	+	-	-	-	-	+	-	-	-
39804 +	+	-	-	-	-	-	-	-	-
41590 +	-	-	-	-	-	-	-	-	-
41479 +	-	-	-	-	-	-	-	-	-
13787 +	+	-	-	-	-	+	–	-	-
40713 +	+	-	-	-	-	-	–	-	-
41439 +	-	-	-	-	-	-	-	-	-
17624 +	+	-	-	-	-	-	-	-	-
41591 +	-	–	+	+	+	-	-	-	-
11404 +	-	-	-	-	-	-	-	-	-
41567 +	-	–	+	+	+	+++	–––	+++	-
18286 +	-	-	-	-	-	-	-	-	-
41529 +	-	-	-	-	-	-	–	-	-
18686 +	-	-	-	-	-	-	-	-	-
41514 +	-	-	-	-	-	-	-	-	-

18164 +	-	-	-	-	-	-	-	-	-
11869 +	-	-	-	-	-	-	-	-	-
41592 +	-	-	-	-	-	-	-	-	-
13682 +	+	--	++	++	++	+++	---	-	-
17594 +	-	-	-	-	-	-	-	-	-
19144 +	-	-	-	-	-	-	-	-	-
41255 +	+	--+	+++	+++	+++	-	-	-	-
19124 +	-	-	-	++	+	-	-	-	-
17987 +	+	-	-	-	-	+	-	-	-
17743 +	+	--+	+++	+++	+++	-	-	-	-
19868 +	-	-	-	-	-	-	-	-	-
17713 +	+	-	-	-	+	-	-	-	-
39892 +	+	-	-	-	-	-	-	-	-
40072 +	+	-	+	-	+	+++	---	-	-
41593 +	+	-	-	-	-	-	-	-	-
41594 +	-	-	-	-	-	-	-	-	-
40583 +	-	-	+	+	+	+++	---	-	-
13724 +	+	-	+	+	+	+++	---	-	-
39961 +	+	--+	+++	+++	+++	+	-	-	-
41560 +	-	-	-	-	-	-	-	-	-
41595 +	-	--	++	++	++	-	-	-	-
12417 +	-	-	-	-	-	-	-	-	-
41451 +	-	-	-	-	-	-	-	-	-
41596 +	+	--+	+++	+++	+++	+++	---	-	-
11051 +	+	-	+	-	+	-	-	-	-
13682 +	+	-	++	+	++	+++	---	-	-
17734 +	+	-	-	-	-	-	-	-	-
41500 +	-	-	-	-	-	-	-	-	-
18866 +	-	-	-	-	-	-	-	-	-
41597 +	-	-	-	-	-	-	-	-	-
41598 +	-	-	-	-	-	-	-	-	-
41599 +	+	-	+	+	+	+++	---	-	-
41578 +	-	-	-	-	-	-	-	-	-

13715 +	+	-	-	-	-	++	--	-	-
41600 +	+	-	-	-	-	-	-	-	-
41568 +	+	-	-	-	-	-	-	-	-
41601 +	-	-	-	-	-	-	-	-	-
40640 +	-	--+	+++	+++	+++	-	-	-	-
17734 +	+	-	-	-	-	-	-	-	-
41602 +	-	-	-	-	-	-	-	-	-
12071 +	-	-	-	-	-	-	-	-	-
41570 +	-	-	-	-	-	-	-	-	-
41603 +	+	--+	+++	+++	+++	+	-	-	-
39856 +	+	--+	+++	+++	+++	+	-	-	-
41604 +	-	-	-	-	-	-	-	-	-
41605 +	-	-	+	++	-	-	-	-	-
11248 +	-	-	-	-	-	-	-	-	-
41606 +	+	--+	+++	+++	+++	+	-	-	-
41607 +	-	-	-	-	-	-	-	-	-
40999 +	-	-	-	-	-	-	-	-	-
38834 +	+	-	-	-	-	-	-	-	-
41608 +	-	-	-	-	-	-	-	-	-
18418 +	-	-	-	-	-	-	-	-	-
41609 +	+	--+	+++	+++	+++	-	-	-	-
41610 +	+	--+	+++	+++	+++	+	-	-	-
41569 +	-	-	-	-	-	-	-	-	-
41608 +	-	-	-	-	-	-	-	-	-
14659 +	+	-	-	-	-	+	-	-	-
41611 +	-	-	-	-	-	+	-	-	-
41587 +	-	-	-	-	-	-	-	-	-
41612 +	+	-	-	-	+	-	-	-	-
16644 +	+	-	-	-	-	-	-	-	-
40139 +	+	-	-	-	-	-	-	-	-
41613 +	-	-	-	-	-	-	-	-	-
41594 +	-	-	-	-	-	-	-	-	-
14300 +	+	-	-	-	-	+	-	-	-

41614 +	-	-	-	-	-	-	-	-	-
41615 +	-	-	-	-	-	-	-	-	-
41565 +	-	-	-	-	-	-	-	-	-
41597 +	-	-	-	-	-	-	-	-	-
41616 +	+	-	-	-	-	+	–	-	-
40288 +	++	-	-	-	-	-	-	-	-
11505 +	-	-	-	-	-	-	-	-	-
41617 +	+	–	+	++	+	+++	–––	-	-
41618 +	-	-	-	+	-	-	-	-	-
41619 +	+	––+	+++	+++	+++	-	–	-	-
41620 +	-	-	-	-	-	-	-	-	-
40812 +	+	–	++	+	+++	+++	–––	-	-
39997 +	-	-	-	-	-	-	-	-	-
41592 +	-	-	-	-	-	-	-	-	-
41590 +	-	-	-	-	-	-	-	-	-
41621 +	+	––+	+++	++	+++	+++	–––	-	-
14666 +	+	–	+	+	+	+++	–––	-	-
18605 +	-	-	-	-	-	-	-	-	-
41611 +	-	-	-	-	+	-	-	-	-
41622 +	-	-	-	-	-	-	-	-	-
12943 +	-	-	-	-	-	-	-	-	-
14556 +	+	-	-	+	-	++	––	-	-
41623 +	-	––	-	-	-	-	-	-	-
40072 +	-	-	+	+	-	+++	–––	-	-
15395 +	+	-	+	+	+	++	––	-	-
38330 +	+	-	-	-	-	-	-	-	-
17963 +	+	-	-	-	-	-	-	-	-
18799 +	+	––	++	++	++	-	-	-	-
41624 +	-	-	-	-	-	-	-	-	-
18548 +	-	-	-	-	-	-	-	-	-
41625 +	+	––+	+++	+++	+++	+	-	-	-
18115 +	-	-	-	-	-	-	-	-	-
41626 +	+	––+	+++	+++	+++	+	-	-	-

41627 +	-	-	-	-	-	-	-	-	-
39689 +	+	--+	+++	+++	+++	-	-	-	-
17614 +	+	-	-	-	-	-	-	-	-
41628 +	-	-	-	-	-	-	-	-	-
41629 +	-	-	-	-	-	-	-	-	-
17994 +	-	-	-	-	-	-	-	-	-
41572 +	+	-	-	-	-	-	-	-	-
41602 +	-	-	-	-	-	-	-	-	-
38500 +	-	--	++	++	+++	+++	---	-	-
18064 +	-	--	+	++	+	-	-	-	-
41630 +	-	-	-	-	-	-	-	-	-
41631 +	+	-	-	-	-	-	-	-	-
41614 +	-	-	-	-	-	-	-	-	-
41632 +	-	-	-	-	-	-	-	-	-
17935 +	-	-	-	-	-	-	-	-	-
41633 +	+	--+	+++	+++	+++	+	-	-	-
41634 +	+	-	-	-	-	-	-	-	-
41159 +	+	-	-	-	-	-	-	-	-
41620 +	-	-	-	-	-	-	-	-	-
41315 +	+	-	-	+	-	-	-	-	-
41635 +	+	-	-	-	-	-	-	-	-
41543 +	-	-	-	-	-	-	-	-	-
41636 +	-	-	-	-	-	-	-	-	-
19770 +	-	-	-	-	-	-	-	-	-
41637 +	-	-	-	-	-	-	-	-	-
41628 +	-	-	-	-	-	-	-	-	-
39781 +	+	-	-	-	-	-	-	-	-
38581 +	+	--+	+++	+++	+++	+	-	-	-
41624 +	-	-	-	-	-	-	-	-	-
17550 +	-	-	-	-	-	-	-	-	-
40167 +	-	-	-	-	-	-	-	-	-
19638 +	-	-	-	-	+	+	-	-	-
41638 +	-	-	-	-	-	-	-	-	-

41639 +	+	--+	+++	+++	+++	+	-	-	-
41640 +	-	-	-	-	-	-	-	-	-
41627 +	-	-	-	-	-	-	-	-	-
11540 +	-	-	-	-	-	-	-	-	-
39772 +	-	-	-	-	-	-	-	-	-
41641 +	-	-	-	-	-	-	-	-	-
41642 +	-	-	-	-	-	-	-	-	-
40143 +	+	-	-	-	-	-	-	-	-
18108 +	-	-	-	-	-	-	-	-	-
41643 +	-	-	-	-	-	-	-	-	-
41644 +	-	-	-	-	-	-	-	-	-
41645 +	-	-	-	-	-	-	-	-	-
41646 +	-	-	-	-	-	-	-	-	-
17741 +	-	-	-	-	-	-	-	-	-
40433 +	++	-	-	-	-	-	-	-	-
41454 +	-	-	-	-	-	-	-	-	-
41647 +	-	-	-	-	-	-	-	-	-
41648 +	+	--+	+++	+++	+++	-	-	-	-
41649 +	-	-	+	++	+	-	-	-	-
41585 +	-	-	-	-	-	-	-	-	-
41650 +	-	-	-	-	-	-	-	-	-
11656 +	-	-	-	-	-	-	-	-	-
41651 +	-	-	-	-	+	-	-	-	-
17567 +	-	-	-	-	-	-	-	-	-
40570 +	-	-	-	-	+	-	-	-	-
41647 +	-	-	-	-	-	-	-	-	-
18605 +	-	-	-	-	-	-	-	-	-
20065 +	-	-	-	-	-	-	-	-	-
11313 +	+	-	-	+	-	++	---	-	-
41652 +	-	-	+	+	-	-	-	-	-
41653 +	-	-	-	-	-	-	-	-	-
18278 +	-	-	-	-	-	-	-	-	-
41654 +	-	-	-	-	-	-	-	-	-

41655	+	-	-	-	-	-	-	-	-
41629	+	-	-	-	-	-	-	-	-
41563	+	-	-	-	-	-	-	-	-
11201	+	-	-	-	-	-	-	-	-
41641	+	-	-	-	-	-	-	-	-
18819	+	+	-	-	-	-	-	-	-
41630	+	-	-	-	-	-	-	-	-
41653	+	-	-	-	-	-	-	-	-
41554	+	-	-	-	-	-	-	-	-
13724	+	+	–	+	+	+	+++	---	-	-
15738	+	++	-	+	+	-	++	---	-	-
19161	+	+	-	-	-	-	-	-	-	-
41656	+	+	-	-	-	+	-	-	-	-
41657	-	+	-	-	-	-	-	-	-	-
41618	-	-	-	-	-	-	-	-	-	-
41658	-	-	-	-	-	-	-	-	-	-
41659	-	-	-	-	-	-	-	-	-	-
41660	-	-	-	-	-	-	-	-	-	-
38836	-	+	–+	+++	+++	+++	-	–	-	-
41598	-	-	-	-	-	-	-	-	-	-
18308	-	-	-	-	-	-	-	-	-	-
40831	-	+	-	+	-	+	+++	---	-	-
41583	-	-	-	-	-	-	-	-	-	-
41659	-	-	-	-	-	-	-	-	-	-
41111	-	-	-	-	-	-	-	-	-	-
41661	-	-	-	-	-	-	-	-	-	-
41662	-	-	-	-	+	-	-	–	-	-
18264	-	-	–	-	++	-	-	-	-	-
41658	-	-	-	-	-	-	-	-	-	-
41360	-	-	-	-	-	-	-	-	-	-
41663	-	-	-	-	-	-	-	-	-	-
17354	-	++	-	-	-	-	++	--	-	-
41651	-	-	-	-	-	-	-	-	-	-

41664	-	-	-	-	-	-	-	-	-
41651	-	-	-	-	-	-	-	-	-
41665	-	-	-	-	-	-	-	-	-
12071	-	-	-	-	-	-	-	-	-
41666	-	-	-	-	-	-	-	-	-
41667	-	-	-	-	-	-	–	-	-
41664	-	-	-	-	-	-	-	-	-
41668	-	-	-	-	-	-	-	-	-
41669	-	-	-	-	-	-	-	-	-
17999	-	-	-	-	-	-	-	-	-
11505	-	-	-	-	-	-	-	-	-
41670	-	-	-	-	-	-	-	-	-
41671	-	-	-	-	-	-	-	-	-
41655	-	-	-	-	-	-	-	-	-
40780	-	-	-	-	-	-	-	-	-
18168	-	-	-	-	-	-	-	-	-
19161	+	-	-	-	-	-	-	-	-
41651	-	-	-	-	-	-	-	-	-
41667	-	-	-	-	-	+	–	-	-
41670	-	-	-	-	-	-	-	-	-
41660	-	-	-	-	-	-	-	-	-
41643	-	-	-	-	-	-	-	-	-
18018	-	-	-	-	-	-	-	-	-
41672	-	-	-	-	-	-	-	-	-
41673	-	-	-	-	-	-	-	-	-
41674	-	–+	+++	+++	+++	+++	–	-	-
16566	-	-	-	-	-	-	-	-	-
41665	-	-	-	-	-	-	-	-	-
41675	-	–+	+++	-	-	-	-	-	-
41676	-	-	-	-	-	-	-	-	-
41677	-	–+	+++	+++	+++	-	-	-	-
19122	-	–+	+++	+++	+++	-	-	-	-
41678	-	–+	+++	+++	+++	-	-	-	-

18072	-	-	---+	+++	+++	+++	-	-	-	-
41679	-	+++	-	+++	-	-	+++	---	-	-
41680	-	-	---+	+++	+++	+++	-	-	-	-
41681	-	++	-	-	-	-	-	-	-	-
41682	-	-	---+	+++	+++	-	-	-	-	-
40120	-	-	---+	+++	+++	+++	-	-	-	-
41683	-	+	---+	+++	+++	+++	-	-	-	-
41684	-	+	-	+	-	-	-	-	-	-
41682	-	+++	---+	+++	+++	+++	-	-	-	-
11717	-	-	-	-	-	-	-	-	-	-
38397	-	+++	-	-	-	-	-	-	-	-
40671	-	+	---+	+++	+++	+++	+	-	-	-
20033	-	+	---+	+++	+++	+++	-	–	-	-
41685	-	+	---+	+++	+++	+++	-	-	-	-
17177	-	+	---+	+++	+++	+++	-	-	-	-
17245	-	-	---+	+++	+++	+++	-	-	-	-
41686	-	+	---+	+++	+++	+++	-	-	-	-
41687	-	-	---+	+++	+++	+++	-	-	-	-
41688	-	+	---+	+++	+++	+++	-	-	-	-
41689	-	+	---+	+++	+++	+++	-	-	-	-
41690	-	+	---+	+++	+++	+++	++	-	-	-
38273	-	++	–	-	+	-	-	-	-	-
38116	-	-	–	-	-	-	-	-	-	-
39946	-	+	---+	+++	+++	+++	-	-	-	-
41691	-	++	---+	+++	+++	+++	-	--	-	-
41692	-	-	---+	+++	+++	+++	-	-	-	-
41693	-	-	---+	+++	+++	+++	-	-	-	-
41694	-	+	---+	+++	+++	+++	+	--	-	-
39505	-	+	---+	+++	+++	+++	-	-	-	-
36466	-	-	---+	+++	+++	+++	+	-	-	-
37768	-	+	---+	+++	+++	+++	-	-	-	-
18133	-	+++	-	+	-	-	-	-	-	-
38657	-	++	-	-	-	-	-	--	-	-

41695	-	+	–+	+++	+++	+++	-	-	-	-
41475	-	++	–+	+++	+++	+++	-	-	-	-
14324	-	-	–	-	-	-	-	-	-	-
41696	-	-	–+	+++	+++	+++	-	-	-	-
37065	-	-	––	+	-	-	-	–	-	-
41697	-	-	–+	+++	+++	+++	-	-	-	-
41698	-	-	–+	+++	+++	+++	-	-	-	-
40294	-	+	–+	+++	+++	+++	-	-	-	-
41699	-	-	–+	+++	+++	+++	+	-	-	-
36317	-	+	-	-	-	-	-	-	-	-
37388	-	++	–+	+++	+++	+++	+++	–––	-	-
41700	-	-	-	+	-	-	-	-	-	-
41701	-	-	–+	+++	+++	+++	-	-	-	+
41702	-	+	–+	+++	++	-	+	-	-	-
19964	-	-	–+	+++	+++	+++	-	-	-	-
41703	-	-	–+	+++	+++	+++	-	-	-	-
41704	-	++	–+	+++	+++	+++	-	-	-	-
41705	-	++	–+	+++	+++	+++	-	-	-	-
41706	-	++	-	-	-	-	-	-	-	-
41707	-	++	–+	+++	+++	+++	-	-	-	-
36959	-	+	–+	+++	+++	+++	+	––	-	-
12919	-	+	-	-	-	-	+	-	-	-
41708	-	-	–+	+++	+++	+++	++	-	-	-
37764	-	-	-	-	-	-	-	-	-	-
36273	-	-	-	-	-	-	-	-	-	-
17179	-	+	–+	+++	+++	+++	-	-	-	-
41709	-	-	–+	+++	+++	+++	+	-	-	-
41710	-	+	–+	+++	+++	+++	-	-	-	-
41711	-	+	–+	+++	+++	+++	-	-	-	-
41712	-	++	–+	+++	+++	+++	-	-	-	-
17125	-	++	–+	+++	+++	+++	-	-	-	-
41713	-	-	–	-	+	-	-	-	-	-
41714	-	-	–+	+++	+++	+++	-	––	-	-

41715	+	-	-	-	-	-	-	-	-
41716	-	---+	+++	+++	+++	-	-	-	-
41717	++	---+	+++	+++	+++	-	-	-	-
18932	-	–	-	-	-	-	-	-	-
15204	+	-	+	-	-	-	–	-	-
38595	++	–	-	-	-	-	-	-	-
17504	++	---+	+++	+++	+++	-	–	-	-
41718	+	-	-	-	-	-	-	-	-
39135	++	---+	+++	+++	+++	+	–	-	-
41719	+	---+	+++	+++	+++	-	-	-	-
16618	-	-	-	-	-	-	-	-	-
37095	+	-	+	-	-	-	-	-	-
19043	-	---+	+++	+++	+++	-	-	-	-
37843	+	---+	+++	+++	+++	+	-	-	-
41720	++	---+	+++	+++	+++	-	-	-	-
41721	+	---+	+++	+++	+++	-	–	-	-
41722	+	-	+	-	-	-	––	-	-
41723	+	---+	+++	+++	+++	-	-	-	-
37825	++	---+	+++	+++	+++	-	-	-	-
41724	-	---+	+++	+++	+++	-	-	-	-
41725	+	---+	+++	+++	+++	-	-	-	-
36701	++	–	+	++	+	-	-	-	-
41726	+	---+	+++	+++	+++	-	-	-	-
37965	-	-	-	-	-	-	-	-	-
37433	-	---+	+++	+++	+++	-	-	-	-
41727	-	---+	+++	+++	+++	++	-	-	-
37107	+	–	-	-	-	-	–	-	-
41679	-	-	++	-	-	+++	---	-	-
40722	+	---+	+++	+++	+++	-	-	-	-
17388	++	---+	+++	+++	+++	-	-	-	-
41693	-	---+	+++	+++	+++	-	-	-	-
41728	-	–	+	-	-	-	-	-	-
41729	+	---+	+++	+++	+++	+	–	-	-

41730	+	–+	+++	+++	+++	-	-	-	-
41731	++	–+	+++	+++	+++	-	-	-	-
41340	-	–	-	-	-	-	-	-	-
41732	+	–+	+++	+++	+++	-	–	-	-
39154	++	–+	+++	+++	+++	++	-	-	-
41733	+	–+	+++	+++	+++	-	-	-	-
41734	-	–+	+++	+++	+++	-	-	-	-
41735	++	–	-	-	-	-	-	-	-
40310	++	–+	+++	+++	+++	++	-	-	-
17535	-	–+	++	++	-	-	-	-	-
17509	++	–+	+++	+++	+++	-	-	-	-
41736	+	–+	+++	+++	+++	-	–	-	-
41571	-	-	+	-	+	-	-	-	-
40518	+	–+	+++	+++	+++	-	-	-	-
41737	+	–+	+++	+++	+++	-	-	-	-
37513	+	-	-	-	-	-	-	-	-
41738	+	–+	+++	+++	+++	-	-	-	-
41528	-	-	-	-	-	-	-	-	-
41739	+	–+	+++	+++	+++	-	-	-	-
38482	++	–+	+++	+++	+++	-	-	-	-
41740	-	–+	+++	+++	+++	-	-	-	-
39617	-	––	+++	+++	++	+++	–––	-	-
40828	++	-	-	-	-	-	-	-	-
38356	+	–+	+++	+++	+++	-	-	-	-
41740	+	–+	+++	+++	+++	-	-	-	-
40055	-	-	+	-	-	-	-	-	-
41741	-	–	-	+	-	-	-	-	-
41742	+	–+	+++	+++	+++	-	-	-	-
41743	++	–+	+++	+++	+++	-	––	-	-
38181	+++	-	+	-	-	-	-	-	-
38860	++	–+	+++	+++	+++	+	–	-	-
16663	-	-	-	-	-	-	-	-	-
41744	+	–+	+++	+++	+++	+	-	-	-

11989	-	-	-	-	-	-	-	-	-
40532	++	-	+	+	++	+	–	-	-
38028	++	–+	+++	+++	+++	-	-	-	-
41745	+	-	-	-	-	-	-	-	-
41746	-	-	-	-	-	-	-	-	-
41747	+	–+	+++	+++	+++	+	–	-	-
40555	+	–+	+++	+++	+++	-	-	-	-
41748	+	–	++	++	+	+++	–––	+	-
39752	+	–+	+++	+++	+++	-	-	-	+
41749	+	–+	+++	+++	+++	+	-	-	-
41745	+	-	-	-	-	-	-	-	-
41750	-	–+	+++	+++	+++	-	-	-	-
41751	++	–+	+++	+++	+++	-	-	-	-
39279	+	–+	+++	+++	+++	+	-	-	-
41752	++	–+	+++	+++	+++	+	-	-	-
41753	+	–+	+++	+++	+++	+	-	-	-
41754	-	-	-	+	-	-	-	-	-
17189	+	–+	+++	+++	+++	-	-	-	-
41755	+	–+	+++	+++	+++	+	–	-	-
16614	+	–+	+++	+++	+++	-	-	-	-
41756	+	–+	+++	+++	+++	-	-	-	-
41757	+	–+	+++	+++	+++	-	-	-	-
18136	-	-	-	-	-	-	-	-	-
41758	+	–+	+++	+++	+++	+	-	-	-
41307	+	-	-	-	++	++	-	-	-
41759	+	–+	+++	+++	+++	+	-	-	-
41760	++	–+	+++	+++	+++	-	-	-	-
41761	+	–+	+++	+++	+++	+	-	-	-
39391	+	–+	+++	+++	+++	+	-	-	-
39297	++	–+	+++	+++	+++	++	-	-	-
13625	+	-	-	-	-	+++	-	-	-
37882	++	-	-	-	-	+++	–––	-	-
41762	-	–+	+++	+++	+++	-	-	-	-

40657 -	+	---+	+++	+++	+++	+	-	-	-
41763 -	+	---+	+++	+++	+++	-	-	-	+
41764 -	-	-	-	-	-	-	–	-	-
41765 -	-	---+	+++	+++	+++	+	-	-	-
41766 -	+	---+	+++	+++	+++	-	-	-	-
17685 -	-	–	-	+++	+	-	-	-	-
39951 -	-	-	-	+	-	-	-	-	-
41767 -	+	---+	+++	+++	+++	+	-	-	-
41768 -	+	–	++	+	++	+++	---	-	-
40995 -	-	---+	+++	+++	+++	+++	---	-	-
38085 -	+	---+	+++	+++	+++	+	-	-	-
38793 -	+	–	-	-	+	-	-	-	-
38454 -	-	-	-	-	-	-	-	-	-
40732 -	+	---+	+++	+++	+++	-	-	-	-
36970 -	-	---+	++	++	-	-	-	-	-
38672 -	++	---+	+++	+++	+++	-	-	-	-
19633 -	+	---+	+++	+++	+++	+	-	-	-
41481 -	+	-	-	-	-	-	-	-	-
40947 -	+	---+	+++	+++	+++	-	-	-	-
37338 -	+	-	-	-	-	-	-	-	-
41741 -	+	-	+	-	-	-	-	-	-
37338 -	+	–	-	-	-	-	-	-	-
41769 -	+	---+	+++	+++	+++	-	-	-	-
41770 -	-	-	-	-	-	-	-	-	-
17407 -	+	---+	+++	+++	+++	-	–	-	-
41771 -	++	---+	+++	+++	+++	-	-	-	-
40877 -	-	-	-	-	-	+	-	-	-
41772 -	+	---+	+++	+++	+++	-	-	-	-
16564 -	+	-	-	+	-	-	-	-	-
12920 -	+	-	-	+	-	++	--	-	-
16622 -	+	–	+	-	-	+	-	-	-
41718 -	-	-	+	-	-	-	-	-	-
41773 -	+	---+	+++	+++	+++	-	-	-	-

38977	-	-	-	-	+	-	-	-	-
40100	-	-	-	-	-	-	-	-	-
41774	-	-	-	-	-	-	-	-	-
17643	+	---+	+++	+++	+++	-	-	-	-
38238	++	---+	+++	+++	+++	+	-	-	-
41775	+	---+	+++	+++	+++	-	-	-	-
41027	+	---+	+++	+++	+++	-	-	-	-
20032	+	---+	+++	+++	+++	-	-	-	-
41776	++	---+	+++	+++	+++	-	-	-	-
12518	+	-	++	+	+	+	--	-	-
39442	+	-	+	-	-	-	-	-	-
16618	+	-	-	-	-	-	-	-	-
19760	++	---+	+++	+++	+++	+	-	-	-
17619	-	---+	+	+++	-	-	-	-	-
39428	+	-	+	-	-	-	-	-	-
40097	+	---+	+++	+++	+++	+	-	-	-
40455	+	-	++	++	+	+++	---	-	-
41777	-	-	++	++	++	-	-	-	-
39119	++	---+	+++	+++	+++	+	-	-	-
41489	-	-	+	-	-	++	-	-	-
41778	+	---+	+++	+++	+++	-	-	-	-
39605	++	---+	+++	+++	+++	+	-	-	-
41779	+	---+	+++	+++	+++	+	-	-	-
41780	+	---+	+++	+++	+++	+	-	-	-
41781	++	---+	+++	+++	+++	+	-	-	-
41782	+	---+	+++	+++	+++	+	-	-	-
38546	+	---+	+++	+++	+++	+	--	-	-
19403	+	---+	+++	+++	+++	-	-	-	-
41636	-	-	-	-	-	-	-	-	-
41561	-	-	-	-	-	-	-	-	-
18008	-	-	-	-	-	-	-	-	-
41783	+	-	-	-	-	-	-	-	-
41784	-	---+	+++	+++	+++	+	-	-	-

41785	-	+	−+	+++	+++	+++	-	-	-	-
13925	-	+	−	++	+	+	++	−−−	-	-
18540	-	+	−+	+++	+++	+++	-	-	-	-
19606	-	-	-	-	-	-	-	-	-	-
39164	-	-	−+	+++	+++	+++	+	−	-	-
39480	-	+	−+	+++	+++	+++	-	-	-	-
41542	-	-	-	-	-	-	+	−	-	-
13514	-	+	-	-	-	-	+	-	-	-
17166	-	+	−+	+++	+++	+++	+	-	-	-
16663	-	-	-	-	-	-	-	-	-	-
40209	-	+	−+	+++	+++	+++	++	−−	-	-
39129	-	++	-	-	-	+	++	−	-	-
41786	-	-	−+	+++	+++	+++	-	−	-	-
41787	-	+	−+	+++	+++	+++	-	-	-	-
41788	-	+	−+	+++	+++	+++	-	-	-	-
40105	-	-	-	-	-	-	-	-	-	-
41789	-	+	−+	+++	+++	+++	+	-	-	-
40172	-	-	-	-	-	-	-	-	-	-
40093	-	-	-	-	-	-	-	-	-	-
41790	-	++	−+	+++	+++	+++	+	-	+	-
41791	-	+	−−	-	++	-	+	-	-	-
39981	-	-	−+	-	+++	-	-	-	-	-
41256	-	-	−−	+	+	+	-	−	-	-
41792	-	+	−+	+++	+++	+++	-	-	-	-
41793	-	-	-	-	-	-	+	-	-	-
41447	-	-	−+	+++	+++	+++	-	−	-	-
17685	-	-	−	+	+++	+	-	-	-	-
18524	-	+	−+	+++	+++	+++	-	−	-	-
38671	-	+	-	-	-	-	-	-	-	-
39277	-	+	−+	+++	+++	+++	+	−	-	-
41478	-	+	-	-	-	-	-	-	-	-
41242	-	+	−+	+++	+++	+++	-	−	-	-
17862	-	-	-	+	-	-	-	-	-	-

41794	+	--+	+++	+++	+++	-	-	-	-
41795	+	--+	+++	+++	+++	+	-	-	-
40579	+	-	-	-	-	-	-	-	-
40279	+	--+	+++	+++	+++	-	-	-	-
40502	+	--+	+++	+++	+++	-	-	-	-
41796	-	-	+	+	+	-	-	-	-
41148	+	-	-	-	-	-	-	-	-
40324	-	-	-	-	-	-	-	-	-
41114	+	-	-	-	-	-	-	-	-
41797	-	-	-	-	-	-	-	-	-
19246	-	-	+	-	+	-	-	-	-
41798	-	--	-	+++	-	-	-	-	-
11385	++	-	-	-	-	-	-	-	-
41799	+	--+	+++	+++	+++	+	-	-	-
41800	-	--	+++	++	+++	+++	---	-	-
41801	+	-	-	-	-	-	-	-	-
41802	-	-	-	-	-	-	-	-	-
41803	+	--+	+++	+++	+++	-	-	-	-
16623	+	-	-	-	-	-	-	-	-
41804	+	-	++	++	++	+++	---	-	-
41805	-	-	+	-	-	-	-	-	-
39151	-	-	-	-	-	-	-	-	-
41589	+	-	-	-	-	-	-	-	-
41539	+	-	-	-	-	-	-	-	-
41806	-	-	+	+	+	-	-	-	-
12117	-	-	-	-	-	-	-	-	-
18164	-	-	-	-	-	-	-	-	-
40613	+	--+	+++	+++	+++	+	-	-	-
38502	+	--+	+++	+++	+++	+	-	-	-
41657	+	-	-	-	-	-	-	-	-
41807	+	--+	+++	+++	+++	+	-	-	-
17749	-	-	-	-	-	-	-	-	-
40360	+	--+	+++	+++	+++	-	-	-	-

41808 -	+	--	+++	++	++	+++	---	-	-
41809 -	-	-	-	-	-	-	-	-	-
18438 -	+	-	-	-	-	-	-	-	-
15215 -	+	-	-	-	-	-	-	-	-
41173 -	+	-	+	+	+	+++	---	-	-
20065 -	-	-	-	-	-	-	-	-	-
20203 -	-	-	-	-	-	-	-	-	-
41810 -	+	--+	+++	+++	+++	+	–	-	-
41811 -	+	--+	+++	+++	+++	-	–	-	-
41812 -	-	-	-	-	-	-	-	-	-
41813 -	+	-	-	-	-	-	-	-	-
18933 -	-	-	-	-	-	-	–	-	-
41814 -	-	-	-	-	-	-	-	-	-
18018 -	-	-	-	-	-	-	-	-	-
41815 -	-	--+	+++	+++	+++	+++	-	-	-
41816 -	-	-	+++	+++	-	-	-	-	-
13745 -	-	-	-	-	-	+++	-	-	-
41817 -	-	--+	+++	+++	+++	-	-	-	-
36517 -	++	-	+++	+++	+++	-	-	-	-
41818 -	-	-	-	-	-	-	-	-	-
37543 -	-	-	-	-	-	-	-	-	-
36245 -	+++	--+	+++	+++	+++	-	-	-	-
41819 -	++	-	-	-	-	-	-	-	-
41820 -	-	--+	+++	+++	+++	-	-	-	-
41821 -	-	--+	+++	+++	+++	-	-	-	-
14324 -	++	-	-	-	-	-	-	-	-
41822 -	++	--+	+++	+++	+++	-	-	-	-
37504 -	-	--+	+++	+++	+++	-	-	-	-
41749 -	-	--+	+++	+++	+++	-	-	-	-
41823 -	-	--+	+++	+++	+++	-	-	-	-
41824 -	+	--+	+++	+++	+++	-	-	-	-
41825 -	-	--+	+++	+++	+++	+++	---	-	-
41826 -	-	--+	+++	-	-	-	-	-	-

41827	+	–+	+++	+++	+++	-	-	-	-
39725	+++	–+	+++	+++	+++	-	-	-	-
41828	-	-	-	-	-	-	-	-	-
41099	+	–+	+++	+++	+++	-	-	-	-
41829	-	–+	+++	+++	+++	-	-	-	-
41830	-	-	-	-	-	-	-	-	-
41831	-	–	+++	+++	-	-	-	-	-
41832	-	-	++	++	-	-	-	-	-
18161	-	-	-	-	-	-	-	-	-
41833	-	–+	+++	+++	+++	-	-	-	-
19359	-	–+	+++	+++	-	-	-	-	-
41834	-	–+	+++	+++	+++	-	––	-	-
41835	+	–+	+++	+++	+++	-	-	-	-
41836	+	–+	+++	+++	+++	-	-	-	-
41837	++	–+	+++	+++	+++	-	-	-	-
41838	-	–+	+++	+++	+++	-	-	-	-
41839	++	–+	+++	+++	+++	-	-	-	-
41840	-	–+	+++	+++	+++	-	-	-	-
41841	-	–+	+++	+++	+++	-	-	-	-
41842	-	-	-	-	-	-	-	-	-
41843	-	–+	+++	+++	+++	-	-	-	-
41844	+	–+	+++	+++	+++	-	-	-	-
41845	-	––	-	-	-	-	-	-	-
41846	+	–+	+++	+++	+++	-	-	-	-
41847	-	–+	+++	+++	+++	-	––	-	-
41848	+	–+	+++	+++	++	-	-	-	-
41849	+	–+	+++	+++	+++	-	-	-	-
41850	-	–+	+++	-	++	-	-	-	-
41851	-	–+	+++	+++	+++	-	-	-	-
36999	-	-	-	-	-	-	-	-	-
17324	-	–	+	-	-	-	-	-	-
18028	-	-	-	-	-	-	-	-	-
41852	++	–+	+++	+++	+++	-	-	-	-

11322	-	-	+	+	-	-	-	-	-
41853	-	--	++	+	-	-	-	-	-
41854	++	-	-	-	-	+	-	-	-
41855	-	-	-	-	-	-	-	-	-
39672	-	--+	+++	+++	+++	+	-	-	-
17191	+	--+	+++	+++	+++	-	-	-	-
17122	+	--+	+++	+++	+++	-	-	-	-
18760	+	--+	+++	+++	+++	-	-	-	-
41856	-	-	+	-	-	-	-	-	-
41857	-	--+	+++	+++	+++	-	-	+	-
41858	+	--+	+++	+++	+++	-	-	-	-
17274	++	--+	+++	+++	+++	-	-	-	-
41859	++	--+	+++	+++	+++	-	-	-	-
41860	++	--+	+++	+++	+++	+++	---	-	-
20156	-	--+	+++	+++	+++	-	-	-	-
40009	-	--+	+	+++	-	++	-	-	-
41861	-	-	-	-	-	-	-	-	-
41424	-	--+	+++	+++	+++	-	-	-	-
41862	+	--+	+++	+++	+++	-	-	-	-
41051	-	-	-	++	-	-	-	-	-
38370	++	--+	+++	+++	+++	+	-	-	-
41863	+	-	+	-	-	-	-	-	-
19359	++	--+	+++	+++	+++	-	-	-	-
41864	++	--+	+++	+++	+++	-	-	-	-
41865	-	-	+	+	++	-	-	-	-
41866	-	--+	+++	+++	+++	-	-	-	-
41867	-	--+	+++	+++	+++	-	-	-	-
41868	+	--+	+++	+++	++	-	-	-	-
17108	-	--+	+++	+++	+++	-	-	-	-
41869	-	-	+	-	-	+++	-	-	-
41870	-	--+	+++	+++	+++	-	-	-	-
38742	+	--+	+++	+++	+++	-	-	-	-
17551	+	--+	+++	+++	+++	-	-	-	-

41871	-	-	---+	+++	-	+	-	-	-	-
41872	-	+	---+	+++	+++	+++	-	-	-	-
41873	-	+	-	+	+	+	-	-	-	-
41874	-	+	---+	+++	+++	+++	-	-	-	-
41875	-	+	-	-	-	-	-	-	-	-
41876	-	-	-	+++	-	+	-	-	-	-
41877	-	+	---+	+++	+++	+++	-	-	-	-
19632	-	+	-	++	+	+++	-	-	-	-
41878	-	-	---+	+++	+++	+++	+	-	-	-
36284	-	-	---+	+++	+++	+++	-	-	-	-
39967	-	++	---+	+++	+++	+++	-	-	-	-
41879	-	+	---+	+++	+++	+++	-	-	-	-
41880	-	+	---+	+++	+++	+++	-	-	-	-
41881	-	++	---+	+++	+++	+++	-	-	-	-
41519	-	-	-	-	-	-	-	-	-	-
37462	-	+	---+	+++	+++	+++	-	-	-	-
41882	-	-	-	-	-	-	-	-	-	-
40220	-	+	-	-	-	-	-	-	-	-
41883	-	+	---+	+++	+++	+++	-	-	-	-
41884	-	+	-	+	++	-	-	-	-	-
41885	-	+	---+	+++	+++	+++	-	--	-	-
17794	-	-	---+	++	++	-	+++	-	-	-
41886	-	+	---+	+++	++	+++	-	-	-	-
39499	-	+	---+	+++	+++	+++	-	-	-	-
39106	-	++	---+	+++	+++	+++	-	-	-	-
40562	-	+	---+	+++	+++	+++	-	-	-	-
17321	-	-	---+	+++	+++	+++	-	-	-	-
41887	-	+	---+	+++	+++	+++	+	-	-	-
41888	-	-	-	-	-	-	-	-	-	-
41889	-	-	-	-	-	-	-	-	-	-
38327	-	-	-	-	-	-	-	-	-	-
40495	-	+	---+	+++	+++	+++	-	-	-	-
41890	-	+	---+	+++	+++	+++	-	-	-	-

19781	-	+	-	-	-	-	-	-	-
41891	-	-	--	++	+	+	-	-	-	-
41892	-	+	--+	+++	+++	+++	+	-	-	-
41713	-	+	-	-	+	-	-	-	-	-
39637	-	++	--+	+++	+++	+++	-	-	-	-
41893	-	-	-	+	-	-	+	--	-	-
41894	-	-	-	+++	-	+	-	-	-	-
41895	-	-	-	-	-	-	-	-	-	-
38568	-	-	-	-	-	-	-	-	-	-
41896	-	-	-	-	-	-	-	-	-	-
41897	-	-	-	+	-	-	-	-	-	-
41898	-	-	-	+	+++	+	-	-	-	-
41735	-	+++	-	-	-	-	-	-	-	-
41899	-	-	--+	+++	+++	+++	-	-	-	-
20147	-	-	--+	+++	+++	-	-	-	-	-
41900	-	-	-	+++	+++	+++	-	-	-	-
41901	-	-	-	-	-	-	-	-	-	-
41902	-	-	--+	+++	+++	+++	-	-	-	-
41819	-	++	-	-	-	-	-	-	-	-
41903	-	-	-	+++	-	-	-	-	-	-
38573	-	-	--+	+++	+++	+++	-	-	-	-
41904	-	++	--+	+++	-	-	+++	---	-	-
41905	-	++	--+	+++	+++	+++	-	-	-	-

T15

AA SEQ ID#	human (b)	macaque (b)	marmoset (b)	mouse (b)	control (b)	human (t)	macaque (t)	marmoset (t)	mouse (t)	control (t)
36344	+++	+	+	-	–	+++	+	–	+	++
36344	+++	+	+	+	–	+++	++	––	++	++
36261	+++	+	+	+	–	+++	+	––	++	++
36261	+++	+	+	+	–	+++	++	––	++	++
36243	+++	+	+	+	–	+++	++	––	+	++
36281	+++	+	+	+	–	+++	++	––	++	+
14005	+++	-	-	-	-	+++	+	–	+	++
14005	+++	-	-	-	–	+++	++	–	+	++
36243	+++	+	+	+	–	+++	+	––	++	++
36281	+++	+	+	+	–	+++	++	––	++	++
36347	+++	++	++	+++	––	+++	+	–	+	++
36243	+++	+	+	+	–	+++	++	––	++	++
36252	+++	+	+	+	–	+++	++	––	++	++
36442	+++	++	++	+++	––	+++	+	–	+	+
14461	+++	-	-	+	–	+++	+	–	+	+
36252	+++	+	+	+	–	+++	++	––	+	++
14269	+++	+	+	++	–	+++	+	–	+	+
14269	+++	+	+	++	–	+++	+	–	+	+
36246	+++	+	+	+	–	+++	++	––	++	++
36253	+++	-	+	+	–	+++	+	–	+	++
36260	+++	+	+	+	–	+++	++	––	++	++
36250	+++	+	+	+	–	+++	++	––	++	++
36246	+++	+	+	+	–	+++	++	––	++	++
36243	+++	+	+	+	–	+++	+	––	+	++
36260	+++	-	-	+	–	+++	-	–	+	++
36247	+++	+	+	+	–	+++	+	––	+	++
36413	+++	-	-	-	-	+++	+	–	+	+
14176	+++	-	-	-	-	+++	+	–	+	+
36347	+++	++	++	+++	––	+++	+	–	+	+
14269	+++	+	+	+	–	+++	+	–	+	+
36268	+++	-	+	+	–	+++	+	––	++	++
36268	+++	+	+	+	–	+++	+	–	+	++

36250	+++	+	+	+	-	+++	++	--	++	++
36442	+++	++	++	+++	--	+++	+	-	+	+
36250	+++	+	+	+	-	+++	+	--	++	++
36247	+++	+	+	+	-	+++	++	--	++	++
36268	+++	+	+	+	-	+++	++	--	++	++
36278	+++	+	+	+	-	+++	+	--	++	++
36268	+++	+	+	+	-	+++	++	--	++	++
36278	+++	+	+	+	-	+++	++	--	++	++
36250	+++	+	+	+	-	+++	+	-	++	++
36253	+++	.	+	+	.	+++	+	.	+	+
14176	+++	.	.	.	.	+++	+	-	+	+
36796	+++	++	++	+++	--	+++	+	-	+	+
36316	+++	+	+	+	.	+++	+	-	+	+
36619	+++	.	.	.	.	+++	+	-	+	+
36347	+++	+	+	++	--	+++	+	-	+	+
36316	+++	+	+	+	-	+++	++	-	+	+
14461	+++	.	.	.	.	+++	+	-	+	++
37910	+++	+	+	+	-	+++	++	--	++	++
36413	+++	.	.	.	.	+++	+	-	+	+
37910	+++	+	+	+	-	+++	+	-	++	++
14441	+++	.	.	.	.	+++	+	-	+	+
36257	+++	.	.	.	.	+++	+	-	+	+
37910	+++	+	+	+	-	+++	+	--	+	++
36723	+++	.	.	.	.	+++	+	-	.	+
36723	+++	.	.	.	.	+++	+	.	+	+
36347	+++	++	+	++	-	+++	+	-	+	+
14036	+++	.	.	.	.	+++	+	-	+	+
37910	+++	+	+	+	-	+++	++	--	++	++
14274	+++	.	.	.	.	+++	+	-	+	+
36459	+++	+	+	++	-	+++	+	-	+	+
36305	+++	+	+	.	.	+++	+	-	+	+
36459	+++	+	+	++	-	+++	+	-	+	+
36459	+++	+	+	++	-	+++	+	-	+	+

36305	+++	-	+	-	-	+++	+	–	+	+
36459	+++	+	+	++	–	+++	+	–	+	+
36619	+++	-	-	-	-	+++	-	-	+	+
17658	+++	+	+	-	-	+++	++	–	+	++
14269	+++	+	+	+	–	+++	-	–	+	+
36796	+++	++	++	++	––	+++	+	–	+	++
14958	+++	+++	+++	+++	–––	+++	+	–	+	+
36723	+++	-	-	-	-	+++	+	–	-	+
14574	+++	+	+	+	–	+++	+	–	+	+
14040	+++	-	-	+	-	+++	+	–	+	++
14441	+++	-	-	-	-	+++	+	–	+	+
36387	+++	+	+	+	–	+++	++	–––	++	++
38273	+++	+++	+++	-	-	+++	-	-	-	-
14200	+++	-	-	-	–	+++	+	–	-	+
14441	+++	-	-	-	-	+++	+	–	+	+
14574	+++	+	+	+	–	+++	+	–	++	+
36387	+++	+	+	+	–	+++	++	––	++	++
36723	+++	-	-	-	-	+++	-	-	+	+
36262	+++	+	+	-	-	+++	+	–	+	+
36257	+++	-	-	-	-	+++	+	–	-	+
36257	+++	-	-	-	-	+++	-	-	+	+
14200	+++	-	-	-	-	+++	+	–	+	+
36262	+++	+	+	+	–	+++	+	–	+	+
36257	+++	-	-	-	-	+++	-	–	+	+
36275	+++	-	-	-	-	+++	+	.	+	+
14274	+++	-	-	-	-	+++	-	–	-	+
36251	+++	-	-	-	-	+++	+	–	+	+
14040	+++	-	-	-	–	+++	+	–	+	+
13864	+++	-	-	-	-	+++	+	–	+	+
14059	+++	+	+	+	–	+++	+	–	+	+
14441	+++	-	-	-	-	+++	-	–	+	+
36303	+	+	+	+	-	+++	+	–	+	+
14036	+++	-	-	-	-	+++	++	–	-	+

13864	+++	-	-	-	-	+++	+	–	+	+
36303	+	+	+	-	–	+++	+	–	+	+++
36523	+++	-	-	-	-	+++	+	–	-	+
13537	+++	-	-	-	-	+++	++	–	+	+
38380	+++	-	+	+	–	+++	+	–	+	++
14259	+++	-	-	-	-	+++	-	–	-	+
38225	++	+	+	+	–	+++	++	–	++	++
36778	+++	+	-	-	-	+++	+	–	+	+
36251	+++	-	-	-	-	+++	+	–	-	+
14048	+++	-	-	-	-	+++	+	–	+	+
17658	+++	-	-	-	-	+++	+	–	++	++
14050	+++	-	-	-	-	+++	+	–	+	+
36275	+++	-	-	-	-	+++	+	-	-	+
36523	+++	-	-	-	-	+++	+	-	-	+
36839	+++	-	-	-	-	+++	+	–	+	+
36840	+++	+	-	+	–	+++	++	–	+	++
36682	+++	++	+	+	-	+++	++	––	+	+
14958	+++	+++	++	+++	––	+++	-	–	+	+
36248	+++	-	-	-	-	+++	+	–	+	+
37248	+++	-	-	-	-	+++	+	–	+	+
36778	+++	-	-	-	–	+++	+	–	+	+
14097	+++	-	-	-	-	+++	+	–	+	+
36266	++	+	+	+	–	+++	++	––	++	++
36778	+++	-	-	-	-	+++	+	–	+	+
36778	+++	-	-	-	-	+++	+	––	+	++
14059	+++	+	+	+	–	+++	+	–	+	+
36248	+++	-	-	-	-	+++	+	–	+	+
36839	+++	-	-	+	-	+++	-	-	+	+
36251	+++	-	-	-	-	+++	+	-	+	+
36592	+++	++	++	++	––	+++	-	–	+	+
13526	+++	-	-	-	-	+++	+	–	+	+
36295	+++	+	+	+	–	+++	+	–	+	+
36840	+++	-	-	-	-	+++	+	–	+	+

14048	+++	-	-	-	-	+++	+	–	+	+
36539	+++	-	-	-	-	+++	+	–	+	+
36295	+++	+	+	+	-	+++	+	–	+	+
38380	+++	-	-	+	–	+++	+	–	+	+
14207	+++	-	-	-	-	+++	+	–	+	+
36248	+++	-	-	-	-	+++	+	–	+	+
36539	+++	-	-	-	-	+++	+	–	-	+
14097	+++	-	-	-	–	+++	+	–	+	+
36251	+++	-	-	-	-	+++	-	–	-	+
36539	+++	-	-	-	-	+++	+	–	+	+
36539	+++	-	-	-	-	+++	+	–	+	+
36248	+++	-	-	-	-	+++	-	-	+	+
14050	+++	-	-	-	-	+++	+	–	+	++
38225	++	+	+	+	–	+++	++	––	++	++
36249	+++	-	+	+	–	+++	+	–	+	++
14632	+++	-	-	-	-	+++	+	–	-	+
14388	+++	-	-	-	-	+++	+	–	+	+
36385	+++	-	-	-	-	+++	+	–	+	+
36975	+++	+	++	++	––	+++	++	––	++	++
36385	+++	-	-	-	-	+++	+	–	+	+
37248	+++	-	-	-	-	+++	+	–	+	+
14259	+++	-	-	-	-	+++	-	–	+	+
14388	+++	-	-	-	-	+++	+	–	+	+
36682	+++	++	+	-	-	+++	++	–	+	+
36288	+	-	-	-	-	+++	+	–	+	+
13537	+++	-	-	-	-	+++	-	–	-	+
36592	+++	++	++	++	––	+++	-	-	+	+
14350	+++	-	-	-	-	+++	+	–	+	+
36534	+++	-	-	-	-	+++	-	–	-	+
13517	+++	-	-	-	-	+++	+	–	+	+
36534	+++	+	-	-	-	+++	+	–	+	+
13928	++	-	-	-	–	+++	+	–	+	+
36554	+++	-	-	-	-	+++	+	-	+	+

36534	+++	-	-	-	-	+++	+	-	+	+
36445	+++	+	+	+	–	+++	+	–	+	+
14632	+++	-	-	+	-	+++	+	–	+	+
36554	+++	+	-	-	-	+++	-	–	+	+
36741	+++	-	-	-	-	+++	-	-	-	+
36741	+++	-	-	-	-	+++	-	-	-	+
13745	+++	-	+	+	–	+++	-	–	+	++
36534	+++	-	-	-	-	+++	-	–	-	+
13517	+++	-	-	-	-	+++	+	–	+	+
36844	+++	++	++	++	––	+++	+	––	++	++
13526	+++	-	-	-	-	+++	+	–	+	+
36290	+++	-	-	-	-	+++	+	–	+	+
14378	+++	-	-	-	-	+++	+	–	+	+
14207	+++	-	-	-	-	+++	+	–	+	+
14198	+++	-	-	-	-	+++	-	–	+	+
36391	+++	+	+	+	–	+++	++	–	++	++
17736	+++	-	-	-	-	+++	+	–	+	+
14628	+++	-	-	-	-	+++	-	-	-	+
16667	+++	+	+	++	–	+++	+	–	+	+
36287	+	-	-	-	-	+++	+	–	+	+
13543	+++	-	-	-	-	+++	+	–	-	+
38753	+++	-	-	-	-	+++	+	-	-	+
38764	+++	-	-	-	-	+++	-	-	-	+
36445	+++	-	-	+	–	+++	+	–	-	+
13816	++	-	-	-	-	+++	+	–	+	+
18011	+++	-	+	-	-	+++	-	–	-	-
16619	+++	+	+	+	–	+++	+	–	+	+
37174	+++	+	++	++	––	+++	++	–	++	++
13928	++	-	-	-	-	+++	+	–	+	+
14343	+++	+	+	-	–	+++	+	–	+	+
16619	+++	+	+	+	–	+++	+	–	+	+
36985	+++	-	+	+	––	+++	+	–	-	+
14289	+++	-	-	-	-	+++	+	–	+	+

36290	+++	-	-	-	-	+++	-	–	+	+
14628	+++	-	-	-	-	+++	-	-	-	+
37062	+++	++	+	++	––	+++	+	––	+	+
16612	+++	+	+	+	–	+++	+	–	+	+
13818	++	-	-	-	-	+++	+	–	+	+
14301	++	-	-	-	-	+++	+	–	+	+
38753	+++	-	-	-	-	+++	-	-	+	+
14581	+++	-	-	-	-	+++	-	-	-	+
37174	+++	+	+	++	–	+++	+	–	+	+
36844	+++	++	+	++	––	+++	+	––	+	+
17736	+++	-	-	-	-	+++	+	-	+	+
16577	+++	-	-	+	-	+++	+	–	+	+
38764	+++	-	-	-	-	+++	-	-	-	+
36972	+	-	+	+	-	+++	+	–	+	+
13818	+++	-	-	-	-	+++	+	–	+	+
36975	+++	++	++	++	––	+++	+	–	++	+
13535	++	-	-	-	-	+++	+	–	+	+
37062	+++	++	+	++	––	+++	+	–	+	+
13816	++	-	-	-	-	+++	-	–	+	+
36249	+++	+	+	+	–	+++	+	–	+	+
14350	++	-	-	-	-	+++	+	–	+	+
16613	++	-	-	-	-	+++	+	–	+	+
13517	++	-	-	-	-	+++	+	–	+	+
13762	++	-	-	-	–	+++	++	–	+	+
14301	++	-	-	-	-	+++	+	–	+	+
13844	++	-	-	-	-	+++	+	–	+	+
18011	+++	-	-	-	-	+++	-	-	+	-
14243	++	-	-	-	-	+++	+	–	+	+
36834	+++	++	++	+++	––	+++	+	–	+	++
14379	+++	+++	+++	+++	–––	+++	+	–	+	+
36894	++	-	-	-	-	+++	+	-	+	+
13535	++	-	-	-	-	+++	+	–	+	+
36753	+++	-	-	-	-	+++	+	–	+	+

13844	++	-	-	-	-	+++	+	–	+	+
13517	+++	-	-	-	-	+++	+	–	+	+
14593	+++	+	+	+	–	+++	+	–	+	+
36753	+++	+	-	-	-	+++	+	–	+	+
37649	+++	-	-	-	-	+++	-	–	-	+
14289	+++	-	-	-	-	+++	+	–	+	+
13510	++	-	-	-	-	+++	+	-	+	+
36287	+	-	-	-	-	+++	-	–	+	+
36894	++	-	-	-	-	+++	-	–	-	+
14628	+++	-	-	-	-	+++	-	-	-	+
16667	+++	+	+	+	–	+++	+	–	+	+
16577	+++	-	-	-	-	+++	+	–	+	+
38753	+++	-	-	-	-	+++	+	–	-	+
38980	+++	-	-	-	-	+++	+	–	+	+
37030	+++	-	-	-	-	+++	+	–	+	+
36769	+++	-	-	-	-	+++	-	-	+	-
14301	++	-	-	-	-	+++	-	–	-	+
13848	++	-	-	-	-	+++	+	–	+	+
36972	+	+	-	-	–	+++	+	–	+	+
14079	++	-	-	-	-	+++	+	–	+	+
14581	+++	-	-	-	-	+++	-	-	-	-
38046	+++	+	+	+	–	+++	+	––	+	+
36382	++	++	+	+	–	+++	+	–	+	+
14243	++	-	-	-	-	+++	+	–	+	+
37030	+++	-	-	-	-	+++	+	–	+	+
37081	+++	-	+	-	-	+++	-	-	+	+
36378	+++	-	+	+	–	+++	+	–	+	+
14301	++	-	-	-	-	+++	+	–	+	+
37081	+++	-	+	-	-	+++	++	-	+	-
38046	+++	+	+	-	–	+++	++	–	+++	+
13510	++	-	-	-	-	+++	-	-	-	+
38712	+++	-	-	-	-	+++	-	-	-	+
14060	+++	-	-	-	-	+++	-	-	-	-

36312	+++	+	+	+	–	+++	+	––	++	+
14198	+++	-	-	-	-	+++	+	–	+	+
37562	+++	+	+	+	–	+++	+	–	+	+
36769	+++	-	-	+	-	+++	-	-	-	+
36697	++	+	+	+	–	+++	++	–	+	++
36697	++	+	+	+	–	+++	++	––	++	++
14593	+++	+	+	+	–	+++	+	-	+	+
13751	+++	-	-	-	-	+++	+	–	+	+
36369	+++	-	-	-	-	+++	-	-	-	-
37019	+++	-	-	-	-	+++	+	–	+	+
38654	++	+	+	+	-	+++	+	–	+	+
36369	+++	-	-	-	-	+++	-	-	-	+
36265	+++	-	-	+	-	+++	+	–	-	+
36378	+++	-	+	-	-	+++	+	–	+	+
36382	++	++	+	+	–	+++	+	–	+	+
16575	+	-	-	-	-	+++	+	–	+	+
37562	+++	+	+	++	––	+++	++	–	+	+
36265	+++	-	-	-	-	+++	-	-	-	+
37030	+++	-	-	-	-	+++	+	–	+	+
13898	+	-	-	-	-	+++	+	-	-	+
16613	++	-	-	-	-	+++	+	–	+	+
13934	++	+	+	+	–	+++	+	–	+	+
38712	+++	-	-	-	-	+++	-	–	-	+
37649	+++	-	-	-	-	+++	-	-	-	+
18180	+	-	-	-	-	+++	+	–	+	+
36947	+++	-	-	-	-	+++	-	–	-	-
14079	++	-	-	-	-	+++	+	–	+	+
38223	+++	-	-	-	-	+++	-	–	-	+
36947	+++	-	-	-	-	+++	+	-	+	+
36947	+++	-	-	-	-	+++	+	–	+	-
13848	++	-	-	-	-	+++	+	–	+	+
18180	+	-	-	+	-	+++	-	-	+	+
38753	+++	-	-	-	-	+++	+	-	-	+

14262	+++	-	-	-	-	+++	+	–	+	+
14378	+++	-	-	-	-	+++	+	–	+	+
14379	+++	+++	+++	+++	---	+++	+	–	+	+
36473	+	-	+	+	–	+++	+	–	++	++
13898	+	-	-	-	-	+++	-	–	-	+
36473	+	-	-	-	-	+++	++	–	++	++
14303	+++	-	-	-	-	+++	-	-	-	+
38843	+++	-	-	-	-	+++	++	–	+	++
38980	+++	-	-	-	-	+++	+	–	+	+
16630	+++	-	-	-	-	+++	+	–	+	+
14367	+	+	+	+	–	+++	+	-	+	+
36301	++	-	-	-	-	+++	+	–	+	+
14060	+++	-	-	-	-	+++	-	-	-	-
37019	+++	-	+	-	-	+++	+	–	+	+
36490	++	+	+	+	–	+++	++	––	++	++
38712	+++	-	-	-	-	+++	-	-	-	-
14010	+++	-	-	-	-	+++	+	–	+	+
14367	+	+	+	+	–	+++	+	-	+	+
16013	+++	-	-	-	-	+++	-	–	+	+
36301	++	-	-	-	-	+++	+	–	+	+
38843	+++	-	-	-	-	+++	+	–	++	+
36947	+++	-	-	-	-	+++	+	–	+	+
13623	++	-	-	+	-	+++	+	–	+	+
38712	+++	-	-	-	-	+++	-	-	-	+
14327	+++	-	-	-	-	+++	+	-	-	-
36437	+++	++	+	-	-	+++	+	–	-	+
37024	+	-	+	+	–	+++	+	–	+	+
13990	++	-	-	-	-	+++	+	–	+	+
36391	+++	+	+	+	–	+++	+	–	+	+
16013	+++	-	-	-	-	+++	+	–	+	+
37030	+++	-	-	-	-	+++	+	-	+	-
37655	+++	+	+	+	–	+++	-	-	+	+
36598	+++	+	+	+	–	+++	+	–	+	+

14303	+++	-	-	-	-	+++	-	-	-	-
38654	++	-	+	+	–	+++	+	–	+	+
16613	++	-	-	-	-	+++	+	–	+	+
37488	+++	-	-	-	-	+++	-	-	+	+
14327	+++	-	-	-	-	+++	-	-	-	+
36312	+++	+	+	+	–	+++	++	––	+	++
37031	+++	-	-	-	-	+++	+	–	+	+
37580	+++	-	-	-	-	+++	+	–	-	+
37024	+	-	+	+	–	+++	+	––	+	+
36437	+++	++	+	-	-	+++	+	–	-	+
36985	+++	+	+	+	–	+++	-	–	-	+
36438	+++	++	+	-	-	+++	++	–	-	-
37655	+++	+	+	+	–	+++	-	-	-	-
38654	+	-	+	-	–	+++	+	–	+	+
37031	+++	-	-	-	-	+++	+	–	+	+
38843	+++	-	-	-	-	+++	+	–	++	+
14136	++	-	-	-	-	+++	+	–	+	+
36495	+++	+	+	++	–	+++	+	–	+	+
36438	+++	+++	+	-	–	+++	+	–	+	+
38843	+++	-	-	-	-	+++	+	–	+	+
14222	+++	-	+	-	-	+++	+	–	+	+
37723	+	-	-	+	–	+++	+	–	+	+
14343	++	-	-	-	-	+++	-	–	+	+
14479	+++	-	-	-	-	+++	+	–	+	+
16630	+++	-	-	-	-	+++	+	–	+	-
36490	++	+	+	+	–	+++	++	–	+	++
16612	+++	+	+	+	–	+++	-	–	+	+
37580	+++	-	-	-	-	+++	+	–	+	+
13543	++	-	-	-	-	+++	+	-	+	+
36549	+	-	-	-	-	+++	-	-	-	-
36956	+	-	-	-	-	+++	+	–	+	+
13762	+	-	-	-	–	+++	-	–	-	++
36790	+	-	-	-	-	+++	+	-	+	+

13990	++	-	-	-	-	+++	+	–	+	+
36563	+++	+	+	+	–	+++	+	-	-	-
14262	+++	-	-	-	-	+++	+	–	+	+
36495	+++	+	++	++	–	+++	+	–	+	+
37580	+++	-	-	-	-	+++	+	–	+	+
36598	+++	+	-	+	–	+++	+	-	-	+
14010	+++	-	-	-	-	+++	-	–	+	+
14010	+++	-	-	-	-	+++	-	–	+	+
13688	++	-	-	-	-	+++	+	–	+	+
16613	++	-	-	-	-	+++	+	–	+	+
13948	++	-	-	-	-	+++	+	–	+	+
14628	+++	-	-	-	-	+++	-	-	-	-
36495	+++	+	+	++	–	+++	+	–	+	+
37488	+++	-	-	-	-	+++	+	-	-	+
37580	+++	-	-	-	-	+++	-	–	+	+
38223	+++	-	-	-	-	+++	-	-	-	-
13934	++	+	+	+	–	+++	+	–	+	+
16636	++	-	-	-	-	+++	+	–	+	+
36834	+++	++	+	++	––	+++	+	–	+	+
11947	+	+	-	-	-	+++	+	–	-	+
36540	++	+	-	+	–	+++	+	–	+	+
13715	++	-	-	-	-	+++	+	–	+	+
14192	++	-	-	+	-	+++	-	-	-	-
15980	++	-	+	-	-	+++	-	–	-	-
13623	++	-	-	-	–	+++	+	–	+	+
13688	++	-	-	-	-	+++	+	–	+	+
36563	+++	+	+	+	–	+++	+	-	-	-
36280	++	-	-	-	-	+++	+	–	+	+
36280	++	-	-	-	-	+++	+	–	+	+
36364	++	+++	+	+	–	+++	+	–	-	-
13580	+++	-	-	-	-	+++	+	–	+	+
36495	+++	+	+	++	–	+++	+	–	+	+
36848	+++	-	-	-	-	+++	-	-	-	+

14010	+++	-	-	-	-	+++	+	–	+	+
36563	+++	+	+	+	–	+++	-	-	-	-
14479	++	-	-	-	-	+++	+	-	-	-
14531	++	-	-	+	-	+++	+	–	+	+
36956	+	-	-	-	-	+++	+	-	-	-
16575	+	-	-	-	-	+++	++	–	+	+
36285	++	-	-	-	-	+++	+	–	-	+
13589	++	-	-	+	-	+++	+	–	+	+
14620	++	-	-	-	-	+++	-	–	+	+
14620	++	-	-	-	-	+++	+	–	+	+
14222	+++	-	-	-	–	+++	+	–	+	+
15980	++	-	-	-	–	+++	+	–	+	+
14290	+++	+	+	+	–	+++	+	–	+	+
13553	++	-	-	-	-	+++	+	–	+	+
16636	++	-	-	-	-	+++	+	–	+	+
36317	+++	-	-	-	-	+++	-	-	-	-
14219	++	-	+	-	-	+++	-	–	-	-
36286	++	+	+	-	–	+++	+	–	+	+
36788	++	-	-	-	-	+++	+	–	+	+
13553	++	-	-	-	-	+++	-	–	+	+
16586	+	-	-	+	-	+++	++	––	++	+
13751	+++	-	-	-	-	+++	-	–	-	-
36563	+++	+	+	+	–	+++	-	-	-	+
13874	++	-	-	-	-	+++	+	–	+	+
13772	++	-	-	-	-	+++	-	–	+	+
13772	++	-	-	-	-	+++	-	–	-	+
36790	+	-	-	-	-	+++	-	–	-	+
13580	+++	-	-	-	-	+++	+	–	+	+
36294	+++	-	-	-	-	+++	-	–	+	+
13901	+++	-	-	-	-	+++	+	–	+	+
36540	++	-	-	-	-	+++	+	–	+	+
36286	++	+	+	-	-	+++	+	–	+	+
14136	++	-	-	-	-	+++	+	–	+	+

36848	+++	-	-	-	-	+++	+	-	-	+
36693	+++	-	-	-	-	+++	-	-	-	-
13948	+	-	-	-	-	+++	+	–	+	+
37075	++	+	+	+	–	+++	+	–	+	+
36294	++	-	-	-	-	+++	+	–	+	+
36788	++	-	-	-	-	+++	+	–	-	+
36540	++	-	+	-	-	+++	+	–	+	+
36576	+++	-	-	-	-	+++	+	–	+	+
37075	++	+	+	++	–	+++	+	–	+	+
14219	++	-	+	+	–	+++	+	-	+	+
13901	++	-	-	-	-	+++	+	–	+	+
36435	+++	++	+	-	-	+++	+	–	-	+
14399	+++	-	-	-	-	+++	+	-	+	-
14531	++	+	+	+	-	+++	-	–	+	+
16602	+	-	+	-	–	+++	-	-	-	+
36364	++	++	++	+	–	+++	+	–	-	+
14290	+++	+	+	+	–	+++	+	–	+	+
36493	+++	+++	+	-	-	+++	++	–	+	+
13715	++	-	-	-	-	+++	-	-	+	+
36576	+++	-	+	-	-	+++	-	–	+	-
36286	++	-	-	-	-	+++	-	–	-	+
38827	++	-	-	-	-	+++	+	–	+	+
36727	++	++	++	-	-	+++	-	-	-	-
36576	+++	-	-	+	-	+++	-	–	+	+
14366	++	-	-	-	-	+++	-	-	-	-
14585	++	-	-	-	-	+++	+	–	+	+
11947	+	-	-	+	-	+++	-	–	+	+
13938	+++	-	+	+	–	+++	+	–	+	+
14192	++	-	-	-	-	+++	+	–	-	-
36464	+++	-	-	-	-	+++	-	-	-	-
36280	++	-	+	-	-	+++	+	–	+	+
38654	+	-	-	-	-	+++	+	–	+	+
14344	++	-	-	-	-	+++	+	–	+	+

13830	++	-	-	-	-	+++	-	–	+	+
17775	++	-	-	-	-	+++	+	-	+	+
14115	+++	-	-	-	-	+++	+	–	+	+
14282	+	-	-	-	-	+++	+	–	+	+
16664	+	+	+	+	–	+++	+	–	+	++
14264	+++	-	-	-	-	+++	+	–	+	+
36663	+	-	-	+	-	+++	+	–	+	+
14344	++	-	-	-	-	+++	+	–	+	+
16602	+	-	-	+	-	+++	+	–	+	+
13851	++	-	-	-	-	+++	+	–	+	+
36663	+	-	-	-	-	+++	+	–	+	+
13580	+++	-	-	-	-	+++	+	–	+	+
36496	+++	+	+	+	–	+++	-	–	-	-
36318	++	-	-	-	-	+++	-	–	+	+
14585	++	-	-	-	-	+++	+	–	+	+
14321	+	-	-	-	-	+++	+	–	+	+
36464	+++	-	-	-	-	+++	-	-	-	-
37096	+	-	-	-	-	+++	+	–	-	+
36491	++	-	-	-	-	+++	+	–	+	+
14344	+++	-	-	-	-	+++	+	–	+	+
36435	+++	+++	+	-	-	+++	+	–	+	-
36496	+++	+	+	+	–	+++	-	-	-	-
13938	+++	-	+	+	–	+++	+	–	+	+
13943	+++	-	-	-	-	+++	+	–	+	+
13874	+++	-	-	-	-	+++	-	–	+	+
36826	+	-	-	-	-	+++	-	–	+	+
38827	++	-	-	-	-	+++	+	–	+	+
36576	+++	-	-	-	–	+++	-	–	+	+
13640	++	-	-	-	-	+++	+	-	+	+
37096	+	-	-	-	-	+++	-	-	-	-
13589	++	-	-	-	-	+++	+	–	+	+
36259	+	-	-	-	-	+++	-	-	-	+
14399	+++	-	-	-	-	+++	+	–	+	+

14115	+++	-	-	-	-	+++	+	–	+	+
37750	+++	++	-	-	–	+++	-	-	-	-
38724	+++	-	-	-	-	+++	-	-	-	+
39136	++	-	-	-	-	+++	+	–	+	+
36286	++	+	-	-	–	+++	+	–	+	+
13943	+++	-	-	-	-	+++	+	–	+	+
14264	+++	-	-	-	-	+++	+	-	-	+
13830	++	-	-	-	-	+++	+	–	+	+
36496	+++	+	+	+	–	+++	-	-	-	-
14861	++	-	-	-	-	+++	+	–	+	+
36280	++	-	-	-	-	+++	-	-	+	-
36964	+++	-	-	-	-	+++	-	-	-	+
39136	++	-	-	+	-	+++	+	–	+	+
17775	++	-	-	-	-	+++	+	-	+	+
36932	+++	-	-	-	-	+++	+	–	+	+
14443	+++	-	-	-	-	+++	-	–	+	+
36932	+++	-	-	-	-	+++	+	–	+	+
36496	+++	+	+	+	–	+++	-	-	-	-
13874	++	-	-	-	-	+++	+	–	+	+
14344	++	-	-	-	-	+++	+	–	+	+
36496	+++	+	+	+	–	+++	-	-	-	-
36693	+++	-	-	-	-	+++	-	-	-	-
38724	+++	-	-	-	-	+++	-	-	+	+
37862	++	-	-	-	-	+++	+	–	+	+
36285	++	-	-	-	-	+++	+	–	+	+
14861	++	-	-	-	-	+++	+	–	+	+
36621	++	-	-	-	-	+++	+	–	+	+
36318	++	-	-	-	-	+++	-	–	+	+
36259	+	-	-	-	-	+++	-	-	-	-
14282	+	-	-	-	-	+++	+	–	+	+
36259	+	-	-	-	-	+++	-	-	-	+
36964	+++	-	-	-	-	+++	-	-	-	-
36496	+++	+	+	+	–	+++	-	-	-	-

36540 +	+	-	-	-	+++	+	–	+	+
36293 +	-	-	-	-	+++	-	–	-	+
36491 ++	-	-	-	-	+++	+	–	-	+
36621 ++	-	-	-	-	+++	+	–	+	+
36299 ++	+	+	+	–	+++	++	––	+	++
14443 ++	-	-	-	-	+++	+	–	-	+
16610 +++	-	-	-	-	+++	-	-	-	-
37938 ++	-	-	-	-	+++	-	-	-	-
11947 +	-	-	-	-	+++	-	–	-	+
13938 +++	-	+	-	-	+++	+	–	+	+
36971 +++	-	-	-	-	+++	-	-	-	-
14046 ++	-	-	-	-	+++	+	–	+	+
37806 ++	-	-	-	-	+++	-	-	-	-
14083 +++	-	-	-	-	+++	+	–	+	+
36493 +++	+++	+	+	-	+++	+	-	+	+
37106 +++	-	-	-	-	+++	-	-	-	-
37862 ++	-	-	-	-	+++	-	–	+	+
13640 ++	-	-	-	-	+++	-	-	+	-
14344 ++	-	-	-	-	+++	+	–	+	-
37938 ++	-	-	-	-	+++	-	-	-	+
13995 +++	-	-	-	-	+++	-	-	-	-
37315 ++	+++	++	+	–	+++	+	–	-	++
38229 ++	-	-	-	-	+++	-	-	+	-
14098 ++	-	-	-	-	+++	+	–	-	+
13972 ++	-	-	-	-	+++	+	–	+	+
14344 ++	-	-	-	-	+++	+	–	+	+
36259 +	-	-	-	-	+++	-	-	-	-
14290 +++	+	+	+	–	+++	+	–	+	+
36826 +	-	-	-	-	+++	-	–	-	+
11947 +	-	-	-	-	++	+	–	+	+
14290 +++	+	+	+	–	++	+	–	+	+
17681 +++	-	-	-	-	++	+	–	+	+
36594 +++	-	-	-	-	++	-	-	-	+

36258	+++	-	-	-	-	++	+	–	+	+
17659	++	+++	++	+	–	++	++	-	-	-
36317	+++	-	-	-	-	++	-	-	-	-
36274	++	-	-	-	-	++	-	–	-	-
37818	++	+++	+	+	-	++	+	-	-	+
36274	+++	-	-	-	-	++	+	-	+	+
36299	++	+	+	+	–	++	+	––	+	++
36652	++	-	-	-	-	++	+	–	+	+
37617	+++	+	+	+	–	++	-	–	-	-
14861	++	-	-	-	-	++	+	–	+	+
39265	++	-	-	-	-	++	-	-	-	-
37315	+++	+++	++	+	–	++	+	–	-	+
13930	+++	-	-	-	-	++	-	–	+	+
16608	+++	-	-	-	-	++	-	-	-	-
36299	++	+	+	+	–	++	++	––	+++	+
36258	+++	-	-	-	-	++	+	–	+	+
13745	++	-	-	-	-	++	-	-	-	-
36652	++	-	-	-	-	++	+	–	+	+
13938	+++	-	-	-	-	++	+	–	+	+
36360	+++	+	+	+	–	++	+	–	+	+
13664	++	-	-	-	-	++	+	–	+	+
37617	+++	-	+	+	–	++	+	-	-	-
39265	++	-	-	-	-	++	-	-	-	+
36594	+++	-	-	-	-	++	-	–	-	+
38571	++	-	-	-	-	++	-	-	-	+
36727	++	++	+	+	-	++	+	–	-	-
36274	++	-	-	-	-	++	-	–	-	+
13949	++	-	-	-	-	++	+	–	+	+
13972	++	-	-	-	-	++	-	-	-	-
13580	+++	-	-	-	-	++	+	-	-	+
36360	+++	+	+	+	–	++	+	–	+	+
37806	++	-	-	-	-	++	-	-	-	-
14384	++	-	-	-	-	++	+	–	+	+

37068	+++	-	-	-	-	++	-	-	-	-
37684	+++	+++	+	+	-	++	+	-	+	-
37750	+++	+	+	-	-	++	-	-	-	-
37684	+++	++	-	-	-	++	-	-	-	-
14704	+	-	-	-	-	++	+	–	+	+
37863	+++	-	-	-	-	++	-	-	-	+
13939	++	-	-	-	-	++	+	–	+	+
11887	+	-	-	-	-	++	-	-	-	-
13874	++	-	-	-	-	++	-	-	-	-
38571	++	-	-	-	-	++	-	-	-	+
38352	++	-	-	-	-	++	+	–	-	+
37106	+++	-	-	-	-	++	-	-	-	-
14145	++	-	-	-	-	++	+	–	+	+
36615	+++	-	-	-	-	++	-	-	-	-
13739	++	-	-	-	-	++	+	–	+	+
14083	+++	-	-	-	-	++	+	–	+	+
36411	+++	-	-	-	-	++	+	-	-	+
13828	+	-	-	-	-	++	+	–	+	+
36258	++	-	-	-	-	++	+	–	+	+
37068	+++	-	-	-	-	++	-	-	-	-
14858	++	-	-	-	-	++	+	–	+	+
13851	++	-	-	-	-	++	-	-	-	-
36299	++	+	+	+	–	++	++	–	++	++
37818	++	+++	+	+	–	++	+	–	+	-
13949	++	-	-	-	-	++	+	–	-	+
36553	++	++	+	-	–	++	++	–	-	+
16610	+++	-	-	-	-	++	-	-	-	-
14018	+	-	+	+	-	++	+	–	+	+
13739	++	-	-	-	-	++	-	-	-	+
14618	++	+++	++	+++	––	++	+++	–	+	-
36971	+++	-	-	-	-	++	-	-	-	-
36343	+	-	-	-	-	++	+	–	+	+
38352	++	-	-	-	-	++	+	–	+	+

36688	++	++	+	-	-	++	+	–	-	-
37863	+++	-	-	-	-	++	-	-	-	-
13995	++	-	-	-	-	++	-	-	+	-
13828	+	-	-	-	-	++	-	–	+	-
36258	++	-	-	-	-	++	+	–	-	+
14298	++	-	-	-	-	++	+	–	+	+
38615	++	-	-	-	-	++	+	–	+	+
36274	+++	-	-	-	-	++	-	-	+	+
36434	++	++	+	-	–	++	++	-	-	-
13939	++	-	-	-	-	++	+	–	+	+
36434	+++	++	+	-	-	++	-	-	-	+
36571	+++	+	+	-	–	++	+	–	+	+
37762	+	++	+	+	-	++	+	–	-	+
36603	+++	-	-	-	-	++	-	-	-	-
11385	+	-	-	-	-	++	-	–	+	-
14098	++	-	-	-	-	++	-	-	-	-
14018	+	+	+	-	-	++	+	–	+	+
36441	++	+++	+	-	-	++	+	–	-	-
36423	+++	-	-	-	-	++	-	-	-	-
38254	++	-	-	-	-	++	-	-	-	-
38254	++	-	-	-	-	++	-	-	-	-
37824	+++	-	-	-	-	++	-	-	-	-
14018	+	-	-	-	–	++	+	–	+	+
36649	+++	-	-	-	-	++	-	-	-	-
36411	+++	-	-	-	-	++	-	–	-	+
14366	++	-	-	-	–	++	-	-	-	+
13930	++	-	-	-	-	++	-	–	-	-
36965	++	-	-	-	-	++	-	–	+	+
13892	++	-	-	-	-	++	+	–	+	+
37831	+	-	-	-	-	++	-	-	-	-
16017	+	-	-	-	-	++	+	–	-	+
37095	++	-	-	-	-	++	-	-	-	-
37831	+	-	-	-	-	++	-	-	-	-

36971	+++	-	-	-	-	++	-	-	-	-
36441	++	+++	++	+	–	++	+	–	-	-
14704	+	-	-	-	-	++	-	–	-	+
40141	++	-	-	-	-	++	-	-	-	-
14018	+	-	-	+	-	++	+	–	+	+
36971	+++	-	-	-	-	++	-	-	-	-
14298	++	-	-	-	-	++	+	–	+	+
37536	+++	-	-	-	-	++	-	-	-	-
13992	+++	-	-	-	-	++	+	–	+	+
13664	++	-	-	-	-	++	+	-	-	+
14384	++	-	-	-	-	++	+	–	+	+
14034	+	-	-	-	-	++	+	–	+	+
11887	+	-	-	-	-	++	-	-	+	+
14191	++	-	-	-	-	++	+	–	+	+
17687	+++	-	-	-	-	++	+	–	-	+
36519	+++	+	+	+	––	++	-	-	+	-
36416	+++	-	-	-	-	++	-	-	-	-
37521	+	+++	+	+	-	++	++	-	-	-
17681	+++	-	-	-	-	++	+	–	+	+
11385	+	-	-	-	-	++	-	-	-	-
15945	++	-	-	-	-	++	+	–	+	+
13991	+++	-	-	-	-	++	++	–	+	+
14602	++	-	-	-	-	++	+	–	+	+
14858	++	-	-	-	–	++	+	–	+	+
38615	++	-	-	-	-	++	+	-	+	+
37824	+++	-	-	-	-	++	-	-	-	-
36571	+++	-	-	-	–	++	+	–	+	+
16608	+++	-	-	-	-	++	+	-	-	-
14556	+	-	-	-	-	++	-	-	-	-
36640	+++	-	-	-	-	++	-	-	-	-
36546	+++	-	-	-	-	++	+	-	-	+
13538	+	-	-	-	-	++	+	-	+	-
13538	+	-	-	-	-	++	+	–	-	+

36416	+++	-	-	-	-	++	-	-	-	-
36416	+++	-	-	-	-	++	-	-	-	-
37824	+++	-	-	-	-	++	-	–	-	+
14191	++	-	-	-	-	++	-	–	+	+
36411	+++	-	-	-	-	++	-	–	+	+
13802	+	-	-	-	-	++	+	–	-	+
37824	+++	-	-	-	-	++	-	-	-	-
36965	++	-	-	-	-	++	-	–	-	+
14066	+	-	-	-	-	++	+	–	+	+
36640	+++	-	-	-	-	++	-	-	-	-
36615	+++	-	-	-	-	++	-	-	-	-
16017	+	-	-	-	-	++	+	–	-	-
37568	+++	-	-	-	-	++	-	-	-	-
36820	++	+++	+	+	-	++	++	-	-	+
15945	++	-	-	-	-	++	+	–	-	-
36416	+++	-	-	-	-	++	-	-	-	-
37095	+++	+	-	-	-	++	-	-	-	-
36936	+++	++	+	-	-	++	-	-	-	-
14861	++	-	-	-	-	++	+	–	-	+
36519	+++	+	+	+	–	++	-	-	-	-
14018	+	+	+	-	-	++	+	–	+	+
14034	+	-	-	-	-	++	+	–	+	+
37762	+	++	+	-	-	++	+	-	-	-
37824	+++	-	-	-	-	++	-	–	-	+
38229	++	+	-	-	-	++	-	–	-	-
13636	++	-	-	-	-	++	+	–	+	+
14704	+	-	-	-	-	++	+	–	+	+
14122	++	-	-	-	-	++	+	–	+	+
36343	+	-	+	-	-	++	+	–	+	+
36603	+++	-	-	-	-	++	-	-	-	-
36553	++	+++	+	-	-	++	+	–	-	-
39593	++	-	-	-	-	++	-	-	-	-
40141	++	-	-	-	–	++	-	-	-	-

14704 +	-	-	-	-	++	+	–	+	+
14145 ++	-	-	-	-	++	+	–	+	+
14122 ++	-	-	-	-	++	-	–	-	+
36603 +++	-	-	-	-	++	-	-	-	-
13892 ++	-	-	-	-	++	+	–	+	+
36681 ++	++	+	+	-	++	++	–	-	-
36317 +++	-	-	-	-	++	-	-	-	-
14521 ++	-	-	+	-	++	-	–	+	-
13557 ++	-	+	-	-	++	+	–	+	+
36411 +++	-	-	-	-	++	-	-	-	+
39593 ++	-	-	-	-	++	-	–	-	-
36820 ++	+++	+	-	-	++	+	-	-	-
37173 +++	-	-	-	-	++	-	-	-	-
36603 +++	-	-	-	-	++	-	-	-	-
36423 +++	-	-	-	-	++	-	-	-	-
14444 ++	-	-	-	-	++	+	–	+	+
36688 +	+++	+	+	–	++	++	–	-	+
13636 ++	-	-	-	-	++	+	–	+	+
13599 +	-	-	-	-	++	+	–	-	-
36354 +	+	+	+	-	++	+	–	+	+
13886 +	+	+	+	–	++	+	––	+	+
14602 ++	-	-	-	-	++	+	–	+	+
36640 +++	-	-	-	-	++	-	-	-	-
14126 ++	-	-	-	-	++	-	–	-	-
14521 +	-	-	-	-	++	+	–	+	+
14126 ++	-	-	-	–	++	-	-	-	-
36936 +++	++	+	+	–	++	+	–	-	-
13802 ++	-	-	-	-	++	-	–	-	+
36639 ++	++	+	+	–	++	+	–	-	+
36486 +++	-	-	-	-	++	-	-	-	-
16064 ++	-	-	-	-	++	-	-	-	-
36649 +++	-	-	-	-	++	-	-	-	-
36350 ++	-	-	-	-	++	-	-	-	+

17687	+++	-	-	-	-	++	-	–	-	-
39375	++	-	-	-	-	++	-	-	-	-
14216	++	-	-	-	-	++	+	–	+	+
13599	+	-	-	-	-	++	+	–	-	+
36420	+++	-	-	-	-	++	-	-	-	-
17796	+++	-	-	-	-	++	+	–	+	+
37118	++	-	-	-	-	++	-	-	-	-
14046	+	-	-	-	-	++	-	-	-	-
36420	+++	-	-	-	-	++	-	-	-	-
37411	++	+++	+	+	–	++	+	–	-	+
14224	+++	+	+	+	–	++	+	–	+	+
17701	+++	-	-	-	-	++	-	-	-	+
14273	+	-	-	-	-	++	+	–	+	+
37824	+++	-	-	-	-	++	-	-	-	-
37173	++	-	-	-	-	++	-	-	-	-
37102	++	-	-	-	-	++	-	-	-	-
37118	++	-	-	-	-	++	-	-	-	-
38061	++	-	-	-	-	++	-	-	-	+
36308	+++	-	-	-	-	++	-	-	-	-
13605	++	-	-	-	-	++	-	–	+	+
14444	++	-	-	-	-	++	-	–	+	+
14776	+	-	-	-	-	++	-	–	-	+
36317	+++	-	-	-	-	++	-	-	-	-
36640	+++	-	-	-	-	++	-	-	-	-
14018	+	-	+	-	-	++	+	–	+	+
14776	+	-	-	-	-	++	+	–	+	+
37652	+++	-	-	-	-	++	-	-	-	-
36354	+	+	+	-	–	++	+	––	+	+
17659	+	++	++	+	–	++	+	–	-	-
39375	+	-	-	-	-	++	-	-	-	-
14807	+++	-	-	-	-	++	+	–	+	+
37746	+++	-	-	-	-	++	-	-	-	-
13992	++	-	-	-	-	++	+	-	-	-

14807	+++	-	-	+	-	++	+	-	+	+
36546	+++	-	-	-	-	++	-	-	-	-
14342	+	-	-	+	–	++	+	–	+	++
37661	+	-	-	-	-	++	-	-	-	-
36308	+++	-	-	-	-	++	-	-	-	-
14216	++	-	-	-	-	++	+	–	-	+
36458	++	+	+	+	–	++	-	-	-	-
16064	++	-	-	-	-	++	-	-	-	-
13857	+	-	-	-	-	++	+	–	+	-
13841	+	-	-	-	-	++	-	-	-	-
36659	+	++	+	-	-	++	++	–	-	-
37102	++	-	-	-	-	++	-	-	-	-
14556	+	-	-	-	-	++	-	-	-	+
38061	++	-	-	-	-	++	-	-	-	-
14293	++	-	-	-	-	++	-	-	-	-
36497	+	-	-	-	-	++	+	–	+	+
14273	+	-	-	-	-	++	-	–	+	-
13899	+	-	-	-	-	++	+	–	+	+
36486	+++	-	-	-	-	++	-	-	-	-
36458	++	+	+	+	–	++	-	-	-	-
14503	+++	-	+	-	-	++	+	–	+	+
14445	++	-	-	-	-	++	+	-	+	-
14342	+	-	+	-	–	++	+	–	+	++
36486	+++	-	-	-	-	++	-	-	-	-
36486	+++	-	-	-	-	++	-	-	-	-
37536	+++	-	-	-	-	++	-	-	-	-
16018	+++	-	-	-	–	++	+	–	+	+
13991	+++	-	-	-	-	++	+	–	-	+
37661	+	-	-	-	-	++	-	-	-	-
13556	+	-	-	-	-	++	+	–	+	+
13882	++	-	-	-	-	++	+	–	+	+
37653	+++	-	-	-	-	++	-	-	-	-
36486	+++	-	-	-	-	++	-	-	-	-

13556	+	-	-	-	-	++	-	–	-	+
37584	++	-	-	-	-	++	+	-	-	+
13946	++	-	-	-	-	++	-	–	-	-
37912	+++	-	-	-	-	++	-	-	-	-
16134	++	-	-	-	-	++	-	-	-	-
36626	++	+	+	-	–	++	+	–	-	-
36639	+	+++	+	+	–	++	+	-	+	+
14576	+++	-	-	-	-	++	-	-	-	-
36497	+	-	+	-	-	++	+	–	+	+
36635	++	-	-	-	-	++	-	–	+	+
13557	++	-	-	-	-	++	+	–	+	+
36453	+++	-	-	-	-	++	-	-	-	-
37653	+++	-	-	-	-	++	-	-	-	-
14265	+	-	-	-	-	++	-	–	+	+
37912	+++	-	-	-	-	++	-	-	-	-
36453	+++	-	-	-	-	++	-	-	-	-
37809	++	-	-	-	-	++	-	-	-	-
13858	++	-	-	-	-	++	-	-	-	+
37666	+++	-	-	-	-	++	-	-	-	-
17796	+++	-	-	-	-	++	-	-	+	-
37854	+++	+	+	++	–	++	-	-	-	-
38144	+++	-	-	-	-	++	-	-	-	-
37641	+++	-	-	-	-	++	-	-	-	-
37854	+++	+	+	++	–	++	-	-	-	-
14346	++	-	-	-	-	++	-	–	-	-
13858	++	-	-	-	-	++	+	-	+	-
38107	++	-	-	-	-	++	+	–	+	+
14346	++	-	-	-	-	++	-	-	+	+
36681	+	++	+	-	-	++	-	-	-	-
17701	+++	-	-	-	-	++	-	–	-	+
36957	+++	-	-	-	-	++	-	-	-	-
13857	+	-	-	-	-	++	+	-	-	+
14183	++	-	-	-	-	++	-	-	-	+

38272	+++	-	-	-	-	++	-	-	-	+
36626	++	-	+	+	–	++	+	–	+	+
36957	+++	-	-	-	-	++	-	-	-	-
36982	+++	-	-	-	-	++	-	-	-	-
14066	+	+	-	-	-	++	-	–	-	+
37652	+++	-	-	-	-	++	-	-	-	-
13605	++	-	-	-	-	++	+	–	+	+
36489	++	-	-	-	-	+	-	-	-	-
36350	++	-	-	-	-	+	-	-	-	-
13841	+	+	-	+	-	+	-	-	-	-
36701	+++	-	-	-	-	+	-	-	-	-
13937	+	-	-	-	-	+	+	-	+	+
36701	+++	-	-	-	-	+	-	-	-	-
37809	++	-	-	-	-	+	-	-	-	-
37641	+++	-	-	-	-	+	-	-	-	-
36328	+++	-	-	-	-	+	-	-	-	-
36458	++	+	+	+	–	+	-	-	-	-
14445	++	-	-	-	-	+	-	-	-	-
37197	+++	-	-	-	-	+	-	-	-	-
38144	+++	-	+	+	-	+	-	-	-	-
12333	+++	-	-	-	-	+	-	-	-	-
37521	+	++	-	-	-	+	-	-	-	-
37568	+++	-	-	-	-	+	-	-	-	-
36458	++	+	+	+	–	+	-	-	-	+
37970	+++	-	-	-	-	+	-	-	-	-
36957	+++	-	-	-	-	+	-	-	-	-
36298	++	++	+	-	-	+	-	-	-	-
37213	+++	-	-	-	-	+	-	-	-	-
38272	+++	-	-	-	-	+	-	-	-	-
19087	++	-	-	-	-	+	-	-	-	-
36701	+++	-	-	-	-	+	-	-	-	-
36486	+++	-	-	-	-	+	-	-	-	-
36982	+++	-	-	-	-	+	-	-	-	-

37029 +++	-	-	-	-	+	-	-	-	-
19087 +++	-	-	-	-	+	-	-	-	-
38160 +++	-	-	-	-	+	-	-	-	-
37641 +++	-	-	-	-	+	-	-	-	-
36933 ++	+++	++	-	–	+	-	-	-	-
14085 +++	-	-	-	-	+	+	–	+	+
36457 +	-	+	-	-	+	+	-	-	-
36912 ++	-	-	-	-	+	-	-	-	-
36361 +++	-	-	-	-	+	-	-	-	-
37991 +	++	+	-	-	+	++	-	-	-
37661 +	-	-	-	-	+	-	-	-	-
13937 +	-	-	-	-	+	+	-	-	+
36389 +++	-	-	-	-	+	-	-	-	-
13923 +	-	-	-	-	+	+	–	-	+
14224 ++	+	+	+	–	+	-	–	+	-
36695 +++	-	-	-	-	+	-	-	-	-
11078 +	-	-	-	-	+	+	–	+	+
14576 +++	-	-	-	-	+	-	-	-	-
13596 +	+	+	+	–	+	-	-	-	+
37939 +++	-	-	-	-	+	-	-	-	-
36456 ++	-	-	-	-	+	+	-	-	+
36328 +++	-	-	-	-	+	-	-	-	-
37641 +++	-	-	-	-	+	-	-	-	-
36457 +	-	-	-	-	+	-	-	-	-
12037 +++	-	-	-	-	+	-	-	-	-
37029 +++	-	-	-	-	+	-	-	-	-
11875 ++	-	-	-	-	+	-	-	-	-
36328 +++	-	-	-	-	+	-	-	-	-
36851 ++	++	+	-	–	+	+	-	-	-
12333 +++	-	-	-	-	+	-	-	-	-
37939 +++	-	-	-	-	+	-	-	-	-
36632 ++	-	-	-	-	+	-	-	-	-
37302 ++	-	-	-	-	+	-	-	-	-

37970	+++	-	-	-	-	+	-	-	-	-
38107	++	-	-	-	-	+	+	–	-	-
14085	+++	-	-	-	-	+	+	–	+	+
37213	+++	-	-	-	-	+	-	-	-	-
37197	+++	-	-	-	-	+	-	-	-	-
12190	++	-	-	-	-	+	-	-	-	-
36749	+	++	-	-	-	+	-	-	-	-
14293	++	-	-	-	-	+	-	–	-	-
13181	++	-	-	-	-	+	-	-	-	-
13946	++	-	-	-	-	+	+	–	+	-
13181	+++	-	-	-	-	+	-	-	-	+
36635	++	-	-	+	-	+	-	–	-	+
13899	+	-	-	-	-	+	-	–	+	-
14495	++	-	-	-	-	+	-	-	-	-
37584	+	-	-	-	-	+	+	-	-	-
36851	++	+++	+	+	-	+	++	-	-	-
16134	++	-	-	-	-	+	-	-	-	+
17593	++	+	+	-	–	+	+	–	+	+
37302	++	-	-	-	-	+	-	-	-	-
13764	+	-	-	-	-	+	+	–	-	+
14416	++	-	-	-	–	+	+	–	++	++
16631	+	-	-	-	-	+	-	-	-	-
16018	+++	-	+	+	-	+	+	–	+	+
36504	+	-	-	-	-	+	-	–	+	-
17737	+	-	-	-	-	+	-	-	-	-
37666	+++	-	-	-	-	+	-	-	-	-
37295	+++	-	-	-	-	+	-	-	-	-
36328	+++	-	-	-	-	+	-	-	-	-
16045	++	-	-	-	-	+	-	–	-	+
14416	++	-	+	+	–	+	+	–	+	+
37963	+	-	-	-	-	+	-	-	-	-
11078	+	-	-	-	-	+	+	–	+	+
39428	++	-	-	-	-	+	-	-	-	-

14103 ++	-	-	-	-	+	+	-	+	+
13960 +	-	-	-	-	+	+	–	+	+
37759 +	+++	+	-	–	+	+	-	-	-
37295 +++	-	-	-	-	+	-	-	-	-
37197 +++	-	-	-	-	+	-	-	-	-
17593 ++	-	-	+	-	+	+	–	+	+
16045 ++	-	+	-	-	+	+	–	+	+
14495 ++	-	-	-	-	+	-	-	-	-
36695 +++	-	-	-	-	+	-	-	-	-
14183 ++	-	-	-	-	+	+	–	-	-
13181 +++	-	-	-	-	+	-	–	-	-
13629 ++	+	+	+	–	+	+	––	+	+
36489 ++	-	-	-	-	+	-	-	-	-
37029 +++	-	-	-	-	+	-	-	-	-
38718 +	-	-	-	-	+	+	–	-	-
13856 +	-	-	-	-	+	+	–	-	-
37302 ++	-	-	-	-	+	-	-	-	-
37168 ++	-	-	-	-	+	-	-	-	+
11974 ++	-	-	-	-	+	-	-	-	-
14087 +	-	-	-	-	+	+	-	+	-
14061 +	-	-	-	-	+	-	–	-	+
13181 ++	-	-	-	-	+	-	-	-	-
37197 +++	-	-	-	-	+	-	-	-	-
38311 +++	-	-	-	-	+	-	-	-	-
36426 ++	-	-	-	-	+	-	-	-	-
37168 ++	-	-	-	-	+	-	-	-	-
14087 +	-	-	-	-	+	+	–	-	+
14265 +	-	-	-	-	+	+	–	+	+
14082 ++	-	-	-	-	+	+	–	+	+
36695 +++	-	-	-	-	+	-	-	-	-
36982 +++	-	-	-	-	+	-	-	-	-
13764 +	-	-	-	-	+	+	–	-	-
36367 +++	-	-	-	-	+	-	-	-	-

14416 ++	-	-	-	–	+	+	–	+	+
37029 +++	-	-	-	-	+	-	-	+	-
14370 ++	+	+	+	–	+	+	–	+	+
36389 +++	-	-	-	-	+	-	-	-	-
36982 +++	-	-	-	-	+	-	-	-	-
37338 +++	-	-	-	-	+	-	-	-	-
37302 ++	-	-	-	-	+	-	-	-	-
37411 +	+++	+	+	–	+	+	-	-	-
11875 ++	-	-	-	-	+	-	-	-	-
16614 +++	-	-	-	-	+	-	-	-	-
14082 ++	-	-	-	-	+	-	–	+	+
36456 ++	-	-	-	-	+	+	-	-	+
16016 ++	-	-	-	-	+	-	-	-	-
14416 ++	-	-	-	–	+	+	–	+	+
36504 +	-	-	-	-	+	-	-	+	+
38672 +	++	+	-	-	+	-	-	-	-
37338 +++	-	-	-	-	+	-	-	-	-
14109 +	-	-	-	-	+	+	–	+	+
14174 +	-	-	-	-	+	+	–	+	+
37659 +	-	-	-	-	+	-	–	-	+
14576 +++	-	-	-	-	+	-	-	-	-
36415 +++	-	-	-	-	+	-	-	+	+
36361 +++	-	-	-	-	+	-	-	-	-
36509 +++	-	-	-	-	+	-	-	-	-
13856 +	-	-	-	-	+	+	–	+	+
14370 ++	+	-	+	–	+	+	–	+	+
14061 +	-	-	-	-	+	-	–	+	+
16016 ++	-	-	-	-	+	+	-	-	-
37095 ++	-	-	-	-	+	-	-	-	-
13795 +++	-	-	-	-	+	-	-	-	-
13603 +	-	-	-	-	+	+	–	+	-
41217 +	++	+	-	-	+	++	–	-	-
36367 +++	-	-	-	-	+	-	-	-	-

36695	+++	-	-	-	-	+	-	-	-	-
37571	++	-	-	-	-	+	-	-	-	-
36730	++	-	-	-	-	+	-	-	-	-
19906	++	-	-	-	-	+	-	-	-	-
12190	++	-	-	-	-	+	-	-	-	-
14502	+	-	-	-	-	+	+	-	-	-
11292	++	-	-	-	-	+	-	-	-	-
37568	+++	-	-	-	-	+	-	-	-	-
37659	+	-	-	-	-	+	+	–	-	+
37661	+	-	-	-	-	+	-	-	-	-
36509	+++	-	-	-	-	+	-	-	-	-
14267	+	-	-	-	-	+	-	-	-	-
38356	+	++	+	+	-	+	-	-	-	-
37516	++	-	-	-	-	+	-	-	-	-
13923	+	-	-	-	-	+	-	-	+	-
17013	++	-	-	-	-	+	-	-	-	-
39271	+++	-	-	-	-	+	-	-	-	-
38090	++	-	-	-	-	+	-	-	-	-
16016	++	-	-	-	-	+	-	-	-	-
36429	++	-	-	-	-	+	-	–	-	+
14218	+	-	-	-	-	+	+	-	+	+
14218	+	-	-	-	-	+	+	–	+	+
36407	+++	-	-	-	-	+	-	-	-	-
14174	++	-	-	-	-	+	+	–	-	+
14267	+	-	-	-	-	+	+	–	+	-
38378	++	-	-	-	-	+	-	-	-	-
14552	++	-	-	-	-	+	+	–	+	+
36511	+++	-	-	-	-	+	-	-	-	-
36511	+++	-	-	-	-	+	-	-	-	-
12006	++	-	-	-	-	+	+	-	+	+
37970	+++	-	-	-	-	+	-	-	-	-
18270	+	-	-	-	-	+	-	-	-	-
13181	++	-	-	-	-	+	-	-	-	-

39428 +	-	-	-	-	+	-	-	-	-
16074 ++	-	-	-	-	+	-	-	-	-
16016 ++	-	-	-	-	+	-	-	-	+
14374 +	-	-	-	-	+	+	–	+	+
36390 +++	-	-	-	-	+	-	-	-	-
13795 +++	-	-	-	-	+	-	-	-	-
36407 +++	-	-	-	-	+	-	-	-	-
38356 ++	-	-	-	-	+	-	-	-	-
38432 ++	-	-	-	-	+	-	-	-	-
19496 +	-	+	+	–	+	+	–	+	+
36362 +++	-	-	-	-	+	+	-	+	+
36362 +++	-	-	-	-	+	+	–	-	-
36911 +++	-	-	-	-	+	-	-	-	-
13882 ++	-	-	-	-	+	+	-	-	-
39271 +++	-	-	-	-	+	-	-	-	-
36612 +++	-	-	-	-	+	-	-	-	-
14503 ++	-	-	-	-	+	+	–	+	+
14447 ++	-	-	-	-	+	+	–	+	+
11522 +++	-	-	-	-	+	-	-	-	-
36431 +++	-	-	-	-	+	-	-	-	-
17013 ++	-	-	-	-	+	-	-	-	-
36426 ++	-	-	-	-	+	-	-	-	-
14026 +	-	-	-	-	+	+	–	+	+
17752 +++	-	-	-	-	+	-	-	-	-
14325 +	-	-	-	-	+	+	–	+	+
17752 +++	-	-	-	-	+	-	–	-	-
13976 +	-	-	-	-	+	-	-	-	-
11522 +++	-	-	-	-	+	-	-	-	-
38103 ++	-	-	-	-	+	-	-	-	-
14576 +++	-	-	-	-	+	-	-	+	-
14109 +	-	-	-	-	+	-	–	+	-
37592 ++	+	-	-	-	+	-	–	-	-
11522 +++	-	-	-	-	+	-	-	-	-

13904 ++	-	-	-	-	+	+	–	+	+
36409 ++	-	-	-	-	+	-	-	-	-
14552 ++	-	-	-	-	+	+	–	+	+
13181 ++	-	-	-	-	+	-	-	-	-
36390 +++	-	-	-	-	+	-	-	-	-
37419 +++	-	-	-	-	+	-	-	-	-
36415 +++	-	-	-	-	+	+	–	+	-
38672 +	++	++	-	-	+	-	-	-	-
36562 +++	-	-	-	-	+	-	-	-	-
36361 +++	-	-	-	-	+	-	-	-	-
13638 +	-	-	-	-	+	+	–	+	-
41300 +	+	-	+	-	+	-	-	-	-
14325 +	-	-	-	-	+	-	-	+	+
14502 +	-	-	-	-	+	-	-	-	-
14614 +	-	-	-	-	+	+	–	+	+
36431 +++	-	-	-	-	+	-	-	-	-
36390 +++	-	-	-	-	+	-	-	-	-
37568 +++	-	-	-	-	+	-	-	-	-
36409 ++	-	-	-	-	+	+	-	-	-
36562 +++	-	-	-	-	+	-	-	-	-
14103 ++	-	-	-	-	+	+	-	+	-
13981 ++	-	+	-	-	+	+	–	+	+
37642 +	+	-	+	-	+	-	-	-	-
36338 +++	-	-	-	-	+	-	-	-	-
12037 +++	-	-	-	-	+	-	-	-	-
38182 +++	+	+	+	–	+	-	-	-	+
36766 +++	-	-	-	-	+	-	-	-	-
13960 +	-	-	-	-	+	-	-	+	-
11826 +	-	-	-	-	+	-	-	-	-
37565 +++	-	-	-	-	+	-	-	-	-
17737 +	-	-	-	-	+	-	-	-	-
37079 +++	-	-	-	-	+	-	-	-	-
37419 +++	-	-	-	-	+	-	-	-	-

38182 +++	+	+	+	–	+	-	–	-	-
36433 +++	-	-	-	-	+	-	–	-	-
40053 +	-	-	-	-	+	-	-	-	-
38378 ++	-	-	-	-	+	-	-	-	-
36429 ++	-	-	-	-	+	-	–	+	-
37746 +++	-	-	-	-	+	-	-	-	-
36939 +++	-	-	-	–	+	-	-	-	-
11826 +	-	-	-	-	+	-	-	-	-
37592 ++	-	-	-	-	+	-	-	-	-
36613 +++	-	-	-	-	+	-	-	-	-
13981 ++	-	-	-	-	+	-	–	+	+
36824 +++	-	-	-	-	+	-	-	-	-
36730 ++	-	-	-	-	+	-	-	-	-
12037 ++	-	-	-	-	+	-	-	-	-
11766 +	-	-	-	-	+	+	–	+	+
38090 ++	-	-	-	-	+	-	-	-	-
36933 ++	+++	++	-	-	+	-	-	-	-
36745 +++	-	-	-	-	+	-	-	-	-
14502 +	-	-	-	-	+	-	-	-	-
37677 +++	+	++	+	–	+	-	-	-	-
36633 ++	-	-	-	-	+	-	-	-	-
37091 +	-	+	-	-	+	+	–	+	+
39056 +	-	-	-	-	+	-	-	-	-
36874 +++	-	-	-	-	+	-	-	-	-
14502 +	-	-	-	-	+	-	-	-	-
13638 +	-	-	-	-	+	-	-	-	-
36429 ++	-	-	-	-	+	-	–	+	-
36431 +++	-	-	-	-	+	-	-	-	-
37007 ++	-	-	-	-	+	-	-	-	-
36613 ++	-	-	-	-	+	-	-	-	-
12037 ++	-	-	-	-	+	-	-	-	-
37182 +++	-	-	-	-	+	-	-	-	-
36745 +++	-	-	-	-	+	-	-	-	-

38690 ++	-	-	-	-	+	-	-	-	-
39056 +	-	-	-	-	+	-	-	-	-
16025 +++	-	-	-	-	+	+	–	+	+
37182 +++	-	-	-	-	+	-	-	-	-
14074 +	-	-	-	-	+	+	–	+	+
37970 +++	-	-	-	-	+	-	-	-	-
37140 ++	+	+	+	–	+	+	–	++	+
13635 ++	-	-	-	-	+	+	–	+	+
37991 +	-	-	-	-	+	-	-	-	-
14614 +	-	-	-	-	+	-	–	+	-
19688 +	-	-	-	-	+	-	-	-	-
38761 +++	-	-	-	-	+	-	-	-	-
37039 ++	-	-	-	-	+	-	-	-	-
11974 ++	-	-	-	-	+	-	-	-	-
36479 +++	-	-	-	-	+	-	-	-	-
36390 +++	-	-	-	-	+	-	-	-	-
36874 +++	-	-	-	-	+	-	-	-	-
13629 ++	-	-	-	-	+	+	–	+	+
19496 +	-	+	+	–	+	+	–	+	+
36338 ++	-	-	-	-	+	-	-	-	-
16573 ++	-	-	-	-	+	-	-	-	-
13635 +	-	-	-	-	+	+	-	-	-
38083 +++	-	-	-	-	+	-	-	-	-
14175 +	-	-	-	-	+	+	–	-	+
13795 ++	-	-	-	-	+	-	-	-	-
37091 +	-	+	-	-	+	-	–	+	+
39881 +	+	-	+	-	+	-	-	-	-
38640 +	-	-	-	–	+	+	-	-	+
36632 ++	-	-	-	-	+	-	-	-	-
36302 +++	-	-	-	-	+	-	–	-	-
38083 +++	-	-	-	-	+	-	-	-	-
39807 +	-	-	-	-	+	-	-	-	-
36925 +	-	-	-	-	+	-	-	-	-

13795 ++	-	-	-	-	+	-	-	-	-
14619 +++	-	-	-	-	+	+	–	+	+
11522 +++	-	-	-	-	+	-	-	-	-
12006 +	-	-	-	-	+	+	–	-	+
36925 +	-	-	-	-	+	-	-	-	-
14211 +	-	-	-	-	+	+	-	-	+
39225 +	+	+	+	–	+	-	-	-	-
37622 ++	-	-	-	-	+	-	-	-	-
39225 +	+	+	+	-	+	-	-	-	-
14502 +	-	-	-	-	+	-	-	-	-
36359 +++	-	-	-	-	+	+	–	+	+
36521 +	-	+	+	-	+	+	–	+	+
13904 ++	-	+	-	-	+	+	–	+	+
15973 +	-	-	-	-	+	+	–	-	+
13642 +	-	-	+	-	+	-	–	+	-
36336 +++	-	-	-	-	+	-	-	-	-
37511 ++	-	-	-	-	+	-	-	-	-
16112 +++	-	-	-	-	+	-	-	-	-
37511 ++	-	-	-	-	+	-	-	-	-
36429 ++	-	-	-	-	+	-	-	+	-
38690 ++	-	-	-	-	+	-	-	-	-
40053 +	-	-	-	-	+	-	-	-	-
11927 +	-	-	-	-	+	+	–	+	-
36912 ++	-	-	-	-	+	-	-	-	-
17801 +	-	-	-	-	+	-	–	-	-
13976 +	-	-	-	-	+	+	–	+	+
36613 +++	-	-	-	-	+	-	-	-	-
11559 +	-	-	-	-	+	+	-	+	-
14092 ++	-	-	-	-	+	+	–	+	+
16595 ++	-	-	-	-	+	+	–	+	+
37079 +++	-	-	-	-	+	-	-	-	-
14447 ++	-	-	-	-	+	-	–	+	-
11292 ++	-	-	-	-	+	-	-	-	-

38432	++	-	-	-	-	+	-	-	-	-
14074	+	-	-	-	-	+	+	–	+	+
12043	+	-	-	-	-	+	-	–	+	-
39807	+	-	-	-	-	+	-	-	-	-
38582	++	-	-	-	-	+	-	-	-	-
14374	+	-	-	-	-	+	-	-	+	+
12043	+	-	-	-	-	+	+	–	+	+
36361	+++	-	-	-	-	+	-	-	-	-
37217	+	-	-	-	-	+	+	–	+	+
36801	++	-	-	-	-	+	-	-	-	-
37338	+++	-	-	-	-	+	-	-	-	-
36911	+++	-	-	-	-	+	-	-	-	-
37516	++	-	-	-	-	+	-	-	-	-
36425	++	-	-	-	-	+	-	-	-	-
37875	+	-	-	-	-	+	-	-	+	-
36371	+++	-	-	-	-	+	-	-	-	-
36353	+++	-	-	-	-	+	-	–	-	-
36408	+	-	-	-	-	+	-	-	-	-
19906	+	-	-	-	-	+	-	-	-	-
14619	+++	-	-	-	-	+	-	–	+	-
39779	++	-	-	-	-	+	-	-	-	-
39043	+	-	-	-	-	+	-	-	-	-
14074	+	-	-	-	-	+	+	–	+	+
37140	++	+	+	+	–	+	+	–	+	+
37095	+	-	-	-	-	+	-	-	-	-
16112	+++	-	-	-	-	+	+	-	-	-
38690	++	-	-	-	-	+	-	-	-	-
36612	+++	-	-	-	-	+	-	-	-	-
36366	+++	-	-	-	-	+	-	-	-	-
11927	+	-	-	-	-	+	-	-	+	+
13642	+	+	+	+	-	+	-	-	+	++
36673	++	-	-	-	-	+	-	-	-	-
38103	+	-	-	-	-	+	-	-	-	-

37007 ++	-	-	-	-	+	-	-	-	-
16074 +	-	-	-	-	+	+	–	+	-
38582 ++	-	-	-	-	+	-	-	-	-
38690 ++	-	-	-	-	+	-	-	-	-
11826 +	-	-	-	-	+	-	-	-	-
36957 +++	-	-	-	-	+	-	-	-	-
39225 +	-	-	-	-	+	-	-	-	-
36477 ++	-	-	-	-	+	+	–	+	+
18345 ++	-	-	-	-	+	-	-	-	-
36366 +++	-	-	-	-	+	-	-	-	-
36739 +++	-	-	-	–	+	-	-	-	-
14038 +	-	-	-	-	+	+	-	-	-
37622 ++	-	-	-	-	+	-	-	-	-
36701 ++	-	-	-	-	+	-	-	-	-
14074 +	-	-	-	-	+	+	–	+	+
36801 ++	-	-	-	-	+	-	-	-	-
36924 +	-	-	-	-	+	-	-	-	-
14234 +	-	-	-	-	+	+	–	+	+
11559 +	-	-	-	-	+	+	–	+	+
36631 ++	-	-	-	–	+	-	-	-	-
13952 +	-	-	-	-	+	+	–	+	+
37466 ++	-	-	-	-	+	-	–	-	-
36320 ++	-	-	-	-	+	+	–	+	-
16025 +++	-	-	-	-	+	-	–	-	-
36898 ++	-	-	-	-	+	-	-	-	-
36613 ++	-	-	-	-	+	-	-	-	-
36371 +++	-	-	-	-	+	-	–	-	-
14483 +	-	-	-	-	+	+	–	+	-
14211 +	-	-	-	-	+	+	–	+	+
36320 ++	-	-	-	-	+	-	–	-	-
36397 ++	-	-	-	-	+	-	-	-	-
36397 ++	-	-	-	-	+	-	-	-	-
37140 ++	+	+	+	–	+	+	––	+	+

16573 ++	-	-	-	-	+	-	-	-	-
39881 +	-	+	-	-	+	-	-	-	-
36336 +++	-	-	-	-	+	-	-	-	-
36479 +++	-	-	-	-	+	-	-	-	+
14234 +	-	-	-	-	+	+	--	+	-
13814 +	-	-	-	-	+	+	-	-	+
39041 +++	-	-	-	-	+	-	-	-	-
38780 +	-	-	-	-	+	-	-	-	-
36766 +++	-	-	-	-	+	-	-	-	-
37079 +++	-	-	-	-	+	-	-	-	-
14074 +	-	-	-	-	+	+	-	+	+
38640 +	-	-	+	-	+	-	-	-	-
11766 +	-	-	-	-	+	+	-	+	+
36479 +++	-	-	-	-	+	-	-	-	-
36408 +	-	-	-	-	+	-	-	-	-
17801 ++	-	-	-	-	+	+	-	+	-
38160 +++	-	-	-	-	+	-	-	-	-
38281 ++	-	-	-	-	+	-	-	-	-
39067 +	-	-	-	-	+	-	-	-	-
18345 ++	-	-	-	-	+	-	-	-	-
36604 +++	-	-	-	-	+	-	-	-	-
36289 +++	-	-	-	-	+	-	-	-	-
36336 +++	-	-	-	-	+	-	-	-	-
14094 ++	-	-	+	-	+	+	-	+	+
37217 +	-	-	-	-	+	-	-	+	+
37430 ++	-	-	-	-	+	-	-	-	+
18133 +++	-	-	-	-	+	-	-	-	-
37039 +	-	-	-	-	+	-	-	-	-
36477 ++	-	+	-	-	+	-	-	+	-
11553 +	-	-	-	-	+	+	-	-	-
36302 +++	-	-	-	-	+	+	-	-	-
14094 ++	-	+	+	-	+	+	-	+	+
36631 +	-	-	-	-	+	-	-	-	-

36633 ++	-	-	-	-	+	-	-	-	-
18133 +++	-	-	-	-	+	-	-	-	-
14038 +	-	-	-	-	+	+	–	+	-
36659 +	-	+	-	-	+	-	-	-	-
36744 +	-	-	-	-	+	-	-	-	-
36709 +++	-	-	-	-	+	-	-	-	-
16621 ++	-	-	-	-	+	-	-	-	-
40946 +	+	+	-	-	+	-	-	-	-
36386 +++	-	-	-	-	+	-	-	-	-
39225 +	+	+	-	–	+	-	-	-	-
37347 +++	-	-	-	-	+	-	-	-	-
13837 +++	-	+	+	–	+	-	-	-	-
37677 +++	+	+	+	––	+	-	-	-	-
16595 +++	-	-	-	-	+	+	-	-	+
38456 ++	-	-	-	-	+	-	-	-	-
36978 +++	-	-	-	-	+	-	–	-	+
37045 +++	-	-	-	-	+	-	-	-	-
37565 +++	-	-	-	-	+	-	-	-	-
12038 +	-	-	-	-	+	-	-	-	-
14074 +	-	-	-	-	+	+	–	+	+
36864 +++	-	-	-	-	+	-	-	-	-
37571 ++	-	-	-	-	+	-	-	-	-
37238 +	-	-	-	-	+	-	-	-	-
36939 +++	-	-	-	-	+	-	-	-	-
14001 +	-	-	-	-	+	-	-	-	-
14175 +	-	-	-	-	+	+	–	+	+
37140 ++	+	+	+	–	+	+	–	++	+
36786 ++	+	+	+	–	+	+	–	+	+
38957 ++	-	-	-	-	+	+	-	+	-
38311 +++	-	-	-	-	+	-	-	-	-
14092 ++	-	-	-	-	+	+	–	+	+
37963 ++	-	-	-	-	+	-	-	-	-
38305 ++	-	-	-	-	+	-	-	-	-

11927 +	-	-	-	-	+	+	–	+	+
18291 +++	-	-	-	-	+	-	-	-	-
39823 +	-	-	-	-	+	-	-	-	-
38957 +	-	-	-	-	+	+	–	+	+
39263 +	-	-	-	-	+	-	-	-	-
13894 +	-	-	-	-	+	+	–	+	+
14137 +	-	-	-	-	+	-	-	+	-
16112 +++	-	-	-	-	+	-	-	-	-
37347 +++	-	-	-	-	+	-	-	-	-
37642 +	+	-	-	–	+	-	-	-	-
37079 +++	-	-	-	-	+	-	-	-	-
41467 +	+	+	-	-	+	-	-	-	-
36264 +++	-	-	-	-	+	-	-	-	-
36425 ++	-	-	-	-	+	-	-	-	-
12239 ++	-	-	-	-	+	-	-	-	-
13863 +	-	-	-	–	+	+	–	+	+
19688 ++	-	+	-	-	+	-	-	-	-
16621 ++	-	-	-	-	+	-	-	-	-
14074 +	-	-	-	-	+	+	–	+	+
38456 ++	-	-	-	-	+	-	-	-	-
36388 +++	-	-	-	-	+	+	-	+	+
39807 ++	-	-	-	-	+	-	-	-	-
38274 +++	-	-	-	-	+	-	-	-	-
36744 +	-	-	-	-	+	-	-	-	-
38305 +++	-	-	-	-	+	-	-	-	-
37109 ++	-	-	-	-	+	-	-	-	-
37454 ++	-	-	-	-	+	-	-	-	-
36738 +	-	-	-	-	+	-	-	-	-
14483 +	-	-	-	-	+	+	-	+	-
36336 +++	-	-	-	-	+	-	-	-	-
41156 +	-	-	-	-	+	-	-	-	-
13593 +	-	-	-	-	+	-	–	-	-
14094 ++	-	-	-	-	+	+	–	+	+

14074 +	-	-	-	-	+	-	-	-	-
13593 +	-	+	+	–	+	+	–	+	+
39225 +	-	-	+	-	+	-	-	-	-
16112 +++	-	-	-	-	+	-	-	-	-
37238 +	-	-	-	-	+	-	-	-	-
39807 +	-	-	-	-	+	-	-	-	-
14137 +	-	-	-	-	+	+	–	-	+
11296 +	-	-	-	-	+	-	–	+	+
36864 +++	-	-	-	-	+	-	-	-	-
39043 +	-	-	-	-	+	-	-	-	-
36386 +++	-	-	-	-	+	-	-	-	-
11663 +++	-	-	-	-	+	-	-	-	-
11785 +	-	-	-	-	+	-	-	-	-
37204 ++	-	-	-	-	+	-	-	-	-
37498 ++	-	-	-	-	+	-	-	-	-
14607 +++	-	-	-	-	+	-	-	-	-
36712 +++	+++	+	++	––	+	-	-	-	-
13814 +	-	-	-	-	+	+	–	-	-
38305 +++	-	-	-	-	+	-	-	-	-
36431 +++	-	-	-	-	+	-	-	-	-
38578 ++	-	-	-	-	+	-	-	-	-
37204 ++	-	-	-	-	+	-	-	-	-
13863 +	-	-	-	-	+	+	–	+	+
39823 +	-	-	-	-	+	-	-	-	-
37129 +++	-	-	-	-	+	-	-	-	-
37454 ++	-	-	-	-	+	-	-	-	-
36824 +++	-	-	-	-	+	-	-	-	-
38305 +++	-	-	-	-	+	-	-	-	-
36424 +	-	-	-	-	+	+	-	-	-
38305 +++	-	-	-	-	+	-	-	-	-
36583 +	-	-	-	-	+	-	-	-	-
36738 +	-	-	-	-	+	-	-	-	-
13837 +++	-	+	+	–	+	-	-	-	-

38456 ++	-	-	-	-	+	-	-	-	-
11765 +	-	-	-	-	+	-	-	-	-
12458 +	-	-	-	-	+	-	–	-	-
16158 ++	-	-	-	-	+	-	-	-	-
14359 ++	-	-	-	-	+	+	-	+	-
14094 ++	-	+	-	-	+	+	–	+	+
38456 ++	-	-	-	-	+	-	-	-	-
36310 +++	-	-	-	-	+	-	-	-	-
38761 +++	-	-	-	-	+	-	-	-	-
38281 ++	-	-	-	-	+	-	-	-	-
11891 +	-	-	-	-	+	+	–	-	+
37448 +++	-	-	-	-	+	+	-	-	-
37215 +++	-	-	-	-	+	-	-	-	-
36359 +++	-	-	-	-	+	+	–	+	+
37430 +	-	-	-	-	+	-	-	-	-
36353 +++	-	-	-	-	+	-	-	-	-
14681 +	-	-	-	-	+	-	-	+	-
13894 +	-	-	-	-	+	-	–	-	-
37109 ++	-	-	-	-	+	-	-	-	-
14359 ++	-	-	-	-	+	+	–	+	+
16158 ++	-	-	-	-	+	-	-	-	-
17605 +++	-	-	-	-	+	-	-	-	-
36786 ++	+	+	+	–	+	+	–	++	+
12038 +	-	-	-	-	+	-	-	-	-
36898 ++	-	-	-	-	+	-	-	+	-
12055 +	-	-	-	-	+	-	-	-	-
16158 ++	-	-	-	-	+	-	-	-	-
36583 ++	-	-	-	-	+	-	-	-	-
11472 +	-	-	-	-	+	-	-	-	-
37650 ++	-	-	-	-	+	-	-	-	-
36479 +++	-	-	-	-	+	-	-	-	-
38087 +	++	-	-	-	+	-	-	-	-
37911 +	+	+	-	–	+	-	-	-	-

18291 +++	-	-	-	-	+	-	-	-	-
36289 +++	-	-	-	-	+	-	-	-	-
39263 +	-	-	-	-	+	-	-	-	-
36604 +++	-	-	-	-	+	-	-	-	-
36550 ++	-	+	-	-	+	-	-	-	-
14607 +++	-	-	-	-	+	-	-	-	-
11826 +	-	-	-	-	+	-	-	-	-
37498 ++	-	-	-	-	+	-	-	-	-
36978 +++	-	-	+	-	+	+	–	-	-
37122 ++	-	-	-	-	+	-	–	+	+
37275 +++	-	-	-	-	+	-	-	-	-
11609 +	-	-	+	-	+	-	-	+	+
15996 +	-	-	-	-	+	+	–	-	+
37288 ++	-	-	-	-	+	-	-	-	-
36783 +++	-	-	-	–	+	+	–	-	-
11609 +	-	-	-	-	+	+	–	+	+
39579 ++	-	-	+	-	+	-	-	-	-
36310 +++	-	-	-	-	+	-	-	-	-
36323 ++	-	-	-	-	+	-	-	-	-
37045 +++	-	-	-	-	+	-	-	-	-
37650 ++	-	-	-	-	+	-	-	-	-
40010 +	+	+	+	-	+	-	-	-	-
14607 ++	-	-	-	-	+	+	-	-	-
37204 ++	-	-	-	-	+	-	-	-	-
41264 +	-	-	-	-	+	-	-	-	-
14452 ++	-	+	+	–	+	-	–	+	+
40010 +	-	-	-	-	+	-	-	-	-
38110 ++	-	-	-	-	+	-	-	-	-
11891 +	-	-	-	-	+	+	-	+	+
37288 ++	-	-	-	-	+	-	-	-	-
36805 ++	-	-	-	-	+	-	-	-	-
36691 +	+	+	-	-	+	-	–	+	+
14452 ++	-	+	+	–	+	+	–	-	+

38872	+++	-	-	-	-	+	-	-	-	-
14607	++	-	-	-	-	+	-	-	-	-
14607	+++	-	-	-	-	+	-	-	-	-
37911	+	-	-	-	-	+	-	-	-	-
36636	++	-	-	-	-	+	-	-	-	-
36424	+	-	-	-	-	+	-	-	-	-
37215	+++	-	-	-	-	+	-	-	-	-
37044	+++	-	+	-	-	+	-	-	-	-
40062	+	-	-	-	-	+	-	-	-	-
36550	++	-	-	-	-	+	++	-	-	+
13767	+	-	-	-	-	+	+	–	+	+
11663	++	-	-	-	-	+	-	-	-	-
36264	+++	-	-	-	-	+	-	-	-	-
14167	+	-	-	-	-	+	+	–	+	+
37286	+	++	++	-	-	+	-	-	-	-
39366	++	-	-	-	-	+	-	-	-	-
16077	+	-	-	-	-	+	-	-	-	-
37589	+	-	-	-	-	+	-	-	-	-
37483	+	-	-	-	-	+	-	–	-	-
11052	+	-	-	-	-	+	-	-	-	-
39041	+++	-	-	-	-	+	-	-	-	-
37598	+++	+++	-	+++	–	+	-	-	-	-
36552	+	-	-	-	-	+	-	-	+	-
39966	++	-	-	-	-	+	-	-	-	-
14167	+	-	-	-	-	+	+	–	+	+
36783	++	-	+	+	-	+	-	–	-	-
12239	++	-	-	-	-	+	-	-	-	-
17547	+	-	-	-	-	+	-	-	-	-
38364	++	-	-	-	–	+	-	-	-	-
14391	+	-	-	-	-	+	+	–	-	-
11077	+	-	-	-	-	+	-	-	-	-
37611	+	-	-	-	-	+	-	-	-	-
38443	++	-	-	-	-	+	-	-	-	-

37313 +++	-	-	-	-	+	-	-	-	-
36443 +++	-	-	-	-	+	-	-	-	-
17558 +++	-	-	-	-	+	-	-	-	-
14607 ++	-	-	-	-	+	-	-	-	-
37204 ++	-	-	-	-	+	-	-	-	-
37747 +	+	+	-	–	+	-	–	-	-
36388 +++	-	-	-	-	+	-	-	+	-
37448 +++	-	-	-	-	+	-	-	-	-
11384 +	-	-	-	-	+	+	–	+	-
12055 +	-	-	-	-	+	-	-	-	-
15956 +	-	-	-	-	+	+	–	+	++
37654 +++	+++	+	-	-	+	+	-	-	-
38305 +++	-	-	-	-	+	-	-	-	-
36620 ++	-	-	-	-	+	-	-	-	-
37128 +	-	+	+	-	+	+	–	+	+
36974 ++	-	-	-	-	+	-	-	-	-
37658 +	-	-	-	-	+	-	-	-	-
11841 +	-	-	-	-	+	-	-	-	-
37144 ++	-	-	-	-	+	-	-	-	-
11203 +	-	-	-	-	+	+	-	+	+
36724 ++	-	-	-	-	+	+	–	+	+
37275 +++	-	-	-	-	+	-	-	-	-
38462 +++	-	-	-	-	+	-	-	-	-
36555 ++	-	-	-	-	+	-	–	-	-
37747 +	+	+	+	–	+	+	–	+	-
18518 +	-	-	-	-	+	-	-	-	-
37328 +	-	-	-	-	+	-	-	-	-
39267 +++	-	-	-	-	+	-	-	-	-
37067 +++	-	-	-	-	+	-	-	-	-
36888 +	-	-	-	-	+	-	-	-	-
37219 ++	-	-	-	-	+	+	-	-	+
37219 ++	-	-	-	-	+	+	–	+	-
37067 +++	-	-	-	-	+	-	-	-	-

36620 ++	-	-	-	-	+	-	-	-	-
36694 ++	+	-	-	–	+	-	-	+	+
36298 +	++	-	-	-	+	-	-	-	-
14179 +	-	-	-	-	+	+	–	+	-
36376 +	-	-	-	-	+	-	-	-	-
14391 +	-	-	-	-	+	+	–	-	-
36443 +++	-	-	-	-	+	-	-	-	-
37747 +	+	+	+	–	+	-	–	+	+
36787 +	-	-	-	-	+	-	-	-	-
37144 ++	-	-	-	-	+	-	-	-	-
36691 +	-	-	-	-	+	+	–	+	+
37522 ++	+++	+	++	––	+	-	-	-	-
36608 +	-	-	-	-	+	-	-	-	-
11853 ++	-	-	-	-	+	-	-	-	-
38104 +	-	+	+	–	+	+	––	+	+
37122 ++	-	-	+	–	+	-	-	-	-
16113 ++	-	-	-	-	+	-	-	-	-
36579 ++	-	-	-	-	+	-	-	-	-
37747 +	-	+	+	–	+	+	–	+	-
11927 +	-	-	-	-	+	+	–	+	+
37598 ++	+++	+	+++	–	+	-	-	-	-
39267 +++	-	-	-	-	+	-	-	-	-
36356 ++	-	-	-	-	+	-	-	-	-
36384 ++	-	-	-	-	+	-	-	-	-
14179 +	-	-	-	-	+	+	–	+	+
39322 ++	+	+	+	–	+	-	-	-	-
37181 ++	-	-	-	-	+	-	-	-	-
37152 +	-	-	-	-	+	-	-	-	-
17018 ++	-	+	+	–	+	+	–	+	+
37930 +	-	-	-	-	+	+	–	-	+
18015 +	-	-	-	-	+	-	-	+	-
37044 +++	-	-	-	-	+	-	-	-	-
17657 +	-	-	-	-	+	-	-	-	-

17558	+++	-	-	-	-	+	-	-	-	-
12707	+++	-	-	-	-	-	-	-	-	-
13913	++	-	-	-	-	-	-	–	-	+
37472	++	-	-	-	-	-	-	-	-	-
16158	++	-	-	-	-	-	-	-	-	-
11841	+	-	-	-	-	-	-	-	-	-
36922	+++	-	-	-	-	-	-	-	-	+
11528	+	-	-	-	-	-	+	–	+	+
37045	+++	-	-	-	-	-	-	-	-	-
12206	+	-	-	-	-	-	-	-	-	-
37472	++	-	-	-	-	-	-	-	-	-
36850	++	-	-	-	-	-	+	–	+	+
36636	+	-	-	-	-	-	-	-	-	-
11955	+	-	-	-	-	-	-	-	-	-
38525	+	-	-	-	-	-	-	-	-	-
15996	+	-	-	-	-	-	+	–	+	-
37930	+	-	-	-	-	-	-	–	-	-
14499	++	-	-	-	-	-	-	-	-	-
17605	+++	-	-	-	-	-	-	-	-	-
36627	+++	-	-	-	-	-	-	-	-	-
37425	+	-	-	-	-	-	-	–	-	+
38794	+++	-	-	-	-	-	-	-	-	-
36922	+++	-	-	-	-	-	-	-	-	-
14607	++	-	-	-	-	-	-	–	-	-
11757	+	-	-	-	-	-	-	–	-	-
16077	+	-	-	-	-	-	-	-	-	-
37045	+++	-	-	-	-	-	-	-	-	-
17613	++	-	-	-	-	-	-	-	-	-
11845	+	-	-	-	-	-	+	-	+	+
36579	++	-	-	-	-	-	-	-	-	-
37045	+++	-	-	-	-	-	-	-	-	-
37141	+++	+++	++	+	–	-	-	-	-	-
37141	+++	+++	++	+	–	-	-	-	-	-

36692 +++	-	-	-	-	-	-	-	-	-
11785 +	-	-	-	-	-	-	-	-	-
36555 ++	-	-	-	-	-	-	–	-	-
37425 ++	-	+	-	-	-	+	–	-	-
39966 ++	-	-	-	-	-	-	-	-	-
36709 +++	-	+	-	-	-	-	-	-	-
36724 +	-	-	-	-	-	+	–	+	+
13850 ++	-	-	-	-	-	-	-	-	-
38438 +	-	-	-	-	-	-	-	-	-
13913 ++	+	-	+	-	-	-	-	-	+
37353 ++	-	-	-	-	-	-	-	-	-
39322 ++	-	+	-	-	-	-	-	-	-
37693 ++	-	-	-	–	-	-	-	-	-
36787 +	-	-	-	-	-	-	-	-	-
11757 +	-	-	-	-	-	-	-	-	-
36636 +	-	-	-	-	-	-	-	-	-
38122 +	-	-	-	-	-	-	–	+	+
14681 +	-	-	-	-	-	-	-	-	-
38438 +	-	-	-	-	-	-	-	-	-
14042 +	-	-	-	–	-	-	-	-	-
36805 ++	-	-	-	-	-	-	-	-	-
12570 +	-	-	-	-	-	-	-	-	-
36488 ++	+	+	-	–	-	-	-	-	-
38188 +	-	+	-	-	-	+	–	+	+
36678 +++	-	-	-	-	-	-	-	-	-
36319 ++	-	-	-	-	-	-	-	-	-
14042 +	-	-	-	-	-	-	–	+	+
11841 +	-	-	-	-	-	-	-	-	-
15956 +	-	-	-	-	-	+	–	+	+
36463 +	-	-	-	-	-	-	-	-	-
37088 ++	-	+	-	–	-	-	-	-	-
17035 +++	+	+	-	-	-	-	-	-	-
36627 +++	-	-	-	-	-	-	-	-	-

36675 ++	-	-	-	-	-	-	-	-	-
37196 ++	-	-	-	-	-	-	-	-	-
16638 ++	-	-	-	–	-	-	-	-	-
36550 ++	-	-	-	-	-	-	–	+	-
38872 +++	-	-	-	-	-	-	-	-	-
36593 +++	-	-	-	-	-	-	-	-	-
37129 +++	-	-	-	-	-	-	-	-	-
37658 +	-	-	-	-	-	-	-	-	-
14499 ++	-	-	-	-	-	-	-	-	-
37468 +	-	-	-	-	-	-	-	-	-
16113 ++	-	-	-	-	-	-	-	-	-
36883 ++	-	-	-	-	-	+	–	+	-
16071 ++	-	-	-	-	-	-	-	-	-
37275 ++	-	-	-	-	-	-	-	-	-
37260 +	-	-	-	-	-	-	-	-	-
36463 +	-	-	-	-	-	-	-	-	-
37223 ++	-	-	-	-	-	-	-	-	-
36461 +++	-	-	-	-	-	-	-	-	-
36396 ++	-	-	-	-	-	-	–	+	-
37468 +	-	-	-	-	-	-	-	-	-
36636 +	-	-	-	-	-	-	-	-	-
36675 +	-	-	-	-	-	-	-	-	-
12206 +	-	-	-	-	-	-	-	-	-
36264 +++	-	-	-	-	-	-	-	-	-
36942 ++	-	-	-	-	-	-	-	-	-
38019 +	-	-	-	-	-	-	-	-	-
36396 ++	-	-	-	-	-	-	-	-	-
11841 +	-	-	-	-	-	-	-	-	-
36264 +++	-	-	-	-	-	-	-	-	-
11472 +	-	-	-	-	-	-	-	-	-
38122 +	-	-	-	-	-	+	-	+	+
39103 +	-	+	+	-	-	-	-	-	-
38525 +	-	-	-	-	-	-	-	-	-

16158 ++	-	-	-	-	-	-	-	-	-
37896 +	-	-	-	-	-	-	-	-	-
37045 +++	-	-	-	-	-	-	-	-	-
38012 +	-	-	+	–	-	-	-	-	-
36791 ++	-	-	-	-	-	-	-	-	-
39557 +	-	-	-	-	-	-	-	-	-
36694 ++	-	+	-	-	-	+	–	-	+
36768 +	-	-	-	-	-	-	-	-	-
37115 ++	-	-	-	-	-	-	-	-	-
11996 ++	-	-	-	-	-	-	-	-	-
12148 ++	-	-	-	-	-	-	-	+	+
11230 +	-	-	-	-	-	-	-	-	-
37654 +++	+++	+	-	-	-	-	-	-	-
37537 ++	+	+	+	–	-	-	-	-	-
37275 +++	-	-	-	-	-	-	-	-	-
13850 +	-	-	-	-	-	-	-	-	-
19603 ++	-	-	-	-	-	-	-	-	-
16014 +	-	-	-	-	-	-	-	-	-
36791 ++	-	-	-	-	-	-	-	-	-
38794 +++	-	-	-	-	-	-	-	-	-
11366 +	-	-	-	-	-	-	-	-	-
37537 ++	-	+	-	–	-	-	-	-	-
12148 ++	-	-	-	-	-	-	-	-	-
37990 ++	-	-	-	-	-	-	-	-	-
37482 +	-	-	-	-	-	-	-	+	-
37402 +	-	-	-	-	-	-	-	-	-
19089 +	-	-	-	-	-	-	–	-	-
36692 +++	-	-	-	-	-	-	-	-	-
16158 ++	-	-	-	-	-	-	-	-	-
41277 +	+	+	-	-	-	-	-	-	-
19089 +	-	-	-	-	-	-	-	-	-
36989 +	-	-	-	-	-	-	-	-	-
38364 ++	+	++	-	–	-	-	-	-	-

36564 ++	-	-	-	-	-	-	-	-	-
37693 +	-	-	-	-	-	-	-	-	-
36757 +	-	-	-	-	-	-	-	-	-
41801 ++	-	-	-	-	-	-	-	-	-
36739 +++	-	-	-	–	-	-	-	-	-
18659 ++	-	-	-	-	-	-	-	-	-
36850 ++	-	-	-	-	-	+	–	+	+
36940 +	-	-	-	-	-	-	-	-	-
38578 +	-	-	-	-	-	-	-	-	-
16186 +	-	-	-	-	-	-	-	-	-
36296 +++	-	-	-	-	-	-	-	-	-
36451 +++	-	-	-	-	-	+	–	+	+
37482 +	-	-	-	-	-	-	-	-	-
38012 +	-	-	-	-	-	-	-	-	-
38188 +	-	-	-	-	-	+	–	+	+
37781 +	-	+	+	–	-	+	–	+	+
36608 +	-	-	-	-	-	-	-	-	-
12069 +	-	-	-	-	-	-	-	-	-
38786 +	+	-	+	–	-	+	-	-	+
37990 ++	-	-	-	-	-	-	-	-	-
36572 ++	-	-	-	-	-	-	-	-	-
36593 ++	-	-	-	-	-	-	–	-	-
12737 +++	-	-	-	-	-	-	-	-	-
37522 ++	+++	++	+	––	-	-	-	-	-
18112 +++	-	-	+	-	-	-	-	-	-
11531 +	-	-	-	-	-	-	–	-	-
36888 +	-	-	-	-	-	-	-	-	-
36481 ++	-	-	-	-	-	-	-	-	-
37611 +	-	-	-	-	-	-	-	-	-
36638 +++	-	-	-	-	-	-	-	-	-
18659 ++	-	-	-	-	-	-	-	-	-
38438 +	-	-	-	-	-	-	-	-	-
12570 +	-	-	-	-	-	-	-	-	-

38012 +	-	-	-	–	-	-	-	-	-
36896 ++	-	-	-	-	-	-	-	-	-
16186 +	-	-	-	-	-	-	-	-	-
38462 +++	-	-	-	-	-	-	-	-	-
14607 ++	-	-	-	-	-	-	-	-	-
38572 +++	-	-	-	-	-	-	-	-	-
36488 ++	+	+	+	–	-	-	–	-	-
17725 ++	-	-	-	-	-	-	-	-	-
37534 +	-	-	-	-	-	+	–	+	+
36451 +++	-	-	-	–	-	+	–	-	+
36893 +++	+++	++	+++	–––	-	-	-	-	-
37482 +	-	-	-	-	-	+	–	+	-
38438 +	-	-	-	-	-	-	-	-	-
11451 ++	-	-	-	-	-	-	-	-	-
12737 +++	-	-	-	-	-	-	-	-	-
38835 +	-	-	-	-	-	-	-	-	-
37223 ++	-	-	-	-	-	-	-	-	-
38473 ++	-	-	-	-	-	+	–	+	+
37920 +	-	-	-	-	-	-	-	-	-
36768 +	-	-	-	-	-	-	-	-	+
36940 +	-	-	-	-	-	-	-	-	-
36940 +	-	-	-	-	-	-	-	-	-
36319 +++	-	-	-	-	-	-	-	-	-
37633 ++	-	-	-	-	-	-	-	-	-
38473 ++	-	-	-	-	-	+	–	+	+
37438 ++	+	+	+	-	-	-	-	-	-
36323 ++	-	-	-	-	-	-	-	-	-
12144 +	-	-	-	-	-	-	-	-	-
11757 +	-	-	-	-	-	-	-	-	-
37553 +	-	-	-	-	-	-	-	-	+
38443 ++	-	-	-	-	-	-	-	-	-
36638 +++	-	-	-	-	-	-	-	-	-
36655 +	-	-	-	-	-	-	-	-	-

37234 +	-	-	-	-	-	-	-	-	-
37937 +	-	-	-	-	-	-	-	-	-
36564 ++	-	-	-	-	-	-	-	-	-
36398 +	-	-	-	-	-	+	–	+	+
37181 ++	-	-	-	-	-	-	-	-	-
39103 +	-	+	+	-	-	-	-	-	+
11996 ++	-	-	-	-	-	-	-	-	-
36777 +	-	-	-	-	-	-	-	+	+
36484 +++	-	-	-	-	-	-	-	-	-
38731 +	-	-	-	-	-	-	-	-	-
16588 +	-	-	-	-	-	-	–	+	+
37542 +	-	-	-	-	-	-	–	-	-
11853 ++	-	-	-	-	-	-	-	-	-
36852 +++	-	-	-	-	-	-	-	-	-
36433 +++	-	-	-	-	-	-	-	-	-
16071 ++	-	-	-	-	-	-	-	-	-
38042 ++	-	-	-	-	-	-	-	-	-
12069 +	-	-	-	-	-	-	-	-	-
37313 ++	-	-	-	-	-	-	-	-	-
37544 +	-	-	-	-	-	+	-	-	+
38019 +	-	-	-	-	-	-	-	-	-
38089 +	-	-	-	-	-	+	-	+	+
36974 ++	-	-	-	-	-	-	-	-	-
37631 ++	-	-	-	-	-	-	-	-	-
38835 +	-	-	-	-	-	-	-	-	-
18191 +++	-	-	-	-	-	-	-	-	-
36384 +	-	-	-	-	-	-	-	-	-
36902 +++	+++	+	+	––	-	-	-	-	-
37674 +	-	-	-	-	-	-	-	-	-
12707 +++	-	-	-	-	-	-	-	-	-
37553 +	-	-	-	-	-	-	-	-	-
36843 ++	-	-	-	-	-	-	-	-	-
37502 +	-	-	-	–	-	-	-	-	-

11757 +	-	-	-	-	-	-	-	-	-
37681 +	-	-	-	-	-	-	-	-	-
37482 +	-	-	-	-	-	+	–	+	-
38731 +	-	-	-	-	-	-	-	-	-
37534 +	-	-	-	-	-	+	–	+	+
36923 +	-	-	-	-	-	-	–	-	-
38457 +++	-	-	-	-	-	-	-	-	-
38042 ++	-	-	-	-	-	-	-	-	-
36843 ++	-	-	-	-	-	-	-	-	-
36484 +++	-	-	-	-	-	-	-	-	-
39557 +	-	-	-	-	-	-	-	-	-
17729 +	-	-	-	-	-	-	-	-	-
16588 ++	-	-	-	-	-	-	-	+	-
36760 +++	-	-	-	-	-	-	-	-	-
18191 +++	-	-	-	-	-	-	-	-	-
36867 ++	-	-	-	-	-	-	–	-	-
36393 ++	-	-	-	-	-	-	-	-	-
38731 +	-	-	-	-	-	-	-	-	-
17596 +	-	-	-	-	-	-	-	-	-
37330 +++	+++	++	++	––	-	-	-	-	-
38589 ++	-	-	-	-	-	-	-	-	-
36484 +++	-	-	-	-	-	-	-	-	-
36940 +	-	-	-	-	-	-	-	-	-
37674 +	-	-	-	-	-	-	-	-	-
36481 ++	-	-	-	-	-	-	-	-	-
37614 +	-	-	-	–	-	+	–	-	+
36588 +++	+++	++	+	––	-	-	-	-	-
38492 +	-	-	-	-	-	-	-	-	-
37176 +	-	-	-	-	-	-	-	-	-
37183 +++	+++	++	++	–	-	-	-	-	-
37130 +	-	-	-	-	-	-	-	-	-
12027 +	-	-	-	-	-	-	-	-	-
36818 +	-	-	-	-	-	-	-	-	-

18112 +++	-	-	-	-	-	-	-	-	-
37844 ++	-	-	-	-	-	-	-	-	-
38280 ++	-	-	-	-	-	-	-	-	-
36895 +	-	-	-	-	-	-	-	-	-
36393 ++	-	-	-	-	-	-	-	-	-
37234 +	-	-	-	-	-	-	-	-	-
36474 ++	+++	+	-	–	-	-	-	-	-
18573 +	-	-	-	-	-	-	-	-	-
36895 +	-	-	-	-	-	-	-	-	-
37542 +	-	-	-	-	-	+	-	-	-
36296 +++	-	-	-	-	-	-	-	-	-
38731 +	-	-	-	-	-	-	-	-	-
39421 ++	-	-	-	-	-	-	-	-	-
19230 +	-	-	-	-	-	-	-	-	-
36687 ++	-	-	-	-	-	-	-	-	-
12100 +	-	-	-	-	-	-	-	-	-
36942 ++	-	-	-	-	-	-	-	-	+
37636 ++	-	-	-	-	-	-	-	-	-
37219 ++	-	-	-	-	-	-	-	+	-
17759 ++	-	-	-	-	-	-	–	+	-
11531 +	-	-	-	-	-	+	-	-	-
11366 +	-	-	-	-	-	-	-	-	-
37330 +++	+++	++	++	–	-	-	-	-	-
36942 ++	-	-	-	-	-	-	-	-	-
36791 +	-	-	-	-	-	-	-	-	-
37340 +++	+++	++	+	–	-	-	-	-	-
36852 ++	-	-	-	-	-	-	-	-	-
36319 +++	-	-	-	-	-	-	-	-	-
12707 +++	-	-	-	-	-	-	-	-	-
11765 +	-	-	-	-	-	-	-	-	-
37844 ++	-	-	-	-	-	-	-	-	-
37119 +	-	-	-	-	-	-	-	-	-
37060 +	-	+	-	-	-	+	-	+	-

37076 +	-	-	-	-	-	-	-	-	-
37937 +	-	-	-	-	-	-	–	-	-
38491 +	-	-	-	-	-	-	-	-	-
19603 +	-	-	-	-	-	-	-	-	-
36339 ++	-	-	-	-	-	-	-	-	-
37781 +	+	-	+	–	-	-	––	+	+
36630 ++	-	-	-	-	-	-	-	-	-
38499 +	-	-	-	-	-	-	-	-	-
19710 +++	-	-	-	-	-	-	-	-	-
36671 +	-	-	-	-	-	-	-	-	-
36319 ++	-	-	-	-	-	-	-	-	-
16607 +++	+++	+++	+	–	-	-	-	-	-
37544 +	-	-	-	-	-	-	-	-	-
37744 +	-	-	-	-	-	-	-	-	-
37969 +	-	+	-	–	-	-	–	+	+
37892 ++	+++	+++	++	–	-	-	-	-	-
37307 +	-	-	-	-	-	-	-	-	-
18812 +	-	-	-	-	-	+	–	+	-
37815 ++	-	-	-	-	-	-	-	-	-
37575 +	-	-	-	-	-	-	-	-	-
38177 ++	-	-	-	-	-	-	-	-	+
40982 +	-	-	-	-	-	-	-	-	-
11408 +	-	-	-	-	-	-	-	-	-
36867 ++	-	-	-	-	-	-	-	-	-
36777 +	-	-	-	-	-	+	-	+	+
36444 ++	+	+	-	-	-	-	-	-	-
36892 +++	-	-	-	-	-	-	-	-	-
36849 +	-	-	-	-	-	-	-	-	-
36699 +++	+++	++	++	–	-	-	-	-	-
37544 +	-	-	-	-	-	-	-	+	-
11878 +	-	-	-	-	-	-	-	-	-
36919 +++	-	-	-	-	-	-	-	-	-
37681 +	-	-	-	-	-	-	-	-	-

36699 +++	+++	++	+++	--	-	-	-	-	-
38141 +	-	-	-	-	-	-	-	-	-
36406 +	-	-	-	-	-	-	-	-	-
36531 ++	-	-	-	-	-	-	-	-	-
38572 +++	-	-	-	-	-	-	-	-	-
17946 ++	-	-	-	-	-	-	-	-	-
38012 +	-	-	-	-	-	-	-	-	-
17729 +	-	-	-	-	-	-	-	-	-
13657 +	-	-	-	-	-	-	-	-	-
36436 +	-	-	-	-	-	-	-	-	-
11908 +	-	-	-	-	-	-	-	-	-
11531 +	-	-	-	-	-	-	-	-	-
36484 +++	-	-	-	-	-	-	-	-	-
37009 ++	-	-	-	-	-	-	-	-	-
38125 +	-	-	-	-	-	-	-	-	-
17547 +	-	-	-	-	-	-	-	-	-
38058 +	-	-	-	-	-	-	-	+	-
38001 +	-	+	+	-	-	-	-	-	-
37517 +	-	-	-	-	-	-	-	-	-
36522 +++	++	+	++	--	-	-	-	-	-
37636 +++	-	-	-	-	-	-	-	-	-
39743 +	-	-	-	-	-	+	-	-	-
12027 +	-	-	-	-	-	-	-	-	-
37219 ++	-	-	+	-	-	+	-	-	-
12481 +	-	-	-	-	-	-	-	-	-
36454 +++	+++	+++	+	-	-	-	-	-	-
17033 +	+	-	+	-	-	-	-	-	+
17573 +	-	-	-	-	-	-	-	-	-
17018 ++	-	-	+	-	-	+	-	+	-
37196 +++	-	-	-	-	-	-	-	-	-
11878 +	-	-	-	-	-	-	-	-	-
39421 ++	-	-	-	-	-	-	-	-	-
36642 +++	+++	++	+	-	-	-	-	-	-

37176 +	-	-	-	-	-	-	-	+	-
37022 +++	+++	+++	++	--	-	-	-	-	-
17830 ++	-	-	-	-	-	-	-	-	-
37086 +	-	-	-	-	-	-	-	-	-
37203 +	-	-	-	-	-	-	-	-	-
36883 +	-	-	-	-	-	-	-	-	-
16088 +	-	-	-	-	-	-	-	-	-
36678 +++	-	-	-	-	-	-	-	-	-
37575 +	-	-	-	-	-	-	-	-	+
36551 +	-	-	-	-	-	-	-	-	-
38809 +	-	-	-	-	-	-	-	+	-
37043 +	-	-	-	-	-	-	-	-	-
38314 +	-	-	-	-	-	-	-	-	-
37381 +++	+++	+	++	--	-	-	-	-	-
11707 +	-	-	-	-	-	+	-	-	-
38903 ++	-	-	-	-	-	-	-	-	-
36365 +++	+	+++	+	-	-	-	-	-	-
37084 ++	+	-	-	-	-	-	-	-	-
37139 +++	+++	+	+	-	-	-	-	-	-
18812 +	-	-	-	-	-	-	-	+	+
37614 +	-	-	-	-	-	-	-	+	-
37402 +	-	-	-	-	-	-	-	-	-
36713 ++	-	-	-	-	-	-	-	-	-
18015 ++	-	-	-	-	-	+	-	-	-
12205 +	-	-	-	-	-	-	-	-	-
36673 +++	-	-	-	-	-	-	-	-	-
37517 +	-	-	-	-	-	-	-	-	-
37969 +	-	-	-	-	-	+	-	+	-
11846 ++	-	-	-	-	-	-	-	-	-
36352 ++	-	-	-	-	-	-	-	-	-
39421 ++	-	-	-	-	-	-	-	-	-
15994 +	-	-	-	-	-	-	-	-	-
36545 +++	+++	+++	+	-	-	-	-	-	-

36818 +	-	-	-	-	-	-	-	-	-
37896 +	-	-	-	-	-	-	-	-	-
38280 +++	-	-	-	-	-	-	-	-	-
36402 +	-	-	-	-	-	-	-	-	-
37966 +++	+++	+	++	–	-	-	-	-	-
36866 ++	-	-	-	-	-	-	-	-	-
36461 +++	-	-	-	-	-	-	-	-	-
37267 +	-	-	-	-	-	-	-	-	-
36902 +++	+++	+	+	–	-	-	-	-	-
12205 +	-	-	-	-	-	-	-	-	-
36760 +++	-	-	-	-	-	-	-	-	-
37015 ++	-	-	-	-	-	-	-	-	-
38809 +	-	-	-	-	-	-	–	-	+
18966 +	-	-	-	-	-	-	-	-	-
36614 ++	-	-	-	-	-	-	-	-	-
37060 +	-	-	-	-	-	+	-	+	+
38132 ++	-	-	-	-	-	-	-	-	-
37230 +	+	+	-	-	-	-	-	-	-
37018 +++	+++	++	+++	––	-	-	-	-	-
17759 ++	-	-	-	–	-	-	–	+	-
36942 ++	-	-	-	-	-	-	-	-	-
36337 ++	-	-	-	-	-	-	-	-	-
11846 +	-	-	-	-	-	-	-	-	-
19998 ++	-	-	-	-	-	-	-	-	-
36335 +	-	-	-	-	-	-	-	-	-
36896 ++	-	-	-	-	-	+	-	+	-
37340 +++	+++	++	+	–	-	-	-	-	-
16567 +	-	-	-	-	-	-	-	-	-
37544 +	-	-	-	-	-	-	-	-	+
37167 ++	-	-	-	-	-	-	-	-	-
36427 ++	-	-	-	-	-	-	-	-	-
17890 +	-	-	-	-	-	-	-	-	-
39421 ++	-	-	-	-	-	-	-	-	-

38177 ++	-	-	-	-	-	-	-	-	-
18354 ++	-	-	-	-	-	-	-	-	-
38449 ++	+	+	+	–	-	+	-	-	-
38499 +	-	-	-	-	-	-	-	-	-
20365 +	-	-	-	-	-	-	-	+	+
36550 ++	-	+	-	-	-	+	-	-	-
36614 ++	-	-	-	-	-	-	-	-	-
12162 +	-	-	-	-	-	-	-	-	-
37218 ++	-	-	-	–	-	-	-	-	-
18772 ++	+	-	-	-	-	-	-	-	-
38132 ++	-	-	-	-	-	-	-	-	-
36567 +++	-	-	-	-	-	-	-	-	-
12206 +	-	-	-	-	-	-	-	-	-
11423 +	-	-	-	-	-	+	-	-	+
17946 ++	-	-	-	-	-	-	-	-	-
37744 +	-	-	-	-	-	-	-	-	-
39390 ++	-	-	-	-	-	-	-	-	-
36699 +++	+++	++	+++	––	-	-	-	-	-
37681 +	-	-	-	-	-	-	-	-	-
38908 +	+	-	-	–	-	-	-	-	-
36860 +	-	-	-	-	-	-	-	-	-
19288 +++	-	-	-	-	-	-	-	-	-
38650 +	-	-	-	-	-	-	-	-	-
36740 +	-	-	-	-	-	-	-	-	-
16671 +	-	-	-	-	-	-	-	-	-
36696 ++	+++	++	-	–	-	-	-	-	-
38141 ++	-	-	-	-	-	-	-	-	-
37307 +	-	-	-	-	-	-	-	-	-
37942 +	-	-	-	-	-	-	-	-	-
12737 +++	-	-	-	-	-	-	-	-	-
37115 ++	-	-	-	-	-	-	-	-	-
38903 ++	-	-	-	-	-	-	-	-	-
11230 +	-	-	-	-	-	-	-	-	-

37920 +	-	-	-	-	-	-	-	-	-
37047 ++	+++	+	+	-	-	-	-	-	-
38589 ++	-	-	-	-	-	-	-	-	-
37660 ++	-	-	-	–	-	-	-	-	-
36876 ++	+	+	+	–	-	-	-	-	-
36866 ++	-	-	-	-	-	-	-	-	-
36531 ++	-	-	-	-	-	-	-	-	-
17666 +	-	-	-	-	-	-	-	-	-
38064 ++	+++	+	+	–	-	-	-	-	-
36808 ++	-	-	-	-	-	-	-	-	-
16652 +	++	+	-	-	-	-	-	-	-
37228 +	-	-	-	-	-	-	-	-	-
17710 +	-	-	-	-	-	-	-	-	-
39471 +	-	-	-	-	-	-	–	-	-
37884 ++	-	-	-	-	-	-	-	-	-
37043 +	-	-	-	-	-	-	-	-	-
18835 +++	++	+++	+	–	-	-	-	+	-
36860 ++	-	-	-	-	-	-	-	-	-
39670 +	-	-	-	-	-	-	-	-	-
36282 +	+	+	-	-	-	-	-	-	-
39160 +	-	-	-	-	-	-	-	-	-
37336 +	-	-	-	-	-	-	-	-	-
36334 +++	+	+++	-	–	-	-	-	-	-
37319 ++	+++	+	+++	–	-	-	-	-	-
37458 +++	+++	++	++	–	-	-	-	-	-
36560 +++	-	-	-	-	-	-	-	-	-
39160 +	-	-	-	-	-	-	-	-	-
37052 +	-	-	-	-	-	-	-	-	-
38331 +++	+++	+	++	–	-	-	-	-	-
36798 ++	+++	-	-	-	-	-	-	-	-
11451 +	-	-	-	-	-	-	-	-	-
37502 +	-	-	-	-	-	-	-	-	-
36671 +	-	-	-	-	-	-	-	-	-

11408 ++	-	-	-	-	-	-	-	-	-
36531 ++	-	-	-	-	-	-	-	-	-
11423 +	-	-	-	-	-	-	-	-	-
36713 ++	-	-	-	-	-	-	-	-	-
17613 ++	-	-	-	-	-	-	-	-	-
36721 +	-	-	-	-	-	-	-	-	-
11955 +	-	-	-	-	-	-	-	-	-
37466 ++	-	-	-	-	-	-	-	-	-
37532 ++	-	-	-	-	-	-	-	-	-
37681 +	-	-	-	-	-	-	-	-	-
37267 +	-	-	-	-	-	-	-	-	+
36836 +	-	-	-	-	-	-	-	-	-
37633 ++	-	-	-	-	-	-	-	-	-
37249 +	-	-	-	-	-	-	-	-	-
37514 +++	+++	++	+	−−	-	-	-	-	-
37575 +	-	-	-	-	-	-	-	+	-
37966 +++	+++	+	++	−	-	-	-	-	-
36363 +++	++	+++	+	−	-	-	-	-	-
37353 ++	-	-	-	-	-	-	-	-	-
17986 +++	++	+++	+	-	-	-	-	-	-
37575 +	-	-	-	-	-	-	-	+	-
37212 +	-	-	-	-	-	-	-	-	-
18152 +	-	-	-	-	-	-	-	-	-
12255 +	-	-	-	-	-	-	-	-	-
15994 +	-	-	-	-	-	-	-	-	-
38089 +	-	-	-	-	-	-	-	+	-
37335 ++	+++	++	++	−	-	-	-	-	-
36412 +++	+++	+++	++	−−	-	-	-	-	-
36822 +	+	-	-	−	-	-	−	-	-
17485 ++	-	-	-	-	-	-	-	+	-
38556 ++	++	-	+	-	-	-	-	-	-
36410 ++	-	-	-	-	-	-	-	-	-
36356 ++	-	-	-	-	-	-	-	-	-

36696 ++	+++	++	-	–	-	-	-	-	+
18303 +	-	-	-	-	-	-	-	-	-
36505 +++	+	+++	-	–	-	-	-	-	-
39350 +	-	-	-	-	-	-	–	-	-
37381 +++	+++	+	++	––	-	-	-	-	-
36732 +	-	-	-	-	-	-	-	-	-
36402 +	-	-	-	-	-	-	-	-	-
37203 +	-	-	-	-	-	-	-	-	-
36989 +	-	-	-	-	-	-	-	-	-
12206 +	-	-	-	-	-	-	-	-	-
39710 +	-	-	-	-	-	-	-	-	-
37212 ++	-	-	-	-	-	-	-	-	-
38331 +++	+++	+	++	––	-	-	-	-	-
37086 +	-	-	-	-	-	-	-	-	-
37004 ++	+	-	-	-	-	-	-	-	-
12361 +	-	-	-	-	-	-	-	-	-
36757 +	-	-	-	-	-	-	-	-	-
36945 +	-	-	-	-	-	-	-	-	-
37203 +	-	-	-	-	-	-	-	-	-
16607 +++	+++	+++	+	–	-	-	-	-	-
37994 +	-	+	+	–	-	-	-	-	+
36525 +	-	-	-	-	-	-	-	-	-
37933 ++	+++	++	++	–	-	-	-	-	-
39350 +	-	-	-	-	-	+	-	-	-
17573 +	-	-	-	-	-	-	-	-	-
37514 +++	+++	++	+	––	-	-	-	-	-
38059 +	-	-	-	-	-	-	-	-	-
14376 ++	-	-	-	-	-	-	-	-	-
18079 ++	-	-	-	-	-	-	-	-	-
37153 ++	+++	+	++	–	-	-	-	-	-
36572 ++	-	-	-	-	-	-	-	-	-
18173 +++	++	+	+	–	-	-	-	-	-
37052 +	-	-	-	-	-	-	-	-	-

17666 +	-	-	-	-	-	-	-	-	-
36808 ++	-	-	-	-	-	-	-	-	-
36506 ++	-	-	-	-	-	-	-	-	-
36699 +++	+++	++	++	--	-	-	-	-	-
38457 +++	-	-	-	-	-	-	-	-	-
36547 +	-	-	-	-	-	-	-	-	-
36963 +++	+++	+	++	-	-	-	-	-	-
36376 +	-	-	-	-	-	-	-	-	-
37766 ++	+++	+	++	-	-	-	-	-	-
37278 +	-	++	-	-	-	-	-	-	-
37567 +	-	-	-	-	-	-	-	-	-
36814 +	-	-	-	-	-	-	-	-	-
37793 +	-	-	-	-	-	-	-	-	-
17023 ++	-	-	-	-	-	-	-	-	-
11586 +	-	-	-	-	-	-	-	-	-
37319 ++	+++	+	+++	-	-	-	-	-	-
36948 ++	-	-	-	-	-	-	-	-	-
38650 +	-	-	-	-	-	-	-	-	-
11707 +	-	-	-	-	-	-	-	-	-
38806 +	-	-	-	-	-	-	-	-	-
37359 ++	+++	++	-	-	-	-	-	-	-
37914 +	-	-	-	-	-	-	-	-	-
37942 +	-	-	-	-	-	-	-	-	-
17063 +	-	-	-	-	-	-	-	-	-
36628 ++	-	-	-	-	-	-	-	-	-
36342 +	-	+	-	-	-	-	-	-	-
36653 ++	+	-	-	-	-	-	-	+	-
37310 ++	-	-	-	-	-	-	-	-	-
39072 +	+	-	-	-	-	-	-	-	-
17637 +	+	-	-	-	-	-	-	-	-
19304 ++	++	-	-	-	-	-	-	-	-
11942 +	-	-	-	-	-	-	-	-	-
17049 ++	+++	++	+	-	-	-	-	-	-

37262 ++	-	-	-	-	-	-	-	-	-
36533 +	+++	+	-	–	-	-	-	-	-
17046 +	-	-	-	-	-	-	-	-	-
38556 +	++	-	+	-	-	-	-	-	-
37332 ++	-	-	-	-	-	-	-	-	-
39147 ++	-	-	-	-	-	-	-	-	-
11586 +	-	-	-	-	-	-	-	-	-
36930 ++	+++	+	-	–	-	-	-	-	-
18036 ++	-	-	-	-	-	-	-	-	-
36653 +	+	+	-	-	-	-	-	-	-
36836 +	-	-	-	-	-	-	-	-	-
16671 +	-	-	-	-	-	-	-	-	-
38834 +	-	-	-	-	-	-	-	-	-
38214 +	-	-	-	-	-	-	-	-	-
37994 +	+	+	+	–	-	-	-	-	+
37574 ++	+++	-	-	-	-	-	-	-	-
36399 +++	+++	++	+	–	-	-	-	-	-
18420 +	-	-	-	-	-	-	-	-	-
36684 +++	+++	+	-	-	-	-	-	-	-
17049 ++	+++	+	-	–	-	-	-	-	-
37793 +	-	-	-	-	-	-	-	-	-
37384 +	-	-	-	-	-	-	-	-	-
37884 ++	-	-	-	-	-	-	-	-	-
36797 +++	+++	+	+	–	-	-	-	-	-
12113 ++	-	-	-	-	-	-	-	-	-
38387 +	-	-	-	-	-	-	-	-	-
17039 ++	-	-	-	-	-	-	-	-	-
39007 +	-	-	-	-	-	-	-	-	-
37018 +++	+++	++	+++	––	-	-	-	-	-
37429 ++	+++	++	++	–	-	-	-	-	-
36740 +	-	-	-	-	-	-	-	-	-
37616 +	-	-	-	-	-	-	-	-	-
37892 ++	+++	+++	++	–	-	-	-	-	-

36368 ++	-	+	+	–	-	-	-	-	-
37383 +	-	-	-	-	-	-	-	-	-
17485 +	-	-	-	-	-	-	-	+	-
38157 ++	+++	+	-	–	-	-	-	-	++
36669 ++	+++	-	-	-	-	-	-	-	-
37660 ++	-	-	-	–	-	-	–	-	-
37989 +	-	-	-	–	-	-	-	-	-
37578 +	-	-	-	–	-	-	-	-	-
12796 +	-	-	-	-	-	-	-	-	-
20014 +++	+++	+	+	–	-	-	-	-	-
36918 ++	+++	-	-	–	-	-	-	-	-
37578 +	-	-	-	–	-	-	-	-	-
38518 ++	+	+	+	–	-	-	-	-	-
17576 +	-	+	-	-	-	-	-	-	-
36798 ++	+++	-	-	-	-	-	-	-	-
37036 +	+++	-	-	-	-	-	-	-	-
36577 ++	-	-	-	-	-	-	-	-	+
19136 +	-	-	-	-	-	-	-	-	-
37332 ++	-	-	-	-	-	-	-	-	-
19543 ++	-	-	-	-	-	-	-	-	-
38157 ++	+++	++	+	–	-	-	–	-	-
37379 +	-	-	-	-	-	-	-	-	-
37501 +++	+++	+++	+++	––	-	-	-	-	-
37270 +	-	-	-	-	-	-	-	-	-
37458 ++	+++	++	++	–	-	-	–	-	-
38071 +	-	-	-	-	-	-	-	-	-
37310 ++	-	-	-	-	-	-	-	-	-
37599 +	-	-	-	-	-	-	-	-	-
36393 ++	-	-	-	-	-	-	-	-	-
37296 +	-	-	-	-	-	-	-	-	-
37218 +	-	-	-	–	-	-	-	-	-
38524 +	-	-	-	-	-	-	-	-	-
36392 +++	+++	+	++	––	-	-	-	-	-

37742 +	-	-	-	-	-	-	-	-	-
37284 ++	+	-	-	-	-	-	-	-	-
37852 +	-	-	-	-	-	-	-	-	-
37905 +	-	-	-	-	-	-	-	-	-
38095 ++	-	-	-	-	-	-	-	-	-
37931 +	-	-	-	-	-	-	-	-	-
36462 +++	+	+++	-	–	-	-	-	-	-
36450 ++	-	+	-	-	-	-	-	-	-
36351 +++	+++	+++	+	–	-	-	-	-	-
38908 +	+	-	+	–	-	-	-	-	-
39390 ++	-	-	-	-	-	-	-	-	-
18573 +	-	-	-	-	-	-	-	-	-
36918 ++	+++	+	-	–	-	-	-	-	-
37994 +	-	+	+	–	-	+	-	-	-
36567 +++	-	-	-	-	-	-	-	-	-
18566 ++	-	-	-	-	-	-	-	-	-
38064 ++	+++	+	+	–	-	-	-	-	-
37384 +	-	-	-	-	-	-	-	-	-
37201 ++	-	-	-	-	-	-	-	-	-
38201 ++	-	-	-	-	-	-	-	-	-
37310 ++	-	-	-	-	-	-	-	-	-
37285 +	-	-	-	-	-	-	-	-	-
36412 +++	+++	++	++	––	-	-	-	-	-
18079 ++	-	-	-	-	-	-	-	-	-
11720 ++	-	-	-	-	-	-	-	-	-
37610 ++	+++	+	-	–	-	-	-	-	-
17025 ++	-	-	-	-	-	-	-	-	-
37349 ++	-	+	+	–	-	-	-	-	-
36363 +++	++	+++	+	–	-	-	-	-	+
37914 +	-	-	-	-	-	-	-	-	-
36937 ++	+++	+	-	–	-	-	-	-	-
36335 +	-	-	-	-	-	-	-	-	-
37048 +	-	+	-	-	-	-	-	-	-

17025 ++	-	-	-	-	-	-	-	-	-
37675 +	+	+	+	-	-	-	-	-	-
18385 +	-	-	-	-	-	-	-	-	-
36393 ++	-	-	-	-	-	-	-	-	-
37574 +++	+++	-	-	–	-	-	-	-	-
37867 +	+	+	-	–	-	-	-	-	-
40083 +	-	-	-	–	-	-	-	-	-
17557 +	-	-	-	-	-	-	-	-	-
36775 +	-	+	-	-	-	-	-	-	-
36799 +	-	-	-	-	-	-	-	-	-
37929 +	-	-	-	-	-	-	-	-	-
36400 +++	-	-	-	-	-	-	-	-	-
38877 +	+	-	-	-	-	-	-	-	-
36767 ++	+++	+	+	-	-	-	-	-	-
36355 +	-	-	-	-	-	-	-	-	-
36842 +	-	-	-	-	-	-	-	-	-
37718 ++	+++	+++	+++	––	-	-	-	-	-
11480 +	-	-	-	-	-	-	-	-	-
37429 ++	+++	++	++	–	-	-	-	-	-
36630 ++	-	-	-	-	-	-	-	-	-
12144 +	-	-	-	-	-	-	-	-	-
36454 +++	+++	+++	+	––	-	-	-	-	-
37725 +++	-	-	-	-	-	-	-	-	-
37070 ++	-	-	-	-	-	-	-	-	-
36930 ++	+++	+	-	–	-	-	-	+	-
36846 +	-	-	-	-	-	-	-	-	-
37352 ++	+++	+	-	–	-	-	-	-	-
36610 ++	-	-	-	-	-	-	-	-	-
36756 ++	++	-	-	-	-	-	-	-	-
36591 +	-	-	-	-	-	-	-	-	-
38524 +	-	-	-	-	-	-	-	-	-
36256 +++	-	-	-	-	-	-	-	-	-
38553 ++	-	-	-	-	-	-	-	-	-

36934 +	-	-	-	-	-	-	-	-	-
36392 +++	+++	+	++	--	-	-	-	-	-
37383 +	-	-	-	-	-	-	-	-	-
37766 ++	+++	+	++	-	-	-	-	-	-
36587 +++	-	-	-	-	-	-	-	-	-
37528 ++	+++	+	+	-	-	-	-	-	-
39431 +	-	-	-	-	-	-	-	-	-
37114 ++	+	+	+	-	-	-	-	-	-
39714 ++	+	+	-	-	-	-	-	-	-
17937 +	-	-	-	-	-	-	-	-	-
37224 ++	+++	-	-	-	-	-	-	-	-
17036 +++	+++	+	++	--	-	-	-	-	-
36881 +++	-	-	-	-	-	-	-	-	-
37331 +++	+++	+++	+++	--	-	-	-	-	-
36432 +++	-	-	-	-	-	-	-	-	-
37309 ++	+++	+	-	-	-	-	-	-	-
18210 +	-	-	-	-	-	-	-	-	-
37576 +	-	-	-	-	-	-	-	-	-
36866 ++	-	-	-	-	-	-	-	-	-
36948 ++	-	-	-	-	-	-	-	-	-
17020 +++	+++	+++	+	-	-	-	-	-	-
36577 ++	-	-	-	-	-	-	-	-	-
36427 ++	-	-	-	-	-	-	-	-	-
36881 +++	-	-	-	-	-	-	-	-	-
37108 ++	+++	+	-	-	-	-	-	-	-
37927 +	-	-	-	-	-	-	-	-	-
17968 +	-	-	-	-	-	-	-	-	-
37365 +++	++	+	-	-	-	-	-	-	-
37285 +	-	-	-	-	-	-	-	-	-
38518 ++	+	+	+	-	-	-	-	-	-
17637 ++	+	-	-	-	-	-	-	-	-
37049 ++	+++	+++	+	-	-	-	-	-	-
18772 ++	+	+	-	-	-	-	-	-	-

37036 +	+++	+	-	-	-	-	-	-	-
37009 ++	-	-	-	-	-	-	-	-	-
37838 +	-	-	-	-	-	-	-	-	-
37532 ++	-	-	-	-	-	-	-	-	-
17888 ++	+++	+	-	–	-	-	-	-	-
37119 +	-	-	-	-	-	-	-	-	-
37520 ++	+++	+	+	–	-	-	-	-	-
38931 +++	+++	+	++	––	-	-	-	-	-
17890 +	-	-	-	-	-	-	-	-	-
39272 +	-	+	-	–	-	+	-	-	-
37833 +++	++	+	+	–	-	-	-	-	-
38944 +	-	-	-	-	-	-	-	-	-
38682 +	-	-	-	–	-	-	-	-	-
38286 +	+	-	-	-	-	-	-	-	-
37556 ++	+++	+	+	–	-	-	-	-	-
36531 +	-	-	-	-	-	-	-	-	-
38125 +	-	-	-	-	-	-	-	-	-
37713 ++	-	-	-	-	-	-	-	-	-
37119 +	-	-	-	-	-	-	-	-	-
37290 ++	+	+	+	–	-	-	-	-	-
37108 ++	+++	+	-	–	-	-	-	-	-
40868 +	-	-	-	-	-	-	-	-	-
38840 ++	+	+	-	–	-	-	-	-	-
36690 ++	+++	+	-	–	-	-	-	-	-
36703 +	-	-	-	–	-	-	-	-	-
11720 ++	-	-	-	-	-	-	-	-	-
36734 +++	+++	+++	+++	––	-	-	-	-	-
36800 +++	+++	+	+	–	-	-	-	-	-
37394 +	-	-	-	-	-	-	-	-	-
18831 +	-	-	-	-	-	-	-	-	-
38455 +	-	-	-	-	-	-	-	-	-
37108 ++	+++	+	-	–	-	-	-	-	-
39272 +	-	+	-	–	-	-	-	-	-

38172 +	-	-	-	-	-	-	-	-	-
37218 +	-	-	-	-	-	-	-	-	-
37116 ++	-	-	-	-	-	-	-	-	-
37556 ++	+++	+	+	–	-	-	-	-	-
37708 +++	+++	-	+	-	-	-	-	-	-
37327 +++	+	-	-	-	-	-	–	+	-
36370 ++	+	-	-	–	-	-	-	-	-
38911 +++	-	-	-	-	-	-	-	-	-
36794 +	-	-	-	-	-	-	-	-	-
37224 ++	+++	-	-	–	-	-	-	-	-
37578 +	-	+	+	–	-	-	-	-	-
37559 ++	+++	+	+	–	-	-	-	-	-
36447 +++	+	++	-	-	-	-	-	-	-
11840 +	-	-	-	-	-	-	-	-	-
36462 +++	+	+++	-	-	-	-	-	-	-
18831 +	-	-	-	-	-	-	-	-	-
37272 +++	+++	+++	+	––	-	-	-	-	-
39570 +	++	+	+	–	-	-	-	-	-
38393 ++	-	-	-	-	-	-	-	-	-
38017 +	-	-	-	-	-	-	-	-	-
38648 +	-	-	-	-	-	-	-	-	-
11920 +	-	-	-	-	-	-	-	-	-
36762 ++	+++	+	+	–	-	-	-	-	-
36365 +++	++	+++	-	–	-	-	-	-	-
37047 ++	+++	+	++	-	-	-	-	-	-
36602 ++	+++	+	+	–	-	-	-	-	-
36842 ++	-	-	-	-	-	-	-	-	-
17023 ++	-	-	-	-	-	-	-	-	-
37280 ++	-	-	-	-	-	-	-	-	-
17020 +++	+++	+++	+	–	-	-	-	-	-
38280 +++	-	-	-	-	-	-	-	-	-
36792 ++	-	-	-	-	-	-	-	-	-
37218 ++	-	-	-	-	-	-	-	-	-

36832 ++	+	-	-	-	-	-	-	-	-
36586 ++	+++	++	+	–	-	-	-	-	-
38697 ++	-	-	-	-	-	-	-	-	-
36917 ++	++	++	+	–	-	-	-	-	-
37974 ++	+++	-	-	-	-	-	-	-	-
12796 +	-	-	-	-	-	-	-	-	-
37846 +	-	-	-	-	-	-	-	-	-
37725 +++	-	-	-	-	-	-	-	-	-
37283 ++	-	-	-	-	-	-	-	-	-
36446 ++	+++	+	+	–	-	-	-	-	-
37833 +++	++	+	+	–	-	-	-	-	-
36326 +++	-	-	-	-	-	-	-	-	-
37349 +	-	-	-	-	-	-	-	-	-
37394 +	-	-	-	-	-	-	-	-	-
37974 ++	+++	-	-	-	-	-	-	-	-
36587 +++	-	-	-	-	-	-	-	-	-
36674 +++	+++	+++	-	–	-	-	-	-	-
37203 +	-	-	-	-	-	-	-	+	-
36432 +++	-	-	-	-	-	-	-	-	-
38868 ++	+++	+	-	-	-	-	-	-	-
36876 ++	+	+	-	–	-	-	-	-	-
37049 ++	+++	++	+	–	-	-	-	-	-
36660 ++	+++	+	-	-	-	-	-	-	-
12523 +	-	-	-	-	-	-	-	-	-
37817 ++	+	-	+	–	-	-	-	-	-
37439 ++	++	-	-	-	-	-	-	-	-
39195 ++	++	-	-	-	-	-	-	-	-
38868 ++	+++	+	-	–	-	-	-	-	-
37989 +	-	-	-	-	-	-	-	-	-
37116 ++	-	-	-	-	-	-	-	-	-
38685 ++	+	+	-	-	-	-	-	-	-
36560 +++	-	-	-	-	-	-	-	-	-
37905 +	-	-	-	-	-	-	-	-	-

38130 +	-	+++	-	-	-	+	-	-	-
37994 +	-	+	-	–	-	-	-	-	-
37249 +	-	-	-	-	-	-	-	-	-
37559 ++	+++	+	+	–	-	-	-	-	-
38931 +++	+++	++	+++	––	-	-	-	-	-
37272 +++	+++	++	+	––	-	-	-	-	-
38972 +	+	-	-	-	-	-	-	-	-
38806 +	-	-	-	-	-	-	-	-	-
37616 +	-	-	-	-	-	-	-	-	-
38095 ++	-	-	-	-	-	-	-	-	-
37625 ++	+++	+	++	-	-	-	-	-	-
36500 ++	++	-	-	-	-	-	-	-	-
36368 ++	-	+	-	–	-	-	-	-	-
37487 +	-	-	-	-	-	-	-	-	-
37823 +	++	+	-	-	-	-	-	-	-
37036 +	+++	+	-	-	-	-	-	-	-
37280 ++	-	-	-	-	-	-	-	-	-
38873 +	+	+	-	–	-	-	-	-	-
37708 +++	+++	-	+	-	-	-	-	-	-
39631 +	++	+	-	-	-	-	-	-	-
36945 +	-	-	-	-	-	-	-	-	-
36589 +++	+++	++	-	–	-	-	-	-	-
39634 +	-	-	-	-	-	-	-	-	-
38961 +	-	-	-	-	-	-	-	-	-
20377 +	+	+	-	–	-	-	-	-	-
37989 +	-	-	-	–	-	-	-	-	-
17821 +	-	-	-	-	-	-	-	-	-
37013 +++	-	-	-	-	-	-	-	-	-
36674 +++	+++	+++	-	–	-	+	–	+	-
37846 +	-	-	-	-	-	-	-	-	-
37022 +++	+++	+++	++	–	-	-	-	-	-
17499 +	+	+	-	–	-	-	-	-	-
12255 +	-	-	-	-	-	-	-	-	-

37850 +	-	-	-	-	-	-	-	-	-
40285 +	+	-	-	-	-	-	-	-	-
36938 ++	+++	++	+	–	-	-	-	-	-
37929 +	-	-	-	-	-	-	-	-	-
37349 ++	-	-	-	-	-	-	-	-	-
39545 +	-	-	-	-	-	-	-	-	-
11920 +	-	-	-	-	-	-	-	-	-
37041 ++	-	-	-	-	-	-	-	-	-
37439 ++	++	-	-	-	-	-	-	-	-
39261 +	-	-	-	-	-	-	-	-	-
38251 +++	++	+	+	–	-	-	-	-	-
37501 +++	+++	+++	+++	––	-	-	-	-	-
11720 ++	-	-	-	-	-	-	-	-	-
37675 +	+	+	-	-	-	-	-	-	-
36937 ++	+++	+	-	–	-	-	-	-	-
37528 ++	+++	+	+	–	-	-	-	-	-
41722 +	-	-	-	-	-	-	-	-	-
39134 ++	+	+	+	–	-	-	-	-	-
37593 ++	++	+	+	–	-	-	-	-	-
37520 ++	+++	+	+	–	-	-	-	-	-
38130 +	-	+++	-	-	-	-	-	-	-
38025 +++	+++	+	+	––	-	-	-	-	-
12162 +	-	-	-	-	-	-	-	-	-
37429 ++	+++	++	+	–	-	-	-	-	-
38553 ++	-	-	-	-	-	-	-	-	-
38286 +	-	-	-	-	-	-	-	-	-
37218 +	-	-	-	-	-	-	-	-	-
36410 ++	-	-	-	-	-	-	-	-	-
37113 ++	+++	-	-	-	-	-	-	-	-
38265 +++	-	-	-	-	-	-	-	-	-
36865 +++	-	-	-	-	-	-	-	-	-
37199 ++	++	-	-	-	-	-	-	-	-
37487 +	-	-	-	-	-	-	-	-	-

37437 ++	+	-	-	-	-	-	-	-	-
12441 ++	-	-	-	-	-	-	-	-	-
39145 +	-	-	-	-	-	-	-	-	-
17882 +	+	-	-	-	-	-	-	-	-
37712 +	+++	+	+	–	-	-	-	-	-
39229 +	+	-	-	-	-	-	-	-	-
38911 +++	-	-	-	-	-	-	-	-	-
37848 +	-	-	-	-	-	-	-	-	-
38286 +	-	-	-	-	-	-	-	-	-
39570 +	++	+	+	–	-	-	-	-	-
40823 +	-	-	-	-	-	-	-	-	-
37578 +	+	+	-	–	-	-	–	-	-
18899 +	+	-	-	-	-	-	-	-	-
37817 ++	+	-	+	-	-	-	-	-	-
40462 ++	-	-	-	-	-	-	-	-	-
17986 +++	++	+++	+	–	-	-	-	-	-
37273 +	+	-	-	-	-	-	-	-	-
37713 ++	-	-	-	-	-	-	-	-	-
37352 ++	+++	+	-	–	-	-	-	-	-
38312 ++	++	+	-	–	-	-	-	-	-
36862 +	+	+	-	-	-	-	-	-	-
36245 ++	-	-	-	-	-	-	-	-	-
37335 ++	+++	++	++	–	-	-	-	-	-
36721 ++	-	-	-	-	-	-	-	-	-
18173 +++	++	+	+	–	-	-	-	-	-
39954 +	++	+	-	-	-	-	-	-	-
38944 +	-	-	-	-	-	-	–	+	-
37338 +++	-	-	-	-	-	-	-	-	-
40667 +	-	-	-	–	-	-	-	-	-
36684 +++	+++	+	-	-	-	-	-	-	-
37097 +	-	-	-	-	-	-	–	-	-
12361 +	-	-	-	-	-	-	-	-	-
39431 +	-	-	-	-	-	-	-	-	-

38081 +	-	-	-	-	-	-	-	-	-
40344 +	+	+	+	–	-	-	-	-	-
38209 +	++	-	-	-	-	-	-	-	-
39203 +	-	-	-	-	-	-	-	-	-
36545 +++	+++	+++	+	-	-	-	-	-	-
37718 ++	+++	+++	+++	–	-	-	-	-	-
36597 +	-	-	-	-	-	-	-	-	-
37327 +++	+	+	-	-	-	-	-	-	-
38873 +	+	+	+	–	-	-	-	-	-
37119 +	-	-	-	-	-	-	-	-	-
37625 +++	+++	++	+	–	-	-	-	-	-
40344 +	+	+	+	–	-	-	-	-	-
12796 +	-	-	-	-	-	-	-	-	-
11707 +	-	-	-	-	-	-	-	-	-
37581 ++	+++	+	-	-	-	-	-	-	-
39848 ++	-	-	-	-	-	-	-	-	-
37280 ++	-	-	-	-	-	-	-	-	-
37145 ++	+	-	-	-	-	-	-	-	-
37850 +	-	-	-	-	-	-	-	-	-
37933 ++	+++	+	++	–	-	-	-	-	-
37359 ++	++	+	-	-	-	-	-	-	-
37184 ++	++	+	-	-	-	-	-	-	-
38081 +	-	-	-	-	-	-	-	-	-
36515 +	-	-	-	-	-	-	-	-	-
36586 +++	+++	+++	-	–	-	-	-	-	-
36781 ++	-	+	-	-	-	-	-	-	-
36887 ++	-	-	-	-	-	-	-	-	-
37741 +++	+++	+	++	–	-	-	-	-	-
36734 +++	+++	+++	+++	––	-	-	-	-	-
36472 +++	+++	++	-	-	-	-	-	-	-
37599 +	-	-	-	-	-	-	-	-	-
17590 +	++	-	-	–	-	-	-	-	-
17711 +	+++	+	+	–	-	-	-	-	-

37529 +++	-	-	+	-	-	-	-	-	-
19043 +	+++	++	-	-	-	-	-	-	-
12113 ++	-	-	-	-	-	-	-	-	-
11516 +	-	-	-	-	-	-	-	-	-
37113 ++	+++	-	-	-	-	-	-	-	-
37759 +	+	-	-	-	-	-	-	-	-
36589 +++	+++	++	-	–	-	-	-	-	-
20014 +++	+++	+	+	–	-	-	-	-	-
17038 ++	+++	+	-	-	-	-	-	-	-
11440 +	-	-	-	-	-	-	-	-	-
37712 +	+++	+	+	–	-	-	-	-	-
37626 ++	+	-	-	-	-	-	-	-	-
39782 +	++	-	-	-	-	-	-	-	-
38008 +	-	-	-	-	-	-	-	-	-
38692 +	-	-	-	–	-	-	-	-	-
38251 +++	++	+	-	–	-	-	-	-	-
36853 ++	-	+	-	-	-	-	-	-	-
36865 +++	-	-	-	-	-	-	-	-	-
36781 ++	-	+	-	-	-	+	-	-	-
18899 ++	+	+	-	–	-	-	-	-	-
37616 +	-	-	-	-	-	-	-	-	-
37850 +	-	-	-	-	-	-	-	-	-
37177 ++	+	-	-	-	-	-	-	-	-
37153 +++	+++	++	+++	––	-	-	-	-	-
39889 +	+++	++	+	–	-	-	-	-	-
38744 +	-	-	-	-	-	-	-	-	-
38391 +	+	-	-	-	-	-	-	-	-
37616 +	-	-	-	-	-	-	-	-	-
11516 +	-	-	-	-	-	-	-	-	-
38972 +	++	-	-	-	-	-	-	-	-
39634 +	-	-	-	-	-	-	-	-	-
12523 ++	-	-	-	-	-	-	-	-	-
38343 ++	+++	+	+	–	-	-	-	-	+

38840 ++	+	+	-	–	-	-	-	-	-
39547 ++	+	-	-	-	-	-	-	-	-
39134 ++	+	+	+	—	-	-	-	-	-
36501 +++	-	+	-	-	-	-	-	-	-
37226 +	-	-	-	-	-	-	-	-	-
38245 ++	-	-	-	-	-	-	-	-	-
36505 +++	++	+++	-	–	-	-	-	-	-
38025 +++	+++	+	+	—	-	-	-	-	-
39547 ++	+	-	-	-	-	-	-	-	-
37927 +	-	-	-	-	-	-	-	-	-
36812 +++	+	+++	+	–	-	-	-	-	-
37015 ++	-	-	-	-	-	-	-	-	-
38294 ++	++	+	-	–	-	-	-	-	-
38278 +	-	-	-	-	-	-	-	-	-
37108 ++	+++	+	-	-	-	-	-	-	-
39080 +	-	-	-	-	-	-	-	-	-
12796 +	-	-	-	-	-	-	-	-	-
17038 ++	+++	+	-	-	-	-	-	-	-
37716 ++	+	-	-	-	-	-	-	-	-
41713 ++	-	-	-	-	-	-	-	-	-
37838 +	-	-	-	-	-	-	-	-	-
37323 +	+	-	-	-	-	-	-	-	-
37624 ++	-	-	-	-	-	-	-	-	-
17835 +	-	-	-	-	-	-	-	-	-
37741 +++	+++	-	++	-	-	-	-	-	-
38798 +	-	-	-	-	-	-	-	-	-
39779 +	-	-	-	-	-	-	-	-	-
37506 ++	-	+	-	–	-	-	-	-	-
17882 +	+	+	-	-	-	-	-	-	-
17535 ++	++	+	-	-	-	-	-	-	-
17060 +	+++	-	-	-	-	-	-	-	-
38442 +	-	-	-	-	-	-	-	-	-
38209 +	++	-	-	-	-	-	-	-	-

37581 ++	+++	+	-	–	-	-	-	-	-
39848 +	-	-	-	-	-	-	-	-	-
38371 ++	++	-	-	-	-	-	-	-	-
36450 ++	-	++	-	-	-	-	-	-	-
20423 +	+	-	-	-	-	-	-	-	-
36690 ++	+++	+	-	-	-	-	-	-	-
39603 +	+++	+	-	-	-	-	-	-	-
18089 +++	+	-	-	-	-	-	-	-	-
37010 +++	+	-	-	-	-	-	-	-	-
38081 +	-	-	-	-	-	-	-	-	-
39077 +	-	-	-	-	-	-	-	-	-
37626 ++	+	-	-	-	-	-	-	-	-
37693 +	-	-	-	-	-	-	-	-	-
39473 +	-	-	-	-	-	-	-	-	-
40490 +	-	-	-	-	-	-	-	-	-
36668 +	+	+	-	-	-	-	-	-	-
37529 +++	-	+	+	-	-	-	-	-	-
37541 ++	-	-	-	-	-	-	-	-	-
38442 +	-	-	-	-	-	-	-	-	-
39115 ++	-	-	-	-	-	-	-	-	-
39261 +	-	-	-	-	-	-	-	-	-
40647 +	+	-	++	-	-	-	-	-	-
37284 ++	+	-	-	-	-	-	-	-	-
36339 ++	+	-	-	-	-	-	-	-	-
37541 ++	-	-	-	-	-	-	-	-	-
37920 +	+	-	-	-	-	-	-	-	-
37161 +++	+	++	+++	––	-	-	-	-	-
40065 +	++	-	-	-	-	-	-	-	-
37437 ++	+	-	-	-	-	-	-	-	-
40521 ++	+	+	-	-	-	-	-	-	-
12737 +++	-	-	-	-	-	-	-	-	-
39889 +	++	++	+	–	-	-	-	-	-
36791 ++	-	-	-	-	-	-	-	-	-

39389 +	-	-	-	-	-	-	-	-	-
36352 ++	-	-	-	-	-	-	-	-	-
38110 +	-	-	-	-	-	-	-	-	-
38883 +	+++	+	+	–	-	-	-	-	-
17637 ++	-	-	-	-	-	-	-	-	-
41713 +	-	-	-	-	-	-	-	-	-
38150 ++	+++	+++	-	-	-	-	-	-	-
17657 +	-	-	-	-	-	-	-	-	-
38274 +	-	-	-	-	-	-	-	-	-
41340 +	-	-	-	-	-	-	-	-	-
13925 +	-	-	-	-	-	-	-	-	-
38166 +	+	-	-	-	-	-	-	-	-
36919 +++	-	-	-	-	-	-	-	-	-
37693 +	+	+	-	-	-	-	-	-	-
37409 +	+	+	-	-	-	-	-	-	-
39063 +	-	-	-	-	-	-	-	-	-
37164 ++	-	+	-	-	-	-	-	-	-
41889 ++	-	-	-	-	-	-	-	-	-
36757 +	-	-	-	-	-	-	-	-	-
39850 +	-	-	-	-	-	-	-	-	-
18789 +	-	-	-	-	-	-	-	-	-
38834 ++	-	-	-	-	-	-	-	-	-
37399 +	+	-	-	–	-	-	-	-	-
38454 +	-	-	-	-	-	-	-	-	-
38576 ++	-	-	+	-	-	-	-	-	-
36757 +	-	-	-	-	-	-	-	-	-
36547 +	-	-	-	-	-	-	-	-	-
37604 ++	-	-	-	-	-	-	-	-	-
37604 +	-	-	-	-	-	-	-	-	-
37494 ++	+++	+++	-	–	-	-	-	-	-
12030 +	-	-	-	-	-	-	-	-	-
38608 +++	-	-	-	-	-	-	-	-	-
38554 +	-	-	+	-	-	-	-	-	-

18354 +	-	-	-	-	-	-	-	-	-
37270 +	-	-	-	-	-	-	-	-	-
36771 +	-	-	-	-	-	-	-	-	-
36892 +++	-	-	-	-	-	-	-	-	-
19710 +++	-	-	-	-	-	-	-	-	-
38035 +	-	-	-	-	-	-	-	-	-
36794 +	-	-	-	-	-	-	-	-	-
17035 +++	+	+	-	-	-	-	-	-	-
37960 +	-	+	-	-	-	-	-	-	-
18857 ++	-	+	-	-	-	-	-	-	-
38812 +	-	+	-	-	-	-	-	-	-
36400 ++	-	-	-	-	-	-	-	-	-
37057 +++	-	-	-	-	-	-	-	-	-
17830 ++	-	-	-	-	-	-	-	-	-
37228 +	-	-	-	-	-	-	-	-	-
37178 +	+++	+	-	-	-	-	-	-	-
38001 +	-	-	-	-	-	+	-	+	-
38608 ++	+	-	-	-	-	-	-	-	-
36322 ++	+	+	-	-	-	-	-	-	-
38162 +	-	-	-	-	-	-	-	-	-
36267 ++	-	-	-	-	-	-	-	-	-
37130 +	-	-	-	-	-	-	-	-	-
41308 +	++	+	+	–	-	-	-	-	-
18765 +	-	-	-	-	-	-	-	-	-
12707 +++	-	-	-	-	-	-	-	-	-
38043 +	-	-	-	-	-	-	-	-	-
38162 +	-	-	-	-	-	-	-	-	-
36846 +	-	-	-	-	-	-	-	-	-
38314 +	-	-	-	-	-	-	-	-	-
36436 +	-	-	-	-	-	-	-	-	-
37167 ++	-	-	-	-	-	-	-	-	-
36494 ++	+	+	+	–	-	-	-	-	-
36870 +	-	-	-	–	-	-	-	-	-

17754 ++	+	-	-	-	-	-	-	-	-
20377 +	+	+	-	-	-	-	-	-	-
37510 +	+++	+	-	-	-	-	-	-	-
37120 +	++	+++	+	–	-	-	-	-	-
37742 +	-	-	-	-	-	-	-	-	-
36799 +	-	-	-	-	-	-	-	-	-
37150 +	-	-	-	-	-	-	-	-	-
37563 +	-	-	-	-	-	-	-	-	-
36785 +	-	-	-	-	-	-	-	-	-
36821 +	-	-	-	-	-	-	-	-	-
36506 ++	-	-	-	-	-	-	-	-	-
37177 ++	+	-	-	-	-	-	-	-	-
17672 +	+	-	-	-	-	-	-	-	-
37201 +	-	-	-	-	-	-	-	-	-
37379 +	-	-	-	-	-	-	-	-	-
41674 ++	-	-	-	-	-	-	-	-	-
39150 +	-	-	-	-	-	-	-	-	-
36797 ++	+++	+	-	–	-	-	-	-	-
40437 +	-	-	-	-	-	-	-	-	-
17968 +	-	-	-	-	-	-	-	-	-
40083 +	+	-	-	-	-	-	-	-	-
18036 ++	-	-	-	-	-	-	-	-	-
37576 +	-	-	-	-	-	-	-	-	-
11707 +	-	-	-	-	-	-	-	-	-
17675 ++	+++	+++	+++	–	-	-	-	-	-
37414 +	+	+	-	-	-	-	-	-	-
37150 +	-	-	-	-	-	-	-	-	-
17039 ++	-	+	-	-	-	-	-	-	-
38186 +	++	+	+	–	-	-	-	-	-
36472 +++	+++	+	-	–	-	-	-	-	-
36624 ++	+++	+	-	–	-	-	-	-	-
18765 +	-	-	-	-	-	-	-	-	-
36843 ++	-	-	-	-	-	-	-	-	-

36642	+++	+++	++	+	–	-	+	-	-	-
36846	+	-	-	-	-	-	-	-	-	-
37902	+	-	-	-	-	-	-	-	-	-
17711	+	+++	+	-	–	-	-	-	-	-
17826	++	+	-	-	–	-	-	-	-	-
36849	+	-	-	-	-	-	-	-	-	-
37679	++	+++	-	-	–	-	-	-	-	-
36846	+	-	-	-	-	-	-	-	-	-
36877	+	+++	+	-	–	-	-	-	-	-
36558	++	-	++	-	–	-	-	-	-	-
38453	++	-	-	-	-	-	-	-	-	-
36597	+	-	-	-	-	-	-	-	-	-
36370	++	+	+	-	–	-	-	-	-	-
36917	++	+++	++	+	–	-	-	-	-	-
20423	++	+	-	-	-	-	-	-	-	-
37014	++	++	+	+	–	-	-	-	-	-
12441	++	-	-	-	-	-	-	-	-	-
37664	+++	+++	+	+	–	-	-	-	-	-
36913	++	+++	++	+++	–	-	-	-	-	-
37401	++	+++	+	+	–	-	-	-	-	-
36624	++	+++	+	-	-	-	-	-	-	-
36954	+	-	-	-	-	-	-	-	-	-
36334	+++	+	++	-	-	-	-	-	-	-
36446	++	+++	+	+	–	-	-	-	-	-
37084	++	+	-	-	-	-	-	-	-	-
37262	++	-	+	-	–	-	-	-	-	-
38071	+	-	-	-	-	-	-	-	-	-
19288	++	-	-	-	-	-	-	-	-	-
37616	+	-	-	-	-	-	-	-	-	-
18789	+	-	-	-	-	-	-	-	-	-
36963	+++	+++	+	+++	–	-	-	-	-	-
36830	+	+	-	-	-	-	-	-	-	-
38693	+	+	+	-	-	-	-	-	-	-

36877 +	+++	+	+	–	-	-	-	-	-
17926 +	-	-	-	-	-	-	-	-	-
36597 +	-	-	-	-	-	-	-	-	-
37114 ++	+	+	+	–	-	-	-	-	-
36381 +	-	-	-	-	-	-	-	-	-
36756 ++	++	-	-	-	-	-	-	-	-
38692 +	-	-	-	–	-	-	-	-	-
17047 ++	+	-	-	-	-	-	-	-	-
36597 +	-	-	-	-	-	-	-	-	-
37309 ++	+++	+	+	–	-	-	-	-	-
36938 ++	+++	++	+	–	-	-	-	-	-
38961 +	-	-	-	–	-	-	-	-	-
38886 +	+	-	+	–	-	-	-	-	-
36602 ++	+++	+	-	–	-	-	-	-	-
36444 +++	+	-	-	–	-	-	-	-	-
38697 ++	-	-	-	-	-	-	-	-	-
19125 +++	+++	+	++	–	-	-	-	-	-
17036 +++	+++	+	+	––	-	-	-	-	-
19575 ++	++	-	-	-	-	-	-	-	-
38214 +	+	-	-	-	-	-	-	-	-
36326 +++	-	-	-	-	-	-	-	-	-
18225 +	-	-	-	-	-	-	-	-	-
41308 +	++	+	+	-	-	-	-	-	-
38697 +	-	-	-	-	-	-	-	-	-
37218 ++	-	-	-	-	-	-	-	-	-
37510 +	+++	+	+	-	-	-	-	-	-
36544 ++	+	+	-	-	-	-	-	-	-
38554 +	-	-	-	–	-	-	–	-	-
17708 ++	+++	++	+	–	-	-	-	-	-
37283 ++	-	-	-	-	-	-	-	-	-
36399 +++	+++	++	-	–	-	-	-	-	-
36680 ++	+++	+	-	-	-	-	-	-	-
38363 +	-	-	-	-	-	-	-	-	-

38453 ++	+	+	-	-	-	-	-	-	-
36500 ++	+	-	-	-	-	-	-	-	-
36785 +	-	-	-	-	-	-	-	-	-
38130 +	-	++	-	–	-	-	-	-	-
17602 +	-	-	+	-	-	-	-	-	-
37664 +++	+++	+	-	–	-	-	-	-	-
36669 ++	+++	-	-	–	-	-	-	-	-
39714 ++	+	+	-	–	-	-	-	+	-
37143 +++	+++	+	+	–	-	-	-	-	-
37431 +	-	-	-	-	-	-	-	-	-
36440 +++	+++	+	+	–	-	-	-	-	-
37139 +++	+++	+	+	–	-	-	-	-	-
17060 +	++	-	-	-	-	-	-	-	-
38387 +	-	-	-	-	-	-	-	-	-
37412 ++	+++	++	+	–	-	-	-	-	-
37902 +	-	-	-	-	-	-	-	-	-
37848 +	-	-	-	-	-	-	-	-	-
37429 ++	+++	+	++	–	-	-	-	-	-
36337 ++	-	-	-	-	-	-	-	-	-
36720 +++	+++	++	+	––	-	-	-	-	-
18566 ++	-	-	-	-	-	-	-	-	-
36428 +	-	-	-	-	-	-	-	-	-
37278 +	+	++	+	–	-	-	-	-	-
36827 +	-	+	-	–	-	+	-	-	-
38964 +	-	-	-	-	-	-	-	-	-
36756 ++	+	-	-	-	-	-	-	-	-
37036 +	+++	+	-	-	-	-	-	-	-
38285 +	-	-	-	-	-	-	-	-	-
39640 +	-	+	-	-	-	-	-	-	-
37716 +	+	-	-	-	-	-	-	-	-
37084 ++	+	-	-	-	-	-	-	-	-
14376 ++	-	-	-	-	-	-	-	-	-
17590 +	++	+	-	–	-	-	-	-	-

36812 +++	+	+++	+	–	-	-	-	-	-
36887 ++	-	-	-	-	-	-	-	-	-
39195 +	++	-	-	-	-	-	-	-	-
37097 +	-	-	-	-	-	-	-	-	-
36846 +	-	-	-	-	-	-	-	-	-
36762 +++	+++	+	+	–	-	-	-	-	+
36838 +	-	-	-	-	-	-	-	-	-
36502 +++	-	-	-	-	-	-	-	-	-
37616 +	-	-	-	-	-	-	-	-	-
18065 +	-	-	+	-	-	-	-	-	-
19755 +	+	-	-	-	-	-	-	-	-
39203 +	-	-	-	-	-	-	-	-	-
41839 +	+++	-	-	-	-	-	-	-	-
37291 +	-	-	-	-	-	-	-	-	-
36680 ++	+++	-	-	-	-	-	-	+	-
36501 ++	-	+	-	-	-	-	-	-	-
37456 +	-	-	-	-	-	-	-	-	-
39640 +	-	-	-	-	-	-	-	-	-
12113 ++	-	-	-	-	-	-	-	-	-
37823 +	+++	+	-	-	-	-	-	-	-
38014 ++	+++	-	+	-	-	-	-	-	-
20365 +	-	-	-	-	-	-	-	+	-
37365 +++	++	++	+	–	-	-	-	-	-
14376 ++	-	-	-	-	-	-	-	-	-
37631 ++	-	-	-	-	-	-	-	-	-
38201 ++	-	-	-	-	-	-	-	-	-
37183 ++	+++	++	++	–	-	-	-	-	-
37084 ++	+	-	-	-	-	-	-	-	-
37072 +++	+	+++	-	-	-	-	-	-	-
36832 ++	+	+	-	-	-	-	-	+	-
37593 ++	++	+	+	–	-	-	-	-	-
36558 ++	+	++	+	-	-	-	-	-	-
36792 ++	-	-	-	-	-	-	-	-	-

19125 +++	+++	+	++	--	-	-	-	-	-
38123 +	-	-	-	-	-	-	-	-	-
36800 +++	+++	+	+	-	-	-	-	-	-
39203 +	-	-	-	-	-	-	-	-	-
36934 +	-	-	-	-	-	-	-	-	-
38648 +	-	-	-	-	-	-	-	-	-
39548 +	+	-	-	-	-	-	-	-	-
37070 ++	-	-	-	-	-	-	-	-	-
38265 +++	-	-	-	-	-	-	-	-	-
38216 +	-	-	-	-	-	-	-	-	-
37280 ++	-	-	-	-	-	-	-	-	-
17535 ++	++	-	-	-	-	-	-	-	-
37349 +	-	-	-	-	-	-	-	-	-
37137 ++	+	-	-	-	-	-	-	-	-
38017 +	-	-	-	-	-	-	-	-	-
14376 ++	-	-	-	-	-	-	-	-	-
17694 +	-	-	-	-	-	-	-	-	-
37394 +	-	-	-	-	-	-	-	-	-
37401 ++	+++	+	++	-	-	-	-	-	-
36835 +	+	-	-	-	-	-	-	-	-
37903 +	-	-	-	-	-	-	-	-	-
37310 ++	-	-	-	-	-	-	-	-	-
40490 +	-	-	-	-	-	-	-	-	-
39072 +	+	-	-	-	-	-	-	-	-
37934 ++	-	-	-	-	-	-	-	-	-
37230 +	+	+	-	-	-	-	-	-	-
11720 ++	-	-	-	-	-	-	-	-	-
38245 ++	-	-	-	-	-	-	-	-	-
38371 +	++	-	-	-	-	-	-	-	-
38540 +	-	-	-	-	-	-	-	-	-
38744 +	-	-	-	-	-	-	-	-	-
36322 ++	+	+	-	-	-	-	-	-	-
39207 +	-	-	-	-	-	-	-	-	-

37010 ++	++	-	-	-	-	-	-	-	-
38393 ++	-	-	-	-	-	-	-	-	-
38130 +	-	+++	-	-	-	-	-	-	-
38540 +	-	-	-	-	-	-	-	-	-
37148 +++	+++	+++	++	--	-	-	-	-	-
18708 +	-	-	-	-	-	-	-	-	-
18708 +	-	-	-	-	-	-	-	-	-
38391 +	+	-	-	-	-	-	-	-	-
41706 ++	-	-	-	-	-	-	-	-	-
36660 ++	+++	+	-	-	-	-	-	-	-
38312 +	++	+	-	-	-	-	-	-	-
37871 +	-	-	-	-	-	-	-	-	-
11720 ++	-	-	-	-	-	-	-	-	-
38845 +	-	-	-	-	-	-	-	-	-
36720 +++	++	++	+	--	-	-	-	-	-
41340 +	-	-	-	-	-	-	-	-	-
40521 ++	-	+	-	-	-	-	-	-	-
18712 +	-	-	-	-	-	-	-	-	-
36273 ++	-	-	-	-	-	-	-	-	-
17694 +	-	-	-	-	-	-	-	-	-
38286 +	+	-	-	-	-	-	-	-	-
17590 ++	++	+	-	-	-	-	-	-	-
38685 ++	+	+	-	-	-	-	-	-	-
11720 ++	-	-	-	-	-	-	-	-	-
36981 ++	-	-	-	-	-	-	-	-	-
36998 +	-	-	-	-	-	-	-	-	-
38455 +	-	-	-	-	-	-	-	-	-
37107 +	-	-	-	-	-	-	-	-	-
18696 +	-	-	-	-	-	-	-	-	-
38877 +	-	-	-	-	-	-	-	-	-
38624 +	+++	-	-	-	-	-	-	-	-
37072 ++	-	+++	-	-	-	-	-	-	-
37900 +	++	-	-	-	-	-	-	-	-

36447	+++	+	+++	-	-	-	-	-	-	-
38278	+	-	-	-	-	-	-	-	-	-
36543	++	+++	-	++	-	-	-	-	-	-
39631	+	++	-	-	-	-	-	-	-	-
36525	+	-	-	-	-	-	-	-	-	-
36821	+	-	-	-	-	-	-	-	-	-
38880	+	+	-	-	-	-	-	-	-	-
16600	+	-	-	-	-	-	-	-	-	-
39203	+	-	-	-	-	-	-	-	-	-
36816	+++	-	-	-	-	-	-	-	-	-
17578	++	+++	-	-	-	-	-	-	-	-
37616	+	-	-	-	-	-	-	-	-	-
41844	+	-	-	+++	-	-	-	-	-	-
38880	+	+	-	-	-	-	-	-	-	-
38278	+	-	-	-	-	-	-	-	-	-
39669	+	-	-	-	-	-	-	-	-	-
38166	+	-	-	-	-	-	-	-	-	-
19339	+	-	-	-	-	-	-	-	-	-
40823	+	-	-	-	-	-	-	-	-	-
18231	+++	++	-	-	-	-	-	-	-	-
17324	+	-	-	-	-	-	-	-	-	-
17821	+	-	-	-	-	-	-	-	-	-
37323	+	+	-	-	-	-	-	-	-	-
37493	++	-	-	-	-	-	-	-	-	-
39738	+	+	+	-	-	-	-	-	-	-
39147	+	-	-	-	-	-	-	-	-	-
40036	+	-	-	-	-	-	-	-	-	-
40462	++	-	-	-	-	-	-	-	-	-
17726	+	-	-	-	-	-	-	-	-	-
39063	++	-	-	-	-	-	-	-	-	-
39738	+	+	+	-	-	-	-	-	-	-
38989	+	+++	++	-	-	-	-	-	-	-
39135	+	+++	-	-	-	-	-	-	-	-

38647 +	-	-	-	-	-	-	-	-	-
40943 +	-	-	+	-	-	-	-	-	-
18513 +	-	-	-	-	-	-	-	-	-
38576 +	-	-	-	-	-	-	-	-	-
40285 +	+	-	-	-	-	-	-	-	-
18518 +	-	-	-	-	-	-	-	-	-
17047 ++	++	-	-	-	-	-	-	-	-
36267 ++	-	-	-	-	-	-	-	-	-
36843 +++	-	-	-	-	-	-	-	-	-
40002 +	+	-	-	-	-	-	-	-	-
38159 +	-	-	-	-	-	-	-	-	-
36725 ++	+	-	-	-	-	-	-	-	-
37925 +	-	-	-	-	-	-	-	-	-
17535 +	++	-	-	-	-	-	-	-	-
16652 +	++	-	-	-	-	-	-	-	-
37339 ++	-	-	-	-	-	-	-	-	-
18835 ++	++	+++	-	–	-	-	-	-	-
17675 ++	+++	+++	++	–	-	-	-	-	-
36522 ++	-	+	++	–	-	-	-	-	-
37925 +	-	+	-	-	-	-	-	-	-
38285 +	-	-	-	-	-	-	-	-	-
17034 ++	-	-	-	-	-	-	-	-	-
40659 +	+++	++	-	-	-	-	-	-	-
36351 +++	+++	+++	-	–	-	-	-	-	-
36327 +	+	-	-	-	-	-	-	-	-
37014 ++	+	+	-	-	-	-	-	-	-
36440 +++	+++	-	+	–	-	-	-	-	-
37438 ++	+	+	+	–	-	-	-	-	-
19005 +	-	-	-	-	-	-	-	-	-
37001 ++	-	-	+	–	-	-	-	-	-
37606 +	-	-	-	-	-	-	-	-	-
36532 +	-	-	-	-	-	-	-	-	-
36474 +	+++	+	-	–	-	-	-	-	-

39850 +	-	-	-	-	-	-	-	-	-
16638 ++	-	-	-	–	-	-	-	-	-
37233 +	-	-	-	-	-	-	-	-	-
38205 +	+	+	-	-	-	-	-	-	-
38092 +	-	-	-	-	-	-	-	-	-
37184 ++	++	+	+	–	-	-	-	-	-
38584 +	-	+	+	-	-	-	-	-	-
18231 +++	+	+	-	–	-	-	-	-	-
37967 +	-	-	-	-	-	-	-	-	-
37127 +	-	-	-	-	-	-	-	-	-
39596 +	-	-	-	-	-	-	-	-	-
38961 +	-	-	-	-	-	-	-	-	-
36624 ++	+++	+	-	-	-	-	-	-	-
38043 +	-	-	-	-	-	-	-	-	-
37143 ++	+++	+	-	–	-	-	-	-	-
37057 +++	-	-	-	-	-	-	-	-	-
38961 +	-	-	-	-	-	-	-	-	-
39531 +	-	-	-	-	-	-	-	-	-
36628 +	-	-	-	-	-	-	-	-	-
18857 +++	+	++	-	-	-	-	-	-	-
37902 +	-	-	+	-	-	-	-	-	-
18210 +	-	-	-	-	-	-	-	-	-
19761 +	-	-	-	-	-	-	-	-	-
36846 +	-	-	-	-	-	-	-	-	-
19230 +	-	-	-	-	-	-	-	-	-
38156 +	-	-	-	-	-	-	-	-	-
36282 +	-	+	-	–	-	-	-	-	-
17826 +	+	-	-	-	-	-	-	-	-
37842 ++	-	-	-	-	-	-	-	-	-
37226 ++	-	-	-	-	-	-	-	-	-
37619 ++	+++	+	+	–	-	-	-	-	-
38697 +	-	-	-	-	-	-	-	-	-
36732 +	-	-	-	-	-	-	-	-	-

36271 +	-	+	-	-	-	-	-	-	-
36624 +	+++	-	-	-	-	-	-	-	-
38549 +	-	-	-	-	-	-	-	-	-
37525 +	-	-	-	-	-	-	-	-	-
18314 +	-	-	++	-	-	-	-	-	-
36272 +++	++	++	-	–	-	-	-	-	-
19337 +	-	-	-	-	-	-	-	-	-
36329 +	-	-	-	–	-	-	-	-	-
37956 +	+	-	-	-	-	-	-	-	-
37572 ++	+++	++	-	–	-	-	-	-	-
36610 ++	-	-	-	-	-	-	-	-	-
16567 +	-	-	-	-	-	-	-	-	-
17600 ++	+	-	-	-	-	-	-	-	-
36835 ++	++	+	-	-	-	-	-	-	-
37525 +	-	-	-	-	-	-	-	-	-
36643 ++	++	+	-	-	-	-	-	-	-
19561 +	-	-	-	-	-	-	-	-	-
36643 ++	++	+	-	-	-	-	-	-	-
36428 ++	-	-	-	-	-	-	-	-	-
17888 ++	+++	-	+	–	-	-	-	-	-
36256 +++	-	-	+	-	-	-	-	-	-
17619 ++	-	-	-	-	-	-	-	-	-
38534 +	++	+	-	–	-	-	-	-	-
39077 +	+	-	-	-	-	-	-	-	-
17637 +	-	-	-	-	-	-	-	-	-
38682 +	-	-	-	-	-	-	-	-	-
40437 +	-	-	-	-	-	-	-	-	-
17576 +	+	+	-	-	-	-	-	-	-
41819 ++	-	-	-	-	-	-	-	-	-
38186 +	+	+	-	–	-	-	-	-	-
37393 +	-	-	-	-	-	-	-	-	-
36272 +++	+++	++	-	–	-	-	-	-	-
37048 +	-	-	-	–	-	-	-	-	-

17754 ++	-	-	-	-	-	-	-	-	-
39669 +	-	-	-	-	-	-	-	-	-
36756 ++	++	-	-	-	-	-	-	-	-
19543 ++	-	-	-	-	-	-	-	-	-
38670 +	-	-	-	-	-	-	-	-	-
37094 +	-	-	-	-	-	-	-	-	-
37290 ++	+	+	-	–	-	-	-	-	+
19998 +	-	-	-	-	-	-	-	-	-
38670 +	-	-	-	-	-	-	-	-	-
36687 ++	-	-	-	-	-	-	-	-	-
17588 +	-	-	-	-	-	-	-	-	-
17514 ++	-	-	-	-	-	-	-	-	-
37038 +	-	+	-	-	-	-	-	-	-
38964 +	-	-	-	-	-	-	-	-	-
37148 +++	+++	+++	+	––	-	-	-	-	-
37394 +	-	-	-	-	-	-	-	-	-
38363 +	-	-	-	-	-	-	-	-	-
38081 +	-	-	-	-	-	-	-	-	-
37004 ++	+	-	-	-	-	-	-	-	-
17625 +	-	-	-	-	-	-	-	-	-
39286 +	-	-	-	-	-	-	-	-	-
18712 +	-	-	-	-	-	-	-	-	-
39170 +	-	-	-	-	-	-	-	-	-
37934 ++	-	-	-	–	-	-	-	-	-
36882 +	-	-	+	-	-	-	-	-	-
36668 ++	+	+	-	–	-	-	-	-	-
36428 +	-	-	-	-	-	-	-	-	-
36271 +	-	+	-	-	-	-	-	-	-
36866 ++	-	-	-	-	-	-	-	-	-
40837 +	-	-	-	-	-	-	-	-	-
17835 +	-	-	-	-	-	-	-	-	-
37137 ++	+	-	-	-	-	-	-	-	-
36743 +	+	+	-	-	-	-	-	-	-

38123 +	-	-	-	-	-	-	-	-	-
36502 +++	-	-	-	-	-	-	-	-	-
40954 +	++	-	-	-	-	-	-	-	-
17563 +	++	-	-	-	-	-	-	-	-
36578 +	-	-	-	-	-	-	-	-	-
37771 +	-	-	-	-	-	-	-	-	-
36428 ++	-	-	-	-	-	-	-	-	-
36870 +	-	+	-	–	-	-	-	-	-
37964 +	-	-	-	-	-	-	-	-	-
36862 +	+	+	-	-	-	-	-	-	-
36355 +	+	-	-	-	-	-	-	-	-
39175 +	-	-	-	-	-	-	-	-	-
38397 +++	-	-	-	-	-	-	-	-	-
39175 +	-	-	-	-	-	-	-	-	-
37456 +	-	-	-	-	-	-	-	-	-
40036 +	-	-	-	-	-	-	-	-	-
37349 +	-	-	-	-	-	-	-	-	-
17686 ++	+	-	+	–	-	-	-	-	-
17048 +	-	-	-	-	-	-	-	-	-
12113 ++	-	-	-	-	-	-	-	-	-
39609 +	+	+	-	-	-	-	-	-	-
38883 +	+++	+	+	–	-	-	-	-	-
36830 +	-	-	-	-	-	-	-	-	-
38014 ++	+++	-	+	-	-	-	-	-	-
37774 +	-	-	-	-	-	-	-	-	-
17514 ++	+	-	-	–	-	-	-	-	-
38915 +	-	+	-	-	-	-	-	-	-
38824 +	++	-	-	-	-	-	-	-	-
37123 +	++	-	-	-	-	-	-	-	-
37420 ++	+++	+	+	–	-	-	-	-	-
41690 +	-	-	-	-	-	-	-	-	-
38280 +++	-	-	-	-	-	-	-	-	-
39556 +	-	-	-	-	-	-	-	-	-

37624 +++	-	-	-	-	-	-	-	-	-
37199 ++	++	-	-	-	-	-	-	-	-
37380 +	-	-	-	-	-	-	-	-	-
38343 ++	+++	+	+	–	-	-	-	-	-
40936 +	-	-	-	-	-	-	-	-	-
40379 +	-	-	-	-	-	-	-	-	-
36814 +	-	-	-	-	-	-	-	-	-
37065 +	-	-	-	-	-	-	-	-	-
41691 +	+++	++	-	-	-	-	-	-	-
38397 +++	-	-	-	-	-	-	-	-	-
37900 +	++	-	-	-	-	-	-	-	-
36981 ++	-	-	-	-	-	-	-	-	-
36381 +	-	-	-	-	-	-	-	-	-
38008 +	-	-	-	-	-	-	-	-	-
39725 +	+++	-	-	-	-	-	-	-	-
37349 ++	-	+	-	–	-	-	-	-	-
36853 ++	-	-	-	-	-	-	-	-	-
38294 ++	++	+	-	–	-	-	-	-	-
37983 +	-	-	-	-	-	-	-	-	-
17686 ++	++	-	+	-	-	-	-	-	-
39545 +	-	-	-	-	-	-	-	-	-
41840 +	-	-	-	-	-	-	-	-	-
40667 +	+	+	-	-	-	-	-	-	-
38172 +	-	-	-	-	-	-	-	-	-
19005 ++	-	-	-	-	-	-	-	-	-
37838 +	-	-	-	-	-	-	-	-	-
37594 +	++	-	-	-	-	-	-	-	-
39219 +	+++	+++	-	-	-	-	-	-	-
38278 +	-	-	-	-	-	-	-	-	-
39006 +	-	-	-	-	-	-	-	-	-
41699 +	+++	-	-	-	-	-	-	-	-
36970 ++	++	-	-	-	-	-	-	-	-
17535 ++	++	-	-	-	-	-	-	-	-

17590 +	++	-	-	–	-	-	-	-	-
39672 +	++	+	-	-	-	-	-	-	-
37981 ++	-	-	-	-	-	-	-	-	-
37981 ++	++	-	-	-	-	-	-	-	-
18641 ++	-	-	-	-	-	-	-	-	-
39115 ++	-	-	-	-	-	-	-	-	-
37610 ++	+++	+	-	–	-	-	-	-	-
37065 ++	-	-	-	-	-	-	-	-	-
41884 +	-	++	-	-	-	-	-	-	-
38845 +	-	-	-	-	-	-	-	-	-
36276 +++	+++	++	+++	––	-	-	-	-	-
36970 +++	+++	-	-	-	-	-	-	-	-
37065 +	-	-	-	-	-	-	-	-	-
37065 ++	-	-	-	–	-	-	-	-	-
39548 +	+	-	-	-	-	-	-	-	-
19339 +	-	+	-	–	-	-	-	-	-
16600 ++	-	-	-	-	-	-	-	-	-
17725 ++	-	-	-	-	-	-	-	-	-
18089 +++	++	-	-	-	-	-	-	-	-
38454 +	-	-	-	-	-	-	-	-	-
16647 ++	-	-	-	-	-	-	-	-	-
16663 +	-	-	-	-	-	-	-	-	-
37164 ++	-	-	-	-	-	-	-	-	-
38824 ++	++	-	-	-	-	-	-	-	-
17874 +	-	-	-	-	-	-	-	-	-
37940 ++	++	-	-	–	-	-	-	-	-
37740 +	-	-	-	-	-	-	-	-	-
36890 ++	++	-	-	-	-	-	-	-	-
37493 +	-	-	-	-	-	-	-	-	-
19305 +	+++	-	-	-	-	-	-	-	-
37940 ++	+	-	-	-	-	-	-	-	-
37494 ++	+++	-	+	–	-	-	-	-	-
36890 +	++	-	-	-	-	-	-	-	-

37289 +	+	-	-	-	-	-	-	-	-
17571 +++	+	-	+	-	-	-	-	-	-
37632 +	-	-	-	-	-	-	-	-	-
36276 +++	+++	+	++	-	-	-	-	-	-
36529 +++	+++	++	-	-	-	-	-	-	-
38205 +	-	-	-	-	-	-	-	-	-
36529 ++	+++	++	-	-	-	-	-	-	-
36599 ++	++	-	-	-	-	-	-	-	-
18969 +	-	-	-	-	-	-	-	-	-
17874 ++	-	-	-	-	-	-	-	-	-
37339 ++	-	+	-	-	-	-	-	-	-
39951 +	-	-	-	-	-	-	-	-	-
37679 ++	+++	-	-	-	-	-	-	-	-
17499 ++	+	-	-	-	-	-	-	-	-
36599 ++	++	-	-	-	-	-	-	-	-
37233 +	-	-	-	-	-	-	-	-	-
17871 +	+	-	-	-	-	-	-	-	-
36771 +	-	+	-	-	-	-	-	-	-
37606 +	-	-	-	-	-	-	-	-	-
17619 ++	-	-	-	-	-	-	-	-	-
19136 +	+	-	-	-	-	-	-	-	-
36532 +	-	-	-	-	-	-	-	-	-
39133 +	+	+	-	-	-	-	-	-	-
19221 +	-	+	-	-	-	-	-	-	-
37001 ++	-	-	-	-	-	-	-	-	-
36767 ++	+++	-	-	-	-	-	-	-	-
19761 +	-	-	-	-	-	-	-	-	-
17600 ++	+	-	-	-	-	-	-	-	-
17034 ++	-	-	-	-	-	-	-	-	-
18641 ++	-	+	-	-	-	-	-	-	-
36643 +	++	+	-	-	-	-	-	-	-
17048 +	-	-	-	-	-	-	-	-	-
39186 +	-	-	-	-	-	-	-	-	-

19337 +	-	-	-	-	-	-	-	-	-
20420 +	+	-	-	-	-	-	-	-	-
37037 +	-	+	-	-	-	-	-	-	-
40119 +	-	++	-	-	-	-	-	-	-
37038 +	+	++	-	–	-	-	-	-	-
37127 +	-	-	-	-	-	-	-	-	-
18409 +	-	-	-	-	-	-	-	-	-
39133 +	+	-	-	-	-	-	-	-	-
36329 +	-	-	-	-	-	-	-	-	-
38782 +	-	-	-	-	-	-	-	-	-
38534 +	++	-	-	-	-	-	-	-	-
37572 ++	++	+	-	-	-	-	-	-	-
19561 +	-	-	-	-	-	-	-	-	-
18284 +	+	+	-	–	-	-	-	-	-
37037 +	-	+	-	-	-	-	-	-	-
37902 +	-	-	-	-	-	-	-	-	-
36643 +	++	-	+	–	-	-	-	-	-
18065 +	+	+	-	-	-	-	-	-	-
17711 +	+++	-	-	-	-	-	-	-	-
19755 +	-	-	-	-	-	-	-	-	-
39609 +	+	-	-	-	-	-	-	-	-
39556 +	-	-	-	-	-	-	-	-	-
37867 +	+	-	-	-	-	-	-	-	-
37380 +	-	-	-	-	-	-	-	-	-
37842 ++	-	-	-	-	-	-	-	-	-
39574 +	+	-	-	-	-	-	-	-	-
37871 +	-	-	-	-	-	-	-	-	-
17571 ++	+	+	-	-	-	-	-	-	-
17625 +	-	-	-	-	-	-	-	-	-
17578 ++	++	-	-	-	-	-	-	-	-
37420 +	+++	+	+	-	-	-	-	-	-
37273 ++	+	-	-	-	-	-	-	-	-
37619 ++	+++	+	+	-	-	-	-	-	-

36703 +	-	+	-	-	-	-	-	-	-
37989 +	-	-	-	–	-	-	-	-	-
18385 +	-	-	-	-	-	-	-	-	-
37953 +	-	-	-	-	-	-	-	-	-
39574 +	++	+	-	–	-	-	-	-	-
37041 ++	-	-	-	-	-	-	-	-	-
41545 +	-	-	-	-	-	-	-	-	-
17563 +	++	-	-	-	-	-	-	-	-
37414 +	+	-	-	-	-	-	-	-	-
40379 +	-	-	-	-	-	-	-	-	-
37983 +	-	-	-	-	-	-	-	-	-
39592 ++	+++	++	+	–	-	-	-	-	-
37145 ++	-	-	-	-	-	-	-	-	-
36544 ++	+	+	+	-	-	-	-	-	-
39006 +	-	-	-	-	-	-	-	-	-
37013 +++	-	-	-	-	-	-	-	-	-

T16

NT SEQ ID#	AA SEQ ID#	NT sequence	AA sequence	hCMEC binding	hCMEC-hTFRC binding
35371	40332	AAAGACGACTATATGTACTAC	KDDYMYY	+++	---
35064	41478	AAGGACGGATCAAGCTATTGG	KDGSSYW	+++	---
36050	41478	AAAGATGGGAGTTCTTACTGG	KDGSSYW	+++	---
31878	40332	AAGGATGATTACATGTATTAT	KDDYMYY	+++	---
30620	39882	CGTGATGACTACCAATATTAC	RDDYQYY	+++	---
30746	39882	AGGGACGATTATCAGTACTAT	RDDYQYY	+++	---
35653	18548	ATTGAACGCCGTGGCTGGGAC	IERRGWD	+++	---
31306	40122	GATCAAGAGATCAAGAGACGC	DQEIKRR	+++	---
30426	39825	ACGGTGTACGATTCTTTCGCT	TVYDSFA	+++	---
32019	40385	CGAGACGAGTTTATGTCTTTT	RDEFMSF	+++	---
31229	39588	AAGGATGACTACTCCTATTAC	KDDYSYY	+++	---
33220	40385	AGGGATGAATTCATGAGCTTC	RDEFMSF	+++	--
22700	37011	AAAGACGAATTTATGTCCTAC	KDEFMSY	+++	---
29766	39588	AAAGACGACTATAGTTACTAT	KDDYSYY	+++	---
32137	40423	AAGGATGGCCTTTCGAGGTGG	KDGLSRW	+++	--
21815	36784	GTTATGGAAAGCAGGAAATGG	VMESRKW	+++	---
23638	37463	ATTGCCAAGAGGGGGTGGGAT	IAKRGWD	+++	---
23653	37463	ATAGCTAAACGAGGATGGGAC	IAKRGWD	+++	---
30677	39904	ATTCAGTTCAGTCCGCTTGAT	IQFSPLD	+++	---
32473	40423	AAAGATGGATTAAGTCGCTGG	KDGLSRW	+++	--
24243	36784	GTCATGGAGTCTCGTAAGTGG	VMESRKW	+++	---
27772	38921	TGGTGCAGGTCCCAGGCGGGG	WCRSQAG	+++	---
29772	39138	GACATGGCAAGTCGTATGTGG	DMASRMW	+++	---
23998	17966	GAAATGGCCGCATATGACTGG	EMAAYDW	+++	---
34728	41386	CGGGAAGGCAGTTCATATTGG	REGSSYW	+++	--
25803	37642	CGTTCGGAATTCAAGGTTTTC	RSEFKVF	+++	---
22808	36960	ATCATGGAGTCACGTAAATGG	IMESRKW	+++	---
24167	37642	CGAAGTGAGTTTAAAGTCTTT	RSEFKVF	+++	---
20572	36276	CCCATGGAAGCCAGATCCTGG	PMEARSW	+++	---
35639	41621	AAGGTAGAGCACGTCCGGTGG	KVEHVRW	+++	---
35542	40423	AAAGACGGATTGAGTCGTTGG	KDGLSRW	+++	--
22260	36960	ATTATGGAAAGTAGGAAGTGG	IMESRKW	+++	---

24481	37735	GCCTTCGAATGTACCCCTGGT	AFECTPG	+++	--
22321	36893	GCCTTGGAATCTCGTACTTGG	ALESRTW	+++	---
28446	39138	GATATGGCGTCCAGAATGTGG	DMASRMW	+++	---
32889	17905	TATAGTAGATTAAATGTTGGT	YSRLNVG	+++	---
33056	38747	AAGGTAGACCATGTGCGCTGG	KVDHVRW	+++	--
27178	38710	GGTAGCGAATTCATGAGCTAT	GSEFMSY	+++	---
32188	17905	TATTCACGTCTTAATGTGGGG	YSRLNVG	+++	--
36111	14324	TACAGTCGTGTAAACCCTAAT	YSRVNPN	+++	---
36141	41845	AACTCAGCTTACGGGTTGCGC	NSAYGLR	+++	--
30568	39863	TGCAATAAACCCATGCACGCA	CNKPMHA	+++	--
22070	36893	GCACTTGAGAGCAGGACGTGG	ALESRTW	+++	---
22390	37011	AAGGATGAGTTCATGAGTTAT	KDEFMSY	+++	---
21927	36834	TTACATCGCTTGGGCCCAAAC	LHRLGPN	+++	---
24482	37736	GTAATGTCCGACAGAACTTGG	VMSDRTW	+++	---
25456	12553	CTGGCCAGGATGGGGTACAAT	LARMGYN	+++	--
25121	37736	GTCATGAGTGATCGTACGTGG	VMSDRTW	+++	---
30796	39063	AAGGACGACTGGAGCTCATGG	KDDWSSW	+++	---
35665	38500	GGAGGAGCCACAAGTAGATGG	GGATSRW	+++	--
22207	36834	CTCCACAGGCTCGGGCCTAAT	LHRLGPN	+++	---
25612	38158	AGGGATGAGTTCATGAGTTAT	RDEFMSY	+++	--
31405	40025	CGCGAGGGGGCAAGCTACTGG	REGASYW	+++	--
28850	39284	AGGGTCGGCGGAGATTGTCCG	RVGGDCP	+++	---
28673	39225	AGGTCTGAATTTACCTCGTAT	RSEFTSY	+++	---
36204	41884	AGAAGTGAGTTCAGCGCATTC	RSEFSAF	+++	--
30070	38468	GGCGCCGGGACCAGCCGTTGG	GAGTSRW	+++	--
23110	17032	AAGATGGATAGTCGCCTATGG	KMDSRLW	+++	---
21810	36782	GACATGTCCAGCCACAAATGG	DMSSHKW	+++	---
23202	37306	GATATGGAAAGCCGCAAATGG	DMESRKW	+++	---
24424	37712	ATAATGGCAGACCGTACTTGG	IMADRTW	+++	---
25857	38158	CGTGACGAATTTATGTCCTAC	RDEFMSY	+++	--
29726	39579	AAGAAATACGAAATCAATAAC	KKYEINN	+++	--
25765	17281	TTAGCGAGGAGTGCCGTTAAT	LARSAVN	+++	--
24443	37718	GTAATGTCCGACAGACTCTGG	VMSDRLW	+++	---

23727	37306	GACATGGAGTCGAGGAAGTGG	DMESRKW	+++	---
34479	41279	AAGAATGAATACGTGAAATGG	KNEYVKW	+++	--
23996	17675	ATTATGAGTGACCGCTTATGG	IMSDRLW	+++	---
34634	41344	TTCGCAAAGAGTAAGGCTAAC	FAKSKAN	+++	--
24316	37491	AGTCTCGAGTCCAGGAAATGG	SLESRKW	+++	---
21057	36307	CCACTGATGAGTCGTGATTGG	PLMSRDW	+++	---
35909	39617	GGGGGGGCAAGTAGTCGTTGG	GGASSRW	+++	--
24440	37717	GTTATGAGCAGCAGATCCTGG	VMSSRSW	+++	---
25877	38239	TGCGGAGGGGGTACGGCAGGC	CGGGTAG	+++	--
25702	38182	ATTGCCCATCGGGGTTGGGAC	IAHRGWD	+++	---
33653	40968	GGTAGCGGTAATCAACGATGG	GSGNQRW	+++	--
32406	40525	AAATCCGATCATGTCAGGTGG	KSDHVRW	+++	--
24883	37892	GTCATGTCCGATAGGCACTGG	VMSDRHW	+++	---
23272	37331	CCCATGGCCGATAGAAAGTGG	PMADRKW	+++	---
31313	16639	ATTATGAGTTCGCGTTCCTGG	IMSSRSW	+++	---
25151	37892	GTTATGAGTGACCGCCATTGG	VMSDRHW	+++	---
24047	37423	CGCAGCGAGTTCATGTCTTAT	RSEFMSY	+++	---
31018	40025	AGGGAAGGTGCGTCTTATTGG	REGASYW	+++	--
33098	40763	AAGGGCGATCATGTACGCTGG	KGDHVRW	+++	--
28894	39256	CTCCCGGGCGTAAAGTGCCCG	LPGVKCP	+++	--
30114	38466	AAAGATGAATATAAATACTAT	KDEYKYY	+++	---
35610	18418	AACTCGGAGTTTATGAGCTAT	NSEFMSY	+++	--
25801	37712	ATCATGGCTGATAGGACCTGG	IMADRTW	+++	---
33725	40995	AAGAACGATCACGTGCGTTGG	KNDHVRW	+++	---
26492	38466	AAGGACGAGTACAAGTATTAC	KDEYKYY	+++	---
31375	39598	TTAGCCAGGTCAGGGTGGGAC	LARSGWD	+++	--
21272	36588	GACCTGGCGAGCTACAAGTGG	DLASYKW	+++	---
25755	37718	GTGATGAGTGACCGTTTATGG	VMSDRLW	+++	---
30049	39625	CGCAATGGTACGTCCGCATGG	RNGTSAW	+++	--
30765	39598	CTGGCTCGAAGCGGATGGGAT	LARSGWD	+++	--
31478	39873	AAGTATGAGTCCTCGGTATGG	KYESSVW	+++	--
28662	17854	GGATCGGAATTTCTTGGGTGG	GSEFLGW	+++	--
21576	36392	ATATTAGAGTCGAGAACTTGG	ILESRTW	+++	---

23918	37331	CCAATGGCTGACCGCAAATGG	PMADRKW	+++	---
32267	18513	ACGGATGATTGGAGTACATGG	TDDWSTW	+++	---
20818	36392	ATCCTGGAAAGCCGCACGTGG	ILESRTW	+++	---
27298	38182	ATAGCACACAGAGGATGGGAT	IAHRGWD	+++	---
35509	40525	AAAAGTGATCATGTCAGGTGG	KSDHVRW	+++	--
23785	37513	GGAGGGGAGTTCTCCCGCTGG	GGEFSRW	+++	--
33728	40525	AAGAGTGACCACGTTCGCTGG	KSDHVRW	+++	--
23086	36782	GACATGAGTTCGCATAAGTGG	DMSSHKW	+++	---
25996	37688	CTCGCCCGTGCGGGCTATAAC	LARAGYN	+++	--
22194	36936	TTGTGTAAGCCCTGCCTCAAC	LCKPCLN	+++	---
26589	38500	GGGGGTGCAACCTCACGGTGG	GGATSRW	+++	--
34781	41406	AAAAACGACCACGTTAAGTGG	KNDHVKW	+++	--
32221	40450	TACTACAGCGGTTACAAAGAC	YYSGYKD	+++	--
34750	38710	GGATCTGAGTTTATGTCATAC	GSEFMSY	+++	--
29743	39583	GGGAGCAATACATCAAGATGG	GSNTSRW	+++	--
21153	36543	CCAATGGAATCGCACTCTTGG	PMESHSW	+++	---
24033	17675	ATTATGTCGGACAGGTTATGG	IMSDRLW	+++	---
23370	37366	GTAATGGCCGATCGCAAGTGG	VMADRKW	+++	---
29873	39625	CGCAATGGCACTTCAGCATGG	RNGTSAW	+++	--
23418	36913	GTTATGTCGGATCGTATATGG	VMSDRIW	+++	---
32714	40626	ATTAAAGCTATGATAAAACAG	IKAMIKQ	+++	--
25987	17281	CTCGCCCGCTCCGCGGTTAAC	LARSAVN	+++	--
32853	40681	CGTGGGGAGTTCTCGTATCCA	RGEFSYP	+++	--
35635	40812	GGAGGCGGAGTGAGCAGGTGG	GGGVSRW	+++	--
28346	12553	TTAGCACGGATGGGTTATAAC	LARMGYN	+++	--
25609	38157	GAAGGAATCTCACGCTCATGG	EGISRSW	+++	---
34564	40228	TGTGCAGATAGAAAACAGGGC	CADRKQG	+++	---
27307	38747	AAAGTTGATCACGTCAGGTGG	KVDHVRW	+++	---
22123	36913	GTAATGAGCGACCGCATCTGG	VMSDRIW	+++	---
34831	39666	GGGGGAGGAGTCGTGCGTTGG	GGGVVRW	+++	--
24238	37366	GTGATGGCTGACAGAAAATGG	VMADRKW	+++	---
30899	39625	AGAAACGGCACTAGTGCGTGG	RNGTSAW	+++	--
28202	39063	AAAGATGATTGGTCTAGTTGG	KDDWSSW	+++	---

21556	36712	GATTTGGCCTCCCGGGAATGG	DLASREW	+++	---
23632	37460	CAAATGGAGTCAAGGATGTGG	QMESRMW	+++	---
23368	36936	CTCTGCAAACCATGTTTAAAT	LCKPCLN	+++	---
23818	37528	GCTATGGCCGACAGAACGTGG	AMADRTW	+++	---
31399	39068	TATTATACTGGTAAGTGCGAT	YYTGKCD	+++	--
34209	40968	GGCTCTGGCAACCAGAGGTGG	GSGNQRW	+++	--
29573	39041	AAGGACGATTGGACAAGCTAC	KDDWTSY	+++	---
28692	39231	TGCAGGATGGATAGTGTACCT	CRMDSVP	+++	--
26502	38468	GGAGCGGGAACTTCAAGATGG	GAGTSRW	+++	--
29796	39598	TTAGCGAGATCGGGGTGGGAC	LARSGWD	+++	--
24358	37688	TTGGCAAGAGCCGGATACAAT	LARAGYN	+++	--
30604	39245	TGCAAACCCTACTTACACGAG	CKPYLHE	+++	--
28872	39295	AGGGAAGAGTATACAGCATAT	REEYTAY	+++	--
23460	37399	AAGAGTGAGTTTAAAATCTTC	KSEFKIF	+++	---
26342	38397	AGAGACGAGTACAGCCCATGG	RDEYSPW	+++	---
23517	37423	AGGTCTGAATTTATGAGTTAC	RSEFMSY	+++	---
26924	38610	CGTATGGAAGACAGAAAATGG	RMEDRKW	+++	---
24168	37314	GATCTTCAATCTAGGAGTTGG	DLQSRSW	+++	---
28082	18032	CTAGGAGGGACAAGCAGGTAT	LGGTSRY	+++	--
34909	41437	AGACAGGAAGGAGTGAGGTGG	RQEGVRW	+++	--
31950	37318	ATAATGAGTAGCAGGGGATGG	IMSSRGW	+++	---
24561	37766	AATATGGCAGACAGGACGTGG	NMADRTW	+++	---
24183	37460	CAGATGGAAAGCCGTATGTGG	QMESRMW	+++	---
22430	36770	GACCTTGAATCTCGAAAATGG	DLESRKW	+++	---
23223	37314	GACTTGCAGAGCCGCTCGTGG	DLQSRSW	+++	---
30239	39753	GGGAACGGTACAAGTAGGTGG	GNGTSRW	+++	--
23882	37528	GCCATGGCAGATCGTACTTGG	AMADRTW	+++	---
23731	37491	TCATTAGAAAGTCGGAAGTGG	SLESRKW	+++	---
35588	41598	ACAGTTTGGGGAGACCCGGCT	TVWGDPA	+++	---
29469	18032	TTAGGCGGTACCTCACGTTAC	LGGTSRY	+++	--
23466	37401	GTTATGGCTGACAGAATATGG	VMADRIW	+++	---
29123	39371	AATGGGAACGCATGCCGCCCT	NGNACRP	+++	--
35679	41636	AAGGAGGACTTCTTGTCATGG	KEDFLSW	+++	--

32917	39625	AGAAACGGAACGAGTGCTTGG	RNGTSAW	+++	--
30355	39796	AAGGATGACTGGAATACATGG	KDDWNTW	+++	--
25735	37766	AACATGGCGGATCGTACATGG	NMADRTW	+++	---
30617	39753	GGTAATGGGACGTCGCGGTGG	GNGTSRW	+++	--
30988	39350	ATAGCTCGGACCGGGTGGGAC	IARTGWD	+++	--
25394	17016	TACGTGAAAAATGACGCTAGG	YVKNDAR	+++	--
25977	38157	GAGGGCATTAGCAGAAGCTGG	EGISRSW	+++	---
23237	17032	AAAATGGACTCCCGATTATGG	KMDSRLW	+++	---
26860	38610	AGAATGGAGGATCGGAAGTGG	RMEDRKW	+++	---
36086	41808	GGCCGCGATGGGGTACGTTGG	GRDGVRW	+++	--
35882	41679	TACGTAAAAAGCCAGAAATTA	YVKSQKL	+++	--
29246	36276	CCTATGGAGGCTCGCAGTTGG	PMEARSW	+++	---
35462	41567	GGAGCCAATACTAGCAGATGG	GANTSRW	+++	--
23518	37289	ATAATGCATGCTCGGGACTGG	IMHARDW	+++	---
22213	36699	ATTATGGAATCACGTAACTGG	IMESRNW	+++	---
35034	40946	CGTAACGAATTTACAGCCTAC	RNEFTAY	+++	--
34472	41277	AGATCGGAATATACGGTGTAT	RSEYTVY	+++	--
30589	39873	AAATACGAAAGTAGCGTCTGG	KYESSVW	+++	---
35070	14210	TTTGCAAAATCGGGATGGAAC	FAKSGWN	+++	--
34399	41251	CGCGAACCGACCTGCCCGAGA	REPTCPR	+++	--
23768	17675	ATCATGTCGGATAGACTCTGG	IMSDRLW	+++	---
25694	38180	AGAAGCGAGTTTATGTCATTT	RSEFMSF	+++	---
25661	37968	ACCGAGTACATGTGCAGACCA	TEYMCRP	+++	---
32768	40647	CGCGATGCGTTTACAAGTTTT	RDAFTSF	+++	--
27722	38180	CGGTCTGAATTCATGAGTTTC	RSEFMSF	+++	--
33094	39598	CTCGCACGGAGTGGTTGGGAT	LARSGWD	+++	--
23217	37312	AGGGATGGCGTGTCCCGATGG	RDGVSRW	+++	--
34666	41359	TGTAACAAGCCGATGACCTAC	CNKPMTY	+++	--
26365	37312	CGTGACGGTGTAAGTAGGTGG	RDGVSRW	+++	--
35933	41751	TCTGATTGGACGGATCGATGT	SDWTDRC	+++	--
25436	38092	GGTGATGGCTACTCAAAGTGG	GDGYSKW	+++	--
27843	38934	GTGATGAGTGATAGACGCTGG	VMSDRRW	+++	---
29876	17982	ATTTCAAAGACGTGTGGGAGC	ISKTCGS	+++	--

34589	40056	TGTAAGCCGCAGTGGCCGAGT	CKPQWPS	+++	--
31929	40349	GGGGGGGGTGTAGTACGGTAC	GGGVVRY	+++	--
24680	37717	GTGATGTCTTCGCGTAGTTGG	VMSSRSW	+++	---
23221	17037	GAAATGCAGTCTCGCGCCTGG	EMQSRAW	+++	---
30846	39583	GGCTCGAACACGAGTCGTTGG	GSNTSRW	+++	--
36003	40455	GGTTCGGGGACGAGTAGGTGG	GSGTSRW	+++	--
31581	39327	TGTAGAGAGGGGACTCGCCTC	CREGTRL	+++	--
28146	39041	AAAGATGACTGGACTTCATAT	KDDWTSY	+++	---
28176	16605	AGTATGGAGAGTCGCCTATGG	SMESRLW	+++	---
23271	37330	CAGATGGCCAGCCGTGACTGG	QMASRDW	+++	---
26625	38519	GCTAGGCAGTGTCTTCCTATG	ARQCLPM	+++	--
29544	17276	CACGAGACATGTGTTCGCGGA	HETCVRG	+++	--
33392	40010	AGAAACGAGTTCACATCATAC	RNEFTSY	+++	---
33324	40450	TATTATTCAGGCTATAAGGAT	YYSGYKD	+++	--
24538	37755	CGCCCAGAGGCTCGCTCATGG	RPEARSW	+++	---
21762	36770	GATTTAGAGAGCCGGAAGTGG	DLESRKW	+++	---
24451	17016	TATGTAAAGAACGATGCCAGA	YVKNDAR	+++	--
25651	37755	AGACCTGAAGCGAGGAGTTGG	RPEARSW	+++	---
33610	40946	AGGAATGAGTTCACGGCTTAT	RNEFTAY	+++	---
36178	41867	GTCCCTGAGTTCTGTCCGTAT	VPEFCPY	+++	--
28493	39161	TGCAAGCCGCGCATGCTCGAG	CKPRMLE	+++	--
28268	37750	TTATGCAGGCCGTGCTCTAAT	LCRPCSN	+++	---
27811	38934	GTTATGTCCGACCGCAGGTGG	VMSDRRW	+++	---
35052	41277	CGCAGCGAGTACACTGTTTAC	RSEYTVY	+++	--
26806	38593	CGAGACGGGTCAAGTCGGTGG	RDGSSRW	+++	--
30830	39371	AACGGAAATGCGTGTAGACCA	NGNACRP	+++	--
30121	37513	GGCGGCGAATTCAGTAGGTGG	GGEFSRW	+++	---
30894	38558	ATTCCTAGTTCCGTTAGGTGG	IPSSVRW	+++	--
33686	40349	GGTGGCGGCGTTGTCAGATAT	GGGVVRY	+++	--
24244	37401	GTAATGGCCGATCGGATCTGG	VMADRIW	+++	---
35684	38581	TGTAAGCCGCGGCAAGGCGAG	CKPRQGE	+++	--
35896	40310	TGTAAGCCGCCCCCCCTCGCC	CKPPPLA	+++	--
25596	38153	TGCAAGCCCATATGCTGTGAG	CKPICCE	+++	--

21377	36642	GTCATGGAAGCACGGAACTGG	VMEARNW	+++	---
33629	40956	GTGCACAAGCTATGTCCGGTT	VHKLCPV	+++	--
24924	37340	AATATGGCTAGCCGGGACTGG	NMASRDW	+++	---
21553	36711	GCACCCGGATCAGTAAGGTGG	APGSVRW	+++	--
20628	36307	CCTTTAATGTCCAGGGACTGG	PLMSRDW	+++	---
34489	41283	TACAAAGAACCATGTATCTCA	YKEPCIS	+++	--
23485	36699	ATAATGGAAAGCCGGAACTGG	IMESRNW	+++	---
22095	36902	GAAATGGCCAGTAGAGATTGG	EMASRDW	+++	---
24539	37475	ATTATGGAATCGAGGGCCTGG	IMESRAW	+++	---
22456	17036	CAATTAGAGGCAAGGACCTGG	QLEARTW	+++	---
24428	37319	GTTATGAGCGAAAGGACATGG	VMSERTW	+++	---
29419	39470	TGTAAACCCGGTGCGGCATCG	CKPGAAS	+++	--
29734	39225	CGGAGCGAATTCACTAGTTAT	RSEFTSY	+++	---
27055	37338	CGTGATGAGTATAGTAGCTAC	RDEYSSY	+++	---
30149	39718	GTGAGCACACACTCTTGCGCC	VSTHSCA	+++	--
35237	41517	ACACGCTGGGGAGAAAATGCC	TRWGENA	+++	--
27389	38779	TGTTACAAGAAGCTACCTGAT	CYKKLPD	+++	--
25301	37924	GGGAGTCCAGGAGTTCGGTGG	GSPGVRW	+++	--
32875	38969	TATGCTAAGCAAAGCAGAAAT	YAKQSRN	+++	--
29125	39373	TGTACTTCAAAAACCGATCAT	CTSKTDH	+++	--
35421	41279	AAAAACGAGTATGTAAAGTGG	KNEYVKW	+++	--
25495	17037	GAGATGCAAAGCAGGGCATGG	EMQSRAW	+++	---
32468	40525	AAGTCGGACCACGTGCGATGG	KSDHVRW	+++	--
21960	36844	CTCCACAGATTATCTGTGAAC	LHRLSVN	+++	---
22412	37018	GTAATGGAGAGCCGTGTTTGG	VMESRVW	+++	---
24130	37458	GTCATGAGCAGCAGAGATTGG	VMSSRDW	+++	---
23404	37381	GACATGGAATCACGCACATGG	DMESRTW	+++	---
29502	39499	TGTAAGCCTCAAAACTCGAGT	CKPQNSS	+++	--
31742	39225	CGCAGCGAGTTCACGAGCTAC	RSEFTSY	+++	---
28969	39322	AAAGATGAGTTCACAGTTTAT	KDEFTVY	+++	---
24367	37693	AGAGATGAGTTCACAGTCTAT	RDEFTVY	+++	---
22406	36642	GTTATGGAGGCCAGAAATTGG	VMEARNW	+++	---
23171	37297	GTTATGGAATCACGGGCATGG	VMESRAW	+++	---

24996	37933	GTGATGTCGGACAGGGCATGG	VMSDRAW	+++	---
31808	40302	TGTCGTTCGCGCATGGCGGAA	CRSRMAE	+++	--
24672	37598	CCAATGGAGTCGCGTGAGTGG	PMESREW	+++	---
30986	40010	CGCAATGAGTTTACCAGCTAT	RNEFTSY	+++	---
28354	39106	TGCAAGGGCGAGAGTGCTATC	CKGESAI	+++	--
28332	37786	TTCGCCAAAAGTGGTTGTGGG	FAKSGCG	+++	--
28008	38996	TGTAGGCCTGACGTTAAAACT	CRPDVKT	+++	--
23196	37297	GTCATGGAGAGTAGAGCTTGG	VMESRAW	+++	---
30880	39131	TGCAAACCCTTTACTCGTGAG	CKPFTRE	+++	--
30625	39885	CGCAACGAGTTCACATCCTTC	RNEFTSF	+++	---
28982	38365	TACGTACGTAGTGATTTTAGG	YVRSDFR	+++	--
27168	16605	TCAATGGAATCGCGACTTTGG	SMESRLW	+++	---
22466	17714	CAACTAGAAAGTCGTTCGTGG	QLESRSW	+++	---
23281	37183	ATCATGGCAAGCAGAGATTGG	IMASRDW	+++	---
24388	37330	CAAATGGCTTCGAGAGATTGG	QMASRDW	+++	---
21769	36712	GACCTAGCTAGTAGAGAGTGG	DLASREW	+++	---
24138	37381	GATATGGAGAGCAGGACTTGG	DMESRTW	+++	---
25968	17826	GAGGGAATAGCTCGCACGTGG	EGIARTW	+++	---
24092	37153	GTGATGGAAGCGCGTAGCTGG	VMEARSW	+++	---
36216	40495	GGGAACAAACACTGCATGGAC	GNKHCMD	+++	--
34741	40252	CCCTGTAAGCCGCAACCCATG	PCKPQPM	+++	---
21695	36588	GATTTAGCTTCGTATAAATGG	DLASYKW	+++	---
22297	36930	AAGATGGCCGATAGACAGTGG	KMADRQW	+++	---
31013	37693	CGAGATGAATTTACGGTATAC	RDEFTVY	+++	---
25155	37966	AGAATGGAAAGTAGGGACTGG	RMESRDW	+++	---
25122	37976	TGTAAGCCAGATAGTCGTGTA	CKPDSRV	+++	--
22038	17020	AAGATGTCTTCGTCGACATGG	KMSSSTW	+++	---
32150	40154	TGTAGGGGGGACAATGGAGTA	CRGDNGV	+++	--
29552	39516	TGTAAATTCCCAGTAATGGAA	CKFPVME	+++	--
32677	39471	GTAGCTCGCACGGGATGGGAC	VARTGWD	+++	--
35343	17640	CGAGGCGAGTACCATTATCCA	RGEYHYP	+++	--
35838	41704	TGTAAGGGAAGCTATGAGCAA	CKGSYEQ	+++	--
23319	37348	GATATGATGTCTCATAAATGG	DMMSHKW	+++	---

35611	41609	GGCTGTGGCACTAAGTATGGC	GCGTKYG	+++	--
26184	38331	TCAATGGAGAGTCGCACATGG	SMESRTW	+++	---
32283	40320	ACTAGGTGGGGGGACCCGGCC	TRWGDPA	+++	---
22535	37062	TTACACAGGCTGTCGCCTAAC	LHRLSPN	+++	---
23344	17626	CTAAGCCGGTTGGGTGGTGGT	LSRLGGG	+++	--
27621	37693	CGGGACGAGTTCACAGTTTAT	RDEFTVY	+++	---
34444	41266	TGCAGGCCTGAAGCAAAAAGC	CRPEAKS	+++	--
30050	39684	CGCGACGGCAACAGCCGCTGG	RDGNSRW	+++	--
22373	17020	AAAATGAGCAGTAGCACATGG	KMSSSTW	+++	---
25511	37741	CAAGGCGAGTCGAGGCTTTGG	QGESRLW	+++	---
34759	39302	AGAGATTACGAAGTATACCCT	RDYEVYP	+++	--
29056	39350	ATTGCAAGAACAGGATGGGAT	IARTGWD	+++	--
30676	39903	TATAAAGCCGATGCCCCATGC	YKADAPC	+++	--
30889	39225	AGGTCAGAGTTCACGTCGTAC	RSEFTSY	+++	---
22480	37018	GTGATGGAATCTAGGGTATGG	VMESRVW	+++	---
26801	38591	AGGGATGGTACAAGTAGATGG	RDGTSRW	++	--
33224	40817	TGTAAGCCGCAGGCGGGACCT	CKPQAGP	++	--
35750	18264	GACATGCGAAGTCCGAACTGG	DMRSPNW	++	--
23302	37340	AACATGGCGTCAAGAGATTGG	NMASRDW	++	---
21522	36699	ATCATGGAGAGCAGAAATTGG	IMESRNW	++	---
30022	39670	CGGGACCAGTTTACTAGTTAC	RDQFTSY	++	--
33303	40844	TGCAAACCTCAAGCTCTTACT	CKPQALT	++	--
35926	41747	GGTTGTAGGTCAGGGGACATA	GCRSGDI	++	--
24780	14618	TATAGTAAGGTTGGCAAGAAC	YSKVGKN	++	---
28707	39238	TGCTGTAAAGACGAGTGCCCC	CCKDECP	++	--
33194	40806	TGTAAGGGACCGTACAGCGAG	CKGPYSE	++	--
23229	14269	TATGCGCGTACAGGCCCTAAT	YARTGPN	++	---
30905	39982	TGTAAACCAGGCAGCCCGCAC	CKPGSPH	++	--
23625	37458	GTGATGTCATCTCGGGACTGG	VMSSRDW	++	---
22720	37141	GACCTCAGCTCACGCGATTGG	DLSSRDW	++	---
22291	36699	ATTATGGAGTCAAGAAACTGG	IMESRNW	++	---
26901	38622	GGGTGCTACAAAGGACCCCCC	GCYKGPP	++	--
24416	37556	ATCATGAGTAGCAGGGAGTGG	IMSSREW	++	---

32038	40393	GGACGCGAGCATGTTAAGTGG	GREHVKW	++	---
24965	37924	GGTTCCCCTGGCGTGAGATGG	GSPGVRW	++	--
24097	37619	GTGATGGCGGATCGCCTATGG	VMADRLW	++	---
24483	37335	GTTATGTCCGATCGGGTCTGG	VMSDRVW	++	---
23285	37335	GTCATGAGTGACAGAGTTTGG	VMSDRVW	++	---
24564	15352	TACTCCAAGATCGGTAAGAAT	YSKIGKN	++	---
24437	17714	CAGCTTGAGTCCCGGAGCTGG	QLESRSW	++	---
33404	17511	TGCATGAGTGACAAACGCGCA	CMSDKRA	++	--
29993	17141	TGCACGAGGATGGACTACGGT	CTRMDYG	++	--
29786	39079	TGCATGAGCGGCCCTCGTCCC	CMSGPRP	++	--
23676	37475	ATAATGGAGAGTCGAGCGTGG	IMESRAW	++	---
21613	36455	GACATGGCCAGTAAAACATGG	DMASKTW	++	---
26766	15352	TATTCAAAAATAGGGAAAAAC	YSKIGKN	++	--
31846	40320	ACACGCTGGGGAGATCCCGCA	TRWGDPA	++	---
20522	36248	ATAGCATTGAAGGGTTGGGAT	IALKGWD	++	---
33605	40943	ACCCCCTATGACGCTATTGCC	TPYDAIA	++	--
29858	16639	ATTATGAGCAGCCGAAGCTGG	IMSSRSW	++	---
22716	37139	GATATGGAGTCACGCGTTTGG	DMESRVW	++	---
22910	36507	GATCTACAGGCACGCAGCTGG	DLQARSW	++	---
25099	37966	CGCATGGAGTCACGCGACTGG	RMESRDW	++	---
24507	37741	CAGGGGGAAAGTCGTTTATGG	QGESRLW	++	---
33973	40072	AGATCAGAGTTTAGAACTTAT	RSEFRTY	++	--
31108	40058	ATGACTGGTACCTCTTGCCTG	MTGTSCL	++	--
35193	18513	ACTGATGACTGGTCGACCTGG	TDDWSTW	++	--
30651	39422	TGTAAGCCGCAAGCCGGGGGG	CKPQAGG	++	--
23245	37319	GTGATGTCTGAGCGCACGTGG	VMSERTW	++	---
35423	40419	CTAGCTAAGACGGCGTGGAAC	LAKTAWN	++	--
22862	37183	ATTATGGCTTCTCGGGACTGG	IMASRDW	++	---
26864	38581	TGCAAACCTAGACAGGGTGAA	CKPRQGE	++	--
29853	39617	GGCGGAGCTTCCTCCAGGTGG	GGASSRW	++	--
33327	40849	TGCAAGATGCCCGGAATGGAT	CKMPGMD	++	--
21529	36702	CTATGTGCCCCGTGCCTCACA	LCAPCLT	++	--
25011	37610	CTTATGGCAGACAGAACGTGG	LMADRTW	++	---

20532	36248	ATAGCGTTAAAAGGGTGGGAT	IALKGWD	++	---
20957	36455	GATATGGCATCGAAGACTTGG	DMASKTW	++	---
36131	41835	GGTGGCGAGCGCAGTTGCTGG	GGERSCW	++	---
23649	16607	GATCTTAGTTCACATAATTGG	DLSSHNW	++	---
26556	14873	TATAGCAAACTGAACAAAAAT	YSKLNKN	++	--
21551	36545	GATTTAAGCTCGCAGACATGG	DLSSQTW	++	---
31301	40118	TGCAAACCAGGGCAGCAGTCA	CKPGQQS	++	--
29417	39468	GGCTGTGGTACGAAGTTGGGG	GCGTKLG	++	--
30637	39713	ATAGGACGCACTGGGTGGGAC	IGRTGWD	++	--
28121	16593	GACATGTCATCTCGGATTTGG	DMSSRIW	++	---
27745	38462	GGAGGGGAGTACAGTACATGG	GGEYSTW	++	---
32843	40676	TGCAAACCTGGATGGGGAGAG	CKPGWGE	++	--
26594	38331	AGTATGGAATCGAGAACGTGG	SMESRTW	++	---
22014	36871	TTGTGTCGTCCCTGCTCAGCC	LCRPCSA	++	--
36045	41447	TTATTCAAGGAATGCGGCGGC	LFKECGG	++	--
29414	39466	ACGGCGAACTGCCTAAAGCCC	TANCLKP	++	--
22181	36930	AAAATGGCAGACCGTCAATGG	KMADRQW	++	---
35574	40583	GGTGGTGCTGGGGTCAGGTGG	GGAGVRW	++	--
35742	41598	ACCGTATGGGGGGATCCTGCA	TVWGDPA	++	--
35708	41649	CGTTCGGAGTTCACAGCATTT	RSEFTAF	++	--
23486	37412	GATATGTCAGTTAGGACCTGG	DMSVRTW	++	---
26401	37879	ATCATGTCGGGTCGTACCTGG	IMSGRTW	++	---
21798	36412	AAAATGGACTCCGTACGGTGG	KMDSVRW	++	---
23887	37559	GTTATGTCAAGCAGGGAATGG	VMSSREW	++	---
33694	39881	CGGAACGAGTTTACCGTTTAT	RNEFTVY	++	--
22938	37210	TATGTGAAGAGCCAGAAAATA	YVKSQKI	++	--
29363	39451	TGCCCAAGAAACACCCCTCCG	CPRNTPP	++	--
20836	36399	CCAATGGCAAGTAGCACATGG	PMASSTW	++	---
35903	37513	GGCGGTGAATTTAGTAGGTGG	GGEFSRW	++	---
22561	18663	CTAGCCCGTACCGCACTCAAC	LARTALN	++	--
30694	18353	TGTCGTCCAGTAAAGGACGGT	CRPVKDG	++	--
27053	38591	CGAGACGGGACTTCGCGTTGG	RDGTSRW	++	--
24559	37625	GATGGGTCGTCCCGGTTATGG	DGSSRLW	++	---

25320	37985	ACGAGTGAGTATAAGTATTAC	TSEYKYY	++	--
22313	36978	ATAGCGAGTAGGGGTTGGGAT	IASRGWD	++	---
29809	39602	TGCCAAAGCAAGACGGGGCAT	CQSKTGH	++	--
23869	37549	TGCAAGCCCAATAATGGCATC	CKPNNGI	++	--
31827	39225	CGCAGCGAATTTACTAGTTAT	RSEFTSY	++	---
28370	39113	AGGGGGGAGTTCTGCGGTGGA	RGEFCGG	++	--
20526	36248	ATCGCTCTCAAGGGTTGGGAC	IALKGWD	++	---
30857	19193	GCGGGTGCCTGTGATGCCAGC	AGACDAS	++	--
24056	37610	TTAATGGCTGATCGGACCTGG	LMADRTW	++	---
24221	14958	TATAGCCGCACTGGTCCGAAC	YSRTGPN	++	---
26213	38343	AAAATGCAGGATCGTAGCTGG	KMQDRSW	++	---
27603	37874	GTCGGCCATAGAGGATGGGAT	VGHRGWD	++	--
23034	17826	GAAGGTATTGCCAGGACATGG	EGIARTW	++	---
32797	40114	TGTAGGTCCGGGCCAACACCA	CRSGPTP	++	--
34637	41191	TGGAACCCGATGTGCAAGGCG	WNPMCKA	++	--
26764	38177	AAGGACGGCTATTCCAGCTGG	KDGYSSW	++	--
24760	37429	ATCATGTCGGATAGGGTTTGG	IMSDRVW	++	---
22947	16593	GACATGAGCAGTCGAATATGG	DMSSRIW	++	---
32597	40583	GGAGGCGCGGGTGTTCGTTGG	GGAGVRW	++	--
35132	40341	AAATGCGGGAAACAAGAGGGA	KCGKQEG	++	--
30482	39684	AGAGATGGAAATTCTCGGTGG	RDGNSRW	++	--
24108	37625	GACGGCAGTAGTAGACTTTGG	DGSSRLW	++	---
20931	36440	GTCCTCTCCGATCGCATCTGG	VLSDRIW	++	---
21402	36649	CGCCTCATGGACGTCTATCCG	RLMDVYP	++	---
27029	38660	ATATTAGACTCCCGCAAATGG	ILDSRKW	++	---
20954	36454	ATAATGTCGAGTGCCACGTGG	IMSSATW	++	---
26930	14190	TACAGTCGTGCTGGACCCAAC	YSRAGPN	++	---
21494	36440	GTGTTAAGTGACCGAATATGG	VLSDRIW	++	---
21547	17036	CAGCTTGAAGCACGCACATGG	QLEARTW	++	---
21168	36459	CTCGCACGTAGCGGGCCGAAT	LARSGPN	++	---
23572	17626	CTCTCGAGACTCGGGGGAGGT	LSRLGGG	++	--
22204	36938	ATTTTGAGCTCCAGAGACTGG	ILSSRDW	++	---
29840	39611	GGGAAATTGGGTTCTTGTGAT	GKLGSCD	++	--

23447	37062	CTGCACCGCTTAAGTCCAAAT	LHRLSPN	++	---
29267	38779	TGCTATAAAAAATTGCCGGAT	CYKKLPD	++	--
23056	14269	TACGCCCGAACAGGACCGAAT	YARTGPN	++	---
27271	38733	TGCACGAGCGCGACGGGACAC	CTSATGH	++	--
35106	41489	CGCGAATCAACCAACGGCAGA	RESTNGR	++	--
34922	39754	TGCAAGGCGCCGGACAAGGGA	CKAPDKG	++	--
20561	36248	ATCGCCCTCAAAGGATGGGAC	IALKGWD	++	---
33053	40749	TGTAAGCTAGACAAGATGGTC	CKLDKMV	++	--
34332	40788	TGCATGTCTAAGACTGGTCAT	CMSKTGH	++	--
27484	38815	GACTTGAGGGATAGGAAGTGG	DLRDRKW	++	---
22557	37073	TTGATGAGTTCGGCGAAATGG	LMSSAKW	++	---
24855	36937	ATACTCTCAGACAGGAATTGG	ILSDRNW	++	---
29032	37522	GATATGATGTCGCGTGATTGG	DMMSRDW	++	---
34615	41334	TGCAAAATTCCATCTAAGGAA	CKIPSKE	++	--
28331	39103	AAGGATGAGTTTACGATATAC	KDEFTIY	++	---
21098	36459	TTAGCACGTAGCGGCCCGAAT	LARSGPN	++	---
24835	37874	GTAGGACACCGTGGCTGGGAC	VGHRGWD	++	--
30845	39071	TGTGGTCGGGCTGGCAGAGAT	CGRAGRD	++	--
21349	36624	ATAATGACGGACCGCATCTGG	IMTDRIW	++	---
26121	38309	CTCCATAAGCTCCAACCGTGT	LHKLQPC	++	--
30798	38971	TATTCTCGGATAGGGTGTAAC	YSRIGCN	++	--
28500	39164	TGCAAGCCTCCTAGTGACATG	CKPPSDM	++	--
23376	15352	TACAGCAAAATTGGGAAGAAT	YSKIGKN	++	---
20569	36273	GTTAACGATTATACAATCTTC	VNDYTIF	++	---
28240	39071	TGCGGGAGAGCAGGTCGTGAC	CGRAGRD	++	--
28932	17104	CGAGGCAATGAGTGCTGGTCC	RGNECWS	++	--
26402	38343	AAGATGCAAGACAGGTCTTGG	KMQDRSW	++	---
27534	38833	AGGCCCGAGTCGGTCAGGTGG	RPESVRW	++	--
23413	36844	TTACATCGTCTGAGCGTTAAC	LHRLSVN	++	---
32078	40401	TGCAAGCCTATGGCTCCCGAT	CKPMAPD	++	---
31359	40141	CGCACATACGAGGTATACCCA	RTYEVYP	++	---
26370	38413	GTTATGCAGAGTCGAACATGG	VMQSRTW	++	---
23859	16667	CTACACAGATTGGCGGCAAAC	LHRLAAN	++	---

31744	40281	TGTAAGGTAAAGATGCCTCCG	CKVKMPP	++	--
25118	37501	CCGATGGGCGATCGGAAGTGG	PMGDRKW	++	---
35022	41467	AGGAGCGAATTTACGTCCTTT	RSEFTSF	++	--
36028	17166	TGTGATTACGGCAGCCGCTCG	CDYGSRS	++	--
30060	13598	CGTGGCGATGGTCATTACAAT	RGDGHYN	++	--
28680	39227	TGCAGGGACGACAAGAGGTGG	CRDDKRW	++	--
23154	37289	ATCATGCACGCGAGAGATTGG	IMHARDW	++	---
24267	37658	CGCTCGGACTTTGAATACTTT	RSDFEYF	++	---
22137	36918	ATCATGACTAGCAGGGACTGG	IMTSRDW	++	---
22665	37120	AGGTTGTCATCGCAAACATGG	RLSSQTW	++	---
31463	40175	TGCAAACCACCAATGCCTCCT	CKPPMPP	++	--
34843	41423	GGCGTTGGTGGCTGCAAGCCA	GVGGCKP	++	--
24662	37429	ATAATGAGCGATCGTGTCTGG	IMSDRVW	++	---
24560	37559	GTAATGAGTTCTCGAGAGTGG	VMSSREW	++	---
22860	37108	GTCCTCTCTGATAGGAACTGG	VLSDRNW	++	---
28705	39236	TGTAAGCCCCAGACAATCGGG	CKPQTIG	++	--
24625	37352	GTACTCTCCGATAGGAGTTGG	VLSDRSW	++	---
24848	37879	ATAATGAGCGGGAGAACGTGG	IMSGRTW	++	---
23264	37108	GTATTGAGCGACCGCAATTGG	VLSDRNW	++	---
23039	14269	TACGCTAGAACCGGTCCAAAC	YARTGPN	++	---
21656	36711	GCCCCGGGCAGTGTTCGTTGG	APGSVRW	++	--
25316	16667	TTGCACCGGCTCGCAGCCAAC	LHRLAAN	++	---
35631	41617	GGGTCGGGCACGGCGAAGTGG	GSGTAKW	++	--
23754	37501	CCAATGGGAGACAGAAAATGG	PMGDRKW	++	---
33516	40875	TGTAAACCACCGAGCCGCGAC	CKPPSRD	++	--
26558	37619	GTCATGGCAGACAGATTGTGG	VMADRLW	++	---
23139	19688	CGAGAAGGTTACTCGCACTGG	REGYSHW	++	---
22679	36446	ATTTTGGCCTCACGTGATTGG	ILASRDW	++	---
36072	41804	ATCCATAAATATGTAGGGGGG	IHKYVGG	++	--
25214	38014	ATCATGGCAGAGAGAACCTGG	IMAERTW	++	---
29963	39656	TACCACAAAGGCGGGTGCGAA	YHKGGCE	++	--
24291	37139	GACATGGAAAGCAGGGTATGG	DMESRVW	++	---
20977	18857	CTTCTCAGTTCTGCTACATGG	LLSSATW	++	---

23907	36938	ATCCTCTCAAGTCGCGACTGG	ILSSRDW	++	---
29606	39536	TGCGCGCCTATGTTACATGAA	CAPMLHE	++	--
24748	17197	CTTTGTCGCCCTTGTAGGGAG	LCRPCRE	++	--
35121	39917	ATGTGTAGGCCTTGTTCAGAA	MCRPCSE	++	--
28261	17211	GGATGTAATCGCTCAACTGCA	GCNRSTA	++	--
31648	40251	TGCGTGGTTCGTTCCGCAGGG	CVVRSAG	++	--
29164	39392	TGGACTAACATGTGCAAAGCG	WTNMCKA	++	--
33895	39702	TGCAAACCCGGAATGGGAGAA	CKPGMGE	++	--
36219	41891	GTCAGTGAGTTCAACTCCTAC	VSEFNSY	++	--
31962	40360	CTACACCGGCTGTGCCCGGAC	LHRLCPD	++	--
33743	41000	TGCAAACCGTTAGCCAGGGAC	CKPLARD	++	--
23641	20014	CAGCCAGAGTCGAGGAGCTGG	QPESRSW	++	---
24505	37664	GAGATGGAATCGCGGGTCTGG	EMESRVW	++	---
27331	38756	GTAATGAGCAGCCGGACGTGG	VMSSRTW	++	---
34324	40848	TGCCGACCACAAGCTGGAGCC	CRPQAGA	++	--
28109	38414	AGGCTGCCGTCAGTATATCCT	RLPSVYP	++	--
22754	37153	GTGATGGAGGCAAGATCTTGG	VMEARSW	++	---
21053	36459	CTCGCTAGATCAGGGCCCAAC	LARSGPN	++	---
29112	37956	ATACTGGCCGACCGTAATTGG	ILADRNW	++	---
25409	38085	TGCAGAGGCGAGCAGAAGATG	CRGEQKM	++	--
21634	36649	AGGTTAATGGATGTTTACCCT	RLMDVYP	++	---
35581	41596	TGTTCGAAGCGCCCTTGCGGG	CSKRPCG	++	--
24344	16639	ATCATGTCGTCTAGGTCCTGG	IMSSRSW	++	---
25668	38177	AAAGATGGTTACTCTTCTTGG	KDGYSSW	++	--
21156	36545	GACCTGTCCAGTCAAACTTGG	DLSSQTW	++	---
30707	39796	AAAGACGATTGGAACACCTGG	KDDWNTW	++	--
20860	36412	AAGATGGATAGTGTCAGATGG	KMDSVRW	++	---
25639	37933	GTCATGAGCGATCGCGCTTGG	VMSDRAW	++	---
32093	40407	TGCAAGCCCGGTATGGGATCT	CKPGMGS	++	--
31927	38756	GTTATGTCTTCTAGAACATGG	VMSSRTW	++	---
25589	38025	CGCTTGGAGGATCGGAAGTGG	RLEDRKW	++	---
24710	36914	CCGATGGGGTCCGCAATGTGG	PMGSAMW	++	---
24870	37684	CTCTGCAGACCGTGTAGCGAT	LCRPCSD	++	---

22166	16607	GATTTGTCAAGTCACAACTGG	DLSSHNW	++	---
20955	36454	ATTATGAGCTCGGCGACCTGG	IMSSATW	++	---
23420	37141	GATTTGTCGAGCAGGGACTGG	DLSSRDW	++	---
22821	37174	CTCCACAGGCTTTCAAGCAAT	LHRLSSN	++	---
30833	38746	TGTAAAAGCGAACATGTGCGC	CKSEHVR	++	--
28958	38883	GTAATGCAGGACCGGACGTGG	VMQDRTW	++	---
22202	36937	ATCTTAAGTGATCGTAACTGG	ILSDRNW	++	---
35194	40141	AGAACCTATGAAGTGTATCCT	RTYEVYP	++	---
23725	37298	AGGCCCGAGTCCTCACGGTGG	RPESSRW	++	--
24217	36624	ATAATGACCGATAGAATATGG	IMTDRIW	++	---
29420	39471	GTTGCAAGAACTGGCTGGGAT	VARTGWD	++	--
25336	38064	GACATGCAAAGCCGTGATTGG	DMQSRDW	++	---
27416	38789	CTGATGAGACCATGCAGTGAG	LMRPCSE	++	--
27354	38413	GTAATGCAATCAAGGACTTGG	VMQSRTW	++	---
35912	41740	GGCGGAAGCCCGTGTCGACCG	GGSPCRP	++	--
33963	41090	TGCACCTCGCAAACAGGGCAT	CTSQTGH	++	--
32373	40510	TGTAGAGAAGGGAGAAGCTCG	CREGRSS	++	--
22445	18996	CTTCACAGATTAGGAGTATCC	LHRLGVS	++	--
34101	41142	TGCAATCATCCTATGACAGCG	CNHPMTA	++	--
32332	39103	AAAGACGAATTCACTATCTAT	KDEFTIY	++	---
24105	37623	AGAATGGAGAGTCAGTCGTGG	RMESQSW	++	---
32966	40720	TGTGGAGAGTCAGTTAAACCT	CGESVKP	++	--
27958	38975	TGTAAGGAGGGGACCAGAGGC	CKEGTRG	++	--
35236	41516	GGGTGTAGACCCTGCCCTACT	GCRPCPT	++	--
21369	36639	CTATGCAAGCCCTGCATGACT	LCKPCMT	++	--
34372	40338	TGCAAGCCGAGGTCTGCTGAG	CKPRSAE	++	--
30868	39633	GGTGATGAGTGGAAAACTTGG	GDEWKTW	++	--
23119	37276	TACTTCACAGGCTTCAAAGAG	YFTGFKE	++	--
22881	36975	TTGCACAGATTGAGTACTAAC	LHRLSTN	++	---
22307	36975	CTCCATCGCCTCTCAACCAAC	LHRLSTN	++	---
32908	38400	TGCCTCAGGGCTAGACCCGAG	CLRARPE	++	--
22962	36963	CCCTTACAGAGTCGAGACTGG	PLQSRDW	++	---
23736	37494	ATCATGAGCAGTGCCATGTGG	IMSSAMW	++	---

25816	14269	TATGCACGCACTGGTCCCAAC	YARTGPN	++	---
20963	36459	CTAGCCAGATCAGGCCCAAAC	LARSGPN	++	---
22420	37022	GATATGTCGGCCAGGGCTTGG	DMSARAW	++	---
31008	40021	TGTGCACCATACCGACATGAG	CAPYRHE	++	--
32568	40550	GGAGGGGAATTCAGACATTGG	GGEFRHW	++	--
33492	38975	TGTAAAGAAGGGACAAGGGGG	CKEGTRG	++	--
23164	37293	TACTTCACAGGATTTAGAGAG	YFTGFRE	++	--
23943	17888	GTGATGACTGCCAGGGACTGG	VMTARDW	++	---
22187	36933	CTATGTCGCCCGTGCTCGACC	LCRPCST	++	---
27132	14190	TACTCCAGGGCCGGTCCTAAT	YSRAGPN	++	---
20873	36417	TGTAAACCAAGAGAAGGCACA	CKPREGT	++	--
31003	40018	CCTGGAAGCACCAGAACATGG	PGSTRTW	++	--
21451	36674	GTAATGTCGTCAGCGAACTGG	VMSSANW	++	---
29495	39495	TGTAAGGGATTACCCGTACCT	CKGLPVP	++	--
32863	39128	ATTCCCGGTCACAAGTGTGCT	IPGHKCA	++	--
24981	14924	TACTCGAAAATGGGTAAAAAT	YSKMGKN	++	--
20825	36351	ATCTTGTCAAGTAGCACGTGG	ILSSSTW	++	---
34156	41163	GGAGGTGGTACTGTACGCTGG	GGGTVRW	++	--
22734	37148	GATATGGCGAGCAACAGGTGG	DMASNRW	++	---
23534	37429	ATAATGAGCGACCGCGTCTGG	IMSDRVW	++	---
35074	41009	GGTGGAGGCACTAGTAAGTGG	GGGTSKW	++	--
26112	18835	GTATTATCTAGCAAGACATGG	VLSSKTW	++	---
22639	17065	AAAATGCCTAGTAGGGACTGG	KMPSRDW	++	---
26767	17590	ATTCTAAGTGACCGAAGTTGG	ILSDRSW	++	---
23388	37108	GTCCTTTCGGACAGGAATTGG	VLSDRNW	++	---
27676	38640	AAAAATGACTATACGGTTTTC	KNDYTVF	++	--
28347	38422	ATTCTTTCACATGCTACTTGG	ILSHATW	++	---
23899	37174	TTACATCGTCTGAGTTCGAAC	LHRLSSN	++	---
23809	37522	GACATGATGAGTAGAGACTGG	DMMSRDW	++	---
32092	40203	TGCCGTGAAGGAACCCCACCA	CREGTPP	++	--
30960	40001	TGTGGTAAAGGGGGGCCTGTA	CGKGGPV	++	--
32065	38842	TGTAAGCCTCCCAGCGGGGAT	CKPPSGD	++	--
21384	36643	GTCCTCTCAGATCGCCTATGG	VLSDRLW	++	---

26283	38297	AGAGAACCGGGTGTGCGATGG	REPGVRW	++	--
31134	39206	TGCAGCGTCGTTACGGGCTCG	CSVVTGS	++	--
25443	37708	TCGGGCGAATCTCGACTCTGG	SGESRLW	++	---
27959	38976	GGATGCGGTACAAAGGTGGGG	GCGTKVG	++	--
28560	39187	TGCAAGCCGCCAATGGCTCCA	CKPPMAP	++	--
32795	40659	TGTATGCCCCAAGCCGGGAGA	CMPQAGR	++	--
22952	37216	TTGAGTCGGATCGGAAGGGAT	LSRIGRD	++	--
36088	18438	CTCTGGGATGGGACTTTTGCA	LWDGTFA	++	--
29183	37399	AAATCCGAATTCAAGATTTTT	KSEFKIF	++	--
33381	40870	TATGAACCTGGGTGCAAAATT	YEPGCKI	++	--
22636	37108	GTATTGAGCGATCGAAATTGG	VLSDRNW	++	---
24041	37598	CCCATGGAAAGTAGGGAATGG	PMESREW	++	---
23881	37556	ATAATGTCGTCACGAGAATGG	IMSSREW	++	---
22637	36971	AGGGATGAATTCACAAGCTAC	RDEFTSY	++	---
27062	13731	TATGCTAAGAGCGGATGGAAC	YAKSGWN	++	--
25145	37985	ACCTCAGAATACAAATACTAT	TSEYKYY	++	--
28627	39213	GGTTGCCGCCATGGACCCATA	GCRHGPI	++	--
28685	39228	TGTAAAGGGCAAGGTCCAAGC	CKGQGPS	++	--
23179	37298	CGACCGGAGAGTAGTAGATGG	RPESSRW	++	--
29910	38660	ATCTTGGATAGTAGAAAGTGG	ILDSRKW	++	---
32014	40383	TGTGGTAAGCGAGACGCGGAC	CGKRDAD	++	--
26699	38556	CGCGGGGAGAGCAGAGGATGG	RGESRGW	++	---
25813	38214	TTGCTCGCCGATAGAACATGG	LLADRTW	++	---
28100	38556	AGGGGTGAATCGCGGGGCTGG	RGESRGW	++	---
29313	19688	AGGGAAGGATATAGTCATTGG	REGYSHW	++	---
22496	36825	TTAGCACGCCAATCTTATAAC	LARQSYN	++	--
35928	41748	TATAGTAAGCGCAACGTCAAC	YSKRNVN	++	--
24013	37540	CTCCACCGCCTTCATCCTAAT	LHRLHPN	++	--
28255	39079	TGTATGTCGGGTCCGAGGCCG	CMSGPRP	++	--
23561	37437	CTGTTGTCCGATAGGACGTGG	LLSDRTW	++	---
23941	36978	ATCGCATCCCGAGGCTGGGAC	IASRGWD	++	---
22269	36963	CCACTCCAATCGAGGGATTGG	PLQSRDW	++	---
23330	37352	GTCCTAAGTGACCGATCCTGG	VLSDRSW	++	---

24685	37815	GGCGGAGATTATTCATCATGG	GGDYSSW	++	--
26414	38432	CGCGACGAGTATGTCCACTGG	RDEYVHW	++	---
27205	38716	TGTAAAGAAGGCGTGCGTTGG	CKEGVRW	++	--
25385	17708	GATATGGTATCCCGGTCATGG	DMVSRSW	++	---
22646	37113	AAGGGAGAGTCGAGAGAGTGG	KGESREW	++	---
32509	40558	TGCGACTCTAAGACAGGACAT	CDSKTGH	++	--
27276	38735	TTTCCAGGGAGTTGCAAAGAA	FPGSCKE	++	--
34346	39113	CGAGGCGAATTTTGTGGAGGG	RGEFCGG	++	--
31486	39326	CGGGAGGGTACCAGTTACTGG	REGTSYW	++	--
32531	40562	GGCTGCAGGAAGGGGGACATA	GCRKGDI	++	--
24332	37677	AGGGAAGACTTCGTCAGGTGG	REDFVRW	++	---
25197	17708	GACATGGTGAGTCGGAGCTGG	DMVSRSW	++	---
22088	36639	TTGTGTAAACCGTGTATGACG	LCKPCMT	++	--
24220	16593	GATATGTCTTCCAGGATTTGG	DMSSRIW	++	---
26687	38550	TGTCGCCCCAAACAGGTCGAT	CRPKQVD	++	--
34373	41238	TTGTGGAAAGAGTGCAAACCA	LWKECKP	++	--
23832	37429	ATTATGTCGGACAGGGTGTGG	IMSDRVW	++	---
20938	36446	ATACTAGCAAGTAGAGACTGG	ILASRDW	++	---
32503	40556	ATGGACGGTGTCTGCAAAGGA	MDGVCKG	++	--
27712	38894	CTCGCGCGTACAGGTTGCGAC	LARTGCD	++	--
29908	17155	CTAGCGCGCAATGCTTCTAAT	LARNASN	++	--
32304	40481	TGTAAACCCAGCCCCATGCCC	CKPSPMP	++	--
23238	18231	CCGCTCGACTCATACAAGTGG	PLDSYKW	++	---
29658	39555	TGTAAACCTCCATCGGGTCCT	CKPPSGP	++	--
24833	17686	ATTGGTGAGTCACGACTATGG	IGESRLW	++	---
31800	40298	TGCAAGCCACCTATGGATGGT	CKPPMDG	++	--
21911	36825	CTTGCAAGACAATCATACAAC	LARQSYN	++	--
24321	17888	GTAATGACCGCACGAGATTGG	VMTARDW	++	---
21135	36533	ATAATGGCAAGCCATGGCTGG	IMASHGW	++	---
23789	37412	GACATGAGTGTACGCACGTGG	DMSVRTW	++	---
31398	39511	ATTAACGGAGGCAAGTGTGAC	INGGKCD	++	--
34508	41289	TATGAGCCGGGTTGCAAACAA	YEPGCKQ	++	--
31933	40352	TGCAAGCCTGGAACTTGGGAA	CKPGTWE	++	--

22963	37224	GACTTGCAAAGCAGGGAATGG	DLQSREW	++	---
23304	37148	GACATGGCATCGAATCGATGG	DMASNRW	++	---
34043	41123	TGCAAGCCGGGCCCCATCGGA	CKPGPIG	++	--
34704	40855	TGCAAGCCGCCAATGTTTGAG	CKPPMFE	++	--
23298	19988	AAAGATTCCTTCACCTCGTGG	KDSFTSW	++	--
23122	18663	CTTGCAAGGACGGCTCTTAAT	LARTALN	++	--
30682	39322	AAGGACGAATTTACCGTATAC	KDEFTVY	++	---
22211	17986	ATGCTAAGTTCACAGACTTGG	MLSSQTW	++	---
21251	36580	GATTTGAGAGCGGCTACGTGG	DLRAATW	++	---
25378	37120	CGTCTAAGCAGTCAGACTTGG	RLSSQTW	++	---
23465	37073	CTAATGTCGAGCGCCAAGTGG	LMSSAKW	++	---
33851	41048	CCGTGCGGTGGGAAACCAATC	PCGGKPI	++	--
29779	39593	CGAACCTATGACGTCTACCCG	RTYDVYP	++	---
24200	20014	CAACCCGAAAGCCGCTCGTGG	QPESRSW	++	---
23412	36918	ATAATGACCTCTCGTGATTGG	IMTSRDW	++	---
21642	36734	GACATGGGGAGCCACAAGTGG	DMGSHKW	++	---
25084	14219	TATGCGAGGCTAGGTCCGAAC	YARLGPN	++	---
20723	36351	ATACTTAGCTCGTCAACATGG	ILSSSTW	++	---
23853	37541	CGAGATGAATACACTGGTTTT	RDEYTGF	++	--
30471	39840	TGTCGGCCCCAAATGGCCTCG	CRPQMAS	++	--
29848	38214	CTATTGGCTGACCGGACTTGG	LLADRTW	++	---
24758	17065	AAGATGCCGTCGCGCGATTGG	KMPSRDW	++	---
29730	17835	CAGGGTGTCTCAAGGGAGTGG	QGVSREW	++	---
23364	36643	GTACTCTCTGACCGTCTCTGG	VLSDRLW	++	---
23029	37251	GGAAGCGAATTCTCGAGATGG	GSEFSRW	++	--
26622	38518	ATGCTCAGCGATCGCAAATGG	MLSDRKW	++	---
31004	40019	TCTATGCAATCAAGGTCGTGG	SMQSRSW	++	--
22236	36624	ATCATGACTGATAGGATTTGG	IMTDRIW	++	---
28981	39326	AGAGAAGGCACGTCATATTGG	REGTSYW	++	--
27943	38689	GATCTCAGGGACCGTACGTGG	DLRDRTW	++	---
27953	38973	TGTAAGAAAGACGAGGCAGTT	CKKDEAV	++	--
22124	36914	CCAATGGGTAGTGCTATGTGG	PMGSAMW	++	---
24496	36624	ATCATGACGGACCGCATCTGG	IMTDRIW	++	---

25794	14059	TACAGCAGAGTCGGACCAAAC	YSRVGPN	++	---
21121	36529	ATTATGTCATCGAACATTTGG	IMSSNIW	++	---
28071	39018	AGAACTGGAACATCCTGTTTA	RTGTSCL	++	--
27390	38780	AGAGACGGGTATAGTGCCTGG	RDGYSAW	++	--
34811	41415	CCCGGACCTGAGAGAAAGTGG	PGPERKW	++	--
21073	36507	GACTTGCAAGCCAGATCATGG	DLQARSW	++	---
24369	37437	TTACTAAGTGACCGAACCTGG	LLSDRTW	++	---
34833	41420	TGTGCACCTGTCTACCGCGAG	CAPVYRE	++	--
26996	36877	ATCATGTCAAGCCATGGGTGG	IMSSHGW	++	---
28358	38815	GACCTTCGAGACCGTAAATGG	DLRDRKW	++	---
22296	36971	CGAGATGAATTTACTTCTTAT	RDEFTSY	++	---
34218	41181	GGGTGTGGCACGAAGATTGGG	GCGTKIG	++	--
32402	40475	ATCATGGGCGACCGCATATGG	IMGDRIW	++	--
35580	41451	GAGATGGAAAGTGTCCGCTGG	EMESVRW	++	--
22676	36769	CTACATCGTCTGGGTTATGAT	LHRLGYD	++	---
26486	38462	GGTGGAGAATATTCAACTTGG	GGEYSTW	++	---
24601	37309	ATTTTGTCAAGCAGGGAGTGG	ILSSREW	++	---
24705	37823	ATTATGGCCGATCGTGCTTGG	IMADRAW	++	---
25691	37686	CACTGCAAGCCCTGTCTGACC	HCKPCLT	++	--
32688	38804	TGTAAGCCTTACTCACGCGAG	CKPYSRE	++	--
30616	39881	AGGAACGAGTTCACAGTGTAC	RNEFTVY	++	--
33376	18969	GTCTTAACAAGCCAGATTTGG	VLTSQIW	++	--
33649	40965	TGTAAGAATACTAAGGTTGAT	CKNTKVD	++	--
33755	41005	TGTAAGCCTGATAAGCCCCTT	CKPDKPL	++	--
23893	37036	ATTATGGCAGACAGAGGGTGG	IMADRGW	++	---
29819	39605	TACGTGAGAAGCTGCCCGATG	YVRSCPM	++	--
33897	41067	GTGGGACAGCGTTGCGCTGAG	VGQRCAE	++	--
29990	39662	TGCAAGCCCCAGACTCCACAG	CKPQTPQ	++	--
29780	39326	AGGGAGGGTACATCGTATTGG	REGTSYW	++	--
21851	36800	CCCCTCGATAGTAGGTCCTGG	PLDSRSW	++	---
21233	36573	GAGATGGCAAGTCATAGCTGG	EMASHSW	++	---
28578	39195	GCTATGCAGGACCGCAGTTGG	AMQDRSW	++	---
28191	17910	GTAATGAGCAGCGCTGGATGG	VMSSAGW	++	--

20706	36344	TATTCAAAAGCAGGAGGGGGT	YSKAGGG	++	---
23320	37349	AGCGACGGGGTTTCTAGGTGG	SDGVSRW	++	--
30997	39670	AGAGATCAATTCACGTCGTAT	RDQFTSY	++	--
32366	40481	TGCAAGCCTTCTCCGATGCCG	CKPSPMP	++	--
27673	38883	GTTATGCAAGATAGAACCTGG	VMQDRTW	++	---
29877	14265	TACGCTCGAAGCGGACATAAT	YARSGHN	++	--
23781	36824	GGAAGCGAGTTCAGCACCTGG	GSEFSTW	++	---
23756	37438	ATACTTAGCGCACGAGATTGG	ILSARDW	++	---
32858	38735	TTCCCCGGATCGTGTAAGGAG	FPGSCKE	++	--
25123	37623	CGCATGGAATCACAAAGTTGG	RMESQSW	++	---
24135	14574	TACAGCCGTTTGGGACCGAAC	YSRLGPN	++	---
24003	36902	GAGATGGCATCGCGGGACTGG	EMASRDW	++	---
33607	40944	GGCTGCGGTACAAAACAGGGG	GCGTKQG	++	--
30886	39593	AGGACATACGATGTATATCCT	RTYDVYP	++	---
27123	38689	GACTTACGAGATAGGACTTGG	DLRDRTW	++	---
27578	37494	ATTATGTCGTCAGCTATGTGG	IMSSAMW	++	---
30236	17514	GAGAGCAGCAGCAGGACCTGG	ESSSRTW	++	---
20926	36329	ATATTGACAAGCGCGACGTGG	ILTSATW	++	---
26077	38297	AGGGAGCCAGGCGTTAGATGG	REPGVRW	++	--
27459	38805	TGGACTCCCGGTTGTAAGGCT	WTPGCKA	++	--
27774	17300	TACTCGAAGAGTAATTGTAAC	YSKSNCN	++	--
30626	39886	TGTAAAAGTACGAACGGTATA	CKSTNGI	++	--
24463	37036	ATCATGGCCGATCGTGGATGG	IMADRGW	++	---
20999	36363	ATTTTATCATCCCAATCGTGG	ILSSQSW	++	---
34025	41053	TGTAAAGGTGATGCGAAAGCA	CKGDAKA	++	--
36008	39605	TATGTCCGTTCATGTCCAATG	YVRSCPM	++	--
24280	37664	GAAATGGAGAGCAGAGTTTGG	EMESRVW	++	---
23987	14574	TATTCGAGGCTAGGCCCCAAC	YSRLGPN	++	---
24591	37290	ATCCTCGAAAGTAGAGGCTGG	ILESRGW	++	---
24784	18089	GCGGGCGAATCGCGCGGTTGG	AGESRGW	++	---
20788	36344	TACAGCAAGGCCGGTGGAGGG	YSKAGGG	++	---
25389	38064	GATATGCAGTCTAGGGACTGG	DMQSRDW	++	---
22564	37044	GTGGCTACGAGGGGGTGGGAT	VATRGWD	++	---

28231	39070	TATGTTCGTTCACAGATGTTG	YVRSQML	++	--
31602	40229	TGTAGACCACAGACGCCATCG	CRPQTPS	++	--
24628	37652	CGAGAGGATTATGTAAAATGG	REDYVKW	++	---
24412	37708	AGTGGGGAGAGCAGGTTGTGG	SGESRLW	++	---
30179	39734	TGCAAGCGAGATGCCGAAAGC	CKRDAES	++	--
22217	36944	ATAATGAGTAGTTCGATGTGG	IMSSSMW	++	--
26039	37833	AAGGGAGATTCACGTAGTTGG	KGDSRSW	++	---
33388	38447	TGTAAAGCTACTATACCCGGA	CKATIPG	++	--
23806	18996	TTGCACCGCTTGGGTGTGTCT	LHRLGVS	++	--
24340	17590	ATTTTGTCCGACAGGAGTTGG	ILSDRSW	++	---
35108	41491	TGTGGAAAGCCAATGACCGCT	CGKPMTA	++	--
26782	14059	TACTCGCGTGTTGGTCCTAAT	YSRVGPN	++	---
31369	38132	GTGCATGATTACATGTCCTAT	VHDYMSY	++	--
30750	39930	CGCACTCCCACTTGCGCGGGA	RTPTCAG	++	--
34330	41222	CGTGACGGATCATGTAAAGCA	RDGSCKA	++	--
26444	37499	GTGCCCAGCTCAGTTCGCTGG	VPSSVRW	++	--
30184	39736	TTAAGGTCTGGGTGTGGACCA	LRSGCGP	++	--
31412	40154	TGCCGCGGCGATAACGGGGTG	CRGDNGV	++	--
22694	37128	AGGACACCCACAACATACCCA	RTPTTYP	++	--
23062	36917	ATTCCAAGTGACCGGTTGTGG	IPSDRLW	++	---
29102	38041	AGACCTGACAGTGTACGCTGG	RPDSVRW	++	--
22454	37036	ATCATGGCCGATCGTGGTTGG	IMADRGW	++	---
21470	36399	CCGATGGCCTCGTCTACGTGG	PMASSTW	++	---
25234	38025	AGACTCGAAGACCGCAAATGG	RLEDRKW	++	---
29778	39592	AGCATGCAGGATCGAAAATGG	SMQDRKW	++	---
21046	36494	CGAGAGGACATGGTGAGGTGG	REDMVRW	++	--
23564	37438	ATTTTGTCAGCCCGGGACTGG	ILSARDW	++	---
26496	38467	TACTTTACGGGAGTCCGCTCG	YFTGVRS	++	--
23407	37113	AAAGGTGAAAGTCGCGAGTGG	KGESREW	++	---
22791	36734	GATATGGGATCGCATAAATGG	DMGSHKW	++	---
34776	41026	TGCAAGGCCAACGCACCAGAC	CKANAPD	++	--
29270	39422	TGCAAACCACAGGCAGGCGGA	CKPQAGG	++	--
23667	14958	TACTCGCGAACAGGTCCTAAT	YSRTGPN	++	---

35601	39856	TGTAAACCTAAGCAGATAGAG	CKPKQIE	++	--
20985	36468	GGTGGGTTGGGAAGTCATTGG	GGLGSHW	++	--
29199	38825	CGAGACGAGTTTCGGAGCTGG	RDEFRSW	++	--
22483	37047	CCGATGTCCTCGCATGGTTGG	PMSSHGW	++	---
23596	37315	CTATGCCGGCCATGTAGTAGT	LCRPCSS	++	---
35295	41494	TACTACACAGGCTACAAAGAG	YYTGYKE	++	--
34796	41145	AAAGAGGGTACGAGCCGTTGG	KEGTSRW	++	--
29929	39641	TGGACTCAGGCGTGTCCGAAA	WTQACPK	++	--
23155	37290	ATATTGGAGTCCCGCGGGTGG	ILESRGW	++	---
28480	39154	GGCTGTCGGCCGCAAGCTGGC	GCRPQAG	++	--
24931	37911	CTCGCCCGCATCGGTTGGGAC	LARIGWD	++	--
26598	37900	CGCATGGAGGATCGTATCTGG	RMEDRIW	++	---
21585	36720	CAAATGGCAAGCGTCAAATGG	QMASVKW	++	---
33816	41034	TGTCGACCCGGCGCAATTGCC	CRPGAIA	++	--
25063	37956	ATCTTAGCGGATAGGAACTGG	ILADRNW	++	---
32655	40606	TGTACGCGTCTTTCGGCCCCG	CTRLSAP	++	--
24726	37833	AAAGGGGACAGCAGATCATGG	KGDSRSW	++	---
21480	17986	ATGTTGAGCAGTCAAACCTGG	MLSSQTW	++	---
30145	38156	ATATTGAGCGATAGGATGTGG	ILSDRMW	++	---
23133	37022	GACATGAGTGCTCGTGCCTGG	DMSARAW	++	---
24436	37252	CTCAGCCGTATCTCTCACAAC	LSRISHN	++	--
26511	38471	TGTGTCGAAGGAAGGGCTCCC	CVEGRAP	++	--
25231	37818	TTATGCCGCCCTTGCTCGGGG	LCRPCSG	++	--
27885	38952	TACAGCACTAATTGCAAATCC	YSTNCKS	++	--
24237	37652	AGGGAAGACTACGTCAAGTGG	REDYVKW	++	---
32896	40694	TGTAAGCCTCCCCCTTTTGCG	CKPPPFA	++	---
31110	39886	TGCAAGTCCACTAATGGAATC	CKSTNGI	++	--
22026	36877	ATTATGAGCTCGCACGGCTGG	IMSSHGW	++	---
32915	40168	TATTTCCCTGGATGTAAAGAG	YFPGCKE	++	--
22500	36825	CTGGCCCGTCAGAGCTATAAT	LARQSYN	++	--
26049	14185	TATGCGAAAACGGGCTGGAAT	YAKTGWN	++	--
21736	36762	CGACTTGAATCGAGAGAGTGG	RLESREW	++	---
35923	38028	TGCGGTAAGATAAAACCAGGT	CGKIKPG	++	--

21277	36447	CAGTTATCTTCAAGTACATGG	QLSSSTW	++	---
23801	37520	GTGATGCAGAGTAGGGATTGG	VMQSRDW	++	---
25263	17711	GTCATGGCCGACCGAGCATGG	VMADRAW	++	---
29364	17561	AATCTAATGGGGTGTACAGGC	NLMGCTG	++	--
24410	37514	TCATTGGAATCTCGTTCATGG	SLESRSW	++	---
27309	17038	ACAATGAGTGATCGAACATGG	TMSDRTW	++	---
25627	17590	ATCCTTAGTGATCGCTCCTGG	ILSDRSW	++	---
25125	37654	TGGTCAACTCATTGCTGCGCT	WSTHCCA	++	---
25758	37520	GTAATGCAATCACGCGACTGG	VMQSRDW	++	---
27334	14632	TACAGCAGAATAGGGCCAAAC	YSRIGPN	++	---
21280	36592	CTACATCGTTTACTCCCGGAC	LHRLLPD	++	---
23387	36971	AGGGACGAGTTCACCAGCTAC	RDEFTSY	++	---
26127	38311	AGGGACGACTACGTTCACTGG	RDDYVHW	++	---
22771	37158	TATTTGAAAAGTCAGAGCTGT	YLKSQSC	++	--
27565	38844	TGCCCTCAGAAAGGGCAGGAG	CPQKGQE	++	--
29153	39386	TGTAGGTCTGGAGACGCTGCG	CRSGDAA	++	--
23701	37114	AAGCTACAGGAAAGAACTTGG	KLQERTW	++	---
30043	39680	TATTTTACTGGCCGATTTGAC	YFTGRFD	++	--
27656	17675	ATAATGAGCGATCGACTGTGG	IMSDRLW	++	---
31378	40146	GAACCCCAAAGCCGTCATTGG	EPQSRHW	++	---
30086	14620	TACTCACGCATGGGGCCTAAC	YSRMGPN	++	---
28713	39239	CGTGACGGCGAGTCGTACTGG	RDGESYW	++	--
28709	14620	TATTCTAGAATGGGACCCAAT	YSRMGPN	++	--
27570	36876	GACTTAACAGCCAGGAATTGG	DLTARNW	++	---
23225	37315	CTCTGTAGACCTTGCTCTTCT	LCRPCSS	++	--
23751	37499	GTCCCATCTAGCGTAAGGTGG	VPSSVRW	++	--
25120	37069	AGAACAGTGACGGTTTATCCA	RTVTVYP	++	--
26751	38571	CGCACATATGACGCATACCCG	RTYDAYP	++	---
33294	40355	TGTATTAAGCCAATGACCGCA	CIKPMTA	++	--
32901	40697	CTTATGCAGGACCGCAGCTGG	LMQDRSW	++	---
28214	39068	TACTACACGGGAAAATGTGAC	YYTGKCD	++	--
23405	37186	TTACATCGGCTCCAGTCGACC	LHRLQST	++	--
25105	37968	ACAGAATATATGTGTCGGCCC	TEYMCRP	++	--

26951	38640	AAGAACGATTACACTGTCTTT	KNDYTVF	++	--
29341	14384	TACTCCCGGCTGGGCTCGAAC	YSRLGSN	++	--
24659	37804	TGCACCAGCAAAAATGGACAT	CTSKNGH	++	--
20922	36437	CTATGCAAACCTTGCTTAGAT	LCKPCLD	++	---
22468	36709	AGGGAAGATTTCGTGAGCTGG	REDFVSW	++	---
24262	37129	AAAGACGATTACTCTACGTGG	KDDYSTW	++	---
26466	13769	TTCTCCAGGATGGGTCCTAAT	FSRMGPN	++	--
30650	39895	CTGAGAGAGGGGGAATGTAAA	LREGECK	++	--
24028	18089	GCAGGAGAAAGTCGTGGGTGG	AGESRGW	++	---
32505	40557	TGCAAAGCTGTGTCGCACGAT	CKAVSHD	++	--
30217	39746	GATTACGCCAGCCGAGATTGG	DYASRDW	++	---
28790	38492	AAGGATGGTCATAGTTTGTGG	KDGHSLW	++	--
22221	36533	ATTATGGCTTCGCACGGATGG	IMASHGW	++	---
25253	37910	TACTCTAGGGTAGGAGGGGGA	YSRVGGG	++	---
26081	38034	AGAATGGAATCAATAAAATGG	RMESIKW	++	---
32298	40478	ACAAAAAACTCGACCACGTGT	TKNSTTC	++	--
23208	37309	ATCCTCAGTTCGCGCGAATGG	ILSSREW	++	---
21714	16595	AGAACGCCGACAGTTTACCCC	RTPTVYP	++	---
31935	40146	GAGCCTCAGTCGAGGCACTGG	EPQSRHW	++	---
20704	36342	GTTCTTTCGTCTAGCATGTGG	VLSSSMW	++	--
21229	36571	TTATCACGTATTGGGATGAAC	LSRIGMN	++	---
22653	15480	TACAGCAAGTTCGGTCCCAAC	YSKFGPN	++	--
21994	36820	CTGTGTAAGCCGTGTAACACT	LCKPCNT	++	--
35157	41308	GACGGATATTCAAGGGAATGG	DGYSREW	++	---
23172	16628	CTGACTCGTATCAGCCACAAC	LTRISHN	++	--
32946	39881	CGAAATGAATTTACTGTATAT	RNEFTVY	++	---
26439	37911	TTAGCGAGAATTGGCTGGGAT	LARIGWD	++	--
23863	36933	CTGTGCAGGCCCTGTAGCACC	LCRPCST	++	--
27846	38942	TGTAAACCTCAATCAGGTTGG	CKPQSGW	++	--
26530	38160	GGCAACGAATTCTCATCATGG	GNEFSSW	++	---
28113	39032	TGCAAACCACCACCCAAGATC	CKPPPKI	++	--
25167	37910	TATAGCCGTGTCGGTGGAGGC	YSRVGGG	++	---
26852	18173	GATCCAGCTAGCAGAGCTTGG	DPASRAW	++	---

24905	37900	AGAATGGAAGACAGAATTTGG	RMEDRIW	++	---
31697	40264	AAGCATGACTACTGTGCACCG	KHDYCAP	++	---
28749	38098	GGCGTGAATGGCTGTAAACCT	GVNGCKP	++	--
20759	36364	CTGTGCAAACCGTGCCTACAA	LCKPCLQ	++	--
31716	40270	TGCAAGTCACGAAGCCTTGAT	CKSRSLD	++	--
29630	38840	GAAAATGCCTCACGTGCTTGG	ENASRAW	++	---
21351	36626	TTGAGCAGGATAGGGCAGAAT	LSRIGQN	++	---
23236	37318	ATTATGTCATCTCGTGGTTGG	IMSSRGW	++	---
21313	36592	TTGCACAGATTGTTGCCAGAT	LHRLLPD	++	---
32471	40462	CCGGTAGAATCACGAACCTGG	PVESRTW	++	---
24450	17686	ATCGGAGAAAGCCGTCTGTGG	IGESRLW	++	---
34173	40911	TGTAAACCCGTGCCTCCAGAA	CKPVPPE	++	--
22738	36762	CGGTTGGAGAGCCGTGAATGG	RLESREW	++	---
35301	41534	TCGATGCAGGATCGTAGGTGG	SMQDRRW	++	--
23786	37514	AGTCTTGAAAGCAGGAGCTGG	SLESRSW	++	---
36217	41890	TGTAATAAACCCATGTATGCA	CNKPMYA	++	--
22136	36917	ATACCTTCAGATAGACTATGG	IPSDRLW	++	---
24930	37910	TATAGTCGCGTCGGCGGGGGG	YSRVGGG	++	---
35594	41601	GATATGGGAGGATATGATTGG	DMGGYDW	++	--
22394	37014	ATACTTTCGGATCGGATATGG	ILSDRIW	++	---
21330	16612	CTTTCGAGGGTCGGCTTCAAC	LSRVGFN	++	---
32676	38229	TACCATCGCATCGGCCCTAAC	YHRIGPN	++	--
27557	38840	GAGAACGCGAGTAGGGCATGG	ENASRAW	++	---
21955	36783	AATGCTTTACGCGGATGGGAT	NALRGWD	++	---
25141	37529	CGTGAGGAGTCAAGGTCCTGG	REESRSW	++	---
28524	39173	GATATGCGGGATCGCATGTGG	DMRDRMW	++	--
21323	36571	CTTAGCAGAATCGGCATGAAT	LSRIGMN	++	---
24010	36643	GTATTAAGTGACAGGTTGTGG	VLSDRLW	++	---
27849	38761	AGAGAGGAGTGGGTTGCATAT	REEWVAY	++	---
31199	18904	CATGTTACTACCCACTGCAGT	HVTTHCS	++	--
29621	39544	AGGGGGGATAGTAGAAGCTGG	RGDSRSW	++	---
35608	38834	CGCGACGAGTATATGAGTTGG	RDEYMSW	++	--
25365	14632	TACTCTCGGATTGGTCCCAAT	YSRIGPN	++	---

25998	37989	GGAGACGGTACTTCTAGGTGG	GDGTSRW	++	--
32811	40663	AGGTCTGAGTTTCAGGTATTT	RSEFQVF	++	--
24812	36751	TATAGTAAATTGCAGAAGAAT	YSKLQKN	++	--
22011	36869	AACATGGCGTCGCATACCTGG	NMASHTW	++	---
23079	36922	GTTGCGTCTCGCGGTTGGGAT	VASRGWD	++	---
34568	41308	GATGGTTACAGTCGTGAGTGG	DGYSREW	++	--
31938	39326	CGAGAAGGCACGAGTTACTGG	REGTSYW	++	--
34818	41417	GTGGGCGGCACTTGTAAGTAC	VGGTCKY	++	--
31295	39336	CGTGGAGATTACACACCGTGG	RGDYTPW	++	--
27835	38780	CGGGATGGGTACTCAGCGTGG	RDGYSAW	++	--
31801	40018	CCCGGCTCTACTCGGACCTGG	PGSTRTW	++	---
26649	38529	ACAAAAGACGGGCTCTGCGCA	TKDGLCA	++	--
31592	40225	ATGCAGGGAACGAGTTGCTTG	MQGTSCL	++	--
21296	36602	GTTATGGCGTCGTCAAGTTGG	VMASSSW	++	---
25057	37910	TACTCCAGGGTTGGTGGAGGA	YSRVGGG	++	---
27095	38251	GAGCCGGAGTCCAGGAAGTGG	EPESRKW	++	---
23847	37537	GGAAGTGAATATTCCAAATGG	GSEYSKW	++	--
22548	37069	CGGACTGTCACAGTGTACCCG	RTVTVYP	++	---
32294	18885	TGTAACCTGAGTCCTACATCG	CNLSPTS	++	--
29629	38984	CGATATGAGCCCAAATGCCCC	RYEPKCP	++	--
20719	36347	CTATCCCGGATCGGTCCCAAT	LSRIGPN	++	---
27800	38930	TGCAAAGATGAGTATAGAGTC	CKDEYRV	++	--
25082	14367	TTTAGTCGATTGGGTCCTAAT	FSRLGPN	++	--
22485	37049	GTTATGAGCTCACAATCGTGG	VMSSQSW	++	---
23365	37365	GATATGAGCAGTAAGGTGTGG	DMSSKVW	++	---
27873	12327	TTGGCGAAATCAGGCTGTAAT	LAKSGCN	++	--
28431	39134	AGCCTAGCAGACAGAAAATGG	SLADRKW	++	---
24732	37275	AGAGACGAATTCGTCAGTTGG	RDEFVSW	++	---
28534	37537	GGGTCAGAGTACAGTAAGTGG	GSEYSKW	++	--
25078	37049	GTAATGTCAAGTCAGAGCTGG	VMSSQSW	++	---
21267	36586	ATAATGAGCAGCGCTAATTGG	IMSSANW	++	---
28418	39131	TGTAAACCATTCACAAGAGAA	CKPFTRE	++	--
31056	40038	TGTAAGCCCCCCATGGGTGCA	CKPPMGA	++	--

34072	39871	TGCAATTTTAAAGGCCCTCCG	CNFKGPP	++	--
21142	36493	TTGTGTAAACCGTGCGCCACG	LCKPCAT	++	---
21084	36437	TTGTGTAAGCCGTGTCTTGAC	LCKPCLD	++	---
27494	17711	GTAATGGCTGATAGGGCGTGG	VMADRAW	++	---
33786	40958	TGCGGGAAAAGCGGGCCATCG	CGKSGPS	++	--
22335	36725	ATAATGGCAAGTCAGACCTGG	IMASQTW	++	---
25845	38225	TATAGTCGCATAGGCGGCGGT	YSRIGGG	++	---
30379	17882	GACGGGTCGAGTCGCTCCTGG	DGSSRSW	++	---
26939	38571	AGAACTTACGATGCGTATCCT	RTYDAYP	++	---
21809	16650	TTAACGAGGTTAAGTCATAAT	LTRLSHN	++	--
22536	37063	CTATCGCGGACATCCCATAAT	LSRTSHN	++	---
26919	37178	ATTATGTCCCACGCCACCTGG	IMSHATW	++	--
27766	38467	TATTTCACCGGCGTTAGAAGT	YFTGVRS	++	--
25478	37581	GCTATGGCGGATAGACAGTGG	AMADRQW	++	---
25718	38186	AATATGACCAGCCATAGTTGG	NMTSHSW	++	---
20662	36322	ATACTTTCTAGCAGTAATTGG	ILSSSNW	++	---
23957	37578	AGGGACGGGGTCAGCAAATGG	RDGVSKW	++	--
26129	38312	CTAATGAGTGATCGCTCTTGG	LMSDRSW	++	---
28906	39304	ATAATGGGAGATCGCAAATGG	IMGDRKW	++	---
24031	37593	GATCTATCTGATAGGAAGTGG	DLSDRKW	++	---
32490	40550	GGTGGAGAGTTTCGGCACTGG	GGEFRHW	++	--
26737	13874	TACAGCCGTTTGGGTCTTAAT	YSRLGLN	++	---
28591	38432	AGAGATGAATACGTTCATTGG	RDEYVHW	++	---
23862	18899	AGGTTGGAATCACATGGATGG	RLESHGW	++	---
22834	37177	GAAGGTATTTCACGTGATTGG	EGISRDW	++	---
31671	40257	TGCTTGCCAACGCACTGCGGA	CLPTHCG	++	--
23505	36800	CCTTTGGACTCGCGCAGTTGG	PLDSRSW	++	---
21761	36769	TTGCACAGGTTGGGCTACGAC	LHRLGYD	++	---
24457	37276	TATTTTACTGGGTTTAAGGAA	YFTGFKE	++	--
26633	38522	TGCAAACCGCAAAGTGGTGCA	CKPQSGA	++	--
25973	17590	ATCTTGTCCGATAGGTCGTGG	ILSDRSW	++	---
25563	38144	CGGAGTGAATTCATGACGTAT	RSEFMTY	++	---
34724	41385	TGCAAGCCTTGTCCGCTTAGA	CKPCPLR	++	---

33801	41026	TGTAAAGCAAATGCTCCCGAT	CKANAPD	++	--
20714	36347	TTGAGTAGAATTGGGCCGAAT	LSRIGPN	++	---
20936	36444	GACATGGCGTCGGCAAGTTGG	DMASASW	++	---
34429	40913	GGTTGCGGAACTAAAAATGGG	GCGTKNG	++	--
20912	36347	CTCTCACGTATTGGGCCCAAT	LSRIGPN	++	---
31921	39807	AGGGAGTATAATGTTTACCCT	REYNVYP	++	--
21186	36553	TTATGCAAACCATGCCAAACT	LCKPCQT	++	--
29949	36771	GTCCTCTCAAGCAATATTTGG	VLSSNIW	++	--
26524	37358	AAGGATGGCACCTCATACTGG	KDGTSYW	++	--
23953	36643	GTCTTAAGCGACAGATTGTGG	VLSDRLW	++	---
31058	39680	TACTTCACCGGTAGGTTCGAT	YFTGRFD	++	--
29906	39633	GGAGACGAATGGAAGACGTGG	GDEWKTW	++	--
30736	39926	GTGAAGACAGACAGATGTGCA	VKTDRCA	++	--
22389	37010	AAGGGGGAAAGTCGAGACTGG	KGESRDW	++	---
25773	37897	AAGGACGACTTCCTTTCATGG	KDDFLSW	++	--
21969	36851	TTGTGCAAGCCATGCCACACG	LCKPCHT	++	--
26453	38449	CACAACTCAACAAACGGAAGA	HNSTNGR	++	--
36005	39119	GCCTGCAAACCACAAATGGGG	ACKPQMG	++	--
33643	39281	TGTATGAAAAGACCCGAGGTA	CMKRPEV	++	--
35490	40381	GCAGGAATGGACCGTGGATGG	AGMDRGW	++	--
24523	37746	AGGGATGAATTTAGCAGTTGG	RDEFSSW	++	---
33299	17514	GAGTCTTCTTCACGTACATGG	ESSSRTW	++	---
22870	37186	CTTCACAGATTACAAAGCACT	LHRLQST	++	--
22722	37143	GAATTGGAATCACGAAGTTGG	ELESRSW	++	---
30365	39544	AGAGGAGACTCCCGGTCATGG	RGDSRSW	++	---
27988	38748	TATTTTTCAGGAGTTCGCGCG	YFSGVRA	++	--
29988	14265	TATGCGAGGTCTGGCCACAAC	YARSGHN	++	--
22479	37044	GTCGCGACTCGCGGCTGGGAC	VATRGWD	++	---
33035	39572	TGCAAACCAAGTCCTCTGGAG	CKPSPLE	++	--
28875	38868	TCCATGTCTGACAGAACCTGG	SMSDRTW	++	---
22434	36971	AGAGACGAGTTTACGTCATAT	RDEFTSY	++	---
29711	39570	GTAATGGGGGATCGCAAATGG	VMGDRKW	++	---
32986	40724	TGTAAACCCTTCGTGGTTGAG	CKPFVVE	++	--

33084	40758	TGTAAGCCGCAGATGCCCACT	CKPQMPT	++	--
23776	37510	ATCATGATGGATAGAGGTTGG	IMMDRGW	++	---
35033	41470	GGTGTTAATCAGGTCAGGTGG	GVNQVRW	++	--
29472	38311	CGTGATGATTATGTCCATTGG	RDDYVHW	++	---
28312	38535	AGGGGAGACCGCGTATACCCT	RGDRVYP	++	--
30803	39375	AGGACTTACGACTCATACGCC	RTYDSYA	++	---
22648	37114	AAATTGCAAGAGCGTACCTGG	KLQERTW	++	---
35418	17698	CTATATGAGTCCCGCGCATGG	LYESRAW	++	--
23511	37420	ATCATGGCAGATCGTGTGTGG	IMADRVW	++	---
32255	40462	CCAGTTGAGAGTAGGACTTGG	PVESRTW	++	---
28805	39271	AAGGATGACTGGACGACTTAT	KDDWTTY	++	---
34957	41451	GAAATGGAGTCCGTGAGGTGG	EMESVRW	++	--
32133	40421	ATCCCAGGGTGCATGTCGTTC	IPGCMSF	++	--
26641	36522	AGAGAAGACCATGTCTACTGG	REDHVYW	++	--
23944	19125	CTACTTGAAAGCAGGAGTTGG	LLESRSW	++	---
24612	37349	TCTGATGGCGTGAGCCGCTGG	SDGVSRW	++	--
22777	37161	CGCCTCGAATCACAGTCGTGG	RLESQSW	++	---
23286	17049	AAGATGAGCTCTGCAAATTGG	KMSSANW	++	---
23905	37272	GATATGACCTCACACAAATGG	DMTSHKW	++	---
26128	37164	GATATGGCAAGCCAACAGTGG	DMASQQW	++	--
27136	38692	GGGGACGGTTCGAGTCGATGG	GDGSSRW	++	--
22813	36869	AATATGGCCAGCCACACTTGG	NMASHTW	++	---
34192	41175	AGAACTCCAACGTGTAAGGAA	RTPTCKE	++	--
26398	17499	GTCATGGAAGCTCGCGCCTGG	VMEARAW	++	---
29408	14384	TATTCTAGGCTAGGTAGTAAT	YSRLGSN	++	--
22579	36586	ATCATGTCATCAGCAAACTGG	IMSSANW	++	---
23129	37280	AGCGACGGTACTTCGAGATGG	SDGTSRW	++	--
20828	36397	GTTTCAGAGTTCCTCAGCTAC	VSEFLSY	++	--
21718	16628	TTAACGAGAATTTCTCATAAT	LTRISHN	++	--
31438	39319	TGTGGGGGTGGCAAACCACCG	CGGGKPP	++	--
35408	39885	AGAAATGAATTTACCAGTTTT	RNEFTSF	++	--
27632	38868	AGTATGAGCGATCGGACGTGG	SMSDRTW	++	---
31792	40294	GGCGGCGGCACGAAGTGTGGT	GGGTKCG	++	--

27312	38748	TACTTCAGTGGGGTAAGGGCA	YFSGVRA	++	--
24174	37348	GACATGATGAGCCACAAGTGG	DMMSHKW	++	---
27527	38831	CATATGCCAGATAGAAAATGG	HMPDRKW	++	--
24076	17578	AAAATGGAGGACCGGTCTTGG	KMEDRSW	++	---
22674	37122	AGAACCGCACAAGTCTATCCA	RTAQVYP	++	---
25556	16664	ATGCATCGGCTGGCCGTAAAT	MHRLAVN	++	---
35961	41767	ATATGCGATAAGCGGGACCCA	ICDKRDP	++	--
27711	17938	GTGCTCTCCCATGCTACGTGG	VLSHATW	++	--
29443	38931	CCAATGGAGAGCAAAAAATGG	PMESKKW	++	---
30764	39935	TGGGCTCGGGGCTGCGACAAC	WARGCDN	++	--
30201	17050	AGGGAGACATACGTCTACCCC	RETYVYP	++	--
25810	14925	TTCAGTAGAACGGGTCCGAAT	FSRTGPN	++	--
28161	38638	TACGTTAGATCCGACAACCGG	YVRSDNR	++	--
23467	17540	GACCTGAACTCTCGTAGTTGG	DLNSRSW	+	---
30205	39183	AAGGACGATTGGAATAGCTGG	KDDWNSW	+	--
29927	39640	ATGCTGTCTGATCGAACTTGG	MLSDRTW	+	---
23851	37540	TTGCATCGGTTGCACCCAAAC	LHRLHPN	+	--
23040	36957	AAGGACGATTATACCACTTGG	KDDYTTW	+	---
26392	38312	TTGATGTCCGACAGAAGCTGG	LMSDRSW	+	---
31755	39853	AGTTGTAAGGAGAGGATGCCT	SCKERMP	+	--
23624	15352	TATTCTAAGATAGGTAAAAAC	YSKIGKN	+	---
33671	40908	CGAATGCAAGATAGAAGCTGG	RMQDRSW	+	--
28027	38872	CGAGATGACTATGTGAGCTGG	RDDYVSW	+	---
35707	41648	TGGGATCCCATGTGTAAGGCA	WDPMCKA	+	--
22022	36876	GATCTGACTGCACGAAACTGG	DLTARNW	+	---
27452	36939	CGGGAAGATTATGTTCATTGG	REDYVHW	+	---
28778	37536	CGCGACGAATTTACTCATTAT	RDEFTHY	+	---
28710	36871	CTCTGCAGGCCGTGTAGCGCG	LCRPCSA	+	--
23958	37349	TCAGACGGTGTGAGTAGATGG	SDGVSRW	+	--
20934	36442	TTAAGTCGCGTCGGTCCTAAC	LSRVGPN	+	---
22959	37221	CGGATGGATTCGGTCAAGTGG	RMDSVKW	+	---
22308	36798	GTGATGGAAAGTCGGGATTGG	VMESRDW	+	---
25391	13874	TATAGTAGATTAGGTTTAAAC	YSRLGLN	+	--

28290	37823	ATCATGGCAGACAGGGCATGG	IMADRAW	+	---
24287	37666	CGTTCAGAATTTTTGAGTTAT	RSEFLSY	+	---
22101	36906	AATATGGCAAGTGCCAAATGG	NMASAKW	+	---
20758	36363	ATACTTAGTAGTCAGAGTTGG	ILSSQSW	+	---
33058	40750	TGTAACAGACCCATGACGGCC	CNRPMTA	+	--
20566	36272	GTTCTCTCTGCCTCGACGTGG	VLSASTW	+	---
23934	37524	ATAATGAGCGACCGCGGTTGG	IMSDRGW	+	---
23114	37272	GACATGACTAGTCATAAGTGG	DMTSHKW	+	---
26351	38404	ATGCTACCTGGCTGTAAGCCG	MLPGCKP	+	--
20770	36371	ATTGCCCATTTAGGTTGGGAT	IAHLGWD	+	---
25799	38209	AGGATGGCTGACAGAGATTGG	RMADRDW	+	---
21371	36640	CGCTTGATGGACGCGTACCCC	RLMDAYP	+	---
25369	38073	AGAAGTGATTTTAAGATCTAC	RSDFKIY	+	--
24546	37759	CTATGCCGCCCCTGCTTAACC	LCRPCLT	+	--
36019	41784	TGTTACCCGCTTCGCCCTGAA	CYPLRPE	+	--
22063	36682	CTATGCAAACCCTGTTTAAGT	LCKPCLS	+	---
21566	16652	TACGTTAAGAGTGATCGATGT	YVKSDRC	+	--
25392	37989	GGTGATGGCACGAGCCGTTGG	GDGTSRW	+	--
28550	39183	AAAGATGACTGGAACTCATGG	KDDWNSW	+	--
30696	39889	GACTATGCAGACAGGAAATGG	DYADRKW	+	---
22946	37213	AGGGATGACTTCACGAGCTGG	RDDFTSW	+	---
26596	38502	ATTATGGGGAAGTGCCCCGGA	IMGKCPG	+	--
31411	37466	AAGGACGGATACAGTGCATAT	KDGYSAY	+	---
26305	38378	CGAAATGAATTTACGAGTTGG	RNEFTSW	+	---
32803	40551	ATCAAGGGCTCGTGTGAACAG	IKGSCEQ	+	--
31595	39640	ATGTTAAGCGATAGGACGTGG	MLSDRTW	+	---
23437	36573	GAAATGGCGTCCCACTCATGG	EMASHSW	+	---
36083	41807	TGTAAGCCTCTTATGCTGGAA	CKPLMLE	+	--
30259	17835	CAAGGAGTAAGTAGAGAATGG	QGVSREW	+	---
31743	37759	TTGTGTAGGCCGTGTCTCACT	LCRPCLT	+	--
26045	37047	CCCATGAGTAGCCACGGGTGG	PMSSHGW	+	---
24258	37036	ATAATGGCTGACAGAGGCTGG	IMADRGW	+	---
24530	37750	CTTTGTCGACCATGTAGCAAT	LCRPCSN	+	---

21515	36696	ATTATGTCGTCCTCAAGCTGG	IMSSSSW	+	---
35906	41739	TGCACGTCACCCACCGGCCAC	CTSPTGH	+	--
30667	39901	TGTAAGCATCAGCAAGTAGAG	CKHQQVE	+	--
20861	36413	CTACATCGCTTGGGCCCCGAC	LHRLGPD	+	---
34347	17136	TGTACAGGTAATAGCTCCAAA	CTGNSSK	+	--
21544	36709	CGCGAGGACTTTGTTTCTTGG	REDFVSW	+	---
33625	40954	GTGATGCAGGACCGCAGTTGG	VMQDRSW	+	---
32147	39592	TCGATGCAAGATCGCAAGTGG	SMQDRKW	+	---
21625	36720	CAGATGGCCTCTGTTAAGTGG	QMASVKW	+	---
21641	36494	AGGGAAGATATGGTCCGCTGG	REDMVRW	+	--
25249	17035	CTGCGTAGCGAATGCTGCGTA	LRSECCV	+	---
22151	36922	GTGGCAAGCAGAGGGTGGGAC	VASRGWD	+	---
22486	37010	AAAGGCGAGTCCAGGGATTGG	KGESRDW	+	---
27002	38209	CGTATGGCCGATCGTGACTGG	RMADRDW	+	---
33438	40344	AACATGGGAGACCGCAAATGG	NMGDRKW	+	---
32699	38534	GTCATGGAGGACCGTAGGTGG	VMEDRRW	+	---
21485	36682	CTGTGTAAGCCTTGCCTTTCC	LCKPCLS	+	---
30040	39678	TGCAAAAAGTACGGAGGCGAT	CKKYGGD	+	--
28703	38824	AGTATGGCGGATCGTTCGTGG	SMADRSW	+	---
27099	38682	ACAGACGGCTACAGCAGTTGG	TDGYSSW	+	--
27520	38286	CAACTTAGTGACCGCACCTGG	QLSDRTW	+	---
22043	36519	CTACATCGACTGCTCCATGAC	LHRLLHD	+	---
31052	40036	CAGGGGGAATCGAGGGTATGG	QGESRVW	+	---
29560	19136	GCAATGGTCGCTCGTGATTGG	AMVARDW	+	---
33232	40243	TGCCGCCCGCCTATGCCACCA	CRPPMPP	+	--
22163	36640	CGCTTAATGGACGCCTATCCA	RLMDAYP	+	---
23081	37063	CTGAGCAGAACGAGTCACAAC	LSRTSHN	+	---
20616	36298	CTCTGCAAACCCTGCTTGATA	LCKPCLI	+	--
21042	36493	CTATGCAAGCCTTGTGCAACA	LCKPCAT	+	---
24409	37122	CGGACTGCTCAGGTATACCCC	RTAQVYP	+	---
23255	18173	GACCCGGCATCACGCGCGTGG	DPASRAW	+	---
33745	36748	TTAAAGGACGGAACATGCAGT	LKDGTCS	+	--
31766	39147	ACAGATGATTGGAGTTCATAC	TDDWSSY	+	--

25177	37224	GATCTTCAGTCTCGCGAGTGG	DLQSREW	+	---
30386	39807	CGCGAATACAACGTGTATCCC	REYNVYP	+	--
21523	36640	AGGCTCATGGATGCTTACCCG	RLMDAYP	+	---
20947	36442	CTGTCGCGTGTAGGGCCCAAT	LSRVGPN	+	---
29133	39375	CGTACGTATGATAGTTATGCG	RTYDSYA	+	---
28288	39088	CAGAACGAGTTCACAATGTAC	QNEFTMY	+	--
27434	17221	ATCTGCAGGGGATATACCAGT	ICRGYTS	+	---
25944	38225	TACTCAAGAATTGGTGGTGGC	YSRIGGG	+	---
26418	14378	TATAGCCGGGTAGGAGCTAAC	YSRVGAN	+	---
24623	36797	GAAATGGATTCCCGGATGTGG	EMDSRMW	+	---
32203	40019	AGCATGCAAAGCCGATCTTGG	SMQSRSW	+	--
30077	39696	AGATCAGGTCCATGCCCCTTC	RSGPCPF	+	--
30692	39271	AAAGACGATTGGACTACATAC	KDDWTTY	+	---
28619	39195	GCAATGCAAGATAGGTCTTGG	AMQDRSW	+	---
30629	39889	GATTACGCCGATCGCAAGTGG	DYADRKW	+	---
22815	37029	AGGAGTGAGTTCGTTAGTTAT	RSEFVSY	+	---
26329	38389	ATTATGGCGAGTCAATCTTGG	IMASQSW	+	--
29837	39609	AGTATGATGGACCGGAGTTGG	SMMDRSW	+	---
30562	17173	AATTCGTCCGCCTGTAGGACT	NSSACRT	+	--
24943	37913	TGCAAACCCTTAGAACGACCG	CKPLERP	+	--
22575	37081	CTCCATCGGCTGAGTTATGAC	LHRLSYD	+	---
24241	37654	TGGAGCACGCACTGTTGTGCG	WSTHCCA	+	---
31190	40083	GTGATGGAGGCCCGCCAATGG	VMEARQW	+	---
21427	36347	CTGAGTAGAATTGGACCGAAC	LSRIGPN	+	---
28387	39118	TGTAAACCCCCATCTCCGATC	CKPPSPI	+	--
22934	37207	CTTCTTAGCTCGAGTAATTGG	LLSSSNW	+	--
20823	36361	AAGGATGAATTCAGCAGTTGG	KDEFSSW	+	---
31243	40101	TGGCAACCCATGTGTAAGGCT	WQPMCKA	+	--
24983	37626	CAAGGTGAGGCAAGAACATGG	QGEARTW	+	---
28443	39137	ATTATGCAGGACCGTGCATGG	IMQDRAW	+	---
30627	39887	TTTTGCAAGAGTAACGCAAAT	FCKSNAN	+	--
25535	38130	GTACTCAGTTCGCAAGGATGG	VLSSQGW	+	--
33190	39746	GACTATGCATCTAGGGACTGG	DYASRDW	+	---

25045	37949	ACGAGGGACGGGTGTATGGCC	TRDGCMA	+	--
25373	16664	ATGCATAGACTTGCTGTGAAC	MHRLAVN	+	---
20979	36416	AAAGACGACTTCACAAGTTGG	KDDFTSW	+	---
25931	37128	CGAACGCCGACCACTTATCCG	RTPTTYP	+	--
32918	38176	TGTAAATACTTGAAGAGTGAC	CKYLKSD	+	--
29903	39631	CCCATGCAGGATAGATCTTGG	PMQDRSW	+	---
26635	13517	TATAGCCGCTTAAACATCAAC	YSRLNIN	+	---
23488	19125	TTATTGGAGTCTCGCTCATGG	LLESRSW	+	---
29303	13751	TATTCAAGAGTGGGCAATAAC	YSRVGNN	+	---
24189	37411	TTGTGCCGCCCTTGCTCCCAG	LCRPCSQ	+	--
30187	39134	TCTTTGGCGGATCGTAAGTGG	SLADRKW	+	---
25999	38014	ATAATGGCGGAACGTACATGG	IMAERTW	+	---
23916	37568	AGAGACGAGTTTACTTCGTGG	RDEFTSW	+	---
27232	37991	TTATGTAAACCTTGTTTTACG	LCKPCFT	+	--
21409	36652	CTCGCGCGAACGGGAATGAAC	LARTGMN	+	---
26947	38638	TATGTGCGTAGCGATAATAGA	YVRSDNR	+	--
23821	37529	AGGGAGGAAAGTCGAAGTTGG	REESRSW	+	---
27802	38931	CCCATGGAATCAAAGAAGTGG	PMESKKW	+	---
24781	17571	GTTGAATCTAGCAGGTTATGG	VESSRLW	+	---
27198	38378	AGGAACGAGTTCACATCGTGG	RNEFTSW	+	---
22632	36906	AACATGGCGTCCGCAAAGTGG	NMASAKW	+	---
33403	40874	TGCAAGGCTCCCAAGTACGAT	CKAPKYD	+	--
22695	37129	AAGGATGACTATAGCACTTGG	KDDYSTW	+	---
27666	38880	AGAATGGAAGACCGTCAATGG	RMEDRQW	+	---
31402	17711	GTTATGGCGGACAGGGCCTGG	VMADRAW	+	---
26443	38443	CAAAACGACTATGTCAGTTAT	QNDYVSY	+	--
26685	38549	GGTGGGGAGTTCTCTAAGTGG	GGEFSKW	+	--
23031	37252	TTGTCGAGGATAAGTCATAAT	LSRISHN	+	--
24399	19304	GAACCAGAGTCCCGCTCATGG	EPESRSW	+	---
23966	37581	GCGATGGCCGACCGCCAATGG	AMADRQW	+	---
21527	36701	CGGGATGAATTCACAAGTTTT	RDEFTSF	+	---
21582	18291	GAGGCACTCCGGGGCTGGGAC	EALRGWD	+	---
25400	37974	AGGATGGAAGACAGAAACTGG	RMEDRNW	+	---

20928	36282	ATTCTCAGCAGCACCACGTGG	ILSSTTW	+	---
23921	37061	CTCAGCAGGATCTCCAACAAC	LSRISNN	+	--
22819	36733	CTGCATAGATTAAGTGTGGTA	LHRLSVV	+	--
24794	17049	AAAATGTCTAGCGCCAACTGG	KMSSANW	+	---
24242	37521	CTCTGTAAACCTTGTCTGGTG	LCKPCLV	+	--
21623	36727	CTCTGCAAGCCGTGTATAACA	LCKPCIT	+	--
27348	38761	CGCGAAGAATGGGTCGCTTAC	REEWVAY	+	---
34326	40973	TGCACTAGCAAACAAGGGCAC	CTSKQGH	+	--
20533	36253	TTGCACAAGTTATCACCAAAC	LHKLSPN	+	---
22361	36580	GACCTCCGTGCTGCGACCTGG	DLRAATW	+	---
24691	37818	CTGTGCAGGCCGTGTAGCGGA	LCRPCSG	+	--
23484	37411	CTCTGTCGTCCATGTTCGCAG	LCRPCSQ	+	--
25849	38170	TACTTCCATGGTAAATGTGAC	YFHGKCD	+	--
25920	38251	GAACCCGAAAGTCGTAAATGG	EPESRKW	+	---
21901	36822	CGTACTCCCGTGGTGTATCCG	RTPVVYP	+	--
26223	37871	AGGCTGGAAGACCGGTTGTGG	RLEDRLW	+	---
31533	17060	CGCATGTCCGATCACAATTGG	RMSDHNW	+	---
29358	39201	AGCATGGCAAGTGTGAAATGG	SMASVKW	+	--
31662	39267	AGAGACGACTACAGTAGTTAC	RDDYSSY	+	---
26030	14185	TACGCTAAGACAGGTTGGAAT	YAKTGWN	+	--
20872	36416	AAAGATGATTTTACCAGCTGG	KDDFTSW	+	---
28677	39173	GACATGAGAGACAGAATGTGG	DMRDRMW	+	--
31769	39914	CGTGGAGGAGACAGGTCATGG	RGGDRSW	+	--
23898	37562	ATGCACCGGTTAAGCACGAAT	MHRLSTN	+	---
21392	36553	CTCTGTAAGCCCTGCCAAACC	LCKPCQT	+	--
28585	39201	TCAATGGCTTCAGTTAAGTGG	SMASVKW	+	--
25741	17540	GATCTAAATAGCAGGTCGTGG	DLNSRSW	+	---
22822	36696	ATAATGAGCAGTAGCTCTTGG	IMSSSSW	+	---
26095	38303	TATTTTTCAGGGAGGACCGCT	YFSGRTA	+	--
23645	37140	CTGTCGCGCGTGGGCAGGGAC	LSRVGRD	+	--
22939	17637	CGGCTTGAAAGTACGCACTGG	RLESTHW	+	---
20753	36272	GTGTTAAGCGCTAGTACCTGG	VLSASTW	+	---
21200	36371	ATAGCACACCTCGGGTGGGAC	IAHLGWD	+	---

28187	38650	CCGTACGCGCGATCTCCGATG	PYARSPM	+	--
25206	38011	AGAGATGAGTTTACTCGCTGG	RDEFTRW	+	--
20866	17659	TTATGCAAGCCATGTTTGACC	LCKPCLT	+	--
30042	39679	ATTATGCTTGATCGTGGTTGG	IMLDRGW	+	--
26739	38518	ATGTTGTCGGACAGAAAGTGG	MLSDRKW	+	---
26749	38294	GATATGGGTGATAGGAAATGG	DMGDRKW	+	---
22225	36946	TTGTGCAAACCTTGCGGCACA	LCKPCGT	+	--
23033	37184	CGAATGGAGAGCGCGGTCTGG	RMESAVW	+	---
23856	36739	AAGAGCGATTTCGTATCGTGG	KSDFVSW	+	---
31928	40348	TGTTCCACAAATTGGAAATCC	CSTNWKS	+	--
25135	36851	TTATGTAAACCGTGCCATACA	LCKPCHT	+	--
29087	38150	ATTATGAGTTCAAAGTTATGG	IMSSKLW	+	---
30816	39954	ATAATGCAGGACCGTTCCTGG	IMQDRSW	+	---
35095	40667	ATAGAGTCCTCACGGTCGTGG	IESSRSW	+	--
25244	37989	GGGGACGGGACCTCGAGGTGG	GDGTSRW	+	--
29911	39634	CTTGATGATTGGACTACTTAC	LDDWTTY	+	--
31917	40344	AATATGGGTGATCGGAAGTGG	NMGDRKW	+	---
27817	14593	TATTCACGCTCGGGGCCTAAC	YSRSGPN	+	---
29378	38845	CCGTTATCTGACAGGACATGG	PLSDRTW	+	---
29578	39523	TGTAAGACCAAGAGCCAAGAT	CKTKSQD	+	--
23342	37358	AAAGATGGTACAAGTTATTGG	KDGTSYW	+	--
23598	37448	GTTCACTCGACAAATGGACGC	VHSTNGR	+	---
24578	17910	GTCATGTCGTCAGCAGGTTGG	VMSSAGW	+	--
20817	36391	TTCCATAAATTATCACTCAAC	FHKLSLN	+	---
22121	36911	GTGAGTTCGACGAATGGCCGG	VSSTNGR	+	---
20745	36361	AAAGATGAGTTTAGCTCGTGG	KDEFSSW	+	---
21382	36626	CTCTCACGGATTGGTCAAAAC	LSRIGQN	+	--
26165	37902	GGAGGCGAATACTCAAAGTGG	GGEYSKW	+	--
21999	36862	CCTATGGGAAGCAGTAGTTGG	PMGSSSW	+	---
24374	37614	CGAACAAGTACCGTCTATCCG	RTSTVYP	+	--
23942	37574	GATATGACATCAAGAGATTGG	DMTSRDW	+	---
27371	38380	TATTCACGGCTTAGTCCAAAT	YSRLSPN	+	---
21814	36640	AGACTTATGGATGCTTATCCA	RLMDAYP	+	---

24841	37693	CGGGACGAATTTACGGTGTAC	RDEFTVY	+	---
23024	37250	CTGTGCCGTCCGTGCAAAGAA	LCRPCKE	+	--
25963	38265	ATGTGGGACGGCACTGGTCCA	MWDGTGP	+	---
31465	17672	GTAATGCTTGATAGGGGGTGG	VMLDRGW	+	---
27989	38144	AGGTCGGAGTTTATGACTTAC	RSEFMTY	+	---
25282	38043	ATAGATGATTATGTTCATTGG	IDDYVHW	+	--
22398	37016	TTTTGCAAACCGTGTCCGGGC	FCKPCPG	+	--
27033	17033	CGGAATATGAGTGTATATCCG	RNMSVYP	+	--
22523	36957	AAAGATGACTACACTACGTGG	KDDYTTW	+	---
21897	36820	CTATGTAAACCTTGCAATACA	LCKPCNT	+	---
25020	37938	AGGACGTACGATAGTTACCCG	RTYDSYP	+	---
31551	39074	GATTTGAGGGATAGAATTTGG	DLRDRIW	+	--
32268	40468	GATATGAGAGACCACAGATGG	DMRDHRW	+	--
32051	17038	ACCATGTCAGATAGGACGTGG	TMSDRTW	+	---
34094	41140	GTGAAAAGTAGCGAAGCTTGC	VKSSEAC	+	--
28751	38472	GCAGGAGCGGATCGTGGGTGG	AGADRGW	+	--
33511	39807	CGAGAGTACAACGTGTACCCA	REYNVYP	+	--
33256	40826	TCAATGCAAGACAGGATGTGG	SMQDRMW	+	--
21130	16650	CTTACGAGACTGTCGCACAAC	LTRLSHN	+	--
26307	38380	TACAGTAGGCTGTCGCCGAAC	YSRLSPN	+	---
28686	39229	ATAATGAGTGACAGGGAATGG	IMSDREW	+	---
24363	37617	CATAGTAGGATAGGCCCGAAT	HSRIGPN	+	---
33353	40417	TGCAAGCCCGTAAAAGGCGAG	CKPVKGE	+	--
25116	37974	CGCATGGAGGATCGCAATTGG	RMEDRNW	+	---
23266	37327	ATTGAGTCCAGCCGGACGTGG	IESSRTW	+	---
25989	14502	GTGTGGTCGACGAACGGAATT	VWSTNGI	+	--
24376	37349	AGCGATGGCGTATCACGCTGG	SDGVSRW	+	--
35282	41530	TGCAAAACGGAAGCCAGAGGA	CKTEARG	+	--
23380	37024	TTACACCGCTTAAGCCCTATG	LHRLSPM	+	--
33814	40910	ATGATGCAAGATCGGTCGTGG	MMQDRSW	+	--
22237	36911	GTTTCCAGTACCAACGGACGT	VSSTNGR	+	---
21843	36796	CTGAGCCGTTTGTCACCGAAT	LSRLSPN	+	---
23813	37524	ATTATGTCGGATAGAGGCTGG	IMSDRGW	+	---

21812	36783	AACGCACTCAGGGGCTGGGAC	NALRGWD	+	---
30947	39596	ATGTTAAGCGATCGTCTGTGG	MLSDRLW	+	---
25522	37081	CTGCACAGATTATCCTACGAC	LHRLSYD	+	---
21922	36831	TTATCGCGTATTAGTTTCAAT	LSRISFN	+	--
35576	39961	TGCCGGGATGTGAAGCAAGGG	CRDVKQG	+	--
32837	20377	GATATGAGCACCAGGACGTGG	DMSTRTW	+	---
34383	39133	ATAATGGGCGACCGAACCTGG	IMGDRTW	+	---
25034	37221	AGAATGGACAGCGTTAAATGG	RMDSVKW	+	---
21107	36522	CGGGAGGATCACGTATATTGG	REDHVYW	+	---
24913	36843	AGGGACGAGTTCGTGAGCTAC	RDEFVSY	+	--
33500	40910	ATGATGCAGGACCGTAGTTGG	MMQDRSW	+	--
28614	39068	TATTATACTGGGAAGTGTGAC	YYTGKCD	+	--
20932	36441	CTGTGCAAACCCTGTACGACG	LCKPCTT	+	--
23686	14367	TTCTCAAGGCTAGGACCGAAC	FSRLGPN	+	--
26413	38292	ATCATGTCGTCGGCTGGCTGG	IMSSAGW	+	--
24019	37593	GACTTGAGCGATCGTAAATGG	DLSDRKW	+	---
33481	40900	TATGGCAAGAGCACGGAATGC	YGKSTEC	+	--
22469	36878	GAGATGAAGGCTCGTACTTGG	EMKARTW	+	--
22831	37140	TTAAGCAGAGTAGGACGGGAT	LSRVGRD	+	--
23563	37213	CGCGACGATTTTACCTCATGG	RDDFTSW	+	---
22324	36919	AGAGAGGATTTTGTCACTTGG	REDFVTW	+	---
28667	19005	CAAGGGGAAGCTAGGTCGTGG	QGEARSW	+	---
27544	38835	CGTGACGAGTTCAGGTCATAC	RDEFRSY	+	--
22379	37002	ATGTTGGCCAGCTCGACATGG	MLASSTW	+	--
35326	18065	GCAGAGTCAAGTAGGTTGTGG	AESSRLW	+	--
28657	38980	TATCACCGCTTGGGTCAAAAT	YHRLGQN	+	---
34905	40982	ACCCGATGGGGTGACAACGCT	TRWGDNA	+	--
20524	36246	TTACATAAATTGAGCATCAAC	LHKLSIN	+	---
31309	39954	ATCATGCAAGATAGAAGTTGG	IMQDRSW	+	---
21934	36688	CTATGTAAGCCGTGTAGTACC	LCKPCST	+	--
21852	36474	ATAATGGCCAGCGCTAATTGG	IMASANW	+	---
22747	37150	CGCTTGGATGATGTGTACCCC	RLDDVYP	+	--
22085	36598	TTACACCGGCTAAGCCCCCTG	LHRLSPL	+	---

22102	36660	CCTATGAGCAGTTCGTCTTGG	PMSSSSW	+	---
20966	36365	GACTTATCATCAGCTAAATGG	DLSSAKW	+	---
21474	36680	ATTATGAGCGCCTCCAATTGG	IMSASNW	+	---
23402	37140	TTATCGAGGGTAGGACGCGAT	LSRVGRD	+	--
32390	40517	CTTGCGCGCAGTTGCCCTGAT	LARSCPD	+	--
21174	36364	TTGTGTAAACCTTGTTTACAG	LCKPCLQ	+	--
20918	36435	TTATGTAAACCCTGCGTAACG	LCKPCVT	+	---
26386	38420	TATGTCCGCAGCGATACTCGC	YVRSDTR	+	--
30467	19655	GCTAACGACTACATGAGCTAC	ANDYMSY	+	--
36208	39499	TGCAAACCCCAGAATAGCTCG	CKPQNSS	+	--
26113	36835	TTGATGACCGACAGGACATGG	LMTDRTW	+	---
27458	17035	TTAAGGTCTGAATGCTGTGTC	LRSECCV	+	---
30164	38186	AACATGACATCTCACTCCTGG	NMTSHSW	+	--
24522	37248	TTTCATAGACTCGGTCCAGAC	FHRLGPD	+	---
24110	37626	CAGGGAGAAGCGCGTACTTGG	QGEARTW	+	---
24916	37574	GACATGACGAGTCGTGACTGG	DMTSRDW	+	---
25873	38236	TGTGGTCGCCCGCAGATGGAG	CGRPQME	+	--
28441	14074	TATAGCCGCATTGGAGGGAAT	YSRIGGN	+	--
34836	17882	GATGGCTCGTCAAGGAGTTGG	DGSSRSW	+	---
21039	36491	CTTGCTAGAACAGGCCTGAAT	LARTGLN	+	---
25991	38273	CTCCATAGACTTTTACCAAAC	LHRLLPN	+	---
31625	40236	TGTAGGGAGATGGGTGTTGGT	CREMGVG	+	--
35028	38835	AGAGATGAATTTCGCAGTTAT	RDEFRSY	+	--
31479	39137	ATCATGCAAGATAGGGCCTGG	IMQDRAW	+	---
29870	39574	AGTATGCAGGACAGGCTCTGG	SMQDRLW	+	---
20539	18857	TTATTATCCAGCGCGACTTGG	LLSSATW	+	---
36041	39981	GTTGGGTATGATCGCGGGTGG	VGYDRGW	+	--
24462	37725	CTTTGGGACGGTACGGGGCCC	LWDGTGP	+	---
34530	41296	TGTAAACCGGGGGTCCCTCCC	CKPGVPP	+	--
26063	13731	TACGCGAAATCAGGGTGGAAC	YAKSGWN	+	--
22666	37029	CGCTCGGAATTTGTGTCATAC	RSEFVSY	+	---
21829	36723	TTGCACCGGCTAGGAGACAAT	LHRLGDN	+	---
21599	36652	TTAGCCAGGACAGGCATGAAT	LARTGMN	+	--

28041	38880	CGCATGGAGGATAGGCAGTGG	RMEDRQW	+	---
21782	36674	GTCATGAGCAGCGCCAATTGG	VMSSANW	+	---
22013	36870	CGCTTAGAGTCTGCCATGTGG	RLESAMW	+	---
26684	38548	TATTTCAGCGGAGTGCGTTCT	YFSGVRS	+	--
20875	36416	AAGGACGACTTCACATCTTGG	KDDFTSW	+	---
24116	37448	GTGCATAGTACTAACGGCAGG	VHSTNGR	+	---
24121	36757	AGGTCAGATTTTGTTGTTTAT	RSDFVVY	+	--
26965	38305	CGTGATGATTACAGCACCTAT	RDDYSTY	+	---
24086	37617	CATTCACGAATCGGGCCCAAC	HSRIGPN	+	---
22532	37061	TTGTCACGTATAAGCAATAAT	LSRISNN	+	--
28535	14074	TACAGCCGCATCGGCGGGAAT	YSRIGGN	+	--
26029	38286	CAGTTGAGCGATCGCACCTGG	QLSDRTW	+	---
27853	38944	CAGGATGGCTATTCAAAGTAC	QDGYSKY	+	--
28040	38744	AGGGACGGACAGAGTTCGTGG	RDGQSSW	+	--
28876	14048	TATGCTAGGAACGGTCCGAAC	YARNGPN	+	---
23246	37218	ACGGATGGCACGAGTAGGTGG	TDGTSRW	+	--
30710	39914	AGGGGGGGGGATCGAAGCTGG	RGGDRSW	+	--
22146	36920	GATTTGAGAAGTGCGGCGTGG	DLRSAAW	+	---
29854	38968	ATTATGTCGGAAAGAGTTTGG	IMSERVW	+	--
22339	36982	AGAGACGATTTTACAGTATAT	RDDFTVY	+	---
22422	37024	CTCCATAGATTGTCTCCAATG	LHRLSPM	+	--
29875	14191	TATGCTCGGACCGGGCACAAC	YARTGHN	+	--
27850	14048	TACGCACGTAATGGCCCTAAC	YARNGPN	+	---
30227	38775	AGCTTAGAATCACGCGCGTGG	SLESRAW	+	---
21845	36798	GTAATGGAGTCAAGAGACTGG	VMESRDW	+	---
32082	40403	TCGGCCCCCACGTGCAAGGGA	SAPTCKG	+	--
21496	36688	TTGTGCAAACCCTGTTCAACT	LCKPCST	+	--
25618	38160	GGTAATGAGTTTAGTAGCTGG	GNEFSSW	+	---
29279	38286	CAGTTGTCAGATAGGACTTGG	QLSDRTW	+	---
27134	38449	CATAATAGTACGAATGGCCGC	HNSTNGR	+	--
28117	38762	TATTTTACCGGAGTTCGGAAC	YFTGVRN	+	--
27269	38286	CAACTTTCTGACAGAACTTGG	QLSDRTW	+	---
25912	13864	TATGCCCGTTCTGGGCCGAAC	YARSGPN	+	---

32126	40417	TGTAAACCTGTGAAGGGGGAA	CKPVKGE	+	--
23714	14461	TACAGTAAATTGAATTACAAC	YSKLNYN	+	---
25839	38081	AGGCTCGAGGACAGGTCATGG	RLEDRSW	+	---
26272	37963	AGAGGGATGGATGTGTACCCT	RGMDVYP	+	--
27730	38806	AAGGATGAGTGGAAGACATAC	KDEWKTY	+	--
31513	39913	GTAGGAATGAGATGTCCCCCA	VGMRCPP	+	--
23145	37161	AGGTTAGAGTCCCAAAGCTGG	RLESQSW	+	---
21335	36435	CTGTGCAAGCCGTGTGTTACG	LCKPCVT	+	---
35105	40416	AAGAATGATTACGCTACGTGG	KNDYATW	+	--
28058	38616	AATTTAGAATCGAGAGGGTGG	NLESRGW	+	---
31384	40149	TTCTACGAAGGCAAACCGTGT	FYEGKPC	+	--
25509	12827	TACTCTAAGACGGGCTGCAAT	YSKTGCN	+	--
32595	20377	GACATGTCGACTCGCACTTGG	DMSTRTW	+	---
25785	37716	GTCCTATCGGACCGCGCATGG	VLSDRAW	+	---
25401	37230	AGCATGTCATCCTCAACTTGG	SMSSSTW	+	--
23607	37327	ATAGAAAGTTCGCGTACATGG	IESSRTW	+	---
22605	37095	AAAGATGATTATACTGTGTTC	KDDYTVF	+	--
25154	37989	GGTGATGGAACGAGCCGCTGG	GDGTSRW	+	--
21008	36441	CTCTGCAAGCCGTGCACTACA	LCKPCTT	+	--
20747	36299	TTCCACAAATTAGGAATCAAT	FHKLGIN	+	---
21146	36506	CGCATGATAGACGTGTACCCG	RMIDVYP	+	--
32849	40679	TGCAAGCCTGAGAGAATGGGC	CKPERMG	+	--
23902	19221	ATACTTTCAGATCGAGTCTGG	ILSDRVW	+	---
24166	37641	AGATCAGAGTTCACCACGTAT	RSEFTTY	+	---
21848	36680	ATAATGTCTGCGAGTAACTGG	IMSASNW	+	---
21157	36546	CTACACAGACTTGGAATGGAT	LHRLGMD	+	---
21422	36505	AACTTATCATCGTCAACCTGG	NLSSSTW	+	---
22625	37102	CGAACCTACGATTCGTTCGTG	RTYDSFV	+	---
23141	37283	GGCGGGGAAACTAGTCGGTGG	GGETSRW	+	--
21155	36544	CCTATGGGATCTTCCACGTGG	PMGSSTW	+	---
23055	36716	TCAATGTCAAGCGCGATATGG	SMSSAIW	+	--
20720	17701	GTCGCTCTTAAGGGGTGGGAC	VALKGWD	+	---
33667	39848	AGCGGCGAGTCGCGGACCTGG	SGESRTW	+	---

30197	39570	GTGATGGGTGACAGAAAGTGG	VMGDRKW	+	---
27937	38968	ATAATGAGTGAGCGCGTATGG	IMSERVW	+	--
27967	38980	TACCATAGGCTTGGACAGAAC	YHRLGQN	+	---
23075	36870	AGACTCGAAAGCGCGATGTGG	RLESAMW	+	--
27646	38873	CAGATGAAAGACCGTACATGG	QMKDRTW	+	---
25962	14502	GTGTGGTCAACTAATGGGATT	VWSTNGI	+	--
23906	37565	AAGGATGATTACACTAGTTAC	KDDYTSY	+	---
25207	38012	CGTAGTGAGTTCAAAACATAC	RSEFKTY	+	--
27583	38046	TTTCACCGTTTGTCCCCGAAC	FHRLSPN	+	---
21100	36519	TTGCACCGTCTTTTACACGAT	LHRLLHD	+	---
26503	19945	GAAGGACCGTCGCGTGGATGG	EGPSRGW	+	---
27512	38824	TCTATGGCTGACAGGAGTTGG	SMADRSW	+	---
32351	17557	GGCATGGCTGACCGCGCATGG	GMADRAW	+	---
25855	37867	GTAATGGAGAGCACAAGGTGG	VMESTRW	+	--
27222	19603	GATGCTTTAGAGTGGAGGGAT	DALEWRD	+	--
34892	41433	TGGACGCCCATGTGTAAGGGA	WTPMCKG	+	--
21914	36827	GACCTCAGGAGTGCGAACTGG	DLRSANW	+	---
32488	19339	GACAGTGCTTCTCGGGCTTGG	DSASRAW	+	---
21273	36461	AAAGATGAATTCAGTACGTGG	KDEFSTW	+	--
26932	38631	TACTCTCGAATCCAGCTTAAT	YSRIQLN	+	--
29465	39072	GTTATGGAGGCGAGAGGGTGG	VMEARGW	+	---
32819	40667	ATCGAAAGCAGTAGAAGTTGG	IESSRSW	+	--
32011	40381	GCGGGCATGGATCGGGGTTGG	AGMDRGW	+	--
23016	37248	TTCCACCGGTTGGGACCCGAT	FHRLGPD	+	---
26629	38420	TACGTTAGGTCTGACACCAGA	YVRSDTR	+	--
27738	38908	AAATTGACGGATCGGACGTGG	KLTDRTW	+	---
26201	14273	TATGCCAGAATGGGGCCTAAC	YARMGPN	+	--
27826	38303	TACTTCAGTGGACGAACGGCG	YFSGRTA	+	--
27490	38608	CGTCTTGAGTCCTACGACTGG	RLESYDW	+	---
26804	13864	TACGCAAGGAGCGGTCCAAAT	YARSGPN	+	---
22718	37140	CTCAGTCGCGTTGGGAGGGAC	LSRVGRD	+	---
25848	37925	AGGGAAGACCATGTGTTCTGG	REDHVFW	+	--
31212	40091	AAAACTGAGTTCTGTGCTGCT	KTEFCAA	+	--

25593	37969	CGAACGAACACAGTCTATCCC	RTNTVYP	+	--
22981	37233	ACGGACGAGTTTTCAACTTGG	TDEFSTW	+	--
27164	13874	TACTCCCGGCTTGGGCTGAAT	YSRLGLN	+	---
29512	14495	AGGCTATATGATGCTTACGAG	RLYDAYE	+	---
22028	36558	ATTCTTTCCAGTAGTAGTTGG	ILSSSSW	+	---
26842	14628	TATAGTCGTTTGAATGACAAT	YSRLNDN	+	---
28427	39133	ATTATGGGTGATAGGACATGG	IMGDRTW	+	---
27836	38764	TACCATAGGCTCGGCGATAAT	YHRLGDN	+	---
25717	13762	TTTTCGAAACTTAATTATAAT	FSKLNYN	+	--
29810	14298	TATAGCCGAATCGGGTCCAAC	YSRIGSN	+	--
21597	36724	CGAACCCCTTCTGTATACCCC	RTPSVYP	+	--
25376	37562	ATGCATAGACTGTCTACCAAC	MHRLSTN	+	---
25862	37650	AAAGATGAGTGGTCAGTGTAT	KDEWSVY	+	--
27968	38981	TATTCAAGGATCCAAGCCAAT	YSRIQAN	+	--
22904	37197	AGAGATGAGTTTTCCACTTAT	RDEFSTY	+	---
23027	37197	AGGGACGAGTTTTCAACATAT	RDEFSTY	+	---
35284	38364	CGAGATGATTGGGTCAAATGG	RDDWVKW	+	---
27636	19011	TTCCTCGCGAGTCGAGACTGG	FLASRDW	+	--
26849	38605	AGGGGAGATTCCCCCAAGTGG	RGDSPKW	+	--
20546	36263	CTAACTCGCTTAAGTGCCAAC	LTRLSAN	+	--
20927	36438	CTGTGCAAGCCCTGTCCGACC	LCKPCPT	+	---
20742	36359	CTGAGTCGTGTTGGCTTTGAT	LSRVGFD	+	---
24072	37614	AGGACCTCGACTGTGTACCCC	RTSTVYP	+	--
23137	17576	GTCTTAAGCTCGAACGTTTGG	VLSSNVW	+	---
22492	17725	GAGCCCGAACGTGGCTGGTTT	EPERGWF	+	---
28880	14074	TATAGCCGTATAGGTGGTAAC	YSRIGGN	+	--
27567	38845	CCTCTCAGCGATCGTACCTGG	PLSDRTW	+	---
22024	13795	CGTGATGATTTTACGGCCTAT	RDDFTAY	+	---
26989	38305	AGGGACGACTATTCGACTTAC	RDDYSTY	+	---
27028	38605	CGTGGCGACAGTCCGAAGTGG	RGDSPKW	+	--
20998	36474	ATCATGGCGTCAGCAAACTGG	IMASANW	+	---
25768	38012	AGATCAGAGTTTAAGACTTAT	RSEFKTY	+	--
31397	38831	CACATGCCTGACCGCAAGTGG	HMPDRKW	+	--

28841	38873	CAAATGAAGGATAGGACCTGG	QMKDRTW	+	---
31900	39631	CCAATGCAAGATCGCAGCTGG	PMQDRSW	+	---
35413	41230	TCGATGGACAGCAGGAGCTGG	SMDSRSW	+	--
24824	37871	CGATTAGAGGATCGTCTCTGG	RLEDRLW	+	---
24599	37641	AGGAGCGAATTCACCACATAT	RSEFTTY	+	---
25780	37938	CGAACCTATGACTCCTATCCT	RTYDSYP	+	---
28744	38446	GACATGCGAGACAGAATTTGG	DMRDRIW	+	--
30594	39876	TGTGCAGCGGAGCGTCTGGGT	CAAERLG	+	--
28328	38442	CGGATGGAAGAACGTTCATGG	RMEERSW	+	---
29577	13553	TATGCTAGAACAGGCTATAAC	YARTGYN	+	--
21069	36505	AATCTCAGCAGTAGCACGTGG	NLSSSTW	+	---
20941	36447	CAACTGAGTAGCTCCACCTGG	QLSSSTW	+	---
26109	38305	AGGGACGATTACAGCACATAC	RDDYSTY	+	---
28462	39147	ACCGACGACTGGTCAAGTTAT	TDDWSSY	+	--
23227	37280	TCAGATGGGACAAGCCGTTGG	SDGTSRW	+	--
21441	36669	GAACTGGCATCGAGAGAGTGG	ELASREW	+	---
30420	39823	AGAAATGAATATAGCACATAT	RNEYSTY	+	--
22306	36974	GACGCTATTCGTGGTTGGGAT	DAIRGWD	+	---
34687	40962	TGGACGCCCAATTGTAAAGCG	WTPNCKA	+	--
29953	39304	ATTATGGGCGACAGAAAGTGG	IMGDRKW	+	---
25603	18518	ACTGACGAATGGTCCCCATAC	TDEWSPY	+	--
21816	14461	TATTCCAAGCTCAATTATAAT	YSKLNYN	+	---
26760	38576	GGGTCCGAGTATCTAACATGG	GSEYLTW	+	--
36077	41806	GGGACTGAATATGTTAGTTAT	GTEYVSY	+	--
22837	37045	AAAGATGACTATTCAACGTAT	KDDYSTY	+	---
21909	36824	GGTTCAGAATTTTCGACGTGG	GSEFSTW	+	---
21793	16568	TTGCACAGATTACTAAAGGAC	LHRLLKD	+	---
31802	40036	CAAGGTGAGAGTCGAGTGTGG	QGESRVW	+	---
29639	13848	TACTCACGGCTTAATCTGAAT	YSRLNLN	+	---
30191	39738	TCAATGTCCGATCGGAGTTGG	SMSDRSW	+	---
21326	36615	CGTGACGAGTTTACAACGTAT	RDEFTTY	+	---
24006	37014	ATTTTAAGTGACAGAATTTGG	ILSDRIW	+	---
21689	36472	GACATGTCCGCGAGCACGTGG	DMSASTW	+	---

20763	36368	AATTTAGCCTCCGCCACGTGG	NLASATW	+	---
22472	36862	CCCATGGGCTCTTCATCCTGG	PMGSSSW	+	---
22617	37031	TTGCACCGGCTCTCGCACGAT	LHRLSHD	+	---
20794	36382	CTCTGTAAACCTTGCTTGGGC	LCKPCLG	+	--
26465	38457	TTGTGGGACGGCACAAGCCCG	LWDGTSP	+	---
24016	36701	CGAGACGAGTTTACTAGTTTT	RDEFTSF	+	---
26925	14704	TATTCGCGTTTAGGACAAAAC	YSRLGQN	+	--
28406	14704	TACTCGCGACTTGGTCAAAAC	YSRLGQN	+	--
27026	38278	CGACTGGAAGACCGCGCATGG	RLEDRAW	+	---
20568	36253	CTTCATAAACTAAGTCCGAAT	LHKLSPN	+	---
27643	38872	AGGGACGATTACGTTTCTTGG	RDDYVSW	+	---
22433	37029	CGTAGCGAATTTGTCTCTTAT	RSEFVSY	+	---
22534	36796	CTTTCAAGGCTCAGCCCCAAC	LSRLSPN	+	---
21755	36723	CTCCACAGGCTGGGCGACAAT	LHRLGDN	+	---
35522	41537	GATTACGAGAGCCGGAAATGG	DYESRKW	+	---
29996	13517	TACTCCAGGTTGAACATTAAT	YSRLNIN	+	---
24127	37029	AGATCAGAGTTCGTAAGCTAC	RSEFVSY	+	---
33154	40790	AGGACTTATGATACTTACGCT	RTYDTYA	+	--
28598	14074	TATTCTAGAATAGGTGGAAAC	YSRIGGN	+	--
25576	16630	CTAAGTAGGTTAAATCATAAC	LSRLNHN	+	---
21875	36812	GATCTTTCATCACAGAAGTGG	DLSSQKW	+	---
25594	37045	AAGGACGATTATTCTACCTAC	KDDYSTY	+	---
24095	37203	AAAGATGGCTATTCAACTTAT	KDGYSTY	+	--
29114	39353	TACTCCCGCATCCAGCCCAAT	YSRIQPN	+	--
26442	38442	AGAATGGAGGAGAGAAGCTGG	RMEERSW	+	---
27284	37604	AGAGAGGAGTACACGAGCTGG	REEYTSW	+	--
24912	37280	TCGGATGGGACATCGAGGTGG	SDGTSRW	+	--
23516	37217	CGTAAACATGATGTGTATCCT	RKHDVYP	+	---
22972	37230	TCTATGAGCAGTAGTACCTGG	SMSSSTW	+	--
23150	37288	CGCGATGACTTTAGTTCATAC	RDDFSSY	+	--
26139	14010	TATAGTCGGGTCGGCTTAAAC	YSRVGLN	+	---
23195	14219	TACGCCCGCCTGGGACCAAAT	YARLGPN	+	--
21345	14379	TATTCAAAAGCGGGGCCTAAC	YSKAGPN	+	---

24853	36827	GATTTGCGCTCCGCAAATTGG	DLRSANW	+	--
25770	37143	GAGCTAGAGAGTCGCTCATGG	ELESRSW	+	---
34649	40379	GACATGCAGGACCGCAGTTGG	DMQDRSW	+	--
34350	41230	AGCATGGATTCTCGATCATGG	SMDSRSW	+	--
21768	10981	TATTCCAAGGCTGGTTGTAAC	YSKAGCN	+	--
23763	37502	GTGTTCAGTACGAATGGTAGG	VFSTNGR	+	--
25287	38046	TTCCATAGACTTAGTCCCAAC	FHRLSPN	+	---
25870	38234	CATTGTGAGGGTCGCCCCGTA	HCEGRPV	+	--
23920	37280	AGCGACGGCACTAGTCGATGG	SDGTSRW	+	--
21825	13762	TTCAGTAAGTTAAATTACAAC	FSKLNYN	+	--
30312	39463	TGTAAGCCCGGTAGTCCAGGA	CKPGSPG	+	--
21649	36724	AGGACACCAAGCGTGTATCCG	RTPSVYP	+	--
32008	40379	GATATGCAAGATAGGTCTTGG	DMQDRSW	+	---
35876	36701	AGGGATGAATTCACATCGTTC	RDEFTSF	+	---
35969	38672	TTATGCAGACCATGTTCAATG	LCRPCSM	+	--
24690	37283	GGGGGAGAGACATCGAGATGG	GGETSRW	+	--
20530	36252	TTGCACAAGTTGTCAGTGAAC	LHKLSVN	+	---
25250	37817	CGAATGGAGAGCCAGGGATGG	RMESQGW	+	---
23865	37546	GTCCCAGATCATGTGAGATGG	VPDHVRW	+	--
26226	17520	TATTTTTCCGGCCGAGTGGCG	YFSGRVA	+	--
28532	13517	TACAGTCGTCTAAATATAAAC	YSRLNIN	+	---
31260	39823	CGTAACGAGTACTCTACGTAC	RNEYSTY	+	--
22954	37217	AGGAAGCACGACGTATACCCG	RKHDVYP	+	---
27705	13841	TTGCACCGCATGACACCAAAC	LHRMTPN	+	--
22850	37177	GAGGGAATCAGTAGAGACTGG	EGISRDW	+	---
20635	36270	CTAAGTCGTTTGGGGCCTGAC	LSRLGPD	+	--
24317	37655	TATCACAGGCTTTTGCCGGAT	YHRLLPD	+	---
28565	38690	CGAACATTCGACGCATATCCG	RTFDAYP	+	---
27655	38424	TATTTCACAGGCAGGGTCAGC	YFTGRVS	+	--
24172	37420	ATAATGGCTGACAGGGTTTGG	IMADRVW	+	---
28241	39072	GTCATGGAAGCTCGGGGCTGG	VMEARGW	+	--
30479	39782	CCTATGCCGGATAGGAGCTGG	PMPDRSW	+	---
20914	36369	TTGCATCGTCTCGGTCTTGAT	LHRLGLD	+	---

22839	37178	ATAATGAGTCATGCAACATGG	IMSHATW	+	---
28139	14262	TACAGCCGGATAGGCGCTAAT	YSRIGAN	+	---
29021	14378	TACTCAAGAGTAGGGGCAAAT	YSRVGAN	+	---
22945	37187	CTAAGCAGAATCTCACCTAAT	LSRISPN	+	--
35151	38372	GGCGACGGCACAAAGTGCGGG	GDGTKCG	+	--
33141	40783	TGTAAGTCAGACCGCAAGGAA	CKSDRKE	+	--
29360	14399	TACGCCCGCACCGGCAACAAT	YARTGNN	+	---
28063	38908	AAGCTAACTGACAGAACTTGG	KLTDRTW	+	---
25420	37332	AAAGATGATTACGTGTCGTAC	KDDYVSY	+	--
25955	14628	TATTCGCGTTTGAACGATAAT	YSRLNDN	+	---
21751	36766	CGCGACGACTTTACTACTTGG	RDDFTTW	+	---
33486	17602	GTCCTGAGCGAACGAAGTTGG	VLSERSW	+	---
24635	37725	TTATGGGATGGGACCGGCCCA	LWDGTGP	+	---
23005	37197	CGTGATGAATTCAGCACTTAC	RDEFSTY	+	---
27460	38806	AAAGACGAATGGAAAACCTAT	KDEWKTY	+	--
24246	37655	TACCATCGTTTGCTACCTGAC	YHRLLPD	+	---
23717	16112	GTGCAGTCGACTAACGGCAGA	VQSTNGR	+	---
30327	39782	CCGATGCCAGACCGTTCGTGG	PMPDRSW	+	---
25022	37939	CGGAATGAATTTACCACGTAC	RNEFTTY	+	---
21499	36690	CCCATGGATTCCTCCAGATGG	PMDSSRW	+	---
26907	38295	GATATGCGCTCCGCTAACTGG	DMRSANW	+	--
21291	36598	CTGCATAGATTGTCGCCGCTC	LHRLSPL	+	---
27011	38654	TACAGCCGCATTTCTCCCAAT	YSRISPN	+	--
24233	37650	AAGGACGAATGGAGTGTTTAC	KDEWSVY	+	--
20888	36413	TTGCACAGACTAGGGCCGGAT	LHRLGPD	+	---
22376	36495	TTAAGTCGCGTGAGCATTAAC	LSRVSIN	+	---
27355	38764	TATCACCGATTGGGAGACAAC	YHRLGDN	+	---
33974	40609	ATCCTCCAGGACAGGGGGTGG	ILQDRGW	+	--
28587	14262	TATTCTAGAATCGGTGCCAAT	YSRIGAN	+	---
21950	36840	TACCACAAGTTGAACGCAAAT	YHKLNAN	+	---
25670	37585	GTTATGGGAAGCTCGAATTGG	VMGSSNW	+	--
33890	41065	GAAATGCAGGACAGGAGCTGG	EMQDRSW	+	--
22556	37072	ACGTTGAGTAGTCAGACGTGG	TLSSQTW	+	---

25539	38012	AGGAGCGAGTTTAAAACGTAC	RSEFKTY	+	--
21977	36778	TACCACAAGTTGAACAACAAT	YHKLNNN	+	---
29240	19603	GACGCCCTGGAATGGCGCGAC	DALEWRD	+	--
22008	36546	TTGCACCGCTTAGGTATGGAC	LHRLGMD	+	---
23738	37106	TTGCACAGACTCTCCGAAGAT	LHRLSED	+	--
27947	37585	GTAATGGGCTCCTCAAACTGG	VMGSSNW	+	--
20916	36418	CTTCATAAAAAGGGCCCTGAT	LHKKGPD	+	---
27696	13818	TATAGCAGGCTGAATGTCAAC	YSRLNVN	+	---
20992	36416	AAGGATGATTTTACTTCGTGG	KDDFTSW	+	---
23416	37045	AAAGATGACTACAGCACTTAT	KDDYSTY	+	---
30085	13848	TATAGCAGACTAAACCTCAAC	YSRLNLN	+	---
26393	38424	TACTTTACCGGTCGAGTTTCG	YFTGRVS	+	--
31093	17033	AGAAACATGTCGGTGTACCCA	RNMSVYP	+	--
22074	36896	GTAGGACACAAGGGGTGGGAT	VGHKGWD	+	--
25819	38012	CGATCAGAATTCAAGACCTAT	RSEFKTY	+	--
24205	37641	AGGAGCGAATTTACGACATAC	RSEFTTY	+	---
30369	39799	TGCCCTCGCGAAAATGACGGG	CPRENDG	+	--
28808	39272	GACCCATCTTCTAGAGCCTGG	DPSSRAW	+	---
21791	36778	TACCATAAGCTCAATAATAAT	YHKLNNN	+	---
32421	40493	TCTATGCCTGACCGCTCGTGG	SMPDRSW	+	---
26814	13517	TACTCGAGACTCAATATAAAT	YSRLNIN	+	---
28384	14628	TATTCAAGGCTTAACGATAAC	YSRLNDN	+	---
29666	39272	GATCCGAGCAGCCGTGCATGG	DPSSRAW	+	---
21608	36663	TATCACAAACTGAATCCCATG	YHKLNPM	+	--
22866	37184	AGGATGGAATCTGCAGTGTGG	RMESAVW	+	---
31793	39548	TCCATGCAGGACAGGACATGG	SMQDRTW	+	---
21172	36550	AGGACCCCCCAGGTGTTCCCA	RTPQVFP	+	--
21595	36723	CTCCATAGATTGGGTGATAAC	LHRLGDN	+	---
21419	36660	CCAATGTCATCCAGCAGCTGG	PMSSSSW	+	---
21389	36603	AGGACCGAACATGTTTTTCCG	RTEHVFP	+	---
22185	36932	TATCATAAGTTGAATCATAAT	YHKLNHN	+	---
24120	37196	AAGAGTGATTTTGTGAGCTAC	KSDFVSY	+	--
27369	37679	GATATGGAGTCACATAAATGG	DMESHKW	+	---

28245	39074	GACCTTCGCGACCGGATTTGG	DLRDRIW	+	--
27177	38709	GGCTGTAGGCATGGTACCATC	GCRHGTI	+	--
23842	16112	GTTCAGAGCACGAACGGCCGG	VQSTNGR	+	---
26334	38393	CTTTGGAACGGAGAAGGACCG	LWNGEGP	+	---
20543	36260	CTTCACAAATTAAGTATGAAT	LHKLSMN	+	---
27640	38371	AACATGGGGTCGAGAGACTGG	NMGSRDW	+	---
28507	39168	CTGCTCCAAAGTACAACGTGG	LLQSTTW	+	--
25476	13580	TATAGCAGAGTCGGGATAAAC	YSRVGIN	+	---
21274	36589	GATATGTCAAGCAGTAAGTGG	DMSSSKW	+	---
21136	36534	CTACACAGGTTAAGTTTGGAT	LHRLSLD	+	---
25360	37939	AGAAACGAGTTCACGACATAT	RNEFTTY	+	---
23042	36743	AGAATGGAAGTGTCGACCTGG	RMEVSTW	+	--
23128	36831	CTCAGCAGAATCTCCTTTAAC	LSRISFN	+	--
24900	18772	CTTCGGACTGATTGCTGTGTC	LRTDCCV	+	---
23556	37336	CGCGAGGATTTTACCGCCTGG	REDFTAW	+	--
27564	38843	TATCACAGGTTATCCGCCAAC	YHRLSAN	+	---
22351	36710	ATGTCAAGGATTGGACCGAAC	MSRIGPN	+	--
24940	37912	AGAACACATGATGTGTACCCA	RTHDVYP	+	---
29789	39596	ATGCTTTCAGACAGATTATGG	MLSDRLW	+	---
26363	13928	TACGCCCGCATCGGCCCAAAT	YARIGPN	+	--
22404	36972	CTTCACCGCCTCAGCCCGGTA	LHRLSPV	+	--
30180	39735	TGCACTTCTAAAACGACACAT	CTSKTTH	+	--
22608	36812	GACTTGAGCAGTCAAAAATGG	DLSSQKW	+	---
31683	40083	GTTATGGAAGCTAGGCAGTGG	VMEARQW	+	--
23508	36544	CCAATGGGCAGCAGTACATGG	PMGSSTW	+	---
21479	36444	GATATGGCAAGTGCGTCCTGG	DMASASW	+	---
21534	36684	CCCATGGCGAGTAGCAATTGG	PMASSNW	+	---
26866	38611	TATAGCAGAGTCCAGTTAAAT	YSRVQLN	+	--
31656	39043	AGGGACGATTGGACGGTCTTC	RDDWTVF	+	--
26448	38446	GATATGAGGGATCGCATCTGG	DMRDRIW	+	--
30959	40000	TGCAAACTACCGAAGAGTGAG	CKLPKSE	+	--
28096	38654	TACTCGAGAATCAGCCCGAAC	YSRISPN	+	--
27566	38305	CGTGATGATTATTCAACCTAT	RDDYSTY	+	---

27539	38305	CGTGATGATTACTCGACATAC	RDDYSTY	+	---
25843	38223	TACTCTAGGATTGGACCAGAT	YSRIGPD	+	---
21391	36594	CTCCACCGCCTAGGCGCAGAC	LHRLGAD	+	---
27991	14321	TTTAGTCGGCTTAACAATAAT	FSRLNNN	+	--
23696	18772	TTGAGAACTGACTGCTGCGTT	LRTDCCV	+	---
24465	17759	AGGAATTCTACCGTGTACCCT	RNSTVYP	+	--
26064	38294	GACATGGGCGACCGTAAGTGG	DMGDRKW	+	---
20814	14005	TATTCAAAGTTGGGGCCAAAT	YSKLGPN	+	---
26224	13580	TACTCGCGTGTAGGAATCAAT	YSRVGIN	+	---
23722	37310	AGAGATGGAACATCAAGCTGG	RDGTSSW	+	--
32325	40490	GCGCTCTCCGACAGGTCCTGG	ALSDRSW	+	---
21257	14379	TATAGCAAGGCGGGTCCAAAT	YSKAGPN	+	---
21065	14040	TATAGTAAAGTGGGACCGAAT	YSKVGPN	+	---
21639	36615	AGGGATGAATTCACGACATAC	RDEFTTY	+	---
24519	37347	CGTAACATGGATGTCTACCCC	RNMDVYP	+	---
28376	39115	GTTGGCGAAGCGAGGTCGTGG	VGEARSW	+	---
24596	37781	CGTACATCCACTCACGGCGTA	RTSTHGV	+	--
24055	36756	GTCATGGAGGCAAGAGACTGG	VMEARDW	+	---
20520	36246	CTGCACAAGCTATCTATTAAT	LHKLSIN	+	---
22027	36878	GAAATGAAAGCCAGGACCTGG	EMKARTW	+	--
29301	14618	TACTCAAAAGTAGGTAAAAAT	YSKVGKN	+	---
33267	17013	CGGAACGAATACACCACTTAC	RNEYTTY	+	--
26403	14628	TACAGTCGCCTAAATGACAAC	YSRLNDN	+	---
31455	17013	AGAAACGAGTATACGACGTAT	RNEYTTY	+	--
27455	38554	AGAATGGACGCAGTGACGTGG	RMDAVTW	+	--
33322	40847	TGCACTAGCAAGGTAGGGCAC	CTSKVGH	+	--
21834	36790	TACCACAAACTGAATCCCTTG	YHKLNPL	+	--
27616	38582	CGTAACGAGTTCAGCACGTAC	RNEFSTY	+	--
20805	14176	TACAGTAAGATAGGGCCGAAC	YSKIGPN	+	---
27589	38852	GTAAGTACGCATTGCGCCGCT	VSTHCAA	+	--
24829	37275	AGAGATGAATTTGTTAGCTGG	RDEFVSW	+	---
20944	36450	ACACTGTCAAGCGCCACCTGG	TLSSATW	+	---
27466	38809	AGAACCAATAATGTCTATCCG	RTNNVYP	+	--

22896	36668	GACATGAGCAGTAGCGTTTGG	DMSSSVW	+	---
28562	19998	GTATCCGATTATGCGTCGTAT	VSDYASY	+	--
23903	36944	ATCATGTCCTCGAGCATGTGG	IMSSSMW	+	--
29095	14115	TATTCAAGGGTTGGGAGTAAC	YSRVGSN	+	---
23290	37197	CGTGACGAATTCAGTACGTAC	RDEFSTY	+	---
28313	38731	TATTGGAGTGGGGTTCGCGAA	YWSGVRE	+	--
29498	13841	CTACATCGAATGACGCCAAAT	LHRMTPN	+	--
21166	36431	GTCGAAAGCACAAACGGTCGA	VESTNGR	+	---
27131	38690	CGAACGTTTGATGCTTACCCG	RTFDAYP	+	---
22416	36841	CTAAGTAGGATCTCAACTAAT	LSRISTN	+	--
22823	17593	CTCTCACGGATCGGGACCAAT	LSRIGTN	+	--
26658	38534	GTTATGGAAGATAGACGATGG	VMEDRRW	+	---
23846	37536	AGAGATGAGTTCACGCACTAC	RDEFTHY	+	---
23726	37473	TACTTTACCGGAAGGACGGCG	YFTGRTA	+	--
29732	14321	TTTTCAAGGTTAAATAATAAC	FSRLNNN	+	--
27381	38775	TCTCTGGAGAGTAGGGCTTGG	SLESRAW	+	---
27121	14344	TATAGTAGGGTGGGCCAGAAC	YSRVGQN	+	---
28986	38654	TATAGTCGTATATCTCCCAAT	YSRISPN	+	--
27005	38650	CCATATGCTAGGAGCCCAATG	PYARSPM	+	--
27461	14273	TACGCTCGGATGGGTCCGAAT	YARMGPN	+	--
25199	38008	CAGGATGGTAATAGCAGGTGG	QDGNSRW	+	--
28826	19945	GAAGGGCCTAGCAGAGGTTGG	EGPSRGW	+	---
22093	36495	CTTTCTCGCGTAAGCATCAAT	LSRVSIN	+	---
28770	39259	GCAATGCCTGATCGGGGCTGG	AMPDRGW	+	---
29079	13664	TATTCAAGAATAGGCATAAAT	YSRIGIN	+	--
20760	36365	GACCTGAGTAGTGCGAAGTGG	DLSSAKW	+	---
22838	16112	GTACAAAGTACAAATGGTCGC	VQSTNGR	+	---
20997	36473	TACCATAAGTTAGGCCCACAG	YHKLGPQ	+	--
22797	37168	AGAACATTTGACGTGTTTCCG	RTFDVFP	+	---
20689	36334	GTGTTGTCGAGCGCCAACTGG	VLSSANW	+	---
34891	18696	GCCGGTGGTTCCCGCGACTGG	AGGSRDW	+	--
21941	36756	GTAATGGAGGCACGGGACTGG	VMEARDW	+	---
33690	40982	ACTAGGTGGGGAGATAATGCC	TRWGDNA	+	--

24270	37592	ATGCACAGACTCAGTTTCGAC	MHRLSFD	+	--
24155	37635	GTTTTAACGAGCGCAAAATGG	VLTSAKW	+	--
24498	37631	GTGAATGACTATATTTCATAT	VNDYISY	+	--
26920	37967	AGATTAGAAGCCGTTACGTGG	RLEAVTW	+	---
21292	36599	CCCATGGAATCATCAAAATGG	PMESSKW	+	---
20664	36292	TTGACCCGTTTGTCTCCAAAT	LTRLSPN	+	---
24323	37045	AAGGACGATTATAGTACGTAC	KDDYSTY	+	---
22690	36778	TATCACAAATTAAACAACAAC	YHKLNNN	+	---
26514	38472	GCGGGTGCCGACAGAGGTTGG	AGADRGW	+	---
20593	36268	TTACATAAGCTTTCGACGAAT	LHKLSTN	+	---
28741	14136	TACTCTCGACTGGGAGCAAAT	YSRLGAN	+	--
24142	37635	GTACTGACCTCTGCTAAGTGG	VLTSAKW	+	--
23345	36823	TATTTTTCCGGCGTGAAGGCC	YFSGVKA	+	--
28521	38690	AGGACATTCGACGCATATCCA	RTFDAYP	+	---
29103	13990	TATGCAAGACAAGGACCTAAC	YARQGPN	+	---
23117	37275	CGTGACGAGTTCGTGTCATGG	RDEFVSW	+	---
32286	39587	TGCAAGCCCCCTCCCATCGAG	CKPPPIE	+	--
21047	36495	CTCTCGAGGGTTTCAATCAAT	LSRVSIN	+	---
21076	36388	ATAGCTAACAAGGGGTGGGAC	IANKGWD	+	---
29348	14191	TACGCACGAACAGGGCATAAC	YARTGHN	+	--
26992	38278	AGGTTAGAGGATAGGGCTTGG	RLEDRAW	+	---
23289	37235	CTATCAAGGGTTAGTCCTAAC	LSRVSPN	+	--
23946	37576	AAAGATGATTACCTTTCATGG	KDDYLSW	+	--
23142	37284	CGTATGGAGAGCGCGAATTGG	RMESANW	+	---
21707	36576	TTATCTCGGCTTAGTTTCGAC	LSRLSFD	+	---
21679	36723	TTGCATCGCTTAGGTGATAAC	LHRLGDN	+	---
22903	37196	AAATCAGACTTCGTCTCTTAT	KSDFVSY	+	---
27090	14264	TATGCACGGACAGGGGCAAAT	YARTGAN	+	---
25374	37641	CGATCAGAATTTACAACTTAC	RSEFTTY	+	---
20559	36268	CTGCACAAATTAAGCACGAAC	LHKLSTN	+	---
20598	36281	TTGCATAAACTAATGCCGAAC	LHKLMPN	+	---
24682	37674	AAGGATGAGTTCCGATCATAC	KDEFRSY	+	--
27551	14192	TTCTCGCGTCTTAACATAAAC	FSRLNIN	+	--

28336	38843	TATCACAGATTGTCCGCAAAT	YHRLSAN	+	---
20681	36331	TTAGCGCGATTGGGGCCGAAT	LARLGPN	+	---
28679	14495	CGCCTTTACGACGCGTATGAA	RLYDAYE	+	---
28479	14010	TACTCGCGGGTGGGCTTAAAT	YSRVGLN	+	---
30135	39714	ACGTTGAGCAGTCGTGATTGG	TLSSRDW	+	--
24689	37817	AGGATGGAATCTCAAGGTTGG	RMESQGW	+	---
24742	37088	CGCGAAGAAACCGTGTATTGG	REETVYW	+	--
23318	37347	AGAAATATGGACGTATATCCT	RNMDVYP	+	---
35370	40956	GTCCATAAATTGTGCCCAGTA	VHKLCPV	+	--
33496	40908	AGAATGCAGGACCGGTCGTGG	RMQDRSW	+	--
22251	36957	AAGGACGATTATACCACGTGG	KDDYTTW	+	---
25510	14858	TATGCCCGTGCTGGCCCCAAT	YARAGPN	+	--
21134	36532	AGGTTGGAGAGCACCTTGTGG	RLESTLW	+	---
22871	37187	CTGTCGCGCATAAGTCCGAAC	LSRISPN	+	--
25159	37991	CTGTGCAAGCCGTGCTTCACC	LCKPCFT	+	--
28471	14350	TACTCCAGATTGAACGCGAAT	YSRLNAN	+	---
35317	41537	GATTATGAATCAAGAAAGTGG	DYESRKW	+	---
21030	36488	TATGTTAAGTCGGACAGGCAC	YVKSDRH	+	---
20575	36278	CTCCACAAATTGAGCCTCAAT	LHKLSLN	+	---
27782	38073	CGCTCCGACTTCAAAATATAC	RSDFKIY	+	--
30505	39848	TCAGGAGAAAGTCGCACTTGG	SGESRTW	+	---
23678	37476	CGTTCAGAATTTTTGCCTTTT	RSEFLPF	+	--
27476	17663	TCTCTGAGCAGTCGCGATTGG	SLSSRDW	+	---
26388	38422	ATCTTGAGCCACGCCACGTGG	ILSHATW	+	--
21468	36431	GTCGAGTCGACCAATGGCAGA	VESTNGR	+	---
23929	37571	AGGGATGAGTTCAGTAGCTTT	RDEFSSF	+	--
23305	37235	TTGAGCCGTGTATCTCCGAAT	LSRVSPN	+	--
36187	41873	AAGCACGAATTTACAGCGTTC	KHEFTAF	+	--
33978	41096	TGTTCTAGGATCGGTCCAAAT	CSRIGPN	+	--
22725	37030	TTGCATAGATTGAGCCAAGAT	LHRLSQD	+	--
21105	36521	TATGCTAAGCACGGACCGAAT	YAKHGPN	+	--
20893	36427	AGGGAAGATGCCGTGAGATGG	REDAVRW	+	--
30701	38749	TACTTCACTGGGCAATGTGAA	YFTGQCE	+	--

23239	18011	CTTCACCGCTTGATGCCCGAT	LHRLMPD	+	--
32579	40102	GTTGGTTCTGACCGAGGATGG	VGSDRGW	+	--
22955	37218	ACCGACGGGACCTCTAGGTGG	TDGTSRW	+	--
27825	14344	TACAGTCGTGTTGGCCAAAAC	YSRVGQN	+	---
21150	36491	TTAGCACGCACTGGATTAAAT	LARTGLN	+	--
23652	13934	TTCGCTAGGACAGGTCCTAAT	FARTGPN	+	---
22245	14342	TATTCTAAACTGGGTTACAAT	YSKLGYN	+	--
21336	36488	TACGTGAAAAGTGATCGCCAT	YVKSDRH	+	---
27157	38697	ATGTGGGACGGAACTATGGCA	MWDGTMA	+	--
21510	14290	TACAGCAAGGTCGGATACAAC	YSKVGYN	+	---
23712	37488	TATTCCAGGGTAGGTCCGGAT	YSRVGPD	+	---
23230	18899	CGACTTGAGAGTCACGGGTGG	RLESHGW	+	---
25459	37578	CGAGATGGCGTATCGAAGTGG	RDGVSKW	+	--
21627	36603	AGGACTGAACACGTGTTTCCT	RTEHVFP	+	---
24558	13928	TATGCACGTATAGGACCGAAC	YARIGPN	+	---
22431	36932	TACCACAAACTTAACCACAAC	YHKLNHN	+	---
31519	40198	ATTCCTCATCGAAGCTGCGCT	IPHRSCA	+	--
29565	14298	TATTCACGGATAGGTAGTAAT	YSRIGSN	+	--
29323	13857	TATGCTAGGTCAGGTTTCAAT	YARSGFN	+	--
25802	37675	AACATGTCAAGTTCGAGTTGG	NMSSSSW	+	--
30242	13553	TACGCTCGCACCGGGTACAAT	YARTGYN	+	--
25421	37930	TATTGGAGCGGTATAAAAGAC	YWSGIKD	+	---
25619	38039	GATCTGCGCGATCGGGGGTGG	DLRDRGW	+	--
26990	37502	GTTTTTTCGACAAACGGCCGC	VFSTNGR	+	--
24177	14224	TACTCCAAAATTGGATACAAT	YSKIGYN	+	---
34694	38280	TTATGGGATGGAACCAACGCC	LWDGTNA	+	---
28227	13851	TATGCACGGACTGGATTTAAC	YARTGFN	+	--
22846	13629	TACAGTAAACACGGTCCCAAC	YSKHGPN	+	---
31722	40137	TGTATGAAGCCGCGTTTGGAG	CMKPRLE	+	--
26790	16630	CTCTCACGACTTAACCATAAT	LSRLNHN	+	---
23409	37284	AGGATGGAATCGGCTAACTGG	RMESANW	+	---
23067	36766	AGGGATGATTTCACCACATGG	RDDFTTW	+	---
21160	14040	TACTCAAAGGTAGGTCCAAAC	YSKVGPN	+	---

23515	36690	CCTATGGACAGTAGTCGCTGG	PMDSSRW	+	---
21701	36602	GTCATGGCTAGCAGTTCCTGG	VMASSSW	+	---
24350	13623	TTTTCAAGAATTGGACCAAAC	FSRIGPN	+	--
22446	37031	CTCCATAGATTGAGCCACGAC	LHRLSHD	+	---
22355	36991	CTCAGTCGTACCAGTTTAAAT	LSRTSLN	+	--
20579	36281	CTTCACAAGTTGATGCCTAAT	LHKLMPN	+	---
23981	37585	GTCATGGGAAGTAGCAATTGG	VMGSSNW	+	--
20777	36376	AAAGACGAGTTTTTATCGTGG	KDEFLSW	+	--
30271	14443	TACTCCCGAATTGGGTTGAAT	YSRIGLN	+	---
24319	37674	AAAGACGAATTTAGGAGCTAT	KDEFRSY	+	--
25714	37365	GACATGTCATCCAAAGTTTGG	DMSSKVW	+	---
29775	14211	TATAGCAGGACAGGTTCCAAC	YSRTGSN	+	--
25044	37912	CGGACGCACGACGTCTATCCC	RTHDVYP	+	---
23937	37218	ACAGACGGTACCTCACGATGG	TDGTSRW	+	--
28345	17563	GTGATGGAAGATCGTATATGG	VMEDRIW	+	---
20603	36292	CTTACGAGGCTTAGCCCTAAC	LTRLSPN	+	---
21240	36438	TTATGCAAACCTTGCCCTACA	LCKPCPT	+	---
22906	36722	GTGTTGAGTTCTAGTGCCTGG	VLSSSAW	+	--
32951	40716	TGTGGCGCGATTAAGCCCCCT	CGAIKPP	+	--
22235	36920	GACCTCCGTTCGGCAGCATGG	DLRSAAW	+	---
28833	14083	TACAGCAGAGTAGGTGTAAAT	YSRVGVN	+	---
23214	13934	TTTGCGCGTACGGGTCCGAAC	FARTGPN	+	---
20715	36331	CTCGCCAGGCTTGGCCCAAAC	LARLGPN	+	--
25284	37199	GATCTGGAAAGTAGGGAGTGG	DLESREW	+	---
25601	14502	GTCTGGAGTACCAACGGCATC	VWSTNGI	+	--
29802	14479	TACAGTCGTATTGGTAATAAT	YSRIGNN	+	---
23742	37288	AGGGACGATTTCTCAAGTTAT	RDDFSSY	+	--
27245	38724	TACAGTAGACTTAATTATGAC	YSRLNYD	+	---
21685	36745	CTACACCGACTTGGGCAGGAC	LHRLGQD	+	---
22481	37045	AAGGATGACTACTCCACTTAT	KDDYSTY	+	---
21374	36563	ATGCACAGATTGCTCCCAGAC	MHRLLPD	+	---
27400	38753	TATCACCGCCTCAGCGATAAC	YHRLSDN	+	---
21115	14176	TATTCCAAAATCGGTCCTAAT	YSKIGPN	+	---

27672	38690	AGGACTTTTGATGCGTACCCT	RTFDAYP	+	---
26831	38305	AGAGATGACTATAGCACTTAT	RDDYSTY	+	---
21250	36576	TTGAGCCGTTTGTCCTTTGAT	LSRLSFD	+	---
27814	38731	TACTGGTCGGGCGTCAGAGAG	YWSGVRE	+	--
29096	13816	TATTCAAGACTTAACCCAAAC	YSRLNPN	+	--
24330	37323	AGAATGGAGAGTAGCCAGTGG	RMESSQW	+	--
21929	36835	CTCATGACTGATCGAACTTGG	LMTDRTW	+	---
29085	39229	ATCATGTCCGATCGCGAGTGG	IMSDREW	+	---
26462	38455	CCAATGGGTTCGCAGACCTGG	PMGSQTW	+	--
22595	37088	AGAGAGGAGACGGTATACTGG	REETVYW	+	--
25946	37497	CCGATGAGCTCGAGCGGGTGG	PMSSSGW	+	--
21297	36603	CGTACAGAGCATGTATTCCCA	RTEHVFP	+	---
21196	36558	ATCTTGAGTTCGTCTTCATGG	ILSSSSW	+	---
29590	39528	CACTTGGCTTCCCATGATTGG	HLASHDW	+	--
23663	37472	AAAGATGATTATCATACATAT	KDDYHTY	+	--
27553	38724	TATTCCCGCTTGAACTACGAT	YSRLNYD	+	---
29188	17726	CGCGGGGAGTCGCACAGTTGG	RGESHSW	+	--
27727	13858	TACGCACGCACAGGTAGCAAC	YARTGSN	+	--
20696	36263	TTAACGAGACTGTCAGCAAAT	LTRLSAN	+	--
22942	37212	AAGTCTGACTATCTTACCTAC	KSDYLTY	+	--
27536	14858	TACGCCAGGGCTGGGCCTAAC	YARAGPN	+	--
21489	36684	CCGATGGCTTCCTCTAACTGG	PMASSNW	+	---
26671	38540	TTAATGTCGGATCGTGAGTGG	LMSDREW	+	---
20583	36278	TTACATAAACTCTCGTTGAAC	LHKLSLN	+	---
27156	38081	CGTCTTGAGGATAGGAGTTGG	RLEDRSW	+	---
28618	39115	GTAGGGGAGGCACGTAGTTGG	VGEARSW	+	---
24777	37854	TACGTAAGGTCTGACACTAAA	YVRSDTK	+	---
24985	37930	TACTGGTCGGGAATCAAGGAT	YWSGIKD	+	---
23673	37235	TTGTCTCGTGTTTCGCCAAAT	LSRVSPN	+	--
26151	38081	AGGTTAGAAGACCGATCCTGG	RLEDRSW	+	---
22936	14290	TACTCTAAGGTTGGGTATAAT	YSKVGYN	+	---
29200	39378	TACTGGCACGGTGTCAAAGAC	YWHGVKD	+	--
29284	39428	AGGTCGGAGTTTATGGTATAC	RSEFMVY	+	---

22104	18573	CGTGCCCTTGACGGGTGGGAC	RALDGWD	+	--
20544	36261	TTGTCAAAGTTGTCTTATAAT	LSKLSYN	+	---
28839	14264	TACGCCCGCACGGGTGCGAAC	YARTGAN	+	---
28032	39006	ATGTGGGACGGGACTGATGCG	MWDGTDA	+	--
23666	37473	TATTTCACGGGGCGAACAGCT	YFTGRTA	+	--
20909	36334	GTTCTAAGCTCAGCTAATTGG	VLSSANW	+	---
23205	13745	TATTCGCGCGTAGGGTACAAT	YSRVGYN	+	---
35239	16671	TTAACTTATGATGCGTATGAA	LTYDAYE	+	--
25608	38156	ATTCTATCGGACCGTATGTGG	ILSDRMW	+	---
28016	38727	TATTCTAGGCTCCACGCGAAT	YSRLHAN	+	--
24213	16613	TATGCCCGCGGTGGTCCCAAT	YARGGPN	+	---
21839	36793	TTGTCCCGCACGTCGGTGAAT	LSRTSVN	+	---
29710	13543	TACAGCCGACTCAACTTCAAC	YSRLNFN	+	---
22782	36985	TTACACAGGTTGTTGCCGGTG	LHRLLPV	+	---
28351	13688	TTTAGCCGTTTGAATGTCAAT	FSRLNVN	+	--
25269	38034	CGCATGGAGAGCATCAAGTGG	RMESIKW	+	---
28492	13943	TACTCACGAGTCGGAACTAAC	YSRVGTN	+	---
28212	17060	AGGATGAGTGACCATAATTGG	RMSDHNW	+	---
27951	38972	GTTATGGAGGATCGTAATTGG	VMEDRNW	+	---
26189	13764	TATGCTAGGTCGGGCTTAAAC	YARSGLN	+	--
25455	37945	TATTTTACAGGACGTCATGAG	YFTGRHE	+	--
22301	36972	CTCCATAGATTATCACCCGTG	LHRLSPV	+	--
24435	37716	GTATTGAGTGATAGAGCGTGG	VLSDRAW	+	---
21294	36486	CGAACGGAGACAGTGTATCCT	RTETVYP	+	---
26934	38310	AGATTGCAGGATGTTACGTGG	RLQDVTW	+	--
35517	41579	CAGATGGCGTCGCAGGCTTGG	QMASQAW	+	--
20531	36250	TTGCATAAATTAACAGTTAAT	LHKLTVN	+	---
28777	19136	GCCATGGTTGCCAGGGACTGG	AMVARDW	+	--
30723	13772	TATTCGCGGCAAGGGCCAAAT	YSRQGPN	+	--
30330	18284	GATCTCCGGGACCGCGCATGG	DLRDRAW	+	---
21283	36594	TTACATAGGTTAGGTGCTGAT	LHRLGAD	+	---
22461	37038	ATGTTATCTTCAAGCACTTGG	MLSSSTW	+	---
29957	13739	TATAGCCGTATAGGAATGAAC	YSRIGMN	+	--

27749	38843	TACCATCGCCTGAGTGCAAAT	YHRLSAN	+	---
21991	36857	GACATGGGTTCGAGCACATGG	DMGSSTW	+	--
22874	16612	TTGAGCCGCGTAGGTTTTAAT	LSRVGFN	+	---
23795	37516	AGAAATGAGTTCACCACTTTC	RNEFTTF	+	--
22277	36965	TTGTCGAGACTCAACTTTGAT	LSRLNFD	+	--
27453	14216	TATGCGAGGTCGGGTGCAAAT	YARSGAN	+	--
20764	36369	CTACACAGGTTAGGATTAGAC	LHRLGLD	+	---
25782	38201	AGGAATGAATTTGTAACGTAT	RNEFVTY	+	--
22740	19755	ATTATGGAATCGGCGACATGG	IMESATW	+	---
29718	39574	TCAATGCAAGATCGCTTGTGG	SMQDRLW	+	---
31469	18608	CCCTTAGCCGATAGGATGTGG	PLADRMW	+	---
23118	16595	CGTACTCCAACTGTCTACCCC	RTPTVYP	+	---
24820	37867	GTTATGGAATCTACCCGATGG	VMESTRW	+	--
22519	36991	TTGTCGCGGACTTCCCTCAAC	LSRTSLN	+	--
21440	36668	GATATGTCATCGTCTGTGTGG	DMSSSVW	+	---
30623	13851	TACGCTCGAACCGGTTTCAAT	YARTGFN	+	--
21550	36710	ATGAGTCGTATCGGGCCAAAT	MSRIGPN	+	--
22884	36982	AGAGATGACTTTACTGTATAC	RDDFTVY	+	---
24446	37534	TACTTCACTGGAAAGATTAAC	YFTGKIN	+	---
21184	36445	TATCATGCCAAGCTCCCTAAC	YHAKLPN	+	---
27193	14344	TACTCCCGAGTCGGGCAAAAT	YSRVGQN	+	---
24346	37684	TTGTGTCGGCCATGTTCCGAT	LCRPCSD	+	---
29707	14366	TTTTCGAGACTGAATCTTAAC	FSRLNLN	+	--
29138	39378	TATTGGCATGGGGTGAAGGAT	YWHGVKD	+	--
25898	38024	CGCCTCGAATCGACGAGCTGG	RLESTSW	+	--
21584	36382	TTATGCAAGCCGTGTCTAGGG	LCKPCLG	+	--
28897	38285	GACATGGAATCATACGACTGG	DMESYDW	+	---
23550	36965	CTAAGCCGCTTGAATTTCGAC	LSRLNFD	+	--
20542	36252	CTACATAAACTAAGCGTTAAT	LHKLSVN	+	---
33465	19339	GATTCAGCATCCAGAGCATGG	DSASRAW	+	---
26187	14023	TACGCACGAGTCGGGCCCAAT	YARVGPN	+	--
25319	37934	AGAATGGAGTCGGTGTCGTGG	RMESVSW	+	--
22537	36947	TTACATCGACTCAGTATGGAT	LHRLSMD	+	---

20793	36323	AAGGACGATTTTAGCACATGG	KDDFSTW	+	--
24353	17018	CACAGTCGGGTTGGCCACAAC	HSRVGHN	+	--
21268	36587	CTCTTCTCAGGGGATGGGCCA	LFSGDGP	+	---
27788	38685	GACATGACGGACCGAAAATGG	DMTDRKW	+	---
25275	38039	GACTTAAGGGACAGAGGTTGG	DLRDRGW	+	--
29392	39461	CGCTTAGACAGCAGAGAATGG	RLDSREW	+	--
21708	36342	GTATTGAGTAGCTCTATGTGG	VLSSSMW	+	---
26287	38371	AATATGGGAAGCCGTGATTGG	NMGSRDW	+	---
20766	13938	TATTCCAAAATGGGACCGAAT	YSKMGPN	+	---
21189	36554	CTCCATCGGCTTAGCATAGAC	LHRLSID	+	---
23606	37275	CGCGATGAGTTTGTGTCATGG	RDEFVSW	+	---
27142	17563	GTAATGGAGGACAGAATCTGG	VMEDRIW	+	---
31046	13772	TACAGCAGGCAGGGCCCGAAC	YSRQGPN	+	--
28111	14046	TACTCTCGTCTTGGAATGAAC	YSRLGMN	+	--
28666	13664	TACAGCCGTATTGGCATTAAC	YSRIGIN	+	--
28119	38201	CGTAACGAGTTCGTTACATAC	RNEFVTY	+	--
28235	14399	TATGCTAGGACAGGTAATAAT	YARTGNN	+	---
21344	36486	AGGACTGAAACCGTCTACCCG	RTETVYP	+	---
26170	20420	ATCATGAGCTCGAGTGCATGG	IMSSSAW	+	--
22729	37145	GATCCGGCGAGCAGAGAGTGG	DPASREW	+	---
20521	36247	CTATCTAAACTCAGTTTTAAT	LSKLSFN	+	---
21457	36532	CGACTCGAATCAACGCTTTGG	RLESTLW	+	---
23191	37302	AGGTTGCACGATGCTTATCCC	RLHDAYP	+	---
29871	13751	TATAGTCGGGTCGGCAATAAT	YSRVGNN	+	---
22544	36324	CTTCACCGTAAGGGAATAGAC	LHRKGID	+	--
21813	36669	GAGTTAGCTAGTCGTGAATGG	ELASREW	+	---
29526	14115	TACAGCCGAGTCGGTTCCAAC	YSRVGSN	+	---
23748	37498	AAAGATGAGTATCACACTTAT	KDEYHTY	+	---
24117	37218	ACGGATGGCACAAGCCGCTGG	TDGTSRW	+	--
25243	13899	TATTCTAAAATGAATTACAAC	YSKMNYN	+	--
29067	14136	TATAGCCGCCTTGGGGCGAAC	YSRLGAN	+	--
21979	36857	GATATGGGAAGCTCGACGTGG	DMGSSTW	+	--
20902	36387	TTTCATAAACTGTCACCCAAC	FHKLSPN	+	---

20761	36366	GTTGCGTCTAAAGGCTGGGAC	VASKGWD	+	---
23489	37277	TATGTTAGATCTGATAAGAAT	YVRSDKN	+	--
23772	37506	GATTTGAGGGCGCACGACTGG	DLRAHDW	+	---
27630	14010	TACTCCCGAGTAGGACTCAAT	YSRVGLN	+	---
26175	37723	TACACTCGCATAGGGCCTAAT	YTRIGPN	+	--
21244	36502	CTCTTCTCAGGCGAGGGTCCT	LFSGEGP	+	---
27654	38877	GCGATGGCCGATCGCGAATGG	AMADREW	+	---
35476	40833	AGTATGCAGGATCGACACTGG	SMQDRHW	+	---
29144	14531	TATAGTAGAAACGGGCCAAAT	YSRNGPN	+	--
21410	36653	GTTATGTCATCCACGACTTGG	VMSSTTW	+	---
33266	40833	TCCATGCAGGACAGGCATTGG	SMQDRHW	+	---
23574	37218	ACGGACGGCACTTCGCGTTGG	TDGTSRW	+	--
27736	38906	TACTTTTCGGGGAAGCGAGAG	YFSGKRE	+	--
29827	13739	TACTCGAGAATCGGGATGAAT	YSRIGMN	+	--
23883	37557	TACTTCACCGGGAAGAGGGAG	YFTGKRE	+	---
25064	37747	CGGACTAGTACGCATGGTATC	RTSTHGI	+	--
28116	13901	TACTCAAGAGTCGGTATGAAC	YSRVGMN	+	---
25156	37990	AAGGACGATTATAGCCACTAT	KDDYSHY	+	--
23439	37393	GACATGTCGAGCGTCCAATGG	DMSSVQW	+	--
30515	13844	TACAGCCGGTTAAACACTAAC	YSRLNTN	+	---
28262	14140	TATGCTCGATCCGGTAGTAAT	YARSGSN	+	--
35525	41552	AATTTAGAGTCGCATAAATGG	NLESHKW	+	--
26781	38582	AGGAATGAATTTTCCACCTAT	RNEFSTY	+	--
21538	36703	AACCTCGCCAGCGCGTCTTGG	NLASASW	+	---
28066	36912	AGATCGGAGTTTTTAGCGTTC	RSEFLAF	+	--
22069	36892	GTCATGTCGACTAATGGCAGA	VMSTNGR	+	---
23397	37376	TACTGGTCAGCTATAAAAGAG	YWSAIKE	+	--
23206	37235	CTCAGCCGGGTCTCTCCAAAC	LSRVSPN	+	--
29239	14083	TATTCACGTGTTGGAGTGAAC	YSRVGVN	+	---
28877	14444	TACGCTAGATCCGGGAACAAC	YARSGNN	+	--
20917	36434	CTGTGCAAACCATGCGATACA	LCKPCDT	+	---
25393	38081	CGCTTAGAGGATCGTAGCTGG	RLEDRSW	+	---
22967	17874	CCTATGGCATCTTTACAGTGG	PMASLQW	+	---

24856	37806	AGAACGTATGACAGCTTCCCG	RTYDSFP	+	---
28799	39267	CGCGATGACTATTCTTCATAT	RDDYSSY	+	---
34053	40864	AACATGCAGGACCGTAGTTGG	NMQDRSW	+	--
28783	14293	TACTCACGGACGGGTAACAAC	YSRTGNN	+	--
22436	36841	CTCAGTCGCATTTCGACAAAC	LSRISTN	+	--
27530	17520	TACTTCAGTGGGAGGGTGGCA	YFSGRVA	+	--
27482	38611	TACTCACGCGTGCAACTTAAC	YSRVQLN	+	--
28389	38545	TACTCACGTGTGCAACCGAAC	YSRVQPN	+	--
24017	37592	ATGCATCGCTTATCATTTGAT	MHRLSFD	+	--
25171	37624	ATGTTCGATGGTACTAATCCC	MFDGTNP	+	---
33365	40864	AATATGCAAGACCGCTCCTGG	NMQDRSW	+	--
24702	37658	CGGAGCGATTTCGAGTATTTC	RSDFEYF	+	--
24084	18291	GAAGCGTTGAGGGGTTGGGAT	EALRGWD	+	---
27391	38130	GTTTTAAGCAGTCAGGGCTGG	VLSSQGW	+	--
28453	38961	AAGGACGGCTATTCGCTATAT	KDGYSLY	+	--
23045	37235	CTCAGCAGGGTGAGTCCCAAC	LSRVSPN	+	--
20665	36323	AAAGATGACTTCTCGACGTGG	KDDFSTW	+	--
21664	36534	CTTCATCGCCTCTCGCTCGAC	LHRLSLD	+	---
22950	14200	TACTCAAAACTTAACTTTAAC	YSKLNFN	+	---
29813	14211	TACTCACGCACAGGCAGTAAT	YSRTGSN	+	--
27261	38731	TATTGGTCAGGAGTGAGGGAG	YWSGVRE	+	--
21753	36767	CCTATGGCTTCTCAGCAATGG	PMASQQW	+	---
21849	36563	ATGCACAGATTGCTCCCGGAT	MHRLLPD	+	---
22541	14224	TATAGTAAAATCGGGTATAAT	YSKIGYN	+	--
21366	36539	CTACACCGACTTAGTGCAGAC	LHRLSAD	+	---
24749	37844	AAGTCAGAGTACTCAACATAT	KSEYSTY	+	--
29263	14593	TACAGCAGGAGTGGGCCAAAT	YSRSGPN	+	---
21666	36739	AAATCGGACTTTGTGAGCTGG	KSDFVSW	+	--
21478	14416	TATAGCAAAATTGGCCACAAC	YSKIGHN	+	--
22057	36753	TATCATAAACTAAACTCCAAC	YHKLNSN	+	---
22455	37019	CTACATAGGCTAACGGCTGAC	LHRLTAD	+	--
27506	14443	TATAGTAGGATCGGACTAAAC	YSRIGLN	+	---
25722	36623	CGATTGGAATCCGCCGCCTGG	RLESAAW	+	--

23331	16620	CTTTCGCGGATAAGCGTAAAT	LSRISVN	+	--
25743	14861	TACTCGCGTCTAGGGGTGAAT	YSRLGVN	+	--
21108	36523	TACCACAAGTTGAATGATAAC	YHKLNDN	+	---
22105	36501	GATTTGTCGAGCTCAAGCTGG	DLSSSSW	+	---
28104	13939	TATTCTCGGATTGGGACTAAT	YSRIGTN	+	--
22427	36589	GACATGAGCTCATCAAAATGG	DMSSSKW	+	---
24524	37747	AGGACTTCGACGCACGGGATC	RTSTHGI	+	--
26819	17637	AGGCTTGAGTCTACCCACTGG	RLESTHW	+	--
26153	37349	TCGGACGGAGTTAGTCGTTGG	SDGVSRW	+	--
21208	36486	CGCACTGAAACCGTATATCCG	RTETVYP	+	---
28962	17737	CGTACTTATGACAGCTTTGCT	RTYDSFA	+	---
24137	37488	TACAGTCGAGTTGGCCCTGAC	YSRVGPD	+	---
25745	17752	AGGTCAGAATTCGTGAGTTTC	RSEFVSF	+	--
26117	38223	TATAGCCGCATAGGTCCTGAC	YSRIGPD	+	---
21043	36431	GTGGAAAGTACGAACGGTAGG	VESTNGR	+	---
21778	36534	TTGCACAGGTTGAGTTTAGAT	LHRLSLD	+	---
28950	14366	TTCAGTCGGCTAAACTTAAAT	FSRLNLN	+	--
26985	17754	GATCCGTCTAGTCATAGCTGG	DPSSHSW	+	---
28731	13990	TACGCGCGGCAGGGTCCAAAT	YARQGPN	+	--
21279	36496	TACGTGAAGTCAGACACAAGG	YVKSDTR	+	---
28028	38794	ATGTGGGACGGAACCGCGGCG	MWDGTAA	+	---
21482	36627	CGAGAGGATAGTGTGCGTTGG	REDSVRW	+	---
23275	37332	AAGGACGACTATGTTAGTTAT	KDDYVSY	+	--
22084	13886	TTCCACAAGTTGGGTAGTAAT	FHKLGSN	+	--
23475	36982	CGCGACGATTTCACGGTGTAT	RDDFTVY	+	---
24897	37844	AAAAGTGAATATAGTACGTAC	KSEYSTY	+	--
26571	38265	ATGTGGGATGGTACCGGACCT	MWDGTGP	+	---
29966	39203	TCACTGGAATCACGCGACTGG	SLESRDW	+	--
26185	37414	AGGATGGAATCGTCAATGTGG	RMESSMW	+	--
22374	37000	TTGTTAACATCTTCTACGTGG	LLTSSTW	+	--
26038	37510	ATAATGATGGACCGCGGCTGG	IMMDRGW	+	---
24664	37806	CGGACCTACGATTCTTTTCCA	RTYDSFP	+	---
20970	36462	GATTTGTCATCGAGCAAATGG	DLSSSKW	+	---

22547	37068	TACAGTCGCTTAAATGATGAT	YSRLNDD	+	---
20849	36407	AACGCGCTTGAGGGCAGAGAC	NALEGRD	+	---
21680	36743	CGGATGGAGGTAAGTACGTGG	RMEVSTW	+	--
25469	37997	CGACGTACCGATGTGTACCCC	RRTDVYP	+	--
23779	37218	ACCGATGGGACAAGCAGATGG	TDGTSRW	+	--
20576	36268	CTACACAAATTAAGCACTAAT	LHKLSTN	+	---
23312	37226	CACGACGGAACTTCCGCGTGG	HDGTSAW	+	--
27660	13892	TATGCACGTACGGGTATGAAC	YARTGMN	+	--
29450	38809	CGGACTAACAACGTTTACCCT	RTNNVYP	+	--
29883	13580	TACAGTAGAGTTGGGATTAAT	YSRVGIN	+	---
21103	36484	ATGTTCGATGGCACTGCAGCC	MFDGTAA	+	---
26239	37781	AGAACGAGTACACATGGAGTT	RTSTHGV	+	--
31089	18712	AGTCTAAGCGATAGGACATGG	SLSDRTW	+	---
24070	37571	CGTGACGAATTTTCCTCGTTC	RDEFSSF	+	---
27700	13949	TATTCTCGAATAGGCGTAAAT	YSRIGVN	+	--
32660	40609	ATATTGCAAGATCGCGGCTGG	ILQDRGW	+	--
26026	13589	TTCAGCCGTGTGGGTCCCAAT	FSRVGPN	+	--
31910	13830	TATTCTAGAGTGGGCCATAAC	YSRVGHN	+	--
31961	18712	TCTTTGTCGGACCGAACCTGG	SLSDRTW	+	---
21767	36771	GTTTTAAGCTCTAACATCTGG	VLSSNIW	+	--
22007	36866	CGGGAAGAAACCGTCAGGTGG	REETVRW	+	--
34947	38212	TATTATACAGGGAAATGTGAA	YYTGKCE	+	--
22290	36874	CGCGATGAATTTACTGGCTAC	RDEFTGY	+	---
22711	37137	GATTTGGAAAGTCGTGATTGG	DLESRDW	+	---
28304	13688	TTCTCACGCCTAAATGTAAAC	FSRLNVN	+	--
21593	36722	GTTCTTTCCAGCTCCGCGTGG	VLSSSAW	+	--
22232	36947	TTACATCGCCTATCAATGGAT	LHRLSMD	+	---
26518	38474	TATTTTAGCGGCCGCATCGAC	YFSGRID	+	--
25464	38103	TATCTCAAGTCGCAACTTTAT	YLKSQLY	+	--
33941	41086	AATACCCCCATGTGTAAAGCA	NTPMCKA	+	--
23976	37137	GACCTCGAGTCCAGGGACTGG	DLESRDW	+	---
22559	37075	TTATCACGCGTAAGCGTGAAT	LSRVSVN	+	---
24139	37633	AGGGAAGACTACACGACCTGG	REDYTTW	+	--

22034	36881	TTGTATGACGGCACATCAGCT	LYDGTSA	+	---
23167	37295	AGGGATGACTTTACAGTCTGG	RDDFTVW	+	---
28871	37468	AGAGATGAGTTCAACCACTGG	RDEFNHW	+	--
22613	37097	CGTCTCGAAAGTGCGAACTGG	RLESANW	+	--
23827	37532	CATGATGGGACATCTAAATGG	HDGTSKW	+	--
25517	38125	CGGGACTTCGACGCGTACCCG	RDFDAYP	+	--
21675	14290	TATTCGAAAGTAGGGTATAAT	YSKVGYN	+	---
29207	13901	TATTCCCGTGTAGGCATGAAT	YSRVGMN	+	---
27034	14092	TTCTCAAGAGTAGGCGCGAAC	FSRVGAN	+	--
28342	14301	TATAGTAGACTGAATATGAAT	YSRLNMN	+	--
21088	16568	CTCCATCGTCTGTTGAAGGAT	LHRLLKD	+	---
20948	36407	AATGCTTTAGAAGGTCGTGAT	NALEGRD	+	---
29160	39390	ATGTGGGACGGCACAAACGCT	MWDGTNA	+	---
29473	13992	TATTCGCGCGCCGGTGCTAAC	YSRAGAN	+	---
23187	37302	CGTCTTCACGATGCGTACCCA	RLHDAYP	+	---
21936	13886	TTTCATAAGTTAGGCTCAAAC	FHKLGSN	+	--
22772	18112	GCATCGTCCACGAACGGTCGG	ASSTNGR	+	---
21898	36687	GTCGCGGAAAAAGGATGGGAC	VAEKGWD	+	--
21721	36756	GTTATGGAAGCTAGAGATTGG	VMEARDW	+	---
24024	13795	CGCGATGACTTTACCGCGTAC	RDDFTAY	+	--
29596	39531	GATATGCAATCTAACTTGTGG	DMQSNLW	+	--
25534	37544	TACTTCACTGGGCGGATTGAC	YFTGRID	+	---
25571	16613	TACGCACGGGGCGGGCCGAAT	YARGGPN	+	--
25824	14092	TTTAGTCGTGTAGGCGCAAAT	FSRVGAN	+	--
25397	38082	ATGCGAAATACGCATTGCGAT	MRNTHCD	+	--
28753	14301	TACTCACGGCTAAACATGAAC	YSRLNMN	+	--
28658	19998	GTCAGTGACTACGCCAGTTAC	VSDYASY	+	--
25289	37557	TATTTTACTGGAAAACGCGAA	YFTGKRE	+	--
20782	36353	GTCGCTACTAAGGGGTGGGAC	VATKGWD	+	---
21352	36627	AGGGAAGACTCAGTAAGGTGG	REDSVRW	+	---
24902	37898	AAGGATGGGTTTTCACATTAC	KDGFSHY	+	--
24305	37636	AAGTCGGACTATGTCACATAT	KSDYVTY	+	--
23200	37072	ACTCTATCCTCCCAAACATGG	TLSSQTW	+	---

20527	36250	CTTCACAAGCTGACCGTGAAC	LHKLTVN	+	---
23496	37414	CGCATGGAGAGTAGCATGTGG	RMESSMW	+	--
28794	14010	TATAGCAGAGTAGGTCTAAAC	YSRVGLN	+	---
29118	13943	TATAGTCGGGTAGGGACCAAC	YSRVGTN	+	---
21573	36563	ATGCATCGCCTTTTACCAGAT	MHRLLPD	+	---
21574	36694	CGCACCCCACAGGTGTACCCA	RTPQVYP	+	--
25043	37299	TGGTGGAGCGGTATAAGGGAG	WWSGIRE	+	--
30829	14531	TACTCTCGGAATGGTCCGAAC	YSRNGPN	+	--
25450	37677	CGAGAAGATTTTGTGCGCTGG	REDFVRW	+	---
22338	36554	TTACACAGATTGTCTATCGAT	LHRLSID	+	---
23101	37176	TATTTCACGGGTAGAGTCGAG	YFTGRVE	+	---
28140	38727	TACTCGCGTCTACATGCGAAT	YSRLHAN	+	--
20523	36247	CTGAGCAAGTTGTCATTCAAT	LSKLSFN	+	---
21951	36841	CTCTCCCGAATTAGTACGAAC	LSRISTN	+	--
26659	38216	AAAATGAGTGACCATACATGG	KMSDHTW	+	--
22631	37097	AGGTTAGAGTCCGCTAATTGG	RLESANW	+	--
28652	14087	TACGCGAGGAGTGGCACTAAC	YARSGTN	+	--
27282	14344	TATTCCAGAGTTGGACAGAAT	YSRVGQN	+	--
25573	38146	TATTGGTCTGGAGTGGCCGCT	YWSGVAA	+	--
27501	13948	TTCAGTAGATTGAACGCGAAT	FSRLNAN	+	--
31245	40102	GTGGGGAGCGATAGGGGTTGG	VGSDRGW	+	--
20832	36398	TACTTTACGGGTAAAATAGCA	YFTGKIA	+	---
23690	37482	TATTGGAGCGGTGTGAAAGAA	YWSGVKE	+	--
25681	38083	AATACATATGACTCCTACCCT	NTYDSYP	+	---
30000	39263	CGTACGTATGATACATTCCCT	RTYDTFP	+	--
21711	36753	TACCACAAGCTGAATAGTAAT	YHKLNSN	+	---
24701	37557	TACTTCACAGGTAAAAGGGAG	YFTGKRE	+	--
28460	39145	CGAGGCGAGTCACACGGATGG	RGESHGW	+	--
26119	17759	CGCAACTCGACAGTATATCCA	RNSTVYP	+	--
24181	36823	TACTTCTCAGGGGTTAAGGCC	YFSGVKA	+	--
28438	39136	TTCCACAGGCTCAGTACGAAT	FHRLSTN	+	--
22387	37009	AGGGATGGGACATCGGCCTGG	RDGTSAW	+	--
32001	40376	TGTAACCAGCCAATGACTGCG	CNQPMTA	+	--

24588	37525	GAGTTGGCGTCCCACGCCTGG	ELASHAW	+	---
25771	38199	AGGCTGGATGATCGTGGGTGG	RLDDRGW	+	--
24299	37482	TATTGGTCAGGTGTGAAGGAG	YWSGVKE	+	--
28311	20423	AACATGGAGTCTAGAGACTGG	NMESRDW	+	---
22917	37199	GACTTAGAGTCACGTGAATGG	DLESREW	+	---
23626	37295	CGCGACGATTTCACCGTATGG	RDDFTVW	+	---
26834	37690	TATTTCACGGGTCGCATGGAT	YFTGRMD	+	--
23408	37053	GACCTACAAAGCAGTACATGG	DLQSSTW	+	--
21314	17701	GTAGCATTAAAAGGATGGGAT	VALKGWD	+	---
23209	37310	CGCGACGGTACTAGCTCTTGG	RDGTSSW	+	--
28818	38287	TTTTGGAGTGGCGTAAAGGAA	FWSGVKE	+	--
33985	17821	AGGGGAGACGACAGAGGGTGG	RGDDRGW	+	--
25514	13899	TACTCAAAGATGAACTATAAC	YSKMNYN	+	--
25179	37568	AGAGATGAGTTCACCAGCTGG	RDEFTSW	+	---
25108	37970	TATTCCCGGATAGGAGAGAAC	YSRIGEN	+	--
33147	40786	TGCAAACCCGCGATGCATGAA	CKPAMHE	+	--
26548	14576	TACAGCAGAATCGGCGACAAC	YSRIGDN	+	--
29176	39160	CGGACCTTCGATAGTTATGCT	RTFDSYA	+	--
20726	36353	GTTGCAACGAAAGGATGGGAT	VATKGWD	+	---
28779	14391	TTCAGCAGAGTGGGATTAAAC	FSRVGLN	+	--
22048	14342	TACAGTAAGTTGGGGTATAAC	YSKLGYN	+	--
25407	37544	TACTTTACCGGTCGAATCGAT	YFTGRID	+	---
20537	36256	AGACTTGTCGACGTGTTCCCT	RLVDVFP	+	---
23291	14290	TACAGCAAAGTAGGCTACAAT	YSKVGYN	+	---
31139	14374	TATTCAAGGGTCGGGGGAAAC	YSRVGGN	+	--
25798	37747	AGAACATCCACACACGGCATA	RTSTHGI	+	--
26807	13892	TACGCCAGGACCGGCATGAAT	YARTGMN	+	--
31161	39634	TTGGACGACTGGACCACCTAT	LDDWTTY	+	--
31440	40053	AGGACGTATGATACATATCCG	RTYDTYP	+	--
21072	36473	TATCACAAACTGGGACCCCAA	YHKLGPQ	+	--
21773	36772	TATTTTACCGGGAAGAAGGAG	YFTGKKE	+	---
22780	17687	GTTAGGAGTACAAACGGAGTC	VRSTNGV	+	---
27093	38387	AAAGATGATTGGGTCAAGTAC	KDDWVKY	+	--

28002	38731	TACTGGAGTGGCGTCCGTGAA	YWSGVRE	+	--
28671	38903	TACGAGAGCACTAACGGAAGG	YESTNGR	+	--
25838	38221	TACTTTAGCGGTAAGATAAAC	YFSGKIN	+	--
27423	38794	ATGTGGGATGGCACAGCCGCC	MWDGTAA	+	---
21055	36381	CCGTTGGCATCGAGTACGTGG	PLASSTW	+	---
24272	37660	TCTCACTCAACGAATGGGAGG	SHSTNGR	+	--
21033	36256	CGGTTGGTGGATGTTTTTCCG	RLVDVFP	+	---
21475	14416	TACTCTAAGATAGGGCATAAT	YSKIGHN	+	--
23351	14552	TATTCTAAGGCGGGATACAAT	YSKAGYN	+	---
20553	36266	TTACACAAATTGATGAATAAT	LHKLMNN	+	--
23703	13795	AGAGACGACTTCACAGCATAC	RDDFTAY	+	---
23260	37323	CGTATGGAATCATCGCAATGG	RMESSQW	+	--
32358	17663	AGTCTCTCTTCCAGGGATTGG	SLSSRDW	+	---
25176	38001	GTAGCACGACTCGGATGGGAC	VARLGWD	+	--
27779	38843	TACCATCGGCTTAGTGCTAAC	YHRLSAN	+	---
27325	38280	CTGTGGGACGGAACGAACGCC	LWDGTNA	+	---
27535	38834	AGAGATGAATACATGTCATGG	RDEYMSW	+	--
25624	37824	TATAGTCGCGTGGGTGAGAAT	YSRVGEN	+	---
28967	13972	TACAGCCGTATCGGACACAAC	YSRIGHN	+	--
22062	36745	TTGCACAGGTTGGGCCAAGAT	LHRLGQD	+	---
20534	36243	TTACATAAGTTGGCCAATAAC	LHKLANN	+	---
25013	37884	ATAAATTCGACAAATGGTAGA	INSTNGR	+	--
21338	36619	CTACACCGATTGAGCGACAAT	LHRLSDN	+	---
25142	17535	AGGATGGAGTCGTCAGTGTGG	RMESSVW	+	---
30456	14585	TATTCACGACTGGGTAACAAT	YSRLGNN	+	--
27414	38619	TATTTTCATGGGAAGAAAGAC	YFHGKKD	+	--
30714	14350	TATTCACGACTCAATGCTAAC	YSRLNAN	+	---
31169	40079	TGTAAGCCTGATGCGGTAAGA	CKPDAVR	+	--
28232	14267	TACTCGAGGACAGGCATGAAT	YSRTGMN	+	--
22836	14200	TATAGCAAGTTGAACTTCAAT	YSKLNFN	+	---
20800	36299	TTTCATAAATTGGGGATCAAC	FHKLGIN	+	--
21210	36563	ATGCATCGCCTATTACCCGAT	MHRLLPD	+	---
28012	38877	GCTATGGCAGACAGGGAGTGG	AMADREW	+	---

23685	37430	AGGGGGGAATTCACTTACCCC	RGEFTYP	+	--
24051	37607	TATTTCTCGGGGAAAAAGGAT	YFSGKKD	+	---
32919	40521	GATCCCGGAGACAGGAAGTGG	DPGDRKW	+	---
30063	39259	GCTATGCCGGACAGAGGTTGG	AMPDRGW	+	---
23537	36882	ATCGCCAGCTTGGGGTGGGAC	IASLGWD	+	--
27650	17637	CGCTTAGAAAGCACTCATTGG	RLESTHW	+	---
24460	37723	TATACCAGGATCGGACCCAAC	YTRIGPN	+	--
34338	41225	CAATCAGGAAAGAATGAGTGC	QSGKNEC	+	--
27324	38272	TATCACCGCCTCGGCGATGAT	YHRLGDD	+	--
21835	36550	CGCACACCACAAGTCTTTCCG	RTPQVFP	+	--
28455	13960	TATGCAAGAAGTGGGATGAAT	YARSGMN	+	--
26505	38469	TACTTTACTGGAAGGCACGAC	YFTGRHD	+	--
22346	36985	CTCCATCGCCTCCTCCCGGTT	LHRLLPV	+	---
24273	37341	TATTTCTCGGGCATTCACGCA	YFSGIHA	+	--
29386	14861	TACTCACGACTAGGTGTTAAC	YSRLGVN	+	--
22512	17637	AGATTGGAGTCGACACATTGG	RLESTHW	+	---
22432	36866	AGGGAAGAGACCGTTCGATGG	REETVRW	+	--
24908	18112	GCTAGTAGTACTAATGGGCGA	ASSTNGR	+	---
29434	17602	GTTTTATCCGAAAGGTCGTGG	VLSERSW	+	---
26021	19089	TATTGGAGCGGTATCAAGGAG	YWSGIKE	+	---
24452	37575	TATTTCACCGGACAACGCGAA	YFTGQRE	+	--
30189	39136	TTTCATCGATTGTCAACTAAC	FHRLSTN	+	--
20980	12737	ATCGAGTCCACCAACGGGAGG	IESTNGR	+	---
20580	36268	TTGCATAAGCTCTCGACAAAC	LHKLSTN	+	---
21902	36823	TACTTCAGTGGTGTAAAAGCG	YFSGVKA	+	--
22861	37079	AAAGACGATTATACGACCTAC	KDDYTTY	+	---
22444	36793	CTCAGTCGGACAAGTGTCAAC	LSRTSVN	+	---
22765	14452	TACTCAAAAATTGGCTTTAAT	YSKIGFN	+	--
23443	37394	AGAGATGGCATGTCTGCTTGG	RDGMSAW	+	--
21316	36397	GTAAGCGAATTTTTGTCGTAT	VSEFLSY	+	--
28416	13580	TACTCACGCGTAGGTATTAAC	YSRVGIN	+	---
20840	17658	TTACATAAGCTGAGCAATAAT	LHKLSNN	+	---
25150	17034	AGTGCAGAATGGGTGTCTTAC	SAEWVSY	+	--

21615	36496	TATGTCAAGTCAGATACCCGA	YVKSDTR	+	---
23643	37466	AAAGATGGCTATTCCGCTTAC	KDGYSAY	+	--
23521	37425	ATTGCTGGAAGAGGCTGGGAT	IAGRGWD	+	--
20833	36384	AAGGATGATTTCGTCAGTTGG	KDDFVSW	+	--
21158	36453	AAAGATGACTTTACTGCCTGG	KDDFTAW	+	---
26332	38391	ATTATGGAAGACAGAGGCTGG	IMEDRGW	+	---
23371	37030	CTGCACAGACTTTCGCAGGAT	LHRLSQD	+	--
21688	36619	CTTCATAGGCTATCGGATAAC	LHRLSDN	+	---
22784	37030	TTACACCGGCTAAGCCAAGAC	LHRLSQD	+	--
30232	14444	TACGCACGCAGTGGCAATAAC	YARSGNN	+	--
22926	37089	TACTTTTCAGGTAAGAAGGAG	YFSGKKE	+	--
24501	17681	CTGAGTCGCGTTGGCCAGAAT	LSRVGQN	+	---
20661	36316	TTGCATGCTAAATTGCCAAAC	LHAKLPN	+	---
20772	14441	TACGCCAAAAGTGGTCCGAAT	YAKSGPN	+	---
31840	14103	TACAGCAGGGCAGGTTTGAAC	YSRAGLN	+	--
21386	36398	TACTTTACCGGCAAGATAGCA	YFTGKIA	+	--
24085	16613	TACGCTAGGGGGGGACCTAAC	YARGGPN	+	---
26756	38572	ATGTGGGATGGCACTCCGTCA	MWDGTPS	+	---
24360	37690	TACTTTACAGGGAGAATGGAC	YFTGRMD	+	--
26963	38159	GGCAGCGAGTACTTAGCCTGG	GSEYLAW	+	--
22590	37087	GACTTGCGTGCTTCTACGTGG	DLRASTW	+	--
22018	36874	AGGGACGAGTTCACGGGGTAT	RDEFTGY	+	---
29603	14447	TATAGCCGCGCAGGATCCAAT	YSRAGSN	+	--
25198	14023	TACGCTAGGGTGGGTCCAAAC	YARVGPN	+	--
28898	39006	ATGTGGGATGGAACAGACGCA	MWDGTDA	+	--
25348	13181	TACTCCCGATTAGGAGAGAAC	YSRLGEN	+	--
22833	37176	TACTTTACTGGGCGTGTTGAA	YFTGRVE	+	---
24590	37778	AATATGTCAGACCGTGGTTGG	NMSDRGW	+	--
26966	38499	TATTTCACCGGCCAACGCGAC	YFTGQRD	+	--
30837	13818	TACTCCCGACTAAACGTAAAC	YSRLNVN	+	---
29964	17557	GGTATGGCGGATAGAGCGTGG	GMADRAW	+	---
25884	37940	GAGATGACGTCACACATGTGG	EMTSHMW	+	---
24355	17571	GTCGAAAGTTCTCGACTCTGG	VESSRLW	+	---

32329	40493	AGCATGCCCGACCGGAGTTGG	SMPDRSW	+	---
21022	36484	ATGTTTGACGGAACCGCTGCA	MFDGTAA	+	---
25103	37207	TTGTTATCGAGTTCAAACTGG	LLSSSNW	+	--
20781	36378	TTATCTAGAGTCGGTCTTAAC	LSRVGLN	+	---
26975	37109	AGAAGTGAATTCGTAGTGTAC	RSEFVVY	+	--
25712	37747	CGCACCAGCACTCATGGAATA	RTSTHGI	+	--
20740	36299	TTTCATAAGCTCGGGATAAAC	FHKLGIN	+	--
20642	36303	TTGCATAAACTTCAACAAAAC	LHKLQQN	+	--
22853	36866	AGAGAGGAGACTGTACGTTGG	REETVRW	+	--
22138	36841	TTGTCCAGGATCAGTACCAAT	LSRISTN	+	--
30516	13543	TATTCGAGGTTAAATTTTAAT	YSRLNFN	+	--
31088	40053	CGTACTTACGACACGTACCCA	RTYDTYP	+	--
22267	36756	GTTATGGAAGCGCGCGATTGG	VMEARDW	+	---
25267	37876	TATTGGTCAGGAGTGAAAGAT	YWSGVKD	+	--
20950	36391	TTTCACAAGCTGAGCTTAAAT	FHKLSLN	+	---
26978	38524	TACTTTACAGGCCAAATCAAT	YFTGQIN	+	--
21049	36496	TACGTTAAAAGTGACACAAGG	YVKSDTR	+	---
22893	37193	TACTTTAGCGGTAAAATTGCA	YFSGKIA	+	--
22776	36947	CTCCACAGGTTGTCCATGGAC	LHRLSMD	+	---
20811	36388	ATCGCCAATAAAGGCTGGGAT	IANKGWD	+	---
24128	37631	GTTAACGATTACATAAGTTAC	VNDYISY	+	--
26533	19089	TATTGGTCAGGAATTAAAGAA	YWSGIKE	+	--
24740	19221	ATTTTAAGTGATCGGGTGTGG	ILSDRVW	+	---
26016	37633	CGCGAGGATTATACAACATGG	REDYTTW	+	--
27918	38906	TATTTCAGCGGTAAACGTGAA	YFSGKRE	+	--
27909	38753	TATCACAGGCTTAGTGACAAT	YHRLSDN	+	---
27558	38469	TATTTCACCGGCCGCCATGAT	YFTGRHD	+	--
21908	36567	ATGTTCGACGGAACATCCGCT	MFDGTSA	+	---
21662	36738	CGAATGATCGACGCGTACCCT	RMIDAYP	+	--
20956	36378	CTGAGCCGTGTTGGCCTCAAT	LSRVGLN	+	---
30449	14607	TACTCGCGGGCGGGTGATAAC	YSRAGDN	+	--
21148	36540	TTACATAAGATGTCGATGAAC	LHKMSMN	+	--
23322	36942	CGCAACGACGTGGTTTATCCC	RNDVVYP	+	--

25638	37881	TACTTCAGTGGCAAGGTGAGC	YFSGKVS	+	--
22326	36974	GATGCAATAAGGGGCTGGGAC	DAIRGWD	+	---
27150	13930	TATGCTCGTACGGGCTTGAAT	YARTGLN	+	---
30955	13535	TATTCGCGATTAAATAACAAT	YSRLNNN	+	--
22012	36856	TATTTCAGCGGAATCGTGGCA	YFSGIVA	+	--
30671	14126	TACTCAAGGATCGGGTTCAAC	YSRIGFN	+	--
21821	13537	TACAGCAAGCTTAACATAAAT	YSKLNIN	+	---
20562	36261	CTAAGCAAACTCAGCTACAAT	LSKLSYN	+	---
26578	20423	AATATGGAAAGCCGGGATTGG	NMESRDW	+	---
24327	37675	AATATGAGCTCCAGCTCGTGG	NMSSSSW	+	--
21027	36486	AGGACAGAAACCGTGTATCCT	RTETVYP	+	---
22370	36998	ATGATGGAAAGTTCGAAATGG	MMESSKW	+	--
20821	36390	AAGGATGAGTTCAGCACATAT	KDEFSTY	+	---
33275	40837	GATCTCGGTGACAGAAAATGG	DLGDRKW	+	---
23568	37079	AAGGATGACTACACAACGTAT	KDDYTTY	+	---
22128	36673	GGTGATGAGTTCGTCCATTGG	GDEFVHW	+	---
21289	36496	TACGTAAAAAGTGACACAAGG	YVKSDTR	+	---
23240	36896	GTGGGCCATAAAGGTTGGGAC	VGHKGWD	+	--
28362	14344	TATTCCAGAGTCGGGCAGAAC	YSRVGQN	+	--
21787	36621	CTGTCCCGATTGAGTCACGAT	LSRLSHD	+	--
23004	14097	TACAGTAAACTCAATCACAAC	YSKLNHN	+	---
26150	37696	TACTTAAAAAGTCAGATGTAC	YLKSQMY	+	--
26725	16577	TACAGCCGTTTGAACAAGGAT	YSRLNKD	+	--
21340	36621	CTAAGTAGGCTTTCGCATGAT	LSRLSHD	+	--
26054	38292	ATAATGAGCAGTGCAGGTTGG	IMSSAGW	+	--
24310	14502	GTATGGTCTACGAACGGGATT	VWSTNGI	+	--
29977	13802	TATTCGCGCATTGGACAGAAT	YSRIGQN	+	--
32487	17926	TCGATGCAGGACCGAAGTTGG	SMQDRSW	+	--
31547	14585	TACAGCAGGCTTGGAAATAAC	YSRLGNN	+	--
20545	36262	CTTCACAAGTTAGCTCAAAAT	LHKLAQN	-	---
25334	37516	CGGAACGAATTTACGACGTTT	RNEFTTF	-	--
24404	13629	TATTCGAAACATGGACCAAAT	YSKHGPN	-	--
21683	36744	CGGATGTTGGACGCCTATCCC	RMLDAYP	-	--

30961	40002	CAAATGCAAGACCGTTCATGG	QMQDRSW	-	---
26341	16613	TATGCCAGAGGAGGACCTAAT	YARGGPN	-	--
27320	38752	ATTATGCCGAGCCGTAACTGG	IMPSRNW	-	---
32606	17821	CGCGGGGATGATCGGGGATGG	RGDDRGW	-	--
24403	37532	CACGACGGCACTAGCAAGTGG	HDGTSKW	-	--
26694	38553	CTCTGGGACGGAACGCCTAGT	LWDGTPS	-	---
23121	37278	GACTTAAGATCAGCCAGCTGG	DLRSASW	-	---
20749	36305	CTGCATAAAGCAGGACCGAAT	LHKAGPN	-	---
27448	14216	TACGCCCGTAGTGGGGCTAAC	YARSGAN	-	--
31601	14192	TTTAGCAGGTTAAATATTAAT	FSRLNIN	-	--
23436	37193	TATTTCTCGGGCAAGATAGCT	YFSGKIA	-	--
29186	14038	TATAGCAGGGCGGGCACAAAT	YSRAGTN	-	--
28963	38280	TTATGGGATGGGACTAATGCG	LWDGTNA	-	---
25852	37854	TATGTTCGTAGCGATACGAAG	YVRSDTK	-	---
31099	14243	TATTCGCGGCTTAATTCGAAC	YSRLNSN	-	--
21805	14416	TATAGCAAAATTGGTCATAAC	YSKIGHN	-	--
26273	13181	TATAGTCGTCTTGGTGAAAAT	YSRLGEN	-	--
34524	41294	AGCATGGGTGACCGGAGTTGG	SMGDRSW	-	--
25354	16112	GTGCAGTCTACCAATGGGCGC	VQSTNGR	-	---
21056	36500	GTTATGGAGTCATCAAAGTGG	VMESSKW	-	---
24640	37495	GTTATGCGCGATGCCTATCCC	VMRDAYP	-	--
28154	14346	TATTCAAGAACCGGAGCGAAT	YSRTGAN	-	--
29735	38964	ATTCTGGAATCGAGGGATTGG	ILESRDW	-	---
24743	37842	GAACTAGAGAGTAGAGAATGG	ELESREW	-	---
27729	38903	TATGAATCTACCAATGGTCGA	YESTNGR	-	--
24735	37212	AAAAGCGATTACTTAACTTAT	KSDYLTY	-	--
27541	38712	TATCATAGACTAAGCGAAAAC	YHRLSEN	-	---
21519	36697	TTCCACAAATTGTCGAATAAC	FHKLSNN	-	--
28574	14376	ATGTGGGATGGTACCAGCCCC	MWDGTSP	-	--
21509	36694	AGGACGCCGCAAGTTTATCCG	RTPQVYP	-	--
23347	36653	GTAATGAGCAGTACTACATGG	VMSSTTW	-	--
27340	37393	GATATGAGCTCAGTACAGTGG	DMSSVQW	-	--
29413	14346	TACAGCCGCACAGGGGCAAAT	YSRTGAN	-	--

31566	38654	TACTCAAGAATCAGCCCCAAC	YSRISPN	-	--
22009	36867	CGCACGGCAGATGCGTATCCG	RTADAYP	-	--
29082	14861	TATAGCCGGTTGGGAGTTAAT	YSRLGVN	-	--
21332	36398	TATTTCACAGGAAAAATTGCG	YFTGKIA	-	--
30269	39714	ACTCTATCATCAAGGGACTGG	TLSSRDW	-	--
22786	37102	AGGACTTATGACAGTTTTGTA	RTYDSFV	-	---
27505	37356	GACCTCTCGTCGAGTGACTGG	DLSSSDW	-	--
21554	36523	TATCATAAACTCAACGACAAT	YHKLNDN	-	---
23036	36698	CCAATGGCGTCCGCTACTTGG	PMASATW	-	---
21147	36539	TTGCATAGGCTGTCAGCGGAT	LHRLSAD	-	---
27508	18345	AGGAGCGAGTTTTCAACCTAT	RSEFSTY	-	--
27326	38753	TACCATCGGTTATCTGACAAT	YHRLSDN	-	---
35646	41623	TCGATGCAAGACCGTATTTGG	SMQDRIW	-	--
26425	38221	TATTTCTCGGGCAAAATTAAT	YFSGKIN	-	--
28244	38712	TACCACCGGTTGTCGGAGAAC	YHRLSEN	-	--
21017	14441	TACGCGAAGTCGGGCCCAAAC	YAKSGPN	-	---
22494	37053	GATTTGCAGTCATCCACCTGG	DLQSSTW	-	--
22999	36832	GACCTAACATCGAGAGACTGG	DLTSRDW	-	---
31688	14479	TACTCAAGAATAGGTAACAAC	YSRIGNN	-	---
22061	36738	AGGATGATTGATGCCTATCCG	RMIDAYP	-	--
20815	36390	AAGGATGAATTTTCTACTTAT	KDEFSTY	-	---
32002	17633	AGGTTAGAATCTGTACAATGG	RLESVQW	-	--
20688	36289	CGAACGATAGACGTTTTTCCA	RTIDVFP	-	---
21629	36576	TTGTCTAGATTGAGCTTTGAC	LSRLSFD	-	---
25107	37969	AGGACAAATACGGTGTACCCT	RTNTVYP	-	--
23406	14860	CTCAGCCGCACGTCGACTAAC	LSRTSTN	-	--
26583	13863	TACTCTAGACTAGGAAAGGAT	YSRLGKD	-	--
28814	38972	GTAATGGAAGACAGGAACTGG	VMEDRNW	-	---
24577	37702	AGGCTTGAGTCAAGTGCATGG	RLESSAW	-	--
22270	36964	AGGGGTGAGTTCGTCTATCCT	RGEFVYP	-	---
24165	37557	TACTTCACGGGCAAACGAGAG	YFTGKRE	-	--
24694	37557	TATTTTACCGGAAAGCGCGAA	YFTGKRE	-	--
33883	40285	AGCATGCAAGACAGAAACTGG	SMQDRNW	-	--

31642	17737	AGGACCTACGATTCCTTCGCA	RTYDSFA	-	--
21514	36587	TTGTTTAGTGGCGACGGACCT	LFSGDGP	-	---
26862	14473	TTCGCCCGGAACGGGCCTAAC	FARNGPN	-	--
27897	14445	TATGCTAGGACTGGCCAAAAT	YARTGQN	-	--
26097	13636	TATGCACGGACAGGGATCAAT	YARTGIN	-	--
23839	37302	AGATTGCATGACGCCTATCCT	RLHDAYP	-	---
29885	14282	TTCAGCAGGCTTAACACAAAC	FSRLNTN	-	--
20852	14274	TATGCTAAAACTGGACCTAAT	YAKTGPN	-	---
22569	37079	AAAGACGACTACACGACGTAC	KDDYTTY	-	---
21548	36496	TATGTCAAGTCCGATACTCGA	YVKSDTR	-	---
20961	16619	TTGCATAAGGCTGGATACAAC	LHKAGYN	-	---
23931	37572	GTACTATCTAGCAACACATGG	VLSSNTW	-	---
21205	36560	TTGTTTGATGGAACGTCGGCC	LFDGTSA	-	---
29220	38827	TATCATAGATTATCGATTAAT	YHRLSIN	-	--
29970	13946	TACAGTCGTACAGGTTTAAAT	YSRTGLN	-	--
24978	37565	AAAGACGACTATACCTCCTAT	KDDYTSY	-	---
29617	14282	TTTTCGCGTTTAAATACCAAT	FSRLNTN	-	--
31364	13535	TATAGTCGGCTGAACAATAAC	YSRLNNN	-	--
21517	36486	CGAACTGAGACAGTCTACCCA	RTETVYP	-	---
24707	37824	TATTCACGCGTTGGTGAAAAC	YSRVGEN	-	---
26970	37778	AACATGAGTGATAGAGGATGG	NMSDRGW	-	--
30265	13844	TATTCTAGACTTAATACAAAT	YSRLNTN	-	---
29384	13858	TATGCCCGAACTGGGTCGAAT	YARTGSN	-	--
22597	36840	TATCATAAACTTAATGCTAAC	YHKLNAN	-	---
20588	36250	TTGCATAAGCTGACGGTTAAT	LHKLTVN	-	---
23480	37009	CGAGACGGCACCAGTGCGTGG	RDGTSAW	-	--
23895	37454	CGCGATGAGTTTAGTGGGTAT	RDEFSGY	-	--
25431	37648	TACTTCACCGGTAAACCAAAC	YFTGKPN	-	--
30451	13830	TACAGCCGCGTAGGTCACAAT	YSRVGHN	-	--
27237	14145	TATGCCCGCACTGGGACCAAT	YARTGTN	-	--
27415	14607	TATTCAAGAGCTGGTGACAAC	YSRAGDN	-	--
22334	36848	TACGCCCGCACGGGACCAGAC	YARTGPD	-	---
34742	41391	CTCCTGTCTGATCGCGTGTGG	LLSDRVW	-	--

22618	36823	TATTTTAGCGGCGTCAAAGCG	YFSGVKA	-	--
21139	36537	TATTTTACGGGGAAGGTGGCG	YFTGKVA	-	--
22281	14370	TACTCGAAGCTGGGTTTTAAT	YSKLGFN	-	--
32130	39679	ATCATGTTGGACAGAGGATGG	IMLDRGW	-	--
33828	40490	GCTTTAAGTGATAGAAGTTGG	ALSDRSW	-	--
23971	37304	TATTTTACAGGACGCACTGAA	YFTGRTE	-	--
23610	37204	AGAGGAGACAACGTCTATCCC	RGDNVYP	-	--
20552	36243	CTCCACAAGCTCGCTAATAAT	LHKLANN	-	---
21935	17968	CGTGAAGACTTTTCAGCGTGG	REDFSAW	-	--
21877	36778	TATCATAAACTCAATAATAAC	YHKLNNN	-	---
23524	37425	ATAGCGGGGCGTGGGTGGGAC	IAGRGWD	-	--
28258	38130	GTGCTGTCATCGCAAGGATGG	VLSSQGW	-	--
25538	38132	GTACACGACTATATGAGTTAC	VHDYMSY	-	--
21808	36781	GATTTGAGTTCTTCACAGTGG	DLSSSQW	-	---
31751	40285	TCTATGCAGGATAGGAATTGG	SMQDRNW	-	--
24768	37731	TATTTTACGGGAAAGGCTAAT	YFTGKAN	-	--
26777	38456	AGTACATACGATTCGTATCCG	STYDSYP	-	---
20565	36271	AGGCTCGAGTCGGCTATTTGG	RLESAIW	-	---
30638	19575	GAGTTGAGCTCCCGCGAGTGG	ELSSREW	-	---
21884	19263	AGACTAGAGTCTGCAGTATGG	RLESAVW	-	--
29584	39526	CCGATGGGGAGTAATACGTGG	PMGSNTW	-	--
22630	36632	CTTCATAGGTTGGGCGATGAC	LHRLGDD	-	--
23115	37273	ATAATGGAGGCGAGGGACTGG	IMEARDW	-	---
27374	38315	TACTGGTCCGGAGTTAAGCTT	YWSGVKL	-	--
28023	38319	CGTCTCGAGAGCGTCTCATGG	RLESVSW	-	--
20784	36302	AATGCTTTGAAAGGGTGGGAC	NALKGWD	-	---
20647	36316	CTACACGCCAAGCTACCGAAT	LHAKLPN	-	---
29817	38753	TATCATCGCCTGTCGGATAAC	YHRLSDN	-	---
27228	14576	TACAGCAGAATTGGAGACAAC	YSRIGDN	-	---
21112	36484	ATGTTCGATGGCACAGCCGCA	MFDGTAA	-	---
23541	36964	CGCGGAGAATTTGTTTACCCA	RGEFVYP	-	---
23023	37007	AAGGATGATTACAGTGTCTTT	KDDYSVF	-	--
27105	37953	CAGATGGCGGCTCACGATTGG	QMAAHDW	-	--

21476	36537	TATTTTACGGGCAAAGTGGCG	YFTGKVA	-	---
22411	36947	CTGCACAGATTGAGCATGGAC	LHRLSMD	-	---
21853	36801	AGAGACGATTTCACGATGTAT	RDDFTMY	-	--
29898	13972	TACTCCCGGATTGGTCATAAT	YSRIGHN	-	--
28889	14103	TATTCTAGAGCCGGGCTTAAT	YSRAGLN	-	--
21110	16619	TTGCATAAAGCCGGCTATAAT	LHKAGYN	-	---
25440	14082	TACTCTAAAGCTAACTACAAC	YSKANYN	-	--
23490	37310	CGAGATGGTACAAGCTCGTGG	RDGTSSW	-	--
22392	37012	TACTTCACGGGCAGATTAGAA	YFTGRLE	-	--
20904	36431	GTAGAGTCAACGAATGGGAGG	VESTNGR	-	---
26666	38537	TACTTCACTGGGAGACAAGAT	YFTGRQD	-	--
31626	13992	TACTCCAGAGCAGGCGCGAAT	YSRAGAN	-	--
28143	38363	GAACTGGATTCCAGAGAATGG	ELDSREW	-	---
28491	39160	AGAACATTTGACTCATACGCA	RTFDSYA	-	--
20915	14018	TTTAGCAAATTGAACGTTAAC	FSKLNVN	-	--
20959	17658	CTCCACAAACTATCAAACAAC	LHKLSNN	-	---
27922	14087	TATGCCCGTTCCGGTACAAAC	YARSGTN	-	--
21505	17613	GGATCAGAATTCGTGAGTTAT	GSEFVSY	-	--
21322	36612	AGGGATGATTTCACCAGTTAC	RDDFTSY	-	---
22730	14552	TACAGCAAAGCCGGTTATAAC	YSKAGYN	-	--
23735	14097	TACTCTAAGTTAAACCATAAT	YSKLNHN	-	---
23973	37304	TATTTCACGGGCAGGACCGAA	YFTGRTE	-	--
24214	17754	GATCCAAGCTCGCACTCTTGG	DPSSHSW	-	---
23432	37182	CGAAACGAATCAGTGTATCCT	RNESVYP	-	---
22724	12113	TCAGACTCCACTAACGGTAGG	SDSTNGR	-	--
23603	14050	TATAGTAAACTGAACGCTAAT	YSKLNAN	-	---
22506	18191	CGCCTAATCGATGTCTACCCG	RLIDVYP	-	---
22951	37215	CGGAACGATACGGTGTACCCC	RNDTVYP	-	---
21531	36697	TTTCACAAGCTCAGTAACAAT	FHKLSNN	-	--
24206	17775	TTACATCGATTATCCTCTGAC	LHRLSSD	-	--
21083	36511	AAGTCGGAGTTCACGACCTAC	KSEFTTY	-	--
29633	39547	AATATGGAAGACCGCAAGTGG	NMEDRKW	-	---
21690	36458	TACGTGAAGAGCGACAGCAGG	YVKSDSR	-	--

20810	36387	TTCCACAAGTTAAGTCCGAAC	FHKLSPN	-	---
24222	17736	TTGCATCGACTGAGCGTTGAC	LHRLSVD	-	---
21832	36788	CTCCACAGGTTAACGACGGAC	LHRLTTD	-	--
24328	17535	CGTATGGAGTCTAGCGTATGG	RMESSVW	-	---
24861	37557	TATTTTACAGGGAAGAGGGAA	YFTGKRE	-	---
31871	13510	TACAGTCGCCTGAATTACAAT	YSRLNYN	-	--
24475	37731	TACTTCACTGGTAAAGCGAAC	YFTGKAN	-	--
23120	37277	TACGTACGAAGCGACAAAAAC	YVRSDKN	-	--
30396	14301	TATAGTCGATTAAACATGAAT	YSRLNMN	-	--
25567	14925	TTTTCACGGACCGGGCCTAAC	FSRTGPN	-	--
28789	39263	AGAACCTACGACACTTTTCCG	RTYDTFP	-	--
28322	38474	TACTTCTCGGGGCGTATAGAT	YFSGRID	-	--
20953	36453	AAGGACGATTTCACCGCATGG	KDDFTAW	-	---
30587	14243	TACAGCCGCCTAAACAGCAAT	YSRLNSN	-	--
25988	38272	TACCATAGGTTGGGTGACGAC	YHRLGDD	-	--
22439	37030	CTACACCGTCTTTCGCAGGAC	LHRLSQD	-	--
20613	36295	ATGCACAAACTTTCACCAAAT	MHKLSPN	-	---
20654	14503	TACAGCAAAATAGGAGCCAAC	YSKIGAN	-	---
25036	37945	TACTTCACGGGGAGACATGAA	YFTGRHE	-	--
28580	39196	TGTGCTCCATATTTACGTGAA	CAPYLRE	-	--
24789	37544	TATTTTACAGGCAGAATAGAT	YFTGRID	-	---
26835	37349	AGCGATGGTGTGTCCAGATGG	SDGVSRW	-	--
20574	36243	TTGCATAAATTGGCCAACAAC	LHKLANN	-	---
24425	37713	TACGAGTCGACTAATGGGAAG	YESTNGK	-	--
30281	13181	TACTCGAGGTTAGGTGAAAAT	YSRLGEN	-	--
23166	36881	CTCTACGATGGGACGAGCGCA	LYDGTSA	-	---
23457	37012	TATTTTACAGGAAGACTTGAA	YFTGRLE	-	--
31037	37002	ATGCTAGCGTCTAGTACGTGG	MLASSTW	-	--
23654	37468	CGTGATGAATTTAATCATTGG	RDEFNHW	-	--
26006	38278	AGACTAGAAGACCGAGCTTGG	RLEDRAW	-	---
23134	36853	CGATTGGAGAGCTCATCTTGG	RLESSSW	-	---
23356	37012	TATTTTACTGGTCGTCTCGAG	YFTGRLE	-	--
29423	13635	TATTCAAGGGCAGGCATAAAC	YSRAGIN	-	--

25332	38060	TATTTCACGGGGAAGACAAAT	YFTGKTN	-	--
21970	36852	ATAACATCGACTAACGGGCGT	ITSTNGR	-	--
26888	38619	TACTTCCACGGAAAAAAGGAT	YFHGKKD	-	--
28821	14344	TACAGTCGGGTAGGACAAAAC	YSRVGQN	-	--
26234	14122	TACGCACGCACAGGCGTCAAC	YARTGVN	-	--
23857	37544	TATTTCACTGGGAGGATAGAC	YFTGRID	-	---
22795	37167	GATTTGCTATCCAGGGACTGG	DLLSRDW	-	---
24210	37648	TATTTTACAGGCAAGCCTAAT	YFTGKPN	-	--
26639	38524	TATTTCACGGGTCAGATTAAC	YFTGQIN	-	--
22401	36495	TTGAGTAGGGTTTCAATAAAC	LSRVSIN	-	---
22593	14452	TATAGCAAGATAGGGTTTAAC	YSKIGFN	-	--
23955	37228	AGAGAGGATTTTGTCCGTTAT	REDFVRY	-	--
21966	36848	TATGCGAGGACTGGGCCGGAT	YARTGPD	-	---
23424	37302	CGTCTTCATGACGCCTACCCG	RLHDAYP	-	---
20768	36370	GAAATGGCCTCTATAAAGTGG	EMASIKW	-	---
23597	17127	AAGATGTCTTCAAGTGTATGG	KMSSSVW	-	--
33162	18065	GCCGAGAGTTCCCGACTCTGG	AESSRLW	-	---
21198	14005	TATAGTAAACTCGGACCCAAT	YSKLGPN	-	---
20639	36312	ATGCATAAGTTGTCAGTGAAT	MHKLSVN	-	---
20651	36286	CTTCACAAGCTCAATAACAAC	LHKLNNN	-	--
25793	14145	TACGCGCGAACAGGTACAAAC	YARTGTN	-	--
23423	14359	TATAGCAAAGCGGGACATAAC	YSKAGHN	-	--
21437	36603	CGTACAGAGCACGTGTTCCCC	RTEHVFP	-	---
28150	14502	GTCTGGAGCACCAATGGAATA	VWSTNGI	-	--
21653	36539	TTGCACAGGTTAAGCGCAGAT	LHRLSAD	-	---
21429	13938	TACAGCAAGATGGGGCCAAAC	YSKMGPN	-	---
26251	38254	TATTCGAGGCTTAACGATCCG	YSRLNDP	-	--
20516	36243	CTTCATAAACTCGCGAACAAT	LHKLANN	-	---
23778	37511	CGCCGTGAGGATGTATATCCG	RREDVYP	-	---
26722	14607	TACAGCAGAGCCGGTGATAAT	YSRAGDN	-	--
22584	37084	GACCTTACCAGCCGAGAGTGG	DLTSREW	-	---
22588	37075	CTCAGTAGAGTGTCGGTAAAC	LSRVSVN	-	---
32892	13874	TATTCTAGACTCGGATTGAAC	YSRLGLN	-	--

24622	36843	CGCGATGAATTCGTCTCGTAT	RDEFVSY	-	--
28337	16577	TATTCGAGACTAAATAAAGAC	YSRLNKD	-	--
24447	37367	TACTTCACGGGTAAACACGAT	YFTGKHD	-	--
25326	38060	TACTTTACCGGTAAAACCAAC	YFTGKTN	-	--
26848	17493	GACCTCAGTGACAGACGCTGG	DLSDRRW	-	---
29920	39175	ATTATGGAATCACAGAGCTGG	IMESQSW	-	--
26060	17752	CGCAGCGAGTTTGTTTCATTC	RSEFVSF	-	---
28572	14303	TACTCACGATTAAATGAGAAT	YSRLNEN	-	---
26126	14861	TATAGCAGGTTGGGCGTTAAC	YSRLGVN	-	--
28678	18835	GTTCTGAGCTCAAAAACTTGG	VLSSKTW	-	---
21101	36450	ACGTTAAGTTCTGCTACATGG	TLSSATW	-	---
20925	36368	AACCTGGCTAGTGCGACTTGG	NLASATW	-	---
25160	37575	TACTTCACGGGGCAGCGTGAA	YFTGQRE	-	--
20626	36305	TTACACAAGGCTGGTCCCAAC	LHKAGPN	-	---
24218	37341	TATTTTAGTGGCATACATGCT	YFSGIHA	-	--
21213	36434	TTGTGTAAGCCTTGTGACACC	LCKPCDT	-	--
22331	36981	ATGCGTGACGGCACTTCGGCT	MRDGTSA	-	--
22513	16045	TACGCTAAATCGGGATTTAAC	YAKSGFN	-	--
29336	39390	ATGTGGGATGGTACTAATGCG	MWDGTNA	-	---
31522	16636	TACCACCGCCTAAGTAACAAC	YHRLSNN	-	--
26477	16016	TACAGTCGACTAGGAGACAAT	YSRLGDN	-	--
27080	14218	TATAGCCGCACTGGAATTAAC	YSRTGIN	-	--
30442	13816	TATAGTCGCCTGAATCCGAAT	YSRLNPN	-	---
21091	36515	TATTTCACGGGACAGGTAGAA	YFTGQVE	-	--
20802	36384	AAAGACGACTTTGTGTCCTGG	KDDFVSW	-	--
27747	38911	ACCTGGGAGGGGGACGCGGCA	TWEGDAA	-	---
29980	13939	TACAGCCGCATCGGTACCAAC	YSRIGTN	-	--
22130	36790	TATCATAAGTTAAACCCACTC	YHKLNPL	-	--
23374	37367	TATTTCACAGGGAAACACGAC	YFTGKHD	-	--
24202	37606	GTGGATGAGTACTTGTCGTGG	VDEYLSW	-	--
27542	38474	TATTTTAGTGGCCGGATTGAT	YFSGRID	-	--
31123	39807	AGGGAATATAATGTTTATCCT	REYNVYP	-	--
22451	13991	TACTCAAAGGTTGGCGCCAAT	YSKVGAN	-	---

22051	36772	TACTTCACAGGTAAAAAAGAA	YFTGKKE	-	--
23945	37575	TACTTTACAGGGCAGAGGGAG	YFTGQRE	-	--
21460	36638	ATGTTCGATGGGACCCCAGCG	MFDGTPA	-	---
22741	37060	CGCACGAAGGAAGTCTATCCA	RTKEVYP	-	--
24838	37876	TACTGGAGCGGCGTCAAGGAC	YWSGVKD	-	--
25097	16602	GTCCACAGACTACAAGACAAA	VHRLQDK	-	--
21252	36496	TATGTAAAAAGCGATACTCGC	YVKSDTR	-	---
24543	37757	TACTTTTCGGGTAGGAAGGAG	YFSGRKE	-	--
21111	14441	TATGCGAAGTCAGGACCTAAC	YAKSGPN	-	---
29962	18789	TCGGATGAGTACAGTACGTAT	SDEYSTY	-	--
26962	38393	TTATGGAATGGTGAGGGGCCA	LWNGEGP	-	---
25424	38042	CGCGAGGACTATGTTAAATAC	REDYVKY	-	--
22596	37089	TATTTCAGCGGCAAGAAAGAA	YFSGKKE	-	--
27586	13603	TATGCAAGGTCAGGAATTAAC	YARSGIN	-	--
27009	14607	TACTCTCGCGCAGGAGACAAC	YSRAGDN	-	--
22634	37106	CTACACCGTTTGAGTGAGGAC	LHRLSED	-	--
26011	38280	CTGTGGGACGGGACAAATGCG	LWDGTNA	-	---
21368	36638	ATGTTTGACGGCACACCTGCT	MFDGTPA	-	---
22879	16045	TATGCTAAGAGTGGGTTCAAT	YAKSGFN	-	--
24318	14082	TATAGCAAGGCGAATTACAAT	YSKANYN	-	--
32123	40416	AAAAACGACTATGCCACATGG	KNDYATW	-	--
23213	36703	AATTTAGCGTCTGCAAGCTGG	NLASASW	-	--
22175	17681	CTCTCACGGGTCGGTCAAAAC	LSRVGQN	-	---
20937	36445	TACCACGCTAAATTGCCGAAT	YHAKLPN	-	---
29553	19005	CAAGGTGAAGCCCGCAGTTGG	QGEARSW	-	---
31023	14301	TACTCACGCCTCAATATGAAC	YSRLNMN	-	--
22619	36839	CTGCACCGCTTACAGGACAAC	LHRLQDN	-	--
21788	36775	GTTTTAAGTTCAAGCCAATGG	VLSSSQW	-	--
21343	15980	TTTTCTAAGTTGAACTTTAAC	FSKLNFN	-	--
21818	36534	CTGCATCGCCTTTCGCTAGAC	LHRLSLD	-	---
21827	36786	ATTGCTACTAGGGGAATAGGG	IATRGIG	-	--
32571	13715	TATAGCAGGTTAAACCATAAC	YSRLNHN	-	--
20870	36415	TTGAGTCGGGTAGGTTACGAC	LSRVGYD	-	---

31645	40248	CAAATGGAAGATAGAGCTTGG	QMEDRAW	-	--
23783	37482	TACTGGAGCGGCGTCAAAGAA	YWSGVKE	-	--
27108	38685	GATATGACAGATAGGAAGTGG	DMTDRKW	-	---
22987	37235	TTGTCAAGAGTGAGTCCCAAT	LSRVSPN	-	--
23747	37497	CCAATGTCAAGTTCTGGTTGG	PMSSSGW	-	--
29476	14175	TATTCAAGGGCCGGCATGAAT	YSRAGMN	-	--
25792	37863	TACAGTAGATTGAATCTAGAT	YSRLNLD	-	--
21483	36484	ATGTTTGACGGAACCGCGGCT	MFDGTAA	-	---
22640	17558	ACGGAAAGCACTAACGGACGT	TESTNGR	-	---
23629	16620	CTGAGTAGAATTTCAGTAAAT	LSRISVN	-	--
29635	39548	AGTATGCAAGATCGTACCTGG	SMQDRTW	-	---
26473	16016	TATTCACGTTTGGGCGATAAC	YSRLGDN	-	--
25059	37953	CAAATGGCTGCACATGACTGG	QMAAHDW	-	--
25211	37367	TACTTTACCGGCAAGCATGAT	YFTGKHD	-	--
27571	13636	TACGCCAGAACCGGTATTAAC	YARTGIN	-	--
28084	13930	TACGCTAGAACTGGCCTAAAC	YARTGLN	-	---
22788	37084	GATTTGACATCTCGGGAATGG	DLTSREW	-	---
30097	39421	TATGACAGCACCAATGGCCGT	YDSTNGR	-	--
22284	36539	CTCCATAGACTCTCGGCGGAC	LHRLSAD	-	---
20618	36299	TTCCACAAGCTAGGCATTAAT	FHKLGIN	-	--
21151	36458	TATGTCAAGTCGGATTCTCGG	YVKSDSR	-	--
20621	36302	AACGCACTTAAGGGATGGGAT	NALKGWD	-	---
21360	36633	CGCGGAGTTGATGTGTACCCC	RGVDVYP	-	---
22383	37006	TATTGGAGTGGTATTTTGGAA	YWSGILE	-	--
22294	13593	TATAGCAAAACGGGATACAAC	YSKTGYN	-	--
27194	38712	TATCATAGACTGAGTGAGAAT	YHRLSEN	-	---
20986	36367	AAGGACGACTTTACGACTTGG	KDDFTTW	-	---
23836	37534	TATTTTACCGGTAAAATCAAT	YFTGKIN	-	---
28133	38278	CGTTTGGAGGATCGTGCCTGG	RLEDRAW	-	---
24999	37934	CGTATGGAAAGCGTCAGTTGG	RMESVSW	-	--
20813	36389	CGCACGGAGACAGTATTTCCC	RTETVFP	-	---
26574	38491	AAAGACGGATATAGTGTTTAC	KDGYSVY	-	--
25327	38061	TATAGCAGGCTGAACATGGAC	YSRLNMD	-	--

27445	38712	TACCATCGTTTATCAGAAAAC	YHRLSEN	-	---
28301	38540	CTGATGAGCGACAGAGAATGG	LMSDREW	-	--
25574	37945	TACTTTACCGGCCGCCACGAA	YFTGRHE	-	--
21024	12707	GTAGACAGCACCAATGGCAGG	VDSTNGR	-	---
32596	18166	CAAGGTGAGGCGCGAATTTGG	QGEARIW	-	--
23327	37067	AGAGAAGACCATGTCTCCTGG	REDHVSW	-	---
21364	36635	TATGTCAAGTCGGACCGCATG	YVKSDRM	-	--
21258	36486	AGAACGGAGACAGTGTACCCT	RTETVYP	-	---
24887	37482	TACTGGTCAGGAGTTAAGGAG	YWSGVKE	-	--
20756	36362	GTCAAAAGCACGAACGGGGTG	VKSTNGV	-	---
22214	36942	AGAAATGACGTTGTATACCCG	RNDVVYP	-	--
26055	37367	TACTTTACAGGTAAGCATGAC	YFTGKHD	-	--
30134	14614	TACAGTAGGACTGGAACTAAT	YSRTGTN	-	--
23106	17515	CTCAGCCGCGCCAGTGTAAAC	LSRASVN	-	--
27517	38827	TACCACCGCCTGAGTATCAAC	YHRLSIN	-	--
20637	36295	ATGCATAAGTTGAGTCCGAAC	MHKLSPN	-	---
26881	38616	AACCTAGAGAGCCGGGGCTGG	NLESRGW	-	---
22388	16573	CGGAGCGAGCACGTCTTCCCT	RSEHVFP	-	--
22157	36852	ATCACGAGTACAAATGGCAGA	ITSTNGR	-	--
21776	36511	AAAAGCGAATTTACAACTTAT	KSEFTTY	-	--
24490	37004	GATATGGCCTCGAAGGATTGG	DMASKDW	-	---
21512	36695	CGCGGACCGGACGTTTACCCA	RGPDVYP	-	---
22566	17593	TTGAGCAGGATAGGTACGAAC	LSRIGTN	-	--
28843	14445	TACGCACGAACAGGTCAGAAC	YARTGQN	-	--
20878	36420	AAAGATGATTTCACTGTCTAT	KDDFTVY	-	---
23222	37313	AGGACTAATGATGTCTATCCT	RTNDVYP	-	---
26731	37994	AGGGAAGGAACTAGTAAATGG	REGTSKW	-	--
24164	37511	AGAAGGGAAGACGTGTACCCA	RREDVYP	-	---
22851	17535	AGGATGGAAAGCTCGGTTTGG	RMESSVW	-	---
22413	37019	CTGCACCGATTGACAGCCGAT	LHRLTAD	-	--
25363	37607	TATTTTAGCGGCAAGAAAGAC	YFSGKKD	-	--
28251	39077	ATAATGGAAGATAGGGTTTGG	IMEDRVW	-	---
30045	38599	GACCTTGATAGCTATAAGTGG	DLDSYKW	-	--

22262	36635	TACGTGAAAAGCGATAGAATG	YVKSDRM	-	--
22385	37007	AAAGACGACTATTCCGTATTC	KDDYSVF	-	--
23912	37203	AAGGATGGATACAGTACCTAT	KDGYSTY	-	--
23709	37419	CGGAACGATCATGTATTTCCA	RNDHVFP	-	---
30260	39421	TACGATTCGACTAACGGGAGG	YDSTNGR	-	--
20589	36286	TTGCACAAGCTGAATAACAAT	LHKLNNN	-	--
23611	36998	ATGATGGAGTCGAGCAAGTGG	MMESSKW	-	--
29986	14183	TACTCGAGAGCTGGGAATAAT	YSRAGNN	-	--
23600	37145	GACCCAGCCTCTCGGGAATGG	DPASREW	-	---
20827	14018	TTTTCGAAGCTGAATGTAAAC	FSKLNVN	-	--
22292	14441	TATGCTAAAAGCGGTCCTAAT	YAKSGPN	-	---
22071	36894	TTGCACCGGGCCGGTCCGGAT	LHRAGPD	-	--
21035	36490	TTTCACAAGCTGTCAACCAAT	FHKLSTN	-	--
27165	38389	ATCATGGCTTCGCAGAGCTGG	IMASQSW	-	--
29923	14376	ATGTGGGACGGGACTAGCCCA	MWDGTSP	-	---
23990	37439	GATATGGAGTCTAGGGGCTGG	DMESRGW	-	--
23915	17830	AGACTACTAGATGTATACCCT	RLLDVYP	-	---
27762	38915	CGATTAGAATCGCAAGTTTGG	RLESQVW	-	--
20834	18191	AGGCTCATTGACGTTTATCCA	RLIDVYP	-	---
21023	36355	ATAATGGAATCAGCGGTTTGG	IMESAVW	-	---
22381	37004	GACATGGCAAGTAAAGACTGG	DMASKDW	-	---
30806	39547	AACATGGAGGATAGAAAATGG	NMEDRKW	-	---
23982	37575	TATTTTACCGGCCAACGGGAG	YFTGQRE	-	--
21255	36464	AAAGACGATTTCACCCACTTT	KDDFTHF	-	---
30817	39461	AGGCTGGATTCGCGCGAGTGG	RLDSREW	-	--
29995	14681	TATGCCAGAAATGGGGCGAAT	YARNGAN	-	--
35404	41552	AACCTGGAAAGCCACAAGTGG	NLESHKW	-	---
22365	15945	TACGCGAAGAGTGGCTATAAC	YAKSGYN	-	--
24504	17687	GTACGTAGCACTAATGGCGTT	VRSTNGV	-	---
21790	36777	TATTTTACTGGAATACGGGAG	YFTGIRE	-	--
20620	36301	TTTCACAAATTAGGGCCTGAT	FHKLGPD	-	--
22703	37079	AAGGATGATTATACTACTTAT	KDDYTTY	-	---
26280	38147	ACTAAGTGGGGGGACGCGGCC	TKWGDAA	-	--

22859	37182	AGGAATGAGAGTGTTTACCCC	RNESVYP	-	---
20935	36443	AGAACAGATGACGTGTTTCCT	RTDDVFP	-	---
34873	40823	AAAGGGGATTCAAGAGACTGG	KGDSRDW	-	---
25016	37666	AGAAGTGAGTTCCTCTCCTAC	RSEFLSY	-	---
21426	36583	ATCATGATGGATGCGTATCCA	IMMDAYP	-	--
20887	13938	TACAGTAAGATGGGCCCCAAC	YSKMGPN	-	---
21219	16608	TTGCACGCCTTGTCACACAAC	LHALSHN	-	--
21881	36814	ATGAGAGACGGTACGCCAGCC	MRDGTPA	-	--
21665	36608	AAAGATGAATTTTCGGGATAT	KDEFSGY	-	--
28759	14137	TATTCGCGGGCGGGGGTTAAT	YSRAGVN	-	--
21907	36370	GAGATGGCAAGCATCAAATGG	EMASIKW	-	---
24990	18345	CGTTCTGAGTTCAGTACATAT	RSEFSTY	-	--
20582	36282	ATATTATCGTCTACGACCTGG	ILSSTTW	-	---
22580	37038	ATGTTGAGCAGTTCGACGTGG	MLSSSTW	-	---
29268	39421	TATGATTCCACGAACGGGAGG	YDSTNGR	-	--
20799	14581	TACTCTAAATTAAATGATAAT	YSKLNDN	-	---
22549	36901	TATTTCACTGGGAAGTTGGAC	YFTGKLD	-	--
20587	36262	TTACACAAACTGGCGCAGAAC	LHKLAQN	-	---
25924	38254	TACAGCAGATTGAATGACCCC	YSRLNDP	-	--
23226	11875	CATACATCTACGAATGGCGTG	HTSTNGV	-	--
20822	14018	TTCTCGAAACTCAATGTCAAT	FSKLNVN	-	--
25926	37945	TATTTCACGGGGAGACATGAG	YFTGRHE	-	--
20962	36458	TACGTAAAAAGTGACAGCCGT	YVKSDSR	-	--
30215	39745	GGGTTAGCTGATAGGAGCTGG	GLADRSW	-	--
23194	37304	TACTTTACAGGTCGCACAGAG	YFTGRTE	-	--
20622	36303	CTTCACAAGTTACAGCAGAAC	LHKLQQN	-	--
20597	14198	TATGCTAAGAACGGGCCCAAT	YAKNGPN	-	---
26040	38287	TTCTGGTCAGGTGTTAAAGAG	FWSGVKE	-	--
25700	37906	TATTGGAGCGGCGTAGTCGCG	YWSGVVA	-	--
21375	36393	CGAGAAATAGACGTGTACCCC	REIDVYP	-	--
22991	37238	AGGAGCGAGTTTGTGACCTTT	RSEFVTF	-	--
21288	36296	AGAACCCCGGAGGTTTTCCCC	RTPEVFP	-	--
30633	39738	AGTATGAGTGATAGATCTTGG	SMSDRSW	-	---

22531	36398	TATTTCACAGGAAAGATCGCG	YFTGKIA	-	--
24204	37084	GATCTAACCAGCAGAGAATGG	DLTSREW	-	---
22274	13913	TATTCTAAAGCGGGCTTCAAC	YSKAGFN	-	--
22616	36775	GTGCTCTCTAGTTCTCAGTGG	VLSSSQW	-	--
21811	36415	CTATCGAGAGTTGGCTATGAC	LSRVGYD	-	---
21892	11720	TCTGAGTCTACTAATGGTCGG	SESTNGR	-	--
29461	13949	TACAGTAGGATAGGTGTCAAT	YSRIGVN	-	--
28954	39145	AGGGGAGAAAGTCATGGGTGG	RGESHGW	-	--
25065	37580	TACAGTAGGCTCTCGCCCGAC	YSRLSPD	-	---
26752	38455	CCCATGGGAAGTCAAACGTGG	PMGSQTW	-	--
21038	36420	AAGGACGACTTTACCGTATAC	KDDFTVY	-	---
21448	36673	GGGGACGAATTTGTACACTGG	GDEFVHW	-	---
23815	37525	GAACTCGCCAGTCATGCGTGG	ELASHAW	-	--
22229	36829	TACTTTACAGGGCAAAAAGAG	YFTGQKE	-	--
26136	37824	TACAGCAGAGTCGGCGAGAAC	YSRVGEN	-	---
21015	36479	AGGACCGATACCGTATATCCA	RTDTVYP	-	---
24470	37580	TATTCGAGATTAAGTCCTGAT	YSRLSPD	-	--
22188	36744	AGAATGCTAGATGCGTACCCA	RMLDAYP	-	--
30004	13946	TACTCCAGGACCGGCCTGAAC	YSRTGLN	-	--
21401	36361	AAGGACGAATTCTCTAGTTGG	KDEFSSW	-	---
24048	37604	CGCGAAGAATATACCTCATGG	REEYTSW	-	--
28302	14607	TACAGTCGCGCAGGCGATAAT	YSRAGDN	-	--
21324	36613	AGAGGAGAAACAGTCTATCCA	RGETVYP	-	---
25280	38042	AGAGAAGATTACGTCAAGTAT	REDYVKY	-	--
20655	16631	TTGCACGTCTTGGGTCCTAAT	LHVLGPN	-	--
23713	37054	TTTCATAAAAAGGGTCCTGAC	FHKKGPD	-	--
21946	36839	TTACATAGACTGCAAGATAAT	LHRLQDN	-	--
26675	14122	TATGCTAGGACTGGTGTTAAT	YARTGVN	-	--
23569	37439	GACATGGAAAGCCGTGGATGG	DMESRGW	-	--
30699	39421	TACGACAGTACTAATGGTCGC	YDSTNGR	-	--
32320	13898	TATTCGCGCTTGAACCAAAAC	YSRLNQN	-	--
21864	36808	CCTATGGAAAGCGTTAAGTGG	PMESVKW	-	---
29006	38130	GTGCTGTCCAGTCAGGGTTGG	VLSSQGW	-	--

21312	36610	ATAGAAAGTACTCATGGCCGG	IESTHGR	-	--
25293	13795	CGGGACGATTTCACAGCCTAC	RDDFTAY	-	---
21925	36832	GATTTGACCAGCCGTGATTGG	DLTSRDW	-	---
20728	36354	ATGCATAAATTAGGGGTCAAT	MHKLGVN	-	--
22728	13526	TACTCGAAGCTTAACAATAAT	YSKLNNN	-	---
25403	38083	AACACTTACGATAGTTATCCC	NTYDSYP	-	---
22737	14416	TATTCAAAGATAGGGCACAAC	YSKIGHN	-	--
24184	14026	TATTCTAAAATGAACTTCAAT	YSKMNFN	-	--
22550	37070	GTCAATGATTACGTTACATAT	VNDYVTY	-	--
26033	37506	GACCTACGAGCTCATGATTGG	DLRAHDW	-	---
32534	16636	TATCATAGGCTTTCAAATAAC	YHRLSNN	-	--
22886	36612	CGAGATGACTTTACTTCCTAT	RDDFTSY	-	---
24850	37622	AGGATGCAAGACGCATATCCA	RMQDAYP	-	--
21682	36457	TATGTGAAATCCGATGTACGT	YVKSDVR	-	--
22977	17605	ACCGAGAGCACACACGGTCGA	TESTHGR	-	---
21246	14807	TATTCTAAACAGGGTCCTAAC	YSKQGPN	-	---
24923	37906	TACTGGTCAGGTGTGGTGGCC	YWSGVVA	-	--
21260	16013	TATAGCAAGACGGGCCCTAAT	YSKTGPN	-	---
21620	36462	GATCTCAGTAGCTCAAAGTGG	DLSSSKW	-	---
25058	17578	AAAATGGAAGACAGAAGCTGG	KMEDRSW	-	---
27267	38457	CTCTGGGATGGGACTTCGCCC	LWDGTSP	-	---
23962	16602	GTGCATCGCCTCCAGGATAAG	VHRLQDK	-	--
25682	38061	TACTCACGTTTAAATATGGAT	YSRLNMD	-	--
24212	17946	ATACAGTCAACTAACGGACGC	IQSTNGR	-	---
22956	37219	ACGAGATCCACCAATGGCGTG	TRSTNGV	-	--
23011	37204	CGCGGGGATAATGTGTACCCT	RGDNVYP	-	--
24107	36836	CGCACTGATGTCGTATACCCT	RTDVVYP	-	--
30106	14303	TACAGCAGGCTAAACGAAAAC	YSRLNEN	-	---
20960	36457	TACGTTAAGAGTGACGTCAGG	YVKSDVR	-	--
21459	36675	TTGATGAATGATGCGTATCCG	LMNDAYP	-	--
20556	36265	TTGCACAAACTGTCATTTGAC	LHKLSFD	-	---
25863	37660	AGCCATAGCACAAACGGACGT	SHSTNGR	-	--
22040	13904	TATAGTAAGATTGGAAACAAT	YSKIGNN	-	--

21242	36576	TTGAGCCGTCTTTCGTTCGAT	LSRLSFD	-	---
25014	17023	GTTTCCAGTAGCAACGGACGA	VSSSNGR	-	--
25846	38146	TACTGGAGCGGCGTCGCGGCA	YWSGVAA	-	--
21500	36691	AGGAAACTGGATGTCTATCCG	RKLDVYP	-	--
24250	36767	CCGATGGCCAGCCAACAGTGG	PMASQQW	-	---
21903	36489	TACGTCAAGAGTGATATGCGC	YVKSDMR	-	--
23539	37430	CGAGGTGAGTTTACGTATCCT	RGEFTYP	-	--
30943	39745	GGACTTGCCGACCGCTCATGG	GLADRSW	-	---
21140	36424	CGGTTGCTAGACGCATACCCT	RLLDAYP	-	--
25252	37649	TATAGTCGTCTCAATCCTGAT	YSRLNPD	-	--
30974	14614	TATTCACGAACCGGCACTAAC	YSRTGTN	-	--
24038	37580	TACAGTAGACTGTCACCAGAC	YSRLSPD	-	--
28295	38572	ATGTGGGACGGTACGCCAAGT	MWDGTPS	-	---
21882	36760	CGCGAGGATGGTGTCCGGTGG	REDGVRW	-	---
20806	36386	AAGGACGAGTTCACTGGTTAT	KDEFTGY	-	---
20595	36289	AGGACCATTGATGTATTCCCT	RTIDVFP	-	---
20910	36432	TTGTTCGATGGCACTGCGGCA	LFDGTAA	-	---
21216	18641	GTGTTGTCATCCACAACGTGG	VLSSTTW	-	---
28219	14325	TATAGCAGGACTGGGGTGAAT	YSRTGVN	-	--
23507	37419	AGAAATGACCACGTTTTCCCG	RNDHVFP	-	---
23306	37341	TACTTCTCCGGGATTCATGCG	YFSGIHA	-	--
22402	36898	CGCGGTGCAGATGTTTACCCA	RGADVYP	-	--
26463	38456	AGTACTTACGATTCCTACCCG	STYDSYP	-	---
22410	14085	TATTCGAAAGTAGGGCACAAT	YSKVGHN	-	---
20602	36257	TTACACAAGCTTAGTGAGAAC	LHKLSEN	-	---
28078	38911	ACATGGGAAGGAGATGCTGCT	TWEGDAA	-	---
20978	36464	AAGGATGACTTTACACATTTC	KDDFTHF	-	---
21772	14388	TATAGCAAGCTCAATTTGAAC	YSKLNLN	-	---
21766	36695	AGAGGTCCAGATGTCTATCCT	RGPDVYP	-	---
21612	36537	TACTTCACCGGTAAGGTTGCC	YFTGKVA	-	--
22657	36901	TACTTTACAGGGAAGCTTGAC	YFTGKLD	-	--
29944	13898	TACAGCAGACTAAATCAAAAT	YSRLNQN	-	--
20993	13991	TATAGTAAAGTGGGGGCAAAC	YSKVGAN	-	---

24103	37622	CGAATGCAGGATGCTTACCCG	RMQDAYP	-	--
23794	36786	ATCGCAACCCGTGGTATCGGC	IATRGIG	-	--
27285	17730	TATTTTACTGGGCGCTTAGAC	YFTGRLD	-	--
24253	37367	TATTTTACTGGAAAGCATGAC	YFTGKHD	-	--
25806	13181	TATTCCCGTCTGGGGGAAAAC	YSRLGEN	-	--
24866	37884	ATTAACAGTACTAACGGGCGC	INSTNGR	-	--
22526	37060	AGAACCAAAGAGGTATACCCC	RTKEVYP	-	--
21796	14050	TACTCCAAGCTAAATGCCAAT	YSKLNAN	-	---
23614	17039	AGAGAGGATGGGCTAAGATGG	REDGLRW	-	--
21226	36338	AAGGATGACTTCACAACGTTC	KDDFTTF	-	--
28020	38300	TATTTCAGCGGCAAACACGAC	YFSGKHD	-	--
21018	36481	AAGGACGACTTCAGTACGTAT	KDDFSTY	-	--
32235	40248	CAGATGGAGGACCGTGCATGG	QMEDRAW	-	--
22249	36271	CGCTTAGAAAGTGCCATATGG	RLESAIW	-	---
30356	37661	TTGCACAGGATGTCCCCTGAT	LHRMSPD	-	--
25901	37359	GACATGTCGAGCAACAAATGG	DMSSNKW	-	--
25558	37353	GTAATGTTTGACGCCTACCCC	VMFDAYP	-	--
21738	13557	TATGCTAAGACTGGGTATAAC	YAKTGYN	-	--
21704	36741	TACCACAAGTTAAACGAGAAC	YHKLNEN	-	---
21972	36853	AGGCTAGAATCTTCCAGCTGG	RLESSSW	-	---
31749	38697	ATGTGGGATGGCACAATGGCC	MWDGTMA	-	--
20663	36275	TTGCACAAATTAGGAGAAAAT	LHKLGEN	-	---
22794	36515	TACTTTACAGGTCAAGTGGAG	YFTGQVE	-	--
22113	14327	CTTAGTAGGTTAAATGATAAT	LSRLNDN	-	--
32466	14293	TACAGCCGAACCGGAAATAAT	YSRTGNN	-	--
24933	13181	TACAGTAGACTAGGAGAGAAT	YSRLGEN	-	--
26928	38456	TCAACCTACGACAGTTATCCA	STYDSYP	-	---
27845	38714	TACTTTACAGGCAGAACCGAC	YFTGRTD	-	--
24580	37772	TTGCTCCAATCTGCAACCTGG	LLQSATW	-	--
21455	12707	GTTGATTCGACGAACGGACGA	VDSTNGR	-	---
21372	36521	TACGCAAAACATGGGCCTAAC	YAKHGPN	-	--
21182	36322	ATCCTAAGCTCGTCAAACTGG	ILSSSNW	-	---
28368	16016	TACTCCAGATTAGGGGACAAT	YSRLGDN	-	--

21569	14036	TATAGTAAATTAAACCCTAAC	YSKLNPN	-	---
20705	36343	TATGTCAAGAGCCAGACCAAT	YVKSQTN	-	--
26059	14576	TATTCACGTATCGGGGATAAT	YSRIGDN	-	---
26500	37379	GTAGCGATGGAAGGCAGAGAT	VAMEGRD	-	--
23090	13593	TACTCAAAGACCGGTTACAAT	YSKTGYN	-	--
27697	14576	TATTCTCGGATAGGTGATAAT	YSRIGDN	-	--
22746	37012	TACTTCACGGGGCGCTTGGAG	YFTGRLE	-	--
21631	14036	TACTCGAAGCTAAATCCCAAC	YSKLNPN	-	---
20610	36266	CTCCACAAGCTTATGAACAAC	LHKLMNN	-	--
20675	36312	ATGCACAAACTCAGTGTCAAC	MHKLSVN	-	---
20896	18180	TTGAGTAAGTTAAGCTTAAAC	LSKLSLN	-	--
20975	36336	AAGGACGACTTTACGACTTAT	KDDFTTY	-	---
25347	37203	AAGGACGGGTACAGTACCTAC	KDGYSTY	-	--
21949	36633	AGGGGTGTCGACGTATATCCT	RGVDVYP	-	--
24809	37863	TATTCCCGGCTTAACTTGGAT	YSRLNLD	-	--
24429	13623	TTCAGTCGCATCGGTCCGAAT	FSRIGPN	-	--
27000	38648	AAAGAAGATTCCCGCACCTGG	KEDSRTW	-	--
23435	13913	TACAGCAAGGCTGGGTTTAAT	YSKAGFN	-	--
28430	14607	TACAGTAGAGCAGGTGACAAC	YSRAGDN	-	--
26879	38615	TATCATAGACTAAGCGCGGAT	YHRLSAD	-	--
23088	14085	TACAGTAAAGTGGGACATAAC	YSKVGHN	-	---
22323	36781	GACCTATCCAGCAGTCAGTGG	DLSSSQW	-	---
24954	37824	TACAGTCGGGTCGGAGAGAAC	YSRVGEN	-	---
20755	36343	TACGTAAAATCACAAACTAAC	YVKSQTN	-	--
21361	36335	AGATTAGCAGACGTTTTTCCT	RLADVFP	-	--
23140	37167	GACCTATTAAGTCGCGATTGG	DLLSRDW	-	---
23070	37262	GTTCTATCGACGAATGGTAGG	VLSTNGR	-	--
21004	36477	TACTCAAAGGTGGGAACGAAT	YSKVGTN	-	--
21133	36531	AGGACATCAGATGTCTACCCA	RTSDVYP	-	--
22829	13526	TACAGTAAACTCAATAACAAT	YSKLNNN	-	---
28848	13948	TTTTCGCGTCTTAACGCCAAC	FSRLNAN	-	--
21918	15956	TATTCTAAGGCCGGCTCTAAT	YSKAGSN	-	--
35380	41545	AGCATGCAGGACCGCGCATGG	SMQDRAW	-	--

22356	14619	TACTCCAAAGCTGGGGCGAAT	YSKAGAN	-	---
20762	36367	AAAGATGATTTCACCACATGG	KDDFTTW	-	---
22615	37098	TATTTCTCTGGTAAGATTGAA	YFSGKIE	-	--
27726	18270	GTGAGTGACTGGGCCCCATTC	VSDWAPF	-	--
20939	36336	AAAGATGATTTCACCACGTAC	KDDFTTY	-	---
28559	38915	AGGCTCGAGAGCCAGGTATGG	RLESQVW	-	--
30757	39531	GACATGCAGAGCAATCTCTGG	DMQSNLW	-	--
32401	40521	GACCCGGGTGATCGCAAATGG	DPGDRKW	-	---
22393	37013	TTATATTCAGGTGAGGGGCCT	LYSGEGP	-	---
23591	18011	TTACACCGGCTGATGCCGGAC	LHRLMPD	-	---
28620	38453	GAGCCGGAGTCACGCGCATGG	EPESRAW	-	---
21309	36540	CTTCATAAAATGTCGATGAAT	LHKMSMN	-	--
23729	37070	GTGAACGACTATGTGACCTAC	VNDYVTY	-	--
22162	36894	CTTCATAGAGCAGGCCCCGAC	LHRAGPD	-	--
21748	14807	TACTCCAAGCAAGGACCTAAT	YSKQGPN	-	---
22655	37116	AACGATGGGTCGAGCAAGTGG	NDGSSKW	-	--
22280	36593	AGAACCAACGACGTCTTTCCT	RTNDVFP	-	---
27839	12255	CACGATTCAACAAACGGAAGA	HDSTNGR	-	--
21504	13814	TATAGTAAGGCCAATTTCAAC	YSKANFN	-	--
26221	17730	TACTTCACGGGCCGGCTGGAC	YFTGRLD	-	--
27256	37690	TATTTCACCGGCCGAATGGAC	YFTGRMD	-	--
21044	13952	TACGCCAAGAGTGGGATGAAT	YAKSGMN	-	--
29717	14218	TACTCAAGAACCGGGATCAAT	YSRTGIN	-	--
21648	14222	TACAGCAAATCTGGTCCGAAC	YSKSGPN	-	---
22329	36934	GTCGGTCTCGAAGGGCGAGAC	VGLEGRD	-	--
28596	39203	AGCCTTGAGTCACGTGACTGG	SLESRDW	-	--
28529	38474	TACTTCTCAGGAAGAATCGAC	YFSGRID	-	--
33579	40936	GTACCGCAGGATCGGGCATGG	VPQDRAW	-	--
22127	36829	TACTTCACTGGACAGAAGGAA	YFTGQKE	-	--
21074	36359	CTATCGAGAGTCGGTTTTGAC	LSRVGFD	-	--
25053	37367	TATTTCACCGGCAAACACGAT	YFTGKHD	-	--
23288	37058	TATTGGAGCGGAATAATAGAG	YWSGIIE	-	--
21193	14222	TATTCAAAGAGTGGACCCAAC	YSKSGPN	-	---

24910	37757	TATTTCAGTGGGCGTAAAGAA	YFSGRKE	-	--
23891	12113	AGTGATAGTACAAATGGACGC	SDSTNGR	-	--
21490	11559	TATAGTAAAGTTGGAATTAAC	YSKVGIN	-	--
29664	39557	CATAGATCGACCAATGGTGTA	HRSTNGV	-	--
22233	36948	ACAAAATACGGGGACCCCGCG	TKYGDPA	-	--
21388	14274	TATGCAAAGACGGGTCCGAAC	YAKTGPN	-	---
32377	17600	GTGGAGGCCTCGCGGTCCTGG	VEASRSW	-	--
23820	37064	TATTTTACAGGAAAGCACGAA	YFTGKHE	-	--
20841	36328	AAGGATGATTTTACTTCATTT	KDDFTSF	-	---
21435	36458	TATGTCAAATCAGACTCTCGT	YVKSDSR	-	--
21034	36489	TATGTGAAATCCGACATGAGG	YVKSDMR	-	---
26028	38285	GATATGGAGAGCTATGATTGG	DMESYDW	-	---
23978	17946	ATCCAAAGCACGAATGGAAGG	IQSTNGR	-	--
35467	18420	GTCGATGAATGGTCCACGTTT	VDEWSTF	-	--
28915	13596	TATTCTAGGAAAAATGATAAT	YSRKNDN	-	--
24227	37649	TACTCCAGATTGAACCCCGAC	YSRLNPD	-	---
32903	39286	GAGCCAGAAAGCCGCGACTGG	EPESRDW	-	--
23242	37310	CGCGACGGGACCTCAAGTTGG	RDGTSSW	-	--
24057	37181	CGCACGGAGACGACCTATCCC	RTETTYP	-	--
21988	36860	AGATCAGATGTCGTTTACCCG	RSDVVYP	-	--
23532	37428	GATCTGCAGTCCAGCAAGTGG	DLQSSKW	-	--
21937	36777	TACTTCACGGGTATTAGAGAA	YFTGIRE	-	--
23536	36957	AAAGATGACTACACGACTTGG	KDDYTTW	-	---
21643	14207	TACTCAAAGCTTAATACCAAC	YSKLNTN	-	---
27964	38456	TCTACCTATGACAGTTACCCC	STYDSYP	-	---
26587	38499	TACTTTACGGGGCAGAGAGAT	YFTGQRD	-	--
25503	17619	CTTCTAAGCTCGCATGACTGG	LLSSHDW	-	---
20906	36390	AAAGACGAATTTTCTACGTAC	KDEFSTY	-	---
21986	36829	TATTTTACAGGGCAAAAAGAG	YFTGQKE	-	--
20695	11078	TACGCAAAGTTAGGTCCAAAC	YAKLGPN	-	--
20605	36250	CTCCACAAATTAACTGTAAAC	LHKLTVN	-	---
23728	37215	AGAAATGACACAGTATATCCG	RNDTVYP	-	---
23964	37580	TATTCGCGATTAAGCCCCGAT	YSRLSPD	-	--

22844	17558	ACTGAGTCTACAAACGGCAGA	TESTNGR	-	---
21928	19288	AACATTCCTGGGATGATGTAT	NIPGMMY	-	---
20808	36360	CTTCATAAAGCGGGTCATAAC	LHKAGHN	-	---
23057	36867	AGGACTGCCGACGCATACCCT	RTADAYP	-	--
22490	37037	TTGCTCTCCTCTGCCTCCTGG	LLSSASW	-	--
21605	36559	TATTTCACCGGGATTAAAGAT	YFTGIKD	-	--
24143	37636	AAAAGTGATTACGTGACGTAC	KSDYVTY	-	--
27905	38955	GAACTGAGCAGTATAAAGTGG	ELSSIKW	-	--
23769	37204	AGGGGAGATAACGTATATCCA	RGDNVYP	-	--
20640	36301	TTCCATAAGCTGGGTCCAGAC	FHKLGPD	-	--
22287	36923	TATTTTACAGGAAAGATTGAC	YFTGKID	-	--
22054	36630	AACAGCTTAGAGGGCCGTGAT	NSLEGRD	-	--
21676	36741	TATCATAAACTGAATGAGAAT	YHKLNEN	-	---
22865	37068	TATTCGCGACTCAACGACGAC	YSRLNDD	-	---
24304	37006	TACTGGTCCGGCATCCTTGAG	YWSGILE	-	--
29222	13635	TACAGCCGCGCAGGTATCAAT	YSRAGIN	-	--
20571	36275	CTTCATAAGCTGGGCGAGAAT	LHKLGEN	-	---
21187	36411	TATCATAAATTGAACCTGGAT	YHKLNLD	-	--
30561	39556	GTCATGGACAGCAGGGATTGG	VMDSRDW	-	---
20940	36389	AGGACCGAAACGGTCTTCCCG	RTETVFP	-	---
21298	36604	GTCGCGTTGGAAGGCCGGGAC	VALEGRD	-	---
29715	38912	CCCTTGAGTTCCCAATCCTGG	PLSSQSW	-	--
21014	36390	AAGGACGAGTTCAGCACCTAC	KDEFSTY	-	---
20876	36418	TTGCACAAGAAAGGTCCAGAC	LHKKGPD	-	---
24766	37219	ACTCGATCAACGAACGGCGTG	TRSTNGV	-	--
25985	37983	GTCCTCGAGAGTAGGGATTGG	VLESRDW	-	---
24240	37653	TACAGCCGATTAAATGAAGAC	YSRLNED	-	--
22077	36898	AGGGGAGCTGACGTGTATCCC	RGADVYP	-	--
20855	36409	CGTGGCGAACATGTGTTCCCA	RGEHVFP	-	---
23184	37301	TTACGGGATGGTACCAATGCG	LRDGTNA	-	--
21823	36479	CGAACTGATACGGTCTACCCT	RTDTVYP	-	---
21518	16013	TACTCAAAAACCGGTCCCAAC	YSKTGPN	-	---
22463	13557	TACGCAAAAACCGGATACAAT	YAKTGYN	-	--

25498	37990	AAAGATGACTACTCACATTAT	KDDYSHY	-	--
23297	37144	AGAAGCGAAAGCGTGTATCCA	RSESVYP	-	--
26976	38443	CAGAATGATTACGTGTCATAC	QNDYVSY	-	--
29139	14098	TATAGTCGAGTTGGTTTCAAT	YSRVGFN	-	--
21771	36678	CTCCATAGATTGGGCGAAGAT	LHRLGED	-	--
30029	13640	TACAGCCGCATTGGGTACAAT	YSRIGYN	-	--
26057	37611	AGAGGAGATCACGTATACCCC	RGDHVYP	-	--
28091	38553	TTGTGGGATGGTACTCCATCG	LWDGTPS	-	---
20885	36424	AGACTCTTGGATGCCTATCCC	RLLDAYP	-	--
29660	39556	GTAATGGATTCACGCGACTGG	VMDSRDW	-	---
26894	36267	CGTGAGGATTTTGTTCAATGG	REDFVQW	-	--
20563	36257	CTTCATAAGTTGTCGGAGAAT	LHKLSEN	-	---
25266	38019	CGCTCAGATCATGTATATCCT	RSDHVYP	-	--
23211	37278	GATCTTCGGAGTGCTTCTTGG	DLRSASW	-	---
26107	14359	TACTCAAAAGCTGGCCACAAT	YSKAGHN	-	--
28893	13802	TATAGTAGGATTGGTCAAAAC	YSRIGQN	-	--
24058	37611	CGTGGCGACCATGTTTATCCT	RGDHVYP	-	--
23858	17515	TTATCGAGAGCTTCTGTGAAT	LSRASVN	-	--
22460	19288	AACATCCCGGGCATGATGTAC	NIPGMMY	-	---
21432	36396	GTTGCGAACAAAGGCTGGGAT	VANKGWD	-	---
21224	36490	TTCCATAAATTAAGCACAAAC	FHKLSTN	-	--
22484	37048	GAAATGTCGAGTATTAAGTGG	EMSSIKW	-	--
21873	14198	TACGCAAAAAACGGACCGAAT	YAKNGPN	-	---
23493	36577	AGACTCGATAATGTCTATCCC	RLDNVYP	-	--
23824	37219	ACGAGGAGCACCAATGGAGTA	TRSTNGV	-	--
20767	36354	ATGCACAAGCTGGGTGTTAAC	MHKLGVN	-	--
25224	38019	AGAAGCGACCACGTGTATCCC	RSDHVYP	-	--
21412	17047	GTCCCTGGAGATTGCTGCGTC	VPGDCCV	-	---
20739	36274	CTCTCACGCATCGGACCAGAT	LSRIGPD	-	--
22713	13904	TACTCAAAGATCGGCAATAAC	YSKIGNN	-	--
23523	37150	AGACTCGACGATGTTTATCCG	RLDDVYP	-	--
25423	37713	TATGAGAGCACAAACGGAAAA	YESTNGK	-	--
29179	13181	TATAGCCGTCTGGGGGAGAAT	YSRLGEN	-	--

21209	36562	AGGACTGACCATGTATTTCCG	RTDHVFP	-	---
25158	14607	TATAGCCGGGCGGGGGATAAT	YSRAGDN	-	--
21263	36583	ATAATGATGGACGCTTACCCC	IMMDAYP	-	--
29503	38391	ATCATGGAGGATCGCGGTTGG	IMEDRGW	-	---
20729	36355	ATTATGGAGAGTGCTGTGTGG	IMESAVW	-	---
30511	16671	CTAACCTACGACGCTTACGAG	LTYDAYE	-	--
24187	17775	CTACACAGGCTCAGTAGCGAT	LHRLSSD	-	--
26585	12255	CATGACAGTACCAATGGTAGG	HDSTNGR	-	--
34438	41264	CGGGATGACTTCATCTCCTTC	RDDFISF	-	--
26838	12523	CACGAGAGTACAAACGGCCGT	HESTNGR	-	--
22614	15973	TATGCTAAAATGGGCCCTAAT	YAKMGPN	-	--
21957	36842	AAAGATGAGTTCGTATCATAT	KDEFVSY	-	--
27430	12361	TTCGAGAGCACCAACGGTCGC	FESTNGR	-	--
22145	36550	CGTACACCCCAAGTCTTCCCA	RTPQVFP	-	--
24873	37887	TACTTTACGGGTCATCATGAC	YFTGHHD	-	--
20713	36290	CTCCACAAGCTCAGCCCAGAC	LHKLSPD	-	--
21520	36698	CCGATGGCTAGTGCGACATGG	PMASATW	-	---
21883	36691	CGAAAGTTAGACGTATACCCC	RKLDVYP	-	--
23932	13837	TACAGCAAGGTTGGTTTCAAC	YSKVGFN	-	---
20752	36310	CGCACTTTAGACGTTTTTCCT	RTLDVFP	-	---
26179	37970	TACAGTAGAATTGGCGAAAAC	YSRIGEN	-	---
23831	37313	CGCACGAACGACGTATACCCG	RTNDVYP	-	---
22196	36788	CTACATCGCCTCACAACTGAT	LHRLTTD	-	--
21870	36500	GTGATGGAAAGCAGTAAATGG	VMESSKW	-	---
20826	36396	GTGGCCAATAAGGGGTGGGAC	VANKGWD	-	---
24432	37572	GTATTGAGCTCTAATACTTGG	VLSSNTW	-	--
20791	36381	CCCCTTGCGAGCTCGACTTGG	PLASSTW	-	---
23502	12239	CATTCATCGACAAATGGAGTG	HSSTNGV	-	--
31386	14183	TACAGTCGCGCTGGAAACAAC	YSRAGNN	-	--
23793	36942	AGGAATGATGTAGTGTACCCG	RNDVVYP	-	--
21558	36695	AGAGGTCCCGATGTCTATCCT	RGPDVYP	-	---
23174	37223	CGTAATGAGGATGTGTATCCC	RNEDVYP	-	---
28820	16016	TACAGTCGGTTGGGAGATAAC	YSRLGDN	-	--

20682	36274	TTGTCGAGAATAGGTCCAGAC	LSRIGPD	-	--
20525	36249	CTGTCGAAACTATCGATCAAC	LSKLSIN	-	---
24414	37472	AAGGACGACTACCACACCTAC	KDDYHTY	-	--
22499	11720	AGCGAAAGCACAAACGGAAGA	SESTNGR	-	--
21235	14094	TATTCCAAGGTTGGATCGAAT	YSKVGSN	-	--
22514	37057	CTTTACGACGGGACCAATGCC	LYDGTNA	-	---
20692	36336	AAGGACGACTTTACAACCTAT	KDDFTTY	-	---
21247	16018	TACTCCAAAAACGGCCCAAAC	YSKNGPN	-	---
26123	38310	CGGCTCCAAGACGTGACCTGG	RLQDVTW	-	--
22669	14094	TATTCAAAAGTTGGCAGCAAC	YSKVGSN	-	--
21204	19496	CTCTCCAAGATAGGTTACAAC	LSKIGYN	-	--
21844	36797	GAGATGGACAGTAGAATGTGG	EMDSRMW	-	---
24348	37219	ACTCGCAGTACGAACGGGGTC	TRSTNGV	-	--
22768	16025	TATAGCAAAGTAGGGCTCAAC	YSKVGLN	-	--
21626	36728	TACTTTTCAGGGGTGAAGGAG	YFSGVKE	-	--
20838	36386	AAAGATGAATTTACAGGCTAC	KDEFTGY	-	---
21278	36476	TATTTCACGGGTGTAAAAGAA	YFTGVKE	-	--
23777	37262	GTCTTGAGCACTAACGGGCGT	VLSTNGR	-	--
22143	14207	TATAGTAAACTCAACACAAAT	YSKLNTN	-	---
21677	16608	CTACATGCACTCAGCCACAAT	LHALSHN	-	--
32292	40475	ATTATGGGGGATAGAATTTGG	IMGDRIW	-	--
33110	40768	GTAATGGAAGACCGGTCGTGG	VMEDRSW	-	--
24772	11875	CATACGAGCACTAACGGTGTC	HTSTNGV	-	--
21471	36678	TTGCACCGCCTAGGAGAGGAC	LHRLGED	-	--
35591	13715	TACTCACGATTGAACCACAAT	YSRLNHN	-	--
27283	13995	TTTTCGAGGTTAAACGACAAT	FSRLNDN	-	--
21511	36481	AAAGATGATTTTTCAACCTAC	KDDFSTY	-	--
20865	36366	GTAGCAAGCAAGGGATGGGAT	VASKGWD	-	---
23274	18566	ACCCTCTCGACTAATGGTCGT	TLSTNGR	-	--
28237	37824	TATTCCCGCGTGGGAGAAAAT	YSRVGEN	-	---
21792	36540	CTGCACAAGATGAGCATGAAC	LHKMSMN	-	--
23392	14327	CTATCGCGACTGAACGATAAC	LSRLNDN	-	--
20554	36249	TTAAGTAAGCTTAGCATTAAT	LSKLSIN	-	---

27138	37970	TACTCTAGAATAGGGGAGAAT	YSRIGEN	-	--
26873	14607	TATTCTCGGGCAGGGGACAAC	YSRAGDN	-	--
29098	39203	AGTCTCGAGAGTAGGGATTGG	SLESRDW	-	--
22090	16586	TACCACAAGTTAGCGAACAAC	YHKLANN	-	--
33240	40823	AAGGGTGACAGCCGGGATTGG	KGDSRDW	-	--
23301	15956	TACTCAAAGGCGGGGAGCAAC	YSKAGSN	-	--
21989	14388	TACTCTAAATTGAATCTCAAT	YSKLNLN	-	---
20869	36410	TTGTTCGACGGCACGCCCGCG	LFDGTPA	-	---
24015	37408	TATTTCAGCGGTAAAATCGAT	YFSGKID	-	--
22807	14259	TACTCAAAACTCAACGTGAAC	YSKLNVN	-	---
21786	16018	TATAGCAAGAATGGTCCCAAT	YSKNGPN	-	---
22540	37064	TATTTTACTGGAAAGCACGAG	YFTGKHE	-	--
21450	14018	TTTTCAAAGCTGAATGTGAAT	FSKLNVN	-	--
22131	36695	CGCGGACCTGACGTATACCCC	RGPDVYP	-	---
21732	36540	CTTCACAAAATGAGCATGAAT	LHKMSMN	-	--
21231	14521	TTTTCTAAATTGAATATAAAC	FSKLNIN	-	--
25893	38245	TTGTGGGACGGTACTAACCCG	LWDGTNP	-	---
20746	36286	CTTCATAAATTAAACAATAAC	LHKLNNN	-	--
21780	13938	TATTCGAAAATGGGACCTAAC	YSKMGPN	-	---
22726	37144	CGTTCCGAGTCAGTATACCCT	RSESVYP	-	--
22546	37067	CGCGAAGATCACGTAAGTTGG	REDHVSW	-	---
21822	36614	AGAGATGAGACGGTCTACCCT	RDETVYP	-	---
20690	36335	CGTCTGGCTGATGTATTCCCG	RLADVFP	-	--
26274	17729	TCGCGGTCCACCAACGGTGTA	SRSTNGV	-	--
22039	13837	TACTCAAAGGTGGGCTTTAAT	YSKVGFN	-	---
22192	14503	TATTCAAAAATAGGCGCGAAC	YSKIGAN	-	--
26563	38300	TACTTTTCTGGTAAGCATGAT	YFSGKHD	-	--
25069	37553	CGTAGTGAGCATACGTACCCA	RSEHTYP	-	--
24302	37115	AGAGATATGGAGGTGTACCCA	RDMEVYP	-	--
28252	38245	CTCTGGGATGGCACGAATCCC	LWDGTNP	-	---
21913	36693	TACCATGCCGCTGGCCCCAAC	YHAAGPN	-	---
23922	37064	TATTTTACCGGAAAGCATGAG	YFTGKHE	-	--
22888	37013	CTCTACAGCGGCGAAGGACCG	LYSGEGP	-	---

24300	37064	TACTTCACTGGTAAACACGAA	YFTGKHE	-	--
20880	36385	TACCACAAGCTTAACCCAGAC	YHKLNPD	-	---
21588	36721	AGAACGTCGGACGTCTTTCCA	RTSDVFP	-	--
21743	16025	TACTCTAAAGTGGGTTTAAAC	YSKVGLN	-	---
20727	36286	TTACATAAGTTGAACAATAAT	LHKLNNN	-	--
20676	36329	ATCCTAACGTCGGCTACTTGG	ILTSATW	-	---
21177	36393	AGGGAGATCGATGTTTATCCA	REIDVYP	-	--
23180	37299	TGGTGGTCAGGAATCCGTGAA	WWSGIRE	-	--
21190	36555	CTGTCGAGGGTGGGACATGAT	LSRVGHD	-	--
22139	36479	AGGACGGACACCGTGTATCCC	RTDTVYP	-	---
26318	37824	TACTCCCGAGTTGGCGAAAAC	YSRVGEN	-	---
22397	37015	AATGACGGAACTTCAAAATGG	NDGTSKW	-	--
22627	13981	TACTCGAAAATCGGGCTAAAC	YSKIGLN	-	--
21921	36830	GACATGCAGAGCAGCACATGG	DMQSSTW	-	--
22371	36849	ATCGCGCAAGTGGGGTGGGAC	IAQVGWD	-	--
24633	11853	CACCAAAGCACTAATGGCGTC	HQSTNGV	-	--
21430	36509	CGTGGTGAGAACGTATTTCCA	RGENVFP	-	---
20607	36294	CTACATAAGTTGTCCCACGAC	LHKLSHD	-	--
21760	16158	GTAATGTCCACAAATGGGGTC	VMSTNGV	-	--
21301	36411	TACCATAAGCTCAATTTAGAC	YHKLNLD	-	--
23015	36942	CGGAACGATGTCGTCTATCCT	RNDVVYP	-	--
28793	39265	TACAGTCGACTCTCGGATAAT	YSRLSDN	-	--
24487	37737	TACTTTACAGGTAAGCAGGAT	YFTGKQD	-	--
21271	14370	TATAGTAAATTAGGATTCAAC	YSKLGFN	-	--
21212	36564	CGAACCAATGAGGTATTTCCG	RTNEVFP	-	--
22216	11974	GTCTCATCGACTAACGGTATC	VSSTNGI	-	--
25445	37403	TACTTTTCCGGTCGTTTAGAG	YFSGRLE	-	--
27404	38648	AAGGAGGACAGTAGAACATGG	KEDSRTW	-	--
25110	37653	TATTCAAGGCTTAACGAGGAT	YSRLNED	-	--
22384	36531	CGAACCAGTGACGTATATCCT	RTSDVYP	-	--
20656	36320	TATAGCAAGGTAGGCCCAGAC	YSKVGPD	-	--
28277	38281	CGGGACGATTATAGTACGTTC	RDDYSTF	-	--
23338	37356	GATTTAAGCAGTTCGGATTGG	DLSSSDW	-	--

21920	36829	TATTTCACTGGTCAGAAAGAA	YFTGQKE	-	--
21831	16074	TACTCCAAGTTGGGCCTAAAC	YSKLGLN	-	--
27921	38964	ATCCTTGAGAGTCGAGACTGG	ILESRDW	-	---
20804	36385	TATCATAAATTAAATCCGGAT	YHKLNPD	-	---
21889	36555	TTAAGTCGAGTTGGCCACGAC	LSRVGHD	-	--
22273	36829	TATTTCACCGGTCAGAAGGAA	YFTGQKE	-	--
28291	14447	TACTCAAGGGCCGGGAGCAAT	YSRAGSN	-	--
22927	37098	TACTTTAGCGGGAAAATCGAG	YFSGKIE	-	--
21211	36560	CTATTCGACGGCACCAGTGCT	LFDGTSA	-	---
21243	36577	CGTTTGGACAACGTATACCCT	RLDNVYP	-	--
22975	12055	GTTGAATCGACAAACGGCATT	VESTNGI	-	--
22375	36895	CGTATGGAGGATGCATATCCT	RMEDAYP	-	--
23530	36948	ACTAAGTATGGCGATCCTGCA	TKYGDPA	-	--
20859	36411	TATCATAAACTTAATTTGGAC	YHKLNLD	-	--
21684	14234	TACTCAAAGCTAGGGATGAAC	YSKLGMN	-	--
21162	14343	TACAGCAAACTCAATTCCAAT	YSKLNSN	-	--
25229	38024	AGGTTAGAGAGCACTTCCTGG	RLESTSW	-	--
25168	13589	TTTTCAAGAGTTGGGCCTAAC	FSRVGPN	-	--
22134	36814	ATGCGCGATGGAACCCCCGCT	MRDGTPA	-	--
23052	15945	TACGCAAAATCAGGATACAAT	YAKSGYN	-	---
25815	38216	AAGATGTCCGATCACACGTGG	KMSDHTW	-	---
21104	11472	GTCGCCAGCACGAACGGGATT	VASTNGI	-	--
22032	17605	ACAGAATCAACCCACGGGAGA	TESTHGR	-	---
20567	36264	CGTTTGGAGGATGTGTTCCCC	RLEDVFP	-	---
23348	36427	CGCGAGGACGCTGTACGGTGG	REDAVRW	-	--
22223	14079	TACAGTAAGTTGAATCAGAAC	YSKLNQN	-	--
21947	36537	TACTTCACAGGAAAAGTAGCC	YFTGKVA	-	--
22081	11720	AGTGAAAGCACCAACGGCCGG	SESTNGR	-	--
21045	36409	AGGGGTGAGCACGTATTTCCC	RGEHVFP	-	---
20673	36328	AAAGATGATTTTACCAGCTTT	KDDFTSF	-	---
21060	36501	GACCTTAGCTCGAGCTCGTGG	DLSSSSW	-	---
22031	36879	TACTTTTCGGGCAAAGTCGAG	YFSGKVE	-	--
22141	36919	CGGGAAGACTTCGTAACCTGG	REDFVTW	-	---

22152	36923	TACTTCACCGGCAAAATAGAT	YFTGKID	-	---
28194	16610	TATGTGAAATATGAGGATAAA	YVKYEDK	-	--
22528	36792	GTTGAAAGCTTTAACGGCCGT	VESFNGR	-	--
25221	13995	TTTAGCCGTCTCAATGATAAT	FSRLNDN	-	--
29039	39077	ATCATGGAGGACCGCGTATGG	IMEDRVW	-	---
21218	36567	ATGTTTGATGGGACGAGTGCA	MFDGTSA	-	---
22925	37203	AAAGACGGCTATTCCACATAC	KDGYSTY	-	--
21261	36411	TACCACAAGTTAAACCTCGAT	YHKLNLD	-	--
21783	36774	ATACTTGCCTCGGCAACTTGG	ILASATW	-	--
22340	36879	TATTTCAGCGGAAAGGTTGAA	YFSGKVE	-	--
24154	17736	CTTCACCGATTATCTGTAGAT	LHRLSVD	-	---
22403	36636	CGCGGGGACAATGTTTTTCCC	RGDNVFP	-	--
23000	36352	CGAGATGATTTTGTCACGTGG	RDDFVTW	-	--
22315	36805	AGGGGCGAAAGCGTATATCCT	RGESVYP	-	--
20837	36400	GAAGCGTTGGAAGGTCGTGAT	EALEGRD	-	---
21124	36477	TATAGTAAAGTTGGCACCAAC	YSKVGTN	-	--
21396	36336	AAAGATGATTTCACTACATAC	KDDFTTY	-	---
22974	37084	GACTTGACTTCTCGTGAGTGG	DLTSREW	-	---
20551	12165	CTTAGCAAAATCGGTCCCAAC	LSKIGPN	-	--
21506	36693	TATCACGCAGCCGGTCCAAAT	YHAAGPN	-	---
21481	11720	TCCGAGTCTACAAATGGTCGT	SESTNGR	-	--
25133	37980	TATTGGAGTGGAATACACGAA	YWSGIHE	-	--
23326	36531	AGAACTTCGGATGTGTACCCG	RTSDVYP	-	--
21214	11846	ACCGAAAGTACTAACGGTGTT	TESTNGV	-	--
20570	36274	TTGAGTAGAATTGGGCCGGAC	LSRIGPD	-	---
21982	36829	TACTTTACGGGACAAAAGGAG	YFTGQKE	-	--
24514	37744	AAATCAGAATTCAAGACGTAC	KSEFKTY	-	--
31853	14137	TACAGCAGAGCGGGCGTTAAC	YSRAGVN	-	--
21905	15973	TACGCGAAAATGGGACCAAAC	YAKMGPN	-	--
24703	17694	ATGCGCGACGGCACTAACGCG	MRDGTNA	-	--
22570	15996	TACAGCAAAGTTGGTCAAAAT	YSKVGQN	-	--
21899	12707	GTCGACAGTACTAATGGAAGA	VDSTNGR	-	---
25809	37842	GAGTTGGAATCCCGTGAGTGG	ELESREW	-	---

30807	39528	CATCTAGCAAGTCACGACTGG	HLASHDW	-	--
20780	36328	AAAGACGACTTCACCAGCTTC	KDDFTSF	-	---
27244	12361	TTTGAATCTACGAATGGCAGA	FESTNGR	-	--
20996	36472	GATATGAGTGCATCTACTTGG	DMSASTW	-	---
21001	19087	ACCAGTGAAAATGTGTATTTT	TSENVYF	-	---
21362	14581	TATAGTAAGCTCAACGATAAC	YSKLNDN	-	---
20540	36258	TATTCTAAATTAGGTCCCGAC	YSKLGPD	-	--
20741	36288	CTGAGCAAGTTGAGTCCGAAT	LSKLSPN	-	--
22929	37204	CGTGGCGACAATGTCTACCCG	RGDNVYP	-	--
23620	37454	AGAGACGAATTCTCGGGTTAT	RDEFSGY	-	--
22443	36860	CGTAGCGACGTTGTGTATCCT	RSDVVYP	-	--
21259	36582	TACTTCACAGGCAAAGTTGAA	YFTGKVE	-	--
21939	18133	AAGGATGATTATACTACCTTC	KDDYTTF	-	---
21195	36463	CGCGGTGAGACAGTGTTTCCG	RGETVFP	-	--
24421	37025	TATTTCACGGGTAAAACAGAT	YFTGKTD	-	--
22739	37091	TACTTGAAGTCACAGTCAAAT	YLKSQSN	-	--
22574	36864	CGTGGTGAAGACGTCTACCCC	RGEDVYP	-	---
24071	37045	AAGGACGATTACAGCACCTAC	KDDYSTY	-	---
21445	36671	CGCGAAGACTCCGTATACTGG	REDSVYW	-	--
25404	36892	GTAATGAGCACAAACGGGCGC	VMSTNGR	-	--
21421	14289	TATTCAAAACTGAACATGAAT	YSKLNMN	-	---
23584	37064	TACTTCACAGGGAAACATGAA	YFTGKHE	-	--
29046	14325	TACTCTCGCACAGGAGTAAAC	YSRTGVN	-	--
20617	36251	TTACATAAGCTAGGGGACAAT	LHKLGDN	-	---
20891	36426	TATGTTAAATCAGATATGAAG	YVKSDMK	-	---
30046	39265	TATTCGCGTTTGAGTGACAAT	YSRLSDN	-	--
20831	13981	TATAGTAAAATTGGATTGAAT	YSKIGLN	-	--
25191	12523	CATGAGTCAACCAACGGAAGG	HESTNGR	-	--
25658	36821	CGTGAGGACGGCGTTAGCTGG	REDGVSW	-	--
22649	37115	CGTGACATGGAAGTTTATCCG	RDMEVYP	-	--
25143	37983	GTGTTAGAATCACGCGACTGG	VLESRDW	-	---
21306	36426	TACGTCAAGAGCGACATGAAA	YVKSDMK	-	--
22848	37181	AGGACTGAAACAACGTACCCT	RTETTYP	-	--

20652	36258	TATAGCAAGCTGGGACCTGAT	YSKLGPD	-	--
23204	37307	GTGGGGCTCAAAGGTTGGGAC	VGLKGWD	-	--
30075	38697	ATGTGGGATGGTACGATGGCG	MWDGTMA	-	--
20958	36456	TACGTAAAGTCGGATAAGATG	YVKSDKM	-	--
21079	36509	CGAGGGGAAAATGTGTTCCCC	RGENVFP	-	---
20722	36320	TACTCAAAAGTCGGACCTGAT	YSKVGPD	-	--
20743	36360	TTACACAAGGCAGGGCACAAT	LHKAGHN	-	---
20973	11927	TATAGCAAGGTCGGTGTAAAC	YSKVGVN	-	--
20972	36433	TATAGCGCTATCGGGCCAAAT	YSAIGPN	-	--
22354	14619	TATAGCAAGGCGGGAGCAAAC	YSKAGAN	-	---
23434	37173	TACCACGCACAGGGCCCGAAC	YHAQGPN	-	--
20564	36270	TTGTCGAGGCTAGGACCAGAT	LSRLGPD	-	--
23753	14094	TACAGCAAGGTAGGCTCCAAC	YSKVGSN	-	--
22601	37091	TATCTAAAAAGTCAGAGCAAT	YLKSQSN	-	--
21638	36579	CGCGCGCTTGAAGGTTATGAC	RALEGYD	-	--
20623	12165	TTATCTAAGATAGGGCCAAAT	LSKIGPN	-	--
21487	36582	TATTTTACCGGGAAGGTCGAG	YFTGKVE	-	--
21114	16158	GTTATGAGCACCAACGGAGTG	VMSTNGV	-	--
21125	14499	GTCATAAGCACAAATGGAGTC	VISTNGV	-	--
30234	37970	TATAGCCGTATCGGTGAAAAT	YSRIGEN	-	--
21458	36432	CTTTTTGACGGGACGGCAGCC	LFDGTAA	-	---
22055	36887	AGGGAAGAGGGTGTCGCATGG	REEGVAW	-	--
20644	36251	CTTCACAAATTAGGAGATAAT	LHKLGDN	-	---
22465	14259	TATAGCAAGTTGAATGTCAAC	YSKLNVN	-	---
20596	36290	TTACATAAATTGTCACCCGAC	LHKLSPD	-	--
21866	36613	AGAGGCGAAACAGTATACCCT	RGETVYP	-	---
22003	36864	AGAGGCGAGGATGTATATCCA	RGEDVYP	-	---
21287	11663	GTGGCCAGTACGAATGGGGTT	VASTNGV	-	--
21355	36429	GTGAAATCTACTAATGGTATC	VKSTNGI	-	--
21632	36730	CGTGATGATTTTACGACTTTC	RDDFTTF	-	--
21325	36614	CGTGACGAAACAGTTTATCCG	RDETVYP	-	--
20604	36257	CTTCATAAATTGTCCGAAAAT	LHKLSEN	-	---
24804	37421	TACTGGTCTGGAGTTATCGAG	YWSGVIE	-	--

21672	17801	TTGAGTAAAGTAGGGCACAAT	LSKVGHN	-	--
20851	11522	GTTGAATCCACCAATGGGGTT	VESTNGV	-	---
21756	14094	TACAGTAAAGTCGGGAGCAAC	YSKVGSN	-	--
20678	36318	CTCGCGAGGACAGGGCCCGAT	LARTGPD	-	--
20711	13882	TATGCGAAGGCCGGGCCTAAT	YAKAGPN	-	--
24995	14860	TTGTCAAGGACAAGCACAAAT	LSRTSTN	-	--
20858	36410	CTTTTTGATGGAACACCTGCT	LFDGTPA	-	---
20624	36294	TTGCACAAGCTTAGTCATGAT	LHKLSHD	-	--
21724	11292	GTGCAAAGTACGAATGGGATC	VQSTNGI	-	--
20738	36308	AAAGATGAGTTTACAACTTTT	KDEFTTF	-	---
22072	13882	TACGCGAAAGCTGGTCCAAAC	YAKAGPN	-	--
20697	36338	AAAGACGATTTTACGACATTT	KDDFTTF	-	---
22006	36865	ATGTTCGATGGAACGATGGCC	MFDGTMA	-	---
21159	15980	TTCTCCAAACTCAATTTCAAC	FSKLNFN	-	--
21876	36479	CGAACGGACACGGTTTACCCT	RTDTVYP	-	---
24476	16610	TACGTAAAGTACGAAGATAAG	YVKYEDK	-	--
27014	38381	TATTGGACCGGAAAGGTGGAA	YWTGKVE	-	--
23343	37359	GATATGAGTTCAAATAAGTGG	DMSSNKW	-	--
20835	16586	TATCATAAGTTGGCCAATAAT	YHKLANN	-	--
21061	36502	TTGTTTAGCGGAGAAGGGCCG	LFSGEGP	-	---
21799	36692	AGGACAGATGATGTCTATCCT	RTDDVYP	-	---
20921	36436	CGCCTTGATGATGTCTTCCCG	RLDDVFP	-	--
21365	36636	CGAGGTGACAATGTTTTCCCC	RGDNVFP	-	--
20984	36456	TATGTCAAAAGTGACAAAATG	YVKSDKM	-	--
21207	14499	GTAATTTCAACGAACGGTGTA	VISTNGV	-	--
20594	36288	TTATCAAAACTGTCCCCAAAC	LSKLSPN	-	--
24607	19263	CGGTTGGAAAGCGCTGTCTGG	RLESAVW	-	--
20732	36274	CTTAGTCGTATTGGGCCTGAT	LSRIGPD	-	--
21282	36593	CGCACGAATGATGTTTTCCCC	RTNDVFP	-	---
23035	36901	TATTTCACCGGCAAACTGGAT	YFTGKLD	-	--
23479	37408	TACTTTTCGGGGAAGATAGAC	YFSGKID	-	--
22542	12037	GTCAACAGCACAAATGGCGTC	VNSTNGV	-	--
21930	36730	AGGGACGACTTCACCACCTTT	RDDFTTF	-	--

20886	36425	AAGGACGATTTCACAATGTTC	KDDFTMF	-	--
20846	36356	CGTGGTCTGGAAGGCTTCGAT	RGLEGFD	-	--
32976	18284	GACTTAAGGGATCGGGCCTGG	DLRDRAW	-	---
22036	36883	GTTGGGACGAAAGGATGGGAT	VGTKGWD	-	--
23130	37116	AATGACGGAAGTTCTAAATGG	NDGSSKW	-	--
21050	12037	GTAAATAGCACCAATGGCGTC	VNSTNGV	-	--
23030	11765	GTAGGAAGTACAAACGGGGTC	VGSTNGV	-	--
20807	11927	TACTCGAAAGTGGGCGTGAAT	YSKVGVN	-	--
21995	36362	GTGAAGTCGACAAATGGAGTT	VKSTNGV	-	--
21222	36569	CGCCTCATGGACGCCTTTCCC	RLMDAFP	-	--
21397	18659	AGAGGTGACAACATTTTCCCC	RGDNIFP	-	--
21175	36328	AAGGACGACTTCACGTCGTTC	KDDFTSF	-	---
29269	13510	TACTCAAGATTAAATTATAAT	YSRLNYN	-	--
20693	36264	CGACTTGAGGATGTTTTTCCC	RLEDVFP	-	---
21763	36515	TACTTTACAGGGCAAGTTGAG	YFTGQVE	-	--
24106	37624	ATGTTTGACGGAACCAACCCG	MFDGTNP	-	---
20614	36296	CGGACACCTGAAGTGTTTCCA	RTPEVFP	-	--
21071	36506	AGGATGATCGATGTCTATCCA	RMIDVYP	-	--
21552	12043	TACGCCAAGACCGGTAACAAC	YAKTGNN	-	--
23454	17023	GTTAGTTCCTCAAATGGTCGC	VSSSNGR	-	--
21413	11766	TACGCTAAAACAGGAGCGAAC	YAKTGAN	-	--
22345	14289	TACAGCAAATTAAATATGAAT	YSKLNMN	-	---
22759	11516	GCTGAATCAACTAACGGTAGA	AESTNGR	-	--
21051	36497	TACACTAAAAGCCAGACCAAC	YTKSQTN	-	--
23149	14174	TATAGTAAGCTTGGTGCTAAC	YSKLGAN	-	--
20650	36318	TTAGCTCGAACCGGACCGGAC	LARTGPD	-	--
20538	36257	TTGCACAAACTAAGCGAAAAC	LHKLSEN	-	---
21502	14602	TACGCGAAGCAGGGCCCTAAT	YAKQGPN	-	--
21339	36620	AGGGGCCCAGACGTTTTTCCG	RGPDVFP	-	--
20560	36269	TTAGCGAAGACGGGCTATAAT	LAKTGYN	-	--
22790	37015	AACGATGGTACAAGCAAGTGG	NDGTSKW	-	--
22817	37173	TATCATGCTCAAGGACCTAAT	YHAQGPN	-	--
22785	36865	ATGTTTGACGGCACTATGGCT	MFDGTMA	-	---

26263	38363	GAGTTAGACAGTCGCGAGTGG	ELDSREW	-	---
26188	12239	CACAGCAGTACCAACGGTGTG	HSSTNGV	-	--
26429	37690	TACTTTACGGGAAGGATGGAT	YFTGRMD	-	--
22552	18079	AGAGCCCTCGAGGGGCGTGAC	RALEGRD	-	--
20812	14018	TTCAGCAAACTTAACGTGAAT	FSKLNVN	-	--
21733	36760	AGAGAAGACGGCGTTCGATGG	REDGVRW	-	--
22310	13537	TATTCAAAATTAAACATTAAC	YSKLNIN	-	---
22504	12333	GTGTCGAGTACCAACGGAGTG	VSSTNGV	-	---
24761	37304	TACTTCACTGGCAGAACCGAG	YFTGRTE	-	--
25854	37498	AAGGACGAATACCATACCTAC	KDEYHTY	-	--
20586	36285	CTACATAAGTTGAGCGTCGAC	LHKLSVD	-	--
21281	36425	AAAGATGACTTTACTATGTTT	KDDFTMF	-	--
21453	12037	GTAAATTCAACTAACGGAGTA	VNSTNGV	-	--
21234	36515	TATTTCACTGGACAGGTCGAA	YFTGQVE	-	--
21225	36504	TACCATAAGATGTTACCCGAT	YHKMLPD	-	--
21712	36550	AGGACCCCGCAGGTGTTTCCG	RTPQVFP	-	--
23872	18659	CGCGGCGATAATATCTTCCCG	RGDNIFP	-	--
21179	17796	CTCTCGCGTGTGGGGCCCGAT	LSRVGPD	-	--
21501	36692	CGTACTGACGACGTGTACCCA	RTDDVYP	-	---
20632	36310	AGAACACTCGATGTGTTCCCA	RTLDVFP	-	--
21106	36423	GTGCAGAGCACCAACGGAGTA	VQSTNGV	-	---
21077	16158	GTTATGTCCACCAATGGAGTT	VMSTNGV	-	--
28533	39175	ATCATGGAGAGTCAATCTTGG	IMESQSW	-	--
23234	14079	TATTCCAAACTAAACCAAAAT	YSKLNQN	-	--
20863	12148	TATTCGAAAGTTGGCGAAAAT	YSKVGEN	-	--
20995	12737	ATTGAAAGTACGAATGGTCGT	IESTNGR	-	---
22489	13983	TATGCTAAAACAGGGCACAAC	YAKTGHN	-	--
21545	36361	AAAGACGAGTTTTCGTCATGG	KDEFSSW	-	---
20670	16575	CTATCTAAGCTTTCTGCCAAC	LSKLSAN	-	--
23566	16573	CGTTCCGAACACGTATTTCCG	RSEHVFP	-	--
28496	14376	ATGTGGGATGGAACCTCGCCT	MWDGTSP	-	---
21197	12190	GTAACGTCTACGAATGGTGTT	VTSTNGV	-	--
20900	36429	GTAAAAAGCACCAACGGGATT	VKSTNGI	-	--

31024	14376	ATGTGGGACGGCACGTCACCT	MWDGTSP	-	--
34677	40800	AATCTCGAGAGTAGAGAGTGG	NLESREW	-	--
22507	16113	ACCCACTCAACCAATGGGGTA	THSTNGV	-	--
24014	36981	ATGAGGGATGGGACCAGCGCA	MRDGTSA	-	--
34856	19648	GACTTAAGCAGCAATAGCTGG	DLSSNSW	-	--
26954	14024	TATTCTCGCAAAAACGAAAAT	YSRKNEN	-	--
23249	16113	ACGCATAGCACCAACGGAGTC	THSTNGV	-	--
21002	36476	TACTTTACTGGCGTGAAGGAG	YFTGVKE	-	--
22907	12113	TCAGACAGTACTAACGGCCGA	SDSTNGR	-	--
21559	36713	AGGAATGATGACGTTTTTCCT	RNDDVFP	-	--
21359	36632	TTACACCGTCTCGGTGACGAT	LHRLGDD	-	--
22073	36895	AGAATGGAAGACGCGTACCCC	RMEDAYP	-	--
24326	36924	TATTTGAAAAGCCAAATCTAC	YLKSQIY	-	--
25203	37862	TTCCACCGTCTTTCGCCAGAT	FHRLSPD	-	--
23440	11292	GTTCAGTCGACAAACGGAATA	VQSTNGI	-	--
21353	36628	CTAGAAAGCAGAGAGGGTATT	LESREGI	-	--
20765	36258	TACTCAAAGCTCGGTCCAGAC	YSKLGPD	-	--
21710	36620	CGTGGTCCCGATGTCTTCCCC	RGPDVFP	-	--
20592	36287	CTGGCAAAAAGCGGCCCAAAT	LAKSGPN	-	--
21567	36675	CTCATGAATGACGCTTACCCT	LMNDAYP	-	--
31467	38702	ATGTGGGATGGAACGATTGCA	MWDGTIA	-	--
20907	12037	GTCAACTCGACAAACGGGGTT	VNSTNGV	-	--
22190	14602	TATGCGAAACAGGGTCCGAAC	YAKQGPN	-	---
22824	36982	CGCGATGACTTCACTGTTTAC	RDDFTVY	-	---
32562	39545	CAACTGGATAGCCGTGACTGG	QLDSRDW	-	--
22228	16134	GTTCACAGTACGAATGGTATT	VHSTNGI	-	--
21895	36819	GACTTAACGAGCGCTAAGTGG	DLTSAKW	-	--
21059	14054	CTCGCGAAAACCGGGCCTAAT	LAKTGPN	-	--
23764	37334	AAACTTGAGTCAAGCATGTGG	KLESSMW	-	--
20669	36326	TTATTCGATGGAACTGGCCCT	LFDGTGP	-	---
21248	36579	AGGGCTTTAGAGGGGTACGAT	RALEGYD	-	--
20897	36429	GTAAAGAGCACGAACGGGATA	VKSTNGI	-	--
21640	36613	CGGGGAGAGACGGTTTATCCC	RGETVYP	-	---

20648	36280	CTGCACAAGTTGAGTATCGAT	LHKLSID	-	--
21141	36451	GTAGCGACGAAAGGTGCTGGG	VATKGAG	-	--
21446	36393	AGGGAGATTGATGTTTACCCT	REIDVYP	-	--
30496	19561	GAACTAGATAGCAGGGACTGG	ELDSRDW	-	--
21561	16158	GTGATGTCAACCAATGGCGTC	VMSTNGV	-	--
22515	36713	CGTAACGACGATGTGTTCCCG	RNDDVFP	-	--
22592	36319	CGTGACGAAACCGTTTTTCCA	RDETVFP	-	--
20819	36393	CGAGAAATAGACGTCTACCCG	REIDVYP	-	--
25303	37086	AAGAGCGACTTTGTGACGTAC	KSDFVTY	-	--
21586	12006	TATGCCAAGAGTGGTGCAAAT	YAKSGAN	-	--
21154	14060	CTTCACGCGGCTTTGCCTAAT	LHAALPN	-	--
20549	36265	CTCCATAAGTTAAGTTTTGAT	LHKLSFD	-	--
22961	37223	AGAAACGAAGACGTTTATCCG	RNEDVYP	-	---
20945	36451	GTCGCTACTAAGGGCGCGGGT	VATKGAG	-	--
23362	18079	CGTGCATTGGAAGGAAGGGAT	RALEGRD	-	--
20923	14060	TTACATGCTGCGCTCCCGAAC	LHAALPN	-	--
22025	12737	ATAGAGAGCACAAACGGACGA	IESTNGR	-	--
21742	11766	TATGCGAAGACTGGGGCTAAT	YAKTGAN	-	--
20548	36264	AGGCTCGAAGACGTTTTTCCA	RLEDVFP	-	---
27770	16064	TTTAGTCGTTTGAACGAGAAT	FSRLNEN	-	--
21113	16575	CTTTCCAAATTAAGCGCAAAT	LSKLSAN	-	--
20844	11887	CTATCTAAAGTAGGTCCTAAT	LSKVGPN	-	--
21943	36564	AGGACAAACGAAGTGTTTCCA	RTNEVFP	-	--
21654	11927	TATTCCAAGGTGGGGGTAAAT	YSKVGVN	-	--
22161	36721	CGGACCAGTGATGTATTCCCT	RTSDVFP	-	--
27166	38702	ATGTGGGACGGGACTATAGCG	MWDGTIA	-	--
23273	14174	TACTCTAAATTGGGAGCGAAT	YSKLGAN	-	--
20581	36258	TATAGCAAATTAGGACCGGAT	YSKLGPD	-	--
20730	36356	AGGGGATTAGAGGGGTTTGAC	RGLEGFD	-	--
20691	36287	TTAGCTAAGTCAGGTCCGAAC	LAKSGPN	-	--
20684	11947	CTGAGTAAGTTAAATCTGAAC	LSKLNLN	-	--
21660	16017	TATGCCAAGGGGGGTCCAAAC	YAKGGPN	-	--
21779	36337	TTATTCGATGGGACTGCGAGC	LFDGTAS	-	---

21452	36636	AGGGGAGATAACGTGTTCCCA	RGDNVFP	-	--
20694	36337	CTTTTTGACGGCACAGCCTCA	LFDGTAS	-	---
23041	18036	ACTGATGAGACCGTTTACAGA	TDETVYR	-	--
20555	11947	TTATCTAAGCTGAACTTAAAT	LSKLNLN	-	--
26197	16567	AGGAACGACATGGTGTTCCCC	RNDMVFP	-	--
21317	11663	GTCGCATCAACAAACGGGGTG	VASTNGV	-	--
36102	13745	TACAGTCGTGTTGGTTATAAT	YSRVGYN	-	---
20528	36251	CTTCACAAATTGGGAGATAAC	LHKLGDN	-	---
20645	36277	TTGCACAAGTTGTCCCCCTTA	LHKLSPL	-	--
31259	39526	CCCATGGGTTCGAACACCTGG	PMGSNTW	-	--
23956	12113	TCGGATTCCACAAACGGGAGG	SDSTNGR	-	--
21614	11559	TATTCCAAGGTCGGTATAAAT	YSKVGIN	-	--
20883	36423	GTTCAATCTACTAATGGCGTT	VQSTNGV	-	---
20787	36264	AGGTTAGAAGACGTCTTCCCG	RLEDVFP	-	---
21348	36604	GTGGCTCTTGAGGGGAGAGAT	VALEGRD	-	---
21580	36718	TACTTCACGGGAAAATTAGAA	YFTGKLE	-	--
32018	39203	TCATTAGAAAGCAGGGATTGG	SLESRDW	-	--
29509	12162	TCGGCATCAACTAATGGGAGG	SASTNGR	-	--
23533	36613	CGGGGTGAGACTGTGTACCCC	RGETVYP	-	--
29627	39545	CAGTTAGACTCAAGAGATTGG	QLDSRDW	-	--
21005	16158	GTCATGAGTACGAACGGTGTA	VMSTNGV	-	--
23551	12144	ACCGCCTCGACTAATGGAGTT	TASTNGV	-	--
22219	16584	CGAGGGATAGATTTCTATCCC	RGIDFYP	-	--
21859	36805	CGCGGGGAGTCAGTTTACCCC	RGESVYP	-	--
20578	36280	CTACATAAACTTTCTATCGAC	LHKLSID	-	--
24667	11423	ACTAAATCGACTAACGGGGTA	TKSTNGV	-	--
21006	18180	CTCTCCAAACTGTCACTTAAC	LSKLSLN	-	--
20653	36319	CGTGATGAAACGGTTTTCCCC	RDETVFP	-	---
21564	16017	TACGCGAAAGGTGGACCTAAT	YAKGGPN	-	--
33181	40800	AACTTAGAATCACGTGAATGG	NLESREW	-	--
21495	36687	GTAGCTGAGAAGGGGTGGGAT	VAEKGWD	-	---
21003	36443	CGCACTGACGATGTCTTCCCA	RTDDVFP	-	---
20924	16158	GTTATGAGCACAAACGGAGTA	VMSTNGV	-	--

23562	11720	TCAGAGAGTACTAATGGACGC	SESTNGR	-	--
20857	11947	CTGTCAAAACTTAACCTTAAC	LSKLNLN	-	--
22259	17025	GTCGAGAGCAGCAATGGTCGA	VESSNGR	-	--
23708	37487	AATGATGGCGTAAGCAAATGG	NDGVSKW	-	--
24518	11720	AGCGAATCCACGAATGGGAGG	SESTNGR	-	--
20611	36280	TTACATAAACTTTCAATAGAC	LHKLSID	-	--
22799	18036	ACCGACGAAACAGTGTACCGG	TDETVYR	-	--
21378	11927	TACAGTAAAGTGGGCGTGAAC	YSKVGVN	-	--
20712	36319	AGGGACGAGACCGTGTTTCCG	RDETVFP	-	---
21621	14018	TTCAGTAAATTGAATGTCAAC	FSKLNVN	-	--
24251	17025	GTTGAGTCATCTAACGGGAGA	VESSNGR	-	--
21012	36326	CTGTTTGACGGTACCGGGCCC	LFDGTGP	-	---
24230	12707	GTTGATTCCACCAACGGGCGT	VDSTNGR	-	---
20899	36285	TTGCACAAACTCTCGGTTGAT	LHKLSVD	-	--
25091	37964	GTGATGGAGTTCAATGCATTC	VMEFNAF	-	---
23007	18225	GACCTCGCCTCCTCGGCGTGG	DLASSAW	-	--
21932	36836	AGGACAGACGTAGTCTATCCG	RTDVVYP	-	--
20949	36402	CGCGGCCTAGAGGGATACGAT	RGLEGYD	-	--
20964	11522	GTAGAATCTACGAATGGTGTA	VESTNGV	-	---
21868	11996	ACAAGTTCTACCAACGGTGTA	TSSTNGV	-	--
22029	12190	GTTACCAGCACTAACGGTGTA	VTSTNGV	-	--
25748	37487	AACGATGGTGTTTCAAAGTGG	NDGVSKW	-	--
29266	17625	AAGATGGAGGCAATGACATGG	KMEAMTW	-	--
21019	36429	GTTAAGTCTACGAATGGTATC	VKSTNGI	-	--
21078	36319	AGAGATGAGACTGTGTTCCCC	RDETVFP	-	--
22182	12441	GTGGTTAGCACAAATGGGAGG	VVSTNGR	-	--
20529	36251	TTGCATAAACTCGGCGACAAC	LHKLGDN	-	---
23078	12006	TATGCGAAATCCGGAGCCAAC	YAKSGAN	-	--
22068	19906	GTTAGCGAGTTCACCACTTAT	VSEFTTY	-	--
35810	38273	TTGCACCGGTTACTTCCTAAT	LHRLLPN	-	--
20590	36280	TTGCACAAGCTAAGCATTGAT	LHKLSID	-	--
22764	37065	CCAATGGAGTCATTGAAATGG	PMESLKW	-	--
36135	41839	CGCACGCCCTGCCTCGGGCCA	RTPCLGP	-	--

21143	11522	GTGGAGAGTACTAACGGCGTA	VESTNGV	-	--
28464	39149	TGCGGTCCAGGCTGCTGTGAA	CGPGCCE	-	--
30159	18238	TGCGGCCCTAGAAACCCGGAA	CGPRNPE	-	--
24430	37714	TGCGCGCCCGACTATGAAGAG	CAPDYEE	-	---
21188	11522	GTCGAGAGCACCAATGGAGTA	VESTNGV	-	--
35841	41707	TTCGCCAAGTGCAACTATAAC	FAKCNYN	-	--
33427	40879	CCATGCCCGGTAAAGCCTGAC	PCPVKPD	-	--
33592	19612	TGTGGGCGCTCCGGAACCCAC	CGRSGTH	-	--
33288	38262	TATGAGAACGGTTGTAAGGAG	YENGCKE	-	--
35963	40995	AAAAATGACCATGTTAGGTGG	KNDHVRW	-	--
27507	38823	TGTAAGGAGGGGAGCGCATGG	CKEGSAW	-	--
35874	41724	TGCGCACCGTCGCTTCATGAG	CAPSLHE	-	--
35879	37433	TGTGGAACTAAGTGCTGTCCT	CGTKCCP	-	--
28019	39002	AAGGAAGAGTACTGTAAGCCC	KEEYCKP	-	--
27890	37251	GGTTCCGAGTTTAGTCGGTGG	GSEFSRW	-	--
30786	37513	GGAGGTGAGTTTTCGCGCTGG	GGEFSRW	-	---
29500	39497	GGTAGTGGGACGAAATGCGGA	GSGTKCG	-	--
29124	39372	TGTACGTACAAAACAGGCCAT	CTYKTGH	-	--
29319	17237	TGCACTAATAACGGGAATCGC	CTNNGNR	-	--
36203	41883	TGGTCTGCTATTACTTGCAAT	WSAITCN	-	--
36167	40009	GCTGGCTATGACCGCCACTGG	AGYDRHW	-	--
36116	41824	TACTGGCCAGGTTGTAAGGAA	YWPGCKE	-	---
36143	41847	TGCGCGCCGGATTACCGAGAT	CAPDYRD	-	--
35993	41027	TTCGCGCGTGCATGTCAAAAC	FARACQN	-	--
27939	38969	TACGCCAAACAGTCTCGAAAC	YAKQSRN	-	--
35919	16663	GAAATGGAATCGTTTAATTGG	EMESFNW	-	---
36136	41840	TACTCAAAATATAATTGTAAT	YSKYNCN	-	--
31806	14873	TACTCAAAGTTAAATAAAAAC	YSKLNKN	-	--
35920	41744	TGCGCTCCTCACTTGCATGAA	CAPHLHE	-	--
29934	39644	GAACGAAAAGTGCATCCACAA	ERKVHPQ	-	--
25061	37954	TGTGCTCCAGATTATCACGAG	CAPDYHE	-	--
29057	39351	GGATGTATGACAAAATGTGGG	GCMTKCG	-	--
22789	37164	GACATGGCCTCACAGCAATGG	DMASQQW	-	---

27748	17329	CAAACCGATTGTGTTAATCAG	QTDCVNQ	-	--
26264	38364	AGGGACGACTGGGTGAAGTGG	RDDWVKW	-	--
29862	39527	TACCATAGGCTCGATCCTAAC	YHRLDPN	-	--
29320	36317	TTGCATCGCCTTAACCCAGAC	LHRLNPD	-	---
32326	40491	TGTGTCGACAAGAGACATCCG	CVDKRHP	-	--
31317	40126	ATGACTGGCACTAGTTGCATG	MTGTSCM	-	--
35892	39154	GGATGCAGACCCCAGGCAGGA	GCRPQAG	-	--
31738	40279	GGGGGACCGTCATGCAAGCCA	GGPSCKP	-	--
36024	39164	TGTAAGCCACCCTCAGATATG	CKPPSDM	-	--
26313	38385	TACTCTCGCATTGGTCCTTGC	YSRIGPC	-	--
25255	38028	TGTGGCAAAATTAAGCCCGGA	CGKIKPG	-	--
27519	38828	GGGTCTGATTTCGTCAGGTGG	GSDFVRW	-	--
31285	39169	TATTGTAAAGACAACCGACCG	YCKDNRP	-	--
32032	40390	GAAGAGCCTGGGTGTAAGGAG	EEPGCKE	-	--
33959	40186	TGTAACAAGCCGTACACTGCC	CNKPYTA	-	--
29062	39356	GGCTGCAGGCCCGGTGACATT	GCRPGDI	-	---
28644	39214	ATTGCGGAGCGTGGATGCGCG	IAERGCA	-	--
30257	39761	CCCGAGGCAGGGTGTAAGGAT	PEAGCKD	-	--
29307	39434	TACCTAAAGTCACAATCCAAG	YLKSQSK	-	--
22295	36970	CCCATGGAGAGCCAAAAATGG	PMESQKW	-	---
36214	41889	CGGGACGAGTATACGAGCTTC	RDEYTSF	-	--
21602	36725	ATTATGGCCTCACAAACTTGG	IMASQTW	-	---
28676	38153	TGCAAGCCAATATGTTGTGAG	CKPICCE	-	--
34709	41377	ATGACGGGTAGTAGTTGTCTC	MTGSSCL	-	--
35968	36970	CCCATGGAATCACAGAAGTGG	PMESQKW	-	---
31011	40022	TGCAAGAGTGACAAAATCATG	CKSDKIM	-	--
33268	40834	TACGTTGCACAATGCCAAGTC	YVAQCQV	-	--
21461	36676	GTGAGTACCCATTGCAGGGCT	VSTHCRA	-	--
29535	38725	GTACCCGACTTTGTCCGTTAC	VPDFVRY	-	--
25027	37940	GAAATGACAAGCCATATGTGG	EMTSHMW	-	---
35093	41483	TGCAATTCTAAAACTGGGCAC	CNSKTGH	-	--
31464	40176	TGTAGACCGGGAACTCCTGGC	CRPGTPG	-	--
31848	36417	TGCAAACCGAGGGAGGGAACT	CKPREGT	-	--

24845	37877	TGCAAACCTGATGCTATAAGA	CKPDAIR	-	--
31883	17203	TGCGGCCGTGGGGCGGGAATA	CGRGAGI	-	--
30861	39464	TGTAAGCGCCAGAGTCCTGAG	CKRQSPE	-	--
35299	39565	TGTGGTAAGAGGGATCCTGAC	CGKRDPD	-	--
33099	17853	TGTGGCGAGGGAAGCAAAGCC	CGEGSKA	-	--
36149	17324	CTCGCCTATAACGTTTCAACA	LAYNVST	-	--
21693	18641	GTACTTTCCAGTACGACATGG	VLSSTTW	-	---
30599	39878	TATGCGCGCGGCTCATGCGAT	YARGSCD	-	--
31468	40177	TGCACCAGTGATACAGGGCAT	CTSDTGH	-	--
30417	19192	CTGGCTAGCGCCTGTCTCTCT	LASACLS	-	--
27795	38576	GGAAGTGAATACTTGACCTGG	GSEYLTW	-	--
23294	37338	AGGGACGAGTACAGTTCCTAT	RDEYSSY	-	---
31152	40073	TATTGGACGGGCTGCATGGAG	YWTGCME	-	--
31934	40353	ATTCCAAAAGGTCCCTGTGCG	IPKGPCA	-	--
29185	38274	CGCGATGATTACACGAGCTGG	RDDYTSW	-	---
35979	41771	GTTTCGACACATTGTGACGCG	VSTHCDA	-	--
29834	39608	ATGACGGGTATAAGCTGCTTA	MTGISCL	-	--
27871	38948	TGTAAGCGACAGTCGGAATGG	CKRQSEW	-	--
33183	40801	ATGAAGGGTAGTTGTGAACAA	MKGSCEQ	-	--
34871	41430	TGCACTTCGGAAACGGGGCAT	CTSETGH	-	--
32902	40698	TACTACGCGGGAAAATGTGCC	YYAGKCA	-	--
31947	40356	GTTAGTACTCACTGCGTAGCG	VSTHCVA	-	--
35978	17407	GGCCCCATAAATTGCAAATCA	GPINCKS	-	--
22543	37065	CCTATGGAATCGTTGAAATGG	PMESLKW	-	---
36042	41256	CGTCTCGAGTCTAGTCTTTGG	RLESSLW	-	--
36029	16663	GAGATGGAGAGCTTTAACTGG	EMESFNW	-	--
35722	41654	AAAGATGAATACATGGTATGG	KDEYMVW	-	--
34040	17325	TATTCGGGGCAAGGATGCGTA	YSGQGCV	-	--
32588	40579	TTTGACGGTTATTCCGCGTAC	FDGYSAY	-	--
26461	38454	CGAGATGAGTTTGTCACGTAC	RDEFVTY	-	--
30735	39925	TGTGCCCCTGACTATGTGGAG	CAPDYVE	-	--
33502	40911	TGCAAACCAGTCCCGCCAGAG	CKPVPPE	-	--
30996	17611	GGGTGCCGCCATGGAGACATA	GCRHGDI	-	--

31006	40020	ATGACGGGGACTTCTTGTCAG	MTGTSCQ	-	--
28292	39090	CAGCATCCAATATGTAAGCCT	QHPICKP	-	--
35863	39135	TTCTGCTCCACGAATGGCGTC	FCSTNGV	-	--
32319	40487	TTGCTGGCTTCGCAAACGTGG	LLASQTW	-	--
34380	19296	TGCGGCGAGGCCATCCTTATG	CGEAILM	-	--
34962	41452	TGCGATGGGTCCGCTAAAGCA	CDGSAKA	-	--
35967	40732	GGGGTAGGAACCAAATGTGGA	GVGTKCG	-	--
21824	36701	AGAGACGAGTTTACGTCGTTC	RDEFTSF	-	---
33975	16638	AATGAGGACTGGGTAAAATGG	NEDWVKW	-	---
20609	36260	TTGCATAAACTCTCGATGAAC	LHKLSMN	-	---
27723	38899	CGTGGTGAGTTTTCAACCTGG	RGEFSTW	-	--
34468	17355	TGTAACAAAACCTCTGTCACA	CNKTSVT	-	--
23300	37339	TCAATGGAGTCGCATGGTTGG	SMESHGW	-	---
25787	38205	CGCATGGAGAGCGTGATATGG	RMESVIW	-	--
25585	38150	ATAATGTCAAGTAAACTTTGG	IMSSKLW	-	---
22206	36939	AGAGAGGACTACGTACACTGG	REDYVHW	-	---
27216	36317	CTACACAGACTGAATCCTGAT	LHRLNPD	-	---
34642	41348	GTTCCAGAAGGATGCCACGGT	VPEGCHG	-	--
27118	38688	TGTAAACCCCCGAGTGACTAC	CKPPSDY	-	--
26917	38628	TGCGATGGCTCCCACAAGGCT	CDGSHKA	-	--
36221	41713	AAGGACGAGTATACTATGTAT	KDEYTMY	-	--
30279	38173	TTCGCGAAGCACGGATGTGGG	FAKHGCG	-	--
33205	40813	ACGGAGCCGGGGTGTAAAGAA	TEPGCKE	-	--
35445	17183	TATCAGAGACAGTGTGAATCA	YQRQCES	-	--
31675	18789	TCTGATGAATATTCAACCTAC	SDEYSTY	-	--
26357	36890	GTTATGAGTAGCCAATTGTGG	VMSSQLW	-	---
35658	39689	TGCAAGGACTCTGCCCGTTTG	CKDSARL	-	--
31650	40252	CCATGCAAACCCCAGCCGATG	PCKPQPM	-	--
35831	36317	CTCCACAGGCTAAATCCGGAT	LHRLNPD	-	---
20698	36339	ATTGCAACGTTGGGATGGGAT	IATLGWD	-	--
32957	17871	GCTCTCGGAGATCGGACGTGG	ALGDRTW	-	---
29801	39600	CCAGTCCCTGACTGTCTGGCG	PVPDCLA	-	--
22767	17493	GATTTATCGGATCGCCGGTGG	DLSDRRW	-	---

36047	18524	CATAAAGAGGGATGTGGCTTA	HKEGCGL	-	--
34624	41340	CGCGACGACTGGAGCACCTGG	RDDWSTW	-	--
30309	37057	TTGTATGATGGAACTAACGCG	LYDGTNA	-	---
22234	16600	CGGGCGCTCGAATGTTGTTAT	RALECCY	-	---
22459	37037	CTCTTGAGTAGCGCGAGCTGG	LLSSASW	-	--
31764	17912	GAGCTAGAGTCTTGGTCATGG	ELESWSW	-	--
21575	36529	ATCATGAGCAGTAATATCTGG	IMSSNIW	-	---
31000	40016	TGTAAGCCGCCGCCATTGCCC	CKPPPLP	-	--
24023	20420	ATTATGTCTAGTTCAGCCTGG	IMSSSAW	-	--
22982	37234	GGAAGCGACTATGTAGCGTGG	GSDYVAW	-	--
32619	37746	CGTGACGAGTTCTCTTCATGG	RDEFSSW	-	---
22882	37189	GCCCCCGGCTCTATTAAATGG	APGSIKW	-	--
25090	37963	CGTGGTATGGACGTATATCCA	RGMDVYP	-	--
31189	18883	TGCAAGGCAAATCGTGTTGAA	CKANRVE	-	--
26857	38608	AGGTTAGAGAGTTATGATTGG	RLESYDW	-	---
31203	40090	TGGACGCCTATCTGCAAAGCC	WTPICKA	-	--
25101	37967	CGCCTCGAGGCTGTCACATGG	RLEAVTW	-	--
28199	39062	CAAAGTCCTGGATGCAAAGAT	QSPGCKD	-	--
29001	39168	TTATTACAGTCGACGACCTGG	LLQSTTW	-	--
30425	38205	AGGATGGAATCGGTAATCTGG	RMESVIW	-	--
20558	36267	AGAGAAGACTTCGTGCAGTGG	REDFVQW	-	--
33406	39667	TACCATGCCAAATCACCATGC	YHAKSPC	-	--
27234	18354	GGGGATGAGTATCATTCGTGG	GDEYHSW	-	--
25858	16584	AGAGGCATTGACTTTTATCCA	RGIDFYP	-	--
23804	37521	TTATGCAAACCATGCTTAGTC	LCKPCLV	-	--
27444	14343	TATTCAAAGTTGAATTCCAAC	YSKLNSN	-	--
23720	17968	AGAGAGGATTTTAGTGCGTGG	REDFSAW	-	--
29000	37095	AAGGACGACTACACAGTTTTT	KDDYTVF	-	---
22766	36400	GAGGCACTCGAGGGACGGGAC	EALEGRD	-	--
21145	36339	ATCGCTACCCTCGGGTGGGAC	IATLGWD	-	---
22672	18074	TTGTTGCAAAGTAGTACATGG	LLQSSTW	-	--
23332	37353	GTGATGTTCGATGCTTATCCG	VMFDAYP	-	--
24079	37001	AGAATGGAAAGTGTAATGTGG	RMESVMW	-	---

35283	39609	TCTATGATGGATCGCTCGTGG	SMMDRSW	-	---
32264	17499	GTGATGGAAGCCAGAGCGTGG	VMEARAW	-	---
30821	39956	ATGCTCACTGGCAAGTGCGAA	MLTGKCE	-	--
26017	38281	AGAGATGACTACTCGACCTTT	RDDYSTF	-	--
28698	16638	AACGAAGATTGGGTCAAGTGG	NEDWVKW	-	--
29620	39543	AGTATGCAGGCCCGGTCTTGG	SMQARSW	-	--
26459	38453	GAACCAGAAAGCAGAGCCTGG	EPESRAW	-	---
25940	38141	CTGGAGGACTGGGTGAAATAC	LEDWVKY	-	--
27063	38670	TTGTGGGACGGAACTATGGCT	LWDGTMA	-	---
23396	17576	GTACTTTCGAGCAATGTCTGG	VLSSNVW	-	--
24160	36801	CGCGATGACTTTACCATGTAC	RDDFTMY	-	--
22378	37001	CGTATGGAGTCAGTCATGTGG	RMESVMW	-	--
21096	16074	TATAGTAAGCTCGGACTTAAC	YSKLGLN	-	--
36000	17619	CTGTTGTCAAGCCACGATTGG	LLSSHDW	-	---
24102	36808	CCGATGGAGTCTGTGAAATGG	PMESVKW	-	---
23267	37273	ATTATGGAAGCTCGAGATTGG	IMEARDW	-	---
28611	39207	ACCTGGATGGGCGATAACGCG	TWMGDNA	-	--
21836	36791	AGGGGGGACGATGTGTACCCG	RGDDVYP	-	--
22508	36791	CGCGGCGATGACGTCTATCCC	RGDDVYP	-	--
26510	37896	AAAGATGATTACAGTGCCTAT	KDDYSAY	-	--
24042	37599	GGTGAAGATCACGTACGCTGG	GEDHVRW	-	--
22525	36562	CGTACCGATCACGTTTTCCCC	RTDHVFP	-	---
28853	39286	GAACCCGAGTCGAGAGATTGG	EPESRDW	-	--
26696	38554	CGTATGGATGCCGTAACTTGG	RMDAVTW	-	--
28708	19561	GAGCTCGATTCTCGAGATTGG	ELDSRDW	-	---
20968	36461	AAGGATGAGTTTTCCACATGG	KDEFSTW	-	---
33241	19638	GAGCTTGGGTCGCATACGTGG	ELGSHTW	-	--
24499	37738	GACCTCTTATCTGCTAAGTGG	DLLSAKW	-	--
27329	38670	CTCTGGGATGGCACCATGGCC	LWDGTMA	-	--
22641	37109	CGGTCCGAGTTTGTGGTTTAT	RSEFVVY	-	--
22222	19710	ATTGAATCCAGAGAGGGGATA	IESREGI	-	---
21998	36846	CGCGAGGAGGACGTTTATCCG	REEDVYP	-	--
21775	11996	ACCTCGTCAACTAATGGCGTC	TSSTNGV	-	--

23450	37395	CGTTTGGAAAGTAGCGGCTGG	RLESSGW	-	--
22359	36610	ATCGAGTCCACGCACGGTCGA	IESTHGR	-	--
22594	36774	ATCTTAGCAAGCGCTACATGG	ILASATW	-	--
35353	41540	GAAATGGAGTCAGTAAAGTGG	EMESVKW	-	--
21993	19755	ATTATGGAGAGTGCTACGTGG	IMESATW	-	--
21604	17796	CTTAGTAGGGTAGGTCCTGAC	LSRVGPD	-	--
23069	11707	AGGGCATTAGAAGGCGCCGAC	RALEGAD	-	--
27914	18573	CGGGCATTGGATGGTTGGGAT	RALDGWD	-	--
20911	36433	TACTCGGCGATAGGACCCAAT	YSAIGPN	-	--
21861	19087	ACTTCAGAGAACGTCTACTTC	TSENVYF	-	---
26865	36757	CGTAGTGACTTTGTAGTCTAC	RSDFVVY	-	--
21622	17127	AAAATGAGCAGTTCAGTTTGG	KMSSSVW	-	--
20630	36308	AAGGACGAATTCACCACATTC	KDEFTTF	-	---
21633	19710	ATCGAGAGTCGCGAGGGCATA	IESREGI	-	---
22953	18385	ACAAGGGAAGGCGATCCTGCC	TREGDPA	-	--
22692	12206	GTAGACAGCACAAACGGCGTA	VDSTNGV	-	--
20733	16631	CTACATGTTCTCGGACCCAAC	LHVLGPN	-	--
27525	17485	AACGCCCTCGTGGGTCGGGAC	NALVGRD	-	--
21357	36630	AATTCTCTTGAAGGTAGAGAC	NSLEGRD	-	--
32926	40705	GCCGGCCCAGACCGCGGTTGG	AGPDRGW	-	--
25895	18225	GATTTAGCAAGTAGCGCCTGG	DLASSAW	-	--
21524	11974	GTGAGTAGCACCAATGGAATT	VSSTNGI	-	--
30601	38697	ATGTGGGACGGAACCATGGCG	MWDGTMA	-	--
22502	36887	CGAGAGGAAGGGGTGGCTTGG	REEGVAW	-	--
23892	11516	GCTGAGAGTACCAATGGCCGA	AESTNGR	-	--
22108	36856	TACTTTTCAGGGATTGTAGCC	YFSGIVA	-	--
22474	11408	GTTGTAAGCACAAACGGTGTG	VVSTNGV	-	--
35788	41678	TGCGCGTTGTATTTACACGAA	CALYLHE	-	--
22172	19543	GTTGCGACTGAAGGCAGAGAT	VATEGRD	-	--
21171	36549	TGTGGTAAACGTTGTGTGCCG	CGKRCVP	-	---
25413	17230	TCCTGTAAATCCTCTTACACA	SCKSSYT	-	--
21891	36816	CGGGACGAATTTACGGCTTGG	RDEFTAW	-	---
30315	17377	AGCTGCGATTCAGGAAAGGCT	SCDSGKA	-	--

24713	37825	TACTTTGCCGGCGTATGCCCA	YFAGVCP	-	--
35867	19043	CGTTGCCCTGACTGTCACCTA	RCPDCHL	-	--
35824	14324	TACAGTCGTGTGAACCCTAAC	YSRVNPN	-	--
28463	39148	TGCATGCCGTGTACTCCGTGT	CMPCTPC	-	--
30411	39819	TGTCGTCCCCCGGAGGTAGAG	CRPPEVE	-	--
35847	17179	TTAAAACTTTGTGCTCATAAC	LKLCAHN	-	--
25216	38016	GGTGGGGCGGGGTCTTGCTGG	GGAGSCW	-	--
28138	18651	TATGTTGCGGGATGCAAAGAA	YVAGCKE	-	--
28625	37095	AAAGACGATTATACAGTTTTT	KDDYTVF	-	---
35812	39946	AAATTTGATAATTGCGGATCC	KFDNCGS	-	--
31349	40138	GGGTGCCGTCATGGCGATGTT	GCRHGDV	-	--
35907	38482	TGCGGGAGCAAGACCGGTCAC	CGSKTGH	-	--
35890	41340	AGAGATGATTGGTCTACATGG	RDDWSTW	-	--
29084	39362	CTCTTTTCTGGACCTAAATGT	LFSGPKC	-	--
23733	37493	GACGACGGCGTAAGTAGATGG	DDGVSRW	-	--
22924	17725	GAGCCAGAGCGGGGTTGGTTC	EPERGWF	-	---
20843	36403	CGCACACCGCTCGTGTTCCCT	RTPLVFP	-	--
35973	37338	AGGGACGAATACTCCTCTTAT	RDEYSSY	-	---
34409	39966	AAGGACGACTACACAAGCTTT	KDDYTSF	-	--
24621	37789	TGCAAGACCACGAAGTGCTGC	CKTTKCC	-	--
21980	36858	TTATGTAAGCCGAGCCTTACC	LCKPSLT	-	--
22109	12737	ATCGAATCGACGAACGGGAGG	IESTNGR	-	--
25136	37981	AGCATGGAAAGTCATCAGTGG	SMESHQW	-	---
35910	40828	TGGTGGAGTGCTATTAGAGAG	WWSAIRE	-	--
28722	37568	CGTGACGAATTTACGTCATGG	RDEFTSW	-	---
35866	37095	AAGGATGACTACACTGTGTTC	KDDYTVF	-	---
36032	41786	TGCACATCGAAAACTAATCAT	CTSKTNH	-	--
32798	39962	TTTTTCACTGGATTCATTGAT	FFTGFID	-	--
29203	37981	TCTATGGAGTCACACCAATGG	SMESHQW	-	--
35917	38181	TACTTTACAGGAATGGTTGAT	YFTGMVD	-	--
35120	41121	CGGTCCGAGTACCACTTCCCT	RSEYHFP	-	--
22064	36890	GTCATGTCGTCACAGCTCTGG	VMSSQLW	-	---
29892	39628	CGTGCCTTTGACTCTTACCCA	RAFDSYP	-	--

35975	37338	CGAGATGAGTATTCAAGTTAC	RDEYSSY	-	---
35043	17966	GAGATGGCTGCTTACGATTGG	EMAAYDW	-	--
26816	38406	GGGGTCGAGACCTGTAAGCCA	GVETCKP	-	--
35940	16614	CATTGTGGCAAATGCCTGAAT	HCGKCLN	-	---
24506	37740	GCCCCCGAAAGCGTTCGGTGG	APESVRW	-	--
35897	17535	CGAATGGAAAGTAGTGTCTGG	RMESSVW	-	---
29737	38870	GGCAGTGAGTTTAGTACCTAC	GSEFSTY	-	--
23830	18231	CCACTGGACAGCTATAAATGG	PLDSYKW	-	---
35820	18133	AAAGACGACTACACAACTTTT	KDDYTTF	-	---
30258	17755	GTATTAGCGAGTGTCACTTGG	VLASVTW	-	--
21959	36843	CGAGACGAGTTCGTGAGTTAT	RDEFVSY	-	--
27379	19261	GACTTGGAAAGTTCGTACTGG	DLESSYW	-	--
25479	38110	AAGGATGATTGGACTCCATTC	KDDWTPF	-	--
24337	37679	GACATGGAAAGTCACAAGTGG	DMESHKW	-	---
20649	36317	CTACATCGCTTGAACCCCGAC	LHRLNPD	-	---
36001	39428	CGCAGCGAATTCATGGTCTAT	RSEFMVY	-	--
28201	38110	AAAGACGACTGGACCCCCTTT	KDDWTPF	-	--
33319	39779	CGCGGGCACGACGTTTTCCCG	RGHDVFP	-	--
32071	37339	AGCATGGAAAGCCACGGCTGG	SMESHGW	-	---
34705	17600	GTAGAGGCGAGTCGCAGTTGG	VEASRSW	-	---
33277	40315	GGAATAGATGTCGTACGATGG	GIDVVRW	-	--
23710	36599	CCGATGGAGAGCAGCAAGTGG	PMESSKW	-	---
23308	36791	AGGGGGGACGATGTTTACCCT	RGDDVYP	-	--
21262	17047	GTCCCCGGTGACTGTTGTGTG	VPGDCCV	-	---
24050	37606	GTTGACGAATATCTAAGCTGG	VDEYLSW	-	--
22201	36791	CGTGGCGATGACGTGTATCCA	RGDDVYP	-	--
35960	39951	GATCTCGAGAGTTACAAATGG	DLESYKW	-	--
35688	19638	GAACTCGGAAGTCACACCTGG	ELGSHTW	-	--
20600	17830	CGTTTGCTCGACGTGTATCCG	RLLDVYP	-	---
27262	37168	CGCACTTTCGATGTCTTCCCT	RTFDVFP	-	---
21857	12333	GTAAGTTCCACTAATGGAGTA	VSSTNGV	-	---
22002	11366	GTGAGTAGTTCAAATGGAGTA	VSSSNGV	-	--
26867	12441	GTAGTGTCCACCAACGGTCGC	VVSTNGR	-	--

26701	38557	TTATTGGCCTCTAGTAGCTGG	LLASSSW	-	--
22154	17801	CTATCCAAGGTAGGACATAAT	LSKVGHN	-	--
26590	16644	AGATTGTACGACGCATATCAA	RLYDAYQ	-	--
25900	17625	AAAATGGAAGCGATGACTTGG	KMEAMTW	-	--
21624	11707	CGCGCGCTCGAGGGGGCAGAT	RALEGAD	-	--
35782	16566	TATTTTACCGGAGTCGTTGCT	YFTGVVA	-	---
36101	41816	TGTAAAGATGGGTGCTGCTCT	CKDGCCS	-	---
22897	37195	ATTCCCCGTTTCTGTGCACCG	IPRFCAP	-	--
21238	17067	ATGTACAACGACTGTTGTGTG	MYNDCCV	-	--
27903	36516	CGTAATGAGTTCTGCACGTTC	RNEFCTF	-	--
24953	37918	TGCACGTCATTAACTGGACAT	CTSLTGH	-	---
23636	37462	TATAAGGGTAGCTGCGAACAG	YKGSCEQ	-	--
26438	38440	TATGAACCGAACTGCAAAGAG	YEPNCKE	-	--
34059	41127	TGCAAAATGTCTTGCCCTCTT	CKMSCPL	-	--
24278	17755	GTTCTTGCATCAGTGACCTGG	VLASVTW	-	--
30080	39698	CGCCCAGAGACATGCTCGCCG	RPETCSP	-	--
28184	37568	CGTGATGAATTCACAAGCTGG	RDEFTSW	-	---
26532	17874	CCCATGGCGAGTCTTCAATGG	PMASLQW	-	---
25463	36727	TTATGTAAACCTTGTATTACG	LCKPCIT	-	--
25212	18932	CTCCTCGCGTCCGCTACTTGG	LLASATW	-	--

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NT SEQ ID#	AA SEQ ID#	NT sequence	AA sequence	hCMEC transdu	hCMEC-hTFRC transduction
27334	14632	TACAGCAGAAT	YSRIGPN	+++	+++
21960	36844	CTCCACAGATT	LHRLSVN	+++	+++
20593	36268	TTACATAAGCT	LHKLSTN	+++	+++
20664	36292	TTGACCCGTTT	LTRLSPN	+++	+++
23859	16667	CTACACAGATT	LHRLAAN	+++	+++
22194	36936	TTGTGTAAGCC	LCKPCLN	+++	+++
21084	36437	TTGTGTAAGCC	LCKPCLD	+++	+++
20922	36437	CTATGCAAACC	LCKPCLD	+++	+++
20523	36247	CTGAGCAAGTT	LSKLSFN	+++	+++
22535	37062	TTACACAGGCT	LHRLSPN	+++	+++
20788	36344	TACAGCAAGGC	YSKAGGG	+++	+++
25816	14269	TATGCACGCAC	YARTGPN	+++	+++
23229	14269	TATGCGCGTAC	YARTGPN	+++	+++
22207	36834	CTCCACAGGCT	LHRLGPN	+++	+++
20661	36316	TTGCATGCTAA	LHAKLPN	+++	+++
20530	36252	TTGCACAAGTT	LHKLSVN	+++	+++
23056	14269	TACGCCCGAAC	YARTGPN	+++	+++
20568	36253	CTTCATAAACT	LHKLSPN	+++	+++
23039	14269	TACGCTAGAAC	YARTGPN	+++	+++
20706	36344	TATTCAAAAGC	YSKAGGG	+++	+++
21584	36382	TTATGCAAGCC	LCKPCLG	+++	+++
20603	36292	CTTACGAGGCT	LTRLSPN	+++	+++
22307	36975	CTCCATCGCCT	LHRLSTN	+++	+++
23447	37062	CTGCACCGCTT	LHRLSPN	+++	+++
20575	36278	CTCCACAAATT	LHKLSLN	+++	+++
25020	37938	AGGACGTACGA	RTYDSYP	+++	+++
21816	14461	TATTCCAAGCT	YSKLNYN	+++	+++
20714	36347	TTGAGTAGAAT	LSRIGPN	+++	+++
20583	36278	TTACATAAACT	LHKLSLN	+++	+++
20531	36250	TTGCATAAATT	LHKLTVN	+++	+++
20719	36347	CTATCCCGGAT	LSRIGPN	+++	+++
20542	36252	CTACATAAACT	LHKLSVN	+++	+++
25794	14059	TACAGCAGAGT	YSRVGPN	+++	+++
20580	36268	TTGCATAAGCT	LHKLSTN	+++	+++
20544	36261	TTGTCAAAGTT	LSKLSYN	+++	+++
25167	37910	TATAGCCGTGT	YSRVGGG	++	+++
24930	37910	TATAGTCGCGT	YSRVGGG	++	+++
20552	36243	CTCCACAAGCT	LHKLANN	++	+++
21280	36592	CTACATCGTTT	LHRLLPD	++	+++
20852	14274	TATGCTAAAAC	YAKTGPN	++	+++
31364	13535	TATAGTCGGCT	YSRLNNN	++	+++
21053	36459	CTCGCTAGATC	LARSGPN	++	+++

25365	14632	TACTCTCGGAT	YSRIGPN	++	+++
26814	13517	TACTCGAGACT	YSRLNIN	++	+++
20534	36243	TTACATAAGTT	LHKLANN	++	+++
20947	36442	CTGTCGCGTGT	LSRVGPN	++	+++
23413	36844	TTACATCGTCT	LHRLSVN	++	+++
20560	36269	TTAGCGAAGAC	LAKTGYN	++	++
26635	13517	TATAGCCGCTT	YSRLNIN	++	+++
29996	13517	TACTCCAGGTT	YSRLNIN	++	+++
26751	38571	CGCACATATGA	RTYDAYP	++	+++
20647	36316	CTACACGCCAA	LHAKLPN	++	+++
21330	16612	CTTTCGAGGGT	LSRVGFN	++	+++
20524	36246	TTACATAAATT	LHKLSIN	++	+++
20520	36246	CTGCACAAGCT	LHKLSIN	++	+++
21519	36697	TTCCACAAATT	FHKLSNN	++	++
20912	36347	CTCTCACGTAT	LSRIGPN	++	+++
25057	37910	TACTCCAGGGT	YSRVGGG	++	+++
27371	38380	TATTCACGGCT	YSRLSPN	++	+++
25845	38225	TATAGTCGCAT	YSRIGGG	++	+++
21843	36796	CTGAGCCGTTT	LSRLSPN	++	+++
23291	14290	TACAGCAAAGT	YSKVGYN	++	++
20543	36260	CTTCACAAATT	LHKLSMN	++	+++
20559	36268	CTGCACAAATT	LHKLSTN	++	+++
21927	36834	TTACATCGCTT	LHRLGPN	++	+++
24221	14958	TATAGCCGCAC	YSRTGPN	++	+++
25912	13864	TATGCCCGTTC	YARSGPN	++	+++
23899	37174	TTACATCGTCT	LHRLSSN	++	+++
28532	13517	TACAGTCGTCT	YSRLNIN	++	+++
25780	37938	CGAACCTATGA	RTYDSYP	++	+++
20861	36413	CTACATCGCTT	LHRLGPD	++	+++
30442	13816	TATAGTCGCCT	YSRLNPN	++	+++
21688	36619	CTTCATAGGCT	LHRLSDN	++	+++
22057	36753	TATCATAAACT	YHKLNSN	++	++
27532	38832	TATTCTCGTCT	YSRLSPT	++	++
26774	38461	TACCATAGATT	YHRLSPV	++	++
26307	38380	TACAGTAGGCT	YSRLSPN	++	+++
25253	37910	TACTCTAGGGT	YSRVGGG	++	+++
30515	13844	TACAGCCGGTT	YSRLNTN	++	+++
23714	14461	TACAGTAAATT	YSKLNYN	++	+++
20516	36243	CTTCATAAACT	LHKLANN	++	+++
31871	13510	TACAGTCGCCT	YSRLNYN	++	+++
20532	36248	ATAGCGTTAAA	IALKGWD	++	+++
28572	14303	TACTCACGATT	YSRLNEN	++	+++
20579	36281	CTTCACAAGTT	LHKLMPN	++	+++
20521	36247	CTATCTAAACT	LSKLSFN	++	+++
28384	14628	TATTCAAGGCT	YSRLNDN	++	+++

20605	36250	CTCCACAAATT	LHKLTVN	++ +++
20574	36243	TTGCATAAATT	LHKLANN	++ +++
22534	36796	CTTTCAAGGCT	LSRLSPN	++ +++
20594	36288	TTATCAAAACT	LSKLSPN	++ ++
28471	14350	TACTCCAGATT	YSRLNAN	++ +++
26939	38571	AGAACTTACGA	RTYDAYP	++ +++
22807	14259	TACTCAAAACT	YSKLNVN	++ +++
24135	14574	TACAGCCGTTT	YSRLGPN	++ +++
23987	14574	TATTCGAGGCT	YSRLGPN	++ +++
28336	38843	TATCACAGATT	YHRLSAN	++ ++
24870	37684	CTCTGCAGACC	LCRPCSD	++ +++
25955	14628	TATTCGCGTTT	YSRLNDN	++ +++
22881	36975	TTGCACAGATT	LHRLSTN	++ +++
28083	39022	TATAGTCGGCT	YSRLQMN	++ ++
21051	36497	TACACTAAAAC	YTKSQTN	++ ++
20622	36303	CTTCACAAGTT	LHKLQQN	++ +++
21548	36496	TATGTCAAGTC	YVKSDTR	++ +++
21142	36493	TTGTGTAAACC	LCKPCAT	++ +++
26782	14059	TACTCGCGTGT	YSRVGPN	++ +++
20959	17658	CTCCACAAACT	LHKLSNN	++ +++
27132	14190	TACTCCAGGGC	YSRAGPN	++ +++
23667	14958	TACTCGCGAAC	YSRTGPN	++ +++
22093	36495	CTTTCTCGCGT	LSRVSIN	++ ++
21796	14050	TACTCCAAGCT	YSKLNAN	++ +++
24213	16613	TATGCCCGCGC	YARGGPN	++ ++
21950	36840	TACCACAAGTT	YHKLNAN	++ +++
21168	36459	CTCGCACGTAC	LARSGPN	++ +++
30587	14243	TACAGCCGCCT	YSRLNSN	++ +++
22299	36825	CTGGCCCGTCA	LARQSYN	++ ++
20599	36291	TTAACTAAGTT	LTKLSPN	++ ++
20937	36445	TACCACGCTAA	YHAKLPN	++ +++
20888	36413	TTGCACAGACT	LHRLGPD	++ +++
20963	36459	CTAGCCAGATC	LARSGPN	++ +++
24154	17736	CTTCACCGATT	LHRLSVD	++ ++
26930	14190	TACAGTCGTGC	YSRAGPN	++ +++
20810	36387	TTCCACAAGTT	FHKLSPN	++ +++
20749	36305	CTGCATAAAGC	LHKAGPN	++ +++
21485	36682	CTGTGTAAGCC	LCKPCLS	++ +++
20772	14441	TACGCCAAAAC	YAKSGPN	++ +++
23652	13934	TTCGCTAGGAC	FARTGPN	++ ++
23735	14097	TACTCTAAGTT	YSKLNHN	++ +++
21772	14388	TATAGCAAGCT	YSKLNLN	++ +++
20563	36257	CTTCATAAGTT	LHKLSEN	++ +++
20576	36268	CTACACAAATT	LHKLSTN	++ +++
20934	36442	TTAAGTCGCGT	LSRVGPN	++ +++

24085	16613	TACGCTAGGGC	YARGGPN	++ ++
21338	36619	CTACACCGATT	LHRLSDN	++ +++
27121	14344	TATAGTAGGGT	YSRVGQN	++ ++
20626	36305	TTACACAAGGC	LHKAGPN	++ +++
28876	14048	TATGCTAGGAA	YARNGPN	++ +++
20553	36266	TTACACAAATT	LHKLMNN	++ +++
26804	13864	TACGCAAGGAC	YARSGPN	++ +++
21065	14040	TATAGTAAAGT	YSKVGPN	++ +++
20814	14005	TATTCAAAGTT	YSKLGPN	++ +++
27400	38753	TATCACCGCCT	YHRLSDN	++ ++
20612	36259	CTCCATAGACT	LHRLLDD	++ ++
20533	36253	TTGCACAAGTT	LHKLSPN	++ +++
22821	37174	CTCCACAGGCT	LHRLSSN	++ +++
26363	13928	TACGCCCGCAT	YARIGPN	++ +++
32320	13898	TATTCGCGCTT	YSRLNQN	++ ++
20812	14018	TTCAGCAAACT	FSKLNVN	++ ++
21098	36459	TTAGCACGTAC	LARSGPN	++ +++
21792	36540	CTGCACAAGAT	LHKMSMN	++ ++
21162	14343	TACAGCAAACT	YSKLNSN	++ ++
21110	16619	TTGCATAAAGC	LHKAGYN	++ ++
25300	16655	CTAAGTAGGAC	LSRSSYN	++ ++
26737	13874	TACAGCCGTTT	YSRLGLN	++ ++
30516	13543	TATTCGAGGTT	YSRLNFN	++ +++
28337	16577	TATTCGAGACT	YSRLNKD	++ ++
26403	14628	TACAGTCGCCT	YSRLNDN	++ +++
20587	36262	TTACACAAACT	LHKLAQN	++ +++
21309	36540	CTTCATAAAAT	LHKMSMN	++ ++
21343	15980	TTTTCTAAGTTC	FSKLNFN	++ ++
29118	13943	TATAGTCGGGT	YSRVGTN	++ ++
22416	36841	CTAAGTAGGAT	LSRISTN	++ ++
20588	36250	TTGCATAAGCT	LHKLTVN	++ +++
21825	13762	TTCAGTAAGTT	FSKLNYN	++ ++
25936	16655	TTGTCCCGATC	LSRSSYN	++ ++
30265	13844	TATTCTAGACT	YSRLNTN	++ +++
21820	36708	CTGACGAGACT	LTRLHID	++ ++
22090	16586	TACCACAAGTT	YHKLANN	++ ++
21072	36473	TATCACAAACT	YHKLGPQ	++ ++
22413	37019	CTGCACCGATT	LHRLTAD	++ ++
20592	36287	CTGGCAAAAAC	LAKSGPN	++ +++
21160	14040	TACTCAAAGGT	YSKVGPN	++ +++
22836	14200	TATAGCAAGTT	YSKLNFN	++ +++
30396	14301	TATAGTCGATT	YSRLNMN	++ +++
24856	37806	AGAACGTATGA	RTYDSFP	++ +++
29944	13898	TACAGCAGACT	YSRLNQN	++ +++
22292	14441	TATGCTAAAAC	YAKSGPN	++ +++

22284	36539	CTCCATAGACT	LHRLSAD	++ ++
20620	36301	TTTCACAAATT	FHKLGPD	++ ++
26341	16613	TATGCCAGAGC	YARGGPN	++ ++
21269	11397	CTTAGCAAGCT	LSKLNPN	++ ++
28666	13664	TACAGCCGTAT	YSRIGIN	++ ++
31099	14243	TATTCGCGGCT	YSRLNSN	++ +++
20546	36263	CTAACTCGCTT	LTRLSAN	++ ++
21017	14441	TACGCGAAGTC	YAKSGPN	++ +++
21111	14441	TATGCGAAGTC	YAKSGPN	++ +++
20820	36394	TACAGCAAGCT	YSKLQAN	++ ++
22619	36839	CTGCACCGCTT	LHRLQDN	++ +++
21615	36496	TATGTCAAGTC	YVKSDTR	++ +++
22063	36682	CTATGCAAACC	LCKPCLS	++ +++
22690	36778	TATCACAAATT	YHKLNNN	++ +++
30837	13818	TACTCCCGACT	YSRLNVN	++ +++
26418	14378	TATAGCCGGGT	YSRVGAN	++ ++
27696	13818	TATAGCAGGCT	YSRLNVN	++ +++
20527	36250	CTTCACAAGCT	LHKLTVN	++ +++
22175	17681	CTCTCACGGGT	LSRVGQN	++ ++
20549	36265	CTCCATAAGTT	LHKLSFD	++ ++
21260	16013	TATAGCAAGAC	YSKTGPN	++ ++
21371	36640	CGCTTGATGGA	RLMDAYP	++ +++
29021	14378	TACTCAAGAGT	YSRVGAN	++ +++
21255	36464	AAAGACGATTT	KDDFTHF	++ +++
21791	36778	TACCATAAGCT	YHKLNNN	++ +++
28235	14399	TATGCTAGGAC	YARTGNN	++ ++
20895	13777	TACGCGAAAAT	YAKIGPN	++ ++
21027	36486	AGGACAGAAAC	RTETVYP	++ ++
25571	16613	TACGCACGGGC	YARGGPN	++ ++
22728	13526	TACTCGAAGCT	YSKLNNN	++ +++
22519	36991	TTGTCGCGGAC	LSRTSLN	+ ++
20677	36330	TATTCTAAACT	YSKLNPL	+ ++
21977	36778	TACCACAAGTT	YHKLNNN	+ +++
27564	38843	TATCACAGGTT	YHRLSAN	+ ++
30955	13535	TATTCGCGATT	YSRLNNN	+ +++
20805	14176	TACAGTAAGAT	YSKIGPN	+ +++
21154	14060	CTTCACGCGGC	LHAALPN	+ +++
25743	14861	TACTCGCGTCT	YSRLGVN	+ ++
20796	11154	CTTTCAAAACT	LSKLGPN	+ ++
20680	36291	CTGACCAAACT	LTKLSPN	+ ++
21082	14054	TTAGCCAAGAC	LAKTGPN	+ ++
27909	38753	TATCACAGGCT	YHRLSDN	+ +++
21049	36496	TACGTTAAAAC	YVKSDTR	+ +++
20715	36331	CTCGCCAGGCT	LARLGPN	+ ++
22950	14200	TACTCAAAACT	YSKLNFN	+ +++

28342	14301	TATAGTAGACT	YSRLNMN	+ +++
29096	13816	TATTCAAGACT	YSRLNPN	+ +++
27150	13930	TATGCTCGTAC	YARTGLN	+ ++
20958	36456	TACGTAAAGTC	YVKSDKM	+ ++
26234	14122	TACGCACGCAC	YARTGVN	+ ++
29639	13848	TACTCACGGCT	YSRLNLN	+ +++
22559	37075	TTATCACGCGT	LSRVSVN	+ ++
30803	39375	AGGACTTACGA	RTYDSYA	+ ++
20590	36280	TTGCACAAGCT	LHKLSID	+ ++
21115	14176	TATTCCAAAAT	YSKIGPN	+ +++
30714	14350	TATTCACGACT	YSRLNAN	+ +++
20840	17658	TTACATAAGCT	LHKLSNN	+ +++
30456	14585	TATTCACGACT	YSRLGNN	+ ++
26224	13580	TACTCGCGTGT	YSRVGIN	+ ++
20637	36295	ATGCATAAGTT	MHKLSPN	+ +++
27011	38654	TACAGCCGCAT	YSRISPN	+ ++
27237	14145	TATGCCCGCAC	YARTGTN	+ ++
22500	36825	CTGGCCCGTCA	LARQSYN	+ ++
28731	13990	TACGCGCGGCA	YARQGPN	+ ++
20902	36387	TTTCATAAACT	FHKLSPN	+ +++
27282	14344	TATTCCAGAGT	YSRVGQN	+ ++
28753	14301	TACTCACGGCT	YSRLNMN	+ +++
24530	37750	CTTTGTCGACC	LCRPCSN	+ +++
20573	36277	CTTCACAAGTT	LHKLSPL	+ ++
22831	37140	TTAAGCAGAGT	LSRVGRD	+ ++
23214	13934	TTTGCGCGTAC	FARTGPN	+ ++
20781	36378	TTATCTAGAGT	LSRVGLN	+ +++
20528	36251	CTTCACAAATT	LHKLGDN	+ +++
30106	14303	TACAGCAGGCT	YSRLNEN	+ +++
20705	36343	TATGTCAAGAC	YVKSQTN	+ ++
21232	36566	TATACGAAGCT	YTKLSPN	+ ++
23128	36831	CTCAGCAGAAT	LSRISFN	+ +++
21279	36496	TACGTGAAGTC	YVKSDTR	+ +++
36102	13745	TACAGTCGTGT	YSRVGYN	+ +++
20597	14198	TATGCTAAGAA	YAKNGPN	+ +++
27517	38827	TACCACCGCCT	YHRLSIN	+ ++
20891	36426	TATGTTAAATC	YVKSDMK	+ ++
27628	38727	TACAGCCGTCT	YSRLHAN	+ ++
27749	38843	TACCATCGCCT	YHRLSAN	+ ++
20780	36328	AAAGACGACTT	KDDFTSF	+ ++
20624	36294	TTGCACAAGCT	LHKLSHD	+ ++
20642	36303	TTGCATAAACT	LHKLQQN	+ +++
23187	37302	CGTCTTCACGA	RLHDAYP	+ ++
20880	36385	TACCACAAGCT	YHKLNPD	+ +++
27850	14048	TACGCACGTAA	YARNGPN	+ +++

20727	36286	TTACATAAGTT	LHKLNNN	+ ++
23387	36971	AGGGACGAGTT	RDEFTSY	+ +++
20927	36438	CTGTGCAAGCC	LCKPCPT	+ +++
26026	13589	TTCAGCCGTGT	FSRVGPN	+ ++
24501	17681	CTGAGTCGCGT	LSRVGQN	+ ++
21903	36489	TACGTCAAGAC	YVKSDMR	+ ++
20794	36382	CTCTGTAAACC	LCKPCLG	+ +++
29802	14479	TACAGTCGTAT	YSRIGNN	+ ++
20604	36257	CTTCATAAATT	LHKLSEN	+ +++
27825	14344	TACAGTCGTGT	YSRVGQN	+ ++
24558	13928	TATGCACGTAT	YARIGPN	+ ++
20774	36374	CTGTCGAAGTT	LSKLHTN	+ ++
27255	38727	TATAGTAGATT	YSRLHAN	+ ++
27553	38724	TATTCCCGCTT	YSRLNYD	+ ++
21421	14289	TATTCAAAACT	YSKLNMN	+ +++
28416	13580	TACTCACGCGT	YSRVGIN	+ ++
31023	14301	TACTCACGCCT	YSRLNMN	+ +++
22270	36964	AGGGGTGAGTT	RGEFVYP	+ ++
21289	36496	TACGTAAAAAC	YVKSDTR	+ +++
22355	36991	CTCAGTCGTAC	LSRTSLN	+ ++
21437	36603	CGTACAGAGCA	RTEHVFP	+ ++
28794	14010	TATAGCAGAGT	YSRVGLN	+ ++
21427	36347	CTGAGTAGAAT	LSRIGPN	+ +++
21595	36723	CTCCATAGATT	LHRLGDN	+ +++
22185	36932	TATCATAAGTT	YHKLNHN	+ ++
22871	37187	CTGTCGCGCAT	LSRISPN	+ ++
27991	14321	TTTAGTCGGCT	FSRLNNN	+ ++
22113	14327	CTTAGTAGGTT	LSRLNDN	+ ++
22697	36968	CGCATGCCAGA	RMPDAYP	+ ++
20525	36249	CTGTCGAAACT	LSKLSIN	+ +++
29871	13751	TATAGTCGGGT	YSRVGNN	+ ++
28104	13939	TATTCTCGGAT	YSRIGTN	+ ++
30085	13848	TATAGCAGACT	YSRLNLN	+ +++
29263	14593	TACAGCAGGAC	YSRSGPN	+ ++
20617	36251	TTACATAAGCT	LHKLGDN	+ +++
22987	37235	TTGTCAAGAGT	LSRVSPN	+ ++
21653	36539	TTGCACAGGTT	LHRLSAD	+ ++
20538	36257	TTGCACAAACT	LHKLSEN	+ +++
27967	38980	TACCATAGGCT	YHRLGQN	+ ++
21877	36778	TATCATAAACT	YHKLNNN	- +++
29526	14115	TACAGCCGAGT	YSRVGSN	- ++
22183	36931	CGGGATGAGTT	RDEFHSY	- ++
28139	14262	TACAGCCGGAT	YSRIGAN	- ++
27445	38712	TACCATCGTTT	YHRLSEN	- ++
20545	36262	CTTCACAAGTT	LHKLAQN	- +++

20962	36458	TACGTAAAAAC	YVKSDSR	-	++
21829	36723	TTGCACCGGCT	LHRLGDN	-	+++
20916	36418	CTTCATAAAAA	LHKKGPD	-	++
21755	36723	CTCCACAGGCT	LHRLGDN	-	+++
23289	37235	CTATCAAGGGT	LSRVSPN	-	++
22061	36738	AGGATGATTGA	RMIDAYP	-	++
25476	13580	TATAGCAGAGT	YSRVGIN	-	++
27355	38764	TATCACCGATT	YHRLGDN	-	++
28492	13943	TACTCACGAGT	YSRVGTN	-	++
22609	15977	TACTCAAAGGC	YSKANLN	-	++
21554	36523	TATCATAAACT	YHKLNDN	-	+++
20827	14018	TTTTCGAAGCT	FSKLNVN	-	++
22597	36840	TATCATAAACT	YHKLNAN	-	+++
20581	36258	TATAGCAAATT	YSKLGPD	-	++
28821	14344	TACAGTCGGGT	YSRVGQN	-	++
21186	36553	TTATGCAAACC	LCKPCQT	-	++
23964	37580	TATTCGCGATT	YSRLSPD	-	++
20675	36312	ATGCACAAACT	MHKLSVN	-	++
27622	38863	TACTCCAGATT	YSRLQSN	-	++
28657	38980	TATCACCGCTT	YHRLGQN	-	++
23305	37235	TTGAGCCGTGT	LSRVSPN	-	++
20961	16619	TTGCATAAGGC	LHKAGYN	-	++
21523	36640	AGGCTCATGGA	RLMDAYP	-	+++
21873	14198	TACGCAAAAAA	YAKNGPN	-	+++
21252	36496	TATGTAAAAAC	YVKSDTR	-	+++
25510	14858	TATGCCCGTGC	YARAGPN	-	++
25576	16630	CTAAGTAGGTT	LSRLNHN	-	++
20957	36455	GATATGGCATC	DMASKTW	-	++
23234	14079	TATTCCAAACT	YSKLNQN	-	++
20923	14060	TTACATGCTGC	LHAALPN	-	+++
20681	36331	TTAGCGCGATT	LARLGPN	-	++
28096	38654	TACTCGAGAAT	YSRISPN	-	++
21042	36493	CTATGCAAGCC	LCKPCAT	-	++
21362	14581	TATAGTAAGCT	YSKLNDN	-	+++
21120	36395	TTGACCAGACT	LTRLHPD	-	+++
25252	37649	TATAGTCGTCT	YSRLNPD	-	+++
20606	36293	CTACACAAATT	LHKLNPD	-	++
26679	38545	TATAGTAGGGT	YSRVQPN	-	++
25022	37939	CGGAATGAATT	RNEFTTY	-	++
21151	36458	TATGTCAAGTC	YVKSDSR	-	++
21388	14274	TATGCAAAGAC	YAKTGPN	-	+++
21966	36848	TATGCGAGGAC	YARTGPD	-	++
21599	36652	TTAGCCAGGAC	LARTGMN	-	++
20613	36295	ATGCACAAACT	MHKLSPN	-	++
22401	36495	TTGAGTAGGGT	LSRVSIN	-	++

28140	38727	TACTCGCGTCT	YSRLHAN	- ++
28986	38654	TATAGTCGTAT	YSRISPN	- ++
26842	14628	TATAGTCGTTT	YSRLNDN	- +++
28244	38712	TACCACCGGTT	YHRLSEN	- ++
21675	14290	TATTCGAAAGT	YSKVGYN	- ++
32534	16636	TATCATAGGCT	YHRLSNN	- ++
24599	37641	AGGAGCGAATT	RSEFTTY	- ++
27090	14264	TATGCACGGAC	YARTGAN	- ++
25110	37653	TATTCAAGGCT	YSRLNED	- ++
21934	36688	CTATGTAAGCC	LCKPCST	- ++
20598	36281	TTGCATAAACT	LHKLMPN	- +++
20602	36257	TTACACAAGCT	LHKLSEN	- +++
27836	38764	TACCATAGGCT	YHRLGDN	- ++
25240	37831	TATTCCCGACT	YSRLQDN	- ++
29957	13739	TATAGCCGTAT	YSRIGMN	- ++
21345	14379	TATTCAAAAGC	YSKAGPN	- ++
28116	13901	TACTCAAGAGT	YSRVGMN	- ++
21034	36489	TATGTGAAATC	YVKSDMR	- ++
25391	13874	TATAGTAGATT	YSRLGLN	- ++
23081	37063	CTGAGCAGAAC	LSRTSHN	- ++
24664	37806	CGGACCTACGA	RTYDSFP	- +++
20644	36251	CTTCACAAATT	LHKLGDN	- +++
22588	37075	CTCAGTAGAGT	LSRVSVN	- ++
22826	37118	CTCCATAGGCT	LHRLTED	- ++
20741	36288	CTGAGCAAGTT	LSKLSPN	- +++
21643	14207	TACTCAAAGCT	YSKLNTN	- +++
23016	37248	TTCCACCGGTT	FHRLGPD	- +++
21043	36431	GTGGAAAGTAC	VESTNGR	- ++
27779	38843	TACCATCGGCT	YHRLSAN	- ++
22436	36841	CTCAGTCGCAT	LSRISTN	- ++
32571	13715	TATAGCAGGTT	YSRLNHN	- ++
20522	36248	ATAGCATTGAA	IALKGWD	- +++
22444	36793	CTCAGTCGGAC	LSRTSVN	- ++
22067	11043	CTCAGCAAATT	LSKLNSN	- ++
21366	36539	CTACACCGACT	LHRLSAD	- +++
29114	39353	TACTCCCGCAT	YSRIQPN	- ++
24777	37854	TACGTAAGGTC	YVRSDTK	- ++
25316	16667	TTGCACCGGCT	LHRLAAN	- +++
20992	36416	AAGGATGATTT	KDDFTSW	- +++
28227	13851	TATGCACGGAC	YARTGFN	- ++
23290	37197	CGTGACGAATT	RDEFSTY	- ++
27501	13948	TTCAGTAGATT	FSRLNAN	- ++
24429	13623	TTCAGTCGCAT	FSRIGPN	- ++
21732	36540	CTTCACAAAAT	LHKMSMN	- ++
20670	16575	CTATCTAAGCT	LSKLSAN	- ++

21683	36744	CGGATGTTGGA	RMLDAYP	-	++
29817	38753	TATCATCGCCT	YHRLSDN	-	++
20601	36259	TTACATCGTTT	LHRLLDD	-	+++
21083	36511	AAGTCGGAGTT	KSEFTTY	-	++
20596	36290	TTACATAAATT	LHKLSPD	-	++
28479	14010	TACTCGCGGGT	YSRVGLN	-	++
29787	13828	TATGCGCGAAC	YARSGYN	-	++
28084	13930	TACGCTAGAAC	YARTGLN	-	++
23712	37488	TATTCCAGGGT	YSRVGPD	-	++
27326	38753	TACCATCGGTT	YHRLSDN	-	++
22439	37030	CTACACCGTCT	LHRLSQD	-	++
26725	16577	TACAGCCGTTT	YSRLNKD	-	++
20652	36258	TATAGCAAGCT	YSKLGPD	-	++
22870	37186	CTTCACAGATT	LHRLQST	-	++
20571	36275	CTTCATAAGCT	LHKLGEN	-	+++
21031	36330	TACAGCAAGCT	YSKLNPL	-	++
21435	36458	TATGTCAAATC	YVKSDSR	-	++
21531	36697	TTTCACAAGCT	FHKLSNN	-	++
26097	13636	TATGCACGGAC	YARTGIN	-	++
29885	14282	TTCAGCAGGCT	FSRLNTN	-	++
21237	36497	TATACGAAGTC	YTKSQTN	-	++
20561	36248	ATCGCCCTCAA	IALKGWD	-	+++
31566	38654	TACTCAAGAAT	YSRISPN	-	++
23673	37235	TTGTCTCGTGT	LSRVSPN	-	++
29323	13857	TATGCTAGGTC	YARSGFN	-	++
24166	37641	AGATCAGAGTT	RSEFTTY	-	++
23392	14327	CTATCGCGACT	LSRLNDN	-	++
20878	36420	AAAGATGATTT	KDDFTVY	-	+++
23823	37530	TATCTAAAATC	YLKSQTY	-	++
21257	14379	TATAGCAAGGC	YSKAGPN	-	++
25421	37930	TATTGGAGCGC	YWSGIKD	-	++
21573	36563	ATGCATCGCCT	MHRLLPD	-	++
21198	14005	TATAGTAAACT	YSKLGPN	-	+++
28304	13688	TTCTCACGCCT	FSRLNVN	-	++
28793	39265	TACAGTCGACT	YSRLSDN	-	++
24205	37641	AGGAGCGAATT	RSEFTTY	-	++
23603	14050	TATAGTAAACT	YSKLNAN	-	+++
20887	13938	TACAGTAAGAT	YSKMGPN	-	++
21989	14388	TACTCTAAATT	YSKLNLN	-	+++
27453	14216	TATGCGAGGTC	YARSGAN	-	++
21510	14290	TACAGCAAGGT	YSKVGYN	-	++
27506	14443	TATAGTAGGAT	YSRIGLN	-	++
21832	36788	CTCCACAGGTT	LHRLTTD	-	++
29095	14115	TATTCAAGGGT	YSRVGSN	-	++
23206	37235	CTCAGCCGGGT	LSRVSPN	-	++

29067	14136	TATAGCCGCCT	YSRLGAN	- ++
21946	36839	TTACATAGACT	LHRLQDN	- +++
24809	37863	TATTCCCGGCT	YSRLNLD	- ++
29239	14083	TATTCACGTGT	YSRVGVN	- ++
31046	13772	TACAGCAGGCA	YSRQGPN	- ++
27630	14010	TACTCCCGAGT	YSRVGLN	- ++
22504	12333	GTGTCGAGTAC	VSSTNGV	- ++
20562	36261	CTAAGCAAACT	LSKLSYN	- +++
25374	37641	CGATCAGAATT	RSEFTTY	- ++
28016	38727	TATTCTAGGCT	YSRLHAN	- ++
21328	36596	TATAGTAAATT	YSKLDRN	- ++
22338	36554	TTACACAGATT	LHRLSID	- +++
22637	36971	AGGGATGAATT	RDEFTSY	- +++
24954	37824	TACAGTCGGGT	YSRVGEN	- ++
27193	14344	TACTCCCGAGT	YSRVGQN	- ++
21297	36603	CGTACAGAGCA	RTEHVFP	- ++
28848	13948	TTTTCGCGTCT	FSRLNAN	- ++
31910	13830	TATTCTAGAGT	YSRVGHN	- ++
20556	36265	TTGCACAAACT	LHKLSFD	- ++
29139	14098	TATAGTCGAGT	YSRVGFN	- ++
21313	36592	TTGCACAGATT	LHRLLPD	- +++
20554	36249	TTAAGTAAGCT	LSKLSIN	- +++
22455	37019	CTACATAGGCT	LHRLTAD	- ++
21821	13537	TACAGCAAGCT	YSKLNIN	- +++
28877	14444	TACGCTAGATC	YARSGNN	- ++
21558	36695	AGAGGTCCCGA	RGPDVYP	- ++
22228	16134	GTTCACAGTAC	VHSTNGI	- ++
21676	36741	TATCATAAACT	YHKLNEN	- +++
21679	36723	TTGCATCGCTT	LHRLGDN	- +++
30086	14620	TACTCACGCAT	YSRMGPN	- ++
26386	38420	TATGTCCGCAC	YVRSDTR	- ++
21517	36486	CGAACTGAGAC	RTETVYP	- ++
28709	14620	TATTCTAGAAT	YSRMGPN	- ++
21215	36565	TTGACTAGGTT	LTRLHAD	- ++
26251	38254	TATTCGAGGCT	YSRLNDP	- ++
22143	14207	TATAGTAAACT	YSKLNTN	- +++
21849	36563	ATGCACAGATT	MHRLLPD	- ++
20720	17701	GTCGCTCTTAA	VALKGWD	- ++
22163	36640	CGCTTAATGGA	RLMDAYP	- ++
21108	36523	TACCACAAGTT	YHKLNDN	- +++
21748	14807	TACTCCAAGCA	YSKQGPN	- ++
24240	37653	TACAGCCGATT	YSRLNED	- ++
28969	39322	AAAGATGAGTT	KDEFTVY	- +++
24317	37655	TATCACAGGCT	YHRLLPD	- ++
21711	36753	TACCACAAGCT	YHKLNSN	- ++

28351	13688	TTTAGCCGTTT	FSRLNVN	-	++
28521	38690	AGGACATTCGA	RTFDAYP	-	++
26675	14122	TATGCTAGGAC	YARTGVN	-	++
21014	36390	AAGGACGAGT	KDEFSTY	-	++
22288	36968	CGAATGCCCG	RMPDAYP	-	++
30829	14531	TACTCTCGGAA	YSRNGPN	-	++
22162	36894	CTTCATAGAGC	LHRAGPD	-	++
29883	13580	TACAGTAGAG	YSRVGIN	-	++
21639	36615	AGGGATGAATT	RDEFTTY	-	++
23067	36766	AGGGATGATTT	RDDFTTW	-	++
20906	36390	AAAGACGAAT	KDEFSTY	-	++
29577	13553	TATGCTAGAAC	YARTGYN	-	++
25360	37939	AGAAACGAGT	RNEFTTY	-	++
31547	14585	TACAGCAGGC	YSRLGNN	-	++
30723	13772	TATTCGCGGCA	YSRQGPN	-	++
21690	36458	TACGTGAAGAC	YVKSDSR	-	++
29133	39375	CGTACGTATGA	RTYDSYA	-	++
23626	37295	CGCGACGATTT	RDDFTVW	-	++
27245	38724	TACAGTAGACT	YSRLNYD	-	++
28587	14262	TATTCTAGAAT	YSRIGAN	-	++
20540	36258	TATTCTAAATT.	YSKLGPD	-	++
20815	36390	AAGGATGAATT	KDEFSTY	-	++
23005	37197	CGTGATGAATT	RDEFSTY	-	++
21038	36420	AAGGACGACT	KDDFTVY	-	++
22784	37030	TTACACCGGCT	LHRLSQD	-	++
24038	37580	TACAGTAGACT	YSRLSPD	-	++
20529	36251	TTGCATAAACT	LHKLGDN	-	+++
20746	36286	CTTCATAAATT	LHKLNNN	-	++
25991	38273	CTCCATAGACT	LHRLLPN	-	+++
24850	37622	AGGATGCAAG	RMQDAYP	-	++
20872	36416	AAAGATGATTT	KDDFTSW	-	+++
29207	13901	TATTCCCGTGT	YSRVGMN	-	++
33404	17511	TGCATGAGTGA	CMSDKRA	-	++
21631	14036	TACTCGAAGCT	YSKLNPN	-	+++
20609	36260	TTGCATAAACT	LHKLSMN	-	+++
21374	36563	ATGCACAGATT	MHRLLPD	-	+++
22782	36985	TTACACAGGTT	LHRLLPV	-	++
26995	38011	CGCGACGAATT	RDEFTRW	-	++
20629	11154	TTAAGCAAATT	LSKLGPN	-	++
20979	36416	AAAGACGACT	KDDFTSW	-	+++
25522	37081	CTGCACAGATT	LHRLSYD	-	++
24841	37693	CGGGACGAATT	RDEFTVY	-	++
21569	14036	TATAGTAAATT	YSKLNPN	-	+++
20733	16631	CTACATGTTCT	LHVLGPN	-	++
21518	16013	TACTCAAAAAC	YSKTGPN	-	++

22196	36788	CTACATCGCCT	LHRLTTD	- ++
27551	14192	TTCTCGCGTCT	FSRLNIN	- ++
21150	36491	TTAGCACGCAC	LARTGLN	- ++
24150	13998	TACTCAAAAAT	YSKMNMN	- ++
20640	36301	TTCCATAAGCT	FHKLGPD	- ++
22627	13981	TACTCGAAAAT	YSKIGLN	- ++
23489	37277	TATGTTAGATC	YVRSDKN	- ++
23424	37302	CGTCTTCATGA	RLHDAYP	- ++
20673	36328	AAAGATGATTT	KDDFTSF	- ++
30029	13640	TACAGCCGCAT	YSRIGYN	- ++
21306	36426	TACGTCAAGAC	YVKSDMK	- ++
23629	16620	CTGAGTAGAAT	LSRISVN	- ++
27194	38712	TATCATAGACT	YHRLSEN	- ++
24086	37617	CATTCACGAAT	HSRIGPN	- ++
32332	39103	AAAGACGAATT	KDEFTIY	- ++
29197	13720	TTCTCGAGGCT	FSRLNMN	- ++
23406	14860	CTCAGCCGCAC	LSRTSTN	- ++
22780	17687	GTTAGGAGTAC	VRSTNGV	- ++
20824	36395	CTTACGCGGTT	LTRLHPD	- +++
21428	18591	TTAACCAGGTT	LTRLSPD	- ++
21247	16018	TACTCCAAAAA	YSKNGPN	- ++
29498	13841	CTACATCGAAT	LHRMTPN	- ++
21175	36328	AAGGACGACTT	KDDFTSF	- ++
22561	18663	CTAGCCCGTAC	LARTALN	- ++
20956	36378	CTGAGCCGTGT	LSRVGLN	- ++
22345	14289	TACAGCAAATT	YSKLNMN	- ++
21778	36534	TTGCACAGGTT	LHRLSLD	- ++
21660	16017	TATGCCAAGGC	YAKGGPN	- ++
27020	37810	TATTCGCGTTT.	YSRLQPL	- ++
21409	36652	CTCGCGCGAAC	LARTGMN	- ++
20817	36391	TTCCATAAATT	FHKLSLN	- ++
21634	36649	AGGTTAATGGA	RLMDVYP	- ++
21793	16568	TTGCACAGATT	LHRLLKD	- ++
20547	36259	CTCCACCGGCT	LHRLLDD	- ++
22296	36971	CGAGATGAATT	RDEFTSY	- +++
23686	14367	TTCTCAAGGCT	FSRLGPN	- ++
20682	36274	TTGTCGAGAAT	LSRIGPD	- ++
20684	11947	CTGAGTAAGTT	LSKLNLN	- ++
28679	14495	CGCCTTTACGA	RLYDAYE	- ++
21112	36484	ATGTTCGATGG	MFDGTAA	- ++
20904	36431	GTAGAGTCAAC	VESTNGR	- ++
25924	38254	TACAGCAGATT	YSRLNDP	- ++
28839	14264	TACGCCCGCAC	YARTGAN	- ++
22666	37029	CGCTCGGAATT	RSEFVSY	- ++
25376	37562	ATGCATAGACT	MHRLSTN	- ++

24350	13623	TTTTCAAGAAT	FSRIGPN	- ++
22262	36635	TACGTGAAAAC	YVKSDRM	- ++
20696	36263	TTAACGAGACT	LTRLSAN	- ++
20589	36286	TTGCACAAGCT	LHKLNNN	- ++
29827	13739	TACTCGAGAAT	YSRIGMN	- ++
21136	36534	CTACACAGGTT	LHRLSLD	- ++
25168	13589	TTTTCAAGAGT	FSRVGPN	- ++
24668	37807	CTCCATCGGCT	LHRLSPS	- ++
25221	13995	TTTAGCCGTCT	FSRLNDN	- ++
21340	36621	CTAAGTAGGCT	LSRLSHD	- ++
21224	36490	TTCCATAAATT	FHKLSTN	- ++
24246	37655	TACCATCGTTT	YHRLLPD	- ++
20678	36318	CTCGCGAGGAC	LARTGPD	- ++
21179	17796	CTCTCGCGTGT	LSRVGPD	- ++
21059	14054	CTCGCGAAAAC	LAKTGPN	- +++
23031	37252	TTGTCGAGGAT	LSRISHN	- ++
20907	12037	GTCAACTCGAC	VNSTNGV	- ++
20984	36456	TATGTCAAAAC	YVKSDKM	- ++
20578	36280	CTACATAAACT	LHKLSID	- ++
22188	36744	AGAATGCTAGA	RMLDAYP	- ++
20639	36312	ATGCATAAGTT	MHKLSVN	- ++
25065	37580	TACAGTAGGCT	YSRLSPD	- ++
23225	37315	CTCTGTAGACC	LCRPCSS	- ++
29710	13543	TACAGCCGACT	YSRLNFN	- +++
23578	18116	TTGACAAGGAT	LTRISSN	- ++
23161	36968	AGGATGCCGGA	RMPDAYP	- ++
21261	36411	TACCACAAGTT	YHKLNLD	- ++
20663	36275	TTGCACAAATT	LHKLGEN	- +++
23045	37235	CTCAGCAGGGT	LSRVSPN	- ++
25287	38046	TTCCATAGACT	FHRLSPN	- ++
20875	36416	AAGGACGACTT	KDDFTSW	- ++
22446	37031	CTCCATAGATT	LHRLSHD	- ++
22088	36639	TTGTGTAAACC	LCKPCMT	- ++
26790	16630	CTCTCACGACT	LSRLNHN	- ++
22138	36841	TTGTCCAGGAT	LSRISTN	- ++
28111	14046	TACTCTCGTCT	YSRLGMN	- ++
21129	36383	TACAGTAAACT	YSKLNPT	- ++
25403	38083	AACACTTACGA	NTYDSYP	- ++
21971	14226	TTTTCGAAATT	FSKLNAN	- ++
21543	36708	TTAACACGCTT	LTRLHID	- ++
23962	16602	GTGCATCGCCT	VHRLQDK	- ++
29220	38827	TATCATAGATT	YHRLSIN	- ++
22298	36968	AGGATGCCTGA	RMPDAYP	- ++
21193	14222	TATTCAAAGAC	YSKSGPN	- ++
21707	36576	TTATCTCGGCT	LSRLSFD	- ++

23898	37562	ATGCACCGGTT	MHRLSTN	-	++
26139	14010	TATAGTCGGGT	YSRVGLN	-	++
29103	13990	TATGCAAGACA	YARQGPN	-	++
20857	11947	CTGTCAAAACT	LSKLNLN	-	++
20978	36464	AAGGATGACTT	KDDFTHF	-	+++
21006	18180	CTCTCCAAACT	LSKLSLN	-	++
21834	36790	TACCACAAACT	YHKLNPL	-	++
20785	13777	TACGCTAAGAT	YAKIGPN	-	++
23405	37186	TTACATCGGCT	LHRLQST	-	++
20755	36343	TACGTAAAATC	YVKSQTN	-	++
22884	36982	AGAGATGACTT	RDDFTVY	-	++
25293	13795	CGGGACGATTT	RDDFTAY	-	++
22334	36848	TACGCCCGCAC	YARTGPD	-	++
21430	36509	CGTGGTGAGAA	RGENVFP	-	++
23839	37302	AGATTGCATGA	RLHDAYP	-	++
30242	13553	TACGCTCGCAC	YARTGYN	-	++
22312	36977	AGAGACGAGTT	RDEFHSF	-	++
21704	36741	TACCACAAGTT	YHKLNEN	-	+++
21429	13938	TACAGCAAGAT	YSKMGPN	-	++
21008	36441	CTCTGCAAGCC	LCKPCTT	-	++
20914	36369	TTGCATCGTCT	LHRLGLD	-	++
22431	36932	TACCACAAACT	YHKLNHN	-	++
23674	37303	TTATGTCGCCC	LCRPCPE	-	++
25944	38225	TACTCAAGAAT	YSRIGGG	-	+++
22450	37033	CTAAGCCGAAC	LSRTSYD	-	++
26305	38378	CGAAATGAATT	RNEFTSW	-	++
21766	36695	AGAGGTCCAGA	RGPDVYP	-	++
28893	13802	TATAGTAGGAT	YSRIGQN	-	++
24476	16610	TACGTAAAGTA	YVKYEDK	-	++
24470	37580	TATTCGAGATT	YSRLSPD	-	++
20835	16586	TATCATAAGTT	YHKLANN	-	++
21322	36612	AGGGATGATTT	RDDFTSY	-	++
24693	37447	TACGTCAGGTC	YVRSGPN	-	++
24137	37488	TACAGTCGAGT	YSRVGPD	-	++
21100	36519	TTGCACCGTCT	LHRLLHD	-	++
26932	38631	TACTCTCGAAT	YSRIQLN	-	++
23563	37213	CGCGACGATTT	RDDFTSW	-	++
20997	36473	TACCATAAGTT	YHKLGPQ	-	++
20960	36457	TACGTTAAGAC	YVKSDVR	-	++
21814	36640	AGACTTATGGA	RLMDAYP	-	++
22756	17081	TTCCATAAACT	FHKLMSN	-	++
22404	36972	CTTCACCGCCT	LHRLSPV	-	++
21326	36615	CGTGACGAGTT	RDEFTTY	-	+++
30451	13830	TACAGCCGCGT	YSRVGHN	-	++
28389	38545	TACTCACGTGT	YSRVQPN	-	++

21664	36534	CTTCATCGCCT	LHRLSLD	-	++
21677	16608	CTACATGCACT	LHALSHN	-	++
25097	16602	GTCCACAGACT	VHRLQDK	-	++
27700	13949	TATTCTCGAAT	YSRIGVN	-	++
22778	36663	TATCATAAGTT	YHKLNPM	-	++
23380	37024	TTACACCGCTT	LHRLSPM	-	++
20625	36304	TTAAGTAAATT	LSKLSQN	-	++
20988	13978	CTCTCCAAGCT	LSKLNAN	-	++
22547	37068	TACAGTCGCTT	YSRLNDD	-	+++
22449	17081	TTTCACAAGTT	FHKLMSN	-	++
20691	36287	TTAGCTAAGTC	LAKSGPN	-	+++
21047	36495	CTCTCGAGGGT	LSRVSIN	-	++
23977	37584	TATCACAGGCT	YHRLSVD	-	++
23189	37303	CTTTGCAGACC	LCRPCPE	-	++
21188	11522	GTCGAGAGCAC	VESTNGV	-	++
28833	14083	TACAGCAGAGT	YSRVGVN	-	++
22085	36598	TTACACCGGCT	LHRLSPL	-	++
22018	36874	AGGGACGAGTT	RDEFTGY	-	++
20986	36367	AAGGACGACTT	KDDFTTW	-	++
23595	37447	TATGTTCGAAG	YVRSGPN	-	++
28967	13972	TACAGCCGTAT	YSRIGHN	-	++
26117	38223	TATAGCCGCAT	YSRIGPD	-	++
21174	36364	TTGTGTAAACC	LCKPCLQ	-	++
25681	38083	AATACATATGA	NTYDSYP	-	++
21189	36554	CTCCATCGGCT	LHRLSID	-	++
29461	13949	TACAGTAGGAT	YSRIGVN	-	++
24522	37248	TTTCATAGACT	FHRLGPD	-	++
22904	37197	AGAGATGAGTT	RDEFSTY	-	++
24460	37723	TATACCAGGAT	YTRIGPN	-	++
20804	36385	TATCATAAATT	YHKLNPD	-	++
23550	36965	CTAAGCCGCTT	LSRLNFD	-	++
24237	37652	AGGGAAGACTA	REDYVKW	-	++
25277	37530	TACCTGAAGAC	YLKSQTY	-	++
28805	39271	AAGGATGACTC	KDDWTTY	-	++
23568	37079	AAGGATGACTA	KDDYTTY	-	++
24103	37622	CGAATGCAGGA	RMQDAYP	-	++
22024	13795	CGTGATGATTT	RDDFTAY	-	++
24363	37617	CATAGTAGGAT	HSRIGPN	-	++
21242	36576	TTGAGCCGTCT	LSRLSFD	-	++
21300	13978	TTAAGCAAACT	LSKLNAN	-	++
22703	37079	AAGGATGATTA	KDDYTTY	-	++
22945	37187	CTAAGCAGAAT	LSRISPN	-	++
21787	36621	CTGTCCCGATT	LSRLSHD	-	++
24707	37824	TATTCACGCGT	YSRVGEN	-	++
21468	36431	GTCGAGTCGAC	VESTNGR	-	++

20841	36328	AAGGATGATTT	KDDFTSF	-	++
22433	37029	CGTAGCGAATT	RSEFVSY	-	++
22411	36947	CTGCACAGATT	LHRLSMD	-	++
21623	36727	CTCTGCAAGCC	LCKPCIT	-	++
21662	36738	CGAATGATCGA	RMIDAYP	-	++
28741	14136	TACTCTCGACT	YSRLGAN	-	++
24346	37684	TTGTGTCGGCC	LCRPCSD	-	++
24222	17736	TTGCATCGACT	LHRLSVD	-	++
21039	36491	CTTGCTAGAAC	LARTGLN	-	++
21466	36565	CTCACCCGCCT	LTRLHAD	-	++
20541	36259	TTGCATAGATT	LHRLLDD	-	++
21751	36766	CGCGACGACTT	RDDFTTW	-	++
22029	12190	GTTACCAGCAC	VTSTNGV	-	++
30692	39271	AAAGACGATTC	KDDWTTY	-	++
23205	13745	TATTCGCGCGT	YSRVGYN	-	++
23368	36936	CTCTGCAAACC	LCKPCLN	-	+++
26556	14873	TATAGCAAACT	YSKLNKN	-	++
26807	13892	TACGCCAGGAC	YARTGMN	-	++
21148	36540	TTACATAAGAT	LHKMSMN	-	++
22071	36894	TTGCACCGGGC	LHRAGPD	-	++
22829	13526	TACAGTAAACT	YSKLNNN	-	+++
25852	37854	TATGTTCGTAG	YVRSDTK	-	++
27541	38712	TATCATAGACT	YHRLSEN	-	++
22043	36519	CTACATCGACT	LHRLLHD	-	+++
21912	36826	CTCTCTCGGTT	LSRLSPD	-	++
25990	14473	TTTGCTAGAAA	FARNGPN	-	++
24691	37818	CTGTGCAGGCC	LCRPCSG	-	++
22865	37068	TATTCGCGACT	YSRLNDD	-	++
36089	15215	TATAGCAAATA	YSKYNPN	-	++
22786	37102	AGGACTTATGA	RTYDSFV	-	++
21824	36701	AGAGACGAGTT	RDEFTSF	-	++
20610	36266	CTCCACAAGCT	LHKLMNN	-	++
23517	37423	AGGTCTGAATT	RSEFMSY	-	++
21994	36820	CTGTGTAAGCC	LCKPCNT	-	++
27621	37693	CGGGACGAGTT	RDEFTVY	-	++
30616	39881	AGGAACGAGTT	RNEFTVY	-	++
25135	36851	TTATGTAAACC	LCKPCHT	-	++
20759	36364	CTGTGCAAACC	LCKPCLQ	-	++
35408	39885	AGAAATGAATT	RNEFTSF	-	++
22310	13537	TATTCAAAATT	YSKLNIN	-	+++
21719	17809	TTACATGCCAA	LHANLPN	-	++
21240	36438	TTATGCAAACC	LCKPCPT	-	+++
24047	37423	CGCAGCGAGTT	RSEFMSY	-	++
30623	13851	TACGCTCGAAC	YARTGFN	-	++
35591	13715	TACTCACGATT	YSRLNHN	-	++

24109	37257	TACCTAAAATC	YLKSQVY	-	++
24167	37642	CGAAGTGAGTT	RSEFKVF	-	++
22339	36982	AGAGACGATTT	RDDFTVY	-	++
21389	36603	AGGACCGAAC/	RTEHVFP	-	++
27444	14343	TATTCAAAGTT	YSKLNSN	-	++
22739	37091	TACTTGAAGTC	YLKSQSN	-	++
30009	13982	TTCAGCCGTCT	FSRLNPN	-	++
23028	14004	TACGCGAAGAC	YAKTGVN	-	++
21401	36361	AAGGACGAATT	KDEFSSW	-	++
31688	14479	TACTCAAGAAT	YSRIGNN	-	++
20739	36274	CTCTCACGCAT	LSRIGPD	-	++
21158	36453	AAAGATGACTT	KDDFTAW	-	++
24233	37650	AAGGACGAATC	KDEWSVY	-	++
21335	36435	CTGTGCAAGCC	LCKPCVT	-	++
20577	36279	TTGCATAAGTT	LHKLLND	-	++
21402	36649	CGCCTCATGGA	RLMDVYP	-	++
21922	36831	TTATCGCGTAT	LSRISFN	-	++
21448	36673	GGGGACGAATT	GDEFVHW	-	++
22465	14259	TATAGCAAGTT	YSKLNVN	-	+++
30682	39322	AAGGACGAATT	KDEFTVY	-	+++
20899	36285	TTGCACAAACT	LHKLSVD	-	++
26175	37723	TACACTCGCAT	YTRIGPN	-	++
21187	36411	TATCATAAATT	YHKLNLD	-	++
22320	36681	CTTTGTAAGCC	LCKPCET	-	++
26766	15352	TATTCAAAAAT	YSKIGKN	-	++
22874	16612	TTGAGCCGCGT	LSRVGFN	-	++
22357	11295	TTTAGCAAGCT	FSKLNLN	-	++
25618	38160	GGTAATGAGTT	GNEFSSW	-	++
22301	36972	CTCCATAGATT	LHRLSPV	-	++
23004	14097	TACAGTAAACT	YSKLNHN	-	++
20651	36286	CTTCACAAGCT	LHKLNNN	-	++
20586	36285	CTACATAAGTT	LHKLSVD	-	++
33694	39881	CGGAACGAGTT	RNEFTVY	-	++
27164	13874	TACTCCCGGCT	YSRLGLN	-	++
21564	16017	TACGCGAAAGC	YAKGGPN	-	++
28350	38658	TATTGGAGTGG	YWSGVTD	-	++
20851	11522	GTTGAATCCAC	VESTNGV	-	++
21506	36693	TATCACGCAGC	YHAAGPN	-	++
25672	37951	AAAGATGATTT	KDDFTGF	-	++
21035	36490	TTTCACAAGCT	FHKLSTN	-	++
21853	36801	AGAGACGATTT	RDDFTMY	-	++
33668	39772	ATAGGGGAGCC	IGERGWD	-	++
20713	36290	CTCCACAAGCT	LHKLSPD	-	++
29898	13972	TACTCCCGGAT	YSRIGHN	-	++
21521	11967	TTGGCTAAGAA	LAKNGPN	-	++

29269	13510	TACTCAAGATT	YSRLNYN	-	++
20630	36308	AAGGACGAATT	KDEFTTF	-	++
20618	36299	TTCCACAAGCT	FHKLGIN	-	++
22725	37030	TTGCATAGATT	LHRLSQD	-	++
21726	11967	CTAGCCAAAA/	LAKNGPN	-	++
21460	36638	ATGTTCGATGG	MFDGTPA	-	++
20918	36435	TTATGTAAACC	LCKPCVT	-	+++
20655	16631	TTGCACGTCTT	LHVLGPN	-	+++
27390	38780	AGAGACGGGT/	RDGYSAW	-	++
23040	36957	AAGGACGATT/	KDDYTTW	-	++
30986	40010	CGCAATGAGTT	RNEFTSY	-	++
21897	36820	CTATGTAAACC	LCKPCNT	-	++
21294	36486	CGAACGGAGA(	RTETVYP	-	++
29360	14399	TACGCCCGCA(	YARTGNN	-	++
29617	14282	TTTTCGCGTTT/	FSRLNTN	-	++
21063	36394	TATTCGAAATT	YSKLQAN	-	++
27755	38832	TACAGCAGAC1	YSRLSPT	-	++
22097	17676	TTACACAGTAA	LHSKLPN	-	++
20607	36294	CTACATAAGTT	LHKLSHD	-	++
21839	36793	TTGTCCCGCAC	LSRTSVN	-	++
24127	37029	AGATCAGAGTT	RSEFVSY	-	++
21184	36445	TATCATGCCAA	YHAKLPN	-	++
26343	38398	TACTCCAGGCT	YSRLSPM	-	++
21805	14416	TATAGCAAAAT	YSKIGHN	-	++
20975	36336	AAGGACGACT1	KDDFTTY	-	++
30046	39265	TATTCGCGTTT(	YSRLSDN	-	++
27989	38144	AGGTCGGAGTT	RSEFMTY	-	++
27672	38690	AGGACTTTTGA	RTFDAYP	-	++
27283	13995	TTTTCGAGGTT.	FSRLNDN	-	++
25231	37818	TTATGCCGCCC	LCRPCSG	-	++
20570	36274	TTGAGTAGAAT	LSRIGPD	-	++
20765	36258	TACTCAAAGCT	YSKLGPD	-	++
30886	39593	AGGACATACG/	RTYDVYP	-	++
31522	16636	TACCACCGCC1	YHRLSNN	-	++
26697	37944	CGAAGCGAGT1	RSEFLPY	-	++
20849	36407	AACGCGCTTGA	NALEGRD	-	++
21785	17659	CTGTGTAAACC	LCKPCLT	-	++
29059	39353	TATTCTAGGAT	YSRIQPN	-	++
21147	36539	TTGCATAGGCT	LHRLSAD	-	++
26482	38461	TATCACCGGCT	YHRLSPV	-	++
22946	37213	AGGGATGACTT	RDDFTSW	-	++
23191	37302	AGGTTGCACGA	RLHDAYP	-	++
21210	36563	ATGCATCGCC1	MHRLLPD	-	++
23596	37315	CTATGCCGGC(	LCRPCSS	-	++
21143	11522	GTGGAGAGTAC	VESTNGV	-	++

21106	36423	GTGCAGAGCAC	VQSTNGV	-	++
25862	37650	AAAGATGAGTC	KDEWSVY	-	++
20854	36408	AAAGACGAGTT	KDEFHSF	-	++
20762	36367	AAAGATGATTT	KDDFTTW	-	++
23331	16620	CTTTCGCGGAT	LSRISVN	-	++
28146	39041	AAAGATGACTC	KDDWTSY	-	++
22824	36982	CGCGATGACTT	RDDFTVY	-	++
22817	37173	TATCATGCTCA	YHAQGPN	-	++
20932	36441	CTGTGCAAACC	LCKPCTT	-	++
20798	36383	TATTCCAAGTT	YSKLNPT	-	++
20883	36423	GTTCAATCTAC	VQSTNGV	-	++
22676	36769	CTACATCGTCT	LHRLGYD	-	++
22434	36971	AGAGACGAGTT	RDEFTSY	-	+++
27964	38456	TCTACCTATGA	STYDSYP	-	++
20650	36318	TTAGCTCGAAC	LARTGPD	-	++
30189	39136	TTTCATCGATT	FHRLSTN	-	++
26928	38456	TCAACCTACGA	STYDSYP	-	++
27583	38046	TTTCACCGTTT	FHRLSPN	-	++
22223	14079	TACAGTAAGTT	YSKLNQN	-	++
22936	14290	TACTCTAAGGT	YSKVGYN	-	++
20738	36308	AAAGATGAGTT	KDEFTTF	-	++
21496	36688	TTGTGCAAACC	LCKPCST	-	++
25082	14367	TTTAGTCGATT	FSRLGPN	-	++
21477	36681	TTGTGCAAACC	LCKPCET	-	++
21344	36486	AGGACTGAAAC	RTETVYP	-	++
20953	36453	AAGGACGATTT	KDDFTAW	-	++
21132	36480	CGCATGCTTGA	RMLDAFP	-	++
22130	36790	TATCATAAGTT	YHKLNPL	-	++
21022	36484	ATGTTTGACGG	MFDGTAA	-	++
26060	17752	CGCAGCGAGTT	RSEFVSF	-	++
20754	36277	CTACATAAACT	LHKLSPL	-	++
29779	39593	CGAACCTATGA	RTYDVYP	-	++
21913	36693	TACCATGCCGC	YHAAGPN	-	++
23475	36982	CGCGACGATTT	RDDFTVY	-	++
24227	37649	TACTCCAGATT	YSRLNPD	-	+++
23795	37516	AGAAATGAGTT	RNEFTTF	-	++
20611	36280	TTACATAAACT	LHKLSID	-	++
21113	16575	CTTTCCAAATT	LSKLSAN	-	++
27644	38398	TATAGTCGATT	YSRLSPM	-	++
23027	37197	AGGGACGAGTT	RDEFSTY	-	++
22687	36977	CGTGATGAATT	RDEFHSF	-	++
22003	36864	AGAGGCGAGGA	RGEDVYP	-	++
27928	38863	TATAGTCGTCT	YSRLQSN	-	++
20816	36269	CTTGCAAAAAC	LAKTGYN	-	++
30271	14443	TACTCCCGAAT	YSRIGLN	-	++

21438	36666	CTTCATGCCTC	LHASGPN	-	++
21648	14222	TACAGCAAATC	YSKSGPN	-	++
26463	38456	AGTACTTACGA	STYDSYP	-	++
22886	36612	CGAGATGACTT	RDDFTSY	-	++
22232	36947	TTACATCGCCT	LHRLSMD	-	++
21368	36638	ATGTTTGACGG	MFDGTPA	-	++
20697	36338	AAAGACGATTT	KDDFTTF	-	++
31806	14873	TACTCAAAGTT	YSKLNKN	-	+++
25334	37516	CGGAACGAATT	RNEFTTF	-	++
29980	13939	TACAGCCGCAT	YSRIGTN	-	++
23916	37568	AGAGACGAGTT	RDEFTSW	-	+++
21818	36534	CTGCATCGCCT	LHRLSLD	-	++
35876	36701	AGGGATGAATT	RDEFTSF	-	+++
22617	37031	TTGCACCGGCT	LHRLSHD	-	++
25179	37568	AGAGATGAGTT	RDEFTSW	-	++
28268	37750	TTATGCAGGCC	LCRPCSN	-	++
21208	36486	CGCACTGAAAC	RTETVYP	-	++
26629	38420	TACGTTAGGTC	YVRSDTR	-	++
25843	38223	TACTCTAGGAT	YSRIGPD	-	++
24812	36751	TATAGTAAATT	YSKLQKN	-	+++
24016	36701	CGAGACGAGTT	RDEFTSF	-	++
32619	37746	CGTGACGAGTT	RDEFSSW	-	++
35340	40380	CCGTTAAAGTC	PLKSSLW	-	++
36068	41801	TTTGAAGAACA	FEEHPSW	-	++
31313	16639	ATTATGAGTTC	IMSSRSW	-	++
23804	37521	TTATGCAAACC	LCKPCLV	-	++
22153	36924	TATCTTAAGTC	YLKSQIY	-	++
20745	36361	AAAGATGAGTT	KDEFSSW	-	+++
20823	36361	AAGGATGAATT	KDEFSSW	-	+++
24287	37666	CGTTCAGAATT	RSEFLSY	-	++
28778	37536	CGCGACGAATT	RDEFTHY	-	++
34430	41262	ATCTCGGAGTT	ISEFKIY	-	++
35194	40141	AGAACCTATGA	RTYEVYP	-	++
20896	18180	TTGAGTAAGTT	LSKLSLN	-	+++
28318	13982	TTTTCGAGATT	FSRLNPN	-	++
24344	16639	ATCATGTCGTC	IMSSRSW	-	++
22346	36985	CTCCATCGCCT	LHRLLPV	-	++
26295	17842	ATGGATGATTT	MDDFTVY	-	++
23846	37536	AGAGATGAGTT	RDEFTHY	-	++
27849	38761	AGAGAGGAGTC	REEWVAY	-	++
25563	38144	CGGAGTGAATT	RSEFMTY	-	++
26084	14098	TACTCGCGCGT	YSRVGFN	-	++
23748	37498	AAAGATGAGTA	KDEYHTY	-	++
24070	37571	CGTGACGAATT	RDEFSSF	-	++
20917	36434	CTGTGCAAACC	LCKPCDT	-	++

23122	18663	CTTGCAAGGAC	LARTALN	-	++
23541	36964	CGCGGAGAATT	RGEFVYP	-	++
24097	37619	GTGATGGCGGA	VMADRLW	-	++
24275	37661	CTACACAGAAT	LHRMSPD	-	++
26530	38160	GGCAACGAATT	GNEFSSW	-	++
21088	16568	CTCCATCGTCT	LHRLLKD	-	++
23536	36957	AAAGATGACTA	KDDYTTW	-	++
20799	14581	TACTCTAAATT	YSKLNDN	-	+++
27705	13841	TTGCACCGCAT	LHRMTPN	-	++
22575	37081	CTCCATCGGCT	LHRLSYD	-	++
25745	17752	AGGTCAGAATT	RSEFVSF	-	++
21724	11292	GTGCAAAGTAC	VQSTNGI	-	++
26971	38263	TACAGTCGCCT	YSRLNLM	-	++
31712	13640	TATTCTCGGAT	YSRIGYN	-	++
21777	36663	TACCACAAACT	YHKLNPM	-	++
21250	36576	TTGAGCCGTTT	LSRLSFD	-	++
23703	13795	AGAGACGACTT	RDDFTAY	-	++
21213	36434	TTGTGTAAGCC	LCKPCDT	-	++
27917	38167	CGTAGCGAGTT	RSEFHSF	-	++
23696	18772	TTGAGAACTGA	LRTDCCV	-	++
27137	38291	TACTTTACCGG	YFTGYPD	-	++
21222	36569	CGCCTCATGGA	RLMDAFP	-	++
20866	17659	TTATGCAAGCC	LCKPCLT	-	++
21130	16650	CTTACGAGACT	LTRLSHN	-	++
29622	13538	TTTTCGCGCTT	FSRLNHN	-	++
23458	19906	GTCTCTGAATT	VSEFTTY	-	++
31359	40141	CGCACATACGA	RTYEVYP	-	++
21070	11477	CTCGCGAAGGC	LAKGGPN	-	++
20964	11522	GTAGAATCTAC	VESTNGV	-	++
20526	36248	ATCGCTCTCAA	IALKGWD	-	+++
22068	19906	GTTAGCGAGTT	VSEFTTY	-	++
23738	37106	TTGCACAGACT	LHRLSED	-	++
21339	36620	AGGGGCCCAGA	RGPDVFP	-	++
21608	36663	TATCACAAACT	YHKLNPM	-	++
21219	16608	TTGCACGCCTT	LHALSHN	-	++
27198	38378	AGGAACGAGTT	RNEFTSW	-	++
20665	36323	AAAGATGACTT	KDDFSTW	-	++
27436	38015	TATTCCCGTTT	YSRLSPI	-	++
26245	38353	TACAGTCGTCT	YSRLNNL	-	++
20806	36386	AAGGACGAGTT	KDEFTGY	-	++
23533	36613	CGGGGTGAGAC	RGETVYP	-	++
27423	38794	ATGTGGGATGC	MWDGTAA	-	++
21627	36603	AGGACTGAACA	RTEHVFP	-	++
28028	38794	ATGTGGGACGC	MWDGTAA	-	++
24069	17903	TACAGCAAGTT	YSKLSDR	-	++

20886	36425	AAGGACGATTT	KDDFTMF	- ++
22993	37185	CTGCACAAGTT	LHKLQVT	- ++
20838	36386	AAAGATGAATT	KDEFTGY	- ++
20948	36407	AATGCTTTAGA	NALEGRD	- ++
21281	36425	AAAGATGACTT	KDDFTMF	- ++
23167	37295	AGGGATGACTT	RDDFTVW	- ++
27817	14593	TATTCACGCTC	YSRSGPN	- ++
22216	11974	GTCTCATCGAC	VSSTNGI	- ++
21661	17676	CTGCACTCCAA	LHSKLPN	- ++
22625	37102	CGAACCTACGA	RTYDSFV	- ++
20821	36390	AAGGATGAGTT	KDEFSTY	- ++
20648	36280	CTGCACAAGTT	LHKLSID	- ++
21396	36336	AAAGATGATTT	KDDFTTY	- ++
20813	36389	CGCACGGAGAC	RTETVFP	- ++
22376	36495	TTAAGTCGCGT	LSRVSIN	- ++
22574	36864	CGTGGTGAAGA	RGEDVYP	- ++
22422	37024	CTCCATAGATT	LHRLSPM	- ++
26777	38456	AGTACATACGA	STYDSYP	- ++

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AA SEQ ID#	AA sequence	CAG-Ly6a	CMV-Cba-Ly6A	CAG-hTFRC	CMV-Cba-hTFR	B-hTFR1-KI Br	B-hTFR1-KI Sp	B-hTFR1-KI Liver
36437	LCKPCLD	-	-	+--	+++	+++	+++	-
36437	LCKPCLD	-	-	+--	+++	+++	+++	-
36413	LHRLGPD	-	-	+--	+++	+++	+++	-
36413	LHRLGPD	-	-	+--	+++	+++	+++	-
36834	LHRLGPN	-	-	+--	+++	+++	+++	-
36936	LCKPCLN	-	-	+--	+++	+++	+++	-
36936	LCKPCLN	-	-	+--	+++	+++	+++	-
36834	LHRLGPN	-	-	+--	+++	+++	+++	-
37684	LCRPCSD	-	-	+--	+++	+++	+++	-
36592	LHRLLPD	-	-	+--	+++	++	+++	-
37684	LCRPCSD	-	-	+--	+++	+++	-	-
36592	LHRLLPD	-	-	+--	+++	++	++	-
14060	LHAALPN	-	-	+--	+++	-	+	-
36316	LHAKLPN	-	-	+--	+++	+++	+++	-
36316	LHAKLPN	-	-	+--	++	+++	+++	-
37062	LHRLSPN	-	-	+--	+++	+++	+++	-
36438	LCKPCPT	-	-	+--	-	++	++	-
14060	LHAALPN	-	-	+--	++	-	-	-
36864	RGEDVYP	-	-	+--	++	+++	+++	-
37062	LHRLSPN	-	-	+--	++	+++	+++	-
36864	RGEDVYP	-	-	+--	+	+++	+++	-
36438	LCKPCPT	-	-	+--	-	++	++	-
36253	LHKLSPN	-	-	+--	++	+++	+++	+
36253	LHKLSPN	-	-	+--	++	+++	+++	-
36619	LHRLSDN	-	-	+--	++	+++	+++	-
36259	LHRLLDD	-	-	+--	-	-	-	-
36975	LHRLSTN	-	-	+--	-	+++	+++	+
36308	KDEFTTF	-	-	+--	++	+++	+++	-
36619	LHRLSDN	-	-	+--	++	+++	+++	-
11522	VESTNGV	-	-	+--	-	+++	+++	-
11522	VESTNGV	-	-	+--	-	+++	+++	-

36723	LHRLGDN	-	-	+--	++	++	++	-
36259	LHRLLDD	-	-	+--	-	-	-	-
39322	KDEFTVY	-	-	+--	+++	+++	+++	-
36308	KDEFTTF	-	-	+--	+++	+++	+++	-
36723	LHRLGDN	-	-	+--	-	++	++	-
36259	LHRLLDD	-	-	+--	-	-	-	-
11522	VESTNGV	-	-	+--	-	+++	+++	-
39322	KDEFTVY	-	-	+--	+	+++	+++	-
36723	LHRLGDN	-	-	+--	-	++	++	-
36431	VESTNGR	-	-	+--	++	+++	+++	-
36723	LHRLGDN	-	-	+--	++	++	++	-
36844	LHRLSVN	-	-	+--	+	+++	+++	-
36431	VESTNGR	-	-	+--	++	+++	+++	-
36844	LHRLSVN	-	-	+--	-	+++	+++	-
36971	RDEFTSY	-	-	+--	-	+++	+++	-
36486	RTETVYP	-	-	+--	+	+++	+++	-
36895	RMEDAYP	-	-	+--	-	+++	+++	-
36486	RTETVYP	-	-	+--	-	+++	+++	-
36486	RTETVYP	-	-	+--	-	+++	+++	-
36389	RTETVFP	-	-	+--	++	+++	+++	-
36259	LHRLLDD	-	-	+--	-	-	-	-
36257	LHKLSEN	-	-	+--	-	+++	+++	-
36431	VESTNGR	-	-	+--	++	+++	+++	-
36257	LHKLSEN	-	-	+--	++	+++	+++	-
36486	RTETVYP	-	-	+--	-	+++	+++	-
36464	KDDFTHF	-	-	+--	++	+++	+++	-
38571	RTYDAYP	-	-	+--	++	+++	+++	-
36420	KDDFTVY	-	-	+--	++	+++	+++	-
36431	VESTNGR	-	-	+--	++	+++	+++	-
36464	KDDFTHF	-	-	+--	++	+++	+++	-
36305	LHKAGPN	-	-	+--	++	+++	+++	-
37652	REDYVKW	-	-	+--	-	+++	+++	-
36971	RDEFTSY	-	-	+--	++	+++	+++	-

36305	LHKAGPN	-	-	+--	++	+++	+++	+
12333	VSSTNGV	-	-	+--	-	+++	+++	-
36975	LHRLSTN	-	-	+--	-	+++	+++	-
36895	RMEDAYP	-	-	+--	-	+++	+++	-
36486	RTETVYP	-	-	+--	-	+++	+++	-
37118	LHRLTED	-	-	+--	-	-	-	-
11522	VESTNGV	-	-	+--	-	+++	+++	-
36257	LHKLSEN	-	-	+--	++	+++	+++	-
36971	RDEFTSY	-	-	+--	++	+++	+++	-
36434	LCKPCDT	-	-	+--	-	+	-	-
16667	LHRLAAN	-	-	+--	-	+++	+++	-
36257	LHKLSEN	-	-	+--	++	+++	+++	-
38571	RTYDAYP	-	-	+--	-	+++	+++	-
36389	RTETVFP	-	-	+--	-	+++	+++	-
36434	LCKPCDT	-	-	+--	-	+	-	-
36509	RGENVFP	-	-	+--	-	+++	+++	-
36423	VQSTNGV	-	-	+--	++	+++	+++	-
36486	RTETVYP	-	-	+--	-	+++	+++	-
37652	REDYVKW	-	-	+--	++	+++	+++	-
12055	VESTNGI	-	-	+--	-	+++	+++	-
36509	RGENVFP	-	-	+--	-	+++	+++	-
36603	RTEHVFP	-	-	+--	-	+++	+++	-
36453	KDDFTAW	-	-	+--	-	++	++	-
36603	RTEHVFP	-	-	+--	-	+++	+++	-
36420	KDDFTVY	-	-	+--	++	+++	++	-
36416	KDDFTSW	-	-	+--	++	+++	++	-
36416	KDDFTSW	-	-	+--	++	+++	++	-
36971	RDEFTSY	-	-	+--	-	+++	+++	-
36493	LCKPCAT	-	-	+--	-	++	++	-
37118	LHRLTED	-	-	+--	++	+	-	-
36727	LCKPCIT	-	-	+--	-	-	-	-
36319	RDETVFP	-	-	+--	-	+++	+++	-
36250	LHKLTVN	-	-	+--	-	++	++	-

17558	TESTNGR	-	-	+--	++	+++	+++	-
36416	KDDFTSW	-	-	+--	++	+++	+++	-
37174	LHRLSSN	-	-	+--	-	+++	+++	+
12055	VESTNGI	-	-	+--	-	+++	+++	-
36328	KDDFTSF	-	-	+--	++	+++	+++	-
36453	KDDFTAW	-	-	+--	-	++	+	-
17558	TESTNGR	-	-	+--	++	+++	+++	-
36328	KDDFTSF	-	-	+--	-	+++	+++	-
37938	RTYDSYP	-	-	+--	-	+++	+++	-
36319	RDETVFP	-	-	+--	-	+++	+++	-
36615	RDEFTTY	-	-	+--	-	+++	+++	-
16667	LHRLAAN	-	-	+--	-	+++	+++	-
36443	RTDDVFP	-	-	+--	-	+++	+++	-
36423	VQSTNGV	-	-	+--	-	+++	+++	-
36692	RTDDVYP	-	-	+--	-	+++	+++	-
36264	RLEDVFP	-	-	+--	-	+++	+++	-
37938	RTYDSYP	-	-	+--	-	+++	+++	-
36681	LCKPCET	-	-	+--	-	-	-	-
36615	RDEFTTY	-	-	+--	-	+++	+++	-
36338	KDDFTTF	-	-	+--	-	+++	+++	-
36328	KDDFTSF	-	-	+--	++	+++	+++	-
36416	KDDFTSW	-	-	+--	-	+++	++	-
36252	LHKLSVN	-	-	+--	++	+++	+++	-
36319	RDETVFP	-	-	+--	-	+++	+++	-
36839	LHRLQDN	-	-	+--	-	++	++	-
36682	LCKPCLS	-	-	+--	++	+	+	-
36328	KDDFTSF	-	-	+--	++	+++	+++	-
37174	LHRLSSN	-	-	+--	-	+++	+++	-
36407	NALEGRD	-	-	+--	-	+++	+++	-
36681	LCKPCET	-	-	+--	-	-	-	-
36338	KDDFTTF	-	-	+--	-	+++	+++	-
37067	REDHVSW	-	-	+--	-	+++	+++	-
36964	RGEFVYP	-	-	+--	-	+++	+++	-

36692	RTDDVYP	-	-	+--	-	+++	+++	-
36250	LHKLTVN	-	-	+--	-	++	++	-
19087	TSENVYF	-	-	+--	-	+++	+++	-
36264	RLEDVFP	-	-	+--	-	+++	+++	-
36682	LCKPCLS	-	-	+--	+	+	++	-
36711	APGSVRW	---	+++	+--	+++	++	-	-
36678	LHRLGED	-	-	+--	-	-	-	-
36435	LCKPCVT	-	-	+--	-	+	+	-
36435	LCKPCVT	-	-	+--	-	+	+	-
36443	RTDDVFP	-	-	+--	-	+++	+++	-
36614	RDETVYP	-	-	+--	-	+++	+++	-
14269	YARTGPN	-	-	+--	++	+++	+++	+
36614	RDETVYP	-	-	+--	-	+++	+++	-
12190	VTSTNGV	-	-	+--	-	++	++	-
37806	RTYDSFP	-	-	+--	-	+++	+++	-
11875	HTSTNGV	-	-	+--	-	+++	+++	-
36839	LHRLQDN	-	-	+--	-	++	++	-
11663	VASTNGV	-	-	+--	-	+++	+++	-
36250	LHKLTVN	-	-	+--	-	++	++	-
11875	HTSTNGV	-	-	+--	-	+++	+++	-
36268	LHKLSTN	-	-	+--	++	+++	+++	-
36336	KDDFTTY	-	-	+--	-	+++	+++	-
12190	VTSTNGV	-	-	+--	-	++	++	-
36613	RGETVYP	-	-	+--	-	+++	+++	-
37106	LHRLSED	-	-	+--	-	-	-	-
36250	LHKLTVN	-	-	+--	++	++	++	-
14269	YARTGPN	-	-	+--	-	+++	+++	-
36268	LHKLSTN	-	-	+--	-	+++	+++	-
11974	VSSTNGI	-	-	+--	-	+++	+++	-
36252	LHKLSVN	-	-	+--	-	+++	+++	-
36563	MHRLLPD	-	-	+--	-	-	-	-
36319	RDETVFP	-	-	+--	-	+++	+++	-
14495	RLYDAYE	-	-	+--	-	++	-	-

36603	RTEHVFP	-	-	+--	-	+++	+++	-
37223	RNEDVYP	-	-	+--	-	+++	+++	-
14269	YARTGPN	-	-	+--	++	+++	+++	-
14495	RLYDAYE	-	-	+--	-	-	-	-
36421	LMADAYP	-	-	+--	-	+++	+++	-
36386	KDEFTGY	-	-	+--	-	++	-	-
17658	LHKLSNN	-	-	+--	-	+++	+++	+
11826	VTSTNGI	-	-	+--	-	-	-	-
36275	LHKLGEN	-	-	+--	++	++	++	-
12206	VDSTNGV	-	-	+--	-	+++	+++	-
36769	LHRLGYD	-	-	+--	-	-	+	-
36563	MHRLLPD	-	-	+--	-	-	-	-
36603	RTEHVFP	-	-	+--	++	+++	+++	-
36613	RGETVYP	-	-	+--	-	+++	+++	-
36563	MHRLLPD	-	-	+--	-	-	-	-
36260	LHKLSMN	-	-	+--	-	+++	+++	+
19087	TSENVYF	-	-	+--	-	+++	+++	-
14628	YSRLNDN	-	-	+--	-	+++	+++	-
36539	LHRLSAD	-	-	+--	-	+	+	-
14269	YARTGPN	-	-	+--	+	+++	+++	-
36390	KDEFSTY	-	-	+--	-	+++	+++	-
37693	RDEFTVY	-	-	+--	-	+++	-	-
36264	RLEDVFP	-	-	+--	-	+++	+++	-
36408	KDEFHSF	-	-	+--	-	++	+++	-
36613	RGETVYP	-	-	+--	-	+++	+++	-
37079	KDDYTTY	-	-	+--	-	+++	++	-
37806	RTYDSFP	-	-	+--	-	+++	+++	-
36563	MHRLLPD	-	-	+--	-	-	-	-
36493	LCKPCAT	-	-	+--	-	++	+	-
36367	KDDFTTW	-	-	+--	-	+++	++	-
12239	HSSTNGV	-	-	+--	-	+++	+++	-
36382	LCKPCLG	-	-	+--	-	+	-	-
36986	RMEDAFP	-	-	+--	-	+++	+++	-

36986	RMEDAFP	-	-	+--	-	+++	+++	-
36390	KDEFSTY	-	-	+--	-	+++	+++	-
37197	RDEFSTY	-	-	+--	-	+++	++	-
37106	LHRLSED	-	-	+--	-	-	-	-
11292	VQSTNGI	-	-	+--	-	+++	+++	-
14628	YSRLNDN	-	-	+--	++	+++	+++	-
37223	RNEDVYP	-	-	+--	-	+++	+++	-
36386	KDEFTGY	-	-	+--	-	++	++	-
17809	LHANLPN	-	-	+--	-	++	++	-
36407	NALEGRD	-	-	+--	-	+++	+++	-
36796	LSRLSPN	-	-	+--	++	++	++	-
36268	LHKLSTN	-	-	+--	++	+++	+++	-
36982	RDDFTVY	-	-	+--	-	++	-	-
36336	KDDFTTY	-	-	+--	-	+++	+++	-
37197	RDEFSTY	-	-	+--	-	+++	++	-
36539	LHRLSAD	-	-	+--	-	++	++	-
12037	VNSTNGV	-	-	+--	-	+++	+++	-
36695	RGPDVYP	-	-	+--	-	++	++	-
13795	RDDFTAY	-	-	+--	-	++	-	-
12037	VNSTNGV	-	-	+--	-	+++	+++	-
12737	IESTNGR	-	-	+--	-	++	++	-
36264	RLEDVFP	-	-	+--	-	+++	+++	-
36539	LHRLSAD	-	-	+--	-	++	-	-
36479	RTDTVYP	-	-	+--	-	+++	+++	-
12737	IESTNGR	-	-	+--	-	+++	++	-
36390	KDEFSTY	-	-	+--	-	+++	+++	-
36539	LHRLSAD	-	-	+--	-	++	++	-
36613	RGETVYP	-	-	+--	-	+++	+++	-
36278	LHKLSLN	-	-	+--	-	+++	++	-
37565	KDDYTSY	-	-	+--	-	+++	++	-
13795	RDDFTAY	-	-	+--	-	++	-	-
36268	LHKLSTN	-	-	+--	-	+++	+++	-
36336	KDDFTTY	-	-	+--	-	+++	+++	-

11826	VTSTNGI	-	-	+--	-	-	-	-
37213	RDDFTSW	-	-	+--	-	+++	++	-
12037	VNSTNGV	-	-	+--	-	+++	+++	-
36408	KDEFHSF	-	-	+--	-	+++	++	-
36511	KSEFTTY	-	-	+--	-	+++	+++	-
36367	KDDFTTW	-	-	+--	-	+++	++	-
36982	RDDFTVY	-	-	+--	-	++	+	-
36695	RGPDVYP	-	-	+--	-	++	++	-
12013	HDSTNGV	-	-	+--	-	+++	+++	-
36511	KSEFTTY	-	-	+--	-	+++	+++	-
37043	RDENVFP	-	-	+--	-	+++	++	-
36695	RGPDVYP	-	-	+--	-	++	++	-
36275	LHKLGEN	-	-	+--	-	++	++	-
12037	VNSTNGV	-	-	+--	-	+++	+++	-
12239	HSSTNGV	-	-	+--	-	+++	+++	-
36390	KDEFSTY	-	-	+--	-	+++	+++	-
36421	LMADAYP	-	-	+--	-	+++	-	-
37565	KDDYTSY	-	-	+--	-	+++	-	-
36278	LHKLSLN	-	-	+--	-	+++	+++	-
37079	KDDYTTY	-	-	+--	-	+++	-	-
16631	LHVLGPN	-	-	+--	-	-	-	-
17736	LHRLSVD	-	-	+--	-	-	+	-
12206	VDSTNGV	-	-	+--	-	+++	+++	-
11663	VASTNGV	-	-	+--	-	+++	+++	-
16631	LHVLGPN	-	-	+--	-	-	-	-
36989	RDEHVFP	-	-	+--	-	+++	+++	-
37081	LHRLSYD	-	-	+--	-	++	-	-
36695	RGPDVYP	-	-	+--	-	++	++	-
37079	KDDYTTY	-	-	+--	-	+++	++	-
17809	LHANLPN	-	-	+--	-	++	++	-
12206	VDSTNGV	-	-	+--	-	+++	+++	-
37079	KDDYTTY	-	-	+--	-	+++	++	-
36594	LHRLGAD	-	-	+--	-	-	-	-

19906	VSEFTTY	-	-	+--	-	+++	++	-
36594	LHRLGAD	-	-	+--	-	-	-	-
36957	KDDYTTW	-	-	+--	-	+++	+	-
11292	VQSTNGI	-	-	+--	-	+++	+++	-
36796	LSRLSPN	-	-	+--	-	++	++	-
37197	RDEFSTY	-	-	+--	-	+++	++	-
36369	LHRLGLD	-	-	+--	+	-	-	-
11826	VTSTNGI	-	-	+--	-	-	-	-
37912	RTHDVYP	-	-	+--	-	+++	+++	-
36463	RGETVFP	-	-	+--	-	+++	+++	-
36349	RLEDAFP	-	-	+--	-	++	++	-
36382	LCKPCLG	-	-	+--	-	-	-	-
36369	LHRLGLD	-	-	+--	-	+	-	-
37197	RDEFSTY	-	-	+--	-	+++	++	-
36820	LCKPCNT	-	-	+--	-	++	-	-
36964	RGEFVYP	-	-	+--	-	++	+++	-
37693	RDEFTVY	-	-	+--	-	+++	++	-
36874	RDEFTGY	-	-	+--	-	++	++	-
14628	YSRLNDN	-	-	+--	-	+++	+++	-
11418	HESTNGV	-	-	+--	-	+++	+++	-
37641	RSEFTTY	-	-	+--	-	++	++	-
36982	RDDFTVY	-	-	+--	-	++	-	-
36977	RDEFHSF	-	-	+--	-	++	++	-
36243	LHKLANN	-	-	+--	-	+++	+++	-
37939	RNEFTTY	-	-	+--	-	+++	-	-
37029	RSEFVSY	-	-	+--	-	++	-	-
36248	IALKGWD	-	-	+--	-	++	++	-
36688	LCKPCST	-	-	+--	-	-	+	-
36243	LHKLANN	-	-	+--	+	+++	+++	+
36459	LARSGPN	-	-	+--	-	+++	+++	++
16134	VHSTNGI	-	-	+--	-	+++	+++	-
14574	YSRLGPN	-	-	+--	-	+	++	-
12312	VDSTNGI	-	-	+--	-	+++	+++	-

14632	YSRIGPN	-	-	+--	-	+++	+++	++
36730	RDDFTTF	-	-	+--	-	+++	++	-
37068	YSRLNDD	-	-	+--	-	+	-	-
12707	VDSTNGR	-	-	+--	-	+++	+++	-
12206	VDSTNGV	-	-	+--	-	+++	+++	-
36572	REDTVKW	-	-	+--	-	+++	++	-
37939	RNEFTTY	-	-	+--	-	+++	-	-
38456	STYDSYP	-	-	+--	-	+++	++	-
16134	VHSTNGI	-	-	+--	-	+++	+++	-
36874	RDEFTGY	-	-	+--	-	++	-	-
17736	LHRLSVD	-	-	+--	-	+	-	-
11866	HTSTNGI	-	-	+--	-	++	++	-
36246	LHKLSIN	-	-	+--	-	+++	+++	-
37622	RMQDAYP	-	-	+--	-	+++	+++	-
12069	SSSTNGV	-	-	+--	-	+++	+++	-
37641	RSEFTTY	-	-	+--	-	++	+++	-
38456	STYDSYP	-	-	+--	-	+++	++	-
14632	YSRIGPN	-	-	+--	-	+++	+++	+
36364	LCKPCLQ	-	-	+--	-	-	-	-
37750	LCRPCSN	-	-	+--	-	+++	+++	-
39103	KDEFTIY	-	-	+--	-	+++	++	-
37641	RSEFTTY	-	-	+--	-	++	++	-
14628	YSRLNDN	-	-	+--	++	+++	+++	-
36347	LSRIGPN	-	-	+--	-	+++	+++	++
12737	IESTNGR	-	-	+--	-	+++	++	-
36441	LCKPCTT	-	-	+--	-	+	+	-
37019	LHRLTAD	-	-	+--	-	+	+	-
36290	LHKLSPD	-	-	+--	-	++	++	-
36336	KDDFTTY	-	-	+--	-	+++	+++	-
36947	LHRLSMD	-	-	+--	-	-	-	-
37019	LHRLTAD	-	-	+--	-	-	+	-
36479	RTDTVYP	-	-	+--	-	+++	+++	-
36441	LCKPCTT	-	-	+--	-	-	-	-

36246	LHKLSIN	-	-	+--	-	+++	+++	-
37641	RSEFTTY	-	-	+--	-	++	++	-
38264	KDEFTKY	-	-	+--	-	++	++	-
36612	RDDFTSY	-	-	+--	-	++	-	-
36738	RMIDAYP	-	-	+--	-	+++	+++	-
36957	KDDYTTW	-	-	+--	-	+++	-	-
36260	LHKLSMN	-	-	+--	-	+++	+++	-
36633	RGVDVYP	-	-	+--	-	+++	+++	-
37045	KDDYSTY	-	-	+--	-	++	++	-
12707	VDSTNGR	-	-	+--	-	+++	+++	-
36251	LHKLGDN	-	-	+--	-	++	++	-
11826	VTSTNGI	-	-	+--	-	-	-	-
36727	LCKPCIT	-	-	+--	-	+	-	-
13841	LHRMTPN	-	-	+-	-	++	++	+
36805	RGESVYP	-	-	+-	-	+++	+++	-
11418	HESTNGV	-	-	+-	-	+++	+++	-
38456	STYDSYP	-	-	+-	-	++	++	-
37081	LHRLSYD	-	-	+-	-	++	-	-
36442	LSRVGPN	-	-	+-	-	+++	+++	++
36769	LHRLGYD	-	-	+-	-	-	-	-
36640	RLMDAYP	-	-	+-	-	+++	+++	-
36787	KDEFKSW	-	-	+-	-	++	++	-
37511	RREDVYP	-	-	+-	-	++	++	-
38753	YHRLSDN	-	-	+-	+	++	++	-
11451	TQSTNGV	-	-	+-	-	+++	++	-
36675	LMNDAYP	-	-	+-	-	+++	+++	-
38712	YHRLSEN	-	-	+-	-	++	++	-
38712	YHRLSEN	-	-	+-	-	++	++	-
37029	RSEFVSY	-	-	+-	-	++	++	-
11418	HESTNGV	-	-	+-	-	+++	++	-
12294	LESTNGI	-	-	+-	-	-	++	-
12038	VNSTNGI	-	-	+-	-	+++	+++	-
37115	RDMEVYP	-	-	+-	-	+++	++	-

36243	LHKLANN	-	-	+-	-	+++	++	-
36425	KDDFTMF	-	-	+-	-	++	++	-
36459	LARSGPN	-	-	+-	-	+++	+++	++
36356	RGLEGFD	-	-	+-	-	++	++	-
12707	VDSTNGR	-	-	+-	-	+++	+++	-
11472	VASTNGI	-	-	+-	-	+++	+++	-
14059	YSRVGPN	-	-	+-	-	+++	+++	++
17605	TESTHGR	-	-	+-	-	+++	+++	-
11846	TESTNGV	-	-	+-	-	++	++	-
37693	RDEFTVY	-	-	+-	-	+++	++	-
36612	RDDFTSY	-	-	+-	-	+++	++	-
38753	YHRLSDN	-	-	+-	-	+	++	-
36251	LHKLGDN	-	-	+-	-	++	++	-
38264	KDEFTKY	-	-	+-	-	++	++	-
37181	RTETTYP	-	-	+-	-	++	++	-
36459	LARSGPN	-	-	+-	-	+++	++	++
11418	HESTNGV	-	-	+-	-	+++	+++	-
17658	LHKLSNN	-	-	+-	-	+++	+++	-
36675	LMNDAYP	-	-	+-	-	+++	+++	-
16158	VMSTNGV	-	-	+-	-	+++	+++	-
37031	LHRLSHD	-	-	+-	-	+	-	-
36620	RGPDVFP	-	-	+-	-	++	-	-
12737	IESTNGR	-	-	+-	-	++	++	-
37029	RSEFVSY	-	-	+-	-	-	-	-
36463	RGETVFP	-	-	+-	-	+++	+++	-
36356	RGLEGFD	-	-	+-	-	++	+	-
36290	LHKLSPD	-	-	+-	-	++	++	-
36347	LSRIGPN	-	-	+-	-	+++	+++	++
36248	IALKGWD	-	-	+-	-	++	++	-
36279	LHKLLND	-	-	+-	-	-	-	-
36479	RTDTVYP	-	-	+-	-	+++	+++	-
36281	LHKLMPN	-	-	+-	-	++	++	-
36578	REENVYP	-	-	+-	-	++	-	-

38083	NTYDSYP	-	-	+-	-	++	++	-
36649	RLMDVYP	-	-	+-	-	++	-	-
36553	LCKPCQT	-	-	+-	-	-	-	-
37302	RLHDAYP	-	-	+-	-	+++	++	-
36243	LHKLANN	-	-	+-	-	+++	++	-
19906	VSEFTTY	-	-	+-	-	+++	+++	-
37213	RDDFTSW	-	-	+-	-	+++	++	-
36977	RDEFHSF	-	-	+-	-	++	-	-
36820	LCKPCNT	-	-	+-	-	-	-	-
36898	RGADVYP	-	-	+-	-	++	++	-
36744	RMLDAYP	-	-	+-	-	+++	++	-
36364	LCKPCLQ	-	-	+-	-	-	-	-
37622	RMQDAYP	-	-	+-	-	+++	+++	-
11472	VASTNGI	-	-	+-	-	++	-	-
37302	RLHDAYP	-	-	+-	-	+++	+++	-
36409	RGEHVFP	-	-	+-	-	+++	++	-
36347	LSRIGPN	-	-	+-	-	+++	+++	++
36479	RTDTVYP	-	-	+-	-	+++	++	-
36459	LARSGPN	-	-	+-	+	+++	++	++
37655	YHRLLPD	-	-	+-	-	+	+	-
11930	IQSTNGI	-	-	+-	-	++	+++	-
38712	YHRLSEN	-	-	+-	-	++	++	-
40923	ESEFKTY	-	-	+-	-	-	-	-
37115	RDMEVYP	-	-	+-	-	+++	-	-
36894	LHRAGPD	-	-	+-	-	++	++	+
14574	YSRLGPN	-	-	+-	-	++	++	-
13795	RDDFTAY	-	-	+-	-	++	++	-
37029	RSEFVSY	-	-	+-	-	++	++	-
11841	HNSTNGV	-	-	+-	-	+++	+++	-
14303	YSRLNEN	-	-	+-	-	++	++	-
36347	LSRIGPN	-	-	+-	-	+++	+++	+
36620	RGPDVFP	-	-	+-	-	++	-	-
36640	RLMDAYP	-	-	+-	-	+++	++	-

38273	LHRLLPN	-	-	+-	-	+++	+	-
37045	KDDYSTY	-	-	+-	-	++	-	-
36897	VSEFKVY	-	-	+-	-	-	-	-
36528	VMPDAFP	-	-	+-	-	-	-	-
36788	LHRLTTD	-	-	+-	-	-	-	-
36292	LTRLSPN	-	-	+-	-	++	++	-
36888	KDDFTMY	-	-	+-	-	++	-	-
11996	TSSTNGV	-	-	+-	-	+++	+++	-
36546	LHRLGMD	-	-	+-	-	-	-	-
36546	LHRLGMD	-	-	+-	-	-	-	-
36248	IALKGWD	-	-	+-	-	++	++	-
11866	HTSTNGI	-	-	+-	-	++	-	-
17752	RSEFVSF	-	-	+-	-	++	++	-
36766	RDDFTTW	-	-	+-	-	+++	++	-
14054	LAKTGPN	-	-	+-	-	++	-	-
36640	RLMDAYP	-	-	+-	-	+++	++	-
36713	RNDDVFP	-	-	+-	-	++	+++	-
37302	RLHDAYP	-	-	+-	-	+++	++	-
36766	RDDFTTW	-	-	+-	-	+++	++	-
11477	LAKGGPN	-	-	+-	-	++	++	-
36968	RMPDAYP	-	-	+-	-	++	+	-
36888	KDDFTMY	-	-	+-	-	++	-	-
36911	VSSTNGR	-	-	+-	-	+++	+++	+
37031	LHRLSHD	-	-	+-	-	+	+	-
38753	YHRLSDN	-	-	+-	-	+	-	-
18966	AHEFGPV	-	-	+-	-	++	-	-
36947	LHRLSMD	-	-	+-	-	-	-	-
36649	RLMDVYP	-	-	+-	-	++	-	-
17659	LCKPCLT	-	-	+-	-	-	++	-
36251	LHKLGDN	-	-	+-	-	++	+	-
14958	YSRTGPN	-	-	+-	-	++	++	++
36911	VSSTNGR	-	-	+-	-	+++	+++	+
36713	RNDDVFP	-	-	+-	-	++	++	-

37030	LHRLSQD	-	-	+-	-	-	-	-
11846	TESTNGV	-	-	+-	-	+++	+++	-
37912	RTHDVYP	-	-	+-	-	+++	-	-
38753	YHRLSDN	-	-	+-	-	+	-	-
11288	VGSTNGI	-	-	+-	-	++	+++	-
37030	LHRLSQD	-	-	+-	-	-	-	-
16112	VQSTNGR	-	-	+-	-	+++	++	+
11160	IESTNGV	-	-	+-	-	-	-	-
36738	RMIDAYP	-	-	+-	-	+++	+++	-
36248	IALKGWD	-	-	+-	-	++	++	-
36442	LSRVGPN	-	-	+-	-	+++	+++	++
37182	RNESVYP	-	-	+-	-	+++	+++	-
36409	RGEHVFP	-	-	+-	-	+++	+++	-
37302	RLHDAYP	-	-	+-	-	+++	+++	-
36262	LHKLAQN	-	-	+-	-	++	++	-
36262	LHKLAQN	-	-	+-	++	++	++	-
38707	GSEFKVF	-	-	+-	-	-	-	-
37204	RGDNVYP	-	-	+-	-	++	++	-
14048	YARNGPN	-	-	+-	-	+++	++	-
14958	YSRTGPN	-	-	+-	-	++	++	+
36947	LHRLSMD	-	-	+-	-	-	-	-
37990	KDDYSHY	-	-	+-	-	+	-	-
36349	RLEDAFP	-	-	+-	-	++	-	-
36285	LHKLSVD	-	-	+-	-	+	+	-
12038	VNSTNGI	-	-	+-	-	+++	++	-
16158	VMSTNGV	-	-	+-	-	++	++	-
11841	HNSTNGV	-	-	+-	-	+++	+++	-
37705	KDEFKVY	-	-	+-	-	+	-	-
11866	HTSTNGI	-	-	+-	-	++	-	-
38903	YESTNGR	-	-	+-	-	+++	++	-
14048	YARNGPN	-	-	+-	-	+++	+++	-
36281	LHKLMPN	-	-	+-	-	++	+	-
38843	YHRLSAN	-	-	+-	-	++	-	-

14303	YSRLNEN	-	-	+-	-	++	++	-
36534	LHRLSLD	-	-	+-	-	+	+	-
36406	KDDFVAW	-	-	+-	-	-	-	-
36344	YSKAGGG	-	-	+-	-	++	++	-
37204	RGDNVYP	-	-	+-	-	++	++	-
11853	HQSTNGV	-	-	+-	-	+++	+++	-
36947	LHRLSMD	-	-	+-	-	-	-	-
11338	ITSTNGI	-	-	+-	-	+	-	-
37030	LHRLSQD	-	-	+-	-	-	-	-
17605	TESTHGR	-	-	+-	-	+++	+++	-
11596	IESTNGI	-	-	+-	-	-	-	-
12229	ISSTNGI	-	-	+-	-	++	++	-
36553	LCKPCQT	-	-	+-	-	-	-	-
11596	IESTNGI	-	-	+-	-	++	++	-
36344	YSKAGGG	-	-	+-	-	+++	++	+
38083	NTYDSYP	-	-	+-	-	+++	++	-
16113	THSTNGV	-	-	+-	-	++	++	+
36556	VMPDAYP	-	-	+-	-	-	-	-
14059	YSRVGPN	-	-	+-	-	+++	+++	++
11633	ASSTNGV	-	-	+-	-	++	++	-
36951	RMADAFP	-	-	+-	-	-	++	-
13795	RDDFTAY	-	-	+-	-	++	+	-
36794	RGDDVFP	-	-	+-	-	++	-	-
36627	REDSVRW	-	-	+-	-	+++	+++	-
12009	SSSTNGI	-	-	+-	-	++	++	-
36788	LHRLTTD	-	-	+-	-	+	-	-
11531	VISTNGI	-	-	+-	-	++	-	-
36534	LHRLSLD	-	-	+-	-	+	-	-
36604	VALEGRD	-	-	+-	-	++	-	-
37121	RSEETYP	-	-	+-	-	-	-	-
11477	LAKGGPN	-	-	+-	-	++	+++	-
36968	RMPDAYP	-	-	+-	-	++	++	-
11714	STSTNGV	-	-	+-	-	++	++	-

37705	KDEFKVY	-	-	+-	-	+	-	-
37068	YSRLNDD	-	-	+-	-	+	+	-
36633	RGVDVYP	-	-	+-	-	+++	+++	-
37655	YHRLLPD	-	-	+-	-	-	-	-
36745	LHRLGQD	-	-	+-	-	-	-	-
36289	RTIDVFP	-	-	+-	-	++	-	-
37181	RTETTYP	-	-	+-	-	++	++	-
14600	IQSTNGV	-	-	+-	-	++	++	-
12229	ISSTNGI	-	-	+-	-	++	+++	-
36968	RMPDAYP	-	-	+-	-	++	-	-
36285	LHKLSVD	-	-	+-	-	++	+	-
14054	LAKTGPN	-	-	+-	-	++	-	-
37419	RNDHVFP	-	-	+-	-	+++	++	-
37144	RSESVYP	-	-	+-	-	++	++	-
36787	KDEFKSW	-	-	+-	-	++	++	-
11338	ITSTNGI	-	-	+-	-	+	-	-
36760	REDGVRW	-	-	+-	-	+++	+++	-
17878	VMADAFP	-	-	+-	-	++	-	-
11531	VISTNGI	-	-	+-	-	-	-	-
36688	LCKPCST	-	-	+-	-	-	-	-
12577	YDSTNGV	-	-	+-	-	+++	+++	-
38712	YHRLSEN	-	-	+-	-	++	++	-
17676	LHSKLPN	-	-	+-	-	++	-	-
12013	HDSTNGV	-	-	+-	-	+++	+++	-
38640	KNDYTVF	-	-	+-	-	++	++	-
36266	LHKLMNN	-	-	+-	-	+	-	-
37204	RGDNVYP	-	-	+-	-	++	+	-
36898	RGADVYP	-	-	+-	-	++	++	-
11531	VISTNGI	-	-	+-	-	-	-	-
36897	VSEFKVY	-	-	+-	-	-	-	-
36745	LHRLGQD	-	-	+-	-	-	-	-
36287	LAKSGPN	-	-	+-	-	++	++	-
37248	FHRLGPD	-	-	+-	-	-	-	-

12265	LHKNLPD	-	-	+-	-	-	-	-
11338	ITSTNGI	-	-	+-	-	-	-	-
14274	YAKTGPN	-	-	+-	+	+	+	-
36640	RLMDAYP	-	-	+-	-	+++	+++	-
36445	YHAKLPN	-	-	+-	-	+	++	-
36562	RTDHVFP	-	-	+-	-	+++	-	-
36940	RGDTVYP	-	-	+-	-	++	-	-
38324	KDDFSAY	-	-	+-	-	-	-	-
36579	RALEGYD	-	-	+-	-	++	-	-
36636	RGDNVFP	-	-	+-	-	++	++	-
37511	RREDVYP	-	-	+-	-	++	++	-
37419	RNDHVFP	-	-	+-	-	++	++	-
36318	LARTGPD	-	-	+-	-	-	-	-
36572	REDTVKW	-	-	+-	-	+++	+++	-
12229	ISSTNGI	-	-	+-	-	++	++	-
37182	RNESVYP	-	-	+-	-	+++	+++	-
36496	YVKSDTR	-	+	+-	+	++	++	-
11164	PQSTNGV	-	-	+-	-	++	-	-
16112	VQSTNGR	-	-	+-	-	++	++	+
16112	VQSTNGR	-	-	+-	-	++	++	-
36556	VMPDAYP	-	-	+-	-	-	-	-
36951	RMADAFP	-	-	+-	-	++	++	-
16113	THSTNGV	-	-	+-	-	++	++	-
37144	RSESVYP	-	-	+-	-	++	++	-
11967	LAKNGPN	-	-	+-	-	+	-	-
40416	KNDYATW	--	-	+-	+++	-	-	-
37296	REETVYP	-	-	+-	-	-	-	-
38224	RDATSSW	-	-	+-	-	-	-	-
14499	VISTNGV	-	-	+-	-	++	++	-
12073	HASTNGV	-	-	+-	-	++	++	-
17596	RLADAYP	-	-	+-	-	++	++	-
37295	RDDFTVW	-	-	+-	-	++	+	-
17704	KDDFSVY	-	-	+-	-	-	-	-

36496	YVKSDTR	-	-	+-	-	++	+	-
36701	RDEFTSF	-	-	+-	-	+++	-	-
36968	RMPDAYP	-	-	+-	-	++	+	-
11878	TNSTNGV	-	-	+-	-	++	++	-
37248	FHRLGPD	-	-	+-	-	-	-	-
36292	LTRLSPN	-	-	+-	-	++	++	-
12176	TSSTNGI	-	-	+-	-	++	+++	-
36554	LHRLSID	-	-	+-	-	+	-	-
36287	LAKSGPN	-	-	+-	-	++	++	-
36562	RTDHVFP	-	-	+-	-	++	++	-
36551	RGPEVFP	-	-	+-	-	-	-	-
36805	RGESVYP	-	-	+-	-	+++	-	-
36534	LHRLSLD	-	-	+-	-	-	-	-
36666	LHASGPN	-	-	+-	-	++	++	-
11644	TESTNGI	-	-	+-	-	++	++	-
16619	LHKAGYN	-	-	+-	-	++	++	-
37440	RNEFTPF	-	-	+-	-	-	-	-
17596	RLADAYP	-	-	+-	-	++	++	-
36945	REDGVKW	-	-	+-	-	++	++	-
16602	VHRLQDK	-	-	+-	-	++	++	+
16158	VMSTNGV	-	-	+-	-	+++	+++	-
14581	YSKLNDN	-	-	+-	-	++	-	-
37951	KDDFTGF	-	-	+-	-	-	-	-
36701	RDEFTSF	-	-	+-	-	+++	+++	-
37303	LCRPCPE	-	-	+-	-	-	-	-
36266	LHKLMNN	-	-	+-	-	+	-	-
36554	LHRLSID	-	-	+-	-	+	-	-
37691	APDSVRW	-	-	+-	-	-	-	-
11996	TSSTNGV	-	-	+-	-	++	++	-
14350	YSRLNAN	-	-	+-	-	++	++	++
11915	ITSTNGV	-	-	+-	-	++	-	-
11338	ITSTNGI	-	-	+-	-	-	-	-
36496	YVKSDTR	-	-	+-	-	++	++	-

36481	KDDFSTY	-	-	+-	-	++	-	-
11866	HTSTNGI	-	-	+-	-	++	+++	-
36318	LARTGPD	-	-	+-	-	-	-	-
36701	RDEFTSF	-	-	+-	-	+++	-	-
13818	YSRLNVN	-	-	+-	-	++	++	+
36711	APGSVRW	---	+++	+-	++	++	-	-
38380	YSRLSPN	-	-	+-	-	-	+	-
11967	LAKNGPN	-	-	+-	-	+	+	-
36606	IHRLGPD	-	-	+-	-	-	-	-
11338	ITSTNGI	-	-	+-	-	+	-	-
11864	TASTNGI	-	-	+-	-	+	-	-
36296	RTPEVFP	-	-	+-	-	++	++	-
41567	GANTSRW	-	-	+-	-	-	-	-
11757	VFSTNGV	-	-	+-	-	++	++	+
37589	RDEFKSW	-	-	+-	-	++	++	-
37313	RTNDVYP	-	-	+-	-	++	++	-
37589	RDEFKSW	-	-	+-	-	++	++	-
36540	LHKMSMN	-	-	+-	-	++	+	-
38843	YHRLSAN	-	-	+-	-	++	+	-
12229	ISSTNGI	-	-	+-	-	++	++	-
11787	THSTNGI	-	-	+-	-	++	++	-
14392	IHSTNGV	-	-	+-	-	++	++	-
11765	VGSTNGV	-	-	+-	-	++	++	-
36481	KDDFSTY	-	-	+-	-	++	-	-
36496	YVKSDTR	-	-	+-	-	++	+	-
11714	STSTNGV	-	-	+-	-	++	++	-
36496	YVKSDTR	-	-	+-	-	+	++	-
36331	LARLGPN	-	-	+-	-	-	-	-
11421	ESSTNGR	-	-	+-	-	+	-	-
14499	VISTNGV	-	-	+-	-	++	++	-
36295	MHKLSPN	-	-	+-	-	++	+	-
13864	YARSGPN	-	-	+-	-	++	++	++
13517	YSRLNIN	-	-	+-	-	++	++	+

37043	RDENVFP	-	-	+-	-	+++	++	-
38843	YHRLSAN	-	-	+-	-	++	++	-
36540	LHKMSMN	-	-	+-	-	++	++	+
36445	YHAKLPN	-	-	+-	-	++	-	-
36280	LHKLSID	-	-	+-	-	++	+	-
36288	LSKLSPN	-	-	+-	-	+	-	-
36295	MHKLSPN	-	-	+-	-	++	++	+
16158	VMSTNGV	-	-	+-	-	++	++	-
36452	LHVKLPD	-	-	+-	-	-	-	-
11451	TQSTNGV	-	-	+-	-	++	++	-
36496	YVKSDTR	-	-	+-	+	++	++	-
14350	YSRLNAN	-	-	+-	-	++	++	++
36940	RGDTVYP	-	-	+-	-	++	-	-
16602	VHRLQDK	-	-	+-	-	++	++	-
36294	LHKLSHD	-	-	+-	-	+	-	-
37067	REDHVSW	-	-	+-	-	+++	+++	-
37536	RDEFTHY	-	-	+-	-	+++	+++	-
17025	VESSNGR	-	-	+-	-	++	-	-
37133	RMSDAYP	-	-	+-	-	+	+	-
11692	TTSTNGV	-	-	+-	-	++	++	-
14394	INSTNGV	-	-	+-	-	++	+	-
12025	TTSTNGI	-	-	+-	-	-	-	-
36987	REETVFP	-	-	+-	-	-	-	-
11867	SDSTNGI	-	-	+-	-	++	+	-
18112	ASSTNGR	-	-	+-	-	++	+	-
36387	FHKLSPN	-	-	+-	-	+	+	-
37498	KDEYHTY	-	-	+-	-	+++	+++	-
13884	TNSTNGI	-	-	+-	-	++	++	-
37030	LHRLSQD	-	-	+-	-	-	-	-
36867	RTADAYP	-	-	+-	-	++	++	-
36693	YHAAGPN	-	-	+-	-	++	-	-
36315	LHKLSTD	-	-	+-	-	+	+	-
36288	LSKLSPN	-	-	+	-	+	-	-

11986	LHSTNGI	-	-	+	-	++	-	-
36791	RGDDVYP	-	-	+	-	+++	-	-
36606	IHRLGPD	-	-	+	-	-	-	-
37693	RDEFTVY	-	-	+	-	+++	-	-
36280	LHKLSID	-	-	+	-	+	-	-
36996	KDDYSIY	-	-	+	-	-	-	-
16004	TQSTNGI	-	-	+	-	++	++	-
36540	LHKMSMN	-	-	+	-	++	++	+
36523	YHKLNDN	-	-	+	-	+	+	-
36425	KDDFTMF	-	-	+	-	++	-	-
38582	RNEFSTY	-	-	+	-	-	-	-
36280	LHKLSID	-	-	+	-	+	-	-
38764	YHRLGDN	-	-	+	-	-	-	-
14274	YAKTGPN	-	-	+	-	++	+	-
37910	YSRVGGG	-	-	+	-	++	+	++
36362	VKSTNGV	-	-	+	-	++	+	+
36291	LTKLSPN	-	-	+	-	+	-	-
37498	KDEYHTY	-	-	+	-	+++	+++	-
17752	RSEFVSF	-	-	+	-	++	-	-
37133	RMSDAYP	-	-	+	-	++	+	-
12289	HSSTNGI	-	-	+	-	++	-	-
36426	YVKSDMK	-	-	+	-	-	-	-
36741	YHKLNEN	-	-	+	-	++	-	-
14441	YAKSGPN	-	-	+	-	+	++	-
37521	LCKPCLV	-	-	+	-	-	-	-
36362	VKSTNGV	-	-	+	-	++	++	-
13934	FARTGPN	-	-	+	-	+	-	-
37133	RMSDAYP	-	-	+	-	++	+	-
37705	KDEFKVY	-	-	+	-	-	-	-
36791	RGDDVYP	-	-	+	-	+++	-	-
17013	RNEYTTY	-	-	+	-	++	-	-
36609	LAKTAPN	-	-	+	-	-	-	-
38380	YSRLSPN	-	-	+	-	-	+	-

36387	FHKLSPN	-	-	+	-	+	+	-
36982	RDDFTVY	-	-	+	-	++	++	-
37516	RNEFTTF	-	-	+	-	++	-	-
36693	YHAAGPN	-	-	+	-	+	+	-
40185	FIKHDTK	-	-	+	-	-	-	-
16619	LHKAGYN	-	-	+	-	++	++	+
12009	SSSTNGI	-	-	+	-	++	++	-
14176	YSKIGPN	-	-	+	-	+	-	-
11633	ASSTNGV	-	-	+	-	++	-	-
36540	LHKMSMN	-	-	+	-	++	+	+
17659	LCKPCLT	-	-	+	-	-	-	-
36778	YHKLNNN	-	-	+	-	-	-	-
37910	YSRVGGG	-	-	+	-	++	++	+
36991	LSRTSLN	-	-	+	-	-	-	+
11684	RESTNGI	-	-	+	-	++	-	-
37056	RMTDAYP	-	-	+	-	++	++	-
17971	WDNGVTG	-	-	+	-	++	++	-
36265	LHKLSFD	-	-	+	-	++	++	-
12034	LHKNTEN	-	-	+	-	-	-	-
13864	YARSGPN	-	-	+	-	++	++	+
37362	RTSDAYP	-	-	+	-	++	-	-
36491	LARTGLN	-	-	+	-	++	+	++
11841	HNSTNGV	-	-	+	-	+++	+++	-
11288	VGSTNGI	-	-	+	-	+++	++	-
14198	YAKNGPN	-	-	+	-	+	-	-
37713	YESTNGK	-	-	+	-	++	-	-
14441	YAKSGPN	-	-	+	-	+	-	-
14200	YSKLNFN	-	-	+	-	++	++	+
12070	RDSTNGI	-	-	+	-	++	++	-
36301	FHKLGPD	-	-	+	-	-	-	-
37045	KDDYSTY	-	-	+	-	++	-	-
39271	KDDWTTY	-	-	+	-	++	-	-
36826	LSRLSPD	-	-	+	-	-	-	-

11418	HESTNGV	-	-	+	-	+++	+++	-
11841	HNSTNGV	-	-	+	-	+++	+++	-
36280	LHKLSID	-	-	+	-	++	+	-
11534	LSSTNGV	-	-	+	-	-	++	-
17775	LHRLSSD	-	-	+	-	-	-	-
38273	LHRLLPN	-	-	+	-	+++	+++	-
16013	YSKTGPN	-	-	+	-	-	-	-
11374	LSSTNGI	-	-	+	-	++	++	-
40141	RTYEVYP	-	-	+	-	++	-	-
14327	LSRLNDN	-	-	+	-	-	-	-
11160	IESTNGV	-	-	+	-	-	-	-
36395	LTRLHPD	-	-	+	-	-	-	-
16186	HHSTNGV	-	-	+	-	++	++	-
37045	KDDYSTY	-	-	+	-	++	-	-
11819	ISSTNGV	-	-	+	-	++	++	-
11915	ITSTNGV	-	-	+	-	-	-	-
19710	IESREGI	-	-	+	-	+++	+++	-
36637	LHKLSSD	-	-	+	-	-	-	-
12707	VDSTNGR	-	-	+	-	+++	++	-
36609	LAKTAPN	-	-	+	-	-	-	-
36523	YHKLNDN	-	-	+	-	+	+	-
36361	KDEFSSW	-	-	+	-	+	-	-
19710	IESREGI	-	-	+	-	++	++	-
36848	YARTGPD	-	-	+	-	-	-	-
36310	RTLDVFP	-	-	+	-	++	-	-
36360	LHKAGHN	-	-	+	-	+	-	-
37322	KDEFRSF	-	-	+	-	++	-	-
14441	YAKSGPN	-	-	+	-	+	-	-
38456	STYDSYP	-	-	+	-	+++	++	-
37402	RDMDVYP	-	-	+	-	-	-	-
37910	YSRVGGG	-	-	+	-	++	++	+
11908	YESTNGV	-	-	+	-	+++	+++	-
36489	YVKSDMR	-	-	+	-	-	-	-

36491	LARTGLN	-	-	+	-	+	++	++
11188	LAKGGFN	-	-	+	-	++	+	++
36989	RDEHVFP	-	-	+	-	+++	+++	-
39421	YDSTNGR	-	-	+	-	+++	++	-
13537	YSKLNIN	-	-	+	-	++	+	+
11684	RESTNGI	-	-	+	-	++	++	-
36579	RALEGYD	-	-	+	-	++	-	-
11586	VLSTNGV	-	-	+	-	++	-	-
14198	YAKNGPN	-	-	+	-	+	-	-
36845	VTSSNGI	-	-	+	-	-	-	-
36636	RGDNVFP	-	-	+	-	-	-	-
39421	YDSTNGR	-	-	+	-	++	-	-
14301	YSRLNMN	-	-	+	-	+	-	+
36655	KDDFHTY	-	-	+	-	++	-	-
37239	RTDDAFP	-	-	+	-	-	++	-
18036	TDETVYR	-	-	+	-	++	-	-
36289	RTIDVFP	-	-	+	-	++	-	-
12030	VESSNGV	-	-	+	-	++	-	-
37315	LCRPCSS	-	-	+	-	-	-	-
12255	HDSTNGR	-	-	+	-	-	-	-
14005	YSKLGPN	-	-	+	-	++	++	-
11765	VGSTNGV	-	-	+	-	+++	+	-
37328	RSEFETF	-	-	+	-	-	-	-
14243	YSRLNSN	-	-	+	-	+	+	+
16112	VQSTNGR	-	-	+	-	++	++	+
39421	YDSTNGR	-	-	+	-	++	++	-
13535	YSRLNNN	-	-	-	-	++	++	++
36744	RMLDAYP	-	-	-	-	+++	++	-
36489	YVKSDMR	-	-	-	-	+	-	-
37750	LCRPCSN	-	-	-	-	+++	+	-
14207	YSKLNTN	-	-	-	-	+	-	+
37322	KDEFRSF	-	-	-	-	++	++	-
11615	TDSTNGI	-	-	-	-	++	-	-

11848	TDSTNGV	-	-	-	-	++	-	-
36608	KDEFSGY	-	-	-	-	++	-	-
36957	KDDYTTW	-	-	-	-	+++	-	-
36400	EALEGRD	-	-	-	-	+	-	-
11279	RESTNGV	-	-	-	-	++	++	-
12381	SESTNGV	-	-	-	-	++	-	-
36608	KDEFSGY	-	-	-	-	++	+	-
36730	RDDFTTF	-	-	-	-	++	+	-
12312	VDSTNGI	-	-	-	-	+++	+++	-
37204	RGDNVYP	-	-	-	-	++	++	-
36791	RGDDVYP	-	-	-	-	++	+++	-
12052	SQSTNGI	-	-	-	-	++	-	-
17775	LHRLSSD	-	-	-	-	+	-	-
11279	RESTNGV	-	-	-	-	++	-	-
16158	VMSTNGV	-	-	-	-	++	++	+
11924	IHSTNGI	-	-	-	-	++	++	-
11940	IISTNGI	-	-	-	-	+	+	-
11487	IDSTNGV	-	-	-	-	++	++	-
14600	IQSTNGV	-	-	-	-	++	++	-
38843	YHRLSAN	-	-	-	-	+	-	-
38903	YESTNGR	-	-	-	-	+++	++	-
39421	YDSTNGR	-	-	-	-	++	++	-
11164	PQSTNGV	-	-	-	-	++	-	-
36627	REDSVRW	-	-	-	-	+++	-	-
36593	RTNDVFP	-	-	-	-	++	++	+
11924	IHSTNGI	-	-	-	-	++	++	-
39271	KDDWTTY	-	-	-	-	++	-	-
36866	REETVRW	-	-	-	-	++	++	-
36397	VSEFLSY	-	-	-	-	++	-	-
12014	VSSQNGV	-	-	-	-	+++	+++	-
16158	VMSTNGV	-	-	-	-	++	++	-
14176	YSKIGPN	-	-	-	-	+	-	-
37133	RMSDAYP	-	-	-	-	+	++	-

14392	IHSTNGV	-	-	-	-	++	++	-
37705	KDEFKVY	-	-	-	-	+	-	-
11338	ITSTNGI	-	-	-	-	+	-	-
11787	THSTNGI	-	-	-	-	++	++	-
36564	RTNEVFP	-	-	-	-	++	-	-
37990	KDDYSHY	-	-	-	-	++	-	-
11908	YESTNGV	-	-	-	-	+++	+++	-
37567	KDEFKSY	-	-	-	-	+	-	-
36801	RDDFTMY	-	-	-	-	++	-	-
16004	TQSTNGI	-	-	-	-	++	++	-
38102	RDEFKSF	-	-	-	-	++	-	-
12113	SDSTNGR	-	-	-	-	+	-	-
37571	RDEFSSF	-	-	-	-	++	-	-
16573	RSEHVFP	-	-	-	-	++	++	-
36578	REENVYP	-	-	-	-	++	++	-
12501	IDSTNGI	-	-	-	-	++	-	-
36636	RGDNVFP	-	-	-	-	++	-	-
11684	RESTNGI	-	-	-	-	++	++	-
11974	VSSTNGI	-	-	-	-	+++	-	-
12205	FQSTNGV	-	-	-	-	++	++	-
36256	RLVDVFP	-	-	-	-	++	-	-
11819	ISSTNGV	-	-	-	-	++	-	-
11455	HVSTNGV	-	-	-	-	+	-	-
36867	RTADAYP	-	-	-	-	++	++	-
36470	RTDDTFP	-	-	-	-	+	-	-
11882	ASSTNGI	-	-	-	-	+	-	-
37536	RDEFTHY	-	-	-	-	+++	+++	-
11774	SQSTNGV	-	-	-	-	++	-	-
36564	RTNEVFP	-	-	-	-	++	++	-
11516	AESTNGR	-	-	-	-	++	++	-
37138	KDEFVSF	-	-	-	-	++	-	-
14581	YSKLNDN	-	-	-	-	++	++	-
12020	PSSTNGV	-	-	-	-	++	-	-

14050	YSKLNAN	-	-	-	-	+	-	-
37844	KSEYSTY	-	-	-	-	++	++	-
37124	RMSDAFP	-	-	-	-	+	-	-
38305	RDDYSTY	-	-	-	-	++	++	-
16636	YHRLSNN	-	-	-	-	++	-	-
36760	REDGVRW	-	-	-	-	++	+++	-
36303	LHKLQQN	-	-	-	-	+	+	-
16573	RSEHVFP	-	-	-	-	++	++	-
37562	MHRLSTN	-	-	-	-	+	-	-
11844	SNSTNGI	-	-	-	-	++	++	-
36957	KDDYTTW	-	-	-	-	+++	-	-
36429	VKSTNGI	-	-	-	-	+	-	-
36945	REDGVKW	-	-	-	-	++	-	-
36261	LSKLSYN	-	-	-	-	+	-	-
12289	HSSTNGI	-	-	-	-	++	++	-
14394	INSTNGV	-	-	-	-	++	++	-
13848	YSRLNLN	-	-	-	-	++	+	+
11878	TNSTNGV	-	-	-	-	++	++	-
36860	RSDVVYP	-	-	-	-	++	++	-
12501	IDSTNGI	-	-	-	-	++	++	-
11729	AASTNGV	-	-	-	-	++	-	-
14461	YSKLNYN	-	-	-	-	++	++	+
18112	ASSTNGR	-	-	-	-	++	+	+
11615	TDSTNGI	-	-	-	-	++	++	-
36583	IMMDAYP	-	-	-	-	++	++	-
37102	RTYDSFV	-	-	-	-	++	++	-
36741	YHKLNEN	-	-	-	-	+	+	-
12030	VESSNGV	-	-	-	-	++	-	-
11366	VSSSNGV	-	-	-	-	++	++	-
11442	HDSSNGV	-	-	-	-	+	-	-
11844	SNSTNGI	-	-	-	-	++	-	-
11684	RESTNGI	-	-	-	-	++	++	-
12098	RDSTNGV	-	-	-	-	++	-	-

11188	LAKGGFN	-	-	-	-	++	+	-
11154	LSKLGPN	-	-	-	-	+	-	-
11720	SESTNGR	-	-	-	-	+	-	-
16186	HHSTNGV	-	-	-	-	++	++	-
36701	RDEFTSF	-	-	-	-	+++	+++	-
12100	VHSSNGV	-	-	-	-	+	-	-
36557	REEHVFP	-	-	-	-	++	-	-
38640	KNDYTVF	-	-	-	-	++	++	-
37472	KDDYHTY	-	-	-	-	++	-	-
11720	SESTNGR	-	-	-	-	+	-	-
36598	LHRLSPL	-	-	-	-	+	-	-
13517	YSRLNIN	-	-	-	-	++	++	+
37454	RDEFSGY	-	-	-	-	++	-	-
36323	KDDFSTW	-	-	-	-	++	-	-
36791	RGDDVYP	-	-	-	-	+++	-	-
11964	HTSSNGV	-	-	-	-	++	-	-
12070	RDSTNGI	-	-	-	-	++	-	-
14207	YSKLNTN	-	-	-	-	+	-	-
12523	HESTNGR	-	-	-	-	++	-	-
11493	SHSTNGV	-	-	-	-	++	+	-
13818	YSRLNVN	-	-	-	-	++	++	++
36303	LHKLQQN	-	-	-	-	++	-	-
38091	LHANGPN	-	-	-	-	+	-	-
38160	GNEFSSW	-	-	-	-	++	-	-
37015	NDGTSKW	-	-	-	-	++	++	-
37045	KDDYSTY	-	-	-	-	++	-	-
36310	RTLDVFP	-	-	-	-	++	-	-
36652	LARTGMN	-	-	-	-	+	-	++
38091	LHANGPN	-	-	-	-	+	-	-
37310	RDGTSSW	-	-	-	-	+	-	-
11684	RESTNGI	-	-	-	-	+	-	-
37571	RDEFSSF	-	-	-	-	+	-	-
11188	LAKGGFN	-	-	-	-	+	-	-

36534	LHRLSLD	-	-	-	-	+	-	-
38223	YSRIGPD	-	-	-	-	+	+	-
36655	KDDFHTY	-	-	-	-	++	-	-
36361	KDEFSSW	-	-	-	-	+	-	-
39179	RDSTHGI	-	-	-	-	+	-	-
11490	FESTNGV	-	-	-	-	++	-	-
17701	VALKGWD	-	-	-	-	+	-	-
18036	TDETVYR	-	-	-	-	++	-	-
36291	LTKLSPN	-	-	-	-	+	+	-
36361	KDEFSSW	-	-	-	-	+	-	-
37056	RMTDAYP	-	-	-	-	++	++	-
37910	YSRVGGG	-	-	-	-	++	++	+
37553	RSEHTYP	-	-	-	-	+	-	-
11490	FESTNGV	-	-	-	-	++	+++	-
36426	YVKSDMK	-	-	-	-	+	+	-
11363	IASTNGI	-	-	-	-	++	-	-
36709	REDFVSW	-	-	-	-	++	-	-
11418	HESTNGV	-	-	-	-	+++	+	-
14481	PTSTNGV	-	-	-	-	++	++	-
14441	YAKSGPN	-	-	-	-	+	-	-
36794	RGDDVFP	-	-	-	-	++	-	-
11106	VFSTNGI	-	-	-	-	++	-	-
37313	RTNDVYP	-	-	-	-	++	-	+
36424	RLLDAYP	-	-	-	-	++	-	-
16011	PASTNGV	-	-	-	-	+	+	+
11864	TASTNGI	-	-	-	-	+	-	-
36251	LHKLGDN	-	-	-	-	++	-	-
11154	LSKLGPN	-	-	-	-	+	-	-
11493	SHSTNGV	-	-	-	-	++	-	-
36931	RDEFHSY	-	-	-	-	+	+	-
13517	YSRLNIN	-	-	-	-	++	++	+
37007	KDDYSVF	-	-	-	-	++	-	-
14388	YSKLNLN	-	-	-	-	+	-	+

36824	GSEFSTW	-	-	-	-	+	-	-
39103	KDEFTIY	-	-	-	-	+++	++	-
17013	RNEYTTY	-	-	-	-	++	++	-
37215	RNDTVYP	-	-	-	-	++	-	-
39369	RDEFTKF	-	-	-	-	+	-	-
37045	KDDYSTY	-	-	-	-	++	-	-
36360	LHKAGHN	-	-	-	-	+	-	-
37516	RNEFTTF	-	-	-	-	++	-	-
12577	YDSTNGV	-	-	-	-	+++	+++	-
11607	PNSTNGV	-	-	-	-	++	++	-
36793	LSRTSVN	-	-	-	-	+	-	+
36866	REETVRW	-	-	-	-	++	++	-
36846	REEDVYP	-	-	-	-	++	-	-
38307	GSSTSTW	-	-	-	-	++	-	-
11447	LHSTNGV	-	-	-	-	+	+	-
17878	VMADAFP	-	-	-	-	++	-	-
11898	TFSTNGV	-	-	-	-	+	-	-
37187	LSRISPN	-	-	-	-	+	-	++
11271	LAKTGFN	-	-	-	-	+	-	-
13841	LHRMTPN	-	-	-	-	++	++	+
38305	RDDYSTY	-	-	-	-	++	-	-
38305	RDDYSTY	-	-	-	-	++	-	-
37021	RGEEVFP	-	-	-	-	++	-	-
14494	YNSTNGV	-	-	-	-	++	++	-
14494	YNSTNGV	-	-	-	-	++	++	-
38200	YDKGTWD	-	-	-	-	+	-	-
36436	RLDDVFP	-	-	-	-	++	+	-
38305	RDDYSTY	-	-	-	-	++	++	-
12069	SSSTNGV	-	-	-	-	+++	-	-
11698	HESTNGI	-	-	-	-	++	++	-
36666	LHASGPN	-	-	-	-	++	++	-
14259	YSKLNVN	-	-	-	-	+	-	+
14860	LSRTSTN	-	-	-	-	+	-	++

39369	RDEFTKF	-	-	-	-	++	-	-
37643	RDDHVYP	-	-	-	-	++	++	-
37643	RDDHVYP	-	-	-	-	++	++	-
36428	REEGVSW	-	-	-	-	++	++	-
36400	EALEGRD	-	-	-	-	+	++	-
18531	GSPSSSW	-	-	-	-	++	++	-
11224	HISTNGV	-	-	-	-	++	-	-
17676	LHSKLPN	-	-	-	-	++	+	-
12144	TASTNGV	-	-	-	-	++	++	-
37713	YESTNGK	-	-	-	-	++	++	-
11720	SESTNGR	-	-	-	-	++	++	-
37288	RDDFSSY	-	-	-	-	+	-	-
11867	SDSTNGI	-	-	-	-	++	-	-
37041	GGESSSW	-	-	-	-	+	-	-
13884	TNSTNGI	-	-	-	-	++	-	-
37844	KSEYSTY	-	-	-	-	+	-	-
11930	IQSTNGI	-	-	-	-	++	++	-
11106	VFSTNGI	-	-	-	-	+	-	-
38046	FHRLSPN	-	-	-	-	+	-	-
37472	KDDYHTY	-	-	-	-	++	-	-
36323	KDDFSTW	-	-	-	-	+	-	-
38079	YDSTNGL	-	-	-	-	++	++	-
13517	YSRLNIN	-	-	-	-	++	-	-
37942	RDEFKSY	-	-	-	-	+	-	-
11720	SESTNGR	-	-	-	-	++	-	-
11720	SESTNGR	-	-	-	-	++	-	-
14481	PTSTNGV	-	-	-	-	++	-	-
36247	LSKLSFN	-	-	-	-	+	++	-
37121	RSEETYP	-	-	-	-	+	-	-
36636	RGDNVFP	-	-	-	-	++	+	-
37488	YSRVGPD	-	-	-	-	+	-	+
12021	KDGNSSW	-	-	-	-	+	-	-
36851	LCKPCHT	-	-	-	-	+	-	-

11529	HNSSNGV	-	-	-	-	+	-	-
12176	TSSTNGI	-	-	-	-	++	++	-
36652	LARTGMN	-	-	-	-	+	-	+
12027	FSSTNGV	-	-	-	-	++	-	-
40717	KTEFTTY	-	-	-	-	+	-	-
36940	RGDTVYP	-	-	-	-	++	++	-
12692	TESSNGV	-	-	-	-	+	-	-
37416	MKDGTNP	-	-	-	-	+	-	-
12796	FDSTNGR	-	-	-	-	++	-	-
36792	VESFNGR	-	-	-	-	+	-	-
12027	FSSTNGV	-	-	-	-	++	-	-
36458	YVKSDSR	-	-	-	-	+	-	-
36569	RLMDAFP	-	-	-	-	++	-	-
37531	RGEEIYP	-	-	-	-	++	-	-
11855	PHSTNGV	-	-	-	-	++	-	-
12179	SNSTNGV	-	-	-	-	++	++	-
12481	VQSSNGV	-	-	-	-	++	-	-
36593	RTNDVFP	-	-	-	-	++	-	-
11986	LHSTNGI	-	-	-	-	++	-	-
36427	REDAVRW	-	-	-	-	++	-	-
36967	KDDFHSY	-	-	-	-	++	-	-
37347	RNMDVYP	-	-	-	-	++	-	-
37095	KDDYTVF	-	-	-	-	+++	-	-
11684	RESTNGI	-	-	-	-	++	-	-
13844	YSRLNTN	-	-	-	-	+	+	-
12097	TMSTNGI	-	-	-	-	+	+	-
36583	IMMDAYP	-	-	-	-	++	-	-
11757	VFSTNGV	-	-	-	-	++	-	-
11675	FDSTNGV	-	-	-	-	+++	-	-
36530	LINDAYP	-	-	-	-	+	-	-
36569	RLMDAFP	-	-	-	-	++	-	-
12570	YSSTNGV	-	-	-	-	++	++	-
36525	VESREGI	-	-	-	-	+	-	-

11955	VYSTNGV	-	-	-	-	++	-	-
36512	RLADAFP	-	-	-	-	++	++	-
36361	KDEFSSW	-	-	-	-	++	-	-
37567	KDEFKSY	-	-	-	-	+	-	-
11452	YESTNGI	-	-	-	-	++	-	-
12113	SDSTNGR	-	-	-	-	+	++	-
11757	VFSTNGV	-	-	-	-	++	-	-
14005	YSKLGPN	-	-	-	-	+	-	-
36598	LHRLSPL	-	-	-	-	+	-	-
36557	REEHVFP	-	-	-	-	++	-	-
14301	YSRLNMN	-	-	-	-	+	+	-
37288	RDDFSSY	-	-	-	-	++	-	-
39179	RDSTHGI	-	-	-	-	+	+	-
38079	YDSTNGL	-	-	-	-	++	-	-
36792	VESFNGR	-	-	-	-	+	-	-
36512	RLADAFP	-	-	-	-	++	++	-
11757	VFSTNGV	-	-	-	-	++	-	-
11690	VLSTNGI	-	-	-	-	+	-	-
36458	YVKSDSR	-	-	-	-	+	-	-
13844	YSRLNTN	-	-	-	-	++	+	-
12070	RDSTNGI	-	-	-	-	++	++	-
12426	RLSDAYP	-	-	-	-	+	-	-
11692	TTSTNGV	-	-	-	-	++	-	-
11615	TDSTNGI	-	-	-	-	++	++	-
14227	LAKAGPN	-	-	-	-	+	-	-
12521	ANSTNGV	-	-	-	-	++	-	-
11956	SHSTNGI	-	-	-	-	++	++	-
38018	GSATSSW	-	-	-	-	+	-	-
14461	YSKLNYN	-	-	-	-	++	++	-
12342	VNSSNGV	-	-	-	-	++	-	-
37150	RLDDVYP	-	-	-	-	++	-	-
36604	VALEGRD	-	-	-	-	+	-	-
39179	RDSTHGI	-	-	-	-	+	-	-

38637	RDGASTW	-	-	-	-	+	+	-
37310	RDGTSSW	-	-	-	-	++	-	-
37674	KDEFRSY	-	-	-	-	+	++	-
19371	GSDTSRW	-	-	-	-	++	++	-
37448	VHSTNGR	-	-	-	-	+	-	+
36828	AGGGLYV	-	-	-	-	++	++	-
17737	RTYDSFA	-	-	-	-	+	-	-
36793	LSRTSVN	-	-	-	-	+	+	++
11586	VLSTNGV	-	-	-	-	++	++	-
37215	RNDTVYP	-	-	-	-	++	++	-
14200	YSKLNFN	-	-	-	-	++	-	-
36436	RLDDVFP	-	-	-	-	++	++	-
36429	VKSTNGI	-	-	-	-	+	-	-
11853	HQSTNGV	-	-	-	-	+++	+++	-
13537	YSKLNIN	-	-	-	-	+	-	-
36429	VKSTNGI	-	-	-	-	+	+	-
39976	GSETSKW	-	-	-	-	++	-	-
36458	YVKSDSR	-	-	-	-	+	-	+
37095	KDDYTVF	-	-	-	-	+++	-	-
36265	LHKLSFD	-	-	-	-	++	-	-
11848	TDSTNGV	-	-	-	-	++	-	-
13848	YSRLNLN	-	-	-	-	++	-	+
40496	WPNGVDG	-	-	-	-	+	-	-
11476	RGSDVFP	-	-	-	-	+	+	-
37423	RSEFMSY	-	-	-	-	++	-	-
16612	LSRVGFN	-	-	-	-	+	-	++
12246	NSSTNGV	-	-	-	-	+	-	-
37616	SDGTSKW	-	-	-	-	+	-	-
14050	YSKLNAN	-	-	-	-	+	-	-
37402	RDMDVYP	-	-	-	-	++	-	-
11690	VLSTNGI	-	-	-	-	++	-	-
36277	LHKLSPL	-	-	-	-	+	-	-
11867	SDSTNGI	-	-	-	-	+	-	-

12361	FESTNGR	-	-	-	-	++	-	-
13990	YARQGPN	-	-	-	-	+	+	++
11664	SDSTNGV	-	-	-	-	++	-	-
12570	YSSTNGV	-	-	-	-	+++	++	-
11675	FDSTNGV	-	-	-	-	+++	+++	-
37603	RDDSVFP	-	-	-	-	++	++	-
12269	NTSTNGI	-	-	-	-	++	-	+
11785	FTSTNGV	-	-	-	-	++	+++	-
18345	RSEFSTY	-	-	-	-	+	+	-
38108	RTEFTTY	-	-	-	-	++	-	-
36597	IESSNGR	-	-	-	-	+	-	-
38305	RDDYSTY	-	-	-	-	++	-	-
13510	YSRLNYN	-	-	-	-	++	-	-
37021	RGEEVFP	-	-	-	-	++	-	-
38623	RESDNGI	-	-	-	-	+	+	-
16613	YARGGPN	-	-	-	-	+	-	++
38144	RSEFMTY	-	-	-	-	++	-	-
37636	KSDYVTY	-	-	-	-	++	-	-
17613	GSEFVSY	-	-	-	-	++	-	-
38223	YSRIGPD	-	-	-	-	+	++	+
37070	VNDYVTY	-	-	-	-	++	-	-
12539	YDSTNGI	-	-	-	-	++	-	-
12294	LESTNGI	-	-	-	-	++	-	-
36836	RTDVVYP	-	-	-	-	++	-	-
36345	RLIDAFP	-	-	-	-	++	-	-
36953	GSEFISF	-	-	-	-	+	-	-
12073	HASTNGV	-	-	-	-	++	++	-
18210	VNSTNGM	-	-	-	-	+	-	-
37518	RLNDAYP	-	-	-	-	++	+	-
11594	SESTNGI	-	-	-	-	+	+	-
11889	INSTNGI	-	-	-	-	++	++	-
14097	YSKLNHN	-	-	-	-	+	-	-
37941	REYDAFP	-	-	-	-	+	-	-

11738	IASTNGV	-	-	-	-	++	-	-
17646	GSPGVSW	-	-	-	-	+	-	-
37616	SDGTSKW	-	-	-	-	+	-	-
11732	TISTNGV	-	-	-	-	+	+	-
37186	LHRLQST	-	-	-	-	+	-	-
12426	RLSDAYP	-	-	-	-	+	+	-
11354	AQSTNGV	-	-	-	-	+	-	-
37202	GSPGVGW	-	-	-	-	++	-	-
37384	GADHVKW	-	-	-	-	++	++	-
12070	RDSTNGI	-	-	-	-	++	-	-
11262	VMSTNGI	-	-	-	-	++	-	-
12088	IGSTNGV	-	-	-	-	+	-	-
11916	SGSTNGV	-	-	-	-	+	-	-
36274	LSRIGPD	-	-	-	-	+	-	+
12050	PGSTNGV	-	-	-	-	++	+	-
36424	RLLDAYP	-	-	-	-	++	-	-
11955	VYSTNGV	-	-	-	-	++	-	-
37362	RTSDAYP	-	-	-	-	+	-	-
12481	VQSSNGV	-	-	-	-	++	-	-
36670	RDIDVYP	-	-	-	-	+	-	-
37360	RGEGVYP	-	-	-	-	+	-	-
11718	HQSTNGI	-	-	-	-	++	-	-
38108	RTEFTTY	-	-	-	-	++	-	-
12113	SDSTNGR	-	-	-	-	++	-	-
36721	RTSDVFP	-	-	-	-	++	-	-
11279	RESTNGV	-	-	-	-	++	+	-
36967	KDDFHSY	-	-	-	-	+	-	-
37636	KSDYVTY	-	-	-	-	++	-	-
11882	ASSTNGI	-	-	-	-	+	-	-
18161	GSPGVAW	-	-	-	-	++	++	-
38637	RDGASTW	-	-	-	-	+	-	-
14259	YSKLNVN	-	-	-	-	+	+	-
36335	RLADVFP	-	-	-	-	+	-	-

11563	TISTNGI	-	-	-	-	+	-	-
11964	HTSSNGV	-	-	-	-	++	++	-
38072	RDMDAYP	-	-	-	-	++	-	-
11416	YQSTNGI	-	-	-	-	++	-	-
36940	RGDTVYP	-	-	-	-	+	++	-
38172	RDGNSSW	-	-	-	-	+	-	-
11973	HGSTNGV	-	-	-	-	++	-	-
12098	RDSTNGV	-	-	-	-	+	+	-
12064	TGSTNGV	-	-	-	-	+	-	-
36597	IESSNGR	-	-	-	-	+	-	-
36842	KDEFVSY	-	-	-	-	+	-	-
41306	KNGTSSW	-	-	-	-	+	-	-
37275	RDEFVSW	-	-	-	-	++	-	-
16054	IISTNGV	-	-	-	-	++	-	-
17097	HGSGNFV	-	-	-	-	+	-	-
11371	LAKQGPN	-	-	-	-	+	-	+
11455	HVSTNGV	-	-	-	-	++	-	-
36480	RMLDAFP	-	-	-	-	++	++	-
11920	PESTNGR	-	-	-	-	++	-	-
39578	GSGQSSW	-	-	-	-	+	-	-
36429	VKSTNGI	-	-	-	-	+	+	-
40853	REGTSSW	-	-	-	-	+	-	-
11776	IMSTNGV	-	-	-	-	+	-	-
14190	YSRAGPN	-	-	-	-	+	+	++
11785	FTSTNGV	-	-	-	-	++	-	-
41306	KNGTSSW	-	-	-	-	+	-	-
36480	RMLDAFP	-	-	-	-	++	-	-
36927	RGTDVFP	-	-	-	-	+	-	-
11771	HNSTNGI	-	-	-	-	++	-	-
36846	REEDVYP	-	-	-	-	+	-	-
12113	SDSTNGR	-	-	-	-	+	-	-
12360	IYSTNGI	-	-	-	-	+	-	-
37063	LSRTSHN	-	-	-	-	+	-	+

12160	HFSTNGV	-	-	-	-	++	++	-
36824	GSEFSTW	-	-	-	-	+	-	-
38501	GGPSSTW	-	-	-	-	+	-	-
36428	REEGVSW	-	-	-	-	++	-	-
36866	REETVRW	-	-	-	-	++	+	-
11664	SDSTNGV	-	-	-	-	+	-	-
36801	RDDFTMY	-	-	-	-	+	-	-
37616	SDGTSKW	-	-	-	-	+	-	-
37448	VHSTNGR	-	-	-	-	+	-	++
39174	GSGTSSW	-	-	-	-	+	-	-
36384	KDDFVSW	-	-	-	-	+	-	-
11334	NTSTNGV	-	-	-	-	+	+	+
11188	LAKGGFN	-	-	-	-	+	-	-
11771	HNSTNGI	-	-	-	-	++	++	-
12913	LESTNGV	-	-	-	-	+	-	-
38160	GNEFSSW	-	-	-	-	++	-	-
16107	TWSTNGV	-	-	-	-	++	-	-
37116	NDGSSKW	-	-	-	-	+	-	-
36591	RTVDTYP	-	-	-	-	+	-	-
36274	LSRIGPD	-	-	-	-	+	-	-
12064	TGSTNGV	-	-	-	-	+	+	-
38305	RDDYSTY	-	-	-	-	++	-	-
16017	YAKGGPN	-	-	-	-	+	+	-
12342	VNSSNGV	-	-	-	-	+	+	-
36828	AGGGLYV	-	-	-	-	++	+	-
39088	QNEFTMY	-	-	-	-	+	-	-
11889	INSTNGI	-	-	-	-	++	-	-
16017	YAKGGPN	-	-	-	-	+	-	-
12100	VHSSNGV	-	-	-	-	+	+	-
37603	RDDSVFP	-	-	-	-	++	-	-
11644	TESTNGI	-	-	-	-	++	++	-
11480	ADSTNGR	-	-	-	-	+	-	-
38224	RDATSSW	-	-	-	-	++	-	-

11452	YESTNGI	-	-	-	-	++	-	-
37618	KDDYTGF	-	-	-	-	+	-	-
37187	LSRISPN	-	-	-	-	+	-	++
13715	YSRLNHN	-	-	-	-	++	-	-
11200	LQSTNGI	-	-	-	-	+	-	-
38072	RDMDAYP	-	-	-	-	+	+	-
37238	RSEFVTF	-	-	-	-	++	-	-
36530	LINDAYP	-	-	-	-	+	-	-
11732	TISTNGV	-	-	-	-	++	-	-
38307	GSSTSTW	-	-	-	-	++	++	-
11279	RESTNGV	-	-	-	-	++	-	-
11783	LESTNGR	-	-	-	-	+	-	-
11615	TDSTNGI	-	-	-	-	++	-	-
12032	SGSTNGI	-	-	-	-	+	-	-
11200	LQSTNGI	-	-	-	-	++	-	-
36296	RTPEVFP	-	-	-	-	++	-	-
16059	VYSTNGI	-	-	-	-	+	-	-
39976	GSETSKW	-	-	-	-	++	+	-
16127	SASTNGV	-	-	-	-	++	-	-
36345	RLIDAFP	-	-	-	-	++	-	-
41395	RDELVFP	-	-	-	-	++	-	-
40010	RNEFTSY	-	-	-	-	++	-	-
36428	REEGVSW	-	-	-	-	+	++	-
36927	RGTDVFP	-	-	-	-	++	-	-
11855	PHSTNGV	-	-	-	-	++	-	-
19288	NIPGMMY	-	-	-	-	+	-	-
12179	SNSTNGV	-	-	-	-	++	-	-
12160	HFSTNGV	-	-	-	-	++	-	-
17737	RTYDSFA	-	-	-	-	+	-	-
39225	RSEFTSY	-	-	-	-	++	-	-
11461	VASSNGV	-	-	-	-	+	-	-
36836	RTDVVYP	-	-	-	-	+	-	-
38293	KDEFKTY	-	-	-	-	+	-	-

38102	RDEFKSF	-	-	-	-	++	-	-
38329	QNEFSTY	-	-	-	-	++	-	-
36860	RSDVVYP	-	-	-	-	++	-	-
14097	YSKLNHN	-	-	-	-	+	-	+
38172	RDGNSSW	-	-	-	-	++	-	-
12513	VDSSNGV	-	-	-	-	+	-	-
17025	VESSNGR	-	-	-	-	++	-	-
14243	YSRLNSN	-	-	-	-	+	++	-
37800	RSSDVYP	-	-	-	-	+	-	-
37517	RTHDTFP	-	-	-	-	+	-	-
11353	HMSTNGV	-	-	-	-	+	-	-
37347	RNMDVYP	-	-	-	-	++	-	-
37102	RTYDSFV	-	-	-	-	++	-	-
38504	RESTHGV	-	-	-	-	+	-	-
37846	RDGASSW	-	-	-	-	+	-	-
36654	RTIDAFP	-	-	-	-	+	-	-
11002	IVSTNGV	-	-	-	-	+	-	-
40717	KTEFTTY	-	-	-	-	+	+	-
11840	TMSTNGV	-	-	-	-	+	-	-
17097	HGSGNFV	-	-	-	-	++	-	-
38503	RDELTSW	-	-	-	-	+	-	-
36531	RTSDVYP	-	-	-	-	++	-	-
39262	KDDFTRY	-	-	-	-	+	++	-
39179	RDSTHGI	-	-	-	-	+	-	-
11353	HMSTNGV	-	-	-	-	+	-	-
39174	GSGTSSW	-	-	-	-	+	-	-
16059	VYSTNGI	-	-	-	-	++	++	-
11973	HGSTNGV	-	-	-	-	++	-	-
11776	IMSTNGV	-	-	-	-	+	-	-
37150	RLDDVYP	-	-	-	-	++	-	-
11690	VLSTNGI	-	-	-	-	++	-	-
11271	LAKTGFN	-	-	-	-	+	-	+
38744	RDGQSSW	-	-	-	-	+	-	-

12185	FNSTNGV	-	-	-	-	++	-	-
37537	GSEYSKW	-	-	-	-	++	-	-
39687	GGSGSTW	-	-	-	-	+	-	-
39262	KDDFTRY	-	-	-	-	+	-	-
36721	RTSDVFP	-	-	-	-	++	-	-
12050	PGSTNGV	-	-	-	-	++	++	-
12205	FQSTNGV	-	-	-	-	++	-	-
16107	TWSTNGV	-	-	-	-	++	++	-
11516	AESTNGR	-	-	-	-	++	++	-
37362	RTSDAYP	-	-	-	-	+	+	-
39593	RTYDVYP	-	-	-	-	++	-	-
37310	RDGTSSW	-	-	-	-	+	-	-
11452	YESTNGI	-	-	-	-	++	+++	-
36709	REDFVSW	-	-	-	-	++	-	-
11452	YESTNGI	-	-	-	-	+++	+++	-
38378	RNEFTSW	-	-	-	-	++	-	-
37616	SDGTSKW	-	-	-	-	+	-	-
11892	LNSTNGV	-	-	-	-	+	-	-
12521	ANSTNGV	-	-	-	-	++	++	-
14286	YTSTNGI	-	-	-	-	++	-	-
13715	YSRLNHN	-	-	-	-	+	-	-
16604	YSSTHGV	-	-	-	-	+	-	-
37870	RESEVRW	-	-	-	-	++	-	-
37202	GSPGVGW	-	-	-	-	+	-	-
36531	RTSDVYP	-	-	-	-	++	-	-
11920	PESTNGR	-	-	-	-	++	-	-
11487	IDSTNGV	-	-	-	-	++	-	-
16604	YSSTHGV	-	-	-	-	+	-	-
12426	RLSDAYP	-	-	-	-	+	-	-
36427	REDAVRW	-	-	-	-	++	-	-
12144	TASTNGV	-	-	-	-	++	-	-
37163	RTLDAFP	-	-	-	-	++	-	-
37337	RTYDSIP	-	-	-	-	+	-	-

38846	RDATSGW	-	-	-	-	+	-	-
39225	RSEFTSY	-	-	-	-	++	-	-
11452	YESTNGI	-	-	-	-	++	-	-
11698	HESTNGI	-	-	-	-	++	-	-
39225	RSEFTSY	-	-	-	-	++	-	-
38597	RDEVTSW	-	-	-	-	++	-	-
18133	KDDYTTF	-	-	-	-	++	-	-
12345	HDSTNGI	-	-	-	-	++	-	-
11840	TMSTNGV	-	-	-	-	++	-	-
12052	SQSTNGI	-	-	-	-	++	-	-
11363	IASTNGI	-	-	-	-	++	-	-
40053	RTYDTYP	-	-	-	-	++	-	-
37454	RDEFSGY	-	-	-	-	+	-	-
16092	HSSSNGV	-	-	-	-	+	-	-
13772	YSRQGPN	-	-	-	-	+	-	++
19961	RDDSSSW	-	-	-	-	++	-	-
12020	PSSTNGV	-	-	-	-	++	++	-
41889	RDEYTSF	-	-	-	-	++	-	-
18890	VDSTHGV	-	-	-	-	+	-	-
12501	IDSTNGI	-	-	-	-	++	-	-
36687	VAEKGWD	-	-	-	-	++	-	-
37015	NDGTSKW	-	-	-	-	++	-	-
36846	REEDVYP	-	-	-	-	++	-	-
11527	LQSTNGV	-	-	-	-	+	-	-
37518	RLNDAYP	-	-	-	-	++	+	-
12345	HDSTNGI	-	-	-	-	++	-	-
11343	MQSTNGV	-	-	-	-	+	-	-
11224	HISTNGV	-	-	-	-	++	-	-
37819	RSVDAYP	-	-	-	-	+	-	-
36591	RTVDTYP	-	-	-	-	+	-	-
19182	REDYVYP	-	-	-	-	+	-	-
11106	VFSTNGI	-	-	-	-	++	-	-
38741	KSDFTSY	-	-	-	-	+	-	-

40559	GSPGSAW	-	-	-	-	+	-	-
11594	SESTNGI	-	-	-	-	+	-	-
38504	RESTHGV	-	-	-	-	+	-	+
11438	TYSTNGV	-	-	-	-	+	+	-
39657	GGSTSTW	-	-	-	-	+	-	-
37226	HDGTSAW	-	-	-	-	++	++	-
12333	VSSTNGV	-	-	-	-	+++	-	-
11534	LSSTNGV	-	-	-	-	+	-	-
38042	REDYVKY	-	-	-	-	+	-	-
37384	GADHVKW	-	-	-	-	++	-	-
36531	RTSDVYP	-	-	-	-	+	-	-
39893	NDATSKW	-	-	-	-	+	-	-
11556	YASTNGV	-	-	-	-	+	-	-
18210	VNSTNGM	-	-	-	-	+	-	-
36597	IESSNGR	-	-	-	-	+	-	-
11476	RGSDVFP	-	-	-	-	+	-	-
38744	RDGQSSW	-	-	-	-	+	-	-
12380	FHSTNGV	-	-	-	-	+	-	-
11690	VLSTNGI	-	-	-	-	+	-	-
38224	RDATSSW	-	-	-	-	+	-	-
18531	GSPSSSW	-	-	-	-	++	-	-
36597	IESSNGR	-	-	-	-	++	-	-
11396	IGSTNGI	-	-	-	-	++	-	-
11776	IMSTNGV	-	-	-	-	+	-	-
11480	ADSTNGR	-	-	-	-	+	-	-
37243	VGSTHGV	-	-	-	-	+	-	-
13535	YSRLNNN	-	-	-	-	++	++	-
38094	KNAEVYP	-	-	-	-	+	-	-
17613	GSEFVSY	-	-	-	-	++	-	-
39770	QDGSSSW	-	-	-	-	+	-	-
37942	RDEFKSY	-	-	-	-	+	-	-
12458	SWSTNGV	-	-	-	-	+	-	-
12134	PDSTNGR	-	-	-	-	+	-	-

36892	VMSTNGR	-	-	-	-	+	-	-
11720	SESTNGR	-	-	-	-	++	-	-
11452	YESTNGI	-	-	-	-	++	-	-
18035	LARSGPD	-	-	-	-	+	-	-
12117	TNSSNGV	-	-	-	-	+	-	-
36654	RTIDAFP	-	-	-	-	+	-	-
38144	RSEFMTY	-	-	-	-	++	-	-
16082	YSSTNGI	-	-	-	-	++	-	-
40948	GSGTSTW	-	-	-	-	+	-	-
14301	YSRLNMN	-	-	-	-	+	-	-
36821	REDGVSW	-	-	-	-	+	-	-
11921	IMSTNGI	-	-	-	-	+	-	-
14286	YTSTNGI	-	-	-	-	++	-	-
37537	GSEYSKW	-	-	-	-	+	-	-
12185	FNSTNGV	-	-	-	-	++	-	-
37202	GSPGVGW	-	-	-	-	++	-	-
37715	RGEHTYP	-	-	-	-	+	-	+
36277	LHKLSPL	-	-	-	-	+	-	+
11941	HYSTNGV	-	-	-	-	+	-	-
37669	QDGTSAW	-	-	-	-	+	-	-
36577	RLDNVYP	-	-	-	-	+	-	-
36866	REETVRW	-	-	-	-	+	-	-
14584	FNSTNGI	-	-	-	-	+	-	-
11776	IMSTNGV	-	-	-	-	+	-	-
37226	HDGTSAW	-	-	-	-	+	-	-
38158	RDEFMSY	-	-	-	-	+	-	-
37643	RDDHVYP	-	-	-	-	++	-	-
36840	YHKLNAN	-	-	-	-	+	-	+
11476	RGSDVFP	-	-	-	-	+	-	+
18161	GSPGVAW	-	-	-	-	++	-	-
11334	NTSTNGV	-	-	-	-	+	+	-
39767	RDEFNSF	-	-	-	-	++	-	-
19371	GSDTSRW	-	-	-	-	++	-	-

11774	SQSTNGV	-	-	-	-	++	-	-
11476	RGSDVFP	-	-	-	-	++	-	+
11235	FASTNGV	-	-	-	-	+	-	-
37124	RMSDAFP	-	-	-	-	++	-	-
14584	FNSTNGI	-	-	-	-	+	-	-
37545	AGGGLFI	-	-	-	-	+	-	-
12361	FESTNGR	-	-	-	-	++	-	-
12295	ISSSNGV	-	-	-	-	+	-	+
38506	ARSTNGV	-	-	-	-	+	-	++
36428	REEGVSW	-	-	-	-	+	-	-
37116	NDGSSKW	-	-	-	-	+	-	-
11607	PNSTNGV	-	-	-	-	++	-	-
36577	RLDNVYP	-	-	-	-	+	-	-
38154	RSHDAFP	-	-	-	-	+	-	-
38827	YHRLSIN	-	-	-	-	+	-	-
40141	RTYEVYP	-	-	-	-	++	-	-
37249	RDQTVYP	-	-	-	-	+	-	-
37202	GSPGVGW	-	-	-	-	++	-	-
37360	RGEGVYP	-	-	-	-	+	-	-
37745	VESTNGW	-	-	-	-	++	-	-
37545	AGGGLFI	-	-	-	-	+	-	-
11450	TGSTNGI	-	-	-	-	+	-	+
16092	HSSSNGV	-	-	-	-	+	-	-
38597	RDEVTSW	-	-	-	-	+	-	-
38744	RDGQSSW	-	-	-	-	+	-	-
11461	VASSNGV	-	-	-	-	+	-	-
13510	YSRLNYN	-	-	-	-	++	-	-
38172	RDGNSSW	-	-	-	-	++	-	-
11361	AHSTNGV	-	-	-	-	+	-	-
39657	GGSTSTW	-	-	-	-	+	-	-
37532	HDGTSKW	-	-	-	-	+	-	-
16042	YMSTNGV	-	-	-	-	++	-	-
37095	KDDYTVF	-	-	-	-	+++	-	-

37370	RSADAYP	-	-	-	-	+	-	-
17646	GSPGVSW	-	-	-	-	+	-	-
37249	RDQTVYP	-	-	-	-	+	-	-
11262	VMSTNGI	-	-	-	-	++	-	-
17942	KDGFSTY	-	-	-	-	+	-	-
37800	RSSDVYP	-	-	-	-	+	-	-
15978	HQSSNGV	-	-	-	-	+	-	-
12246	NSSTNGV	-	-	-	-	+	-	-
12458	SWSTNGV	-	-	-	-	++	-	-
37362	RTSDAYP	-	-	-	-	+	-	-
37370	RSADAYP	-	-	-	-	+	-	-
37631	VNDYISY	-	-	-	-	+	-	-
36942	RNDVVYP	-	-	-	-	+	-	-
36954	RMVDVFP	-	-	-	-	+	-	-
37070	VNDYVTY	-	-	-	-	++	-	-
17937	AGDGLWV	-	-	-	-	++	-	-
39225	RSEFTSY	-	-	-	-	+	-	-
37616	SDGTSKW	-	-	-	-	+	-	-
11447	LHSTNGV	-	-	-	-	+	-	-
36531	RTSDVYP	-	-	-	-	+	-	-
38692	GDGSSRW	-	-	-	-	+	-	-
12539	YDSTNGI	-	-	-	-	++	-	-
38773	REDSSRW	-	-	-	-	+	-	-
37553	RSEHTYP	-	-	-	-	+	-	-
16027	TVSTNGV	-	-	-	-	+	-	-
18576	GGSSSTW	-	-	-	-	+	-	-
17942	KDGFSTY	-	-	-	-	+	-	-
14036	YSKLNPN	-	-	-	-	+	-	-
39267	RDDYSSY	-	-	-	-	++	-	-
18773	VHSFNGV	-	-	-	-	+	-	-
37532	HDGTSKW	-	-	-	-	+	-	-
36942	RNDVVYP	-	-	-	-	+	-	-
37201	REEQVRW	-	-	-	-	+	-	-

39088	QNEFTMY	-	-	-	-	++	-	-
14531	YSRNGPN	-	-	-	-	+	-	-
12222	HESSNGV	-	-	-	-	+	-	-
12087	FQSTNGI	-	-	-	-	++	-	-
38271	KDEFRTY	-	-	-	-	+	-	-
11804	SASTNGI	-	-	-	-	+	-	-
40740	RHEDVYP	-	-	-	-	+	-	-
12426	RLSDAYP	-	-	-	-	++	-	-
39657	GGSTSTW	-	-	-	-	+	-	-
37643	RDDHVYP	-	-	-	-	++	-	-
11201	MTSTNGV	-	-	-	-	+	-	-
12087	FQSTNGI	-	-	-	-	+	-	-
12502	FESTNGI	-	-	-	-	+	-	-
36247	LSKLSFN	-	-	-	-	-	++	-
16613	YARGGPN	-	-	-	-	-	+	++
12255	HDSTNGR	-	-	-	-	-	++	-
36274	LSRIGPD	-	-	-	-	-	+	++
13526	YSKLNNN	-	-	-	-	-	+	-
14040	YSKVGPN	-	-	-	-	-	+	-
13934	FARTGPN	-	-	-	-	-	+	+
39056	WPNGVAG	-	-	-	-	-	+	-
11201	MTSTNGV	-	-	-	-	-	+	-
12417	LNSTNGI	-	-	-	-	-	++	-
37674	KDEFRSY	-	-	-	-	-	++	-
11002	IVSTNGV	-	-	-	-	-	+	+
16575	LSKLSAN	-	-	-	-	-	++	-
12596	MESTNGV	-	-	-	-	-	+	-
17687	VRSTNGV	-	-	-	-	-	+	+
12796	FDSTNGR	-	-	-	-	-	++	-
38980	YHRLGQN	-	-	-	-	-	++	-
37745	VESTNGW	-	-	-	-	-	++	-
36732	KDDFVSY	-	-	-	-	-	+	-
12411	HHSTNGI	-	-	-	-	-	+	-

12575	SSSSNGV	-	-	-	-	-	+	+
37617	HSRIGPN	-	-	-	-	-	+	-
39174	GSGTSSW	-	-	-	-	-	+	-
11776	IMSTNGV	-	-	-	-	-	+	-
37848	NDGNSKW	-	-	-	-	-	++	-
11467	SFSTNGI	-	-	-	-	-	++	-
38071	NDGISKW	-	-	-	-	-	+	-
40416	KNDYATW	-	-	-	++	-	-	-

T19

AA SEQ ID#	hCMEC WT	hCMEC-hTFRC	hCMEC-hTFRC	hCMEC+hTFR(	hCMEC+hTFR(	hCMEC+hTFR(	Holo Tf sensitivity
36248	++	---	+++	+--	+++	+++	Insensitive
36248	++	---	+++	+--	+++	+++	Insensitive
36248	++	---	+++	+--	+++	+++	Insensitive
36248	++	---	+++	+--	+++	+++	Insensitive
17016	++	--	++	+--	++	++	Insensitive
17016	++	--	++	+--	+++	++	Insensitive
36649	++	---	+++	+--	+++	+++	Insensitive
38397	++	---	++	+-	++	++	Insensitive
36649	++	---	+++	+--	+++	+++	Insensitive
36971	++	---	+++	+--	+++	+++	Insensitive
36971	++	---	+++	+--	+++	+++	Insensitive
41489	++	--	++	+-	++	++	Insensitive
37463	+++	--	++	+-	++	++	Insensitive
36971	++	---	+++	+--	+++	+++	Insensitive
36783	++	--	++	+--	+++	+++	Insensitive
37044	++	--	++	+--	+++	+++	Insensitive
36971	++	---	+++	+--	+++	+++	Insensitive
38414	++	--	++	+-	++	++	Insensitive
37463	+++	--	++	+-	++	++	Insensitive
36978	++	--	++	+--	+++	+++	Insensitive
17905	+++	--	++	+--	+++	+++	Insensitive
41478	+++	--	++	+--	+++	+++	Insensitive
17281	++	--	++	+-	++	++	Insensitive
36494	++	--	++	+-	++	++	Insensitive
36922	++	--	++	+--	+++	+++	Insensitive
17281	++	--	++	+-	++	++	Insensitive
37652	++	---	+++	+--	+++	+++	Insensitive
41478	+++	---	++	+--	+++	+++	Insensitive
40419	++	--	++	+-	++	++	Insensitive
37746	++	---	++	+-	+++	++	Insensitive
39322	++	---	+++	+--	+++	+++	Insensitive
37652	++	---	+++	+--	+++	+++	Insensitive

37044	++	--	++	+--	+++	+++	Insensitive
37069	++	--	++	+-	++	++	Insensitive
37122	++	--	++	+--	+++	+++	Insensitive
37128	++	--	++	+-	++	++	Insensitive
40141	++	--	++	+--	+++	+++	Insensitive
36978	++	--	++	+--	+++	+++	Insensitive
37642	+++	--	++	+--	+++	+++	Insensitive
38182	++	---	++	+-	+++	++	Insensitive
18032	++	--	++	+-	++	++	Insensitive
17905	+++	--	+++	+--	+++	+++	Insensitive
40423	+++	--	++	+-	++	++	Insensitive
38432	++	--	++	+-	++	++	Insensitive
37642	+++	--	++	+--	+++	+++	Insensitive
40423	+++	--	++	+-	++	++	Insensitive
39904	+++	--	++	+-	++	++	Insensitive
39471	++	--	++	+-	++	++	Insensitive
17626	++	--	+++	+--	+++	+++	Insensitive
39350	++	--	++	+-	++	++	Insensitive
37280	++	--	++	+-	++	++	Insensitive
36711	++	--	++	+-	++	++	Insensitive
40423	+++	--	++	+-	++	++	Insensitive
37349	++	--	++	+-	++	++	Insensitive
12553	++	--	++	+-	++	++	Insensitive
38182	++	--	++	+-	++	++	Insensitive
37688	++	--	++	+-	++	++	Insensitive
37423	++	--	++	+-	++	++	Insensitive
18996	++	--	++	+-	++	++	Insensitive
39322	++	---	+++	+--	+++	+++	Insensitive
37693	++	--	++	+-	+++	+++	Insensitive
16595	++	--	+++	+--	+++	+++	Insensitive
18996	++	--	++	+-	++	++	Insensitive
39041	++	--	++	+--	++	++	Insensitive
36824	++	--	++	+-	+++	++	Insensitive

38761	++	--	++	+-	++	++	Insensitive
37069	++	--	++	+-	++	++	Insensitive
39471	++	--	++	+-	++	++	Insensitive
39593	++	--	++	+--	+++	++	Insensitive
39375	++	--	++	+-	++	++	Insensitive
38571	++	--	+++	+--	+++	+++	Insensitive
39350	++	--	++	+-	++	++	Insensitive
38311	++	--	++	+-	+++	++	Insensitive
37677	++	--	++	+-	+++	+++	Insensitive
37911	++	--	++	+-	++	++	Insensitive
17626	++	--	+++	+--	+++	+++	Insensitive
37578	++	--	++	+-	++	++	Insensitive
37338	++	--	++	+-	++	++	Insensitive
40010	++	--	++	+-	++	++	Insensitive
39041	++	--	++	+--	++	++	Insensitive
39271	++	--	++	+--	+++	++	Insensitive
40141	++	--	++	+--	+++	++	Insensitive
38041	++	--	++	+-	++	++	Insensitive
38571	++	--	+++	+--	+++	+++	Insensitive
38432	++	--	++	+-	++	++	Insensitive
37693	++	--	++	+-	+++	++	Insensitive
40332	+++	---	++	+-	++	++	Insensitive
39593	++	--	++	+--	++	++	Insensitive
36344	++	---	+++	+--	+++	+++	Insensitive
38160	++	---	+++	+--	+++	+++	Insensitive
13769	++	--	++	+--	++	++	Insensitive
40025	++	--	++	+-	++	++	Insensitive
39225	++	--	++	+-	++	++	Insensitive
38462	++	--	++	+-	++	++	Insensitive
37989	++	--	++	+-	++	++	Insensitive
38311	++	--	++	+-	++	++	Insensitive
37011	+++	--	++	+-	++	++	Insensitive
41386	+++	--	++	+-	++	++	Insensitive

37693	++	--	+++	+--	+++	++	Insensitive
37399	++	--	++	+-	++	++	Insensitive
37216	++	--	++	+-	++	++	Insensitive
37423	++	--	++	+-	++	++	Insensitive
36711	++	--	++	+-	++	++	Insensitive
38462	++	--	++	+-	++	++	Insensitive
39225	++	--	++	+-	++	++	Insensitive
36522	++	--	++	+-	++	++	Insensitive
40025	++	--	++	+-	++	++	Insensitive
39103	++	--	++	+-	++	++	Insensitive
37129	++	--	++	+-	++	++	Insensitive
36344	++	---	+++	+--	+++	+++	Insensitive
36709	++	--	++	+-	++	++	Insensitive
37349	++	--	++	+-	++	++	Insensitive
37358	++	--	++	+-	++	++	Insensitive
39598	++	--	++	+-	++	++	Insensitive
39103	++	--	++	+-	++	++	Insensitive
37688	++	--	++	+-	++	++	Insensitive
37186	++	--	++	+-	++	++	Insensitive
39225	++	--	++	+-	++	++	Insensitive
40010	++	--	++	+-	++	++	Insensitive
39807	++	--	++	+-	++	++	Insensitive
39225	++	--	++	+-	++	++	Insensitive
38692	++	--	++	+-	++	++	Insensitive
38144	++	--	++	+-	++	++	Insensitive
39881	++	--	++	+-	++	+	Insensitive
37011	+++	--	++	+-	++	++	Insensitive
39225	++	--	++	+-	++	++	Insensitive
38180	++	--	++	+-	++	++	Insensitive
36834	+++	---	+++	+--	+++	+++	Insensitive
36834	++	---	+++	+--	+++	+++	Insensitive
37911	++	--	++	+-	++	++	Insensitive
39326	++	--	++	+-	++	+	Insensitive

39680	++	--	++	+	++	++	Insensitive
38449	++	--	++	+-	++	++	Insensitive
36936	++	---	+++	+--	+++	+++	Insensitive
18663	++	--	++	+-	++	+	Insensitive
39881	++	--	++	+	++	+	Insensitive
39680	++	--	++	+-	++	++	Insensitive
38466	++	--	++	+-	++	+	Insensitive
14269	++	---	+++	+--	+++	+++	Insensitive
19688	++	---	++	+-	++	++	Insensitive
14269	++	---	+++	+--	+++	+++	Insensitive
14269	++	---	+++	+--	+++	+++	Insensitive
37275	++	--	++	+-	++	++	Insensitive
14269	++	---	+++	+--	+++	+++	Insensitive
14367	++	--	++	+-	++	++	Insensitive
12553	++	--	++	+-	++	++	Insensitive
36936	++	---	+++	+--	+++	+++	Insensitive
38748	++	--	++	+-	++	++	Insensitive
39063	++	--	++	+-	++	++	Insensitive
38558	++	--	++	+-	++	++	Insensitive
39326	++	--	++	+-	++	+	Insensitive
39063	++	---	++	+--	++	++	Insensitive
40332	+++	---	++	+-	++	++	Insensitive
18663	++	--	++	+-	++	++	Insensitive
39326	++	--	++	+-	++	+	Insensitive
38467	++	--	++	+-	++	++	Insensitive
14632	++	---	+++	+--	+++	+++	Insensitive
14059	++	---	+++	+--	+++	+++	Insensitive
14059	++	---	+++	+--	+++	+++	Insensitive
39885	++	--	++	+	++	+	Insensitive
38748	++	--	++	+-	++	++	Insensitive
37251	++	--	++	+-	++	++	Insensitive
14925	++	--	++	+-	++	++	Insensitive
14620	++	--	++	+-	++	++	Insensitive

14632	++	---	+++	+--	+++	+++	Insensitive
14620	++	--	++	+-	++	++	Insensitive
14958	++	---	+++	+--	+++	+++	Insensitive
37658	++	--	++	+	+	+	Insensitive
37750	++	--	++	+-	++	++	Insensitive
39881	++	--	++	+	++	+	Insensitive
37910	++	---	+++	+--	+++	+++	Insensitive
37910	++	---	+++	+--	+++	+++	Insensitive
14958	++	---	+++	+--	+++	+++	Insensitive
16628	++	--	++	+-	+	+	Insensitive
37910	++	---	+++	+--	+++	+++	Insensitive
14574	++	---	+++	+--	+++	+++	Insensitive
14574	++	---	+++	+--	+++	+++	Insensitive
41467	++	--	++	+	++	++	Insensitive
37910	++	---	+++	+--	+++	+++	Insensitive
14190	++	---	+++	+--	+++	+++	Insensitive
37541	++	--	++	+-	++	++	Insensitive
37499	++	--	++	+-	++	++	Insensitive
14190	++	--	+++	+--	+++	+++	Insensitive
38177	++	--	++	+-	++	++	Insensitive
16650	++	--	++	+	+	+	Insensitive
38492	++	--	++	+	++	+	Insensitive
38225	++	--	++	+-	++	++	Insensitive
36459	++	---	+++	+-	+++	++	Insensitive
36459	++	---	+++	+-	+++	++	Insensitive
36626	++	--	++	+	++	++	Insensitive
14384	++	--	++	+	+	+	Insensitive
37684	++	---	+++	+--	+++	+++	Insensitive
36459	++	---	+++	+-	++	++	Insensitive
36571	++	--	++	+-	++	++	Insensitive
36571	++	--	++	+-	++	++	Insensitive
14384	++	--	++	+	+	+	Insensitive
36459	++	---	+++	+-	++	++	Insensitive

36844 ++	---	+++	+--	+++	+++	Insensitive
36975 ++	---	+++	+--	+++	+++	Insensitive
38833 ++	--	++	+	+	++	Insensitive
36844 ++	---	+++	+--	+++	+++	Insensitive
19688 ++	--	++	+	+	++	Moderate sensitivity
39873 ++	--	++	+-	++	++	Moderate sensitivity
36975 ++	---	+++	+--	+++	+++	Moderate sensitivity
36437 ++	---	+++	+--	+++	+++	Moderate sensitivity
37063 ++	--	++	+	+	+	Moderate sensitivity
39873 ++	--	++	+-	++	++	Moderate sensitivity
37174 ++	---	+++	+--	+++	+++	Moderate sensitivity
36347 ++	---	+++	+--	+++	+++	Moderate sensitivity
36347 ++	---	+++	+--	+++	+++	Moderate sensitivity
37062 ++	---	+++	+--	+++	+++	Moderate sensitivity
36347 ++	---	+++	+--	+++	+++	Moderate sensitivity
36437 ++	---	+++	+--	+++	+++	Moderate sensitivity
36493 ++	--	++	+	+	+	Moderate sensitivity
37062 ++	---	+++	+--	+++	+++	Moderate sensitivity
14219 ++	--	++	+-	++	+	Moderate sensitivity
16612 ++	---	+++	+--	+++	+++	Moderate sensitivity
37174 ++	---	+++	+--	+++	+++	Moderate sensitivity
16667 ++	---	+++	+-	++	++	Moderate sensitivity
14618 ++	--	++	+	+	+	Moderate sensitivity
16667 ++	---	+++	+-	++	++	Moderate sensitivity
36592 ++	---	+++	+--	+++	+++	Moderate sensitivity
36592 ++	---	+++	+--	+++	+++	Moderate sensitivity
36769 ++	---	+++	+-	++	++	Moderate sensitivity
36769 ++	---	+++	+-	++	++	Moderate sensitivity
37298 ++	--	++	+	+	+	Sensitive
37298 ++	--	++	+	+	+	Sensitive
36914 ++	--	++	+	+	++	Sensitive
36914 ++	--	++	+	+	+	Sensitive
37318 ++	--	++	.	.	.	Sensitive

40018	++	--	++	-	-	-	Sensitive
37178	++	--	++	-	+	+	Sensitive
37289	++	--	++	+-	+	++	Sensitive
37289	++	---	++	+-	+	++	Sensitive
37318	++	--	++	-	-	+	Sensitive
16639	++	--	++	+-	+	++	Sensitive
40018	++	--	++	-	-	-	Sensitive
37491	++	---	++	+	-	+	Sensitive
37755	++	--	++	+-	+	++	Sensitive
38756	++	--	++	+-	+	+	Sensitive
17938	++	--	++	+	-	-	Sensitive
40019	++	--	++	-	-	-	Sensitive
16639	++	--	++	+-	-	++	Sensitive
36342	++	--	++	-	-	-	Sensitive
20014	++	---	+++	+-	++	++	Sensitive
37491	++	---	++	+	-	+	Sensitive
37717	++	--	++	+-	+	++	Sensitive
38422	++	--	++	+	-	-	Sensitive
20014	++	---	+++	+-	++	++	Sensitive
39544	++	--	++	-	-	-	Sensitive
37755	++	--	++	+-	+	+	Sensitive
37879	++	--	++	-	-	+	Sensitive
37717	++	---	++	+-	+	++	Sensitive
37494	++	--	++	-	+	-	Sensitive
37879	++	--	++	+	-	+	Sensitive
16639	++	--	++	+-	-	+	Sensitive
40146	++	--	++	-	-	-	Sensitive
38556	++	--	++	-	-	-	Sensitive
38556	++	--	++	-	-	-	Sensitive
38034	++	--	++	-	-	-	Sensitive
40462	++	---	+++	+-	+	++	Sensitive
40146	++	--	++	-	-	-	Sensitive
37073	++	--	+++	+	+	+	Sensitive

40462	++	---	+++	+-	+	++	Sensitive
17910	++	--	++	-	-	-	Sensitive
38815	++	---	++	+	-	+	Sensitive
39544	++	--	++	-	-	-	Sensitive
38413	++	--	++	+	-	+	Sensitive
36784	+++	---	+++	+-	+	++	Sensitive
36960	+++	---	+++	+-	+	++	Sensitive
36784	+++	---	+++	+-	+	++	Sensitive
38934	++	--	++	+-	-	++	Sensitive
17049	++	--	+++	+	-	+	Sensitive
37956	++	--	+++	+	+	++	Sensitive
38815	++	--	++	+	-	+	Sensitive
38660	++	---	+++	+-	+	++	Sensitive
16593	++	---	++	+	-	+	Sensitive
38660	++	---	+++	+-	+	++	Sensitive
36960	+++	---	+++	+-	+	++	Sensitive
37956	++	---	+++	+-	+	++	Sensitive
16593	++	---	++	-	-	+	Sensitive
38214	++	---	+++	+-	+	++	Sensitive
37494	++	--	+++	-	-	-	Sensitive
36322	++	--	+++	-	-	-	Sensitive
37073	++	---	+++	+	-	+	Sensitive
36412	++	---	+++	+	-	+	Sensitive
37522	++	---	+++	+-	-	++	Sensitive
37120	++	--	++	-	-	+	Sensitive
36877	++	--	++	-	-	+	Sensitive
41308	++	--	++	-	-	-	Sensitive
37114	++	---	+++	+	+	-	Sensitive
39304	++	--	++	-	-	-	Sensitive
37438	++	---	+++	+-	+	++	Sensitive
37510	++	--	++	-	-	-	Sensitive
38214	++	---	+++	+-	-	++	Sensitive
37438	++	---	+++	+-	+	++	Sensitive

36877	++	--	++	+	-	+	Sensitive
37900	++	--	++	-	-	-	Sensitive
38934	++	--	++	+-	-	++	Sensitive
36533	++	---	+++	+	-	+	Sensitive
17020	++	---	+++	+-	+	++	Sensitive
36412	++	---	+++	+	-	+	Sensitive
17888	++	---	+++	+	-	+	Sensitive
36918	++	---	+++	+	-	+	Sensitive
17882	++	--	++	-	-	-	Sensitive
17826	++	---	+++	+-	-	++	Sensitive
17708	++	---	+++	+	-	+	Sensitive
39134	++	--	+++	+	-	+	Sensitive
17065	++	---	+++	+-	-	++	Sensitive
36533	++	---	++	+	-	+	Sensitive
36720	++	--	+++	+	-	+	Sensitive
37654	++	--	++	-	-	+	Sensitive
38156	++	--	++	-	-	-	Sensitive
36944	++	--	++	-	-	-	Sensitive
36937	++	---	+++	+-	+	++	Sensitive
37290	++	---	+++	+	-	+	Sensitive
37120	++	--	++	-	-	+	Sensitive
18835	++	---	+++	+-	-	++	Sensitive
36938	++	---	+++	+-	-	++	Sensitive
16593	++	--	++	+	-	+	Sensitive
38186	++	--	++	-	-	-	Sensitive
37712	++	---	+++	+--	-	+++	Sensitive
37437	++	---	+++	+-	-	++	Sensitive
17020	++	---	+++	+-	+	++	Sensitive
37148	++	---	+++	+	-	+	Sensitive
37412	++	---	+++	+	-	+	Sensitive
37148	++	---	+++	+	-	+	Sensitive
38025	++	---	+++	+	-	+	Sensitive
37712	++	---	+++	+-	-	++	Sensitive

37114	++	---	+++	+	-	+	Sensitive
37529	++	---	+++	-	-	+	Sensitive
37437	++	---	+++	+-	-	++	Sensitive
17514	++	--	++	-	-	-	Sensitive
38840	++	--	++	-	-	-	Sensitive
39570	++	--	++	-	-	-	Sensitive
17065	++	---	+++	+-	-	++	Sensitive
17826	++	---	+++	+	-	++	Sensitive
38931	++	---	+++	-	-	-	Sensitive
38518	++	---	+++	+	-	+	Sensitive
36507	++	---	+++	+-	-	++	Sensitive
36586	++	---	+++	-	-	-	Sensitive
36507	++	---	+++	+-	-	+	Sensitive
36876	++	--	+++	+	-	+	Sensitive
37833	++	---	+++	+-	-	+	Sensitive
38756	++	--	++	+-	-	+	Sensitive
37290	++	---	+++	+	-	+	Sensitive
36918	++	---	+++	+	-	+	Sensitive
17499	++	--	++	-	-	-	Sensitive
36937	++	---	+++	+-	-	++	Sensitive
38610	++	---	++	+-	-	++	Sensitive
17708	++	---	+++	+	-	+	Sensitive
37047	++	---	++	-	-	-	Sensitive
36771	++	--	++	-	-	-	Sensitive
37610	++	---	+++	+-	-	++	Sensitive
17514	++	--	++	-	-	-	Sensitive
36938	++	---	+++	+-	-	++	Sensitive
39746	++	--	++	-	-	-	Sensitive
37833	++	---	+++	+-	-	+	Sensitive
38610	++	---	++	+-	-	++	Sensitive
37309	++	---	+++	+	-	+	Sensitive
38840	++	--	++	-	-	-	Sensitive
37556	++	---	++	+	-	+	Sensitive

36624	++	---	+++	+	-	+	Sensitive
39173	++	--	++	-	-	-	Sensitive
38025	++	---	+++	+	-	+	Sensitive
37309	++	---	+++	+-	-	+	Sensitive
36602	++	--	+++	-	-	-	Sensitive
37139	++	---	+++	+-	-	++	Sensitive
17032	++	---	+++	+--	-	+++	Sensitive
36446	++	---	+++	+-	-	+	Sensitive
19125	++	---	+++	+-	-	++	Sensitive
36586	++	---	+++	-	-	-	Sensitive
38413	++	--	++	+	-	+	Sensitive
36392	++	---	+++	+--	+	++	Sensitive
37514	++	---	+++	+-	-	+	Sensitive
39592	++	--	++	+	-	+	Sensitive
17590	++	---	+++	+	-	+	Sensitive
38312	++	--	++	-	-	-	Sensitive
37036	++	--	+++	+	-	+	Sensitive
17888	++	---	+++	+	-	+	Sensitive
36363	++	---	+++	+-	-	++	Sensitive
37177	++	---	++	-	-	-	Sensitive
36588	++	---	+++	+-	-	++	Sensitive
37514	++	---	+++	+-	-	+	Sensitive
37625	++	---	+++	+	-	+	Sensitive
17032	++	---	+++	+--	-	+++	Sensitive
36917	++	---	+++	+-	-	+	Sensitive
36930	++	---	+++	+-	-	++	Sensitive
38343	++	---	+++	+	-	+	Sensitive
18173	++	---	+++	+	-	+	Sensitive
36444	++	---	+++	-	-	-	Sensitive
16605	++	---	+++	+-	-	++	Sensitive
38157	++	---	+++	+-	-	++	Sensitive
37412	++	---	+++	+	-	+	Sensitive
37429	++	---	+++	+	-	+	Sensitive

37108 ++	---	+++	+-	-	++	Sensitive
37314 ++	---	+++	+-	-	++	Sensitive
37501 ++	---	+++	+	-	+	Sensitive
37183 ++	---	+++	+-	-	++	Sensitive
38157 ++	---	+++	+-	-	++	Sensitive
38331 ++	---	+++	+-	-	++	Sensitive
37113 ++	---	+++	+	-	+	Sensitive
37108 ++	---	+++	+-	-	++	Sensitive
37014 ++	---	+++	+	-	+	Sensitive
36529 ++	---	+++	-	-	-	Sensitive
36699 ++	---	+++	+-	-	++	Sensitive
37625 ++	---	+++	+	-	+	Sensitive
17590 ++	---	+++	+	-	+	Sensitive
37610 ++	---	+++	+-	-	++	Sensitive
38064 ++	---	+++	+	-	+	Sensitive
18089 ++	---	+++	+	-	-	Sensitive
17986 ++	---	+++	+-	-	++	Sensitive
39138 +++	---	+++	+--	-	+++	Sensitive
17590 ++	---	+++	+	-	+	Sensitive
36624 ++	---	+++	+	-	+	Sensitive
37501 ++	---	+++	+	-	+	Sensitive
37520 ++	---	+++	+	-	+	Sensitive
36930 ++	---	+++	+-	-	++	Sensitive
36446 ++	---	+++	+	-	+	Sensitive
36642 ++	---	+++	+-	-	++	Sensitive
16605 ++	---	+++	+-	-	++	Sensitive
37823 ++	--	+++	+	-	+	Sensitive
36913 ++	---	+++	+-	-	++	Sensitive
38331 ++	---	+++	+-	-	++	Sensitive
17037 ++	---	+++	+-	-	++	Sensitive
38343 ++	---	+++	+	-	+	Sensitive
37153 ++	---	+++	+-	-	++	Sensitive
37153 ++	---	+++	+-	-	++	Sensitive

37559	++	---	+++	+	-	+	Sensitive
37049	++	---	+++	-	-	-	Sensitive
17036	++	---	+++	+-	-	++	Sensitive
36392	++	---	+++	+--	-	++	Sensitive
37049	++	---	+++	-	-	-	Sensitive
37892	++	---	+++	+-	-	++	Sensitive
37429	++	---	+++	+	-	+	Sensitive
36643	++	---	+++	+	-	+	Sensitive
18231	++	---	+++	+	-	+	Sensitive
37340	++	---	+++	+-	-	++	Sensitive
37108	++	---	+++	+-	-	++	Sensitive
37460	++	---	+++	+-	-	++	Sensitive
37314	++	---	+++	+-	-	++	Sensitive
37108	++	---	+++	+-	-	++	Sensitive
36674	++	---	+++	+	-	+	Sensitive
37598	++	---	+++	+-	-	++	Sensitive
37708	++	---	+++	+	-	+	Sensitive
37559	++	---	+++	+	-	+	Sensitive
18899	++	--	+++	-	-	-	Sensitive
37458	++	---	+++	+-	-	++	Sensitive
37623	++	---	+++	+-	-	++	Sensitive
17037	++	---	+++	+-	-	++	Sensitive
36329	++	--	+++	-	-	-	Sensitive
37556	++	---	+++	+	-	+	Sensitive
36963	++	---	+++	+-	-	++	Sensitive
36440	++	---	+++	+	-	+	Sensitive
36588	++	---	+++	+-	-	++	Sensitive
37429	++	---	+++	+	-	+	Sensitive
36573	++	---	+++	+-	-	+	Sensitive
36699	++	---	+++	+-	-	++	Sensitive
36276	++	---	+++	+-	-	++	Sensitive
37366	++	---	+++	+--	-	+++	Sensitive
38064	++	---	+++	+	-	-	Sensitive

37183	++	---	+++	+-	-	++	Sensitive
37330	++	---	+++	+-	-	++	Sensitive
18089	++	---	+++	+	-	+	Sensitive
36276	+++	---	+++	+--	-	+++	Sensitive
37022	++	---	+++	+	-	+	Sensitive
36917	++	---	+++	+	-	+	Sensitive
36643	++	---	+++	+	-	+	Sensitive
37352	++	---	+++	+-	-	+	Sensitive
37022	++	---	+++	+	-	+	Sensitive
40697	++	--	++	-	-	-	Sensitive
17590	++	---	+++	+-	-	+	Sensitive
36712	++	---	+++	+-	-	++	Sensitive
37664	++	---	+++	+	-	+	Sensitive
36351	++	---	+++	+-	-	++	Sensitive
36869	++	---	+++	+-	-	++	Sensitive
36642	++	---	+++	+-	-	++	Sensitive
37458	++	---	+++	+-	-	++	Sensitive
36643	++	---	+++	+	-	+	Sensitive
37736	++	---	+++	+--	-	+++	Sensitive
17675	++	---	+++	+-	-	++	Sensitive
37933	++	---	+++	+-	-	++	Sensitive
38689	++	--	+++	+	-	+	Sensitive
37352	++	---	+++	+-	-	+	Sensitive
38868	++	--	++	+	-	-	Sensitive
36725	++	--	+++	-	-	-	Sensitive
37741	++	---	+++	+-	-	++	Sensitive
37331	++	---	+++	+-	-	++	Sensitive
17711	++	---	+++	+	-	+	Sensitive
17675	++	---	+++	+-	-	++	Sensitive
37018	++	---	+++	+-	-	++	Sensitive
36800	++	---	+++	-	-	+	Sensitive
37330	++	---	+++	+-	-	++	Sensitive
37736	+++	---	+++	+--	-	+++	Sensitive

37018	++	---	+++	+-	-	++	Sensitive
37718	++	---	+++	+-	-	++	Sensitive
38883	++	--	++	+-	-	++	Sensitive
36800	++	---	+++	+	-	+	Sensitive
17966	+++	---	++	+	-	-	Sensitive
37429	++	---	+++	+	-	+	Sensitive
37892	++	---	+++	+-	-	++	Sensitive
37297	++	---	+++	+-	-	++	Sensitive
36580	++	---	+++	+	-	-	Sensitive
36893	+++	---	+++	+--	-	+++	Sensitive
36902	++	---	+++	+-	-	++	Sensitive
36734	++	---	+++	+	-	+	Sensitive
37708	++	---	+++	+	-	+	Sensitive
17036	++	---	+++	+-	-	++	Sensitive
17714	++	---	+++	+-	-	++	Sensitive
37161	++	---	+++	-	-	-	Sensitive
37010	++	---	+++	-	-	-	Sensitive
36454	++	---	+++	+-	-	++	Sensitive
37460	++	---	+++	+-	-	++	Sensitive
36963	++	---	+++	+-	-	++	Sensitive
37528	++	---	+++	+-	-	++	Sensitive
17686	++	---	+++	+	-	+	Sensitive
38883	++	---	+++	+-	-	++	Sensitive
16607	++	---	+++	+-	-	++	Sensitive
37581	++	---	+++	-	-	-	Sensitive
37036	++	---	+++	+	-	+	Sensitive
36699	++	---	+++	+-	-	++	Sensitive
37036	++	---	++	+	-	+	Sensitive
38689	++	---	+++	+	-	+	Sensitive
17711	++	---	+++	+	-	+	Sensitive
37319	++	---	+++	+-	-	++	Sensitive
37520	++	---	+++	+	-	+	Sensitive
37366	++	---	+++	+--	-	+++	Sensitive

37966	++	---	+++	+-	-	++	Sensitive
37340	++	---	+++	+-	-	++	Sensitive
37619	++	---	+++	+-	-	++	Sensitive
37141	++	---	+++	+-	-	++	Sensitive
37348	++	---	+++	+-	-	++	Sensitive
36762	++	---	+++	+	-	+	Sensitive
37224	++	---	+++	-	-	-	Sensitive
37319	++	---	+++	+-	-	++	Sensitive
36454	++	---	+++	+-	-	+	Sensitive
37741	++	---	+++	+-	-	++	Sensitive
37401	++	---	+++	+-	-	++	Sensitive
36734	++	---	+++	+	-	+	Sensitive
37401	++	---	+++	+-	-	++	Sensitive
37933	++	---	+++	+-	-	++	Sensitive
36893	+++	---	+++	+--	-	+++	Sensitive
16607	++	---	+++	+-	-	++	Sensitive
17714	++	---	+++	+-	-	++	Sensitive
37381	++	---	+++	+-	-	++	Sensitive
18857	++	---	+++	+	-	-	Sensitive
36307	++	---	+++	+-	-	++	Sensitive
36307	++	---	+++	+-	-	++	Sensitive
36447	++	---	+++	-	-	-	Sensitive
36440	++	---	+++	+	-	+	Sensitive
37966	++	---	+++	+-	-	++	Sensitive
38014	++	---	+++	+	-	+	Sensitive
17038	++	---	+++	+	-	+	Sensitive
37528	++	---	+++	+-	-	++	Sensitive
36782	++	---	+++	+--	-	++	Sensitive
36545	++	---	+++	+-	-	++	Sensitive
36399	++	---	+++	+	-	+	Sensitive
37623	++	---	+++	+-	-	++	Sensitive
17675	++	---	+++	+-	-	++	Sensitive
36913	++	---	+++	+-	-	++	Sensitive

37766	++	---	+++	+-	-	++	Sensitive
36399	++	---	+++	+	-	+	Sensitive
37420	++	---	+++	+	-	+	Sensitive
36770	++	---	+++	+-	-	++	Sensitive
37272	++	---	+++	-	-	-	Sensitive
37113	++	---	++	-	-	-	Sensitive
37475	++	---	+++	+-	-	++	Sensitive
36762	++	---	+++	+	-	+	Sensitive
37139	++	---	+++	+	-	+	Sensitive
38868	++	--	++	+	-	+	Sensitive
37331	++	---	+++	+-	-	++	Sensitive
37475	++	---	+++	+-	-	++	Sensitive
36712	++	---	+++	+-	-	++	Sensitive
37619	++	---	+++	+-	-	++	Sensitive
36782	++	---	+++	+--	-	++	Sensitive
37335	++	---	+++	+-	-	++	Sensitive
36545	++	---	+++	+-	-	++	Sensitive
36351	++	---	+++	+-	-	+	Sensitive
17578	++	---	+++	-	-	-	Sensitive
36455	++	---	+++	+-	-	++	Sensitive
17986	++	---	+++	+-	-	++	Sensitive
37306	++	---	+++	+--	-	+++	Sensitive
37766	++	---	+++	+-	-	++	Sensitive
37365	++	---	+++	-	-	-	Sensitive
37306	++	---	+++	+--	-	+++	Sensitive
37143	++	---	+++	+	-	+	Sensitive
36455	++	---	+++	+-	-	++	Sensitive
37141	++	---	+++	+-	-	++	Sensitive
37381	++	---	+++	+-	-	++	Sensitive
37297	++	---	+++	+-	-	++	Sensitive
36869	++	--	+++	+-	-	++	Sensitive
36770	++	---	+++	+-	-	++	Sensitive
37718	++	---	+++	+-	-	++	Sensitive

36902	++	--	++	-	-	-	Sensitive
37164	++	--	++	-	-	-	Sensitive
38251	++	---	+++	+	-	+	Sensitive
17835	++	--	++	-	-	-	Sensitive
40475	++	--	++	-	-	-	Sensitive
36543	++	--	+++	-	-	++	Sensitive
37522	++	--	+++	+-	-	+	Sensitive
36624	++	---	+++	+	-	+	Sensitive
37900	++	--	++	-	-	-	Sensitive
36643	++	---	+++	+	-	++	Sensitive
36624	++	---	+++	+	-	+	Sensitive
17686	++	---	+++	+-	-	++	Sensitive
37598	++	---	++	+	-	+	Sensitive
39195	++	--	++	-	-	-	Sensitive
37335	++	---	+++	+-	-	+	Sensitive
37348	++	---	+++	+-	-	++	Sensitive
37664	++	---	+++	-	-	-	Sensitive
36699	++	---	+++	+-	-	++	Sensitive
37593	++	---	+++	-	-	-	Sensitive
18969	++	--	++	-	-	-	Sensitive
39138	+++	---	+++	+--	-	+++	Sensitive
17675	++	---	+++	+-	-	++	Sensitive

T20

AA SEQ ID#	AA_sequence	Fc-hTFR1 pH7	Fc-macaqueTFR	Fc-marmosetTFR	Fc-mouseTFR1 p	2-step, humanTI	2-step, macaque	2-step, LY6A control
41906	CLKDVNS	---	+++	---	-	-	-	-
41907	CTATVAL	---	+++	-	-	-	-	-
41908	YVKSDRL	---	++	--	++	-	-	-
41909	LHKLTNN	---	++	-	-	+	-	-
41909	LHKLTNN	---	++	-	-	+	-	-
36442	LSRVGPN	---	-	-	++	+	-	-
41910	YVKVDPK	---	++	--	+	-	-	+
41911	LSRVGIN	---	-	-	+	-	-	-
36250	LHKLTVN	---	+	-	+	++	-	-
41912	YVKSDSK	---	++	--	+	-	-	-
41913	LHRLLPT	---	++	--	+++	++	-	-
41914	YSKLNAL	---	+	-	+	-	-	-
41915	LSRLNVN	---	-	-	++	-	-	-
41916	YVKSDKL	---	++	--	-	-	-	-
41917	YVKSDTK	---	++	---	+	-	+	-
41918	YVKSDNK	---	++	---	-	-	++	+
36445	YHAKLPN	---	-	-	+	+	-	-
41919	LSRLSNN	---	-	-	++	-	-	-
14343	YSKLNSN	---	-	-	-	-	-	-
41920	LARTGPN	---	-	-	++	++-	-	-
36442	LSRVGPN	---	-	-	++	+	-	-
41921	YVKSDQR	---	++	--	-	-	+	-
41922	YLKSDNK	---	+	--	-	-	-	-
41918	YVKSDNK	---	++	--	+	-	-	-
36250	LHKLTVN	---	++	-	-	++	+	-
36426	YVKSDMK	---	++	--	-	-	-	+
14269	YARTGPN	---	-	-	++	++	-	-
41923	LSRVGNN	---	-	-	+	-	-	-
16575	LSKLSAN	---	-	-	-	-	-	-
41922	YLKSDNK	---	++	--	-	-	-	-
13526	YSKLNNN	---	+	-	-	+	-	-

41924	LSRTGPN	---	-	-	+++	++	-	-
41925	LSRIGNN	---	-	-	-	-	-	-
41926	LHKNLMN	---	++	-	+	-	-	-
41917	YVKSDTK	---	++	---	+	+	++	+
41927	LTRISTN	---	-	-	++	-	-	-
41919	LSRLSNN	---	-	-	++	+	-	-
41928	LSRVGAN	---	-	-	+	-	-	-
36491	LARTGLN	---	-	-	-	-	-	-
41928	LSRVGAN	---	-	-	++	-	+	-
11947	LSKLNLN	---	-	-	+	-	-	-
41929	LSRTAYN	---	-	-	+++	+	-	-
41930	YHKLNTN	---	++	--	+	-	-	-
41931	YHKLNQN	---	++	-	+	-	+	-
41932	YLKSDTK	---	++	--	+	-	-	-
16599	FVKSDTK	---	++	--	+	-	-	-
41933	YVKSDKQ	---	++	--	+	-	-	-
41920	LARTGPN	---	-	-	++	++-	-	-
41934	IHKLTIN	---	+	-	+	-	-	-
41932	YLKSDTK	---	++	--	+	-	-	-
16619	LHKAGYN	---	+	-	+	-	-	-
16599	FVKSDTK	---	++	--	+	-	+	-
41935	LHRLAVD	---	-	-	+	++	-	-
16112	VQSTNGR	---	-	-	++	++	-	-
41930	YHKLNTN	---	++	--	+	-	-	-
41923	LSRVGNN	---	-	-	+	-	-	-
41936	YIKSDTK	---	++	--	+	-	-	++
14050	YSKLNAN	---	-	-	-	-	-	-
41937	LHKAGIN	---	-	-	+	-	-	-
41915	LSRLNVN	---	-	-	++	-	-	-
41912	YVKSDSK	---	++	--	+	-	++	+
41938	YIKSDIK	---	++	--	+	-	-	-
41939	LHKASLN	---	+	-	+	-	-	-
41911	LSRVGIN	---	-	-	-	-	-	-

36369	LHRLGLD	---	-	-	+	++	-	-
41940	YVKSDKN	---	++	--	+	-	-	-
36911	VSSTNGR	---	-	-	+	-	-	-
41941	LHKTGPN	---	-	-	-	++	-	++
14958	YSRTGPN	---	+	-	+++	++	-	-
41942	LSRLNSN	---	-	-	++	-	-	-
41943	LHKSLTN	---	+	-	+	-	-	-
14207	YSKLNTN	---	-	-	+	-	-	-
41944	YIKNDSK	---	++	--	+	-	-	-
41945	LARTGFN	---	-	-	+	-	-	-
14343	YSKLNSN	---	-	-	-	-	-	-
41946	LSRVSTN	---	-	-	++	-	-	-
41942	LSRLNSN	---	-	-	++	-	-	-
41947	LARTATN	---	-	-	-	-	+	-
41948	LARTGNN	---	-	-	-	-	-	-
41949	YSKLGNN	---	-	-	-	-	-	-
14552	YSKAGYN	---	+	-	-	-	-	-
41950	HSKLNMN	---	+	-	-	-	-	-
41951	LSKLSNN	---	-	-	-	-	-	-
41952	LSRVGVN	---	-	-	++	-	-	-
41924	LSRTGPN	---	-	-	+++	+	-	-
41953	LHKMGLN	---	++	--	-	-	-	-
41954	YLKSDQR	---	+	-	-	-	-	-
41931	YHKLNQN	---	++	-	+	-	-	-
37075	LSRVSVN	---	-	-	++	-	-	-
36491	LARTGLN	---	-	-	-	-	-	-
41955	LHKAGLN	---	+	-	+	-	-	-
14059	YSRVGPN	---	+	-	++	-	-	-
41946	LSRVSTN	---	-	-	++	-	-	-
16575	LSKLSAN	---	-	-	-	-	-	-
36291	LTKLSPN	---	-	-	-	-	-	-
41953	LHKMGLN	---	+	-	+	-	++	-
41956	LARTAAN	---	-	-	+	++	-	-

41957	FVKSDNK	---	+	-	-	-	-	-
41958	YVKNDLK	---	++	-	-	-	-	-
41959	LHKLLHD	---	-	-	-	+	-	-
36343	YVKSQTN	---	+	-	-	-	-	+
13882	YAKAGPN	---	-	-	-	-	-	-
41960	LHRLAND	---	-	-	+	+	-	-
41955	LHKAGLN	---	+	-	-	-	-	-
37061	LSRISNN	---	-	-	++	-	-	-
41961	LHKQGLN	---	+	-	+	-	-	-
41962	LHKQGIN	---	+	-	-	-	-	-
41963	LSRVSAN	---	-	-	++	-	-	-
41937	LHKAGIN	---	+	-	-	-	-	-
14269	YARTGPN	---	+	-	++	++	-	-
41964	LARTGVN	--	+	-	-	-	-	-
41965	YTKSDTK	--	++	-	+	-	-	+
41966	LHRLATD	--	-	-	-	++	-	-
36991	LSRTSLN	--	-	-	+++	-	+	-
41967	LHKASIN	--	++	-	+	-	-	-
36369	LHRLGLD	--	+	-	++	++	-	-
41968	LHKASVN	--	+	-	-	-	-	-
18591	LTRLSPD	--	-	-	+	-	-	-
17775	LHRLSSD	--	-	-	-	+	-	-
36788	LHRLTTD	--	-	-	+	+	-	-
41969	LHRLTHD	--	+	-	-	+	-	-
41970	LHRLTVD	--	-	-	-	++	-	-
41957	FVKSDNK	--	+	--	-	-	-	-
36445	YHAKLPN	--	-	-	-	+	-	-
41971	LHKNLTN	--	+	-	-	-	-	-
41939	LHKASLN	--	+	-	-	-	+	-
41972	LHKMSTN	--	++	-	-	-	-	-
41973	LSKLNNN	--	-	-	-	-	-	-
13844	YSRLNTN	--	-	-	++	-	-	-
13802	YSRIGQN	--	-	-	++	-	-	-

41934	IHKLTIN	--	+	-	+	-	-	-
41974	YVKSDRQ	--	++	--	+	-	-	-
41975	LHKMGNN	--	++	-	-	-	-	-
41968	LHKASVN	--	-	-	-	-	-	-
14059	YSRVGPN	--	+	-	+++	+	-	-
41976	LHKAGVN	--	+	-	-	-	-	-
41977	LSRLSEN	--	-	-	+	++	-	-
41978	LTKLHSN	--	+	-	-	-	-	-
41943	LHKSLTN	--	++	-	-	-	++	-
41969	LHRLTHD	--	+	-	-	+	-	-
36275	LHKLGEN	--	-	-	-	++	-	-
14083	YSRVGVN	--	-	-	+	-	-	-
41966	LHRLATD	--	-	-	-	+	-	-
36793	LSRTSVN	--	-	-	+++	+	-	-
41947	LARTATN	--	-	-	+	-	-	-
41979	VASTNGR	--	-	-	-	-	-	-
41980	VTSTNGR	--	-	-	+	++	-	-
37061	LSRISNN	--	-	-	++	-	-	+
41981	LHRLNEN	--	-	-	-	-	-	-
41982	LHKAGAN	--	+	-	-	-	+	-
16619	LHKAGYN	--	++	-	+	-	-	-
41983	LHKLGPD	--	-	-	-	++-	+	+
41984	LSRTAVN	--	-	-	++	-	-	-
41985	LHKLSLD	--	-	-	-	-	-	-
41986	LSKLSMN	--	-	-	++	-	-	-
36911	VSSTNGR	--	-	-	+	+	-	-
36257	LHKLSEN	--	+	-	-	++	+	-
41987	LHKAGMN	--	+	-	-	-	-	-
36291	LTKLSPN	--	-	-	-	-	-	-
36251	LHKLGDN	--	+	-	-	+	-	-
41961	LHKQGLN	--	+	-	-	-	-	-
14298	YSRIGSN	--	++	--	++	-	-	-
41970	LHRLTVD	--	-	-	+	++	-	-

41988	LHKSLHN	--	+	-	-	-	-	-
41935	LHRLAVD	--	-	-	-	++	-	-
41989	LHKQGYN	--	++	--	+	-	-	-
36991	LSRTSLN	--	-	-	+++	-	-	-
41990	YIKSDRN	--	+	-	-	-	-	-
41991	LSRAGGG	--	-	-	-	-	-	-
36275	LHKLGEN	--	-	-	-	++	-	-
13636	YARTGIN	--	-	-	+	-	-	-
41992	LSRLSDN	--	-	-	-	+	-	-
41993	LHRLQDT	--	-	-	-	+	-	-
41994	YVKSDMF	--	-	-	-	-	-	-
17736	LHRLSVD	--	-	-	-	++	-	-
13535	YSRLNNN	--	+	-	++	-	-	-
36477	YSKVGTN	--	-	-	-	-	-	-
16112	VQSTNGR	--	-	-	+	+	-	-
41995	LHRLGID	--	-	-	-	++	-	-
41996	YSKLQSN	--	-	-	-	-	-	-
41960	LHRLAND	--	-	-	+	+	-	-
41983	LHKLGPD	--	-	-	-	++-	-	-
36285	LHKLSVD	--	-	-	-	-	-	-
41997	LSRVGSN	--	-	-	-	-	-	-
41998	YVKSQVN	--	+	-	-	-	-	-
41999	LHKLGLD	--	-	-	-	+	-	-
41999	LHKLGLD	--	+	-	-	-	-	-
42000	LSRLSLD	--	-	-	-	-	-	-
42001	LHKSGVN	--	+	-	+	-	-	-
13930	YARTGLN	--	-	-	++	-	-	-
42002	LHRLGTD	--	-	-	-	+	-	-
42003	LHRLSTD	--	-	-	-	++	-	-
42004	LHKQSVN	--	++	--	+	-	-	-
14378	YSRVGAN	--	-	-	++	-	-	-
41972	LHKMSTN	--	++	-	+	-	+	-
41995	LHRLGID	--	-	-	-	++	-	-

42005	LHKLGYD	--	-	-	-	+	-	-
42006	LHRLGSD	--	-	-	-	-	-	-
42007	LHKQSLN	--	+	-	+	-	+	-
42008	LSRVGTN	--	-	-	+	-	-	-
14958	YSRTGPN	--	-	-	+++	+	-	-
42009	LHKAGNN	--	+	-	-	-	-	-
42010	LHKLGVD	--	-	-	-	-	-	-
13892	YARTGMN	--	+	-	+	-	-	-
14103	YSRAGLN	--	-	-	++	-	-	-
41989	LHKQGYN	--	+	-	++	-	-	-
42011	YVKSQNH	--	+	-	-	-	-	-
41977	LSRLSEN	--	-	-	-	+	-	-
42012	YHKNSPN	--	+	-	++	-	-	-
42013	YHKTGPN	--	++	-	+	-	-	-
42014	LHKLTDN	--	+	-	-	++	-	-
17889	LSKLSSN	--	+	-	-	-	-	-
41967	LHKASIN	--	+	-	-	-	-	-
14115	YSRVGSN	--	+	-	++	+	-	-
42001	LHKSGVN	--	+	-	-	-	-	-
42015	YHKAGMN	--	+	-	-	-	-	-
42016	LHRLSDD	--	-	-	-	++	-	-
42017	LHKSLSN	--	+	-	-	-	-	-
41991	LSRAGGG	--	-	-	-	-	-	-
11559	YSKVGIN	--	-	-	+	-	-	-
42018	LSRTGLN	--	-	-	+	-	-	-
42019	LHKLSDN	--	-	-	-	++	-	-
13938	YSKMGPN	--	++	-	-	-	+	+
36788	LHRLTTD	--	-	-	+	+	-	-
41941	LHKTGPN	--	-	-	-	+	-	-
42020	LHKQGVN	--	+	-	+	-	-	+
36497	YTKSQTN	--	-	-	+	-	-	-
36594	LHRLGAD	--	-	-	-	++	-	-
16579	YLKSQGN	--	+	-	-	-	-	-

42021	LHKMTTN	--	+	-	-	-	-	-
42022	YHKLGAG	--	++	-	+	-	-	-
13751	YSRVGNN	--	+	-	++	-	-	-
42023	YHKSSPN	--	++	-	+	-	-	-
42024	YVKTDTR	--	+	--	-	-	+	-
42006	LHRLGSD	--	-	-	-	-	-	-
13844	YSRLNTN	--	-	-	++	++	-	-
14190	YSRAGPN	--	+	-	++	-	-	-
42025	LHKASAN	--	+	-	-	-	+	-
42019	LHKLSDN	--	-	-	-	++	-	-
41985	LHKLSLD	--	+	-	-	+	-	-
42026	LHKSTPN	--	+	-	+	-	-	++
42027	LHRALPD	--	-	-	-	++	-	-
37448	VHSTNGR	--	+	-	+	-	-	-
42028	YSALNIN	--	-	-	-	-	-	-
42000	LSRLSLD	--	-	-	++	-	-	-
41987	LHKAGMN	--	+	-	-	-	-	-
42029	WSKAGGG	--	++	--	++	-	-	-
42030	YTKSDTR	--	++	--	-	-	-	-
41962	LHKQGIN	--	-	-	-	-	-	-
42004	LHKQSVN	--	+	-	+	-	-	-
14122	YARTGVN	--	-	-	+	-	-	-
42031	YARNGNN	--	-	-	-	-	-	-
42032	LHKASTN	--	+	-	+	+	-	-
42033	VNSTNGR	--	-	-	+	-	-	-
42034	IHRLTDN	--	-	-	-	-	-	-
42035	LSRAGPN	--	-	-	++	-	-	-
36285	LHKLSVD	--	-	-	-	-	-	-
41975	LHKMGNN	--	++	-	-	-	++	-
42036	YTKSDNK	--	+	-	++	-	-	-
42037	HHKLQEN	--	-	-	-	-	-	-
42038	LSRVSSN	--	-	-	++	-	-	-
42035	LSRAGPN	--	-	-	+++	-	-	-

42037	HHKLQEN	--	-	-	-	-	-	-
36257	LHKLSEN	--	-	-	-	++	-	-
42039	YSKIGPD	--	-	-	-	-	-	-
36793	LSRTSVN	--	-	-	+++	-	-	-
42040	LSRTSAN	--	-	-	+++	-	-	-
36741	YHKLNEN	--	-	-	-	-	-	-
42041	LARTGTN	--	-	-	-	-	-	-
36251	LHKLGDN	--	-	-	-	++	+	-
13898	YSRLNQN	--	-	-	++	-	-	-
42042	KDEMTHW	--	-	-	-	-	-	-
42043	LHKNGVN	--	+	-	-	-	-	-
42007	LHKQSLN	--	++	-	+	-	++	-
41982	LHKAGAN	--	-	-	-	-	-	-
36294	LHKLSHD	--	-	-	-	-	-	-
42044	YSKLNEN	--	-	-	-	-	-	++
17736	LHRLSVD	--	-	-	+	++	-	-
42045	LHRSLEN	--	-	-	-	++	-	-
14399	YARTGNN	--	-	-	+	-	-	-
14593	YSRSGPN	--	+	-	++	-	-	-
42046	LHKNGLN	--	-	-	+	+	-	-
42047	LHKSGIN	--	+	-	-	-	-	-
37030	LHRLSQD	--	-	-	-	+	-	-
17515	LSRASVN	--	-	-	++	-	-	-
42048	LHVRTVN	--	+	-	++	-	-	-
42049	LHSLLPN	--	-	-	+	+	-	-
36294	LHKLSHD	--	+	-	-	-	-	-
14858	YARAGPN	--	-	-	+	-	-	-
42003	LHRLSTD	--	+	-	+	++	-	-
41984	LSRTAVN	--	-	-	++	-	-	-
42050	ISSTNGR	--	-	-	-	-	-	-
42025	LHKASAN	--	+	-	+	-	-	-
14264	YARTGAN	--	-	-	++	-	-	-
37030	LHRLSQD	--	-	-	-	++	-	-

42051	LHRLQTD	--	-	-	-	-	-	-
42052	YHKSQPN	--	+	-	-	-	-	-
42053	YSRLHDN	--	-	-	-	-	-	-
41956	LARTAAN	--	-	-	+	-	-	-
42014	LHKLTDN	--	+	-	-	++	-	-
36741	YHKLNEN	--	+	-	-	-	-	-
42054	LSRTANN	--	-	-	++	-	-	-
41993	LHRLQDT	--	-	-	-	+	-	-
14226	FSKLNAN	--	-	-	-	-	-	-
14860	LSRTSTN	--	-	-	++	-	-	-
42055	YHSLGPN	--	-	-	-	-	-	-
42056	LHKAGTN	--	+	-	+	-	-	-
42057	LHKQGNN	--	+	-	+	-	-	+
17796	LSRVGPD	--	-	-	-	-	-	-
42058	LSKLSEN	--	-	-	-	-	-	++
42059	LSRISSN	--	-	-	++	-	-	-
42018	LSRTGLN	--	-	-	-	-	-	-
42060	LSRTSQN	--	-	-	++	-	-	-
42061	LHKNSIN	--	+	-	-	-	-	-
42062	LHKQGTN	--	-	-	-	-	-	-
14122	YARTGVN	--	-	-	+	-	-	-
18295	LHRLSGD	--	-	-	-	+	-	-
42063	LSRVGEN	--	-	-	-	-	-	-
42064	YVKSDPR	--	++	--	+	-	-	-
36385	YHKLNPD	--	+	-	+	-	-	-
42044	YSKLNEN	--	-	-	-	+	-	-
42065	LHKASNN	--	+	-	+	-	-	-
42066	LHKLSAD	--	-	-	-	-	-	-
42067	YHKLSDN	--	-	-	-	+	-	-
42068	LARSGLN	--	-	-	-	-	-	-
42069	LHKYGEN	--	++	--	++	-	-	-
42026	LHKSTPN	--	++	-	+	-	-	-
42070	YVKSDQN	--	-	-	+	-	-	-

14087	YARSGTN	--	-	-	+	-	-	-
42071	LHRLQDS	--	-	--	-	-	-	-
42012	YHKNSPN	--	+	-	-	-	+	-
42072	YVRSDNN	--	-	-	+	-	-	-
14145	YARTGTN	--	-	-	+	-	-	-
42049	LHSLLPN	--	-	-	+	+	-	-
42073	YLKSQNS	--	-	-	-	-	-	-
42074	YSRVSPN	--	-	-	++	-	-	-
42075	YVKNDPK	--	++	--	-	-	-	-
42061	LHKNSIN	--	+	--	+	-	-	-
42076	LSRTSSN	--	-	-	++	-	-	-
13751	YSRVGNN	--	+	-	++	-	-	-
14628	YSRLNDN	--	-	-	-	++	-	-
42077	LHKQSMN	--	++	-	-	-	-	-
42078	YVKTDTK	--	+	-	-	-	-	++
42079	YSRLNAP	--	-	-	++	-	-	-
42080	YARTSAN	--	-	-	+	-	+	-
42081	LSRTGVN	--	-	-	+	-	-	-
42082	LARAGPN	--	-	-	-	+	-	-
37096	LHRLQLD	--	-	-	-	+	-	-
42083	LHKSSIN	--	+	-	++	-	-	-
42002	LHRLGTD	--	-	-	-	+	-	+
42084	YSRAGGG	--	++	-	++	++	-	-
42085	YVKSDNN	--	-	-	-	-	-	++
42046	LHKNGLN	--	-	-	+	-	-	-
42086	LSRTGNN	--	-	-	+	-	-	-
42087	LSRTGHN	--	-	-	++	-	-	-
42088	YVKSDTT	--	-	-	-	-	-	+
14175	YSRAGMN	--	+	-	++	-	-	-
42089	LSRLNEN	--	-	-	-	+	-	-
36315	LHKLSTD	--	+	-	-	+	+	-
42090	LSRTATN	--	-	-	++	-	-	-
42091	YIKTDTK	--	++	-	+	-	-	++

42045	LHRSLEN	--	-	-	-	++	-	-
42092	YVKSDNT	--	-	-	-	-	-	-
42093	LHARTMN	--	+	-	-	-	++	+
42090	LSRTATN	--	-	-	++	-	-	-
37863	YSRLNLD	--	-	-	-	-	-	-
42094	LHKSGNN	--	+	-	+	-	-	-
14140	YARSGSN	--	-	-	-	-	+	-
17775	LHRLSSD	--	-	-	+	+	-	-
14593	YSRSGPN	--	+	-	++	-	-	-
36594	LHRLGAD	--	-	-	-	++	-	-
42095	RLLDAFP	--	-	-	-	++	-	-
42067	YHKLSDN	--	-	-	-	-	-	-
42096	WVKSDLR	--	++	--	+	-	-	-
41980	VTSTNGR	--	-	-	-	++	-	-
42097	LHRAGTN	--	+	-	+	-	-	-
42098	LARTSIN	--	-	-	++	-	-	-
42099	LHKSQVN	--	+	-	-	-	-	-
42100	LHRSLAN	--	++	-	+	+	-	-
42101	LARTGSN	--	-	-	-	-	-	-
42102	LHRQLEN	--	-	-	-	+	-	-
14218	YSRTGIN	--	-	-	-	-	-	-
42070	YVKSDQN	--	-	-	-	-	+	+
42102	LHRQLEN	--	-	-	-	+	-	-
42103	KNEFSTY	--	-	-	-	-	-	-
14303	YSRLNEN	--	-	-	++	+	-	+
42100	LHRSLAN	--	++	-	++	-	-	-
17515	LSRASVN	--	-	-	++	-	-	-
42104	RLIDAYP	--	-	-	-	+	-	-
13772	YSRQGPN	--	+	-	++	-	-	-
42053	YSRLHDN	--	-	-	-	-	++	-
42105	YVKSDTN	--	-	-	-	-	-	-
42106	IATKGWD	--	-	-	-	-	-	-
42084	YSRAGGG	--	+	-	++	++	-	-

42034	IHRLTDN	--	-	-	-	+	-	-
42107	LAKSAPN	--	-	-	-	-	-	-
42085	YVKSDNN	--	-	-	+	-	-	-
42068	LARSGLN	--	-	-	+	-	-	-
42027	LHRALPD	--	-	-	-	++	-	-
42105	YVKSDTN	--	-	-	-	-	++	-
42108	LSKVSFN	--	-	-	+	-	-	-
14229	YSKLGVN	--	-	-	-	-	-	+
12737	IESTNGR	--	-	-	-	+	-	-
14303	YSRLNEN	--	-	-	-	++	-	-
14038	YSRAGTN	--	-	-	+	-	-	-
42109	LARTSLN	--	-	-	+	-	-	-
42110	YARTSMN	--	-	-	++	-	-	-
42111	YVKSDHT	--	-	-	-	-	-	-
42112	YVKTDNK	--	+	-	-	-	-	+
42113	YIKSDNN	--	-	-	-	-	-	-
11974	VSSTNGI	--	-	-	-	++	-	-
42114	LHKSSLN	--	+	-	-	-	-	-
42088	YVKSDTT	--	-	-	-	-	++	++
42066	LHKLSAD	--	-	-	-	-	-	-
42115	YSRLNTD	--	-	-	-	-	-	-
42116	LARTGQN	--	-	-	-	-	-	-
42117	YTKLHTN	--	+	-	-	-	-	-
42083	LHKSSIN	--	+	-	-	-	-	-
19635	LSKLSYD	--	-	-	-	-	-	-
42118	LHRTGQN	--	+	-	++	-	-	-
42119	LSRAGAN	--	-	-	+	-	-	-
42120	RARTDDH	--	-	-	-	-	-	-
42028	YSALNIN	--	-	-	-	-	-	-
42121	IHRLLND	--	+	-	-	-	-	-
42122	YSKLSNN	--	-	-	-	-	-	-
42123	YLKSQDN	--	-	-	-	-	-	-
42124	LHAKTVN	--	-	-	-	-	-	-

42125	YARNGPD	--	-	-	-	-	-	-
42098	LARTSIN	--	-	-	+	-	-	-
42126	YHKAQSN	--	+	-	-	-	-	+
42127	YHKAGSN	--	+	-	+	-	-	-
42128	YHKAGIN	--	+	-	-	-	-	-
42129	YSRVGDN	--	-	-	+	-	-	-
42016	LHRLSDD	--	-	-	+	++	-	-
42130	YARTGEN	--	-	-	-	-	-	-
36315	LHKLSTD	--	-	-	-	-	-	-
12055	VESTNGI	--	-	-	-	++	-	-
42131	WVKSDTR	--	++	---	++	-	-	-
42132	YVKSDDH	--	-	-	-	-	-	-
42133	YIKSDTN	--	-	-	-	-	-	-
42134	YVKSDAN	--	-	-	-	-	-	-
42135	PGATSGW	--	-	-	-	+	-	-
42136	LHKSSVN	--	+	-	-	-	-	-
42137	LHKSGLN	--	+	-	-	-	-	-
42135	PGATSGW	--	-	-	-	-	-	-
42138	LHKAAAN	--	+	-	+	-	+	-
42139	LHRQGYD	--	-	-	-	-	-	-
42120	RARTDDH	--	-	-	+	-	-	-
42138	LHKAAAN	--	+	-	+	-	-	-
42140	RTEYTYP	--	-	-	-	-	-	-
42141	YHRLSDS	--	+	-	++	-	-	-
42107	LAKSAPN	--	-	-	-	-	-	-
42142	YSRLNAD	--	-	-	-	-	-	+
42143	LSRIGGG	--	-	-	+	-	-	-
42058	LSKLSEN	--	-	-	-	-	-	-
42144	LRTGEGP	--	-	-	-	+	-	-
42113	YIKSDNN	--	-	-	+	-	-	+
42145	LSKLNYD	--	-	-	-	-	-	+
14211	YSRTGSN	--	+	-	++	-	+	-
42052	YHKSQPN	--	+	-	+	-	-	-

42146	YSRISAN	--	-	-	++	-	-	-
42147	LHKAATN	--	+	-	-	-	-	-
38620	YSRLSEN	--	-	-	+	-	-	-
42148	YSRVGAG	--	-	-	++	-	-	-
42149	LHKNGAN	--	+	-	-	-	-	-
42150	YHKSGLN	--	++	-	++	-	++	-
42151	LHKQSTN	--	++	-	+	-	-	-
42071	LHRLQDS	--	-	-	-	-	-	-
42152	LHRNGIN	--	+	-	+	-	-	-
42153	LHKSGTN	--	+	-	+	-	-	-
39265	YSRLSDN	--	-	-	-	-	-	-
11875	HTSTNGV	--	-	-	-	++	-	-
42154	LHRAGEN	--	-	-	-	-	-	-
42123	YLKSQDN	--	-	-	-	-	-	-
42124	LHAKTVN	--	-	-	-	-	-	-
42155	RTAEVYP	--	-	-	-	+	-	-
19635	LSKLSYD	--	-	-	-	-	-	-
37824	YSRVGEN	--	-	-	-	-	-	-
17857	LSRLSQD	--	-	-	-	-	-	-
42134	YVKSDAN	--	-	-	-	-	-	-
42156	LHRQGTN	--	++	-	++	-	-	-
42157	VSDYVTF	--	-	-	-	-	-	-
12055	VESTNGI	--	-	-	+	++	-	-
42158	LHKAQTN	--	+	-	-	-	-	-
42159	LHKQGSN	--	+	-	-	-	-	-
42160	VESTNGK	--	-	-	-	+	+	-
42161	LHKALPI	--	+	-	+	-	-	+
42103	KNEFSTY	--	-	-	-	-	-	-
15967	LHKSGMN	--	+	-	-	-	-	-
11315	YSKANAN	--	-	-	-	-	-	-
42130	YARTGEN	--	-	-	-	-	-	-
42069	LHKYGEN	--	+	-	+	+	-	-
12737	IESTNGR	--	-	-	-	++	-	-

42162	YARTGDN	--	-	-	-	-	-	-
42163	LHRDGPN	--	-	-	-	+	++	-
11955	VYSTNGV	--	-	-	-	-	-	-
42164	VYSTNGR	--	-	-	-	-	-	-
11326	LSKVGLN	--	-	-	-	-	-	-
42165	TADNIYF	--	-	-	+	++	-	-
38122	YSRLGAD	--	-	-	-	-	-	-
42166	LHRALHD	--	-	-	-	-	-	-
42167	YHKMSTN	--	+	-	-	-	-	-
42168	YSRLNSD	--	-	-	-	-	-	-
42169	YSRTQTN	--	-	-	++	-	-	-
11974	VSSTNGI	--	-	-	-	++	-	-
13887	YSRTGQN	--	-	-	+	-	-	-
42170	HHKLSNN	--	++	--	+	-	-	-
16583	YVKSDHH	--	+	-	-	-	-	-
42171	LHKSSTN	--	+	-	+	-	-	-
42172	VGSTNGR	--	-	-	-	-	-	-
16071	YSRAGEN	--	-	-	-	-	-	-
42173	YHKLTEN	--	-	-	-	-	+	-
17025	VESSNGR	--	-	-	-	+	-	+
42174	LHKSTAN	--	+	-	+	-	-	-
42165	TADNIYF	--	-	-	-	+	-	-
11522	VESTNGV	--	-	-	-	++	-	-
11875	HTSTNGV	--	-	-	+	++	-	-
42175	LHKSSAN	--	-	-	-	-	-	+
42176	LARSGMN	--	-	-	-	-	-	-
42177	YVKTDNR	--	-	-	+	-	-	-
39265	YSRLSDN	--	-	-	-	-	-	-
42178	LHRNGVN	--	+	-	++	+	-	-
36388	IANKGWD	--	-	-	-	-	-	-
12707	VDSTNGR	--	-	-	+	+	-	-
11288	VGSTNGI	--	-	-	-	-	-	-
42149	LHKNGAN	--	-	-	-	-	-	-

42179	SSDFVSF	--	-	-	-	-	-	-
42180	LHKNGMN	--	-	-	-	-	-	-
12707	VDSTNGR	--	-	-	-	++	+	-
42155	RTAEVYP	--	-	-	-	-	-	-
38620	YSRLSEN	--	-	-	-	-	-	-
42181	YTKSDMR	--	+	--	-	-	+	-
42182	LHKNGTN	--	-	-	-	-	-	-
42183	TDEFTSY	--	-	-	-	-	-	-
15967	LHKSGMN	--	+	-	+	-	-	-
42184	YHRNGPD	--	-	-	+	-	-	-
42147	LHKAATN	--	+	-	-	-	-	-
42185	YVKSNNS	--	+	-	-	-	-	-
37182	RNESVYP	--	-	-	-	+	-	+
42186	LHKSSYN	--	++	--	-	-	-	-
42187	LHARSVN	--	+	-	-	-	-	-
42188	YSKLNTD	--	-	-	-	-	-	-
42189	LSRTASN	--	-	-	++	-	-	-
42190	YHKNGAN	--	-	-	-	-	-	-
42191	LHRTSVN	--	+	-	+++	-	-	-
42192	LHKAGSN	--	+	-	-	-	-	-
42193	LHRSGVN	--	+	-	++	-	-	-
17857	LSRLSQD	--	-	-	-	-	-	-
42158	LHKAQTN	--	-	-	-	-	-	-
42125	YARNGPD	--	-	-	-	-	-	-
42194	LHRASTN	--	++	-	++	-	-	-
19982	LHRAGID	--	-	-	-	-	-	-
42195	YSKLNLD	--	-	-	-	-	-	-
13912	YSRVNAN	--	-	-	++	-	-	-
42196	LSRTGTN	--	-	-	-	-	-	-
42197	VESTNGM	--	-	-	-	+	-	-
42198	YVHSDLK	--	-	-	-	++	-	-
42199	YALEGRD	--	-	-	-	+	-	-
42200	LHREGPN	--	-	-	-	++	-	-

42201	YHKSGMN	--	+	-	-	-	+	-
42202	YHRTGPD	--	-	-	+	-	-	-
42203	LHRHGDN	--	+	--	-	-	-	-
42160	VESTNGK	--	-	-	-	-	-	-
42204	LHKLGTD	--	-	-	-	-	-	-
42205	LHKLTLD	--	+	-	-	-	-	-
42206	LRSGEGP	--	-	-	-	-	+	++
42207	LARSGTN	--	-	-	+	-	-	-
36414	YVKSDAL	--	-	-	-	-	-	-
42163	LHRDGPN	--	-	-	-	+	-	-
42191	LHRTSVN	--	++	--	+++	-	-	-
42208	LMQDAYP	--	-	-	-	-	-	-
42209	LSRISDN	--	-	-	-	-	-	-
42188	YSKLNTD	--	-	-	-	-	-	-
42210	RTQDSYP	--	-	-	-	-	-	-
11348	YSKTGAN	--	-	-	-	-	-	-
42211	LSRLNTD	--	-	-	-	-	+	-
37182	RNESVYP	--	-	-	-	+	-	-
42212	LHKQTLN	--	+	-	-	-	++	-
42213	YHKAGVN	--	-	-	-	-	-	-
42205	LHKLTLD	--	+	-	-	-	-	-
16186	HHSTNGV	--	-	-	-	+	+	-
42206	LRSGEGP	--	-	-	-	-	-	-
17025	VESSNGR	--	-	-	-	++	-	++
42214	YHKNGPG	--	+	-	-	-	+	-
42215	YVKSQST	--	+	-	-	-	-	-
36297	YLKSDTN	--	-	-	-	-	-	-
42216	FHKLSEN	--	+	-	-	+	-	-
42217	ACVIKPS	--	+++	---	-	-	-	-
38903	YESTNGR	--	-	-	-	+	-	++
16186	HHSTNGV	--	-	-	-	+	-	-
42218	RNDECCF	--	+	-	++	-	-	-
42219	YVKSDAM	--	-	-	-	-	-	-

37636	KSDYVTY	--	+	-	-	-	-	-
42220	LHKASSN	--	+	-	+	-	-	-
42221	RTNEVYP	--	-	-	-	+	-	-
42222	YIKHDTN	--	-	-	+	-	+	-
42184	YHRNGPD	--	-	-	+	-	-	-
11522	VESTNGV	--	-	-	-	++	-	-
42223	KSDFVAY	--	-	-	-	+	-	-
42224	YHKSTPN	--	+	-	+	-	-	-
11223	YSRQGTN	--	-	-	+	-	-	-
42225	LHKHGDN	--	+	-	+	++	-	-
42226	LARGSFN	--	-	-	+	-	-	-
42156	LHRQGTN	--	+	-	++	-	-	-
42227	MHKLSSN	--	++	--	-	-	++	-
42228	VNSTHGR	--	-	-	-	-	-	-
42229	HGNGNFV	--	-	-	-	+	-	-
11388	YSRNGLN	--	-	-	++	-	-	-
42230	YVKSDHK	--	++	--	++	-	-	-
42231	LHRNLDN	--	-	-	-	+	-	-
42232	YSSTNGM	--	-	-	+	-	-	-
14121	YSKSGFN	--	++	-	+	-	-	-
42233	YSRVGTD	--	-	-	+	-	-	-
42234	GDEFKIF	--	-	-	-	++	-	-
42235	RNQDVFP	--	-	-	-	-	-	-
42236	LSRAATN	--	-	-	-	-	-	-
42237	LSKTSFN	--	-	-	-	-	-	-
12523	HESTNGR	--	-	-	-	-	-	-
42238	LSKLHSN	--	-	-	+	-	-	-
42186	LHKSSYN	--	++	-	+	+	-	-
42239	LARTSTN	--	-	-	+	-	-	-
11288	VGSTNGI	--	-	-	-	+	-	-
42240	LHKSTVN	--	+	-	-	-	-	-
12570	YSSTNGV	--	-	-	-	++	-	-
42241	TSENTYF	--	-	-	-	+	-	-

42242	LHKMASN	--	+	-	+	-	++	-
11955	VYSTNGV	--	-	-	+	-	-	-
42243	LHKSLGN	--	++	-	-	-	-	-
42219	YVKSDAM	--	-	-	+	-	-	+
42244	LHRSSEN	--	-	-	-	-	+	-
42245	LHKMGEN	--	-	-	-	-	-	-
42246	YVKSQIT	--	+	-	++	-	-	-
42247	TDEWTGF	--	-	-	-	-	-	-
11930	IQSTNGI	--	-	-	-	-	-	-
42210	RTQDSYP	--	-	-	-	-	-	-
42152	LHRNGIN	--	-	-	+	-	-	-
37636	KSDYVTY	--	-	-	+	+	-	-
42248	LHRQTNN	--	++	-	+	-	-	-
42249	TKWGDNP	--	-	-	-	-	-	-
42237	LSKTSFN	--	-	-	-	-	-	-
38506	ARSTNGV	--	-	-	-	-	-	-
42250	LHRTTAN	--	+	--	++	-	-	-
42251	YHRAGEN	--	-	-	+	-	-	-
42252	YVRNGPN	--	-	-	++	-	-	-
42253	LHAKSTN	--	-	-	-	-	-	-
10995	LSRTSDN	--	-	-	-	-	-	-
42254	LHKNSNN	--	+	-	++	-	-	-
42221	RTNEVYP	--	-	-	+	-	-	-
42255	LHRTTTN	--	++	-	++	-	-	-
12570	YSSTNGV	--	-	-	-	+	-	-
42256	IHDRMCS	--	++	---	-	-	-	-
42257	NALIGFD	--	-	-	-	-	-	-
42258	YLKSDNN	--	-	-	-	-	-	-
42259	RTDQVYP	--	-	-	-	+	-	-
42260	RDDTVFP	--	-	-	-	++	-	-
42261	YVKSDPN	--	-	-	-	-	-	+
42262	LARTSNN	--	-	-	+	-	-	-
42263	LSKSSFN	--	-	-	-	-	-	-

42264	YLKSDTS	--	-	-	-	-	-	-
36811	LHRLSDP	--	-	-	+	-	-	-
42265	YARSSTN	--	-	-	+	-	-	-
14116	YSRQGVN	--	-	-	++	-	-	-
42266	LHKSTIN	--	+	-	+	-	-	-
11930	IQSTNGI	--	-	-	-	+	-	-
42267	KSEYYAH	--	-	-	-	-	-	-
42259	RTDQVYP	--	-	-	-	++	-	-
42241	TSENTYF	--	-	-	-	+	-	-
42229	HGNGNFV	--	-	-	-	+	-	-
42268	YTKTQSN	--	-	-	-	-	-	-
42269	LHRSATN	--	++	-	++	-	-	-
42260	RDDTVFP	--	-	-	-	+	-	-
42270	HSRLSEN	--	-	-	-	-	-	-
42271	DVGDRCK	--	+++	---	-	-	-	-
42272	LHRNGEN	--	-	-	+	+	+	-
42273	LHARGDN	--	-	-	-	-	-	-
42274	RNDMVYP	--	-	-	+	++	-	-
11043	LSKLNSN	--	-	-	-	-	-	-
42272	LHRNGEN	--	-	-	-	-	-	-
42275	YHRSGEN	--	+	-	++	-	-	-
11992	YTSSNGV	--	-	-	-	-	-	-
42276	LHRQTYD	--	-	-	+	-	-	-
11720	SESTNGR	--	-	-	-	-	-	-
11556	YASTNGV	--	-	-	+	-	-	-
42277	FSRAGAN	--	-	-	-	-	-	-
42278	LHRTSTN	--	+	--	+++	-	-	-
42279	LHKSTMN	--	+	--	+	-	+	-
42280	LHRSQDN	--	-	-	-	-	-	-
42281	LHKQATN	--	+	-	+	-	-	-
42282	LHRLGTQ	--	+	--	+	-	-	-
42283	LHKSTLN	--	+	--	-	-	-	-
42283	LHKSTLN	--	+	-	-	-	-	-

42284	LHRSTAN	--	++	-	++	-	-	-
42285	LHAKSNN	--	+	-	-	-	-	-
42286	YHKSGSN	--	+	-	+	-	-	-
42287	LHRLGTG	--	+	-	++	-	-	-
42288	LHKSQSN	--	++	--	+	-	-	-
42289	LHKAAQN	--	+	-	+	-	-	-
42290	LHKSGSN	--	+	-	-	-	-	-
42291	LHKSTTN	--	+	-	-	-	-	-
42292	CPPQRTI	--	+++	---	-	-	-	-
42288	LHKSQSN	--	+	-	+	-	+	-
42293	LHKSSSN	--	+	-	+	-	-	-
42294	LHRTMTN	--	+	-	+++	-	-	-
42295	YTKSDKF	--	++	--	-	-	-	-
42296	IHKLSMN	--	++	-	++	-	-	-
42297	YHKSGQN	--	+	-	-	-	-	-
42298	LHKSATN	--	+	-	+	-	-	-
42299	YVKHDTH	--	+	-	-	-	-	-
42300	LHKTGIN	--	+	-	+	-	-	-
42301	NPTGCET	--	+++	---	-	-	-	-
42302	LHRTSQN	--	++	-	+++	-	-	-
42303	YVKTDMK	--	++	-	-	-	-	+
42304	LHKSMTN	--	+	-	-	-	++	-
42305	YHKLNIV	--	++	---	-	-	-	-
42306	YIKHDLS	--	+	-	-	-	-	-
42307	YVKNDKN	--	+	-	+	-	-	-
42308	YVKTDSR	--	++	-	-	-	-	-
42309	YIKHDQN	--	+	--	-	-	-	-
42310	VEDSNCR	--	+++	-	-	-	-	-
42311	LHKYTVN	--	+++	--	++	-	-	-
13865	YSRINQN	-	+	-	++	-	-	-
42312	LCKTCTN	-	+++	-	-	++	-	-
42313	LHKSAMN	-	+	--	-	-	-	-
42314	YVKNDQK	-	+	-	+	-	+	-

42315	LHKATSN	-	+	-	-	-	-	-
42316	YARGGSG	-	+	-	-	-	-	-
42317	LHKSANN	-	+	-	+	-	-	-
42318	IGTRCFD	-	+++	---	-	-	-	-
42319	WNVLTCN	-	++	---	-	-	-	-
42320	KHGGLCM	-	+++	---	-	+	-	-
42321	FHKAGFN	-	++	--	-	-	-	-
42313	LHKSAMN	-	++	-	-	-	-	-
42322	CRIGKNP	-	+++	---	++	-	-	-
42323	WVKSDTM	-	++	-	-	-	+	-
42324	LHKSALN	-	+	-	+	-	-	-
42325	LHKLQNS	-	+	-	-	-	-	-
42326	DSGTCKA	-	+++	---	-	-	-	-
42327	YHKLSTG	-	+	-	++	-	-	-
42328	YVKTDKY	-	++	--	++	-	-	-
42329	LHKSTNN	-	+	-	-	-	-	-
42330	YVHSNTK	-	+	--	+	-	-	-
42331	LHKSMQN	-	+	-	-	-	-	-
42332	NVRCESE	-	++	-	-	-	-	-
42333	YHKLSAG	-	++	--	-	-	-	-
42334	WNKSGQG	-	+++	---	+	-	-	-
42335	LHKTGNN	-	+	-	-	-	-	-
42336	CDPTKKS	-	+++	---	-	++	-	-
42329	LHKSTNN	-	+	-	+	-	-	-
42337	CKGPEQV	-	+++	---	-	-	-	-
42338	KFDHMGT	-	+++	---	-	-	++	-
42339	GTACGKL	-	+++	---	-	-	-	-
42340	YIKNDKS	-	+	-	-	-	-	-
42341	YHRTNTG	-	+++	--	+	-	-	-
42342	THRLASN	-	+	-	++	-	-	-
42343	SYKNSTY	-	++	-	-	-	-	-
11314	YSKTGGN	-	+++	--	++	-	-	-
42344	YVKHGTT	-	++	--	-	-	-	-

42345	GDSEKCR	-	+++	---	+	-	-	-
42346	YVKSSNQ	-	+	-	-	-	-	-
42347	YLKSMSN	-	+	-	-	-	-	-
42348	LHKHSFD	-	+	-	-	-	-	-
42349	ITGNLKC	-	+++	---	++	-	-	-
42350	WIKSVNT	-	++	--	-	-	-	-
42351	CNNFLSE	-	+++	---	-	-	-	-
42352	IKYITKD	-	+++	--	++	-	-	-
42353	VRDKHGN	-	++	--	++	-	-	-
42354	KWDHAGS	-	+++	---	-	-	-	-
42355	MSCKDTC	-	+++	--	+++	-	-	-
42356	MNKHVHS	-	++	--	++	-	-	-
42357	IKYQTKD	-	++	--	++	-	-	-
42358	IKYSTSA	-	++	--	++	-	-	-
42359	SPSPGCM	-	+++	---	-	+	-	-
42360	MESCAKN	-	+++	---	-	-	-	-
42361	EKFIHSS	-	++	-	-	-	-	-
42362	KYDHMGT	-	+++	---	-	-	-	-
42363	GEKLYRA	-	+++	---	-	-	++	-
42364	INNLCVA	-	+++	---	-	-	-	-
42365	KYDAKGY	-	++	--	+	-	-	-
42366	YYKSSAS	-	++	--	++	-	-	-
42367	RCDKMCS	-	+++	---	+	-	-	-
42368	MHKVTHS	-	++	-	+	-	-	-
42369	SMAYIKQ	-	++	--	-	+	-	-
42370	SSYLQTK	-	++	--	-	-	-	-
42371	YVKHDKS	-	++	---	+++	-	-	-
42372	LSRTTSN	-	++	--	+	-	-	-
42373	KWDHAGA	-	+++	---	-	-	-	-
42374	LTALRKV	-	+++	-	++	-	-	-
42375	KFDHTSK	-	+++	--	++	-	-	-
42376	KFDHTGS	-	+++	---	-	+	++	-
42377	CRANAMP	-	+++	---	-	-	-	-

42378	KFDHMGS	-	+++	---	-	++	+++	-
42379	KFDHRGE	-	+++	---	-	-	++	-
42354	KWDHAGS	-	+++	---	+	-	++	-
42380	CAKFLVS	-	+++	---	+++	-	-	-
42381	KFDHQGV	-	+++	---	-	-	+++	-
42382	AWLKEGT	-	+++	--	-	-	+	-
42362	KYDHMGT	-	+++	---	-	-	-	-
42383	KFDHQGN	-	+++	---	-	-	++	-

T22

SEQ ID #	Family	Log2 production fitness (in vivo)	Log2 production fitness (in vitro)	TFR1 binding, pH sen	hCMEC binding	hCMEC transduction	Tf sensitivity
	AAV9 1x	good	good	insensitive	none	very low	moderate
	AAV9 10x	good	good	insensitive	low	low	insensitive
	AAV9 100x	good	good	insensitive	low	low	insensitive
	AAV-PHP.eB	good	n.p.	n.d.	n.d.	n.d.	n.d.
	AAV-BI28	excellent	n.p.	n.d.	n.d.	n.d.	n.d.
	9P31	poor	n.p.	n.d.	n.d.	n.d.	n.d.
	9P36	good	n.p.	n.d.	n.d.	n.d.	n.d.
	AAV-BI30	low	n.p.	n.d.	n.d.	n.d.	n.d.
36834	Family1	good	good	insensitive	high	high	insensitive
36253	Family1	excellent	good	insensitive	moderate	high	sensitive
36305	Family1	excellent	excellent	reduced	low	high	moderate
37062	Family1	good	good	insensitive	high	high	moderate
14632	Family1	good	excellent	insensitive	high	high	insensitive
36975	Family1	good	good	insensitive	high	high	moderate
16667	Family1	good	excellent	insensitive	high	high	moderate
36619	Family1	excellent	excellent	insensitive	moderate	high	sensitive
36257	Family1	excellent	excellent	reduced	low	low	sensitive
36844	Family1	good	good	insensitive	high	high	moderate
14269	Family1	excellent	excellent	insensitive	high	high	insensitive
37174	Family1	excellent	good	insensitive	high	high	moderate
36268	Family1	excellent	excellent	insensitive	moderate	high	moderate
36413	Family1	excellent	excellent	insensitive	moderate	high	sensitive
36252	Family1	excellent	good	insensitive	moderate	high	sensitive
17658	Family1	excellent	excellent	insensitive	low	high	moderate
36260	Family1	excellent	good	insensitive	low	low	sensitive
36347	Family1	excellent	excellent	insensitive	high	high	moderate
14059	Family1	excellent	excellent	insensitive	high	high	insensitive
14628	Family1	excellent	excellent	insensitive	moderate	high	insensitive
36246	Family1	excellent	good	insensitive	moderate	high	sensitive
36278	Family1	excellent	good	insensitive	moderate	high	sensitive
36243	Family1	excellent	good	reduced	low	high	moderate

36442 Family1	excellent	excellent	insensitive	moderate	high	moderate
14048 Family1	excellent	excellent	insensitive	moderate	high	moderate
36459 Family1	excellent	excellent	insensitive	high	high	moderate
36344 Family1	excellent	excellent	insensitive	high	high	insensitive
36262 Family1	excellent	excellent	reduced	low	moderate	moderate
13841 Family1	good	good	insensitive	moderate	very low	sensitive
36290 Family1	excellent	good	minimal	low	very low	sensitive
36287 Family1	excellent	good	insensitive	low	very low	moderate
36592 Family1	excellent	good	insensitive	high	moderate	moderate
14303 Family1	excellent	excellent	insensitive	low	high	moderate
36275 Family1	excellent	excellent	minimal	low	very low	sensitive
13517 Family1	good	excellent	insensitive	moderate	high	moderate
36281 Family1	good	good	insensitive	moderate	moderate	sensitive
16602 Family1	excellent	excellent	minimal	low	very low	insensitive
14350 Family1	excellent	excellent	insensitive	moderate	high	moderate
13818 Family1	excellent	excellent	insensitive	moderate	high	moderate
36250 Family1	excellent	excellent	insensitive	moderate	high	moderate
36796 Family1	excellent	excellent	insensitive	moderate	high	sensitive
16619 Family1	excellent	excellent	minimal	low	moderate	moderate
38712 Family1	excellent	excellent	insensitive	low	low	sensitive
14054 Family1	excellent	good	insensitive	low	low	moderate
13864 Family1	excellent	excellent	insensitive	moderate	high	moderate
14581 Family1	excellent	excellent	insensitive	low	very low	moderate
14574 Family1	good	good	insensitive	high	high	insensitive
36723 Family1	excellent	excellent	insensitive	moderate	moderate	sensitive
14200 Family1	excellent	excellent	insensitive	moderate	high	insensitive
36839 Family1	excellent	excellent	insensitive	low	low	moderate
37910 Family1	excellent	excellent	insensitive	high	high	insensitive
36251 Family1	excellent	good	minimal	low	low	sensitive
36540 Family1	excellent	excellent	minimal	low	very low	moderate
36295 Family1	excellent	excellent	minimal	low	moderate	sensitive
36539 Family1	excellent	excellent	insensitive	moderate	very low	sensitive
14274 Family1	excellent	excellent	insensitive	low	high	moderate

38843	Family1	good	excellent	insensitive	moderate	moderate	sensitive
13537	Family1	excellent	good	insensitive	low	very low	moderate
36491	Family1	excellent	good	insensitive	moderate	very low	moderate
36280	Family1	good	good	minimal	low	very low	sensitive
36445	Family1	excellent	excellent	insensitive	moderate	very low	moderate
38753	Family1	excellent	excellent	insensitive	moderate	moderate	sensitive
36693	Family1	excellent	good	minimal	low	very low	sensitive
36285	Family1	excellent	good	minimal	low	very low	sensitive
36741	Family1	excellent	good	insensitive	low	very low	moderate
36534	Family1	good	good	insensitive	moderate	very low	sensitive
36387	Family1	excellent	excellent	insensitive	moderate	high	sensitive
14198	Family1	excellent	good	insensitive	low	moderate	moderate
14441	Family1	excellent	excellent	insensitive	low	high	moderate
36523	Family1	excellent	excellent	insensitive	moderate	low	moderate
14176	Family1	excellent	excellent	insensitive	moderate	moderate	insensitive
37031	Family1	good	good	insensitive	moderate	very low	sensitive
37068	Family1	excellent	good	insensitive	low	very low	moderate
11967	Family1	excellent	good	insensitive	low	very low	insensitive
36288	Family1	excellent	excellent	insensitive	low	moderate	sensitive
36266	Family1	excellent	good	reduced	low	very low	moderate
36360	Family1	excellent	good	minimal	low	very low	moderate
36554	Family1	good	good	insensitive	moderate	very low	sensitive
36316	Family2	excellent	excellent	insensitive	low	high	sensitive
36431	Family3	excellent	excellent	insensitive	moderate	very low	insensitive
36423	Family3	excellent	good	insensitive	low	very low	insensitive
17558	Family3	excellent	excellent	insensitive	low	very low	insensitive
11875	Family3	excellent	excellent	insensitive	low	very low	insensitive
12333	Family3	excellent	good	insensitive	very low	very low	insensitive
11292	Family3	good	good	reduced	low	very low	insensitive
12037	Family3	good	good	reduced	low	very low	insensitive
11522	Family3	good	good	insensitive	low	very low	insensitive
12055	Family3	good	good	insensitive	low	very low	insensitive
12239	Family3	excellent	excellent	insensitive	low	very low	insensitive

16134	Family3	excellent	good	minimal	low	very low	insensitive
11974	Family3	excellent	good	reduced	very low	very low	insensitive
11663	Family3	good	good	minimal	low	very low	insensitive
12013	Family3	excellent	good	reduced	very low	very low	insensitive
12707	Family3	good	good	minimal	low	very low	insensitive
17605	Family3	good	good	minimal	low	very low	insensitive
11841	Family3	good	excellent	insensitive	low	very low	insensitive
12038	Family3	excellent	good	minimal	low	very low	insensitive
12069	Family3	good	good	minimal	low	very low	insensitive
11853	Family3	good	good	minimal	low	very low	insensitive
38903	Family3	good	good	reduced	moderate	very low	insensitive
36911	Family3	good	good	reduced	moderate	very low	insensitive
16158	Family3	good	good	minimal	low	very low	insensitive
12737	Family3	good	good	minimal	low	very low	insensitive
16112	Family3	good	excellent	reduced	moderate	very low	insensitive
11866	Family3	good	good	minimal	low	very low	insensitive
11765	Family3	good	low	minimal	low	very low	insensitive
11451	Family3	good	good	minimal	low	very low	insensitive
14499	Family3	good	good	minimal	low	very low	insensitive
39421	Family3	good	excellent	minimal	low	very low	insensitive
12190	Family3	excellent	good	insensitive	low	very low	insensitive
16113	Family3	good	excellent	minimal	low	very low	insensitive
12009	Family3	good	good	minimal	low	very low	insensitive
11878	Family3	excellent	good	minimal	low	very low	insensitive
14392	Family3	good	good	minimal	low	very low	insensitive
16186	Family3	good	good	minimal	low	very low	insensitive
17025	Family3	good	good	minimal	low	very low	insensitive
18112	Family3	good	good	minimal	moderate	very low	insensitive
36362	Family3	excellent	good	minimal	low	very low	insensitive
36895	Family4	good	good	insensitive	low	very low	insensitive
36864	Family4	good	good	insensitive	low	very low	insensitive
37938	Family4	good	excellent	insensitive	moderate	high	insensitive
36486	Family4	excellent	good	insensitive	moderate	very low	insensitive

36389 Family4	good	good	insensitive	low	very low	insensitive
36509 Family4	excellent	good	insensitive	low	very low	insensitive
38571 Family4	good	excellent	insensitive	high	high	insensitive
36603 Family4	good	good	insensitive	moderate	very low	insensitive
37806 Family4	excellent	excellent	insensitive	moderate	moderate	insensitive
37223 Family4	good	good	insensitive	low	very low	insensitive
36319 Family4	good	good	insensitive	low	very low	insensitive
36613 Family4	good	good	insensitive	low	very low	insensitive
36738 Family4	good	good	insensitive	low	very low	insensitive
36692 Family4	good	good	insensitive	low	very low	insensitive
36675 Family4	good	good	insensitive	low	very low	insensitive
36479 Family4	good	good	insensitive	low	very low	insensitive
37622 Family4	excellent	excellent	insensitive	low	very low	insensitive
36805 Family4	good	good	insensitive	low	very low	insensitive
36409 Family4	good	low	insensitive	low	very low	insensitive
36989 Family4	good	good	insensitive	low	very low	insensitive
36463 Family4	good	good	insensitive	low	very low	insensitive
37182 Family4	good	good	insensitive	low	very low	insensitive
36443 Family4	good	good	insensitive	low	very low	insensitive
37302 Family4	good	good	insensitive	moderate	very low	insensitive
37912 Family4	good	excellent	insensitive	moderate	very low	insensitive
36640 Family4	excellent	good	insensitive	moderate	low	insensitive
38456 Family4	good	good	insensitive	low	very low	insensitive
36633 Family4	good	good	insensitive	low	very low	insensitive
36744 Family4	excellent	good	insensitive	low	very low	insensitive
37419 Family4	good	good	insensitive	low	very low	insensitive
38083 Family4	good	good	insensitive	low	very low	insensitive
37511 Family4	good	good	insensitive	low	very low	insensitive
17596 Family4	excellent	good	insensitive	low	very low	insensitive
37144 Family4	good	good	insensitive	low	very low	insensitive
36713 Family4	good	good	insensitive	low	very low	insensitive
36898 Family4	good	good	insensitive	low	very low	insensitive
36867 Family4	good	good	insensitive	low	very low	insensitive

36620	Family4	good	good	insensitive	low	very low	insensitive
37313	Family4	good	good	insensitive	low	very low	insensitive
37204	Family4	good	good	insensitive	low	very low	insensitive
37181	Family4	good	good	insensitive	low	very low	insensitive
36695	Family4	excellent	good	insensitive	low	very low	insensitive
36649	Family4	good	low	insensitive	high	very low	insensitive
36636	Family4	excellent	good	insensitive	low	very low	insensitive
36940	Family4	good	good	insensitive	low	very low	insensitive
37133	Family4	excellent	good	insensitive	low	very low	insensitive
36936	Family5	good	good	insensitive	high	low	insensitive
36437	Family5	excellent	excellent	insensitive	high	high	moderate
37684	Family5	good	good	insensitive	moderate	very low	insensitive
36438	Family5	excellent	good	insensitive	moderate	very low	sensitive
36493	Family5	excellent	good	insensitive	high	moderate	moderate
36434	Family5	good	good	insensitive	moderate	very low	moderate
36682	Family5	excellent	excellent	insensitive	moderate	high	insensitive
36435	Family5	excellent	good	insensitive	moderate	very low	moderate
36464	Family7	excellent	good	minimal	low	very low	insensitive
37652	Family7	good	good	insensitive	high	very low	insensitive
36336	Family7	excellent	good	minimal	low	very low	insensitive
36615	Family7	good	good	insensitive	moderate	very low	insensitive
36328	Family7	excellent	good	insensitive	low	very low	insensitive
36338	Family7	good	good	insensitive	low	very low	insensitive
36390	Family7	excellent	good	minimal	low	very low	insensitive
39322	Family7	good	good	insensitive	high	very low	insensitive
36971	Family7	good	good	insensitive	high	very low	insensitive
36420	Family7	good	good	insensitive	low	low	insensitive
37079	Family7	good	good	insensitive	moderate	very low	insensitive
37213	Family7	good	good	insensitive	moderate	very low	insensitive
19906	Family7	good	good	minimal	low	very low	insensitive
36416	Family7	good	good	insensitive	moderate	low	insensitive
36511	Family7	excellent	good	minimal	low	very low	insensitive
36367	Family7	good	good	insensitive	low	very low	insensitive

37197 Family7	good	excellent	insensitive	moderate	very low	insensitive
36766 Family7	good	good	insensitive	moderate	very low	insensitive
37939 Family7	good	excellent	reduced	moderate	low	insensitive
36612 Family7	good	good	insensitive	low	very low	insensitive
36730 Family7	excellent	good	insensitive	low	very low	insensitive
37641 Family7	good	excellent	minimal	moderate	low	insensitive
36787 Family7	good	good	minimal	low	very low	insensitive
36453 Family7	good	good	insensitive	low	very low	insensitive
36425 Family7	good	low	reduced	low	very low	insensitive
36874 Family7	good	good	minimal	moderate	very low	insensitive
17013 Family7	good	good	insensitive	moderate	very low	insensitive
36982 Family7	good	good	insensitive	low	very low	insensitive
36977 Family7	good	good	reduced	low	very low	insensitive
13795 Family7	good	good	insensitive	moderate	very low	insensitive
17752 Family7	good	good	reduced	moderate	very low	insensitive
37029 Family7	good	good	reduced	moderate	very low	insensitive
36407 Family8	good	good	insensitive	moderate	very low	insensitive
36248 Family8	excellent	good	insensitive	high	low	insensitive
36579 Family8	good	good	insensitive	low	very low	insensitive
36496	excellent	excellent	insensitive	moderate	moderate	insensitive

2-step LY6A	2-Step hTFRC	B-hTFR1 KI brain	B-hTFR1 KI spinal cord	B-hTFR1 KI liver
very low	none	none	none	moderate
moderate	low	low	low	high
high	low	low	low	high
high	none	high	high	very low
high	high	high	high	low
high	high	high	low	very low
moderate	low	low	none	very low
high	low	low	none	high
none	high	high	high	low
none	high	high	high	high
none	high	high	high	high
none	high	high	high	high
none	high	high	high	high
none	high	high	high	high
none	high	high	high	moderate
none	high	high	high	moderate
none	high	high	high	high
none	high	high	high	moderate
none	high	high	high	high
none	high	high	high	high
none	high	high	high	high
none	high	high	high	very low
none	high	high	high	moderate
none	high	high	high	high
none	high	high	high	moderate
none	high	high	high	high
none	high	high	high	high
none	high	high	high	high
none	high	high	high	moderate
none	high	high	high	high
none	high	high	high	high

none	high	high	high	high
none	moderate	high	high	moderate
none	high	high	high	high
none	moderate	high	high	high
none	moderate	high	high	high
none	moderate	moderate	moderate	high
none	high	moderate	moderate	moderate
none	moderate	moderate	moderate	high
none	high	moderate	high	very low
none	high	moderate	moderate	moderate
none	high	moderate	moderate	low
none	low	moderate	moderate	high
none	high	moderate	moderate	low
none	moderate	moderate	moderate	high
none	moderate	moderate	moderate	high
none	low	moderate	moderate	high
none	high	moderate	moderate	moderate
none	high	moderate	high	low
none	moderate	moderate	moderate	high
none	high	moderate	moderate	low
none	moderate	moderate	low	low
none	moderate	moderate	moderate	high
none	moderate	moderate	low	moderate
none	high	moderate	moderate	low
none	high	moderate	moderate	very low
none	low	moderate	none	moderate
none	high	moderate	moderate	moderate
none	low	moderate	moderate	high
none	moderate	moderate	low	low
none	moderate	moderate	moderate	high
none	moderate	moderate	moderate	high
none	high	moderate	moderate	very low
none	moderate	moderate	moderate	moderate

none	moderate	moderate	low	moderate
none	low	moderate	low	high
none	moderate	moderate	moderate	high
none	moderate	moderate	low	moderate
none	moderate	moderate	low	moderate
none	high	moderate	moderate	moderate
none	moderate	moderate	low	high
none	moderate	moderate	moderate	moderate
none	low	moderate	low	high
none	moderate	moderate	none	very low
none	moderate	moderate	moderate	high
none	moderate	moderate	low	moderate
none	low	moderate	low	moderate
none	moderate	moderate	moderate	high
none	moderate	moderate	low	low
none	high	moderate	moderate	low
none	high	moderate	low	low
none	moderate	moderate	low	very low
none	moderate	moderate	low	low
none	moderate	moderate	low	moderate
none	low	moderate	low	moderate
none	moderate	moderate	low	very low
none	high	high	high	moderate
none	high	high	high	moderate
none	high	high	high	moderate
none	high	high	high	low
none	high	high	high	low
none	low	high	moderate	low
none	high	high	high	low
none	high	high	high	moderate
none	high	high	high	very low
none	high	high	high	very low
none	high	high	high	moderate

none	high	high	high	moderate
none	moderate	high	moderate	very low
none	high	high	high	moderate
none	high	high	high	very low
none	high	high	high	low
none	high	high	high	very low
none	high	high	high	moderate
none	high	high	high	low
none	moderate	high	moderate	low
none	low	high	high	very low
none	moderate	high	high	low
none	high	high	high	high
none	moderate	high	high	moderate
none	high	high	high	very low
none	moderate	high	high	high
none	high	high	moderate	low
none	moderate	high	moderate	low
none	moderate	high	moderate	very low
none	moderate	high	high	moderate
none	moderate	high	moderate	very low
none	high	high	moderate	very low
none	moderate	high	moderate	high
none	moderate	moderate	high	moderate
none	moderate	moderate	moderate	moderate
none	moderate	moderate	moderate	high
none	low	moderate	moderate	moderate
none	low	moderate	low	very low
none	low	moderate	moderate	high
none	moderate	moderate	moderate	high
none	high	high	high	very low
none	high	high	high	very low
none	high	high	high	very low
none	high	high	high	moderate

none	high	high	high	very low
none	high	high	high	high
none	high	high	high	very low
none	high	high	high	very low
none	high	high	high	very low
none	high	high	high	very low
none	high	high	high	very low
none	high	high	high	high
none	high	high	high	low
none	high	high	high	very low
none	high	high	high	very low
none	high	high	high	very low
none	high	high	high	high
none	moderate	high	moderate	low
none	high	high	high	high
none	moderate	high	high	very low
none	high	high	high	low
none	moderate	high	high	low
none	high	high	high	very low
none	high	high	high	low
none	high	high	moderate	moderate
none	moderate	high	high	low
none	moderate	high	moderate	very low
none	high	high	high	low
none	moderate	high	high	very low
none	moderate	high	high	low
none	high	high	moderate	very low
none	moderate	high	moderate	low
none	moderate	high	moderate	moderate
none	moderate	high	moderate	high
none	high	high	high	very low
none	moderate	high	moderate	low
none	moderate	high	moderate	low

none	high	moderate	low	very low
none	low	moderate	moderate	high
none	moderate	moderate	moderate	moderate
none	moderate	moderate	high	low
none	high	moderate	moderate	very low
none	high	moderate	low	very low
none	moderate	moderate	low	moderate
none	none	moderate	moderate	very low
none	moderate	moderate	moderate	moderate
none	high	high	high	very low
none	high	high	high	very low
none	high	high	low	very low
none	high	moderate	moderate	very low
none	high	moderate	moderate	very low
none	high	moderate	none	very low
none	high	moderate	moderate	very low
none	high	moderate	moderate	very low
none	high	high	high	very low
none	high	high	high	very low
none	high	high	high	very low
none	high	high	high	very low
none	high	high	high	very low
none	high	high	high	very low
none	high	high	high	very low
none	high	high	high	very low
none	high	high	high	very low
none	high	high	high	very low
none	high	high	high	very low
none	high	high	moderate	very low
none	high	high	high	very low
none	high	high	high	very low
none	high	high	high	very low
none	high	high	high	very low
none	high	high	moderate	very low

none	high	high	moderate	very low
none	high	high	moderate	very low
none	high	high	low	very low
none	high	high	moderate	very low
none	moderate	high	moderate	very low
none	high	high	high	very low
none	high	high	high	very low
none	high	high	moderate	very low
none	moderate	moderate	low	very low
none	high	moderate	moderate	very low
none	low	moderate	low	very low
none	moderate	moderate	low	very low
none	high	moderate	low	very low
none	moderate	moderate	moderate	very low
none	moderate	moderate	low	very low
none	high	moderate	low	very low
none	high	high	high	very low
none	high	moderate	moderate	low
none	moderate	moderate	none	very low
none	moderate	moderate	moderate	moderate

CLAIMS

What is claimed is:

1. A composition comprising a targeting moiety effective to increase transduction of central nervous system (CNS) tissues via binding to a transferrin receptor (TfR1), optionally further comprising a cargo coupled to or otherwise associated with the targeting moiety.

2. The composition of claim 1, wherein the targeting moiety binds to the extracellular domain of TFRC.

3. The composition of claim 2, wherein the targeting moiety binds to one or more of the apical, helical, and/or protease-like domain of the extracellular domain.

4. The composition of claim, 3 wherein the targeting moiety binds to the apical domain.

5. The composition of any of the preceding claims wherein, the wherein the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of X_1-X_2-X_3-X_4-X_5-X_6-X_7 wherein:

X_1 comprises of Y, M, F, and L;

X_2 comprises of S, H, T, and A;

X_3 comprises of K and R;

X_4 comprises of A, G, I, L, M, N, Q, S, T, V and H;

X_5 comprises of N, G, A, L, M, Q, S, and T;

X_6 comprises of A, T, H, N, F, I, P, L, Y, G, S, V, D, E, M, and Q; and

X_7 comprises of D and N.

6. The composition of claim 5, wherein:

X_1 comprises of Y, M, and L;

X_2 comprises of S, H, T, and A;

X_3 comprises of K and R;

X_4 comprises of A, G, I, L, M, N, Q, S, T, and V;

X_5 comprises of N;

X_6 comprises of A, T, H, N, F, I, P, L, and Y; and

X_7 comprises of D and N;

or

X_1 comprises of Y, M, and L;

X_2 comprises of S, H, T, and A;

X_3 comprises of K and R;

X_4 comprises of A, G, I, L, M, N, Q, S, T, and V;

X_5 comprises of G;

X_6 comprises of A, G, F, H, I, L, N, P, S, T, V, and Y; and

X_7 comprises of D and N;

or

X_1 comprises of L and Y;

X_2 comprises of A, H, and S;

X_3 comprises of K and R;

X_4 comprises of A, G, H, I, L, M, N, Q, S, T, and V;

X_5 comprises of G;

X_6 comprises of P; and

X_7 comprises of D;

or

X_1 comprises of L and Y;

X_2 comprises of A, H, and S;

X_3 comprises of K and R;

X_4 comprises of A, G, H, I, L, M, N, Q, S, T, and V;

X_5 comprises of G;

X_6 comprises of P; and

X_7 comprises of N;

or

X_1 comprises of Y;

X_2 comprises of S;

X_3 comprises of K;

X_4 comprises of A, I, L, M, N, Q, S, T, and V;

X_5 comprises of G;

X_6 comprises of X; and

X_7 comprises of Y, P, T, Q, V, F, L, H, S, A, E, D, I, and M;

or

X_1 comprises of L and Y;

X_2 comprises of S;

X_3 comprises of R and K;

X_4 comprises of V, I, T, L, and A;

X_5 comprises of S and A;

X_6 comprises of P, R, Y, F, H, I, K, and W; and

X_7 comprises of D;

or

X_1 comprises of F, L, M, and Y;

X_2 comprises of H;

X_3 comprises of K and R;

X_4 comprises of A, L, and M;

X_5 comprises of A, G, L, M, N, Q, S, and T;

X_6 comprises of A, D, E, F, H, I, L, M, N, Q, P, S, T, V, and Y; and

X_7 comprises of D and N;

or

X_1 comprises of L, M, and Y;

X_2 comprises of H;

X_3 comprises of K and R;

X_4 comprises of A, L, and M;

X_5 comprises of A, G, L, M, N, Q, S, and T;

X_6 comprises of A, D, E, F, H, I, L, M, N, Q, P, S, T, V, and Y; and

X_7 comprises of N;

or

X_1 comprises of L, M, and Y;

X_2 comprises of H;

X_3 comprises of K and R;

X_4 comprises of A, L, and M;

X_5 comprises of A, G, L, M, N, Q, S, and T;

X_6 comprises of A, D, E, F, H, I, L, M, N, Q, P, S, T, V, and Y; and

X_7 comprises of D;

or

X_1 comprises of L, M, and Y;

X_2 comprises of H;

X_3 comprises of K and R;

X_4 comprises of L;

X_5 comprises of S, Q, G, T, N, and L;

X_6 comprises of P, T, V, I, Q, L, and A; and

X_7 comprises of D;

or

X_1 comprises of F;

X_2 comprises of S;

X_3 comprises of R;

X_4 comprises of L;

X_5 comprises of G;

X_6 comprises of A, H, N, L, V, S, P, and T; and

X_7 comprises of N;

or

X_1 comprises of F;

X_2 comprises of A;

X_3 comprises of R;

X_4 comprises of T, S, and N;

X_5 comprises of G;

X_6 comprises of Y, F, H, P, and A; and

X_7 comprises of N;

or

X_1 comprises of F;

X_2 comprises of H;

X_3 comprises of K and R;

X_4 comprises of L;

X_5 comprises of G;

X_6 comprises of I, P, and S; and

X_7 comprises of N and D.

7. The composition of claim 6, wherein the n-mer motif is selected from the group consisting of LHRLGPN (SEQ ID NO: 36834), YSRIGPN (SEQ ID NO: 14632), LHRLGPN (SEQ ID NO: 36834), LHRLGPD (SEQ ID NO: 36413), LHRAGPD (SEQ ID NO: 36894), YSRIGPD (SEQ ID NO: 38223), LSRIGPD (SEQ ID NO: 36274), LARSGPD (SEQ ID NO: 18035), YSRNSDN (SEQ ID NO: 16626), LHKAGPN (SEQ ID NO: 36305), LSRIGPN (SEQ ID NO: 36347), LAKSGPN (SEQ ID NO: 36287), YARNGPN (SEQ ID NO: 14048) and YSRNSDN (SEQ ID NO: 16626).

8. The composition of claim 7, wherein the n-mer motif is YSRIGPN (SEQ ID NO: 14632).

9. The composition of claim 1 to 4, the wherein the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of X_1-X_2-X_3-X_4-X_5-X_6-X_7 wherein:

X_1 comprises of Y or L;

X_2 comprises of H;

X_3 comprises of A;

X_4 comprises of K, R, N, and A;

X_5 comprises of G, Q, L, and S;

X_6 comprises of P, L, I, N, D, and T; and

X_7 comprises of N.

10. The composition of claim 1 to 4, the wherein the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of X_1-X_2-X_3-X_4-X_5-X_6-X_7 wherein:

X_1 comprises of A, F, H, I, L, N, P, R, S, T, V, and Y;

X_2 comprises of A, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, W, and Y;

X_3 comprises of S;

X_4 comprises of S and T;

X_5 comprises of N;

X_6 comprises of G; and

X_7 comprises of I, R, and V.

11. The composition of claim 10, wherein:

X_1 comprises of F, L, and Y;

X_2 comprises of D, E, H, N, Q, S, and T;

X_3 comprises of S;

X_4 comprises of S and T;

X_5 comprises of N;

X_6 comprises of G; and

X_7 comprises of I and V;

or

X_1 comprises of V, P, I, S, T, H, and A;

X_2 comprises of A, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, and Y;

X_3 comprises of S;

X_4 comprises of S and T;

X_5 comprises of N;

X_6 comprises of G; and

X_7 comprises of I and V;

or

X_1 comprises of A, F, I, L, P, S, T, V, and Y;

X_2 comprises of D, E, N, Q, S, and T;

X_3 comprises of S;

X_4 comprises of T and S;

X_5 comprises of N;

X_6 comprises of G; and

X_7 comprises of R;

or

X_1 comprises of R;

X_2 comprises of E, D, Q, and T;

X_3 comprises of S;

X_4 comprises of S and T;

X_5 comprises of N;

X_6 comprises of G; and

X_7 comprises of I and V.

12. The composition of claim 11, wherein the n-mer motif is selected from the group consisting of FRSTNGV (SEQ ID NO: 16070), VESTNGR (SEQ ID NO: 36431), VDSTNGV (SEQ ID NO: 12206), VQSTNGV (SEQ ID NO: 36423), VSSTNGV (SEQ ID NO: 12333), TESTNGR (SEQ ID NO: 17558), VQSTNGI (SEQ ID NO: 11292) and FVSTNGV (SEQ ID NO: 11162).

13. The composition of claim 1 to 4, the wherein the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of X_1-X_2-X_3-X_4-X_5-X_6-X_7 wherein:

X_1 comprises of R and T;

X_2 comprises of T, L, M, S, G, D, N, E, R, K, Y, and W;

X_3 comprises of G, E, D, I, F, H, S, A, M, P, V, Y, W, Q, and T;

X_4 comprises of D, T, E, H, N, and G;

X_5 comprises of A, V, S, T, and D;

X_6 comprises of Y, F, P and A; and

X_7 comprises of A and P.

14. The composition of claim 13, wherein:

X_1 comprises of R;

X_2 comprises of T, M, L, and S;

X_3 comprises of Y, S, A, M, I, F, and P;

X_4 comprises of D;

X_5 comprises of A, V, S, and T;

X_6 comprises of Y and F; and

X_7 comprises of P;

or

X_1 comprises of R;

X_2 comprises of T, M, L, and S;

X_3 comprises of Y, S, A, M, I, F, and P;

X_4 comprises of D;

X_5 comprises of A, V, S, and T;

X_6 comprises of Y and F; and

X_7 comprises of A;

or

X_1 comprises of R;

X_2 comprises of G, T, D, S, N, and E;

X_3 comprises of E, D, P, S, and G;

X_4 comprises of D, T, E, H, and N;

X_5 comprises of V, A, and T;

X_6 comprises of Y and F; and

X_7 comprises of P;

or

X_1 comprises of R;

X_2 comprises of G, L, T, D, and S;

X_3 comprises of D, P, S, and G;

X_4 comprises of D, E, H, and N;

X_5 comprises of V and T;

X_6 comprises of Y and F; and

X_7 comprises of P;

or

X_1 comprises of T;

X_2 comprises of R, K, Y, and W;

X_3 comprises of E, W, Y, Q, S, and T;

X_4 comprises of G;

X_5 comprises of D;

X_6 comprises of P and A; and

X_7 comprises of A and P.

15. The composition of claim 14, wherein the n-mer motif is selected from the group consisting of RGEDVYP (SEQ ID NO: 36864), RLEDVFP (SEQ ID NO: 36264), RTYDSYP (SEQ ID NO: 37938), RTYDAYP (SEQ ID NO: 38571), RTYDSFP (SEQ ID NO: 37806), RTETVYP (SEQ ID NO: 36486), RTETVFP (SEQ ID NO: 36389), and RTEHVFP (SEQ ID NO: 36603).

16. The composition of claim 1 to 4, the wherein the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of X_1-X_2-X_3-X_4-X_5-X_6-X_7 wherein:

X_1 comprises of L;

X_2 comprises of C;

X_3 comprises of K and R;

X_4 comprises of P;

X_5 comprises of C;

X_6 comprises of L, S, D, A, N, Q, H, P, and V; and

X_7 comprises of E, T, G, A, D, N, and S.

17. The composition of claim 16, wherein the n-mer motif comprises of LCKPCLD (SEQ ID NO: 36437) or LCKPCPT (SEQ ID NO: 36438).

18. The composition of claim 1 to 4, the wherein the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of X_1-X_2-X_3-X_4-X_5-X_6-X_7 wherein:

X_1 comprises of Y, and F;

X_2 comprises of W, F, and Y;

X_3 comprises of S, T, H, A and Q;

X_4 comprises of G;

X_5 comprises of I, T, V, Q, M, H, K, and R;

X_6 comprises of I, P, H, L, M, A, Q, T, V, K, and R; and

X_7 comprises of A, S, D, E, and N.

19. The composition of claim 18, wherein:

X_1 comprises of Y and F;

X_2 comprises of W, F, and Y;

X_3 comprises of T and S;

X_4 comprises of G;

X_5 comprises of I, T, V, Q, M, and H;

X_6 comprises of I, P, H, L, M, A, Q, T, and V; and

X_7 comprises of A, S, D, and E;

or

X_1 comprises of Y and F;

X_2 comprises of W, F, and Y;

X_3 comprises of T and S;

X_4 comprises of G;

X_5 comprises of I, T, V, Q, M, and H;

X_6 comprises of K and R; and

X_7 comprises of A, S, D, and E;

or

X_1 comprises of Y and F;

X_2 comprises of W, F, and Y;

X_3 comprises of T and S;

X_4 comprises of G;

X_5 comprises of K and R;

X_6 comprises of I, P, H, L, M, A, Q, T, and V; and

X_7 comprises of A, S, D, and E;

or

X_1 comprises of Y;

X_2 comprises of F;

X_3 comprises of T;

X_4 comprises of G;

X_5 comprises of K, R, Q, M, H, and I;

X_6 comprises of T, R, H, K, V, and L; and

X_7 comprises of E;

or

X_1 comprises of Y;

X_2 comprises of F;

X_3 comprises of T, S, H, and A;

X_4 comprises of G;

X_5 comprises of K, R, and T;

X_6 comprises of I, P, H, L, M, A, Q, and T; and

X_7 comprises of D and N;

or

X_1 comprises of Y;

X_2 comprises of W;

X_3 comprises of T;

X_4 comprises of G;

X_5 comprises of K, M, V, and T;

X_6 comprises of P, V, I, H, Q, T, M, and L; and

X_7 comprises of E and D;

or

X_1 comprises of Y and F;

X_2 comprises of F;

X_3 comprises of S, H, A, and Q;

X_4 comprises of G;

X_5 comprises of K, Q, and R;

X_6 comprises of I, V, L, K, H, R, Q, and M; and

X_7 comprises of E.

20. The composition of claim 1 to 4, the wherein the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of X_1-X_2-X_3-X_4-X_5-X_6-X_7 wherein:

X_1 comprises of K, R, S, G, N, T, M, Q, V, D, I, and E;

X_2 comprises of D, S, N, M, L, G, P, E, and A;

X_3 comprises of E, D, G, S, A, R, Q, T, P, and N;

X_4 comprises of F, Y, T, V, S, N, A, G, and H;

X_5 comprises of T, K, S, R, V, and H;

X_6 comprises of T, S, G, V, A, K, R, N, D, E, and H; and

X_7 comprises of F, W, and Y.

21. The composition of claim 20, wherein:

X_1 comprises of K and R;

X_2 comprises of D, S, and N;

X_3 comprises of E;

X_4 comprises of F;

X_5 comprises of T, K, S, R, and V;

X_6 comprises of T, S, G, and V; and

X_7 comprises of F, W, and Y;

or

X_1 comprises of K and R;

X_2 comprises of D;

X_3 comprises of D;

X_4 comprises of F and Y;

X_5 comprises of T, S, V, and H;

X_6 comprises of T, S, G, V, and A; and

X_7 comprises of F, W, and Y;

or

X_1 comprises of S, R, G, N, T, M, and Q;

X_2 comprises of D;

X_3 comprises of G;

X_4 comprises of T, V, S, N, and Y;

X_5 comprises of S;

X_6 comprises of K and R; and

X_7 comprises of W;

or

X_1 comprises of R, V, D, I, Q, and K;

X_2 comprises of M, L, and G;

X_3 comprises of S, E, A, R, and Q;

X_4 comprises of D;

X_5 comprises of R;

X_6 comprises of T, A, S, G, K, and N; and

X_7 comprises of W;

or

X_1 comprises of D, I, E, Q, V, S, and K;

X_2 comprises of L, M, G, and P;

X_3 comprises of E, A, S, D, Q, and T;

X_4 comprises of S and A;

X_5 comprises of R;

X_6 comprises of D, S, E, T, G, and A; and

X_7 comprises of W;

or

X_1 comprises of G;

X_2 comprises of E, S, P, G, and A;

X_3 comprises of D, E, P, and N;

X_4 comprises of G, H, T, S, and N;

X_5 comprises of V;

X_6 comprises of R, K, and S; and

X_7 comprises of W and Y;

or

X_1 comprises of R;

X_2 comprises of E;

X_3 comprises of D, E, P, and N;

X_4 comprises of G, H, T, S, and N;

X_5 comprises of V;

X_6 comprises of R, K, and S; and

X_7 comprises of W and Y;

or

X_1 comprises of G;

X_2 comprises of G and S;

X_3 comprises of G, E, S, A, P, and D;

X_4 comprises of T, G, and S;

X_5 comprises of S;

X_6 comprises of S, T, H, K, R, A, and N; and

X_7 comprises of W.

22. The composition of claim 21, wherein the n-mer motif is selected from the group consisting of KDEFTTF (SEQ ID NO: 36308), KDDFTTY (SEQ ID NO: 36336), RDEFTTY

(SEQ ID NO: 36615), KDEFSTY (SEQ ID NO: 36390), RDEFTSF (SEQ ID NO: 36701), and REDHVSW (SEQ ID NO: 37067).

23. The composition of claim 1 to 4, the wherein the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of X_1-X_2-X_3-X_4-X_5-X_6-X_7 wherein:

X_1 comprises of V, I, R, N and D;

X_2 comprises of A, G, and S;

X_3 comprises of L, T, S, H, and G;

X_4 comprises of K, R, and E;

X_5 comprises of G;

X_6 comprises of W, R, A, and I; and

X_7 comprises of D and G.

24. The composition of claim 23, wherein the n-mer motif is selected from the group consisiting of IALKGWD (SEQ ID NO: 36248), NALEGRD (SEQ ID NO: 36407), VALEGRD (SEQ ID NO: 36604), and VALKGWD (SEQ ID NO: 17701).

25. The composition of claim 1 to 4, the wherein the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of X_1-X_2-X_3-X_4-X_5-X_6-X_7 wherein:

X_1 comprises of L, M, and W;

X_2 comprises of F, R, W, K, T, and Y;

X_3 comprises of D and S;

X_4 comprises of G;

X_5 comprises of T;

X_6 comprises of P, G, S, N, A, and R; and

X_7 comprises of A, P, S, and Y.

26. The composition of claim 1 to 4, the wherein the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of X_1-X_2-X_3-X_4-X_5-X_6-X_7 wherein:

X_1 comprises of P, N, and K;

X_2 comprises of Y and F;

X_3 comprises of A;

X_4 comprises of R and K;

X_5 comprises of S;

X_6 comprises of P, V, A, R, I, L, S, E; and

X_7 comprises of E, D, M, and L.

27. The composition of claim 1 to 4, wherein the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of Z_1-X_1-Z_2-X_2-X_3-X_4-X_5 wherein Z_1 is selected from the group consisting of Y, F, and L, Z_2 is selected to the group consisting of S, R, and K, $X_1 - X_5$ are independently selected amino acids.

28. The composition of claim 27, wherein X_1 comprises of A, S, or H.

29. The composition of claim 27, wherein X_2 comprises of S, T, L, or I.

30. The composition of claim 27, wherein X_3 comprises N or G.

31. The composition of claim 27, wherein X_4 comprises G.

32. The composition of claim 27, wherein X_5 comprises of N, D, I, V, or R.

33. The composition of claim 1 to 4, wherein the n-mer motif is selected from the group consisting of YSRIGPN (SEQ ID NO: 14632), YSRLNMN (SEQ ID NO: 14301), YSRLNKD (SEQ ID NO: 16577), and YHRLSNN (SEQ ID NO: 16636).

34. The composition of claim 1 to 4, wherein the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of is X_1-H-X_2-L-X_3-X_4-X_5 wherein X_1 – X_5 are independently selected amino acids.

35. The composition of claim 34, wherein the n-mer motif is VHRLQDK (SEQ ID NO: 16602) or LHALSHN (SEQ ID NO: 16608).

36. The composition of claim 1 to 4, wherein the n-mer motif comprises PSATNGV (SEQ ID NO: 20486), QVSTNGI (SEQ ID NO: 16021), SYSSNGV (SEQ ID NO: 16234), HQSSNGV (SEQ ID NO: 15978), VGSINGI (SEQ ID NO: 16199), AMSTNGR (SEQ ID NO: 16000), SASTNGV (SEQ ID NO: 16127), YMSTNGV (SEQ ID NO: 16042), YYSSNGV (SEQ ID NO: 16206), VHSTNGI (SEQ ID NO: 16134), PLSTNGV (SEQ ID NO: 16233), VYSTNGI (SEQ ID NO: 16059), IISTNGV (SEQ ID NO: 16054), RSVSSNGV (SEQ ID NO: 20502), YKSSNGV (SEQ ID NO: 16123), FRSTNGV (SEQ ID NO: 16070), and/or FVSTNGV (SEQ ID NO: 11162).

37. The composition of claim 1 to 27, wherein the n-mer is selected from any one of the amino acid sequences as listed in Tables 1-22, or any combination thereof.

38. The composition of claim 1 to 27, wherein the n-mer motif is selected from the amino acid sequences of SEQ ID NO: 10952-20481 and 36241-42428.

39. The composition of any one of the preceding claims, wherein the targeting moiety is part of a viral capsid protein.

40. The composition of any one of the preceding claims, wherein the targeting moiety is inserted or substituted in loop IV, loop VIII, or both of an AAV capsid protein.

41. The composition of claim 40, wherein the targeting moiety is IPFSRVNPDT (SEQ ID NO: 20285), LGFARTGAAD (SEQ ID NO: 20274), LGFTKSSGSD (SEQ ID NO: 20270), LRYSKTQGES (SEQ ID NO: 20266), SPYARSSAGV (SEQ ID NO: 20271), VGWSRLDLTT (SEQ ID NO: 20262).

42. The composition of any of the preceding claims, wherein targeting moiety is inserted between two amino acids of one or more capsid proteins such that the targeting moiety is external to the AAV capsid.

43. The composition of any of the preceding claims, wherein the viral capsid protein is an AAV viral capsid protein.

44. The composition of any of the preceding claims, wherein the targeting moiety is inserted between amino acids 588 and 589 of a capsid protein of AAV9, or in an analogous position of a capsid protein from AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAVrh8, AAV rh.74, or AAV rh. 10.

45. The composition of any of the preceding claims, wherein the targeting moiety is inserted between two consecutive amino acids within amino acid 451-460 of a capsid protein of AAV9, or in an analogous position of a capsid protein from AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAVrh8, AAV rh.74, or AAV rh. 10.

46. The composition of any of the preceding claims, wherein the capsid protein is VP1, VP2, VP3, or a combination thereof.

47. The composition of any one of the preceding claims, wherein the cargo is a polynucleotide, a recombinant AAV genome comprising a transgene, one or more polypeptides, a ribonucleoprotein complex.

48. The composition of claim 47, wherein the polynucleotide encodes one or more polypeptides and/or a RNAi oligonucleotide.

49. The composition of claim 48, wherein the polynucleotide encodes one or more polypeptides.

50. The composition of claim 49, wherein the one or more polypeptides comprise enzymes or antibodies.

51. The composition of any one of the preceding claims, wherein the polynucleotide encodes a CRISPR-Cas system.

52. The composition of any one of claims 47-51, wherein the polynucleotide is operably linked to a regulatory sequence that promotes expression in the CNS.

53. A viral capsid or viral particle, comprising the composition of any one of claims 1-52.

54. The viral capsid or viral particle of claim 53, further comprising a recombinant viral genome, wherein the recombinant viral genome encodes a therapeutic protein or nucleic acid, control polypeptide or nucleic acid, and/or selectable marker polypeptide or nucleic acid.

55. The viral capsid or viral particle of claim 54, wherein the therapeutic protein or nucleic acid, control polypeptide or nucleic acid, and/or selectable marker polypeptide or nucleic acid is operably linked to a regulatory sequence that promotes expression in the CNS.

56. The viral capsid or viral particle of any one of claims 53-55, wherein the viral capsid or viral particle is an AAV viral capsid or AAV viral particle.

57. The viral capsid or viral particle of claim 54, wherein the recombinant viral genome is a recombinant AAV viral genome.

58. The viral capsid or viral particle of any one of claims 53-57, wherein the targeting moiety is inserted between amino acids of 588 and 589 of a capsid protein of AAV9, or in an analogous position of a capsid protein from AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAVrh8, AAV rh.74, or AAV rh. 10.

59. A vector system comprising one or more vectors, wherein at least one of the one or more vectors encodes a targeting moiety effective to increase transduction of central nervous system tissues (CNS) via binding to a transferrin receptor (TFRC), and optionally wherein at least one of the one or more vectors encodes a recombinant AAV genome comprising a transgene encoding a protein or a polypeptide.

60. The vector system of claim 59, wherein the targeting moiety binds to the extracellular domain of TFRC.

61. The vector system of claim 60, wherein the targeting moiety binds to one or more of the apical, helical, and/or protease-like domain of the extracellular domain.

62. The vector system of claim 61, wherein the targeting moiety binds to the apical domain.

63. The vector system of claim 59 or 62, wherein the targeting moiety comprises any n-mer motif of claims 5-26.

64. The vector system of claim 59 or 62, wherein the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of Z_1-X_1-Z_2-X_2-X_3-X_4-X_5 wherein Z_1 is Y, F, or L, Z_2 is S, R, or K, X_1 – X_5 are independently selected amino acids.

65. The vector of claim 64, wherein X_1 comprises of A, S, or H.

66. The vector of claim 64, wherein X_2 comprises of S, T, L, or I.

67. The vector of claim 64, wherein X_3 comprises N or G.

68. The vector of claim 64, wherein X_4 comprises G.

69. The vector of claim 64, wherein X_5 comprises of N, D, I, V, or R.

70. The vector system of claim 65, wherein the n-mer motif is selected from the group consisting of YSRIGPN (SEQ ID NO: 14632), YSRLNMN (SEQ ID NO: 14301), YSRLNKD (SEQ ID NO: 16577), and YHRLSNN (SEQ ID NO: 16636).

71. The vector system of claim 59 or 60, wherein the targeting moiety comprises a n-mer motif, the n-mer motif comprising or consisting of an amino acid sequence of is X_1-H-X_2-L-X_3-X_4- X_5 wherein X_1 – X_5 are independently selected amino acids.

72. The vector system of claim 71, wherein the n-mer motif is VHRLQDK (SEQ ID NO: 16602) or LHALSHN (SEQ ID NO: 16608).

73. The vector system of claim 59 or 62, wherein the n-mer motif is comprises PSATNGV (SEQ ID NO: 20486), QVSTNGI (SEQ ID NO: 16021), SYSSNGV (SEQ ID NO: 16234), HQSSNGV (SEQ ID NO: 15978), VGSINGI (SEQ ID NO: 16199), AMSTNGR (SEQ ID NO: 16000), SASTNGV (SEQ ID NO: 16127), YMSTNGV (SEQ ID NO: 16042), YYSSNGV (SEQ ID NO: 16206), VHSTNGI (SEQ ID NO: 16134), PLSTNGV (SEQ ID NO: 16233), VYSTNGI (SEQ ID NO: 16059), IISTNGV (SEQ ID NO: 16054), RSVSSNGV (SEQ ID NO: 20502), YKSSNGV (SEQ ID NO: 16123), FRSTNGV (SEQ ID NO: 16070), and/or FVSTNGV (SEQ ID NO: 11162).

74. The vector system of claim 59 or 60, wherein the n-mer is selected from any one as listed in Tables 1-22, or any combination thereof.

75. The vector system of claim 59 or 60, wherein the n-mer motif is selected from SEQ ID NO: 10952-20481 and 36241-42428.

76. The vector system of any one of claims 59 or 75, wherein the targeting moiety is part of a viral capsid protein.

77. The vector system of any one of claims 59 or 76, wherein the targeting moiety is inserted or substituted in loop IV and/or loop VIII.

78. The vector system of any one of claims 77, wherein the targeting moiety is IPFSRVNPDT (SEQ ID NO: 20285), LGFARTGAAD (SEQ ID NO: 20274), LGFTKSSGSD (SEQ ID NO: 20270), LRYSKTQGES (SEQ ID NO: 20266), SPYARSSAGV (SEQ ID NO: 20271), VGWSRLDLTT (SEQ ID NO: 20262).

79. The vector system of claim 76, wherein targeting moiety is inserted between two amino acids of one or more capsid proteins such that the targeting moiety is external to the AAV capsid.

80. The vector system of claim 79, wherein the viral capsid protein is an AAV viral capsid protein.

81. The vector system of claim 79, wherein the targeting moiety is inserted between amino acids 588 and 589 of a capsid protein of AAV9, or in an analogous position of a capsid protein from AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAVrh8, AAV rh.74, or AAV rh. 10.

82. The vector system of claim 79, wherein the targeting moiety is inserted between amino acids 451-460 of a capsid protein of AAV9, or in an analogous position of a capsid protein from AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAVrh8, AAV rh.74, or AAV rh. 10.

83. The vector system of claim 76, wherein the capsid protein is VP1, VP2, VP3, or a combination thereof.

84. The vector system of any one of claims 59 or 83, wherein the cargo is a polynucleotide, a recombinant AAV genome comprising a transgene, one or more polypeptides, a ribonucleoprotein complex.

85. The vector system of claim 84, wherein the polynucleotide encodes one or more polypeptides and/or a RNAi oligonucleotide.

86. The vector system of claim 85, wherein the polynucleotide encodes one or more polypeptides.

87. The vector system of claim 86, wherein the one or more polypeptides comprise enzymes or antibodies.

88. The vector system of any one of claims 59 or 87, wherein the polynucleotide encodes a CRISPR-Cas system.

89. The vector system of any one of claims 84-88, wherein the polynucleotide is operably linked to a regulatory sequence that promotes expression in the CNS.

90. A polypeptide encoded or produced by the vector system of any one of claims 59 or 88.

91. The polypeptide of claim 90, wherein the polypide is a capsid protein, optionally an AAV capsid polypeptide.

92. A particle produced by the vector system of any one of claims 59 or 89.

93. The particle of claim 92, wherein the particle is a viral particle, optionally an AAV particle.

94. A cell comprising the composition, vector, polypeptide, or particle of any of the preceding claims.

95. A method of delivering one or more cargos to the CNS, comprising:

administering, in vivo or in vitro, the capsid and/or viral particle of claim of any one of claims 1 to 58.

96. The method of claim 95, wherein the cargo is recombinant AAV genome comprising a transgene, a polynucleotide which encodes an RNAi oligonucleotide, a polynucleotide encoding a polypeptide, or a polypeptide.

97. The method of claim 96, wherein the polypeptide includes an enzyme or antibody.

98. The method of claim 95, wherein the cargo is a Cas polypeptide, a guide molecule, or both.

99. The method of claim 95, wherein the cargo encodes a nuclease or a nucleic acid component of a RNA-guided nuclease.

100. The method of claim 95, wherein the cargo is one or more polynucleotides encoding the nuclease and nucleic acid component of a RNA-guided nuclease.

101. A method of creating humanized transgenic non-human animals comprising:

delivering to one or more cells of a non-human animal a vector system or a recombinant viral particle comprising a recombinant viral genome, wherein:

the vector system or recombinant viral genome encodes a human transferrin polypeptide, wherein the encoded human transferrin polypeptide is under the control of a tissue-specific promoter or miRNA binding element that has selective activity in the desired cell, tissue, or organ.

102. The method of claim 101, wherein the one or more cells are endothelial cells.

103. The method of claim any one of claims 101-102, wherein the one or more cells are CNS cells.

104. The method of claim 102, wherein the one or more cells are of the CNS vasculature, lungs, kidneys, liver, or any combination thereof.

105. The method of claim 104, wherein the endothelial cells are of the CNS vasculature.

106. The method of any one or claims 101-105, wherein the recombinant viral particle, optionally an AAV viral particle, comprises a capsid polypeptide, optionally an AAV capsid polypeptide, wherein the capsid polypeptide comprises a CNS specific n-mer motif.

107. The method of claim 106, wherein the CNS-specific n-mer motif comprises X1-N-X3-X4-X5-X6-X7, wherein X5 is independently selected from K or R, and X1, X3, X4, X6 and X7 are independently selected from any amino acid, optionally wherein the overall charge of the n-mer motif at neutral pH is between 0 and + 2.

108. The method of claim 106, wherein the CNS-specific n-mer motif comprises or consists of NNSTRGG (SEQ ID NO: 42429), GNSARNI (SEQ ID NO: 42430), and GNSVRDF (SEQ ID NO: 42431).

109. The method of any one of claims 101-108, wherein the transgenic non-human animal is a rodent, optionally a mouse.

110. A humanized transgenic non-human animal comprising:
one or more cells expressing a human transferrin polypeptide, optionally wherein the one or more cells are CNS cells.

111. The humanized transgenic non-human animal of claim 110, wherein the transgenic non-human animal is a rodent, optionally a mouse.

112. A humanized transgenic non-human animal produced by the method of any one of claims 101-109.

113. The humanized transgenic non-human animal of any one of claims 101-112, wherein the humanized non-human animal has a suppressed immune system.

114. A method of screening n-mer motifs capable of conferring transduction of central nervous system (CNS) tissues via binding to a transferrin receptor (TFRC) in humanized transgenic non-human animals comprising:

introducing one or more compositions comprising a candidate n-mer motif to humanized non-human transgenic animal of any one of claims 101-113; and

detecting binding of the compositions that bind to a transferrin receptor (TFRC) and/or detecting transduction or uptake by one or more CNS cells of the humanized transgenic non-human animal.

115. The method of claim 114, wherein the candidate n-mer motif comprises or consists of X1-N-X3-X4-X5-X6-X7, wherein X5 is independently selected from K or R, and X1, X3, X4, X6 and X7 are independently selected from any amino acid, optionally wherein the overall charge of the n-mer motif at neutral pH is between 0 and + 2.

116. The method of any one of claims 114-115, wherein the composition is a viral particle comprising one or more capsid proteins each comprising the candidate n-mer motif.

117. The method of claim 116, wherein the viral particle is an AAV viral particle and the one or more capsid proteins is an AAV capsid protein, optionally wherein the candidate n-mer motif is inserted in between amino acids 588-589 of an AAV9 capsid polypeptide or in an analogous position of a capsid protein from AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAVrh8, AAV rh.74, or AAV rh. 10.

118. The method of claim 114-117, wherein at least one of the one or more compositions furthers comprises a cargo.

119. The method of claim 118, wherein the cargo is or encodes a therapeutic nucleic acid or polypeptide, a selectable marker, or a control polypeptide or nucleic acid.

120. A recombinant AAV particle comprising (1) a recombinant capsid protein having a TFR1-targeting n-mer motif peptide inserted within the capsid protein such that the peptide is displayed on the surface when incorporated into the AAV particle; and (2) a recombinant AAV genome comprising a transgene encoding a therapeutic polypeptide or polynucleotide operably linked to one or more regulatory sequences which promote expression of the transgene in CNS cells, flanked by AAV ITR sequences, wherein the AAV particle has enhanced binding, transduction or transgene expression in CNS cells relative to an AAV particle having a reference capsid that does not contain the targeting n-mer motif.

121. The recombinant AAV particle of claim 120 in which the targeting n-mer motif peptide is a 7-mer peptide having an amino acid sequence of any of those in claims 5-26.

122. The recombinant AAV particle of claim 120, in which the targeting n-mer motif is a 7-mer peptide having an amino acid sequence of SEQ ID NO: 10952-20481 and 36241-42428.

123. The recombinant AAV particle of any of claims 120-122, in which the peptide has an amino acid sequence of claims 7, 12, 15, 17, 22, or 24.

124. The recombinant AAV particle of claims 120-123, in which the recombinant capsid protein is an AAV9 capsid protein (SEQ ID NO: 20506), an AAV9 K449R capsid protein (SEQ ID NO: 20507), or a capsid protein having at least 90%, 90% or 99% sequence identity to the AAV9 capsid protein and forms a capsid that transduces CNS cells.

125. The recombinant AAV particle of any of claims 120-124 in which the peptide is inserted between amino acids 588 and 589 of the AAV9 capsid protein or at a corresponding position of another AAV capsid protein.

126. The recombinant AAV particle of any of claims 120-125 in which the peptide is inserted between two consecutive amino acids within amino acids 451-460 of the AAV9 capsid protein or at a corresponding position within another AAV capsid protein.

127. A method of delivering a therapeutic polypeptide or polynucleotide to the CNS of a subject in need thereof, said method comprising administering to said subject the recombinant AAV particle of any of claims 120-126.

128. A recombinant engineered AAV capsid protein having a TFR1-targeting n-mer motif peptide inserted within the capsid protein such that the peptide is displayed on the surface when incorporated into the AAV particle.

129. The recombinant engineered AAV capsid protein of claim 128 in which the targeting n-mer motif peptide is a 7-mer peptide having an amino acid sequence of any of those in claims 5-26.

130. The recombinant engineered AAV capsid protein of claims 128-129, in which the targeting n-mer motif is a 7-mer peptide having an amino acid sequence of SEQ ID NO: 10952-20481 and 36241-42428.

131. The recombinant engineered AAV capsid protein of any of claims 128-130, in which the peptide has an amino acid sequence of claims 7, 12, 15, 17, 22, or 24.

132. The recombinant engineered AAV capsid protein of any of claims 128-131, in which the recombinant capsid protein is an AAV9 capsid protein (SEQ ID NO: 20506), an AAV9 K449R capsid protein (SEQ ID NO: 20507), or a capsid protein having at least 90%, 90% or 99% sequence identity to the AAV9 capsid protein and forms a capsid that transduces CNS cells.

133. The recombinant engineered AAV capsid protein of any of claims 128-132, in which the peptide is inserted between amino acids 588 and 589 of the AAV9 capsid protein or at a corresponding position of another AAV capsid protein.

134. A host cell for producing the recombinant AAV particles of any of claims 120-127, said host cell comprising a first construct comprising a nucleic acid encoding the recombinant AAV capsid protein and a second construct comprising a nucleic acid encoding the recombinant AAV genome.

135. A method of producing the recombinant AAV particle of any of claims 120-127, said method comprising culturing said host cell under conditions sufficient for production of the recombinant AAV particle and harvesting of said recombinant AAV particle.

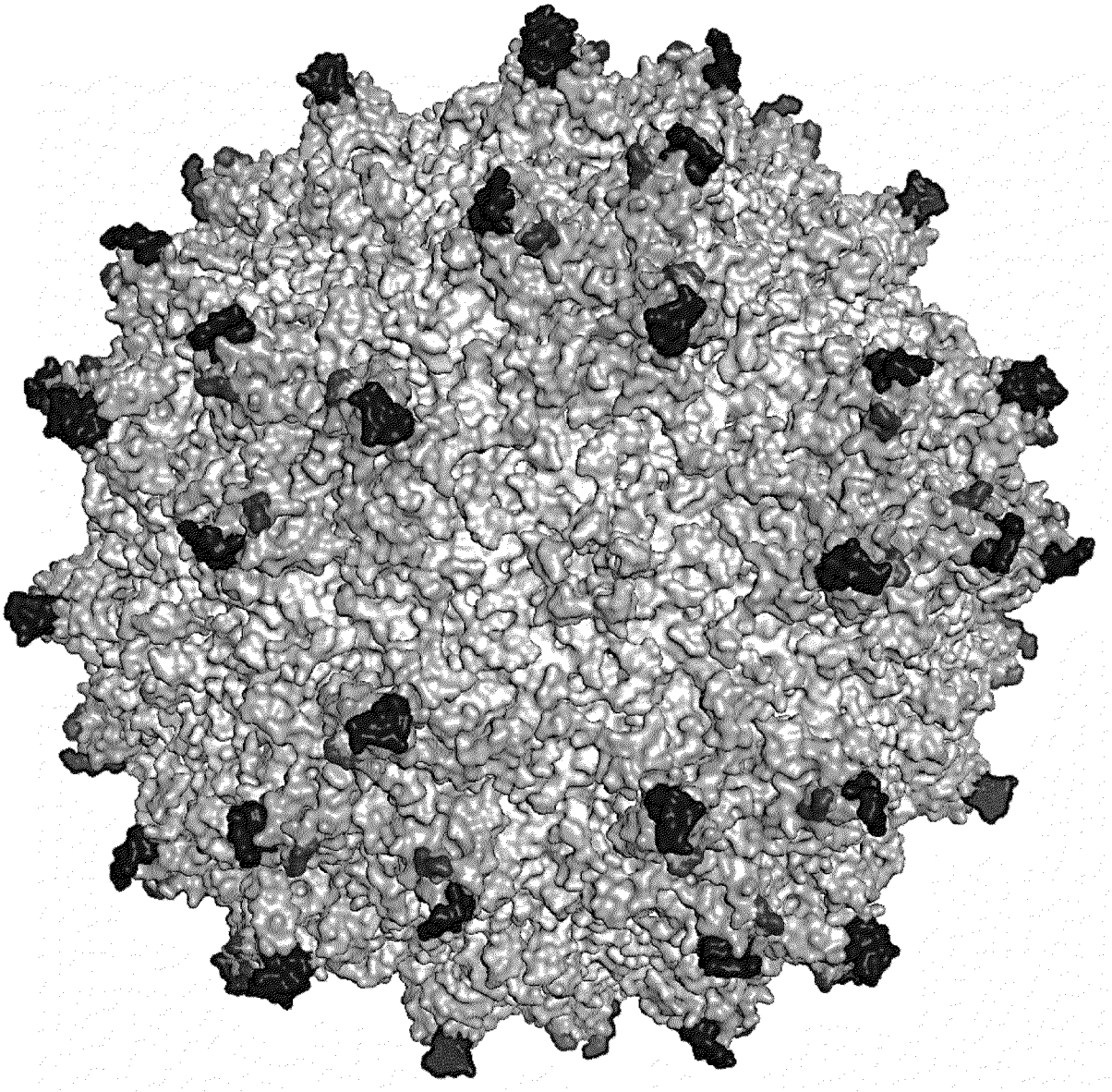


FIG. 1

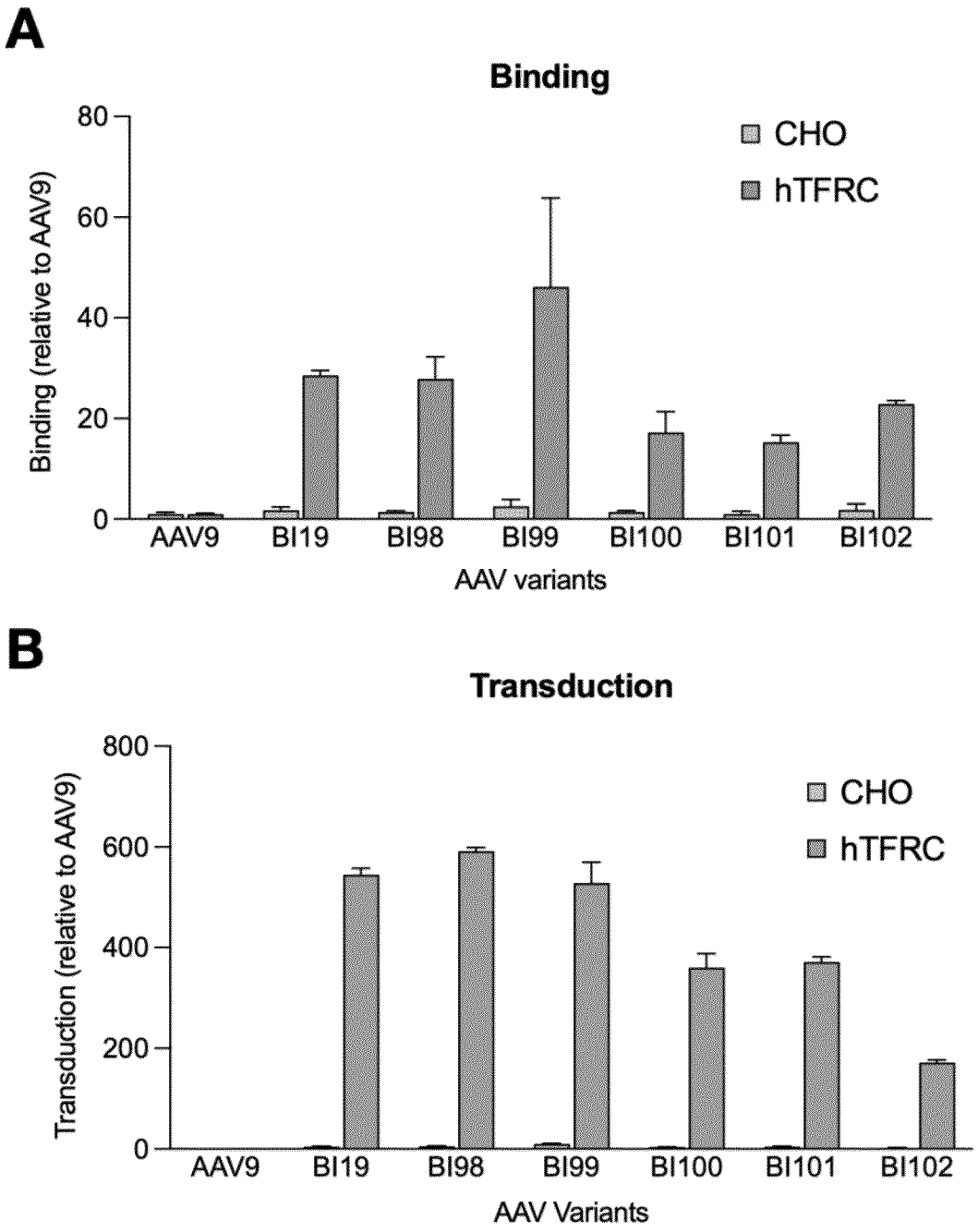

A
Binding
Binding (relative to AAV9)
80
60
40
20
0
CHO
hTFRC
AAV9
BI19
BI98
BI99
BI100
BI101
BI102
AAV variants
B
Transduction
Transduction (relative to AAV9)
800
600
400
200
0
CHO
hTFRC
AAV9
BI19
BI98
BI99
BI100
BI101
BI102
AAV Variants

FIG. 2A-2B

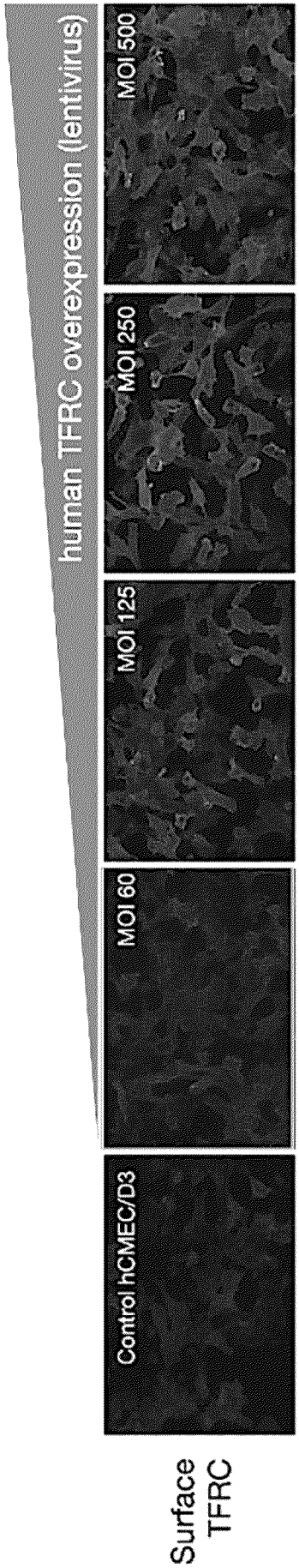

human TFRC overexpression (lentivirus)
Control hCMEC/D3
MOI 60
MOI 125
MOI 250
MOI 500
Surface TFRC

FIG. 3

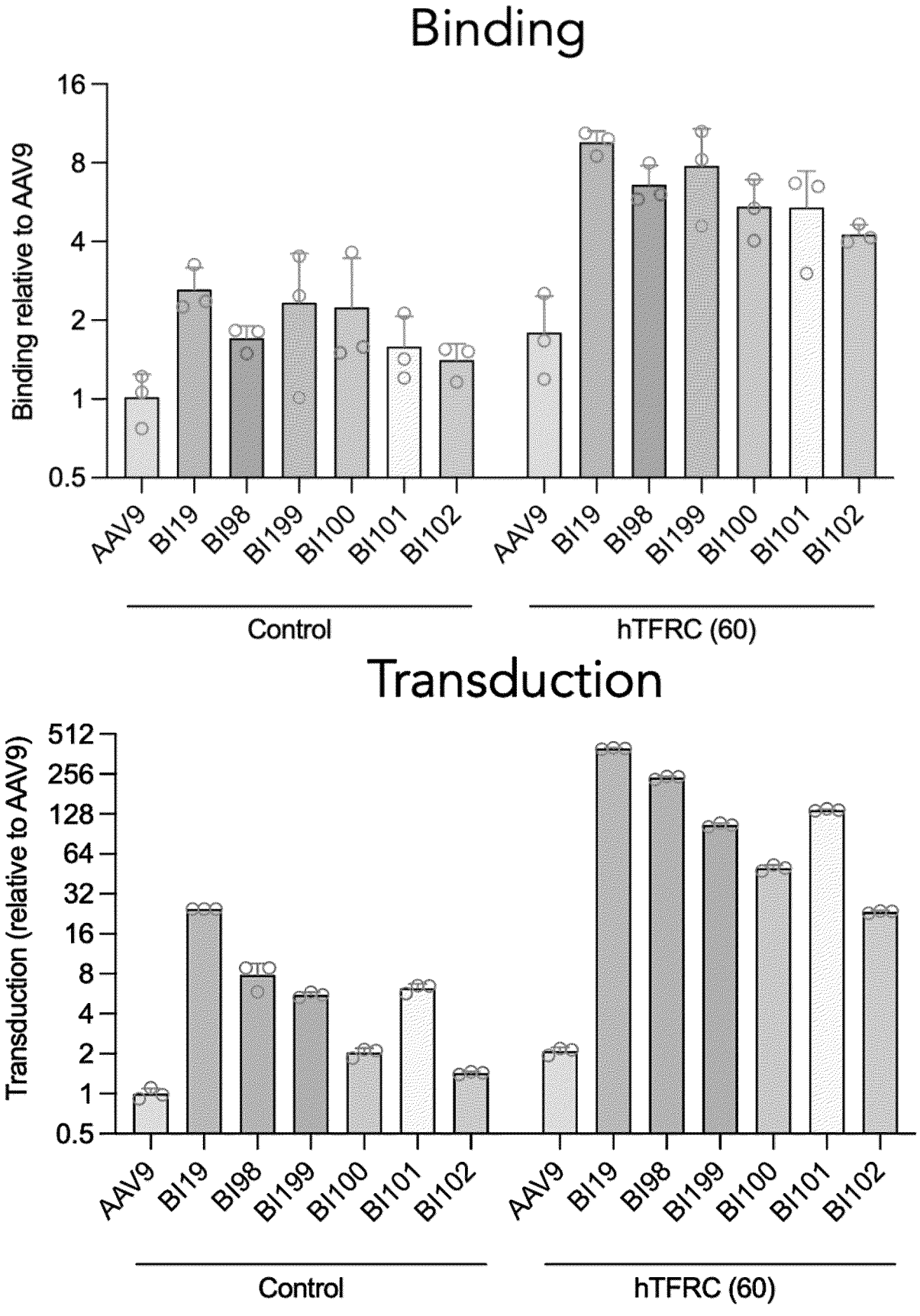
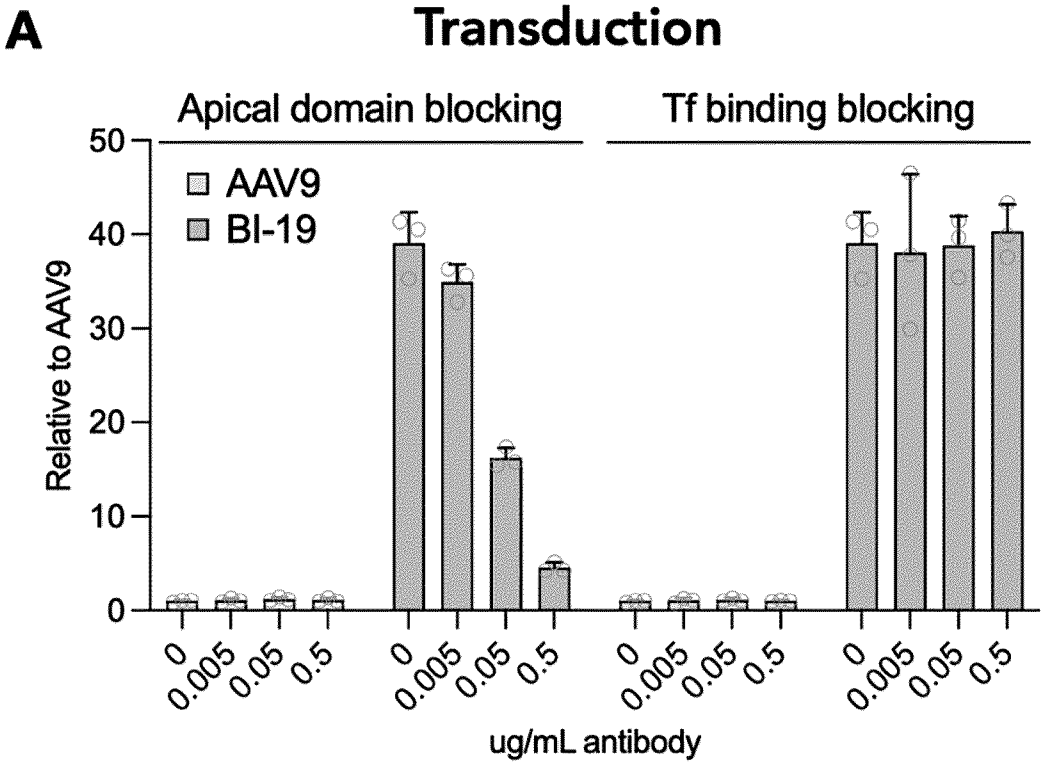

Binding
Binding relative to AAV9
16
8
4
2
1
0.5
AAV9
BI19
BI98
BI199
BI100
BI101
BI102
Control
hTFRC (60)
Transduction
Transduction (relative to AAV9)
512
256
128
64
32
16
8
4
2
1
0.5
AAV9
BI19
BI98
BI199
BI100
BI101
BI102
Control
hTFRC (60)

FIG. 4


A
Transduction
Apical domain blocking
Tf binding blocking
AAV9
BI-19
Relative to AAV9
50
40
30
20
10
0
0
0.005
0.05
0.5
ug/mL antibody

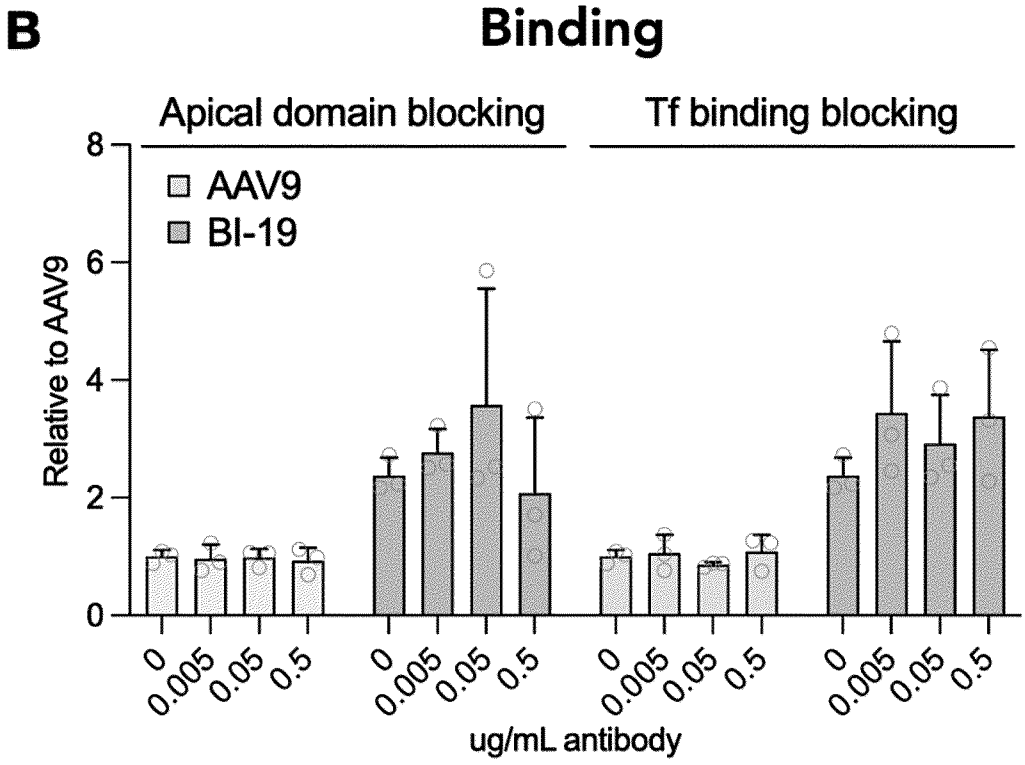
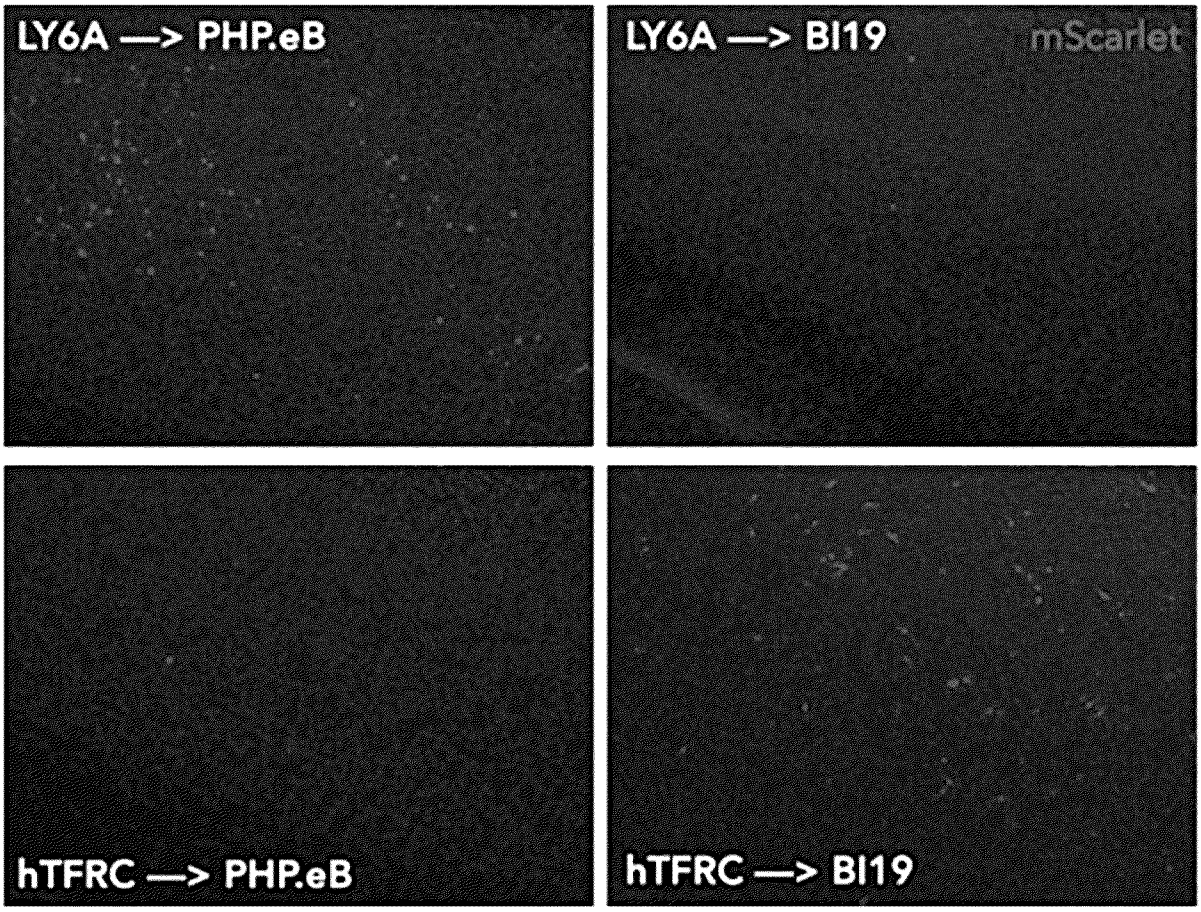
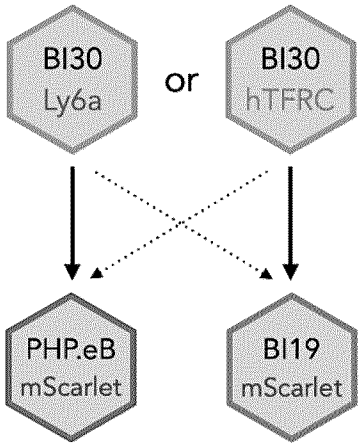

B
Binding
Apical domain blocking
Tf binding blocking
AAV9
BI-19
Relative to AAV9
8
6
4
2
0
0
0.005
0.05
0.5
ug/mL antibody

FIG. 5A-5B



Two-step BBB crossing experiment

Step 1: Express Ly6a or hTFRC



Step 2: administer PHP.eB (LY6A binding) or BI-19 (hTFRC binding)

FIG. 6

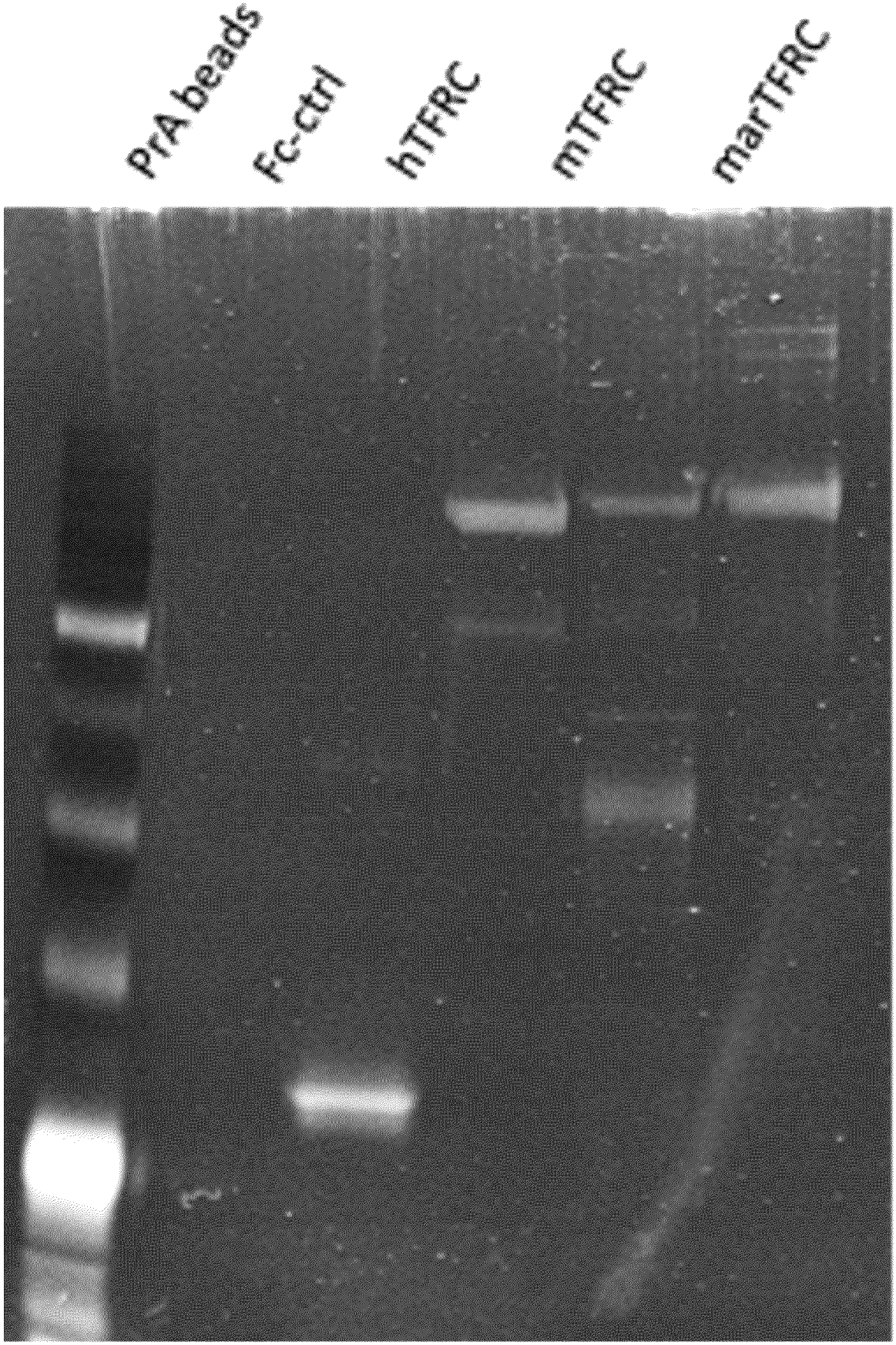


FIG. 7

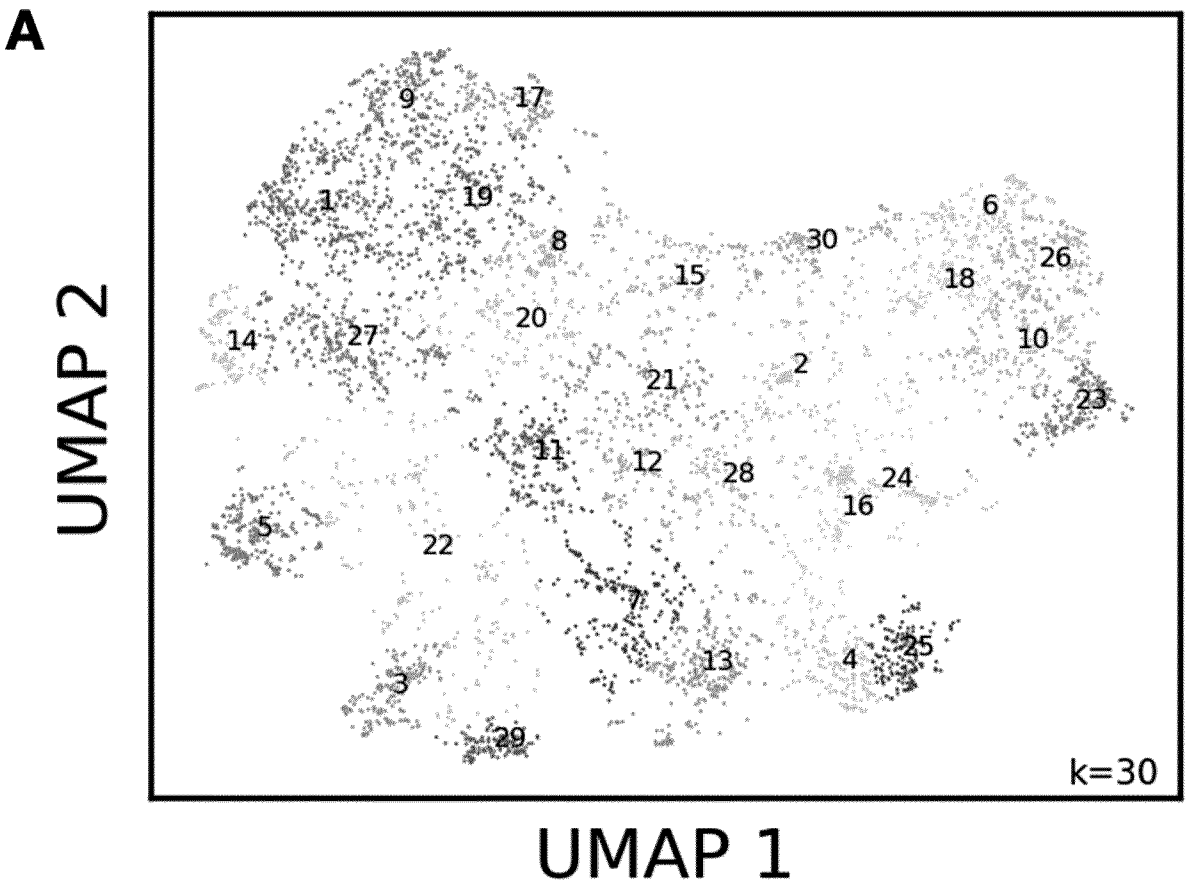

A
UMAP 2
UMAP 1
k=30
9
17
1
19
8
30
6
26
15
18
20
14
27
10
2
21
23
11
12
28
24
16
5
22
7
13
4
25
3
29

FIG. 8A

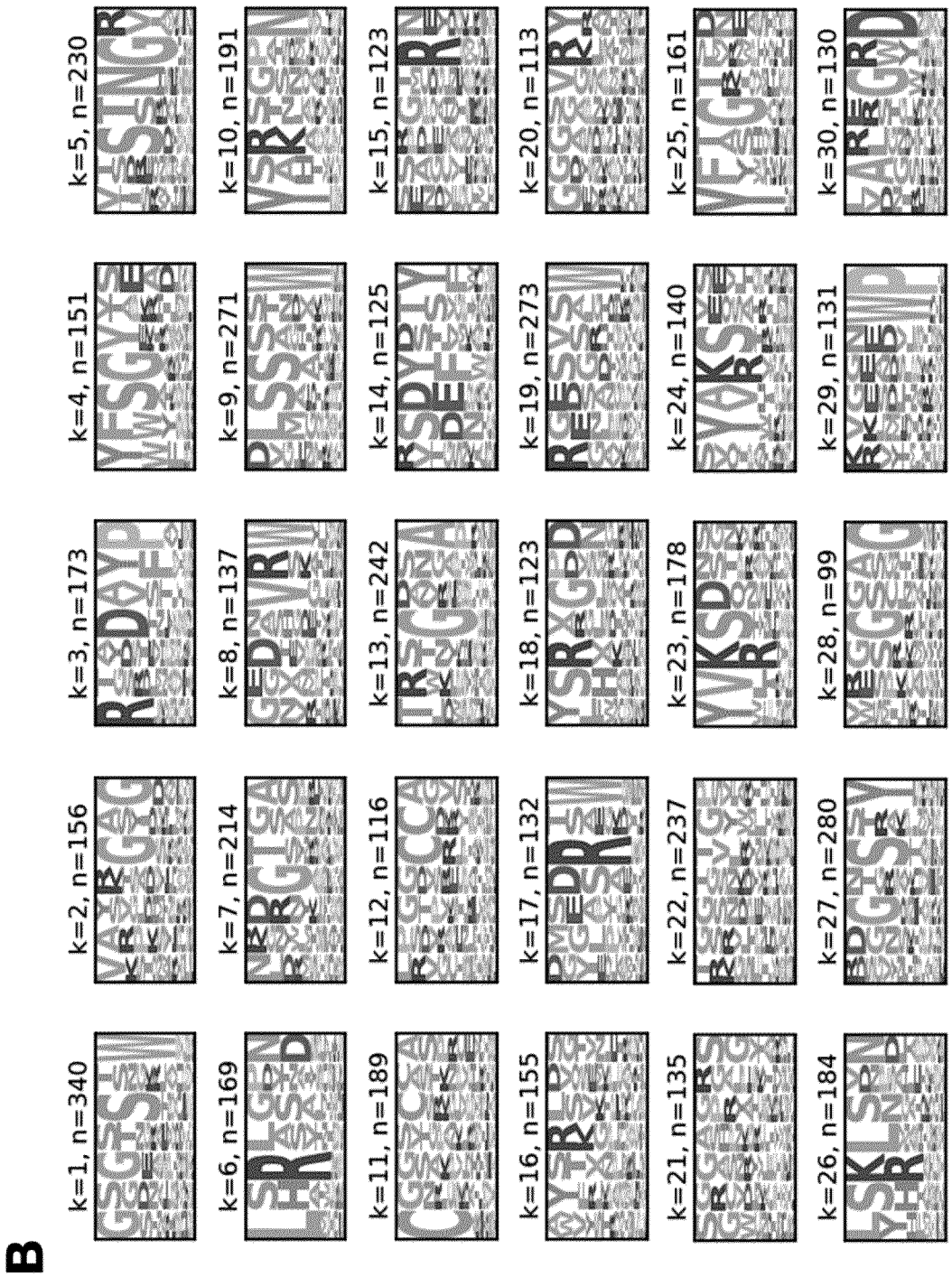
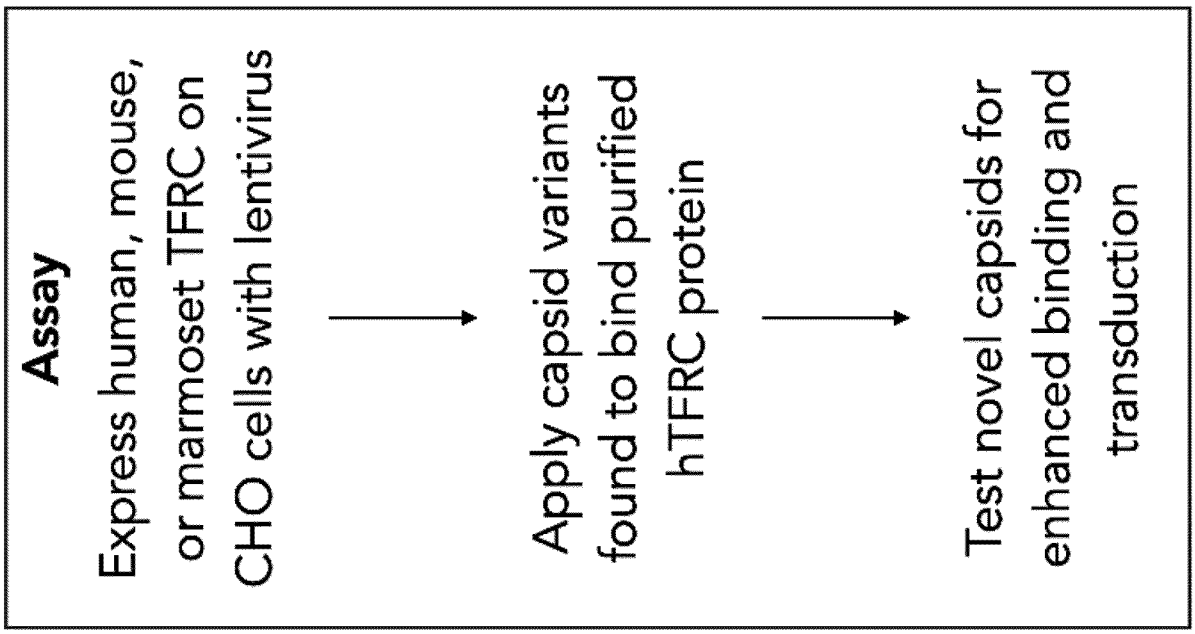

B
k=1, n=340
k=2, n=156
k=3, n=173
k=4, n=151
k=5, n=230
k=6, n=169
k=7, n=214
k=8, n=137
k=9, n=271
k=10, n=191
k=11, n=189
k=12, n=116
k=13, n=242
k=14, n=125
k=15, n=123
k=16, n=155
k=17, n=132
k=18, n=123
k=19, n=273
k=20, n=113
k=21, n=135
k=22, n=237
k=23, n=178
k=24, n=140
k=25, n=161
k=26, n=184
k=27, n=280
k=28, n=99
k=29, n=131
k=30, n=130

FIG. 8B


Assay
Express human, mouse, or marmoset TFRC on CHO cells with lentivirus
Apply capsid variants found to bind purified hTFRC protein
Test novel capsids for enhanced binding and transduction

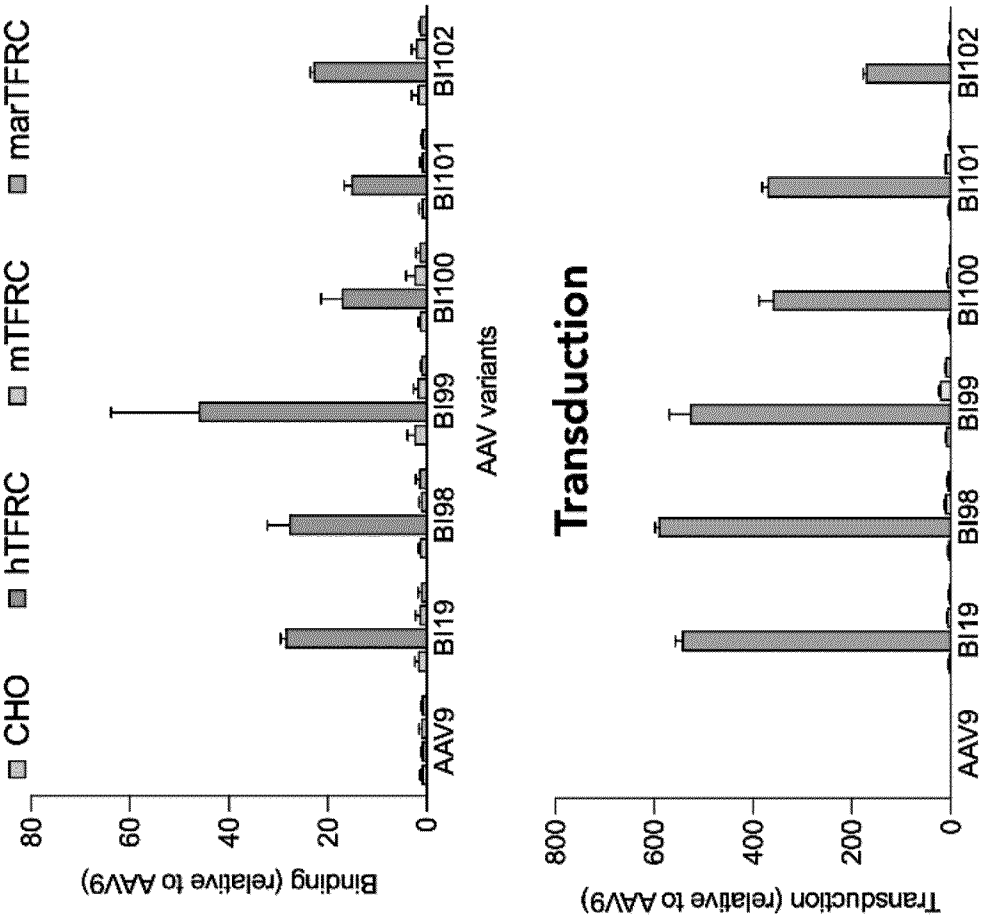
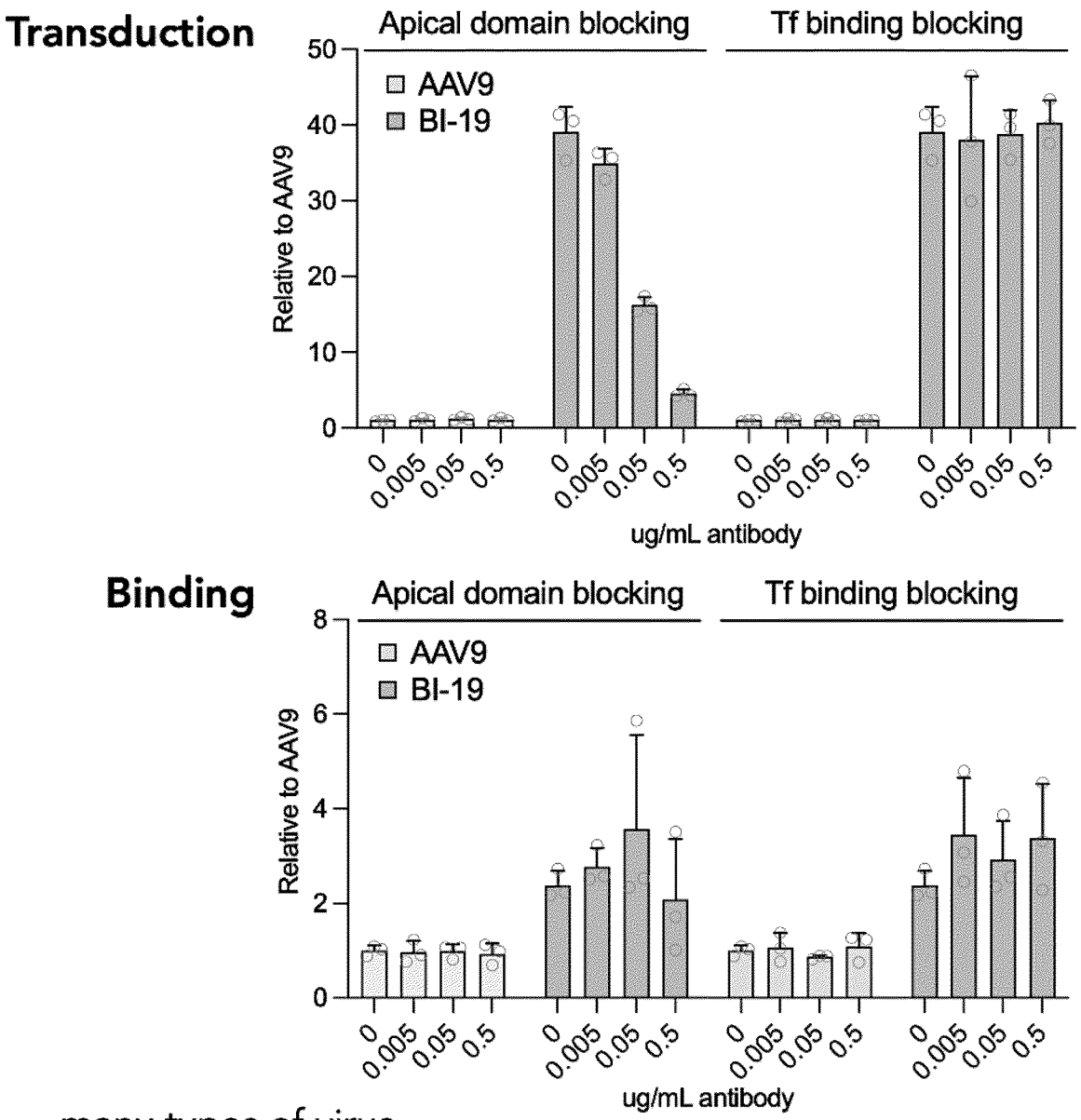

Binding
CHO
hTFRC
mTFRC
marTFRC
Binding (relative to AAV9)
0
20
40
60
80
AAV9
BI19
BI98
BI99
BI100
BI101
BI102
AAV variants
Transduction
Transduction (relative to AAV9)
0
200
400
600
800
AAV9
BI19
BI98
BI99
BI100
BI101
BI102
AAV Variants

FIG. 9



many types of virus internalize using TFRC by binding to the apical domain

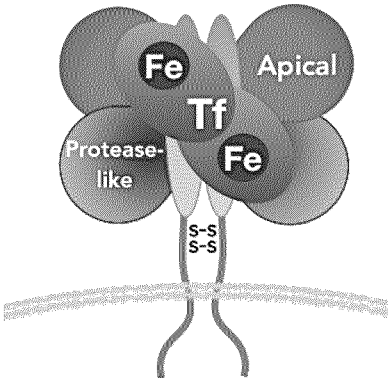
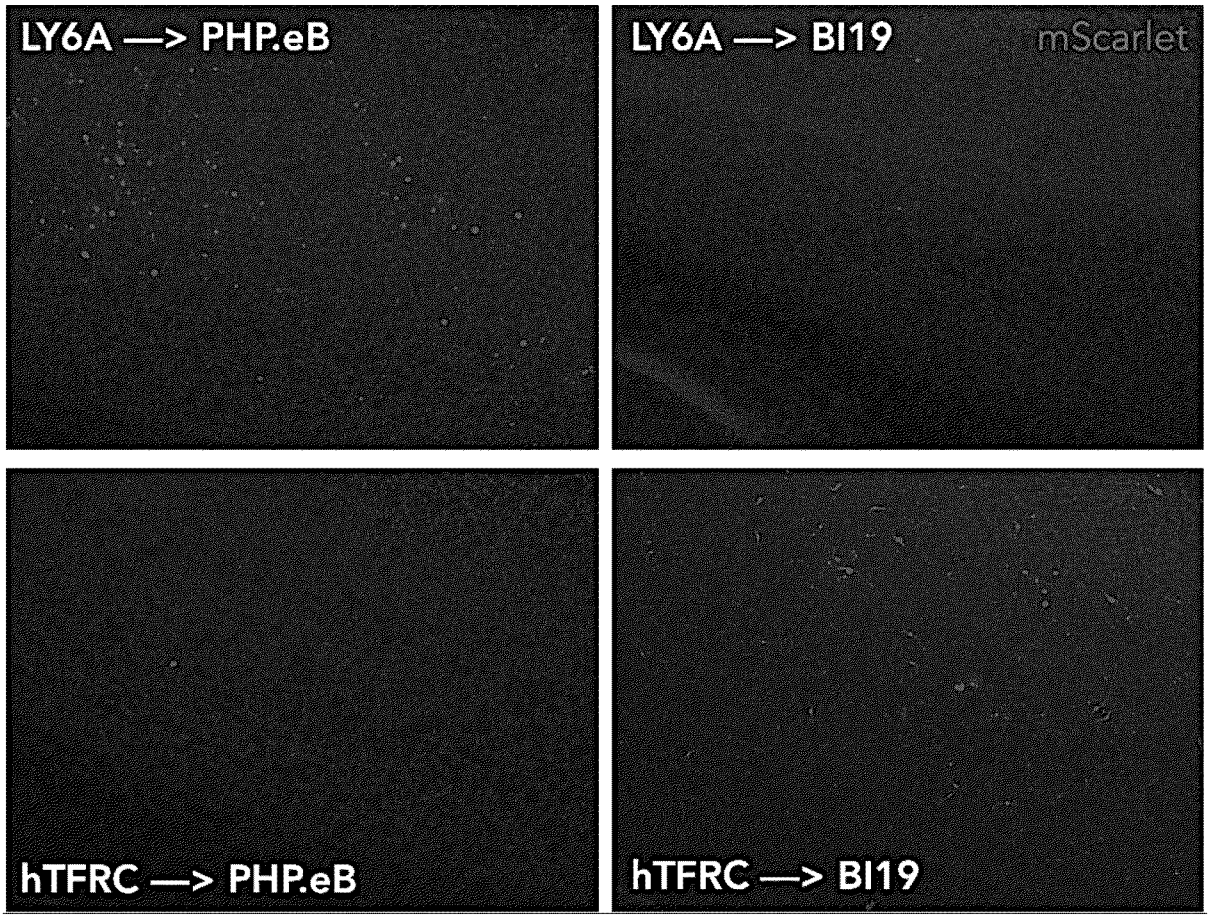
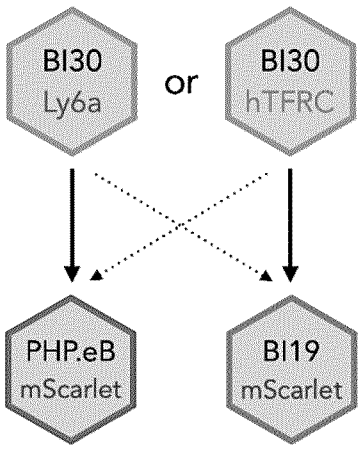


FIG. 10



Two-step BBB crossing experiment

Step 1: Express Ly6a or hTFRC



Step 2: administer PHP.eB (LY6A binding) or BI-19 (hTFRC binding)

Conclusions

- BI19 can meditate increased transduction of brain cells following expression of human TFRC on brain vasculature
- Further assay development is required to make the 2-step in vivo human receptor experiment more convincing
- Ongoing: evaluating this with BI30 expressed huCD59 and multiple huCD59 binding AAVs

FIG. 11

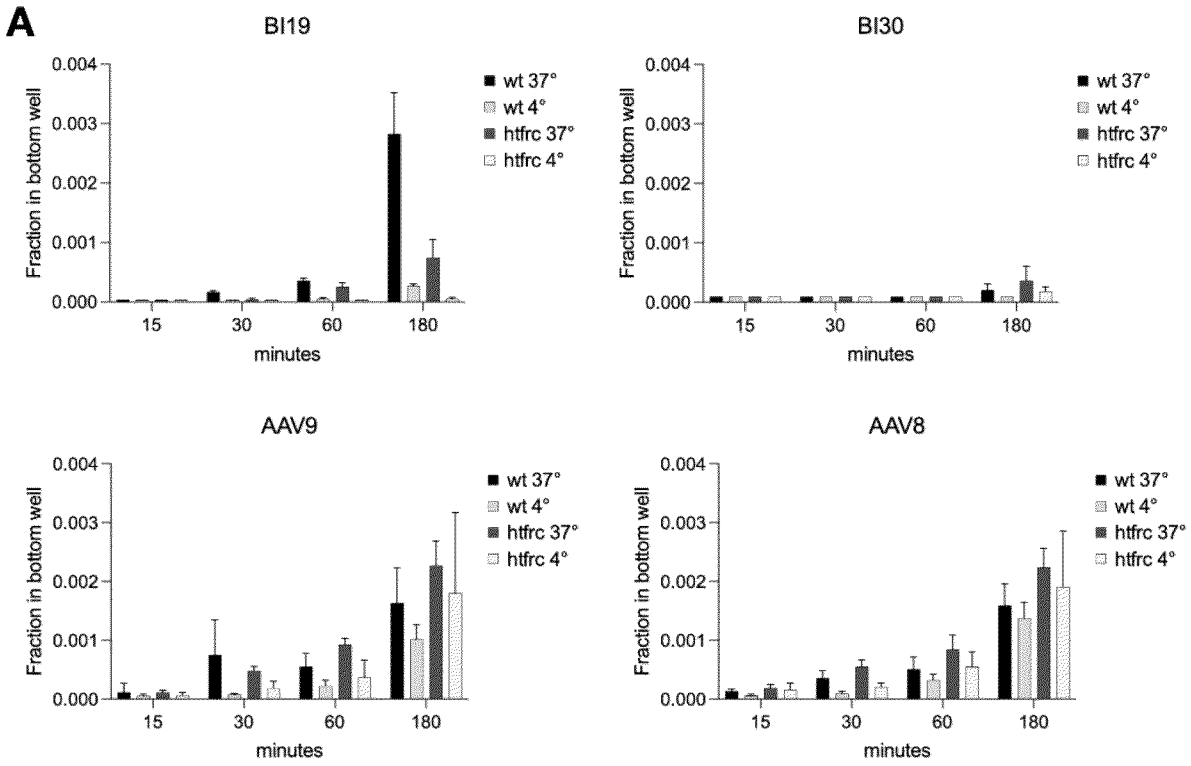

A
BI19
BI30
AAV9
AAV8
Fraction in bottom well
0.004
0.003
0.002
0.001
0.000
15
30
60
180
minutes
wt 37°
wt 4°
htfrc 37°
htfrc 4°

FIG. 12A

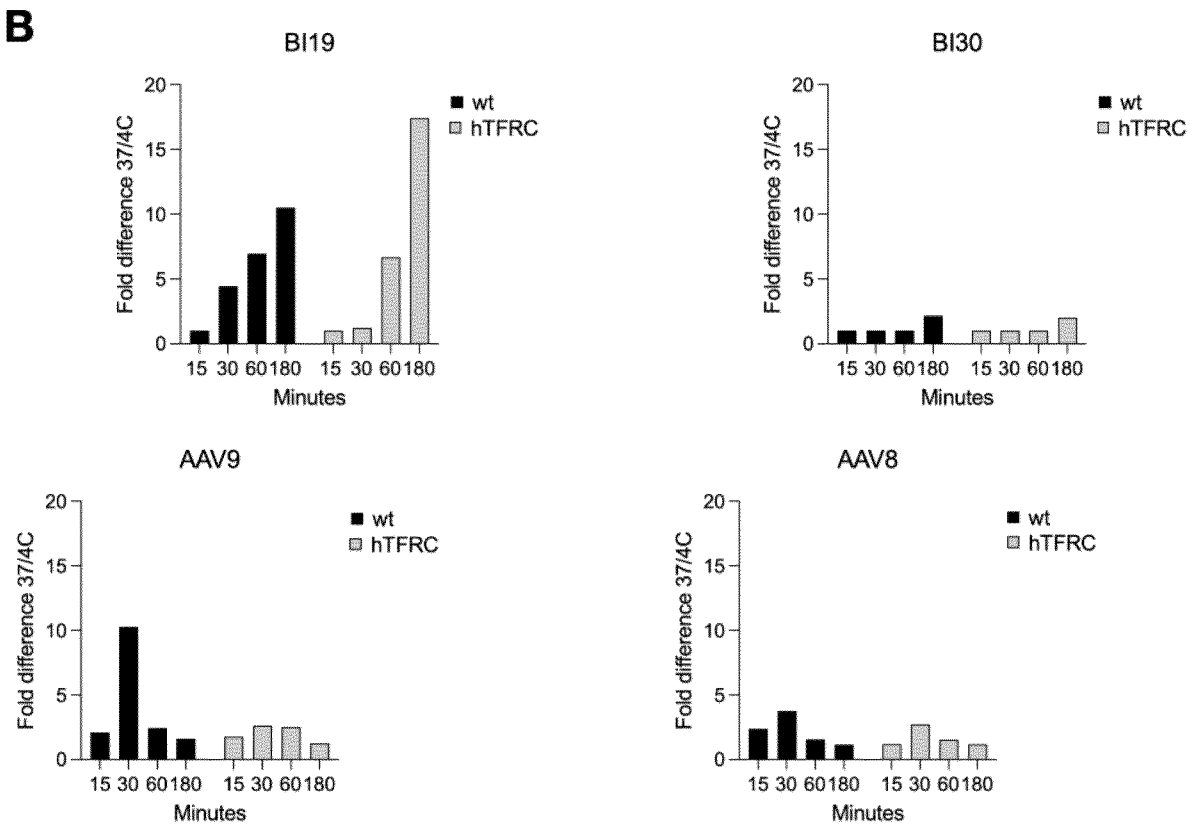

B
BI19
BI30
AAV9
AAV8
wt
hTFRC
Fold difference 37/4C
Minutes
0
5
10
15
20
15 30 60180 15 30 60180

FIG. 12B

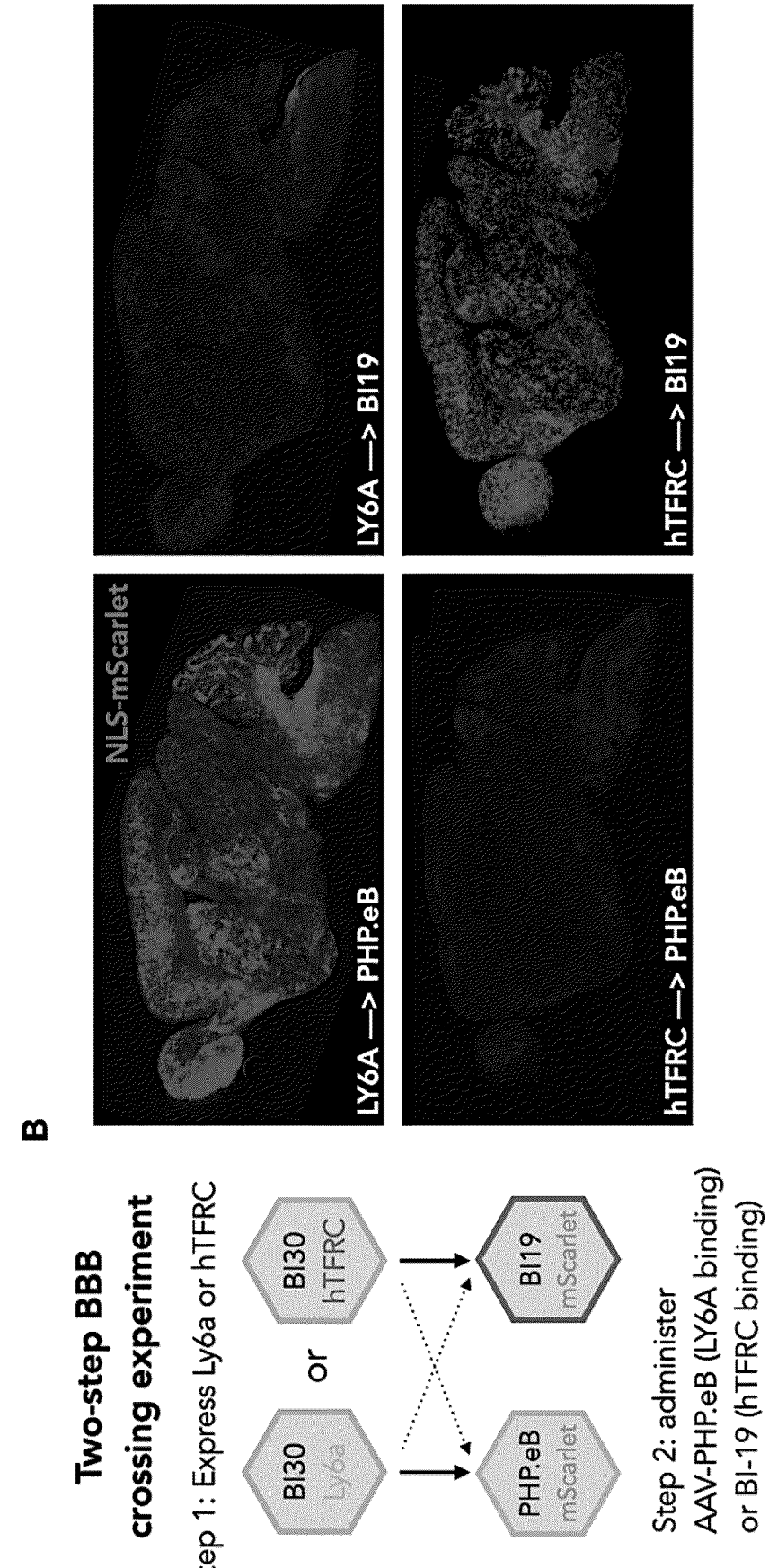

A
Two-step BBB crossing experiment
Step 1: Express Ly6a or hTFRC
BI30 Ly6a
or
BI30 hTFRC
PHP.eB mScarlet
BI19 mScarlet
Step 2: administer AAV-PHP.eB (LY6A binding) or BI-19 (hTFRC binding)
B
NLS-mScarlet
LY6A —> PHP.eB
hTFRC —> PHP.eB
LY6A —> BI19
hTFRC —> BI19

FIG. 13A-13B

C

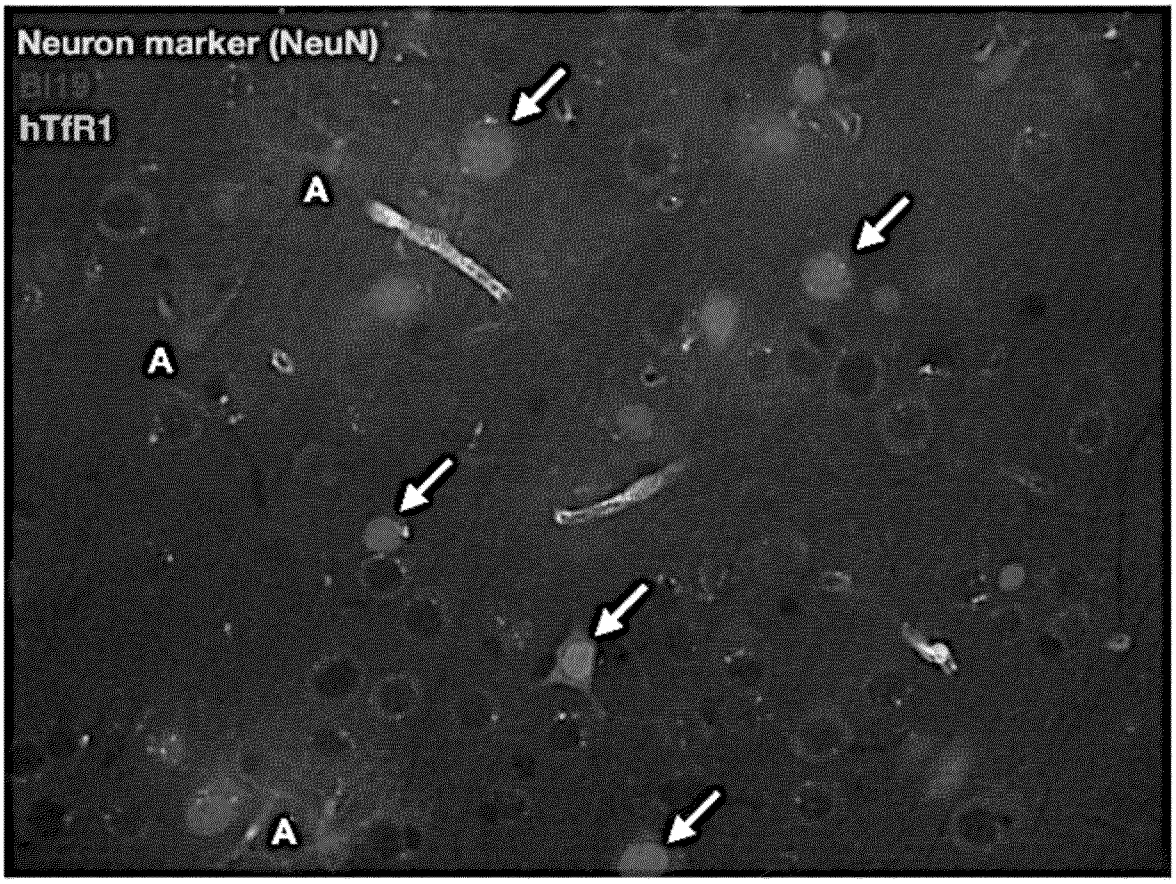


FIG. 13C



A

FIG. 14A



B

FIG. 14B

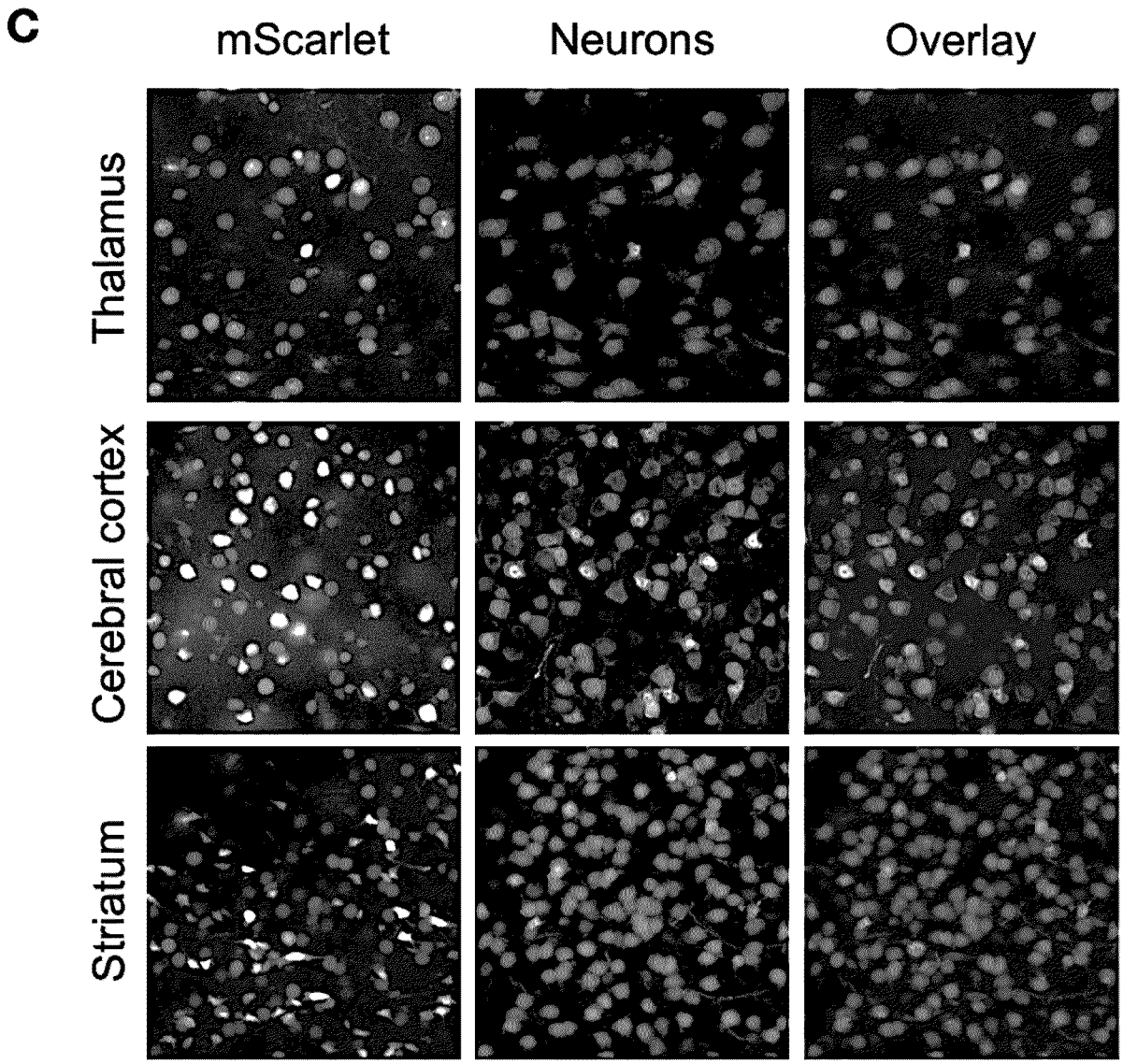

C
mScarlet
Neurons
Overlay
Thalamus
Cerebral cortex
Striatum

FIG. 14C

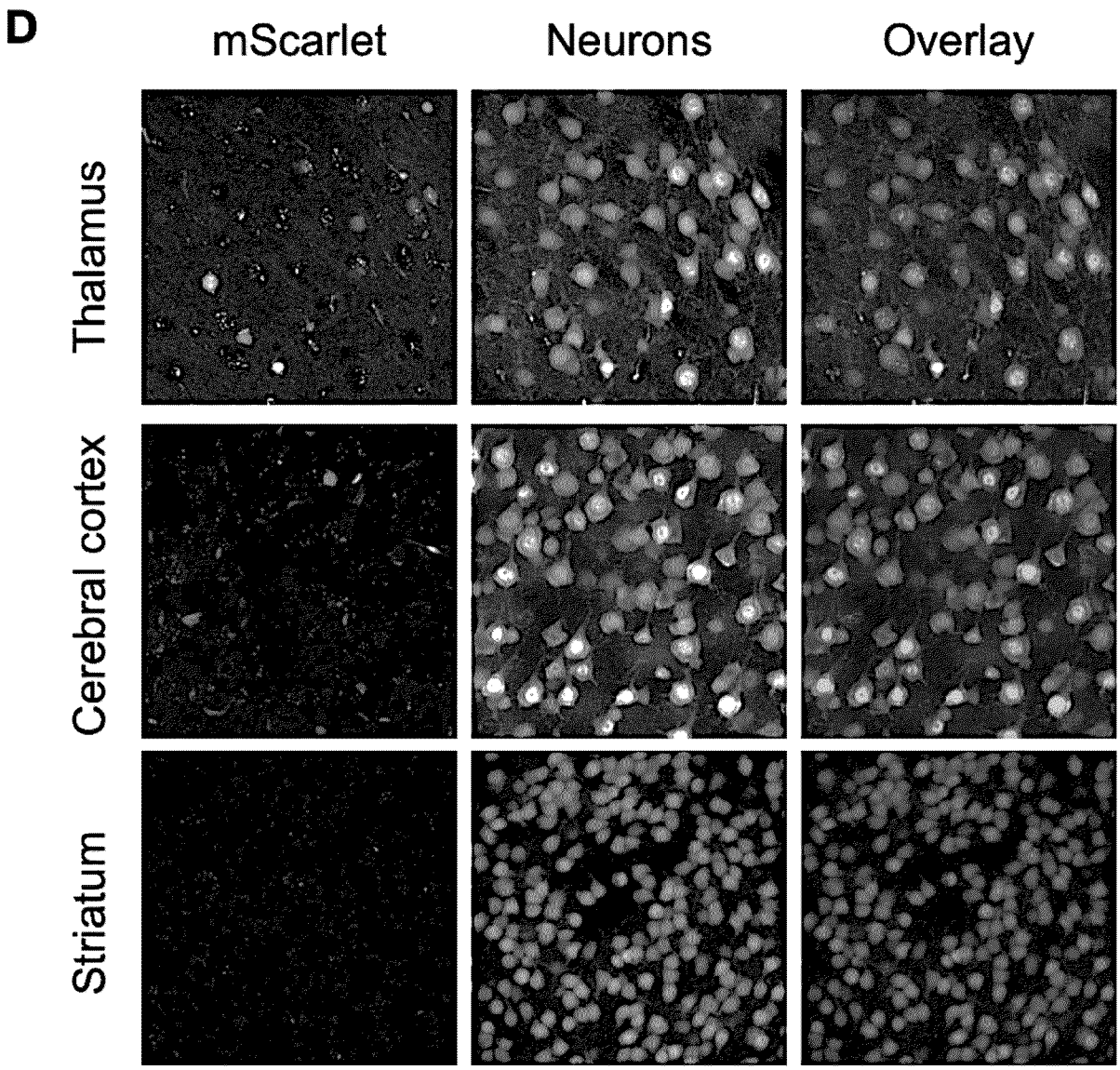

D
mScarlet
Neurons
Overlay
Thalamus
Cerebral cortex
Striatum

FIG. 14D

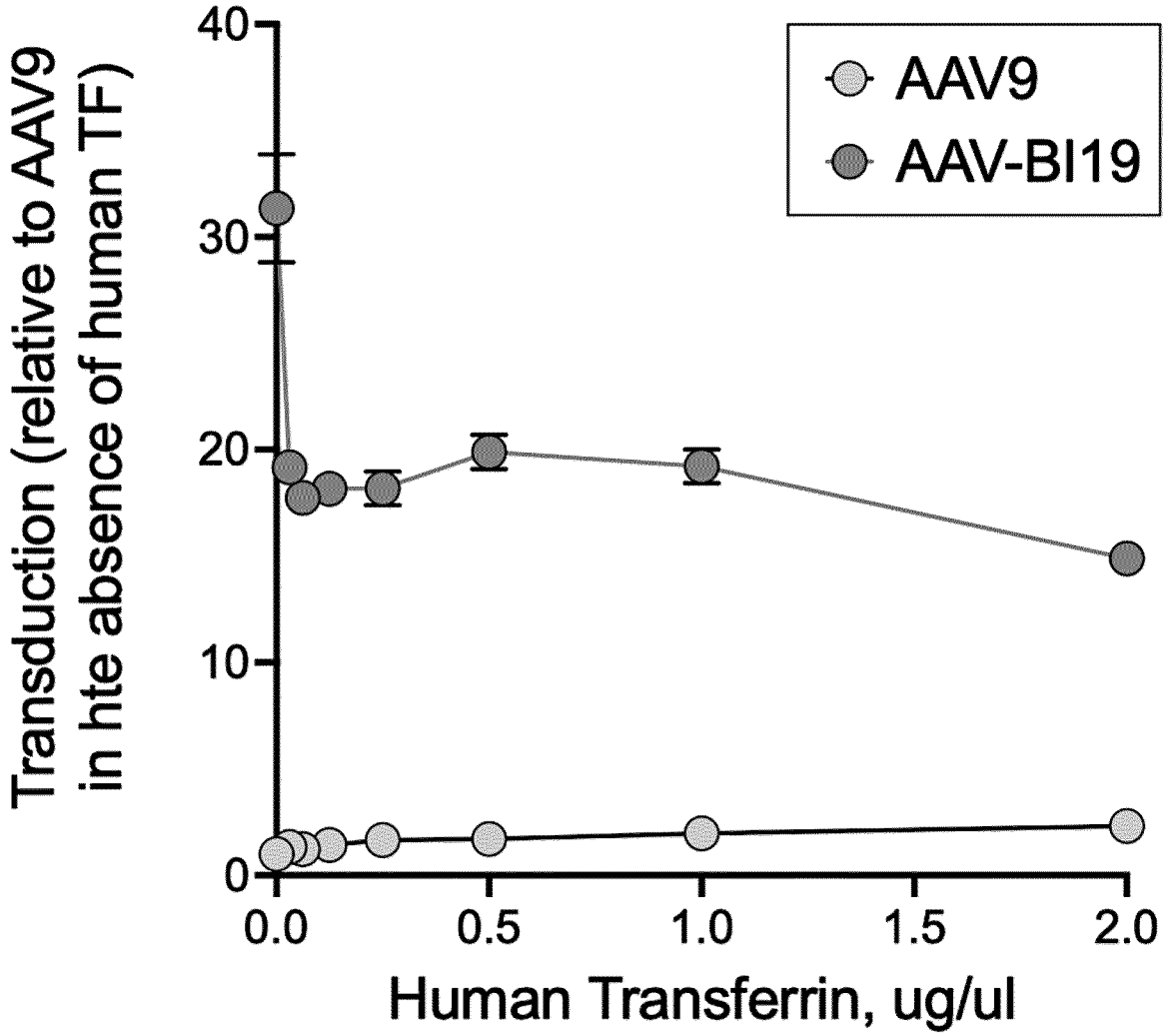

Transduction (relative to AAV9 in hte absence of human TF)
40
30
20
10
0
0.0
0.5
1.0
1.5
2.0
Human Transferrin, ug/ul
AAV9
AAV-BI19

FIG. 15

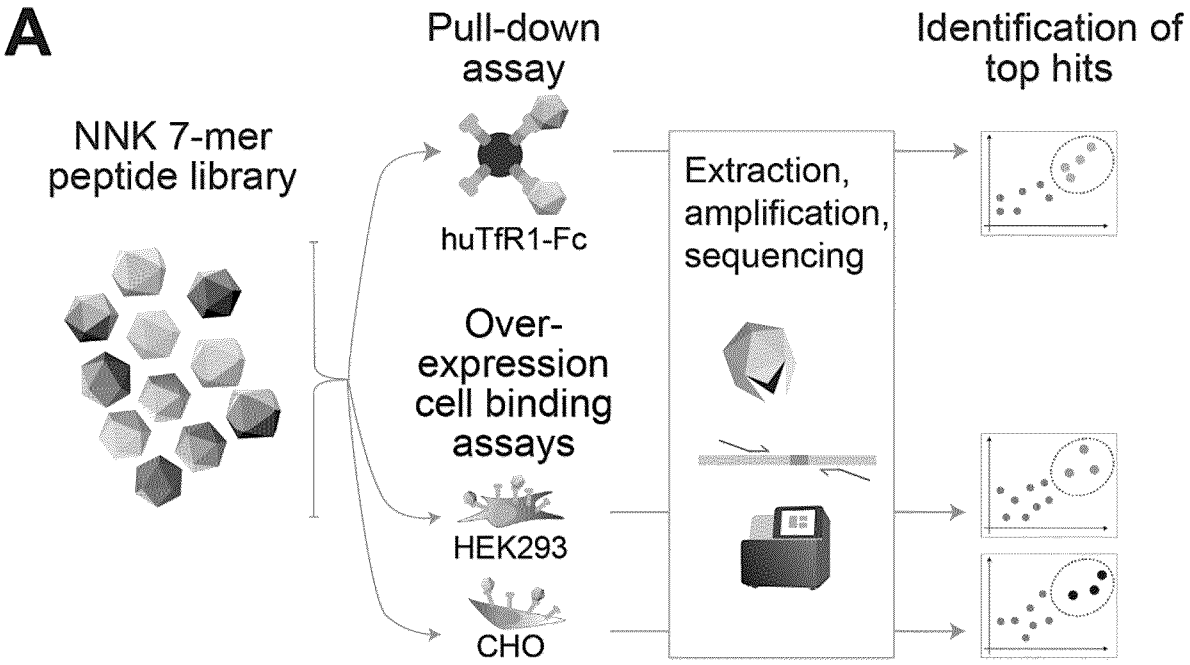


FIG. 16A

B

Selection of top candidates across assays that share a motif

AAV-BI19	YSRIGPN
AAV-BI98	YSRLNMN
AAV-BI99	YSRLNKD
AAV-BI101	YHRLSNN

FIG. 16B

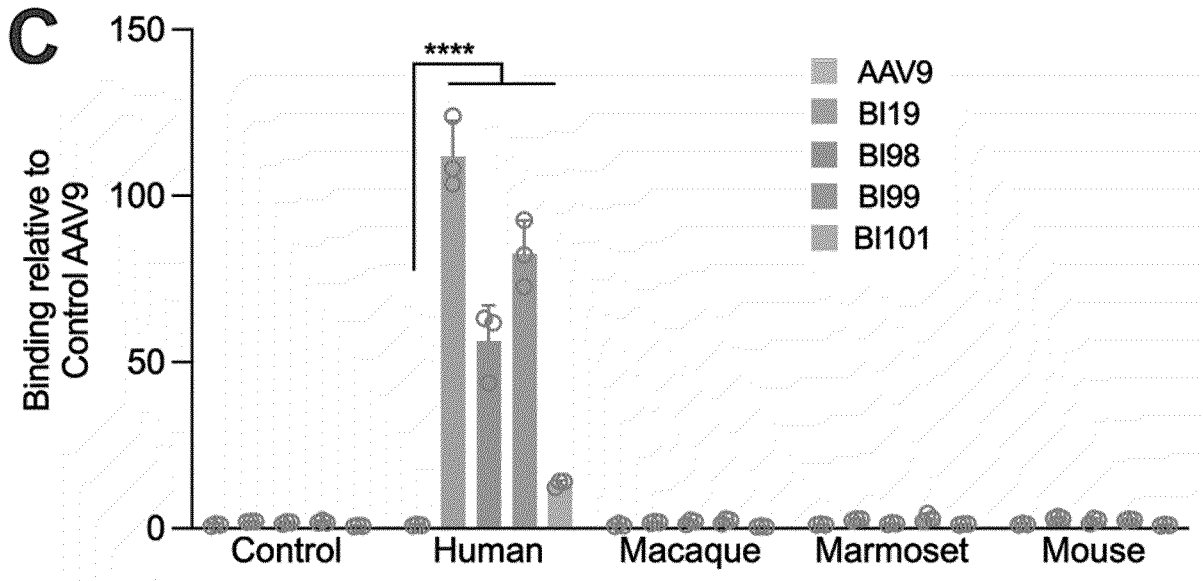


FIG. 16C

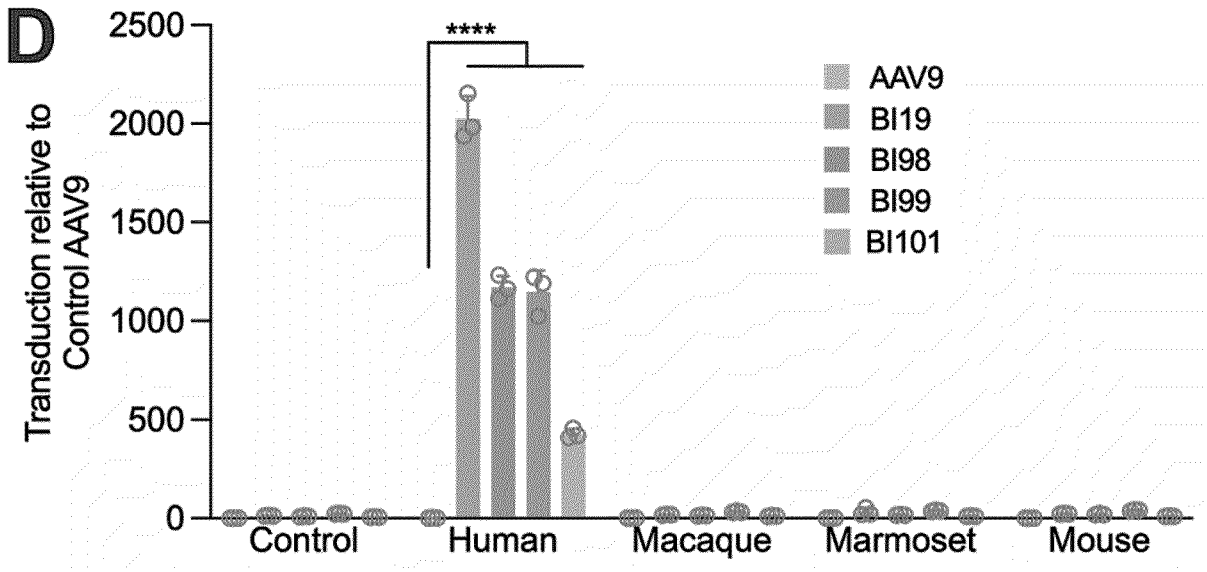


FIG. 16D

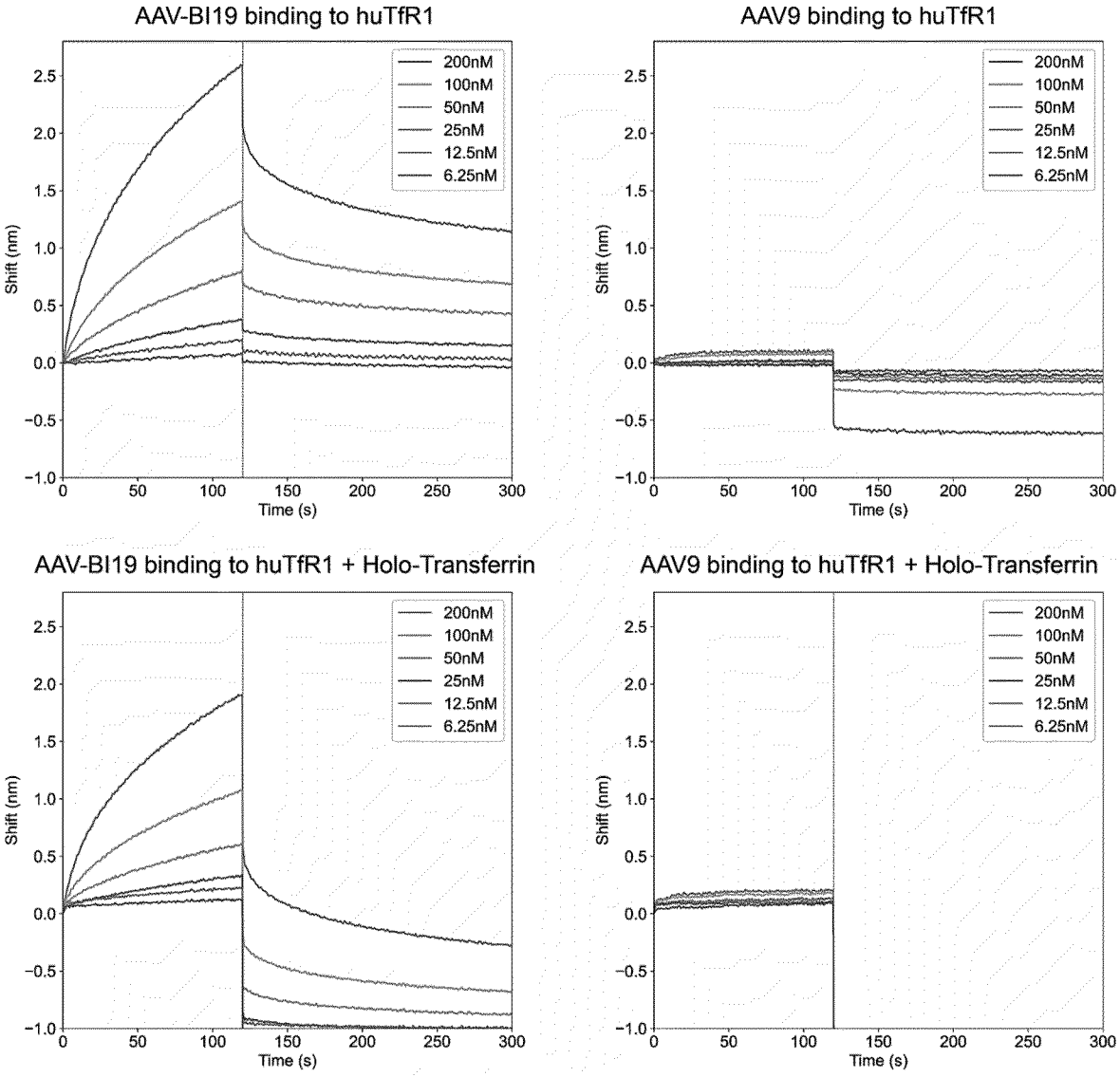

AAV-BI19 binding to huTfR1
AAV9 binding to huTfR1
AAV-BI19 binding to huTfR1 + Holo-Transferrin
AAV9 binding to huTfR1 + Holo-Transferrin
200nM
100nM
50nM
25nM
12.5nM
6.25nM
Shift (nm)
Time (s)

FIG. 16E

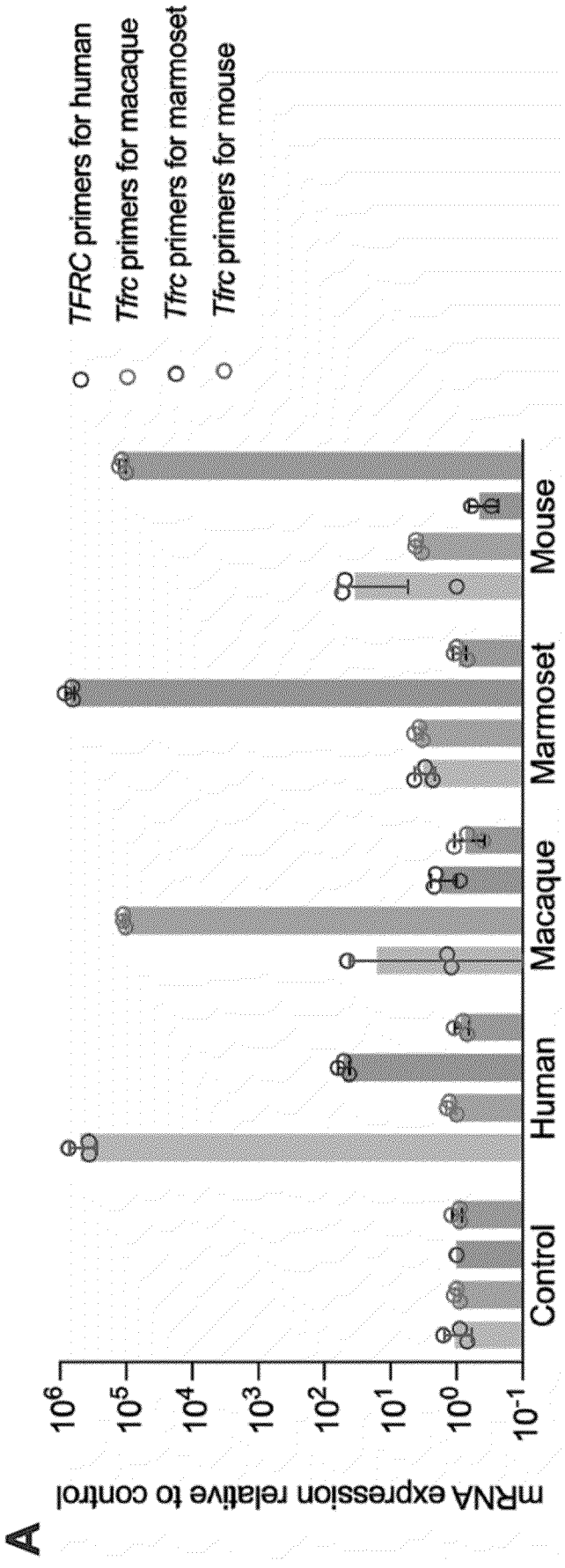

A
mRNA expression relative to control
10^{6}
10^{5}
10^{4}
10^{3}
10^{2}
10^{1}
10^{0}
10^{-1}
Control
Human
Macaque
Marmoset
Mouse
TFRC primers for human
Tfrc primers for macaque
Tfrc primers for marmoset
Tfrc primers for mouse

FIG. 17A

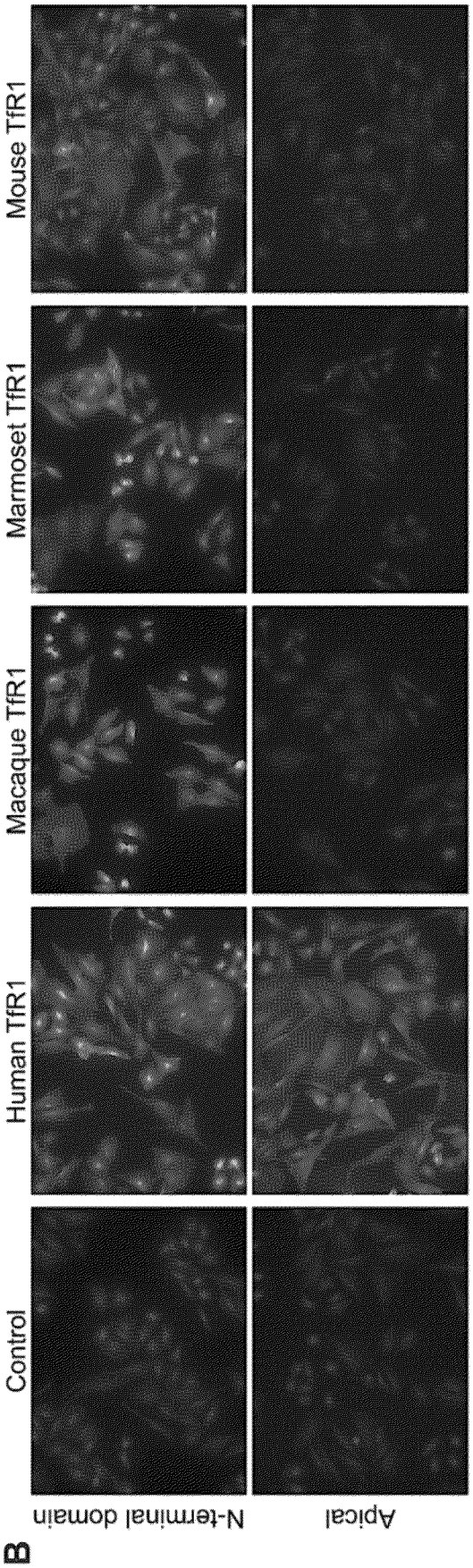

B
N-terminal domain
Apical
Control
Human TfR1
Macaque TfR1
Marmoset TfR1
Mouse TfR1

FIG. 17B

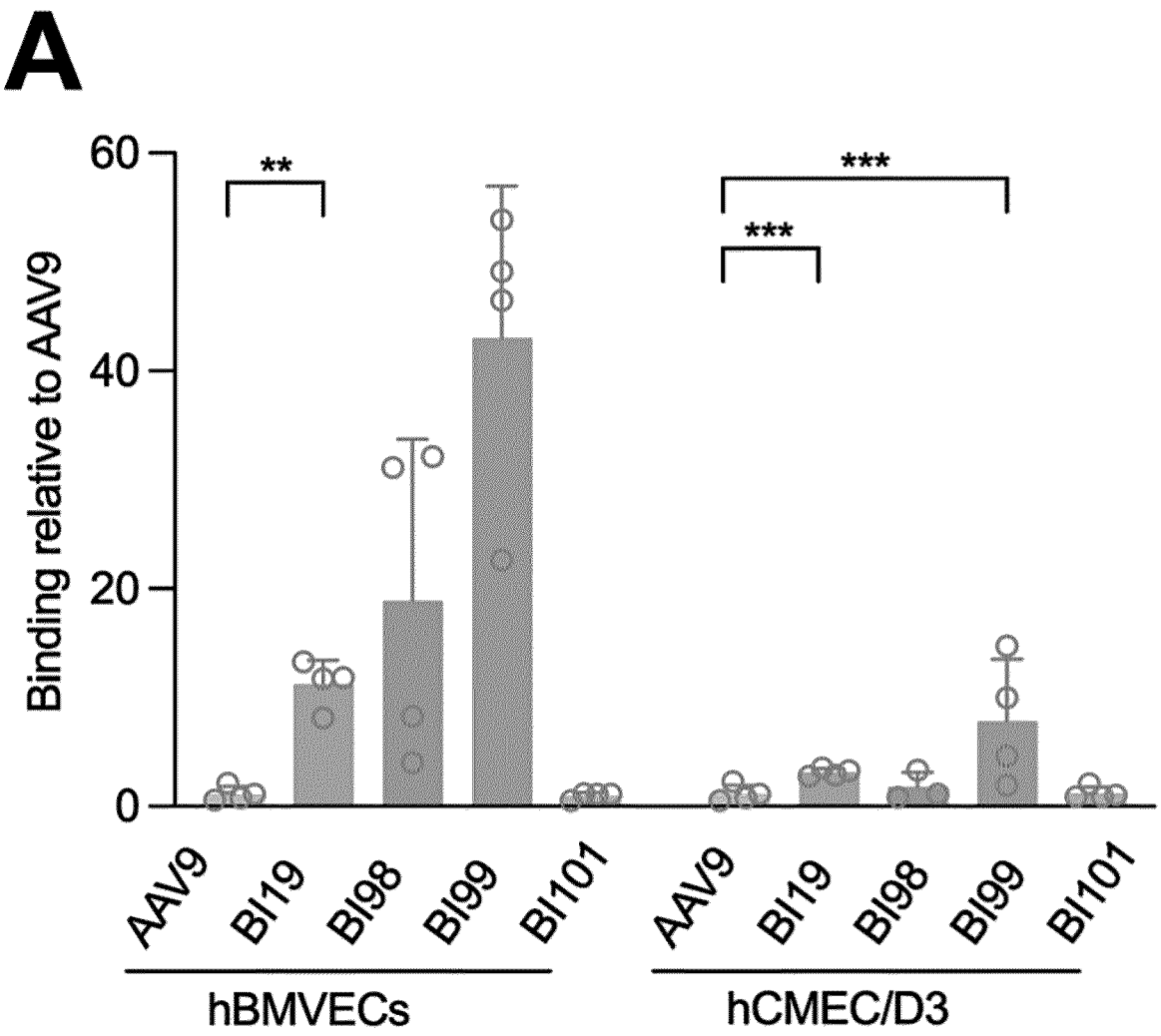

A
Binding relative to AAV9
60
40
20
0
**
***
***
AAV9
BI19
BI98
BI99
BI101
AAV9
BI19
BI98
BI99
BI101
hBMVECs
hCMEC/D3

FIG. 18A

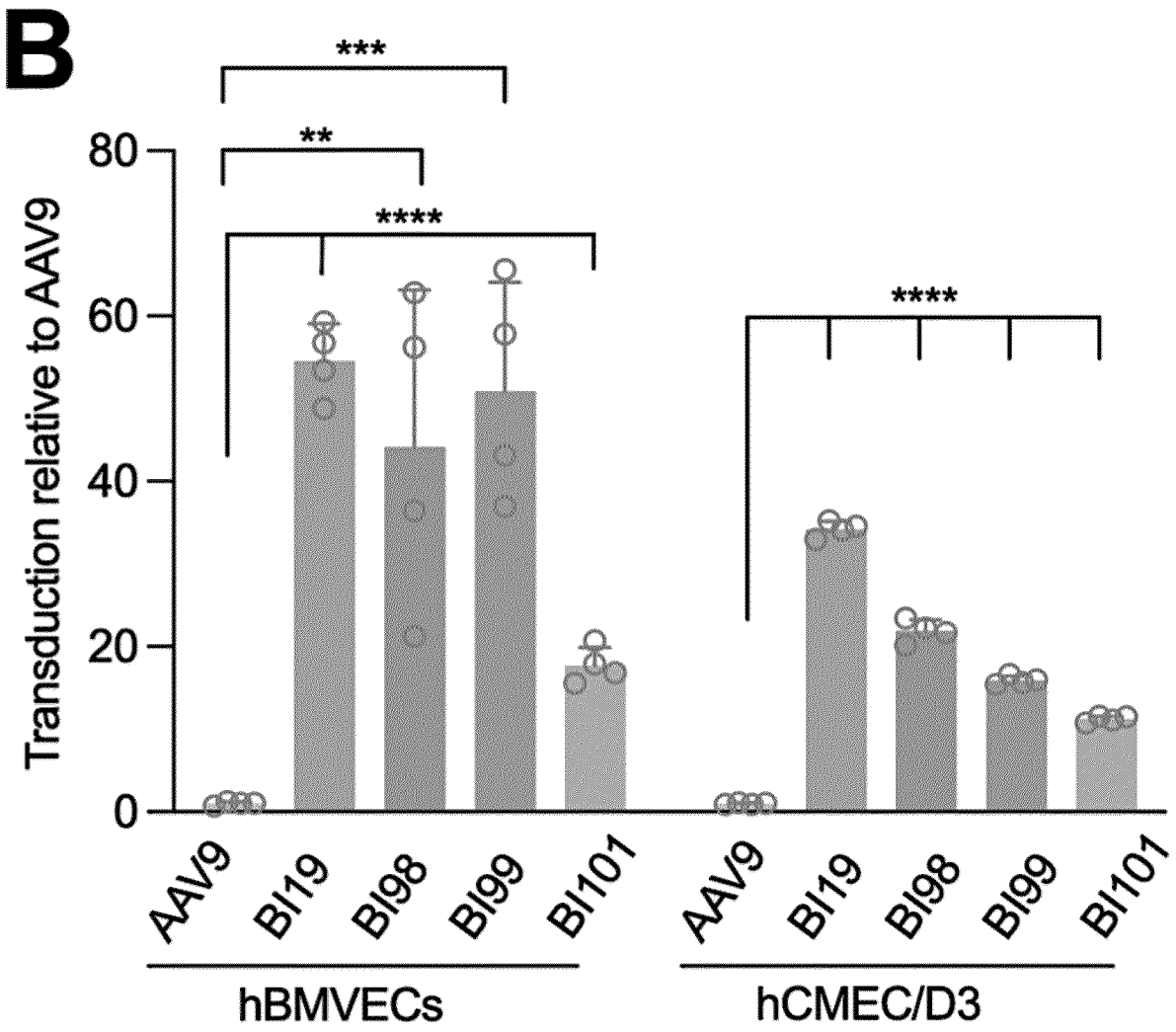

B
***
**
****
****
80
60
40
20
0
Transduction relative to AAV9
AAV9
BI19
BI98
BI99
BI101
AAV9
BI19
BI98
BI99
BI101
hBMVECs
hCMEC/D3

FIG. 18B

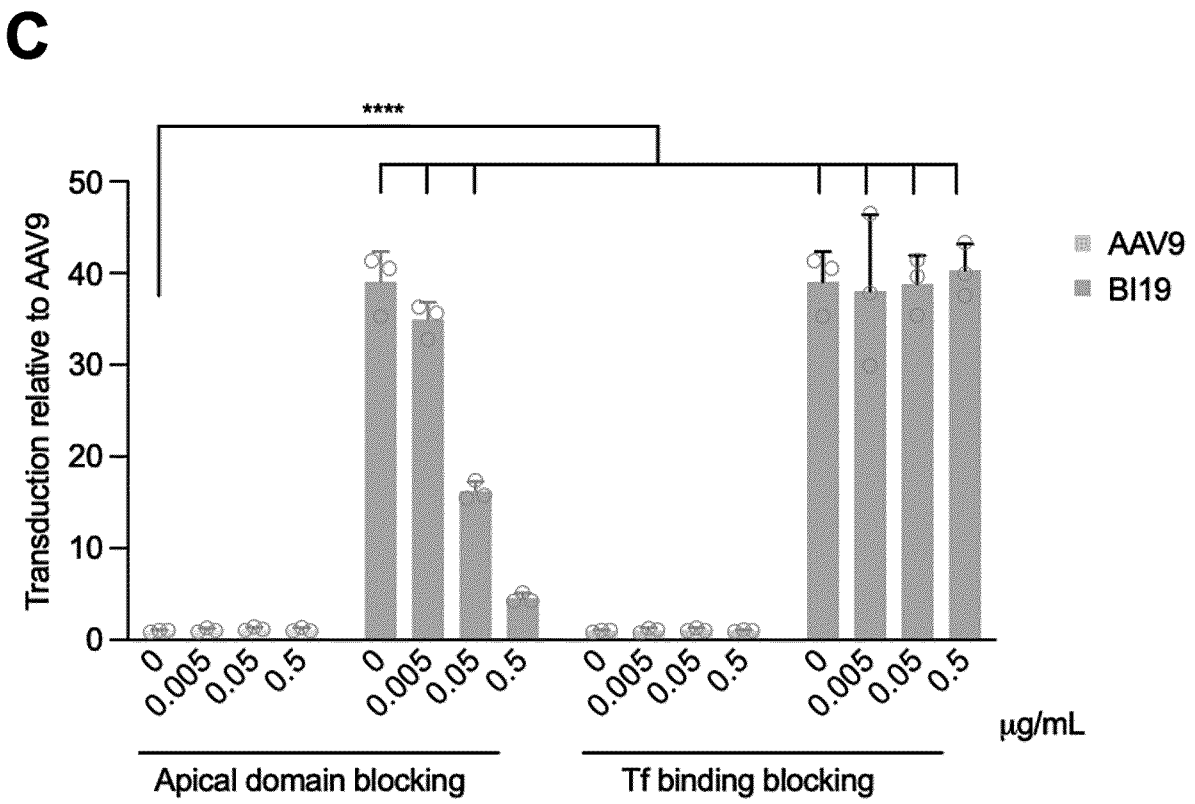

C
****
Transduction relative to AAV9
50
40
30
20
10
0
0
0.005
0.05
0.5
0
0.005
0.05
0.5
0
0.005
0.05
0.5
0
0.005
0.05
0.5
μg/mL
AAV9
BI19
Apical domain blocking
Tf binding blocking

FIG. 18C

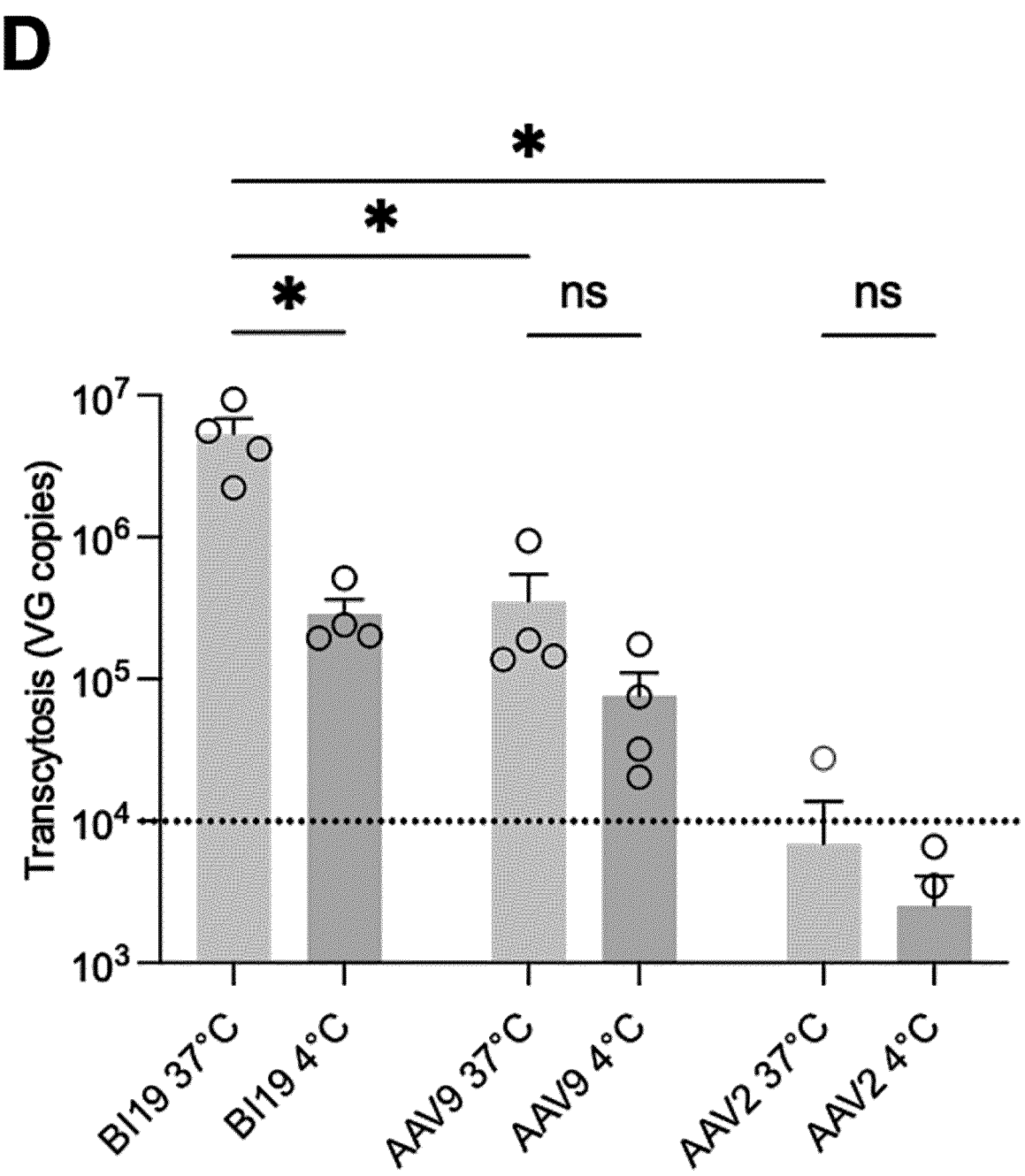

D
*
*
*
ns
ns
Transcytosis (VG copies)
10^7
10^6
10^5
10^4
10^3
BI19 37°C
BI19 4°C
AAV9 37°C
AAV9 4°C
AAV2 37°C
AAV2 4°C

FIG. 18D


A
Human
Macaque
Marmoset
208
247 248
292 294
325
364
370 372
200 VIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKKDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPI 290
200 VIIVDKNGGLVYLVENPGGYVAYSKAATVTGKLVHANFGTKKDFEDLDSPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPI 290
200 VTITGTNSEFVYLVENPGGYVAYSQNATVTGKLVHANFGTEKDFEDLDSPVNGSLVIVRAGKITFAEKVANAESANAIGVLIYMDKTKFPI 290
291 VNAELSFFGHAHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDSTCRMVTSESKNVKLTVSNV 380
291 VKADLSFFGHAHLGTGDPYTPGFPSFNHTQFPPSQSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDSTCKMVTSENKSVKLTVSNV 380
291 VDADVSFFGHAHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAERLFENMEGDCPSDWKTDSSCRMVTSQNKSVKLSVSNV 380

FIG. 19A

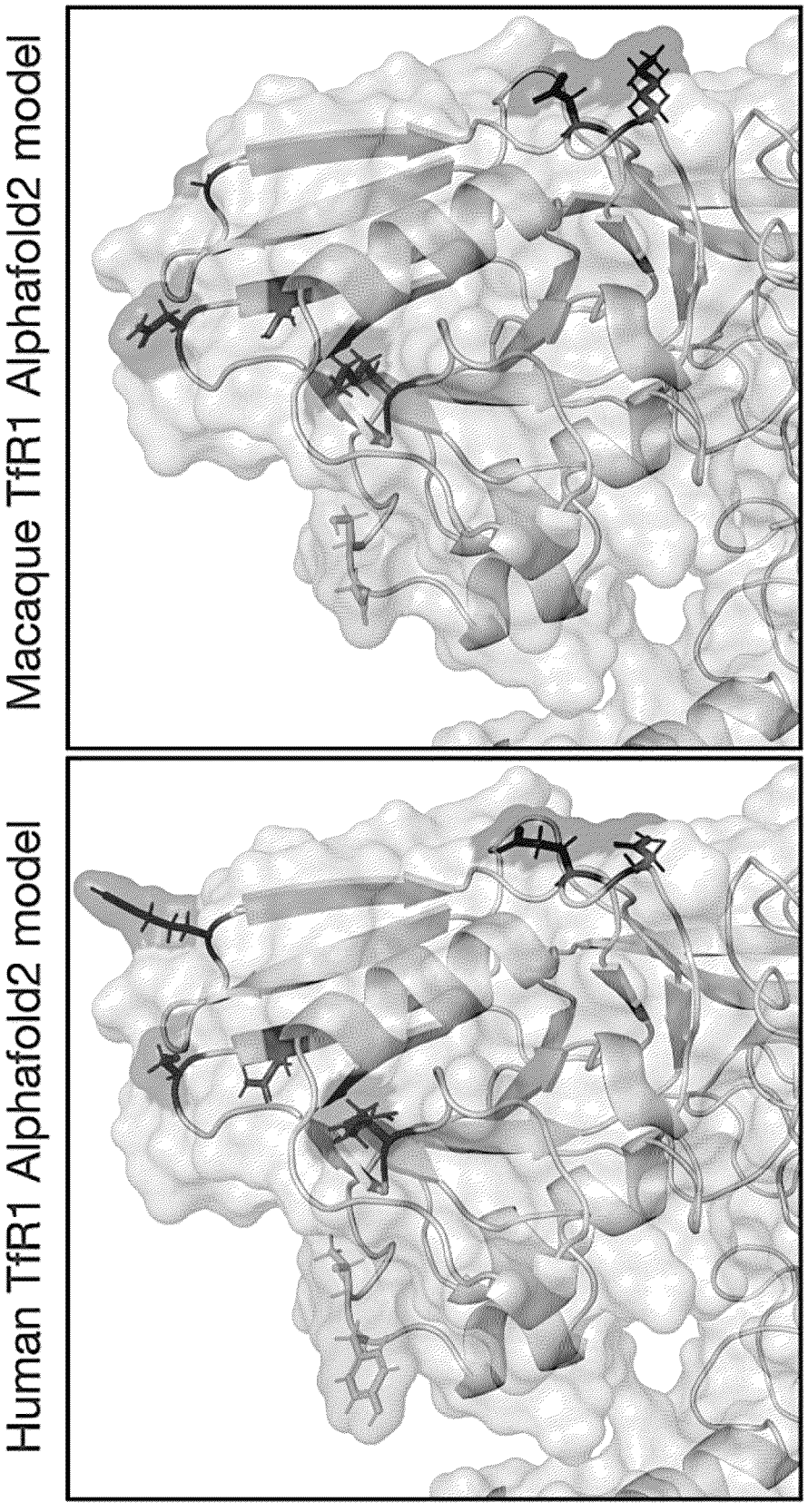

B
Human TfR1 Alphafold2 model
Macaque TfR1 Alphafold2 model

FIG. 19B

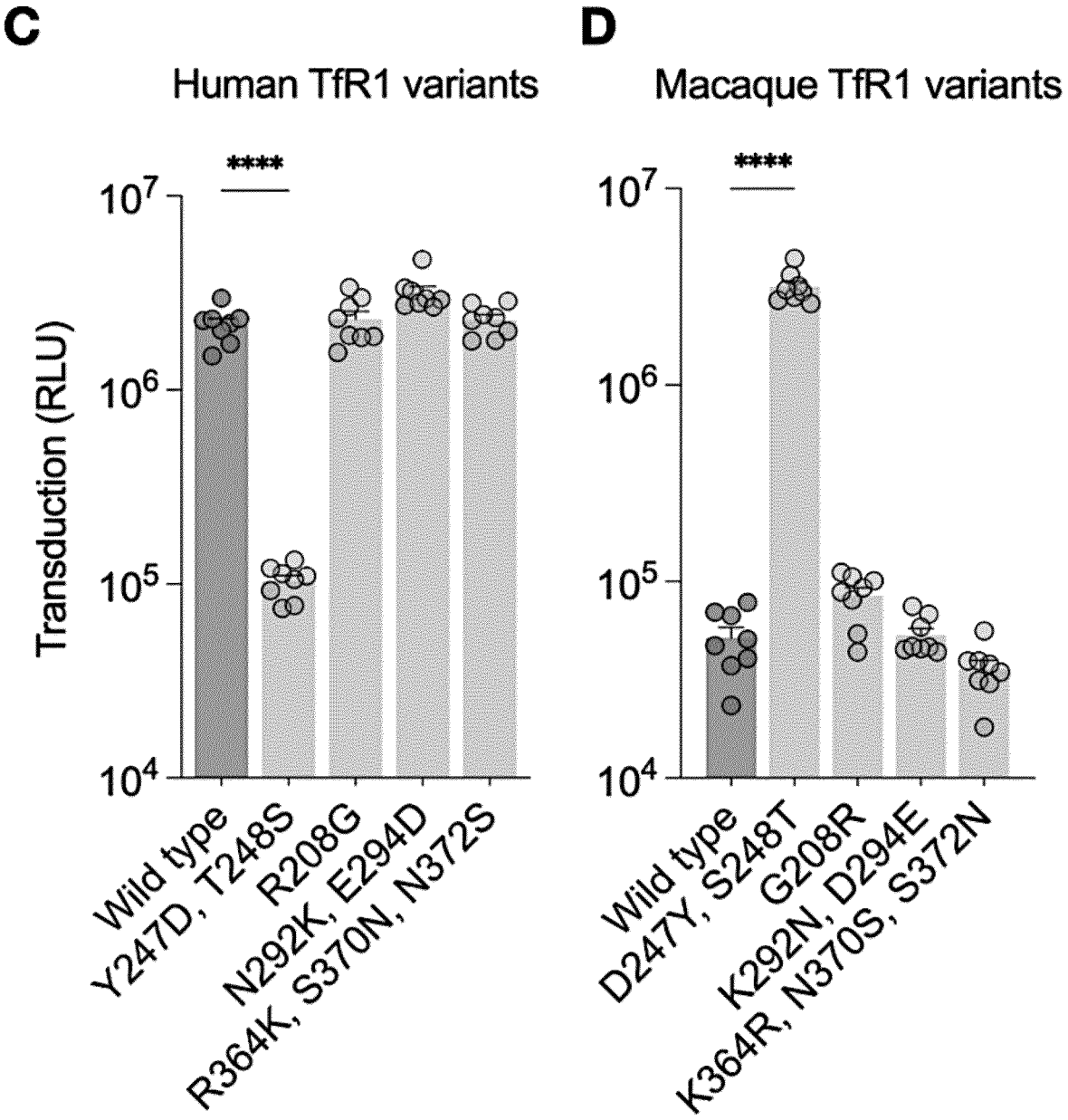

C
Human TfR1 variants
****
10^7
10^6
10^5
10^4
Transduction (RLU)
Wild type
Y247D, T248S
R208G
N292K, E294D
R364K, S370N, N372S
D
Macaque TfR1 variants
****
10^7
10^6
10^5
10^4
Wild type
D247Y, S248T
G208R
K292N, D294E
K364R, N370S, S372N

FIG. 19C-19D

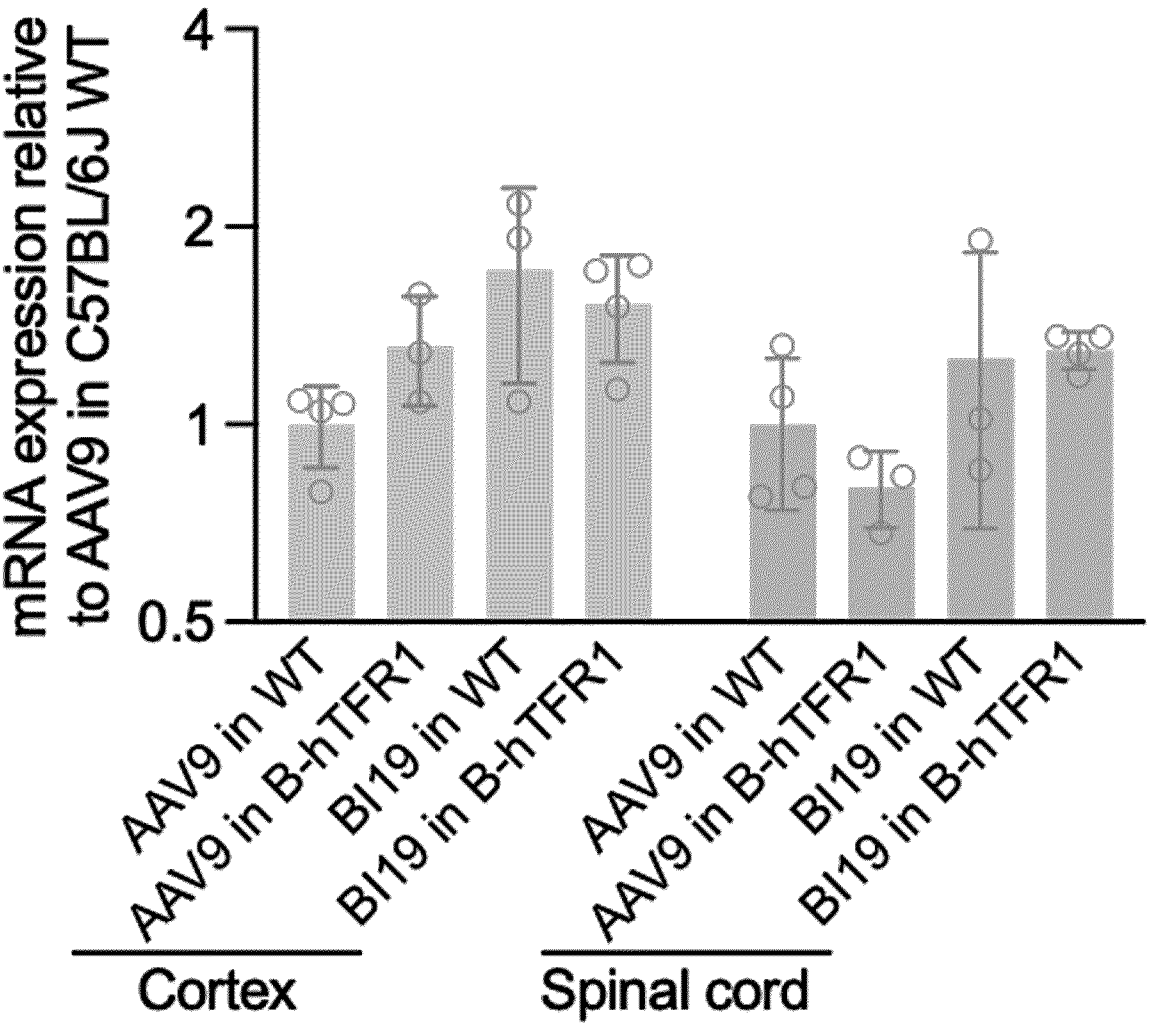

mRNA expression relative to AAV9 in C57BL/6J WT
4
2
1
0.5
AAV9 in WT
AAV9 in B-hTFR1
BI19 in WT
BI19 in B-hTFR1
AAV9 in WT
AAV9 in B-hTFR1
BI19 in WT
BI19 in B-hTFR1
Cortex
Spinal cord

FIG. 20

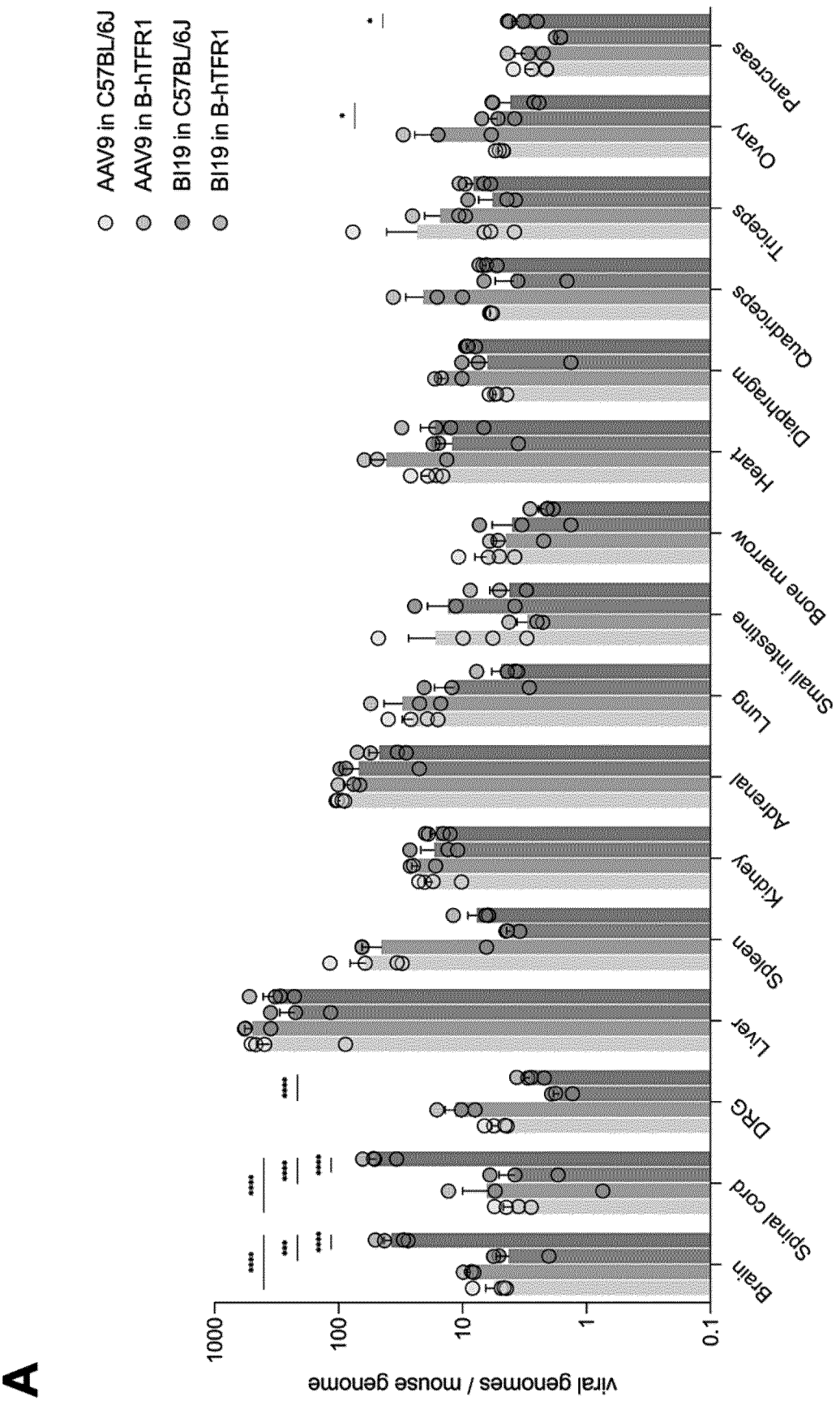

A
AAV9 in C57BL/6J
AAV9 in B-hTFR1
BI19 in C57BL/6J
BI19 in B-hTFR1
viral genomes / mouse genome
1000
100
10
1
0.1
Brain
Spinal cord
DRG
Liver
Spleen
Kidney
Adrenal
Lung
Small intestine
Bone marrow
Heart
Diaphragm
Quadriceps
Triceps
Ovary
Pancreas

FIG. 21A

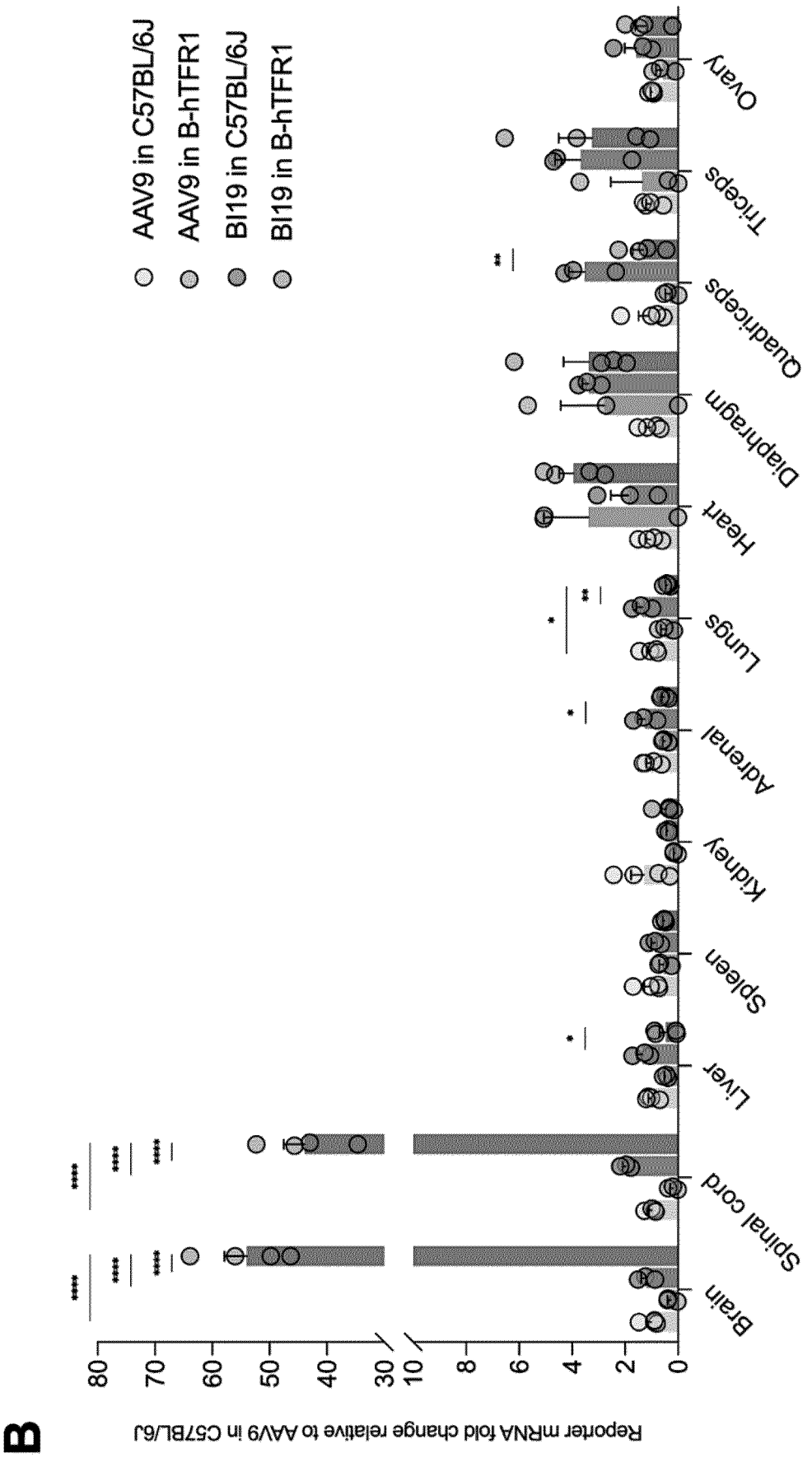

B
Reporter mRNA fold change relative to AAV9 in C57BL/6J
AAV9 in C57BL/6J
AAV9 in B-hTFR1
BI19 in C57BL/6J
BI19 in B-hTFR1
Brain
Spinal cord
Liver
Spleen
Kidney
Adrenal
Lungs
Heart
Diaphragm
Quadriceps
Triceps
Ovary

FIG. 21B


C
Luciferase activity fold change relative to AAV9 in C57BL/6J
250
200
150
100
50
20
10
0
AAV9 in C57BL/6J
AAV9 in B-hTFR1
BI19 in C57BL/6J
BI19 in B-hTFR1
Brain
Spinal cord
Liver
Kidney
Spleen
Lungs
Heart
Quadriceps
Triceps
Small intestine
Pancreas

FIG. 21C

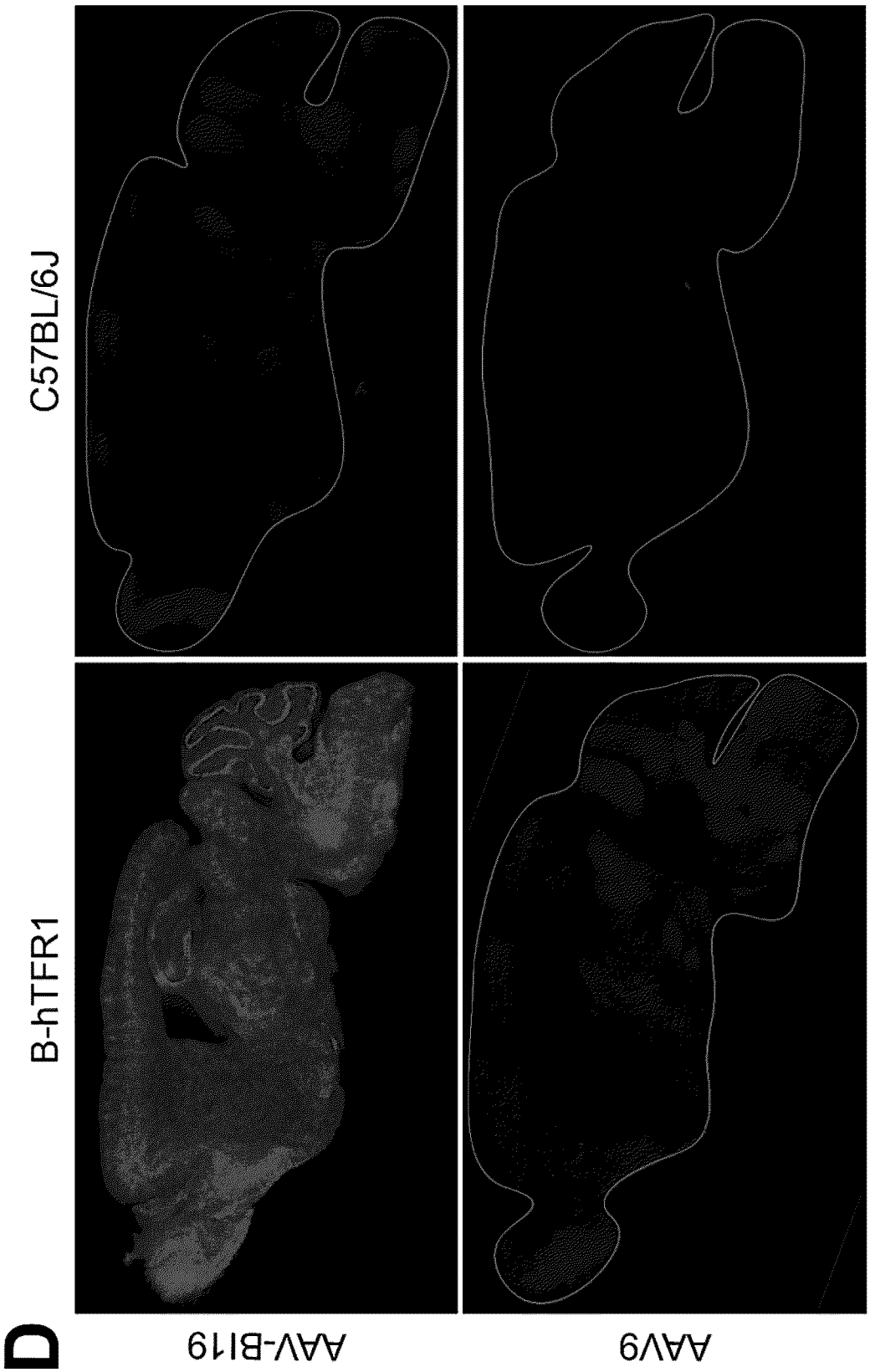


FIG. 21D

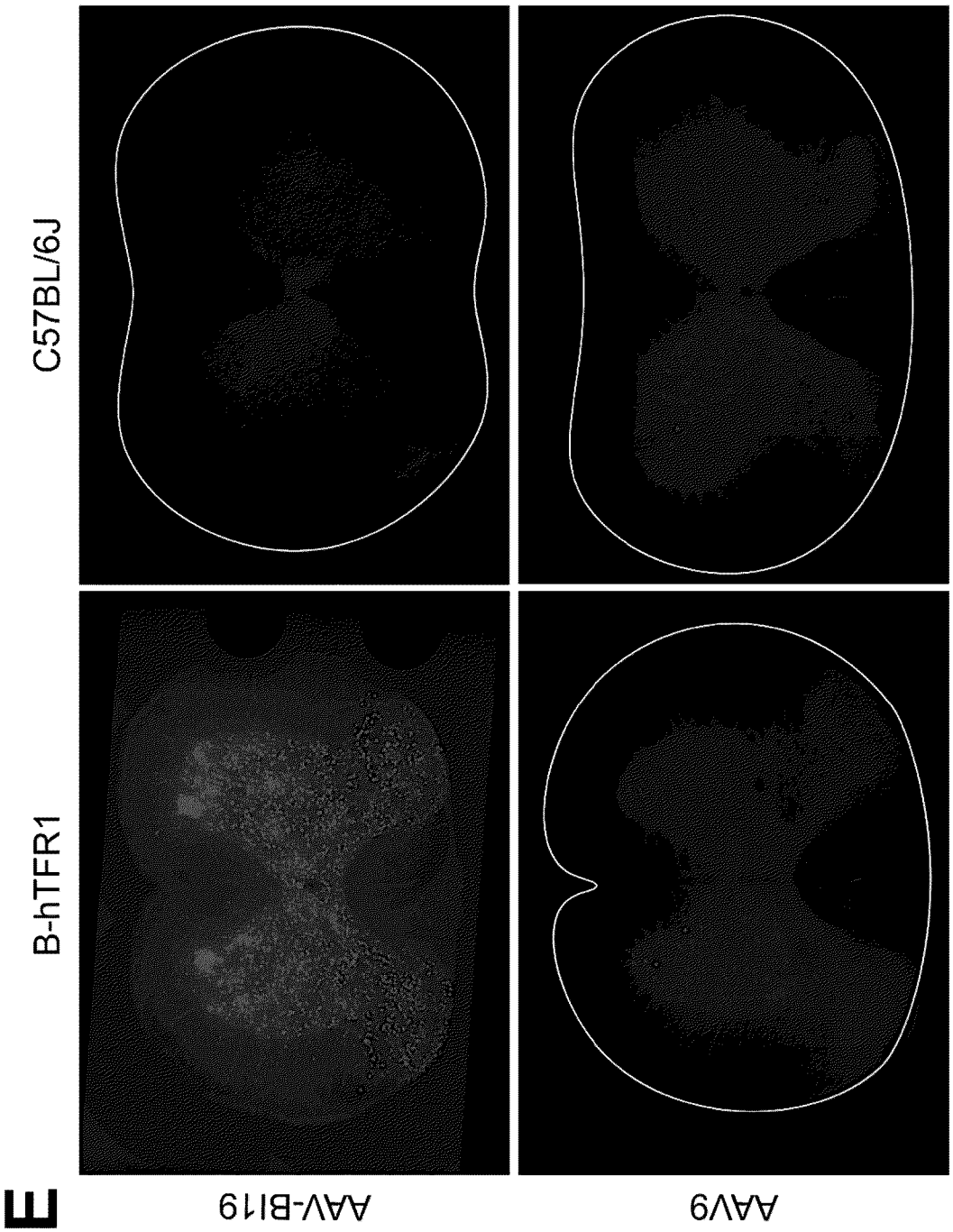


FIG. 21E

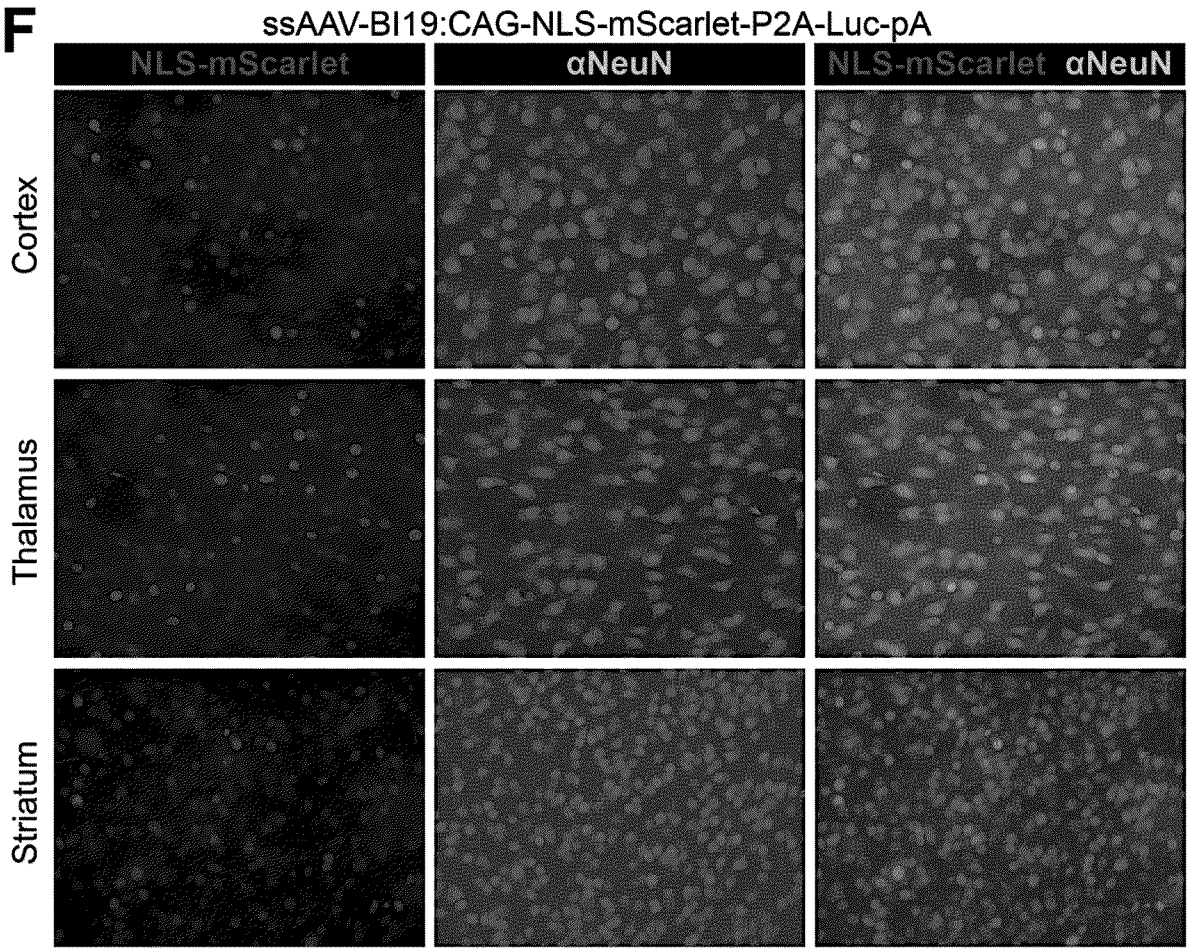

F
ssAAV-BI19:CAG-NLS-mScarlet-P2A-Luc-pA
NLS-mScarlet
αNeuN
NLS-mScarlet αNeuN
Cortex
Thalamus
Striatum

FIG. 21F

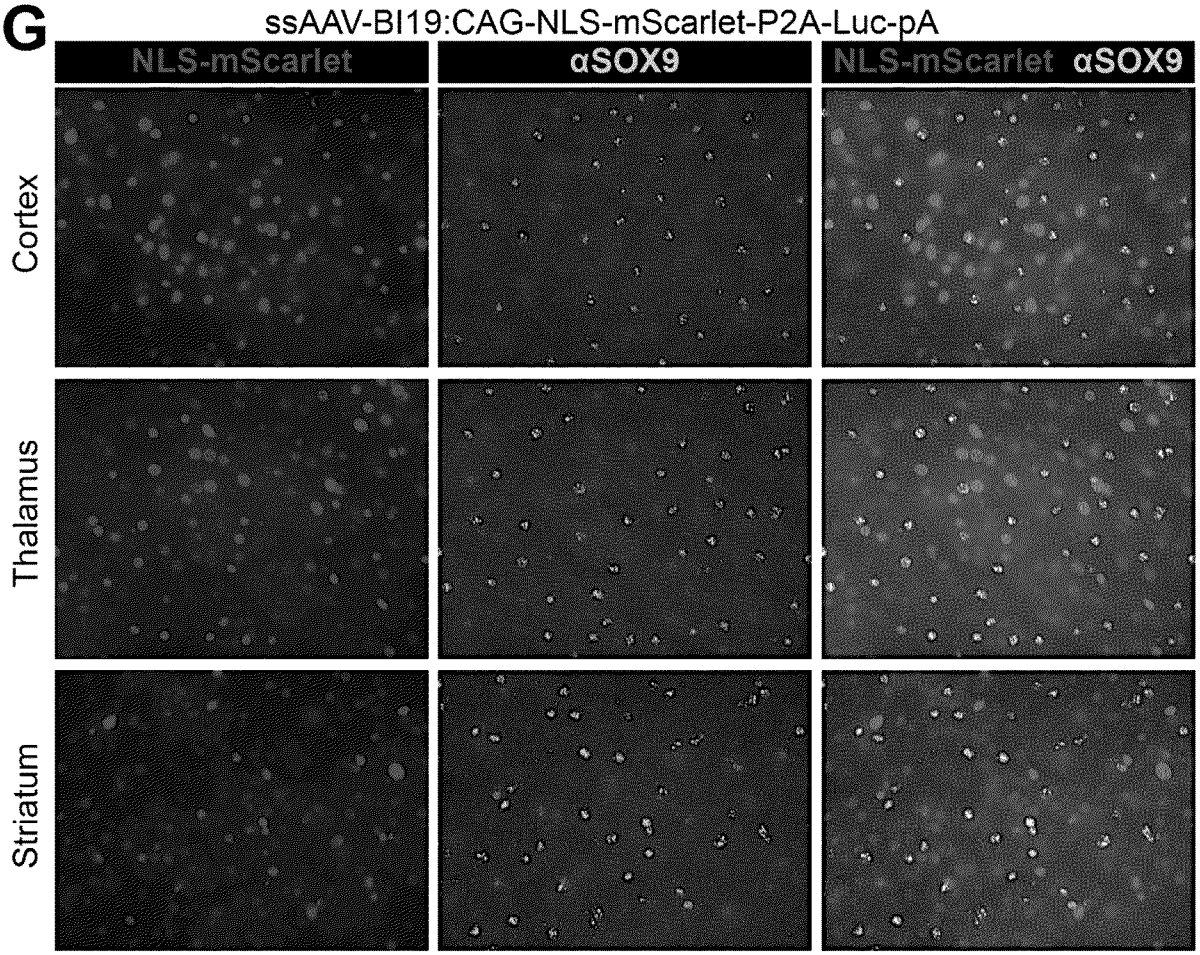

G
ssAAV-BI19:CAG-NLS-mScarlet-P2A-Luc-pA
NLS-mScarlet
αSOX9
NLS-mScarlet αSOX9
Cortex
Thalamus
Striatum

FIG. 21G

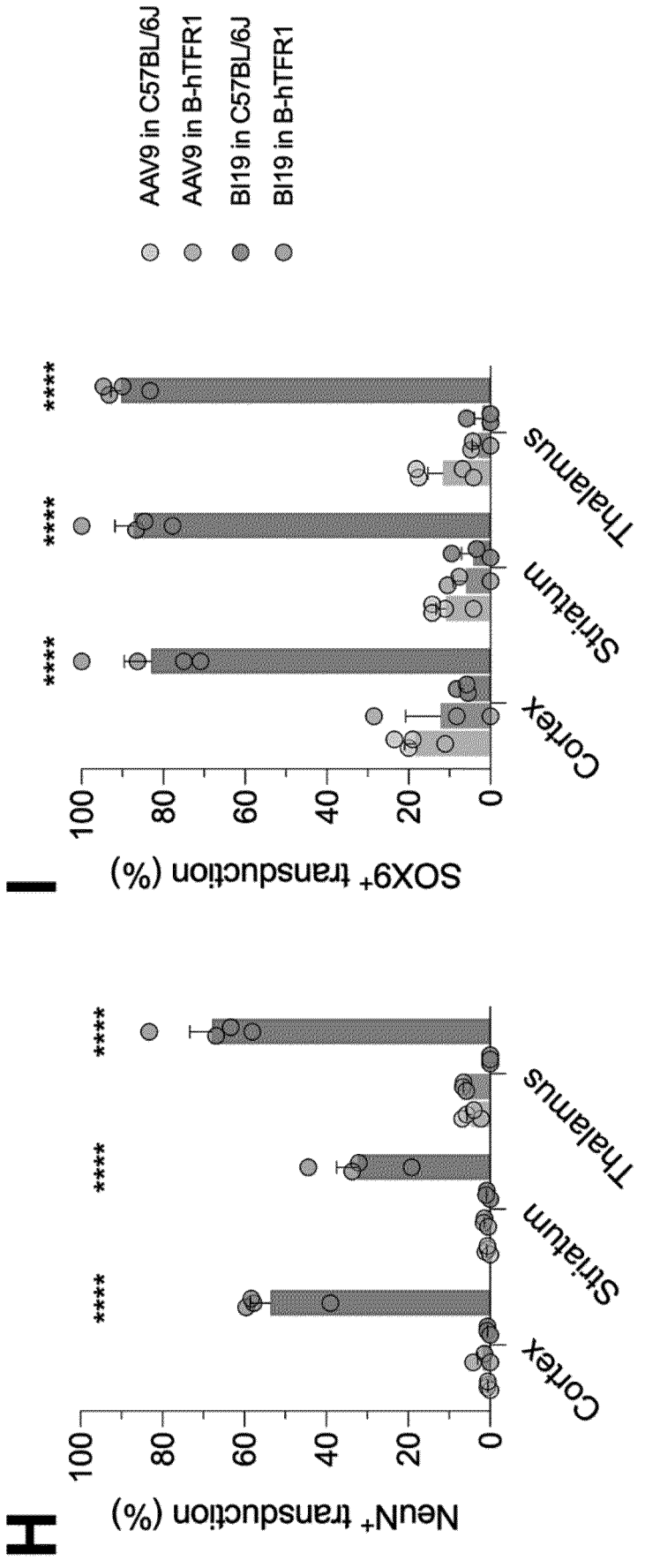

AAV9 in C57BL/6J
AAV9 in B-hTFR1
BI19 in C57BL/6J
BI19 in B-hTFR1
I
SOX9+ transduction (%)
0
20
40
60
80
100
Cortex
Striatum
Thalamus
****
****
****
H
NeuN+ transduction (%)
0
20
40
60
80
100
Cortex
Striatum
Thalamus
****
****
****

FIG. 21H-21I

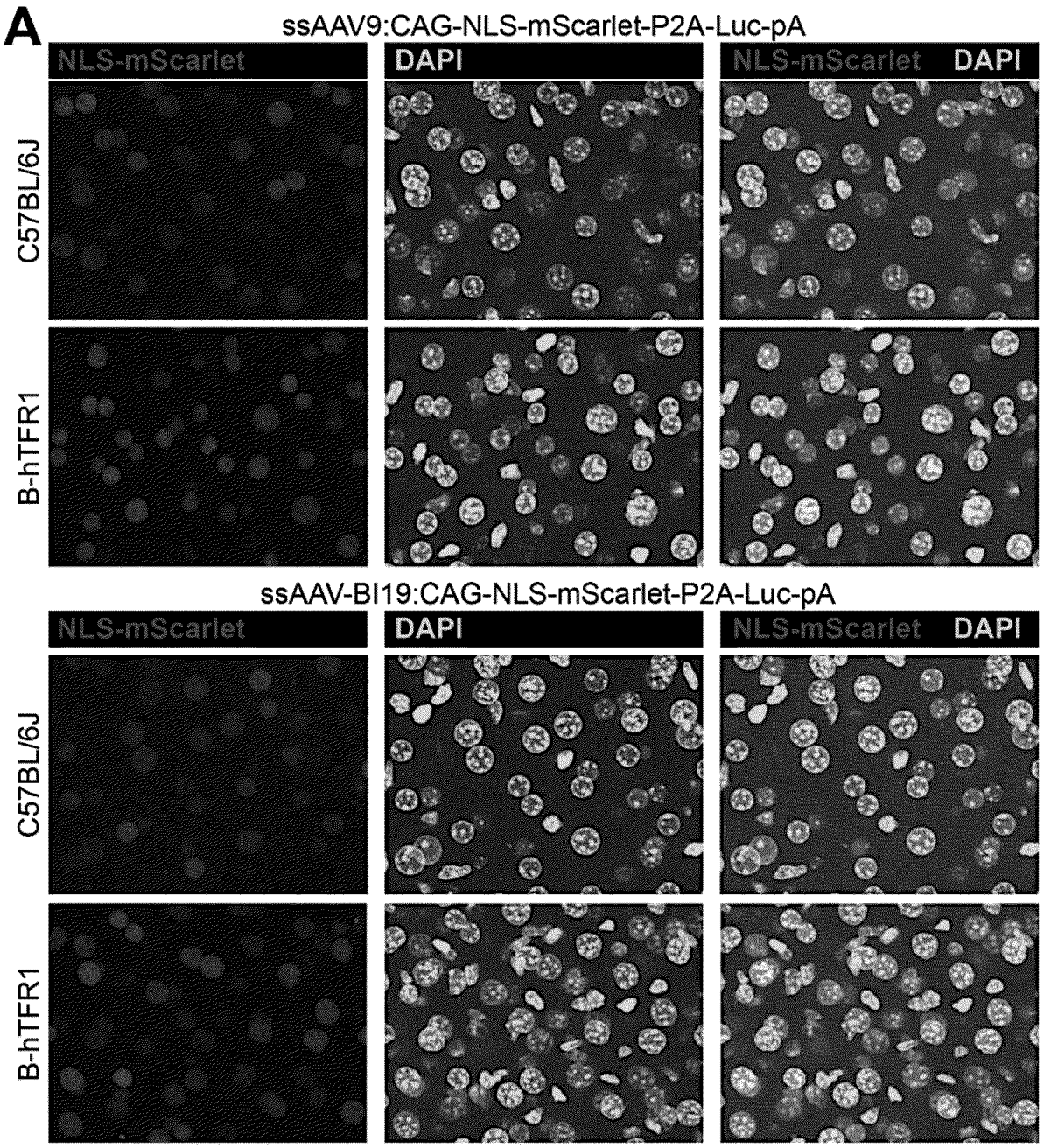

A
ssAAV9:CAG-NLS-mScarlet-P2A-Luc-pA
NLS-mScarlet
DAPI
NLS-mScarlet DAPI
C57BL/6J
B-hTFR1
ssAAV-BI19:CAG-NLS-mScarlet-P2A-Luc-pA
NLS-mScarlet
DAPI
NLS-mScarlet DAPI
C57BL/6J
B-hTFR1

FIG 22A

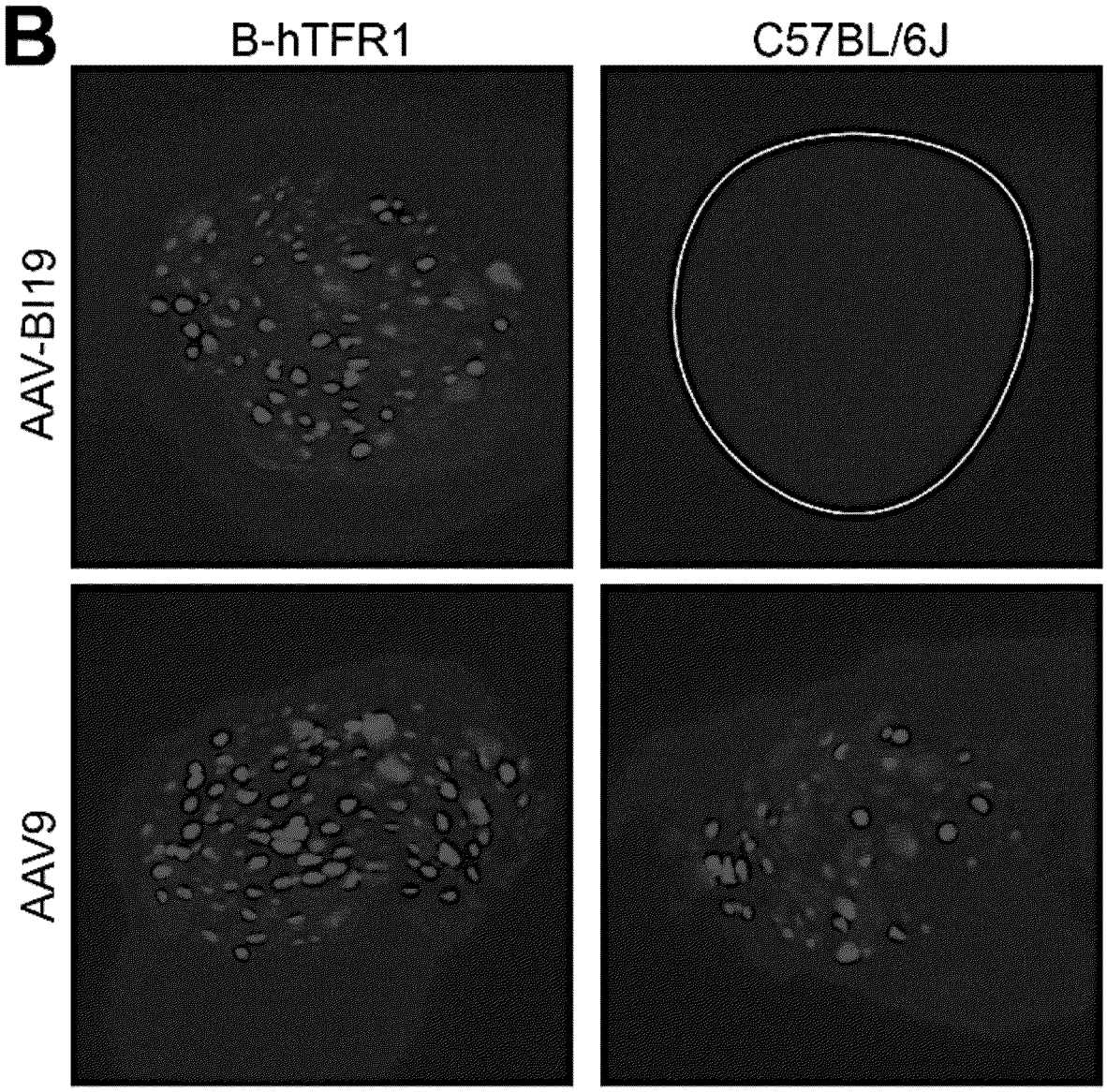


FIG. 22B

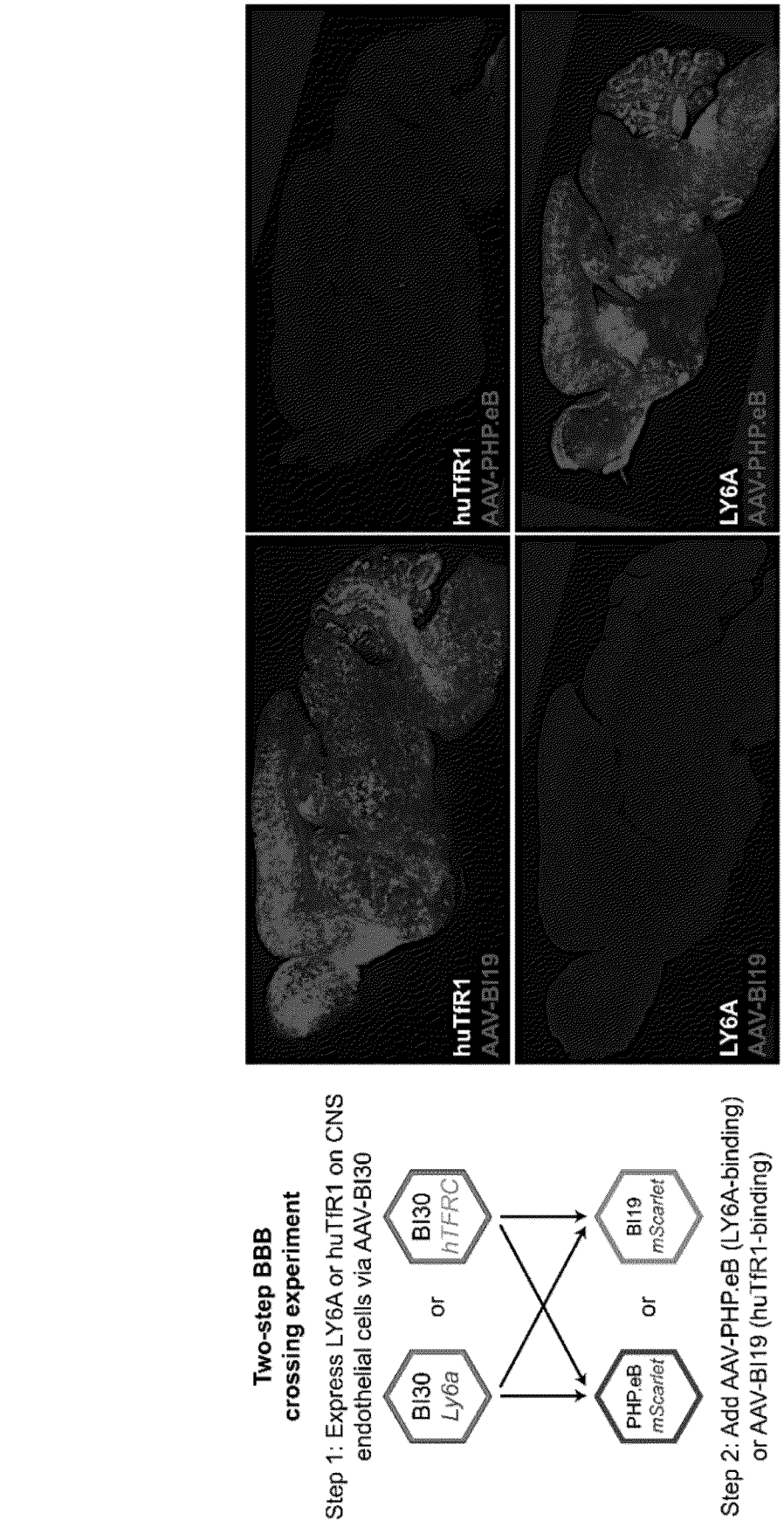
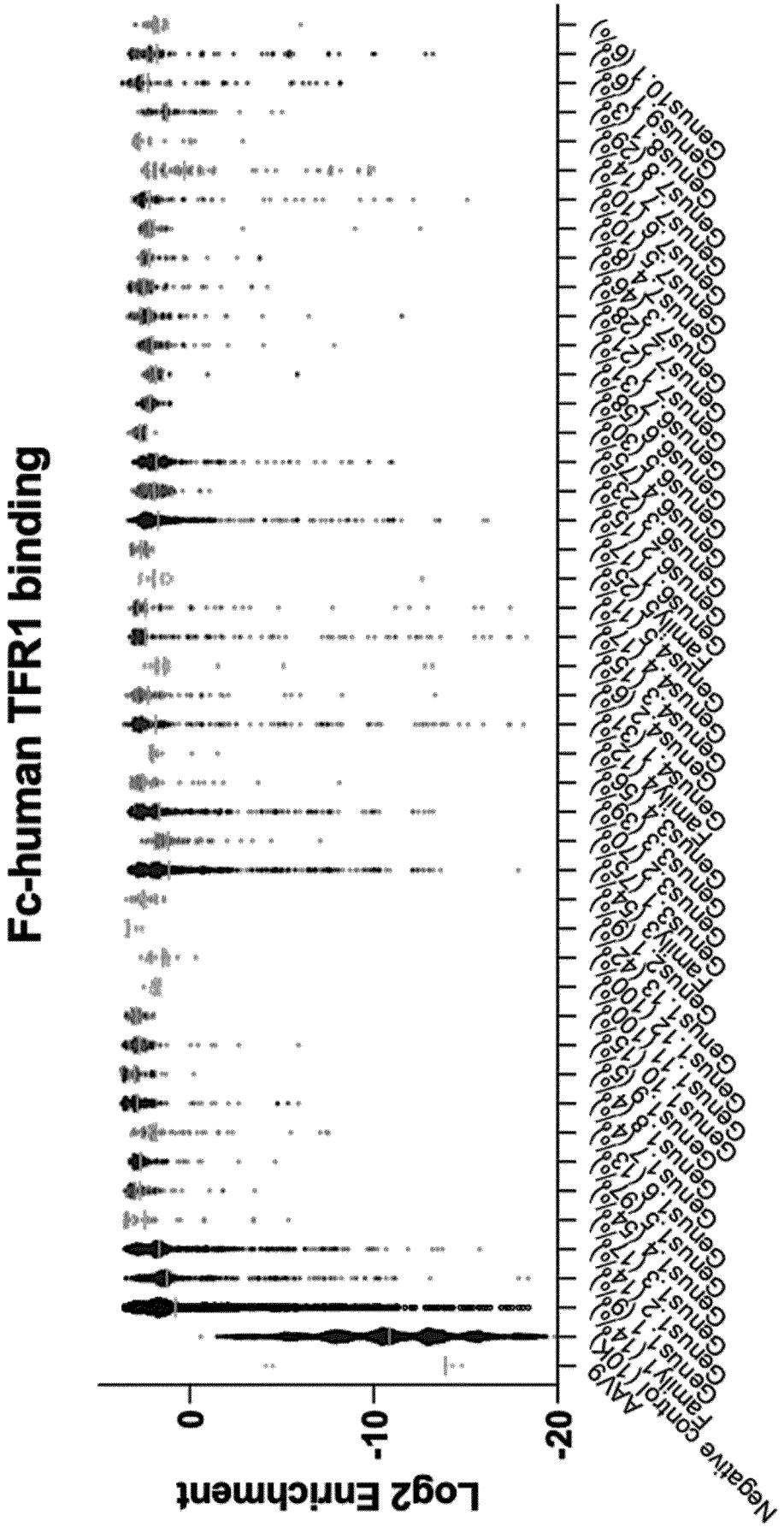

Two-step BBB crossing experiment
Step 1: Express LY6A or huTfR1 on CNS endothelial cells via AAV-BI30
BI30 Ly6a
or
BI30 hTFRC
PHP.eB mScarlet
or
BI19 mScarlet
Step 2: Add AAV-PHP.eB (LY6A-binding) or AAV-BI19 (huTfR1-binding)
huTfR1 AAV-BI19
huTfR1 AAV-PHP.eB
LY6A AAV-BI19
LY6A AAV-PHP.eB

FIG. 23


Fc-human TFR1 binding
Log2 Enrichment
0
-10
-20
Negative control
AAV9
Family1.7(14%)
Genus1.1(74%)
Genus1.2(74%)
Genus1.3(74%)
Genus1.4(53%)
Genus1.6(97%)
Genus1.7(13%)
Genus1.8(94%)
Genus1.9(53%)
Genus1.10(53%)
Genus1.11(53%)
Genus1.12(100%)
Genus1.13(100%)
Family2.1(42%)
Family3.1(54%)
Genus3.1(53%)
Genus3.2(53%)
Genus3.3(70%)
Family4.1(39%)
Genus4.1(37%)
Genus4.2(37%)
Genus4.3(37%)
Genus4.4(53%)
Family5.1(53%)
Genus5.1(53%)
Genus5.2(53%)
Genus5.3(53%)
Genus5.4(53%)
Genus5.5(53%)
Genus5.6(53%)
Genus5.7(53%)
Genus5.8(53%)
Genus5.9(53%)
Genus5.10(53%)
Genus5.11(53%)
Genus5.12(53%)
Genus5.13(53%)
Genus5.14(53%)
Genus5.15(53%)
Genus5.16(53%)
Genus5.17(53%)
Genus5.18(53%)
Genus5.19(53%)
Genus5.20(53%)
Genus5.21(53%)
Genus5.22(53%)
Genus5.23(53%)
Genus5.24(53%)
Genus5.25(53%)
Genus5.26(53%)
Genus5.27(53%)
Genus5.28(53%)
Genus5.29(53%)
Genus5.30(53%)
Genus5.31(53%)
Genus5.32(53%)
Genus5.33(53%)
Genus5.34(53%)
Genus5.35(53%)
Genus5.36(53%)
Genus5.37(53%)
Genus5.38(53%)
Genus5.39(53%)
Genus5.40(53%)
Genus5.41(53%)
Genus5.42(53%)
Genus5.43(53%)
Genus5.44(53%)
Genus5.45(53%)
Genus5.46(53%)
Genus5.47(53%)
Genus5.48(53%)
Genus5.49(53%)

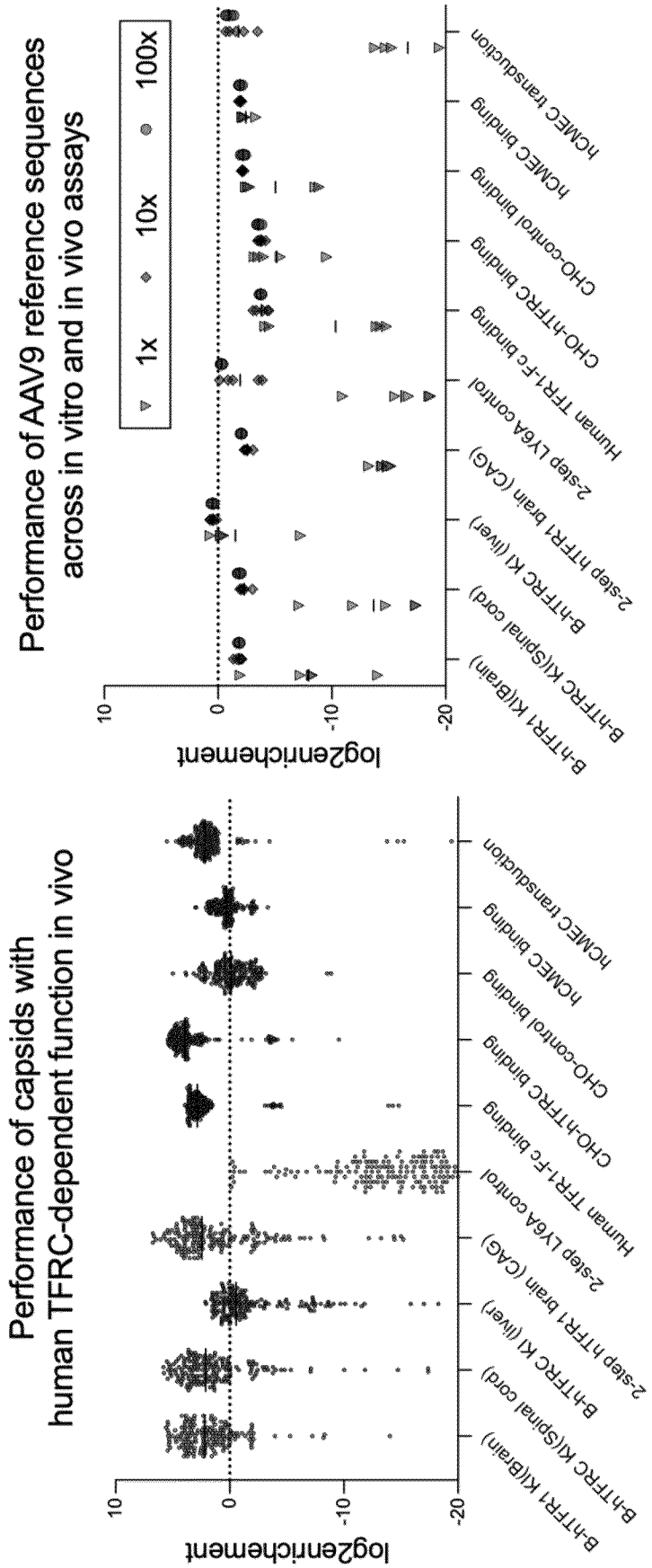

Performance of AAV9 reference sequences
across in vitro and in vivo assays
1x
10x
100x
log2enrichement
10
0
-10
-20
B-hTFR1 KI(Brain)
B-hTFRC KI(Spinal cord)
B-hTFRC KI (liver)
2-step hTFR1 brain (CAG)
2-step LY6A control
Human TFR1-Fc binding
CHO-hTFRC binding
CHO-control binding
hCMEC binding
hCMEC transduction
Performance of capsids with
human TFRC-dependent function in vivo
log2enrichement
10
0
-10
-20
B-hTFR1 KI(Brain)
B-hTFRC KI(Spinal cord)
B-hTFRC KI (liver)
2-step hTFR1 brain (CAG)
2-step LY6A control
Human TFR1-Fc binding
CHO-hTFRC binding
CHO-control binding
hCMEC binding
hCMEC transduction

FIG. 25