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DESCRIPTION

FIELD OF THE INVENTION

[0001] The present invention relates generally to a method of screening for the onset, predisposition to the onset and/or progression of a neoplasm. More particularly, the present invention relates to a method of screening for the onset, predisposition to the onset and/or progression of a neoplasm by screening for changes to the methylation levels of a panel of gene markers. The method of the present invention is useful in a range of applications including, but not limited to, those relating to the diagnosis and/or monitoring of colorectal neoplasms, such as colorectal adenocarcinosis.

BACKGROUND OF THE INVENTION

[0002] Colorectal cancer includes cancerous growths in the colon, rectum and appendix. With 655,000 deaths worldwide per year, it is the fourth most common form of cancer in the United States and the third leading cause of cancer-related death in the Western world. Colorectal cancers arise from adenomatous polyps in the colon. These mushroom-shaped growths are usually benign, but some develop into cancer over time. Localized colon cancer is usually diagnosed through colonoscopy.

[0003] Invasive cancers that are confined within the wall of the colon (stages I and II) are curable with surgery. If untreated, they spread to regional lymph nodes (stage III), where up to 73% are curable by surgery and chemotherapy. Cancer that metastasizes to distant sites (stage IV) is usually not curable, although chemotherapy can extend survival, and in rare cases, surgery and chemotherapy together have seen patients through to a cure (Markowitz and Bertagnolli, 2009, N. Engl. J. Med. 361(25): 2449-60). Radiation is used with rectal cancer.

[0004] Colorectal cancer is preceded by adenomas. Adenomas are benign tumours, or neoplasms, of epithelial origin which are derived from glandular tissue or exhibit clearly defined glandular structures. Some adenomas show recognisable tissue elements, such as fibrous tissue (fibroadenomas) and epithelial structure, while others, such as bronchial adenomas, produce active compounds that might give rise to clinical syndromes.

[0005] Adenomas may progress to become an invasive neoplasm and are then termed adenocarcinomas. Accordingly, adenocarcinomas are defined as malignant epithelial tumours arising from glandular structures, which are constituent parts of many organs of the body. The term adenocarcinoma is also applied to tumours showing a glandular growth pattern. These tumours may be sub-classified according to the substances that they produce, for example mucus secreting and serous adenocarcinomas, or to the microscopic arrangement of their cells into patterns, for example papillary and follicular adenocarcinomas. These carcinomas may be solid or cystic (cystadenocarcinomas). Each organ may produce tumours showing a variety of histological types, for example the ovary may produce both mucinous and cystadenocarcinoma.

[0006] Adenomas in different organs behave differently. In general, the overall chance of carcinoma being present within an adenoma (i.e. a focus of cancer having developed within a benign lesion) is approximately 5%. However, this is related to size of an adenoma. For instance, in the large bowel (colon and rectum specifically) occurrence of a cancer within an adenoma is rare in adenomas of less than 1 centimetre. Such a development is estimated at 40 to 50% in adenomas which are greater than 4 centimetres and show certain histopathological change such as villous change, or high grade dysplasia. Adenomas with higher degrees of dysplasia have a higher incidence of carcinoma. In any given colorectal adenoma, the predictors of the presence of cancer now or the future occurrence of cancer in the organ include size (especially greater than 9mm) degree of change from tubular to villous morphology, presence of high grade dysplasia and the morphological change described as "serrated adenoma". In any given individual, the additional features of increasing age, familial occurrence of colorectal adenoma or cancer, male gender or multiplicity of adenomas, predict a future increased risk for cancer in the organ - so-called risk factors for cancer. Except for the presence of adenomas and its size, none of these is objectively defined and all those other than number and size are subject to observer error and to confusion as to precise definition of the feature in question. Because such factors can be difficult to assess and define, their value as predictors of current or future risk for cancer is imprecise.

[0007] Once a sporadic adenoma has developed, the chance of a new adenoma occurring is approximately 30% within 26 months.

[0008] The symptoms of colorectal cancer depend on the location of tumor in the bowel, and whether is has metastasised. Unfortunately, many of the symptoms may occur in other diseases as well, and hence symptoms may not be conclusively diagnostic of colorectal cancer.

[0009] Local symptoms are more likely if the tumor is located closer to the anus. There may be a change in bowel habit (new-onset constipation or diarrhea in the absence of another cause), a feeling of incomplete defecation and reduction in diameter of stools. Tenesmus and change in stool shape are both characteristic of rectal cancer. Lower gastrointestinal bleeding, including the passage of bright red blood in the stool, may indicate colorectal cancer, as may the increased presence of mucus. Melena, black stool with a tarry appearance, normally occurs in upper gastrointestinal bleeding (such as from a duodenal ulcer), but is sometimes encountered in colorectal cancer when the disease is located in the beginning of the large bowl.

[0010] A tumor that is large enough to fill the entire lumen of the bowel may cause bowel obstruction. This situation is characterized by constipation, abdominal pain, abdominal distension and vomiting. This occasionally leads to the obstructed and distended bowel perforating and causing peritonitis.

[0011] Certain local effects of colorectal cancer occur when the disease has become more advanced. A large tumor is more likely to be noticed on feeling the abdomen, and it may be noticed by a doctor on physical examination. The disease may invade other organs, and may cause blood or air in the urine or vaginal discharge.

[0012] If a tumor has caused chronic occult bleeding, iron deficiency anaemia may occur. This may be experienced as fatigue, palpitations and noticed as pallor. Colorectal cancer may also lead to weight loss, generally due to a decreased appetite.

[0013] More unusual constitutional symptoms are an unexplained fever and one of several paraneoplastic syndromes. The most common paraneoplastic syndrome is thrombosis, usually deep vein thrombosis.

[0014] Colorectal cancer most commonly spreads to the liver. This may go unnoticed, but large deposits in the liver may cause jaundice and abdominal pain (due to stretching of the capsule). If the tumor deposit obstructs the bile duct, the jaundice may be accompanied by other features of biliary obstruction, such as pale stools.

[0015] Colorectal cancer can take many years to develop and early detection of colorectal cancer greatly improves the prognosis. Even modest efforts to implement colorectal cancer screening methods can result in a drop in cancer deaths. Despite this, colorectal cancer screening rates remain low. There are currently several different tests available for this purpose:

- Digital rectal exam: The doctor inserts a lubricated, gloved finger into the rectum to feel for abnormal areas. It only detects tumors large enough to be felt in the distal part of the rectum but is useful as an initial screening test.
- Faecal occult blood test: a test for blood in the stool. Two types of tests can be used for detecting occult blood in stools i.e. guaiac based (chemical test) and immunochemical. The sensitivity of immunochemical testing is superior to that of chemical testing without an unacceptable reduction in specificity (Weitzel JN (December 1999). "Genetic cancer risk assessment. Putting it all together". Cancer 86 (11 Suppl): 2483-92).

- Endoscopy:

  - Sigmoidoscopy: A lit probe (sigmoidoscope) is inserted into the rectum and lower colon to check for polyps and other abnormalities.

  - Colonoscopy: A lit probe called a colonoscope is inserted into the rectum and the entire colon to look for polyps and other abnormalities that may be caused by cancer. A colonoscopy has the advantage that if polyps are found during the procedure they can be removed immediately. Tissue can also be taken for biopsy.

- Double contrast barium enema (DCBE): First, an overnight preparation is taken to cleanse the colon. An enema containing barium sulfate is administered, then air is insufflated into the colon, distending it. The result is a thin layer of barium over the inner lining of the colon which is visible on X-ray films. A cancer or a precancerous polyp can be detected this way. This technique can miss the (less common) flat polyp.
- Virtual colonoscopy replaces X-ray films in the double contrast barium enema (above) with a special computed tomography scan and requires special workstation software in order for the radiologist to interpret. This technique is approaching colonoscopy in sensitivity for polyps. However, any polyps found must still be removed by standard colonoscopy.
- Standard computed axial tomography is an x-ray method that can be used to determine the degree of spread of cancer, but is not sensitive enough to use for screening. Some cancers are found in CAT scans performed for other reasons.
- Blood tests: Measurement of the patient's blood for elevated levels of certain proteins can give an indication of tumor load. In particular, high levels of carcinoembryonic antigen (CEA) in the blood can indicate metastasis of adenocarcinoma. While these tests are frequently false positive or false negative, and are not recommended for screening, they can be useful to assess disease recurrence. CA19-9 and CA 242 biomarkers can indicate e-selectin related metastatic risks, help follow therapeutic progress, and assess disease recurrence. Recently, an assay for detection in plasma of methylated sequences of the Septin 9 gene has also become available to assist in diagnosis of colorectal cancer.
- Positron emission tomography (PET) is a 3-dimensional scanning technology where a radioactive sugar is injected into the patient, the sugar collects in tissues with high metabolic activity, and an image is formed by measuring the emission of radiation from the sugar. Because cancer cells often have very high metabolic rates, this can be used to differentiate benign and malignant tumors. PET is not used for screening and does not (yet) have a place in routine workup of colorectal cancer cases.
- Stool DNA testing is an emerging technology in screening for colorectal cancer. Premalignant adenomas and cancers shed DNA markers from their cells which are not degraded during the digestive process and remain stable in the stool. Capture, followed by PCR amplifies the DNA to detectable levels for assay.
- High C-Reactive Protein levels as risk marker

[0016] Despite the existence of these tests, diagnosis remains problematic. Most of the more sensitive tests are quite invasive and expensive and therefore uptake by patients is low. There is therefore an ongoing need to develop simpler and more informative diagnostic protocols or aids to diagnosis that enable one to direct colonoscopy at people more likely to have developed adenomas or carcinomas. A simple and accurate screening test would enable much more widely applicable screening systems to be set up.

[0017] To this end, more recently there have been identified genetic markers which are modulated, in terms of their expression levels, in individuals who have developed a neoplasm of the large intestine. Some of these markers are upregulated in terms of their level of expression, while others are downregulated. However, a feature common to most of these markers, and the use of genetic marker expression levels in general as a diagnostic, is that they often exhibit only moderate levels of sensitivity and specificity. The development of diagnostic protocols which provide high levels of sensitivity and specificity is highly sought after.

[0018] In work leading up to the present invention, it has been unexpectedly determined that the gene markers BCAT1, IKZF1 IRF4, GRASP and CAHM, although each individually being one of a number of gene markers known to exhibit utility in terms of diagnosing colorectal neoplasia development, have in fact been determined to collectively enable a significantly higher level of sensitivity or specificity to be achieved than where any one of these gene markers is analysed either alone or together with other unrelated gene markers. More specifically, screening for an increase in the level of methylation of any two or more of these five specific markers can be designed so as to achieve a level of specificity or sensitivity not previously achievable.

[0019] Bearing in mind the large number of gene markers which, in differential gene expression analysis studies, have been shown to exhibit modulated expression levels in neoplasia, the identification that five specific markers can in fact collectively provide improved diagnostic outcomes relative either to these markers individually or to other groups of markers is both unexpected and unpredictable

[0020] WO 2012/034170 A1 discloses nucleic acid molecules in respect of which changes to DNA methylation levels are indicative of the onset or predisposition to the onset of a neoplasm. More particularly, WO 2012/034170 A1 discloses nucleic acid molecules in respect of which changes to DNA methylation levels arc indicative of the onset and/or progression of a large intestine neoplasm, such as an adenoma or adenocarcinoma. WO 2012/034170 A1 also discloses a method of screening for the onset, predisposition to the onset and/or progression of a neoplasm by screening for modulation in DNA methylation of one or more nucleic acid molecules.

SUMMARY OF THE INVENTION

[0021] Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" and "comprising", will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integers or steps.

[0022] As used herein, the term "derived from" shall be taken to indicate that a particular integer or group of integers has originated from the species specified, but has not necessarily been obtained directly from the specified source. Further, as used herein the singular forms of "a", "and" and "the" include plural referents unless the context clearly dictates otherwise.

[0023] Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs.

[0024] The subject specification contains nucleotide sequence information prepared using the programme PatentIn Version 3.5, presented herein after the bibliography. Each nucleotide sequence is identified in the sequence listing by the numeric indicator <210> followed by the sequence identifier (e.g. <210>1, <210>2, etc). The length, type of sequence (DNA, etc) and source organism for each sequence is indicated by information provided in the numeric indicator fields <211>, <212> and <213>, respectively. Nucleotide sequences referred to in the specification are identified by the indicator SEQ ID NO: followed by the sequence identifier (e.g. SEQ ID NO:1, SEQ ID NO:2, etc.). The sequence identifier referred to in the specification correlates to the information provided in numeric indicator field <400> in the sequence listing, which is followed by the sequence identifier (e.g. <400>1, <400>2, etc). That is SEQ ID NO:1 as detailed in the specification correlates to the sequence indicated as <400>1 in the sequence listing.

[0025] Described herein is a method of screening for the onset or predisposition to the onset of or monitoring a large intestine neoplasm in an individual, said method comprising assessing the methylation status of a DNA region selected from:
(i) the region, including 2kb upstream of the transcription start site, defined by any two or more of Hg19 coordinates:

1. (1) chr12:24962958..25102393
2. (2) chr7:50344378...50472798
3. (3) chr6:391739..411443;
4. (4) chr12:52400748..52409671; and
5. (5) chr6:163834097..163834982; or

(ii) the gene region, including 2kb upstream of any two or more of:

(1) BCAT1	(2) IKZF1	(3) IRF4	(4) GRASP and	(5) CAHM

in a biological sample from said individual wherein a higher level of methylation of at least one of the DNA regions of group (i) and/or (ii) relative to control levels is indicative of a large intestine neoplasm or a predisposition to the onset of a large intestine neoplastic state One aspect of the present invention is directed to a method of screening for the onset or predisposition to the onset of or monitoring a large intestine neoplasm in an individual, said method comprising assessing the methylation status of: the gene region, including 2kb upstream of: (2) IKZF1; in combination with one or more of the following gene regions, including 2 kb upstream of: (1) BCAT1; (3) IRF4; (4) GRASP; and (5) CAHM

[0026] In another aspect said method is directed to identifying biological samples in which any one of said DNA regions exhibits a higher level of methylation.

[0027] In still another aspect said method is directed to identifying biological samples in which two or more of said DNA regions exhibit a higher level of methylation.

[0028] In yet another aspect there is provided a method of screening for the onset or predisposition to the onset of or monitoring a large intestine neoplasm in an individual, said method comprising assessing the methylation status of:

the gene region, including 2kb upstream of:

1. (1) BCAT1; and
2. (2) IKZF1;

and optionally one or more of (3) IRF4, (4) GRASP and (5) CAHM

in a biological sample from said individual wherein a higher level of methylation of at least one of the DNA regions of group (i) and/or (ii) relative to control levels is indicative of a large intestine neoplasm or a predisposition to the onset of a large intestine neoplastic state.

[0029] In one embodiment of this aspect, the gene marker panel which is screened for is:
the gene region, including 2kb upstream of:
(1) BCAT1, (2) IKZF1 and (3) IRF4.

[0030] In another embodiment of this aspect, the gene marker panel which is screened for is:
the gene region, including 2kb upstream of:
(1) BCAT1, (2) IKZF1; and (4) GRASP.

[0031] In still another embodiment of this aspect, the gene marker panel which is screened for is:
the gene region, including 2kb upstream of:

(1) BCAT1, (2) IKZF1 and (5) CAHM

[0032] In still yet another embodiment of this aspect, the gene marker panel which is screened for is the gene region, including 2kb upstream of:
(1) BCAT1, (2) IKZF1, (3) IRF4 and (4) GRASP.

[0033] In yet still another embodiment of this aspect, the gene marker panel which is screened for is
the gene region, including 2kb upstream of:
(1) BCAT1, (2) IKZF1, (3) IRF4 and (5) CAHM. In a further embodiment of this aspect, the gene marker panel which is screened for is:
gene region, including 2kb upstream of:
(1) BCAT1, (2) IKZF1, (4) GRASP and (5) CAHM.

[0034] In yet another further embodiment of this aspect, the gene marker panel which is screened for is:
the gene region, including 2kb upstream of:
(1) BCAT1, (2) IKZF1, (3) IRF4, (4) GRASP and (5) CAHM.

[0035] In still another embodiment there is provided a method of screening for the onset or predisposition to the onset of or monitoring a large intestine neoplasm in an individual, said method comprising assessing the methylation status of:
the gene region, including 2kb upstream of:

(2) IKZF1; and

(5) CAHM;

and optionally one or more of (1) BCAT1, (3) IRF4 and (4) GRASP
in a biological sample from said individual wherein a higher level of methylation of at least one of the DNA regions of group (i) and/or (ii) relative to control levels is indicative of a large intestine neoplasm or a predisposition to the onset of a large intestine neoplastic state.

[0036] In still another further embodiment there is provided a method of screening for the onset or predisposition to the onset of or monitoring a large intestine neoplasm in an individual, said method comprising assessing the methylation status of:
the gene region, including 2kb upstream of:

(2) IKZF1; and

(3) IRF4;

and optionally one or more of (1) BCAT1, (4) GRASP and (5) CAHM
in a biological sample from said individual wherein a higher level of methylation of at least one of the DNA regions of group (i) and/or (ii) relative to control levels is indicative of a large intestine neoplasm or a predisposition to the onset of a large intestine neoplastic state.

[0037] In yet still another embodiment there is provided a method of screening for the onset or predisposition to the onset of or monitoring a large intestine neoplasm in an individual, said method comprising assessing the methylation status of:
the gene region, including 2kb upstream of:

(2) IKZF1; and

(4) GRASP;

and optionally one or more of (1) BCAT1, (3) IRF4 and (5) CAHM
in a biological sample from said individual wherein a higher level of methylation of at least one of the DNA regions of group (i) and/or (ii) relative to control levels is indicative of a large intestine neoplasm or a predisposition to the onset of a large intestine neoplastic state.

[0038] The subregions which have been determined to exhibit particular utility are listed below with reference to the gene and chromosomal region within which they are found:

1. (1) BCAT subregions chr12:25101992-25102093 (SEQ ID NO:1 or corresponding minus strand) and chr12:25101909-25101995 (SEQ ID NO:2 or corresponding minus strand)
2. (2) IKZF1 subregions: chr7:50343867-50343961 (SEQ ID NO:3 or corresponding minus strand) and chr7:50343804-5033895 (SEQ ID NO:4 or corresponding minus strand)
3. (3) IRF4 subregions chr6:392036-392145 (SEQ ID NO:5 or corresponding minus strand)
4. (4) GRASP subregions: chr12:52399672-52399922, chr12:52400821-52401051 (SEQ ID NO:6 or corresponding minus strand), chr12:52401407-52401664 (SEQ ID NO:7 or corresponding minus strand) chr12:52400866-52400973 and Chr12:52401107-52401664.
5. (5) CAHM subregions: chr6:163834295-163834500 (SEQ ID NO:8 or corresponding minus strand), chr6:163834621-163834906, chr6:163834393-163834455 and chr6:163834393-163834519.

[0039] To the extent that the method of the present invention includes analysing the methylation of GRASP, the subject residues are:

chr12:52399713	chr12:52399731	chr12:52399749	chr12:52399783
chr12:52399796	chr12:52399808	chr12:52399823	chr12:52399835
chr12:52399891			
chr12:52400847	chr12:52400850	chr12:52400859	chr12:52400866
chr12:52400869	chr12:52400873	chr12:52400881	chr12:52400886

chr12:52400893	chr12:52400895	chr12:52400899	chr12:52400902
chr12:52400907	chr12:52400913	chr12:52400919	chr12:52400932
chr12:52400938	chr12:52400958	chr12:52400962	chr12:52400971
chr12:52400973	chr12:52400976	chr12:52400998	chr12:52401008
chr12:52401010	chr12:52401012	chr12:52401016	chr12:52401019
chr12:52401025	chr12:52401041	chr12:52401044	chr12:52401053
chr12:52401060	chr12:52401064	chr12:52401092	chr12:52401118
chr12:52401438	chr12:52401448	chr12:52401460	chr12:52401465
chr12:52401474	chr12:52401477	chr12:52401479	chr12:52401483
chr12:52401504	chr12:52401514	chr12:52401523	chr12:52401540
chr12:52401553	chr12:52401576	chr12:52401588	chr12:52401595
chr12:52401599	chr12:52401604	chr12:52401606	chr12:52401634
chr12:52401640	chr12:52401644	chr12:52401659	
chr12:52401160	chr12:52401165	chr12:52401174	chr12:52401177
chr12:52401179	chr12:52401183	chr12:52401204	chr12:52401215
chr12:52401223	chr12:52401240	chr12:52401253	chr12:52401288
chr12:52401295	chr12:52401299	chr12:52401304	chr12:52401334
chr12:52401340	chr12:52401344	chr12:52401359	

or a corresponding cytosine at position n+1 on the opposite DNA strand.

[0040] To the extent that the method of the present invention includes analysing CAHM, the subject residues are:

chr6:163834330	chr6:163834332	chr6:163834357
chr6:163834373	chr6:163834384	chr6:163834390
chr6:163834392	chr6:163834406	chr6:163834412
chr6:163834419	chr6:163834443	chr6:163834448
chr6:163834452	chr6:163834464	chr6:163834483
chr6:163834653	chr6:163834660	chr6:163834672
chr6:163834675	chr6:163834678	chr6:163834681
chr6:163834815	chr6:163834824	chr6:163834835
chr6:163834840	chr6:163834853	chr6:163834855
chr6:163834858	chr6:163834863	chr6:163834869
chr6:163834872		

or a corresponding cytosine at position n+1 on the opposite DNA strand.

[0041] To the extent that the method of the present invention includes analysing IKZF1, the subject residues are:

chr7:50343869	chr7:50343872	chr7:50343883
chr7:50343889	chr7:50343890	chr7:50343897
chr7:50343907	chr7:50343909	chr7:50343914
chr7:50343934	chr7:50343939	chr7:50343950
chr7:50343959	chr7:50343805	chr7:50343822
chr7:50343824	chr7:50343826	chr7:50343829
chr7:50343831	chr7:50343833	chr7:50343838
chr7:50343847	chr7:50343850	chr7:50343858
chr7:50343864	chr7:50343869	chr7:50343872
chr7:50343890		

or a corresponding cytosine at position n+1 on the opposite DNA strand.

[0042] To the extent that the method of the present invention includes analysing IRF4, the subject residues are:

chr6:392036	chr6:392047	chr6:392049
chr6:392057	chr6:392060	chr6:392066
chr6:392080	chr6:392094	chr6:392102
chr6:392131		

or a corresponding cytosine at position n+1 on the opposite DNA strand.

[0043] There is also described herein a method of screening for the onset or predisposition to the onset of or monitoring a large intestine neoplasm in an individual, said method comprising assessing the level of expression of a DNA region selected from:

(i) the region, including 2kb upstream of the transcription start site, defined by any two or more of Hg19 coordinates:

1. (1) chr12:24962958..25102393
2. (2) chr7:50344378...50472798
3. (3) chr6:391739..411443; or
4. (4) chr12:52400748..52409671; and
5. (5) chr6:163834097..163834982; or

(ii) the gene region, including 2kb upstream of any two or more of:

(1) BCAT1	(2) IKZF1	(3) IRF4	(4) GRASP and	(5) CAHM

in a biological sample from said individual wherein a lower level of expression of at least one of the DNA regions of group (i) and/or (ii) relative to control levels is indicative of a large intestine neoplasm or a predisposition to the onset of a neoplastic state.

BRIEF DESCRIPTION OF THE DRAWINGS

[0044]

Figure 1 depicts the genomic sequence of GRASP.

Figure 2 depicts the genomic sequence of CAHM.

Figure 3 depicts the genomic sequence of IRF4.

Figure 4 depicts the genomic sequence of BCAT1.

Figure 5 depicts the genomic sequence of IKZF1.

DETAILED DESCRIPTION OF THE INVENTION

[0045] The present invention is predicated, in part, on the determination that the change in methylation pattern of a panel of gene markers can provide a higher level of either diagnostic specificity or diagnostic sensitivity when tested collectively than if any one of these markers is tested either in isolation or together with markers other than those specified herein. This finding has therefore now facilitated the development of an improved test for diagnosing, prognosing or monitoring neoplasms of the large intestine based on assessing the methylation of two or more of the gene markers BCAT1, IKZF1, CAHM, GRASP and IRF4.

[0046] In accordance with the present invention, it has been determined that certain specific panels of genes are modulated, in terms of differential changes to their levels of methylation, depending on whether or not the cell in issue is neoplastic or not. It should be understood that the genes in issue are described herein both by reference to their name and their chromosomal coordinates. The chromosomal coordinates are consistent with the human genome database version Hg19 which was released in February 2009 (herein referred to as "Hg19 coordinates").

[0047] Accordingly, one aspect of the present invention is directed to a method of screening for the onset or predisposition to the onset of or monitoring a large intestine neoplasm in an individual, said method comprising assessing the methylation status of the gene region, including 2kb upstream of: (2) IKZF1; in combination with one or more of the following gene regions, including 2 kb upstream of: (1) BCAT1; (3) IRF4; (4) GRASP; and (5) CAHM in a biological sample from said individual wherein a higher level of methylation of at least one of the DNA regions of group (i) and/or (ii) relative to control levels is indicative of a large intestine neoplasm or a predisposition to the onset of a large intestine neoplastic state.

[0048] In one embodiment, said method is directed to identifying biological samples in which any one of said DNA regions exhibits a higher level of methylation.

[0049] In another embodiment, said method is directed to identifying biological samples in which two or more of said DNA regions exhibit a higher level of methylation.

[0050] Without limiting the present invention to any one theory or mode of action, the panel of DNA regions (markers) specified herein provide not only an improved diagnostic outcome relative to prior art methods but, in addition, enable the development of a screening method which can be designed to focus on providing either a high level of diagnostic specificity or a high level of diagnostic sensitivity. As would be understood by the person of skill in the art, in the context of diagnostics "sensitivity" defines the proportion of positive results which are correctly identified, that is, the percentage of individuals correctly identified as having the disease in issue. "Specificity", however, defines the proportion of negative results which are correctly identified, that is, the percentage of individuals correctly identified as not having the disease in issue.

[0051] In the context of the present invention it has been determined that screening a patient sample for the methylation status of the specified panel of markers can be designed to provide either a diagnostic result which exhibits a high level of specificity or a diagnostic result which exhibits a high level of sensitivity.

[0052] Where a high level of sensitivity is sought, the screening method is designed to identify samples in which any one of the markers of the panel exhibits increased methylation relative to control levels. That is, not all of the markers are required to exhibit hypermethylation in order to define the result as positive. Where a higher level of sensitivity is sought, the level of specificity is inherently reduced. However, if it is desired to pursue a higher level of specificity (which may reduce the level of sensitivity) then the method is designed to identify samples in which two or more of the panel of DNA regions exhibit increased methylation.

[0053] Accordingly, to the extent that the present invention is directed to embodiments of the method in which "any one of" the DNA regions (markers) of the specified panel exhibits a higher level of methylation, these embodiments are designed to achieve results exhibiting increased sensitivity based on any one of the markers in the panel being hypermethylated. It should be understood that it need not be the same marker which is hypermethylated in each sample. Rather, it is simply that one of the markers which forms part of the panel is hypermethylated. It should also be understood that in relation to some samples, two or more of the markers of the panel may be hypermethylated. These samples should be understood to nevertheless fall within the scope of this embodiment of the invention since this embodiment is not excluding the situation where multiple markers are hypermethylated but is merely including within its scope all those samples where as few as one marker are hypermethylated. Overall these data will provide increased sensitivity but reduced specificity.

[0054] To the extent that the present invention is directed to embodiments of the method in which "two or more" of the DNA regions (markers) of the specified panel exhibit a higher level of methylation, these embodiments are designed to achieve a higher level of specificity. This is achieved by virtue of the fact that at least two, if not more, of the specified panel of markers are determined to be hypermethylated.

[0055] Reference to "large intestine" should be understood as a reference to a cell derived from one of the eight anatomical regions of the large intestine, which regions commence after the terminal region of the ileum, these being:

1. (i) the cecum;
2. (ii) the ascending colon;
3. (iii) the transverse colon;
4. (iv) the descending colon;
5. (v) the sigmoid colon;
6. (vi) the rectum;
7. (vii) the splenic flexure; and
8. (viii) the hepatic flexure.

[0056] Reference to "neoplasm" should be understood as a reference to a lesion, tumour or other encapsulated or unencapsulated mass or other form of growth which comprises neoplastic cells. A "neoplastic cell" should be understood as a reference to a cell exhibiting abnormal growth. The term "growth" should be understood in its broadest sense and includes reference to proliferation. In this regard, an example of abnormal cell growth is the uncontrolled proliferation of a cell. Another example is failed apoptosis in a cell, thus prolonging its usual life span. The neoplastic cell may be a benign cell or a malignant cell. In a preferred embodiment, the subject neoplasm is an adenoma or an adenocarcinoma. Without limiting the present invention to any one theory or mode of action, an adenoma is generally a benign tumour of epithelial origin which is either derived from epithelial tissue or exhibits clearly defined epithelial structures. These structures may take on a glandular appearance. It can comprise a malignant cell population within the adenoma, such as occurs with the progression of a benign adenoma or benign neoplastic legion to a malignant adenocarcinoma.

[0057] Preferably, said neoplastic cell is an adenoma or adenocarcinoma and even more preferably a colorectal adenoma or adenocarcinoma.

[0058] Reference to "DNA region" should be understood as a reference to a specific section of genomic DNA. These DNA regions are specified either by reference to a gene name or a set of chromosomal coordinates. Both the gene names and the chromosomal coordinates would be well known to, and understood by, the person of skill in the art. As detailed hereinbefore, the chromosomal coordinates correspond to the Hg19 version of the genome. In general, a gene can be routinely identified by reference to its name, via which both its sequences and chromosomal location can be routinely obtained, or by reference to its chromosomal coordinates, via which both the gene name and its sequence can also be routinely obtained.

[0059] Reference to each of the genes/DNA regions detailed above should be understood as a reference to all forms of these molecules and to fragments or variants thereof. As would be appreciated by the person of skill in the art, some genes are known to exhibit allelic variation between individuals or single nucleotide polymorphisms. SNPs encompass insertions and deletions of varying size and simple sequence repeats, such as dinucleotide and trinucleotide repeats. Variants include nucleic acid sequences from the same region sharing at least 90%, 95%, 98%, 99% sequence identity i.e. having one or more deletions, additions, substitutions, inverted sequences etc. relative to the DNA regions described herein. Accordingly, the present invention should be understood to extend to such variants which, in terms of the present diagnostic applications, achieve the same outcome despite the fact that minor genetic variations between the actual nucleic acid sequences may exist between individuals. The present invention should therefore be understood to extend to all forms of DNA which arise from any other mutation, polymorphic or allelic variation.

[0060] It should be understood that the "individual" who is the subject of testing may be any human or non-human mammal. Examples of non-human mammals includes primates, livestock animals (e.g. horses, cattle, sheep, pigs, donkeys), laboratory test animals (e.g. mice, rats, rabbits, guinea pigs), companion animals (e.g. dogs, cats) and captive wild animals (e.g. deer, foxes).

[0061] Preferably the mammal is a human.

[0062] The panel of genes which has been identified demonstrates increased methylation in large intestine neoplastic cells relative to corresponding non-neoplastic cells. This increased methylation is, in some cases, localised to a few specific CpG sites within the DNA region while in other cases it is observed across a wide range of CpG sites. However, although specific regions from all genes exhibit increased methylation and are therefore useful diagnostic markers, it is the analysis of these specific markers as a panel which has provided an independent and very significant improvement over the sensitivity and specificity could be obtainable over these markers are analysed individually. This improvement is also significant even when considered against the sensitivity and specificity obtainable using other markers known to exhibit increased methylation as a marker of the onset of a large intestine neoplasm. Accordingly, the method of the present invention has now provided a means of achieving a higher level of sensitivity and specificity than has been achievable to date.

[0063] In one aspect there is provided a method of screening for the onset or predisposition to the onset of or monitoring a large intestine neoplasm in an individual, said method comprising assessing the methylation status of:

the gene region, including 2kb upstream of:

1. (1) BCAT1; and
2. (2) IKZF1;

and optionally one or more of (3) IRF4, (4) GRASP and (5) CAHM
in a biological sample from said individual wherein a higher level of methylation of at least one of the DNA regions of group (i) and/or (ii) relative to control levels is indicative of a large intestine neoplasm or a predisposition to the onset of a large intestine neoplastic state.

[0064] In one embodiment of this aspect, the gene marker panel which is screened for is:
the gene region, including 2kb upstream of:
(1) BCAT1, (2) IKZF1 and (3) IRF4.

[0065] In another embodiment of this aspect, the gene marker panel which is screened for is:
the gene region, including 2kb upstream of:
(1) BCAT1, (2) IKZF1; and (4) GRASP.

[0066] In still another embodiment of this aspect, the gene marker panel which is screened for is:
the gene region, including 2kb upstream of:
(1) BCAT1, (2) IKZF1 and (5) CAHM

[0067] In still yet another embodiment of this aspect, the gene marker panel which is screened for is:
the gene region, including 2kb upstream of:
(1) BCAT1, (2) IKZF1, (3) IRF4 and (4) GRASP.

[0068] In yet still another embodiment of this aspect, the gene marker panel which is screened for is:
the gene region, including 2kb upstream of:
(1) BCAT1, (2) IKZF1, (3) IRF4 and (5) CAHM.

[0069] In a further embodiment of this aspect, the gene marker panel which is screened for is:
the gene region, including 2kb upstream of:
(1) BCAT1, (2) IKZF1, (4) GRASP and (5) CAHM.

[0070] In yet another further embodiment of this aspect, the gene marker panel which is screened for is:
the gene region, including 2kb upstream of:
(1) BCAT1, (2) IKZF1, (3) IRF4, (4) GRASP and (5) CAHM.

[0071] In still another embodiment there is provided a method of screening for the onset or predisposition to the onset of or monitoring a large intestine neoplasm in an individual, said method comprising assessing the methylation status of:
the gene region, including 2kb upstream of:

(2) IKZF1; and

(5) CAHM;

and optionally one or more of (1) BCAT1, (3) IRF4 and (4) GRASP
in a biological sample from said individual wherein a higher level of methylation of at least one of the DNA regions of group (i) and/or (ii) relative to control levels is indicative of a large intestine neoplasm or a predisposition to the onset of a large intestine neoplastic state.

[0072] In still another further embodiment there is provided a method of screening for the onset or predisposition to the onset of or monitoring a large intestine neoplasm in an individual, said method comprising assessing the methylation status of:
the gene region, including 2kb upstream of:

(2) IKZF1; and

(3) IRF4;

and optionally one or more of (1) BCAT1, (4) GRASP and (5) CAHM
in a biological sample from said individual wherein a higher level of methylation of at least one of the DNA regions of group (i) and/or (ii) relative to control levels is indicative of a large intestine neoplasm or a predisposition to the onset of a large intestine neoplastic state.

[0073] In yet still another embodiment there is provided a method of screening for the onset or predisposition to the onset of or monitoring a large intestine neoplasm in an individual, said method comprising assessing the methylation status of:
the gene region, including 2kb upstream of:

(2) IKZF1; and

(4) GRASP;

and optionally one or more of (1) BCAT1, (3) IRF4 and (5) CAHM
in a biological sample from said individual wherein a higher level of methylation of at least one of the DNA regions of group (i) and/or (ii) relative to control levels is indicative of a large intestine neoplasm or a predisposition to the onset of a large intestine neoplastic state.

[0074] In accordance with these aspects and embodiments, in yet another embodiment said control level is a non-neoplastic level.

[0075] In one embodiment, said method is directed to identifying biological samples in which any one of said DNA regions exhibits a higher level of methylation.

[0076] In another embodiment, said method is directed to identifying biological samples in which two or more of said DNA regions exhibits a higher level of methylation.

[0077] Still further, in another embodiment, said large intestine tissue is preferably colorectal tissue.

[0078] In still another embodiment, the neoplasm is malignant, such as a carcinoma.

[0079] In a further embodiment, the neoplasm is non-malignant, such as an adenoma.

[0080] In terms of screening for the methylation of these gene regions, it should be understood that the assays can be designed to screen either the specific regions listed herein (which correspond to the "plus" strand of the gene) or the complementary "minus" strand. It is well within the skill of the person in the art to choose which strand to analyse and to target that strand based on the chromosomal coordinates provided herein. In some circumstances, assays may be established to screen both strands.

[0081] It should be understood that one may screen for the specified panel of markers exclusively or one may elect to additionally screen for other markers, such as other DNA hypermethylation markers, other RNA expression level markers or other protein markers. These other markers may, for example, provide additional information in relation to the health status of the patient in issue.

[0082] Without limiting the present invention to any one theory or mode of action, although measuring the methylation levels across these DNA regions is diagnostic of a large intestine neoplastic condition, it has been determined that discrete subregions are particularly useful in this regard since these subregions contain a high density of CpG dinucleotides which are frequently hypermethylated in large intestine neoplasias, such as colorectal cancers. This finding renders these subregions a particularly useful target for analysis since it both simplifies the screening process due to a shorter more clearly defined region of DNA requiring analysis and, further, the fact that the results from these regions will provide a significantly more definitive result in relation to the presence, or not, of hypermethylation than would be obtained if analysis was performed across the DNA region as a whole. This finding therefore both simplifies the screening process and increases the sensitivity and specificity of large intestine neoplasia diagnosis.

[0083] The subregions which have been determined to exhibit particular utility are listed below with reference to the gene and chromosomal region within which they are found:

1. (1) BCAT subregions chr12:25101992-25102093 (SEQ ID NO:1 or corresponding minus strand) and chr12:25101909-25101995 (SEQ ID NO:2 or corresponding minus strand)
2. (2) IKZF1 subregions: chr7:50343867-50343961 (SEQ ID NO:3 or corresponding minus strand) and chr7:50343804-5033895 (SEQ ID NO:4 or corresponding minus strand)
3. (3) IRF4 subregions chr6:392036-392145 (SEQ ID NO:5 or corresponding minus strand)
4. (4) GRASP subregions: chr12:52399672-52399922, chr12:52400821-52401051 (SEQ ID NO:6 or corresponding minus strand), chr12:52401407-52401664 (SEQ ID NO:7 or corresponding minus strand) chr12:52400866-52400973 and Chr12:52401107-52401664.
5. (5) CAHM subregions: chr6:163834295-163834500 (SEQ ID NO:8), chr6:163834621-163834906, chr6:163834393-163834455 and chr6:163834393-163834519.

[0084] Without limiting the present invention to any one theory or mode of action, the skilled person may screen one or more subregions for each gene marker.

[0085] In one embodiment, the methylation marker subregions tested for each selected gene marker are:

1. (1) The BCAT subregion defined by SEQ ID NO:1 or SEQ ID NO:2 or corresponding minus strand;
2. (2) The IKZF1 subregion defined by SEQ ID NO:3 or SEQ ID NO:4 or corresponding minus strand;
3. (3) The IRF4 subregion defined by SEQ ID NO:5 or corresponding minus strand;
4. (4) The GRASP subregion defined by SEQ ID NO:6 or 7 or corresponding minus strands; and
5. (5) The CAHM subregion defined by SEQ ID NO:8 or corresponding minus strand.

[0086] Without limiting the present invention to any one theory or mode of action, DNA methylation is universal in bacteria, plants, and animals. DNA methylation is a type of chemical modification of DNA that is stable over rounds of cell division but does not involve changes in the underlying DNA sequence of the organism. Chromatin and DNA modifications are two important features of epigenetics and play a role in the process of cellular differentiation, allowing cells to stably maintain different characteristics despite containing the same genomic material. In eukaryotic organisms DNA methylation occurs only at the number 5 carbon of the cytosine pyrimidine ring. In mammals, DNA methylation occurs mostly at the number 5 carbon of the cytosine of a CpG dinucleotide. CpG dinucleotides comprise approximately 1% human genome.

[0087] 70-80% of all CpGs are methylated. CpGs may be grouped in clusters called "CpG islands" that are present in the 5' regulatory regions of many genes and are frequently unmethylated. In many disease processes such as cancer, gene promoters and/or CpG islands acquire abnormal hypermethylation, which is associated with heritable transcriptional silencing. DNA methylation may impact the transcription of genes in two ways. First, the methylation of DNA may itself physically impede the binding of transcriptional proteins to the gene, thus blocking transcription. Second, methylated DNA may be bound by proteins known as Methyl-CpG-binding domain proteins (MBDs). MBD proteins then recruit additional proteins to the locus, such as histone deacetylases and other chromatin remodelling proteins that can modify histones, thereby forming compact, inactive chromatin termed silent chromatin. This link between DNA methylation and chromatin structure is very important. In particular, loss of Methyl-CpG-binding Protein 2 (MeCP2) has been implicated in Rett syndrome and Methyl-CpG binding domain protein 2 (MBD2) mediates the transcriptional silencing of hypermethylated genes in cancer.

[0088] In humans, the process of DNA methylation is carried out by three enzymes, DNA methyltransferase 1, 3a and 3b (DNMT1, DNMT3a, DNMT3b). It is thought that DNMT3a and DNMT3b are the *de novo* methyltransferases that set up DNA methylation patterns early in development. DNMT1 is the proposed maintenance methyltransferase that is responsible for copying DNA methylation patterns to the daughter strands during DNA replication. DNMT3L is a protein that is homologous to the other DNMT3s but has no catalytic activity. Instead, DNMT3L assists the *de novo* methyltransferases by increasing their ability to bind to DNA and stimulating their activity. Finally, DNMT2 has been identified as an "enigmatic" DNA methylstransferase homolog, containing all 10 sequence motifs common to all DNA methyltransferases; however, DNMT2 may not methylate DNA but instead has been shown to methylate a small RNA.

[0089] "Methylation status" should therefore be understood as a reference to the presence, absence and/or quantity of methylation at a particular nucleotide, or nucleotides, within a DNA region. The methylation status of a particular DNA sequence (e.g. DNA region as described herein) can indicate the methylation state of every base in the sequence or can indicate the methylation state of a subset of the base pairs (e.g., of cytosines or the methylation state of one or more specific restriction enzyme recognition sequences) within the sequence, or can indicate information regarding regional methylation density within the sequence without providing precise information of where in the sequence the methylation occurs. The methylation status can optionally be represented or indicated by a "methylation value." A methylation value can be generated, for example, by quantifying the amount of intact DNA present following restriction digestion with a methylation dependent restriction enzyme. In this example, if a particular sequence in the DNA is quantified using quantitative PCR, an amount of template DNA approximately equal to a mock treated control indicates the sequence is not highly methylated whereas an amount of template substantially less than occurs in the mock treated sample indicates the presence of methylated DNA at the sequence. Accordingly, a value, i.e., a methylation value, for example from the above described example, represents the methylation status and can thus be used as a quantitative indicator of the methylation status. This is of particular use when it is desirable to compare the methylation status of a sequence in a sample to a threshold value.

[0090] The method of the present invention is predicated on the comparison of the level of methylation of specific DNA regions of a biological sample with the control methylation levels of these DNA regions. The "control level" is the "normal level", which is the level of methylation of the DNA region of a corresponding large intestine cell or cellular population which is not neoplastic or in another biological sample from which DNA may be isolated for assay.

[0091] The normal (or "non-neoplastic") methylation level may be determined using non-neoplastic tissues derived from the same individual who is the subject of testing. However, it would be appreciated that this may be quite invasive for the individual concerned and it is therefore likely to be more convenient to analyse the test results relative to a standard result which reflects individual or collective results obtained from individuals other than the patient in issue. This latter form of analysis is in fact the preferred method of analysis since it enables the design of kits which require the collection and analysis of a single biological sample, being a test sample of interest. The standard results which provide the normal methylation level may be calculated by any suitable means which would be well known to the person of skill in the art. For example, a population of normal tissues can be assessed in terms of the level of methylation of the genes of the present invention, thereby providing a standard value or range of values against which all future test samples are analysed. It should also be understood that the normal level may be determined from the subjects of a specific cohort and for use with respect to test samples derived from that cohort. Accordingly, there may be determined a number of standard values or ranges which correspond to cohorts which differ in respect of characteristics such as age, gender, ethnicity or health status. Said "normal level" may be a discrete level or a range of levels. An increase in the methylation level of the subject genes relative to normal levels is indicative of the tissue being neoplastic.

[0092] The term "methylation" shall be taken to mean the presence of a methyl group added by the action of a DNA methyl transferase enzyme to a cytosine base or bases in a region of nucleic acid, e.g. genomic DNA. As described herein, there are several methods known to those skilled in the art for determining the level or degree of methylation of nucleic acid.

[0093] By "higher level" is meant that there are a higher number of methylated CpG dinucleotides in the subject diagnosed than in a control sample, that is, either the proportion of DNA molecules methylated at a particular CpG site is higher or there are a higher number of separate CpG sites methylated in the subject. It should be understood that the terms "enhanced" and "increased" are used interchangeably with the term "higher".

[0094] In relation to detecting a "higher level" of methylation, it should be understood that in some situations the normal/control level will in fact correspond to the absence of any detectable methylation while the neoplastic level will correspond to the presence of methylation, *per se.* In this situation the diagnostic method is relatively simple since one need only screen for the mere presence of methylation (i.e. a qualitative assessment only), rather than assessing the methylation levels relative to a control level of methylation, which analysis necessarily involves a measure of quantification. Without limiting the present invention in any way, it is observed in blood-derived samples, for example, that in the context of some markers the change in methylation of that marker upon the onset of neoplasia is a shift from undetectable levels of methylation to the presence of detectable methylation. In these situations a relatively simple qualitative assessment is enabled where one need only screen a test sample to determine the presence or not of methylation. In the context of the definitions provided herein, reference to "higher level" encompasses both a relative increase in the level of methylation of a marker or the onset of methylation where previously none was evident. As detailed hereinbefore, the control level may be newly assessed for each patient or there may be a standard result against which all test samples are assessed. Where it is known that methylation is not present on the marker of interest, one need only screen for the presence or not of methylation since the control level is the absence of methylation and the "higher level" is thereby the presence of any amount of methylation.

[0095] The present invention is not to be limited by a precise number of methylated residues that are considered to be diagnostic of neoplasia in a subject, because some variation between patient samples will occur. The present invention is also not limited by positioning of the methylated residue.

[0096] Nevertheless, a number of specific cytosine residues which undergo hypermethylation within these subregions have also been identified. In another embodiment, therefore, a screening method can be employed which is specifically directed to assessing the methylation status of one or more of either these residues or the corresponding cytosine at position n+1 on the opposite DNA strand.

[0097] To this end, detailed in Table 1 are the cytosine residues which have been identified in this regard. It should be appreciated by the person of skill in the art that these individual residues are numbered by reference to Hg19, which also corresponds to the numbering of the specific subregions listed hereinbefore and which can be further identified when the coordinate numbering for each subregion is applied to the corresponding subregion sequences which are provided in the sequence listing. It should be understood that these residues have been identified in the context of the subregion DNA. However, there are other residues which are hypermethylated outside the subregions themselves but within the larger DNA region from which the subregions derive. Accordingly, these specified residues represent a particularly useful subset of individual cytosine residues which undergo hypermethylation within the context of the DNA regions and subregions herein disclosed. These individual residues are grouped below according to the DNA region within which they occur. These DNA regions are identified by reference to both the Hg19 chromosomal coordinates and the gene region name.

[0098] To the extent that the method of the present invention includes analysing the methylation of GRASP, the subject residues are:

chr12:52399713	chr12:52399731	chr12:52399749	chr12:52399783
chr12:52399796	chr12:52399808	chr12:52399823	chr12:52399835
chr12:52399891			
chr12:52400847	chr12:52400850	chr12:52400859	chr12:52400866
chr12:52400869	chr12:52400873	chr12:52400881	chr12:52400886
chr12:52400893	chr12:52400895	chr12:52400899	chr12:52400902
chr12:52400907	chr12:52400913	chr12:52400919	chr12:52400932
chr12:52400938	chr12:52400958	chr12:52400962	chr12:52400971
chr12:52400973	chr12:52400976	chr12:52400998	chr12:52401008
chr12:52401010	chr12:52401012	chr12:52401016	chr12:52401019
chr12:52401025	chr12:52401041	chr12: 52401044	chr12:52401053
chr12:52401060	chr12:52401064	chr12: 52401092	chr12:52401118
chr12:52401438	chr12:52401448	chr12:52401460	chr12:52401465
chr12:52401474	chr12:52401477	chr12:52401479	chr12:52401483
chr12:52401504	chr12:52401514	chr12:52401523	chr12:52401540
chr12:52401553	chr12:52401576	chr12:52401588	chr12:52401595
chr12:52401599	chr12:52401604	chr12:52401606	chr12:52401634
chr12:52401640	chr12:52401644	chr12:52401659	
chr12:52401160	chr12:52401165	chr12:52401174	chr12:52401177
chr12:52401179	chr12:52401183	chr12:52401204	chr12:52401215
chr12:52401223	chr12:52401240	chr12:52401253	chr12:52401288
chr12:52401295	chr12:52401299	chr12:52401304	chr12:52401334
chr12:52401340	chr12:52401344	chr12:52401359	

or a corresponding cytosine at position n+1 on the opposite DNA strand.

[0099] To the extent that the method of the present invention includes analysing CAHM, the subject residues are:

chr6:163834330	chr6:163834332	chr6:163834357
chr6:163834373	chr6:163834384	chr6:163834390
chr6:163834392	chr6:163834406	chr6:163834412
chr6:163834419	chr6:163834443	chr6:163834448
chr6:163834452	chr6:163834464	chr6:163834483
chr6:163834653	chr6:163834660	chr6:163834672
chr6:163834675	chr6:163834678	chr6:163834681
chr6:163834815	chr6:163834824	chr6:163834835
chr6:163834840	chr6:163834853	chr6:163834855
chr6:163834858	chr6:163834863	chr6:163834869
chr6:163834872		

or a corresponding cytosine at position n+1 on the opposite DNA strand.

[0100] To the extent that the method of the present invention includes analysing IKZF1, the subject residues are:

chr7:50343869	chr7:50343872	chr7:50343883
chr7:50343889	chr7:50343890	chr7:50343897
chr7:50343907	chr7:50343909	chr7:50343914
chr7:50343934	chr7:50343939	chr7:50343950
chr7:50343959	chr7:50343805	chr7:50343822
chr7:50343824	chr7:50343826	chr7:50343829
chr7:50343831	chr7:50343833	chr7:50343838
chr7:50343847	chr7:50343850	chr7:50343858

chr7:50343864	chr7:50343869	chr7:50343872
chr7:50343890		

or a corresponding cytosine at position n+1 on the opposite DNA strand.

[0101] To the extent that the method of the present invention includes analysing IRF4, the subject residues are:

chr6:392036	chr6:392047	chr6:392049
chr6:392057	chr6:392060	chr6:392066
chr6:392080	chr6:392094	chr6:392102
chr6:392131		

or a corresponding cytosine at position n+1 on the opposite DNA strand.

[0102] The detection method of the present invention can be performed on any suitable biological sample. To this end, reference to a "biological sample" should be understood as a reference to any sample of biological material derived from an animal such as, but not limited to, cellular material, biofluids (e.g. blood), faeces, tissue biopsy specimens, surgical specimens or fluid which has been introduced into the body of an animal and subsequently removed (such as, for example, the solution retrieved from an enema wash). The biological sample which is tested according to the method of the present invention may be tested directly or may require some form of treatment prior to testing. For example, a biopsy or surgical sample may require homogenisation prior to testing or it may require sectioning for *in situ* testing of the qualitative expression levels of individual genes. Alternatively, a cell sample may require permeabilisation prior to testing. Further, to the extent that the biological sample is not in liquid form, (if such form is required for testing) it may require the addition of a reagent, such as a buffer, to mobilise the sample.

[0103] To the extent that the DNA region of interest is present in a biological sample, the biological sample may be directly tested or else all or some of the nucleic acid present in the biological sample may be isolated prior to testing. In yet another example, the sample may be partially purified or otherwise enriched prior to analysis. For example, to the extent that a biological sample comprises a very diverse cell population, it may be desirable to enrich for a sub-population of particular interest. It is within the scope of the present invention for the target cell population or molecules derived therefrom to be treated prior to testing, for example, inactivation of live virus. It should also be understood that the biological sample may be freshly harvested or it may have been stored (for example by freezing) prior to testing or otherwise treated prior to testing (such as by undergoing culturing).

[0104] The choice of what type of sample is most suitable for testing in accordance with the method disclosed herein will be dependent on the nature of the situation. Preferably, said sample is a faecal (stool) sample, enema wash, surgical resection, tissue biopsy or blood sample (e.g. whole blood, serum or plasma).

[0105] More preferably, said biological sample is a blood sample, biopsy sample or stool sample.

[0106] As detailed hereinbefore, the present invention is designed to screen for a neoplastic cell or cellular population, which is located in the large intestine. Accordingly, reference to "cell or cellular population" should be understood as a reference to an individual cell or a group of cells. Said group of cells may be a diffuse population of cells, a cell suspension, an encapsulated population of cells or a population of cells which take the form of tissue.

[0107] Reference to the "onset" of a neoplasm, such as adenoma or adenocarcinoma, should be understood as a reference to one or more cells of that individual exhibiting dysplasia. In this regard, the adenoma or adenocarcinoma may be well developed in that a mass of dysplastic cells has developed. Alternatively, the adenoma or adenocarcinoma may be at a very early stage in that only relatively few abnormal cell divisions have occurred at the time of diagnosis. The present invention also extends to the assessment of an individual's predisposition to the development of a neoplasm, such as an adenoma or adenocarcinoma. Without limiting the present invention in any way, changed methylation levels may be indicative of that individual's predisposition to developing a neoplasia, such as the future development of an adenoma or adenocarcinoma or another adenoma or adenocarcinoma.

[0108] Although the preferred method is to assess methylation levels for the purpose of diagnosing neoplasia development or predisposition thereto, the detection of converse changes in the levels of said methylation may be desired under certain circumstances, for example, to monitor the effectiveness of therapeutic or prophylactic treatment directed to modulating a neoplastic condition, such as adenoma or adenocarcinoma development. For example, where elevated levels of methylation indicate that an individual has developed a condition characterised by adenoma or adenocarcinoma development, screening for a decrease in the levels of methylation subsequently to the onset of a therapeutic treatment regime may be utilised to indicate successful clearance of the neoplastic cells. In another example, one can use this method to test the tissue at the margins of a tumour resection in order to determine whether the full margin of the tumour has been removed.

[0109] The present method can therefore be used in the diagnosis, prognosis, classification, prediction of disease risk, detection of recurrence of disease, selection of treatment of a number of types of neoplasias and monitoring of neoplasias. A cancer at any stage of progression can be detected, such as primary, metastatic, and recurrent cancers.

[0110] The present invention provides methods for determining whether a mammal (e.g., a human) has a neoplasia of the large intestine, whether a biological sample taken from a mammal contains neoplastic cells or DNA derived from neoplastic cells, estimating the risk or likelihood of a mammal developing a neoplasm, monitoring the efficacy of anti-cancer treatment, or selecting the appropriate anti-cancer treatment in a mammal with cancer. Such methods are based on the determination that neoplastic cells have a different methylation status than normal cells in the DNA regions described herein. Accordingly, by determining whether or not a cell contains differentially methylated sequences in the DNA regions as described herein, it is possible to determine that a cell is neoplastic .

[0111] The method of the invention can be used to evaluate individuals known or suspected to have a neoplasia or as a routine clinical test, i.e., in an individual not necessarily suspected to have a neoplasia. Further diagnostic assays can be performed to confirm the status of neoplasia in the individual.

[0112] Further, the present methods may be used to assess the efficacy of a course of treatment. For example, the efficacy of an anti-cancer treatment can be assessed by monitoring DNA methylation of the sequences described herein over time in a mammal having cancer. For example, a reduction or absence of methylation in any of the diagnostic sequences of the invention in a biological sample taken from a mammal following a treatment, compared to a level in a sample taken from the mammal before, or earlier in, the treatment, indicates efficacious treatment.

[0113] The method of the present invention is therefore useful as a one-time test or as an ongoing monitor of those individuals thought to be at risk of neoplasia development or as a monitor of the effectiveness of therapeutic or prophylactic treatment regimes directed to inhibiting or otherwise slowing neoplasia development. In these situations, mapping the modulation of methylation levels in any one or more classes of biological samples is a valuable indicator of the status of an individual or the effectiveness of a therapeutic or prophylactic regime which is currently in use. Accordingly, the method of the present invention should be understood to extend to monitoring for increases or decreases in methylation levels in an individual relative to their normal level (as hereinbefore defined), or relative to one or more earlier methylation levels determined from a biological sample of said individual.

[0114] The methods for detecting neoplasia can comprise the detection of one or more other cancer-associated polynucleotide or polypeptides sequences. Accordingly, detection of methylation by the method of the invention can be used either alone, or in combination with other screening methods for the diagnosis or prognosis of neoplasia.

[0115] Any method for detecting DNA methylation can be used in the methods of the present invention. A number of methods are available for detection of differentially methylated DNA at specific loci in either primary tissue samples or in patient samples such as blood, urine, stool or saliva (reviewed in Kristensen and Hansen Clin Chem. 55:1471-83, 2009; Ammerpohl et al. Biochim Biophys Acta. 1790:847-62, 2009; Shames et al. Cancer Lett. 251:187-98, 2007; Clark et al. Nat Protoc. 1:2353-64, 2006). For analysis of the proportion or extent of DNA methylation in a target gene, DNA is normally treated with sodium bisulfite and regions of interest amplified using primers and PCR conditions that will amplify independently of the methylation status of the DNA. The methylation of the overall amplicon or individual CpG sites can then be assessed by sequencing, including pyrosequencing, restriction enzyme digestion (COBRA) or by melting curve analysis. Alternatively ligation-based methods for analysis of methylation at specific CpG sites may be used. Detection of aberrantly methylated DNA released from tumours and into bodily fluids is being developed as a means of cancer diagnosis. Here, in the case of hypermethylated sequences, it is necessary to use sensitive methods that allow the selective amplification of the methylated DNA sequence from a background of normal cellular DNA that is unmethylated. Such methods based on bisulfite-treated DNA, for example; include methylation selective PCR (MSP), Heavymethyl PCR, Headloop PCR and Helper-dependent chain reaction (PCT/AU2008/001475).

[0116] Briefly, in some embodiments, methods for detecting methylation include randomly shearing or randomly fragmenting the genomic DNA, cutting the DNA with a methylation-dependent or methylation-sensitive restriction enzyme and subsequently selectively identifying and/or analyzing the cut or uncut DNA. Selective identification can include, for example, separating cut and uncut DNA (e.g., by size) and quantifying a sequence of interest that was cut or, alternatively, that was not cut. See, e.g., U.S. Pat. No. 7,186,512. Alternatively, the method can encompass amplifying intact DNA after restriction enzyme digestion, thereby only amplifying DNA that was not cleaved by the restriction enzyme in the area amplified. See, e.g., U.S. patent application Ser. Nos. 10/971,986; 11/071,013; and 10/971,339. In some embodiments, amplification can be performed using primers that are gene specific. Alternatively, adaptors can be added to the ends of the randomly fragmented DNA, the DNA can be digested with a methylation-dependent or methylation-sensitive restriction enzyme, intact DNA can be amplified using primers that hybridize to the adaptor sequences. In this case, a second step can be performed to determine the presence, absence or quantity of a particular gene in an amplified pool of DNA. In some embodiments, the DNA is amplified using real-time, quantitative PCR.

[0117] In some embodiments, the methods comprise quantifying the average methylation density in a target sequence within a population of genomic DNA. In some embodiments, the method comprises contacting genomic DNA with a methylation-dependent restriction enzyme or methylation-sensitive restriction enzyme under conditions that allow for at least some copies of potential restriction enzyme cleavage sites in the locus to remain uncleaved; quantifying intact copies of the locus; and comparing the quantity of amplified product to a control value representing the quantity of methylation of control DNA, thereby quantifying the average methylation density in the locus compared to the methylation density of the control DNA.

[0118] The quantity of methylation of a locus of DNA can be determined by providing a sample of genomic DNA comprising the locus, cleaving the DNA with a restriction enzyme that is either methylation-sensitive or methylation-dependent, and then quantifying the amount of intact DNA or quantifying the amount of cut DNA at the DNA locus of interest. The amount of intact or cut DNA will depend on the initial amount of genomic DNA containing the locus, the amount of methylation in the locus, and the number (i.e., the fraction) of nucleotides in the locus that are methylated in the genomic DNA. The amount of methylation in a DNA locus can be determined by comparing the quantity of intact DNA or cut DNA to a control value representing the quantity of intact DNA or cut DNA in a similarly-treated DNA sample. The control value can represent a known or predicted number of methylated nucleotides. Alternatively, the control value can represent the quantity of intact or cut DNA from the same locus in another (e.g., normal, non-diseased) cell or a second locus.

[0119] By using at least one methylation-sensitive or methylation-dependent restriction enzyme under conditions that allow for at least some copies of potential restriction enzyme cleavage sites in the locus to remain uncleaved and subsequently quantifying the remaining intact copies and comparing the quantity to a control, average methylation density of a locus can be determined. A methylation-sensitive enzyme is one which cuts DNA if its recognition sequence is unmethylated while a methylation-dependent enzyme cuts DNA if its recognition sequence is methylated. If the methylation-sensitive restriction enzyme is contacted to copies of a DNA locus under conditions that allow for at least some copies of potential restriction enzyme cleavage sites in the locus to remain uncleaved, then the remaining intact DNA will be directly proportional to the methylation density, and thus may be compared to a control to determine the relative methylation density of the locus in the sample. Similarly, if a methylation-dependent restriction enzyme is contacted to copies of a DNA locus under conditions that allow for at least some copies of potential restriction enzyme cleavage sites in the locus to remain uncleaved, then the remaining intact DNA will be inversely proportional to the methylation density, and thus may be compared to a control to determine the relative methylation density of the locus in the sample. Such assays are disclosed in, e.g., U.S. patent application Ser. No. 10/971,986.

[0120] Kits for the above methods can include, e.g., one or more of methylation-dependent restriction enzymes, methylation-sensitive restriction enzymes, amplification (e.g., PCR) reagents, probes and/or primers.

[0121] Quantitative amplification methods (e.g., quantitative PCR or quantitative linear amplification) can be used to quantify the amount of intact DNA within a locus flanked by amplification primers following restriction digestion. Methods of quantitative amplification are disclosed in, e.g., U.S. Pat. Nos. 6,180,349; 6,033,854; and 5,972,602, as well as in, e.g., Gibson et al., Genome Research 6:995-1001 (1996); DeGraves, et al., Biotechniques 34(1):106-10, 112-5 (2003); Deiman B, et al., Mol. Biotechnol. 20(2):163-79 (2002). Amplifications may be monitored in "real time."

[0122] Additional methods for detecting DNA methylation can involve genomic sequencing before and after treatment of the DNA with bisulfite. See, e.g., Frommer et al., Proc. Natl. Acad. Sci. USA 89:1827-1831 (1992). When sodium bisulfite is contacted to DNA, unmethylated cytosine is converted to uracil, while methylated cytosine is not modified.

[0123] In some embodiments, restriction enzyme digestion of PCR products amplified from bisulfite-converted DNA is used to detect DNA methylation. See, e.g., Sadri & Hornsby, Nucl. Acids Res. 24:5058-5059 (1996); Xiong & Laird, Nucleic Acids Res. 25:2532-2534 (1997).

[0124] In some embodiments, a methylation-specific PCR ("MSP") reaction is used alone or in combination with other methods to detect DNA methylation. An MSP assay entails initial modification of DNA by sodium bisulfite, converting all unmethylated, but not methylated, cytosines to uracil, and subsequent amplification with primers specific for methylated verses unmethylated DNA. See, Herman et al. Proc. Natl. Acad. Sci. USA 93:9821-9826 (1996); U.S. Pat. No. 5,786,146.

[0125] In some embodiments, a MethyLight assay is used alone or in combination with other methods to detect DNA methylation (see, Eads et al., Cancer Res. 59:2302-2306 (1999)). Briefly, in the MethyLight process genomic DNA is converted in a sodium bisulfite reaction (the bisulfite process converts unmethylated cytosine residues to uracil). Amplification of a DNA sequence of interest is then performed using PCR primers that hybridize to CpG dinucleotides. By using primers that hybridize only to sequences resulting from bisulfite conversion of methylated DNA, (or alternatively to unmethylated sequences) amplification can indicate methylation status of sequences where the primers hybridize. Furthermore, the amplification product can be detected with a probe that specifically binds to a sequence resulting from bisulfite treatment of a unmethylated DNA. If desired, both primers and probes can be used to detect methylation status. Thus, kits for use with MethyLight can include sodium bisulfite as well as primers or detectably-labelled probes (including but not limited to Taqman or molecular beacon probes) that distinguish between methylated and unmethylated DNA that have been treated with bisulfite. Other kit components can include, e.g., reagents necessary for amplification of DNA including but not limited to, PCR buffers, deoxynucleotides; and a thermostable polymerase.

[0126] In some embodiments, a Ms-SNuPE (Methylation-sensitive Single Nucleotide Primer Extension) reaction is used alone or in combination with other methods to detect DNA methylation (see, Gonzalgo & Jones, Nucleic Acids Res. 25:2529-2531 (1997)). The Ms-SNuPE technique is a quantitative method for assessing methylation differences at specific CpG sites based on bisulfite treatment of DNA, followed by single-nucleotide primer extension (Gonzalgo & Jones, *supra).* Briefly, genomic DNA is reacted with sodium bisulfite to convert unmethylated cytosine to uracil while leaving 5-methylcytosine unchanged. Amplification of the desired target sequence is then performed using PCR primers specific for bisulfite-converted DNA, and the resulting product is isolated and used as a template for methylation analysis at the CpG site(s) of interest.

[0127] Typical reagents (e.g., as might be found in a typical Ms-SNuPE-based kit) for Ms-SNuPE analysis can include, but are not limited to: PCR primers for specific gene (or methylation-altered DNA sequence or CpG island); optimized PCR buffers and deoxynucleotides; gel extraction kit; positive control primers; Ms-SNuPE primers for a specific gene; reaction buffer (for the Ms-SNuPE reaction); and detectably-labelled nucleotides. Additionally, bisulfite conversion reagents may include: DNA denaturation buffer; sulfonation buffer; DNA recovery regents or kit (e.g., precipitation, ultrafiltration, affinity column); desulfonation buffer; and DNA recovery components.

[0128] Additional methylation detection methods include, but are not limited to, methylated CpG island amplification (see, Toyota et al., Cancer Res. 59:2307-12 (1999)) and those described in, e.g., U.S. Patent Publication 2005/0069879; Rein, et al. Nucleic Acids Res. 26 (10): 2255-64 (1998); Olek, et al. Nat. Genet. 17(3): 275-6 (1997); and PCT Publication No. WO 00/70090.

[0129] More detailed information in relation to several of these generally described methods is provided below:

(a) Probe or Primer Design and/or Production

[0130] Several methods described herein for the diagnosis of a neoplasia use one or more probes and/or primers. Methods for designing probes and/or primers for use in, for example, PCR or hybridization are known in the art and described, for example, in Dieffenbach and Dveksler (Eds) (In: PCR Primer: A Laboratory Manual, Cold Spring Harbor Laboratories, NY, 1995). Furthermore, several software packages are publicly available that design optimal probes and/or primers for a variety of assays, e.g. Primer 3 available from the Center for Genome Research, Cambridge, Mass., USA.

[0131] Clearly, the potential use of the probe or primer should be considered during its design. For example, should the probe or primer be produced for use in a methylation specific PCR or ligase chain reaction (LCR) assay the nucleotide at the 3' end (or 5' end in the case of LCR) should preferably correspond to a methylated nucleotide in a nucleic acid.

[0132] Probes and/or primers useful for detection of a sequence associated with a neoplasia are assessed, for example, to determine those that do not form hairpins, self-prime or form primer dimers (e.g. with another probe or primer used in a detection assay). Furthermore, a probe or primer (or the sequence thereof) is often assessed to determine the temperature at which it denatures from a target nucleic acid (i.e. the melting temperature of the probe or primer, or Tm). Methods for estimating Tm are known in the art and described, for example, in Santa Lucia, Proc. Natl. Acad. Sci. USA, 95: 1460-1465, 1995 or Bresslauer et al., Proc. Natl. Acad. Sci. USA, 83: 3746-3750, 1986.

[0133] Methods for producing/synthesizing a probe or primer of the present invention are known in the art. For example, oligonucleotide synthesis is described, in Gait (Ed) (In: Oligonucleotide Synthesis: A Practical Approach, IRL Press, Oxford, 1984). For example, a probe or primer may be obtained by biological synthesis (e.g. by digestion of a nucleic acid with a restriction endonuclease) or by chemical synthesis. For short sequences (up to about 100 nucleotides) chemical synthesis is preferable.

[0134] For longer sequences standard replication methods employed in molecular biology are useful, such as, for example, the use of M13 for single stranded DNA as described by Messing, Methods Enzymol, 101, 20-78, 1983. Other methods for oligonucleotide synthesis include, for example, phosphotriester and phosphodiester methods (Narang, et al. Meth. Enzymol 68: 90, 1979) and synthesis on a support (Beaucage, et al. Tetrahedron Letters 22:1859-1862, 1981) as well as phosphoramidate technique, Caruthers, M. H., et al., Methods in Enzymology, Vol. 154, pp. 287-314 (1988), and others described in "Synthesis and Applications of DNA and RNA," S. A. Narang, editor, Academic Press, New York, 1987 , and the references cited therein. Probes comprising locked nucleic acid (LNA) are synthesized as described, for example, in Nielsen et al. J. Chem. Soc. Perkin Trans., 1:3423, 1997; Singh and Wengel, Chem. Commun. 1247, 1998. While, probes comprising peptide-nucleic acid (PNA) are synthesized as described, for example, in Egholm et al., Am. Chem. Soc., 114:1895, 1992; Egholm et al., Nature, 365:566, 1993; and Orum et al., Nucl. Acids Res., 21:5332, 1993.

(b) Methylation-Sensitive Endonuclease Digestion of DNA

[0135] In one example, the increased methylation in a sample is determined using a process comprising treating the nucleic acid with an amount of a methylation-sensitive restriction endonuclease enzyme under conditions sufficient for nucleic acid to be digested and then detecting the fragments produced. Exemplary methylation-sensitive endonucleases include, for example, HhaI or HpaII. Preferably, assays include internal controls that are digested with a methylation-insensitive enzyme having the same specificity as the methylation-sensitive enzyme employed. For example, the methylation-insensitive enzyme MspI is an isoschizomer of the methylation-sensitive enzyme HpaII.

Hybridization Assay Formats

[0136] In one example, the digestion of nucleic acid is detected by selective hybridization of a probe or primer to the undigested nucleic acid. Alternatively, the probe selectively hybridizes to both digested and undigested nucleic acid but facilitates differentiation between both forms, e.g., by electrophoresis. Suitable detection methods for achieving selective hybridization to a hybridization probe include, for example, Southern or other nucleic acid hybridization (Kawai et al., Mol. Cell. Biol. 14:7421-7427, 1994; Gonzalgo et al., Cancer Res. 57:594-599, 1997).

[0137] Suitable hybridization conditions are determined based on the melting temperature (Tm) of a nucleic acid duplex comprising the probe. The skilled artisan will be aware that optimum hybridization reaction conditions should be determined empirically for each probe, although some generalities can be applied. Preferably, hybridizations employing short oligonucleotide probes are performed at low to medium stringency. In the case of a GC rich probe or primer or a longer probe or primer a high stringency hybridization and/or wash is preferred. A high stringency is defined herein as being a hybridization and/or wash carried out in about 0.1 x SSC buffer and/or about 0.1% (w/v) SDS, or lower salt concentration, and/or at a temperature of at least 65°C., or equivalent conditions. Reference herein to a particular level of stringency encompasses equivalent conditions using wash/hybridization solutions other than SSC known to those skilled in the art.

[0138] In accordance with the present example, a difference in the fragments produced for the test sample and a negative control sample is indicative of the subject having a neoplasia. Similarly, in cases where the control sample comprises data from a tumor, cancer tissue or a cancerous cell or pre-cancerous cell, similarity, albeit not necessarily absolute identity, between the test sample and the control sample is indicative of a positive diagnosis (i.e. cancer).

Amplification Assay Formats

[0139] In an alternative example, the fragments produced by the restriction enzyme are detected using an amplification system, such as, for example, polymerase chain reaction (PCR), rolling circle amplification (RCA), inverse polymerase chain reaction (iPCR), in situ PCR (Singer-Sam et al., Nucl. Acids Res. 18:687, 1990), strand displacement amplification (SDA) or cycling probe technology.

[0140] Methods of PCR are known in the art and described, for example, by McPherson et al., PCR: A Practical Approach, (series eds, D. Rickwood and B. D. Hames), IRL Press Limited, Oxford, pp 1-253, 1991 and by Dieffenbach (ed) and Dveksler (ed) (In: PCR Primer: A Laboratory Manual, Cold Spring Harbour Laboratories, NY, 1995), the contents of which are each incorporated in their entirety by way of reference. Generally, for PCR two non-complementary nucleic acid primer molecules comprising at least about 18 nucleotides in length, and more preferably at least 20-30 nucleotides in length are hybridized to different strands of a nucleic acid template molecule at their respective annealing sites, and specific nucleic acid molecule copies of the template that intervene the annealing sites are amplified enzymatically. Amplification products may be detected, for example, using electrophoresis and detection with a detectable marker that binds nucleic acids. Alternatively, one or more of the oligonucleotides are labelled with a detectable marker (e.g. a fluorophore) and the amplification product detected using, for example, a lightcycler (Perkin Elmer, Wellesley, Mass., USA, Roche Applied Science, Indianapolis, IN, USA).

[0141] Strand displacement amplification (SDA) utilizes oligonucleotide primers, a DNA polymerase and a restriction endonuclease to amplify a target sequence. The oligonucleotides are hybridized to a target nucleic acid and the polymerase is used to produce a copy of the region intervening the primer annealing sites. The duplexes of copied nucleic acid and target nucleic acid are then nicked with an endonuclease that specifically recognizes a sequence at the beginning of the copied nucleic acid. The DNA polymerase recognizes the nicked DNA and produces another copy of the target region at the same time displacing the previously generated nucleic acid. The advantage of SDA is that it occurs in an isothermal format, thereby facilitating high-throughput automated analysis.

[0142] Cycling Probe Technology uses a chimeric synthetic primer that comprises DNA-RNA-DNA that is capable of hybridizing to a target sequence. Upon hybridization to a target sequence the RNA-DNA duplex formed is a target for RNaseH thereby cleaving the primer. The cleaved primer is then detected, for example, using mass spectrometry or electrophoresis.

[0143] For primers that flank or are adjacent to a methylation-sensitive endonuclease recognition site, it is preferred that such primers flank only those sites that are hypermethylated in neoplasia to ensure that a diagnostic amplification product is produced. In this regard, an amplification product will only be produced when the restriction site is not cleaved, i.e., when it is methylated. Accordingly, detection of an amplification product indicates that the CpG dinucleotide/s of interest is/are methylated.

[0144] As will be known to the skilled artisan, the precise length of the amplified product will vary depending upon the distance between the primers.

Clearly this form of analysis may be used to determine the methylation status of a plurality of CpG dinucleotides provided that each dinucleotide is within a methylation sensitive restriction endonuclease site. In these methods, one or more of the primers may be labelled with a detectable marker to facilitate rapid detection of amplified nucleic acid, for example, a fluorescent label (e.g. Cy5 or Cy3) or a radioisotope (e.g. ^{32}P).

[0145] The amplified nucleic acids are generally analyzed using, for example, non-denaturing agarose gel electrophoresis, non-denaturing polyacrylamide gel electrophoresis, mass spectrometry, liquid chromatography (e.g. HPLC or dHPLC), or capillary electrophoresis. (e.g. MALDI-TOF). High throughput detection methods, such as, for example, matrix-assisted laser desorption/ionization time of flight (MALDI-TOF), electrospray ionization (ESI), mass spectrometry (including tandem mass spectrometry, e.g. LC MS/MS), biosensor technology, evanescent fiber-optics technology or DNA chip technology (e.g., WO98/49557; WO 96/17958; Fodor et al., Science 767-773, 1991; U.S. Pat. No. 5,143,854; and U.S. Pat. No. 5,837,832, the contents of which are all incorporated herein by reference), are especially preferred for all assay formats described herein. Alternatively, amplification of a nucleic acid may be continuously monitored using a melting curve analysis method as described herein and/or in, for example, U.S. Pat. No. 6,174,670, which is incorporated herein by reference.

(c) Other Assay Formats

[0146] In an alternative example, the increased methylation in a sample is determined by performing a process comprising treating chromatin containing the nucleic acid with an amount of DNaseI under conditions sufficient for nucleic acid to be digested and then detecting the fragments produced. This assay format is predicated on the understanding that chromatin containing methylated DNA, e.g., hyper methylated DNA, has a more tightly-closed conformation than non-hyper methylated DNA and, as a consequence, is less susceptible to endonuclease digestion by DNase I.

[0147] In accordance with this method , DNA fragments of different lengths are produced by DNase I digestion of methylated compared to non-methylated DNA. Such different DNA fragments are detected, for example, using an assay described earlier. Alternatively, the DNA fragments are detected using PCR-SSCP essentially as described, for example, in Gregory and Feil, Nucleic Acids Res., 27, e32i-e32iv, 1999. In adapting PCR-SSCP to the present invention, amplification primers flanking or comprising one or more CpG dinucleotides in a nucleic acid that are resistant to DNase I digestion in a neoplasia sample but not resistant to DNase I digestion in a healthy/normal control or healthy/normal test sample are used to amplify the DNase I-generated fragments. In this case, the production of a specific nucleic acid fragment using DNase I is diagnostic of neoplasia, because the DNA is not efficiently degraded. In contrast, template DNA from a healthy/normal subject sample is degraded by the action of DNase I and, as a consequence, amplification fails to produce a discrete amplification product. Alternative methods to PCR-SSCP, such as for example, PCR-dHPLC are also known in the art and contemplated by the present invention.

(d) Selective Mutagenesis of Non-Methylated DNA

[0148] In an alternative method the increased methylation in a sample is determined using a process comprising treating the nucleic acid with an amount of a compound that selectively mutates a non-methylated cytosine residue within a CpG dinucleotide under conditions sufficient to induce mutagenesis.

[0149] Preferred compounds mutate cytosine to uracil or thymidine, such as, for example, a salt of bisulfite, e.g., sodium bisulfite or potassium bisulfite (Frommer *et al.,* 1992, *supra).* Bisulfite treatment of DNA is known to distinguish methylated from non-methylated cytosine residues, by mutating cytosine residues that are not protected by methylation, including cytosine residues that are not within a CpG dinucleotide or that are positioned within a CpG dinucleotide that is not subject to methylation.

Sequence Based Detection

[0150] In one example, the presence of one or more mutated nucleotides or the number of mutated sequences is determined by sequencing mutated DNA. One form of analysis comprises amplifying mutated nucleic acid using an amplification reaction described herein, for example, PCR. The amplified product is then directly sequenced or cloned and the cloned product sequenced. Methods for sequencing DNA are known in the art and include for example, the dideoxy chain termination method or the Maxam-Gilbert method (see Sambrook et al., Molecular Cloning, A Laboratory Manual (2nd Ed., CSHP, New York 1989) or Zyskind et al., Recombinant DNA Laboratory Manual, (Acad. Press, 1988)).

[0151] As the treatment of nucleic acid with a compound, such as, for example, bisulfite results in non-methylated cytosines being mutated to uracil (and hence thymidine after an amplification process), analysis of the sequence determines the presence or absence of a methylated nucleotide. For example, by comparing the sequence obtained using a control sample or a sample that has not been treated with bisulfite, or the known nucleotide sequence of the region of interest with a treated sample facilitates the detection of differences in the nucleotide sequence. Any thymine residue detected at the site of a cytosine in the treated sample compared to a control or untreated sample may be considered to be caused by mutation as a result of bisulfite treatment. Suitable methods for the detection of methylation using sequencing of bisulfite treated nucleic acid are described, for example, in Frommer *et al.,* 1992, *supra* or Clark et al., Nucl. Acids Res. 22:2990-2997, 1994.

[0152] In another method, the presence of a mutated or non-mutated nucleotide in a bisulfite treated sample is detected using pyrosequencing, such as, for example, as described in Uhlmann et al., Electrophoresis, 23: 4072-4079, 2002. Essentially this method is a form of real-time sequencing that uses a primer that hybridizes to a site adjacent or close to the site of a cytosine that is methylated. Following hybridization of the primer and template in the presence of a DNA polymerase each of four modified deoxynucleotide triphosphates are added separately according to a predetermined dispensation order. Only an added nucleotide that is complementary to the bisulfite treated sample is incorporated and inorganic pyrophosphate (PPi) is liberated. The PPi then drives a reaction resulting in production of detectable levels of light. Such a method allows determination of the identity of a specific nucleotide adjacent to the site of hybridization of the primer.

[0153] Methods of solid phase pyrosequencing are known in the art and reviewed in, for example, Landegren et al., Genome Res., 8(8): 769-776,

1998. Such methods enable the high-throughput detection of methylation of a number of CpG dinucleotides.

[0154] A related method for determining the sequence of a bisulfite treated nucleotide is methylation-sensitive single nucleotide primer extension (Me-SnuPE) or SNaPmeth. Suitable methods are described, for example, in Gonzalgo and Jones, 1997, *supra,* or Uhlmann et al., Electrophoresis, 23:4072-4079, 2002. An oligonucleotide is used that hybridizes to the region of a nucleic acid adjacent to the site of a cytosine that is methylated. This oligonucleotide is then used in a primer extension protocol with a polymerase and a free nucleotide diphosphate or dideoxynucleotide triphosphate that corresponds to either or any of the possible bases that occur at this site following bisulfite treatment (i.e., thymine or cytosine). Preferably, the nucleotide-diphosphate is labelled with a detectable marker (e.g. a fluorophore). Following primer extension, unbound labelled nucleotide diphosphates are removed, e.g. using size exclusion chromatography or electrophoresis, or hydrolyzed, using for example, alkaline phosphatase, and the incorporation of the labelled nucleotide to the oligonucleotide is detected, indicating the base that is present at the site.

[0155] Clearly other high throughput sequencing methods are encompassed by the present invention. Such methods include, for example, solid phase minisequencing (as described, for example, in Southern et al., Genomics, 13:1008-1017, 1992), or minisequencing with FRET (as described, for example, in Chen and Kwok, Nucleic Acids Res. 25:347-353, 1997).

Restriction Endonuclease-Based Assay Format

[0156] In one method, the presence of a non-mutated sequence is detected using combined bisulfite restriction analysis (COBRA) essentially as described in Xiong and Laird, 2001, *supra.* This method exploits the differences in restriction enzyme recognition sites between methylated and unmethylated nucleic acid after treatment with a compound that selectively mutates a non-methylated cytosine residue, e.g., bisulfite.

[0157] Following bisulfite treatment a region of interest comprising one or more CpG dinucleotides that are methylated and are included in a restriction endonuclease recognition sequence is amplified using an amplification reaction described herein, e.g., PCR. The amplified product is then contacted with the restriction enzyme that cleaves at the site of the CpG dinucleotide for a time and under conditions sufficient for cleavage to occur. A restriction site may be selected to indicate the presence or absence of methylation. For example, the restriction endonuclease TaqI cleaves the sequence TCGA, following bisulfite treatment of a non-methylated nucleic acid the sequence will be TTGA and, as a consequence, will not be cleaved. The digested and/or non-digested nucleic acid is then detected using a detection means known in the art, such as, for example, electrophoresis and/or mass spectrometry. The cleavage or non-cleavage of the nucleic acid is indicative of cancer in a subject. Clearly, this method may be employed in either a positive read-out or negative read-out system for the diagnosis of a cancer.

Positive Read-Out Assay Format

[0158] In one embodiment, the assay format of the invention comprises a positive read-out system in which DNA from a sample that has been treated, for example, with bisulfite is detected as a positive signal. Preferably, the non-hypermethylated DNA from a healthy or normal control subject is not detected or only weakly detected.

[0159] In a preferred embodiment, the increased methylation in a subject sample is determined using a process comprising:

1. (i) treating the nucleic acid with an amount of a compound that selectively mutates a non-methylated cytosine residue under conditions sufficient to induce mutagenesis thereby producing a mutated nucleic acid;
2. (ii) hybridizing a nucleic acid to a probe or primer comprising a nucleotide sequence that is complementary to a sequence comprising a methylated cytosine residue under conditions such that selective hybridization to the non-mutated nucleic acid occurs; and
3. (iii) detecting the selective hybridization.

[0160] In this context, the term "selective hybridization" means that hybridization of a probe or primer to the non-mutated nucleic acid occurs at a higher frequency or rate, or has a higher maximum reaction velocity, than hybridization of the same probe or primer to the corresponding mutated sequence. Preferably, the probe or primer does not hybridize to the non-methylated sequence carrying the mutation(s) under the reaction conditions used.

Hybridization-Based Assay Format

[0161] In one embodiment, the hybridization is detected using Southern, dot blot, slot blot or other nucleic acid hybridization means (Kawai *et al.,* 1994, *supra*; Gonzalgo *et al.,* 1997, *supra).* Subject to appropriate probe selection, such assay formats are generally described herein above and apply mutatis mutandis to the presently described selective mutagenesis approach.

[0162] Preferably, a ligase chain reaction format is employed to distinguish between a mutated and non-mutated nucleic acid. Ligase chain reaction (described in EP 320,308 and U.S. Pat. No. 4,883,750) uses at least two oligonucleotide probes that anneal to a target nucleic acid in such a way that they are juxtaposed on the target nucleic acid. In a ligase chain reaction assay, the target nucleic acid is hybridized to a first probe that is complementary to a diagnostic portion of the target sequence (the diagnostic probe) e.g., a nucleic acid comprising one or more methylated CpG dinucleotide(s), and with a second probe that is complementary to a nucleotide sequence contiguous with the diagnostic portion (the contiguous probe), under conditions wherein the diagnostic probe remains bound substantially only to the target nucleic acid. The diagnostic and contiguous probes can be of different lengths and/or have different melting temperatures such that the stringency of the hybridization can be adjusted to permit their selective hybridization to the target, wherein the probe having the higher melting temperature is hybridized at higher stringency and, following washing to remove unbound and/or non-selectively bound probe, the other probe having the lower melting temperature is hybridized at lower stringency. The diagnostic probe and contiguous probe are then covalently ligated such as, for example, using T4 DNA ligase, to thereby produce a larger target probe that is complementary to the target sequence, and the probes that are not ligated are removed by modifying the hybridization stringency. In this respect, probes that have not been ligated will selectively hybridize under lower stringency hybridization conditions than probes that have been ligated. Accordingly, the stringency of the hybridization can be increased to a stringency that is at least as high as the stringency used to hybridize the longer probe, and preferably at a higher stringency due to the increased length contributed by the shorter probe following ligation.

[0163] In another example, one or both of the probes is labelled such that the presence or absence of the target sequence can be tested by melting the target-probe duplex, eluting the dissociated probe, and testing for the label(s). Where both probes are labelled, different ligands are used to permit distinction between the ligated and unligated probes, in which case the presence of both labels in the same eluate fraction confirms the ligation event. If the target nucleic acid is bound to a solid matrix e.g., in a Southern hybridization, slot blot, dot blot, or microchip assay format, the presence of both the diagnostic and contiguous probes can be determined directly.

[0164] Methylation specific microarrays (MSO) are also useful for differentiating between a mutated and non-mutated sequence. A suitable method is described, for example, in Adorjan et al. Nucl. Acids Res., 30: e21, 2002. MSO uses nucleic acid that has been treated with a compound that selectively mutates a non-methylated cytosine residue (e.g., bisulfite) as template for an amplification reaction that amplifies both mutant and non-mutated nucleic acid. The amplification is performed with at least one primer that comprises a detectable label, such as, for example, a fluorophore, e.g., Cy3 or Cy5.

[0165] To produce a microarray for detection of mutated nucleic acid oligonucleotides are spotted onto, for example, a glass slide, preferably, with a degree of redundancy (for example, as described in Golub et al., Science, 286:531-537, 1999). Preferably, for each CpG dinucleotide analyzed two different oligonucleotides are used. Each oligonucleotide comprises a sequence N_2-16CGN_2-16 or N_2-16TGN_2-16 (wherein N is a number of nucleotides adjacent or juxtaposed to the CpG dinucleotide of interest) reflecting the methylated or non-methylated status of the CpG dinucleotides.

[0166] The labelled amplification products are then hybridized to the oligonucleotides on the microarray under conditions that enable detection of single nucleotide differences. Following washing to remove unbound amplification product, hybridization is detected using, for example, a microarray scanner. Not only does this method allow for determination of the methylation status of a large number of CpG dinucleotides, it is also semi-quantitative, enabling determination of the degree of methylation at each CpG dinucleotide analyzed. As there may be some degree of heterogeneity of methylation in a single sample, such quantification may assist in the diagnosis of cancer.

Amplification-Based Assay Format

[0167] In an alternative example, the hybridization is detected using an amplification system. In methylation-specific PCR formats (MSP; Herman et al. Proc. Natl. Acad. Sci. USA 93:9821-9826, 1992), the hybridization is detected using a process comprising amplifying the bisulfite-treated DNA. Accordingly, by using one or more probe or primer that anneals specifically to the unmutated sequence under moderate and/or high stringency conditions an amplification product is only produced using a sample comprising a methylated nucleotide. Alternate assays that provide for selective amplification of either the methylated or the unmethylated component from a mixture of bisulfite-treated DNA are provided by Cottrell et al., Nucl. Acids Res. 32: e10, 2003 (HeavyMethyl PCR), Rand et al. Nucl. Acids Res. 33:e127, 2005 (Headloop PCR), Rand et al. Epigenetics 1:94-100, 2006 (Bisulfite Differential Denaturation PCR) and PCT/AU07/000389 (End-specific PCR).

[0168] Any amplification assay format described herein can be used, such as, for example, polymerase chain reaction (PCR), rolling circle amplification (RCA), inverse polymerase chain reaction (iPCR), in situ PCR (Singer-Sam *et al.,* 1990, *supra),* strand displacement amplification, or cycling probe technology. PCR techniques have been developed for detection of gene mutations (Kuppuswamy et al., Proc. Natl. Acad. Sci. USA 88:1143-1147, 1991) and quantitation of allelic-specific expression (Szabo and Mann, Genes Dev. 9: 3097-3108, 1995; and Singer-Sam et al., PCR Methods Appl. 1: 160-163, 1992). Such techniques use internal primers, which anneal to a PCR-generated template and terminate immediately 5' of the single nucleotide to be assayed. Such as format is readily combined with ligase chain reaction as described herein above. The use of a real-time quantitative assay format is also useful. Subject to the selection of appropriate primers, such assay formats are generally described herein above and apply mutatis mutandis to the presently described selective mutagenesis approach.

[0169] Methylation-specific melting-curve analysis (essentially as described in Worm et al., Clin. Chem., 47:1183-1189, 2001) is also contemplated by the present invention. This process exploits the difference in melting temperature in amplification products produced using bisulfite treated methylated or unmethylated nucleic acid. In essence, non-discriminatory amplification of a bisulfite treated sample is performed in the presence of a fluorescent dye that specifically binds to double stranded DNA (e.g., SYBR Green I). By increasing the temperature of the amplification product while monitoring fluorescence the melting properties and thus the sequence of the amplification product is determined. A decrease in the fluorescence reflects melting of at least a domain in the amplification product. The temperature at which the fluorescence decreases is indicative of the nucleotide sequence of the amplified nucleic acid, thereby permitting the nucleotide at the site of one or more CpG dinucleotides to be determined. As the sequence of the nucleic acids amplified using the present invention

[0170] The present invention also encompasses the use of real-time quantitative forms of PCR, such as, for example, TaqMan (Holland et al., Proc. Natl. Acad. Sci. USA, 88:7276-7280, 1991; Lee et al., Nucleic Acid Res. 21:3761-3766, 1993) to perform this embodiment. For example, the MethylLight method of Eads et al., Nucl. Acids Res. 28: E32, 2000 uses a modified TaqMan assay to detect methylation of a CpG dinucleotide. Essentially, this method comprises treating a nucleic acid sample with bisulfite and amplifying nucleic acid comprising one or more CpG dinucleotides that are methylated in a neoplastic cell and not in a control sample using an amplification reaction, e.g., PCR. The amplification reaction is performed in the presence of three oligonucleotides, a forward and reverse primer that flank the region of interest and a probe that hybridizes between the two primers to the site of the one or more methylated CpG dinucleotides. The probe is dual labelled with a 5' fluorescent reporter and a 3' quencher (or vice versa). When the probe is intact, the quencher dye absorbs the fluorescence of the reporter due to their proximity. Following annealing of to the PCR product the probe is cleaved by 5' to 3' exonuclease activity of, for example, Taq DNA polymerase. This cleavage releases the reporter from the quencher thereby resulting in an increased fluorescence signal that can be used to estimate the initial template methylation level. By using a probe or primer that selectively hybridizes to unmutated nucleic acid (i.e. methylated nucleic acid) the level of methylation is determined, e.g., using a standard curve.

[0171] Alternatively, rather than using a labelled probe that requires cleavage, a probe, such as, for example, a Molecular Beacon is used (see, for example, Mhlanga and Malmberg, Methods 25:463-471, 2001). Molecular beacons are single stranded nucleic acid molecules with a stem-and-loop structure. The loop structure is complementary to the region surrounding the one or more CpG dinucleotides that are methylated in a neoplastic sample and not in a control sample. The stem structure is formed by annealing two "arms" complementary to each other, which are on either side of the probe (loop). A fluorescent moiety is bound to one arm and a quenching moiety that suppresses any detectable fluorescence when the molecular beacon is not bound to a target sequence is bound to the other arm. Upon binding of the loop region to its target nucleic acid the arms are separated and fluorescence is detectable. However, even a single base mismatch significantly alters the level of fluorescence detected in a sample. Accordingly, the presence or absence of a particular base is determined by the level of fluorescence detected. Such an assay facilitates detection of one or more unmutated sites (i.e. methylated nucleotides) in a nucleic acid.

[0172] Fluorescently labelled locked nucleic acid (LNA) molecules or fluorescently labelled protein-nucleic acid (PNA) molecules are useful for the detection of nucleotide differences (e.g., as described in Simeonov and Nikiforov, Nucleic Acids Research, 30(17): 1-5, 2002). LNA and PNA molecules bind, with high affinity, to nucleic acid, in particular, DNA. Fluorophores (in particular, rhodomine or hexachlorofluorescein) conjugated to the LNA or PNA probe fluoresce at a significantly greater level upon hybridization of the probe to target nucleic acid. However, the level of increase of fluorescence is not enhanced to the same level when even a single nucleotide mismatch occurs. Accordingly, the degree of fluorescence detected in a sample is indicative of the presence of a mismatch between the LNA or PNA probe and the target nucleic acid, such as, in the presence of a mutated cytosine in a methylated CpG dinucleotide. Preferably, fluorescently labelled LNA or PNA technology is used to detect at least a single base change in a nucleic acid that has been previously amplified using, for example, an amplification method known in the art and/or described herein.

[0173] As will be apparent to the skilled artisan, LNA or PNA detection technology is amenable to a high-throughput detection of one or more markers by immobilizing an LNA or PNA probe to a solid support, as described in Orum et al., Clin. Chem. 45:1898-1905, 1999.

[0174] Alternatively, a real-time assay, such as, for example, the so-called HeavyMethyl assay (Cottrell *et al.,* 2003, *supra)* is used to determine the presence or level of methylation of nucleic acid in a test sample. Essentially, this method uses one or more non-extendible nucleic acid (e.g., oligonucleotide) blockers that bind to bisulfite-treated nucleic acid in a methylation specific manner (i.e., the blocker/s bind specifically to unmutated DNA under moderate to high stringency conditions). An amplification reaction is performed using one or more primers that may optionally be methylation specific but that flank the one or more blockers. In the presence of unmethylated nucleic acid (i.e., non-mutated DNA) the blocker/s bind and no PCR product is produced. Using a TaqMan assay essentially as described supra the level of methylation of nucleic acid in a sample is determined.

[0175] Other amplification based methods for detecting methylated nucleic acid following treatment with a compound that selectively mutates a non-methylated cytosine residue include, for example, methylation-specific single stranded conformation analysis (MS-SSCA) (Bianco et al., Hum. Mutat., 14:289-293, 1999), methylation-specific denaturing gradient gel electrophoresis (MS-DGGE) (Abrams and Stanton, Methods Enzymol., 212:71-74, 1992) and methylation-specific denaturing high-performance liquid chromatography (MS-DHPLC) (Deng et al. Chin. J. Cancer Res., 12:171-191, 2000). Each of these methods use different techniques for detecting nucleic acid differences in an amplification product based on differences in nucleotide sequence and/or secondary structure. Such methods are clearly contemplated by the present invention.

[0176] As with other amplification-based assay formats, the amplification product is analyzed using a range of procedures, including gel electrophoresis, gel filtration, mass spectrometry, and in the case of labelled primers, by identifying the label in the amplification product. In an alternative embodiment, restriction enzyme digestion of PCR products amplified from bisulfite-converted DNA is performed essentially as described by Sadri and Hornsby, Nucl. Acids Res. 24:5058-5059, 1996; and Xiong and Laird, Nucl. Acids Res. 25:2532-2534, 1997), to analyze the product formed.

[0177] High throughput detection methods, such as, for example, matrix-assisted laser desorption/ionization time of flight (MALDI-TOF), electrospray ionization (ESI), Mass spectrometry (including tandem mass spectrometry, e.g. LC MS/MS), biosensor technology, evanescent fiber-optics technology or DNA chip technology, can also be employed.

[0178] As with the other assay formats described herein that utilize hybridization and/or amplification detection systems, combinations of such processes as described herein above are particularly contemplated by the selective mutagenesis-based assay formats of the present invention. In one example, the increased methylation is detected by performing a process comprising:

1. (i) treating the nucleic acid with an amount of a compound that selectively mutates a non-methylated cytosine residue within a CpG dinucleotide under conditions sufficient to induce mutagenesis thereby producing a mutated nucleic acid;
2. (ii) hybridizing the nucleic acid to two non-overlapping and non-complementary primers each of which comprises a nucleotide sequence that is complementary to a sequence in the DNA comprising a methylated cytosine residue under conditions such that hybridization to the non-mutated nucleic acid occurs;
3. (iii) amplifying nucleic acid intervening the hybridized primers thereby producing a DNA fragment consisting of a sequence that comprises a primer sequence;
4. (iv) hybridizing the amplified DNA fragment to a probe comprising a nucleotide sequence that corresponds or is complementary to a sequence comprising a methylated cytosine residue under conditions such that hybridization to the non-mutated nucleic acid occurs; and detecting the hybridization.

Negative Read-Out Assays

[0179] In another example, the assay format comprises a negative read-out system in which reduced methylation of DNA from a healthy/normal control sample is detected as a positive signal and preferably, methylated DNA from a neoplastic sample is not detected or is only weakly detected.

[0180] In a preferred embodiment, the reduced methylation is determined using a process comprising:

1. (i) treating the nucleic acid with an amount of a compound that selectively mutates a non-methylated cytosine residue within a CpG island under

conditions sufficient to induce mutagenesis thereby producing a mutated nucleic acid;

2. (ii) hybridizing the nucleic acid to a probe or primer comprising a nucleotide sequence that is complementary to a sequence comprising the mutated cytosine residue under conditions such that selective hybridization to the mutated nucleic acid occurs; and
3. (iii) detecting the selective hybridization.

[0181] In this context, the term "selective hybridization" means that hybridization of a probe or primer to the mutated nucleic acid occurs at a higher frequency or rate, or has a higher maximum reaction velocity, than hybridization of the same probe or primer to the corresponding non-mutated sequence. Preferably, the probe or primer does not hybridize to the methylated sequence (or non-mutated sequence) under the reaction conditions used.

Hybridization-Based Assay Format

[0182] In one embodiment the hybridization is detected using Southern, dot blot, slot blot or other nucleic acid hybridization means (Kawai *et al.,* 1994, *supra*; Gonzalgo *et al.,* 1997, *supra).* Subject to appropriate probe selection, such assay formats are generally described herein above and apply mutatis mutandis to the presently described selective mutagenesis approach. Preferably, a ligase chain reaction format is employed to distinguish between a non-mutated and mutated nucleic acid. In this respect, the assay requirements and conditions are as described herein above for positive read-out assays and apply mutatis mutandis to the present format. However the selection of probes will differ. For negative read-out assays, one or more probes are selected that selectively hybridize to the mutated sequence rather than the non-mutated sequence.

[0183] Preferably, the ligase chain reaction probe(s) have 3'-terminal and/or 5'-terminal sequences that comprise a CpG dinucleotide that is not methylated in a healthy control sample, but is hypermethylated in cancer, such that the diagnostic probe and contiguous probe are capable of being ligated only when the cytosine of the CpG dinucleotide is mutated to thymidine e.g., in the case of a non-methylated cytosine residue.

[0184] As will be apparent to the skilled artisan the MSO method described supra is amenable to either or both positive and/or negative readout assays. This is because the assay described detects both mutated and non-mutated sequences thereby facilitating determining the level of methylation. However, an assay detecting only methylated or non-methylated sequences is contemplated by the invention.

Amplification-Based Assay Format

[0185] In an alternative example, the hybridization is detected using an amplification system using any amplification assay format as described herein above for positive read-out assay albeit using primers (and probes where applicable) selectively hybridize to a mutated nucleic acid.

[0186] In adapting the HeavyMethyl assay described supra to a negative read-out format, the blockers that bind to bisulfite-treated nucleic acid in a methylation specific manner bind specifically to mutated DNA under moderate to high stringency conditions. An amplification reaction is performed using one or more primers that may optionally be methylation specific (i.e. only bind to mutated nucleic acid) but that flank the one or more blockers. In the presence of methylated nucleic acid (i.e., mutated DNA) the blocker/s bind and no PCR product is produced.

[0187] In one example, the reduced methylation in the normal/healthy control subject is detected by performing a process comprising:

1. (i) treating the nucleic acid with an amount of a compound that selectively mutates non-methylated cytosine residues under conditions sufficient to induce mutagenesis thereby producing a mutated nucleic acid;
2. (ii) hybridizing the nucleic acid to two non-overlapping and non-complementary primers each of which comprises a nucleotide sequence that is complementary to a sequence in the DNA comprising a mutated cytosine residue under conditions such that hybridization to the mutated nucleic acid occurs;
3. (iii) amplifying nucleic acid intervening the hybridized primers thereby producing a DNA fragment consisting of a sequence that comprises a primer sequence;
4. (iv) hybridizing the amplified DNA fragment to a probe comprising a nucleotide sequence that corresponds or is complementary to a sequence comprising a mutated cytosine residue under conditions such that hybridization to the mutated nucleic acid occurs; and
5. (v) detecting the hybridization.

[0188] As will be apparent to the skilled artisan a negative read-out assay preferably includes a suitable control sample to ensure that the negative result is caused by methylated nucleic acid rather than a reaction failing.

[0189] This invention also provides kits for the detection and/or quantification of the diagnostic sequences of the invention, or expression or methylation thereof using the methods described herein.

[0190] For kits for detection of methylation, the kits of the invention can comprise at least one polynucleotide that hybridizes to at least one of the diagnostic sequences of the invention and at least one reagent for detection of gene methylation. Reagents for detection of methylation include, e.g., sodium bisulfite, polynucleotides designed to hybridize to sequence that is the product of a biomarker sequence of the invention if the biomarker sequence is not methylated (e.g., containing at least one C→U conversion), and/or a methylation-sensitive or methylation-dependent restriction enzyme. The kits may also include control natural or synthetic DNA sequences representing methylated or unmethylated forms of the sequence. The kits can provide solid supports in the form of an assay apparatus that is adapted to use in the assay. The kits may further comprise detectable labels, optionally linked to a polynucleotide, e.g., a probe, in the kit. Other materials useful in the performance of the assays can also be included in the kits, including test tubes, transfer pipettes, and the like. The kits can also include written instructions for the use of one or more of these reagents in any of the assays described herein.

[0191] As detailed hereinbefore, hypermethylation is associated with transcriptional silencing. Accordingly, in addition to the increased level of methylation of these genes providing a basis upon which to screen for the predisposition to or onset of a large intestine neoplasm, the downregulation in the level of expression of these genes is also diagnostically valuable. In accordance with this aspect of the present disclosure reference to a gene "expression product" or "expression of a gene" is a reference to either a transcription product (such as primary RNA or mRNA) or a translation product such as protein. In this regard, one can assess changes to the level of expression of a gene either by screening for changes to the level of expression product which is produced (i.e. RNA or protein), changes to the chromatin proteins with which the gene is associated, for example the presence of histone H3 methylated on lysine at amino acid position number 9 or 27 (repressive modifications) or changes to the DNA itself which acts to downregulate expression, such as changes to the methylation of the DNA. These genes and their gene expression products, whether they be RNA transcripts, changes to the DNA which act to downregulate expression or encoded proteins, are collectively referred to as "neoplastic markers".

[0192] Accordingly, described herein is a method of screening for the onset or predisposition to the onset of or monitoring a large intestine neoplasm in an individual, said method comprising assessing the level of expression of a DNA region selected from:
(i) the region, including 2kb upstream of the transcription start site, defined by any two or more of Hg19 coordinates:

1. (1) chr12:24962958..25102393
2. (2) chr7:50344378...50472798
3. (3) chr6:391739..411443; or
4. (4) chr12:52400748..52409671; and
5. (5) chr6:163834097..163834982; or

(ii) the gene region, including 2kb upstream of any two or more of:

(1) BCAT1	(2) IKZF1	(3) IRF4	(4) GRASP and	(5) CAHM

in a biological sample from said individual wherein a lower level of expression of at least one of the DNA regions of group (i) and/or (ii) relative to control levels is indicative of a large intestine neoplasm or a predisposition to the onset of a neoplastic state.

[0193] In one embodiment, said method is directed to identifying biological samples in which any one of said DNA regions exhibits a higher level of methylation.

[0194] In another embodiment, said method is directed to identifying biological samples in which two or more of said DNA regions exhibits a higher level of methylation.

[0195] The method is predicated on the comparison of the level of the neoplastic markers of a biological sample with the control levels of these markers. The "control level" may be either a "normal level", which is the level of marker expressed by a corresponding large intestine cell or cellular population which is not neoplastic.

[0196] As detailed hereinbefore, the normal (or "non-neoplastic") level may be determined using tissues derived from the same individual who is the subject of testing. However, it would be appreciated that this may be quite invasive for the individual concerned and it is therefore likely to be more convenient to analyse the test results relative to a standard result which reflects individual or collective results obtained from individuals other than the patient in issue.

[0197] There is more particularly described an aspect comprising a method of screening for the onset or predisposition to the onset of or monitoring a large intestine neoplasm in an individual, said method comprising assessing the level of expression of one or more genes or transcripts selected from:

1. (i) the DNA regions, including 2kb upstream of the transcription start site, defined by Hg19 coordinates:
    1. (1) chr12:24962958..25102393; and
    2. (2) chr7:50344378...50472798;

    and optionally one or more of (3) chr6:391739..411443, (4) chr12:52400748..52409671 and (5) chr6:163834097..163834982; or
2. (ii) the gene region, including 2kb upstream or:
    1. (1) BCAT1; and
    2. (2) IKZF1;

and optionally one or more of (3) IRF4, (4) GRASP and (5) CAHM
in a biological sample from said individual wherein a lower level of expression of at least one of the DNA regions of group (i) and/or group (ii) relative to control levels is indicative of a neoplastic large intestine neoplasm or a predisposition to the onset of a neoplastic state.

[0198] Preferably, said control level is a non-neoplastic level.

[0199] In one embodiment of this aspect, the gene marker panel which is screened for is:
(i) the DNA regions, including 2kb upstream of the transcription start site, defined by Hg19 coordinates:

1. (1) chr12:24962958..25102393
2. (2) chr7:50344378...50472798; and
3. (3) chr6:391739..411443; or

(ii) the gene region, including 2kb upstream of:

(1) BCAT1	(2) IKZF1 and	(3) IRF4.

[0200] In another embodiment of this aspect, the gene marker panel which is screened for is:

(i) the DNA regions, including 2kb upstream of the transcription start site, defined by Hg19 coordinates:

(1) chr12:24962958..25102393

(2) chr7:50344378...50472798; and

(4) chr12:52400748..52409671; or

(ii) the gene region, including 2kb upstream of:

(1) BCAT1	(2) IKZF1 and (4) GRASP.

[0201] In still another embodiment of this aspect, the gene marker panel which is screened for is:
(i) the DNA regions, including 2kb upstream of the transcription start site, defined by Hg19 coordinates:

(1) chr12:24962958..25102393

(2) chr7:50344378...50472798; and

(5) chr6:163834097..163834982; or

(ii) the gene region, including 2kb upstream of:

(1) BCAT1	(2) IKZF1 and (5) CAHM

[0202] In still yet another embodiment of this aspect, the gene marker panel which is screened for is:
(i) the DNA regions, including 2kb upstream of the transcription start site, defined by Hg19 coordinates:

1. (1) chr12:24962958..25102393
2. (2) chr7:50344378...50472798
3. (3) chr6:391739..411443; and
4. (4) chr12:52400748..52409671; or

(ii) the gene region, including 2kb upstream of:

(1) BCAT1	(2) IKZF1	(3) IRF4 and	(4) GRASP.

[0203] In yet still another embodiment of this aspect, the gene marker panel which is screened for is:
(i) the DNA regions, including 2kb upstream of the transcription start site, defined by Hg19 coordinates:

(1) chr12:24962958..25102393

(2) chr7:50344378...50472798

(3) chr6:391739..411443; and

(5) chr6:163834097..163834982; or

(ii) the gene region, including 2kb upstream of:

(1) BCAT1	(2) IKZF1	(3) IRF4 and	(5) CAHM.

[0204] In a further embodiment of this aspect, the gene marker panel which is screened for is:
(i) the DNA regions, including 2kb upstream of the transcription start site, defined by Hg19 coordinates:

(1) chr12:24962958..25102393

(2) chr7:50344378...50472798

(4) chr12:52400748..52409671; and

(5) chr6:163834097..163834982; or

(ii) the gene region, including 2kb upstream of any one or more of:

(1) BCAT1	(2) IKZF1	(4) GRASP and	(5) CAHM.

[0205] In yet another further embodiment of this aspect, the gene marker panel which is screened for is:
(i) the DNA regions, including 2kb upstream of the transcription start site, defined by Hg19 coordinates:

1. (1) chr12:24962958..25102393
2. (2) chr7:50344378...50472798
3. (3) chr6:391739..411443; or
4. (4) chr12:52400748..52409671; and
5. (5) chr6:163834097..163834982; or

(ii) the gene region, including 2kb upstream of any one or more of:

(1) BCAT1	(2) IKZF1	(3) IRF4	(4) GRASP and	(5) CAHM.

[0206] In one embodiment, said method is directed to identifying biological samples in which any one of said DNA regions exhibits a higher level of methylation.

[0207] In another embodiment, said method is directed to identifying biological samples in which two or more of said DNA regions exhibits a higher level of methylation.

[0208] As detailed hereinbefore, the present invention is designed to screen for a neoplastic cell or cellular population, which is located in the large intestine. Accordingly, reference to "cell or cellular population" should be understood as a reference to an individual cell or a group of cells. Said group of cells may be a diffuse population of cells, a cell suspension, an encapsulated population of cells or a population of cells which take the form of tissue.

[0209] Reference to "expression" should be understood as a reference to the transcription and/or translation of a nucleic acid molecule. Reference to "RNA" should be understood to encompass reference to any form of RNA, such as primary RNA or mRNA or non-translated RNA (e.g. miRNAs etc.). The modulation of gene transcription leading to increased or decreased RNA synthesis may also correlate with the translation of some of these RNA transcripts (such as mRNA) to produce a protein product. Accordingly, the present disclosure also extends to detection methodology which is directed to screening for modulated levels or patterns of the neoplastic marker protein products as an indicator of the neoplastic state of a cell or cellular population. Although one method is to screen for mRNA transcripts and/or the corresponding protein product, it should be understood that the present disclosure is not limited in this regard and extends to screening for any other form of neoplastic marker expression product such as, for example, a primary RNA transcript.

[0210] In terms of screening for the downregulation of expression of a marker it would also be well known to the person of skill in the art that changes which are detectable at the DNA level are indicative of changes to gene expression activity and therefore changes to expression product levels. Such changes include but are not limited to, changes to DNA methylation. Accordingly, reference herein to "screening the level of expression" and comparison of these "levels of expression" to control "levels of expression" should be understood as a reference to assessing DNA factors which are related to transcription, such as gene/DNA methylation patterns. These have, in part, been described in detail hereinbefore.

[0211] It would also be known to a person skilled in the art that changes in the structure of chromatin are indicative of changes in gene expression. Silencing of gene expression is often associated with modification of chromatin proteins, methylation of lysines at either or both positions 9 and 27 of histone H3 being well studied examples, while active chromatin is marked by acetylation of lysine 9 of histone H3. Thus association of gene sequences with chromatin carrying repressive or active modifications can be used to make an assessment of the expression level of a gene.

[0212] Reference to "nucleic acid molecule" should be understood as a reference to both deoxyribonucleic acid molecules and ribonucleic acid molecules and fragments thereof. The present disclosure therefore extends to both directly screening for mRNA levels in a biological sample or screening for the complementary cDNA which has been reverse-transcribed from an mRNA population of interest. It is well within the skill of the person of skill in the art to design methodology directed to screening for either DNA or RNA. As detailed above, the method of the present disclosure also extends to screening for the protein product translated from the subject mRNA or the genomic DNA itself.

[0213] In one preferred embodiment, the level of gene expression is measured by reference to genes which encode a protein product and, more particularly, said level of expression is measured at the protein level.

[0214] In another particularly preferred embodiment, said gene expression is assessed by the association of DNA with chromatin proteins carrying repressive modifications, for example, methylation of lysines 9 or 27 of histone H3.

[0215] The present disclosure should be understood to encompass methods of detection based on identifying both proteins and/or nucleic acid molecules in one or more biological samples. This may be of particular significance to the extent that some of the neoplastic markers of interest may correspond to genes or gene fragments which do not encode a protein product. Accordingly, to the extent that this occurs it would not be possible to test for a protein and the subject marker would have to be assessed on the basis of transcription expression profiles or changes to genomic DNA.

[0216] The term "protein" should be understood to encompass peptides, polypeptides and proteins (including protein fragments). The protein may be glycosylated or unglycosylated and/or may contain a range of other molecules fused, linked, bound or otherwise associated to the protein such as amino acids, lipids, carbohydrates or other peptides, polypeptides or proteins. Reference herein to a "protein" includes a protein comprising a sequence of amino acids as well as a protein associated with other molecules such as amino acids, lipids, carbohydrates or other peptides, polypeptides or proteins.

[0217] The proteins encoded by the neoplastic markers of the present disclosure may be in multimeric form meaning that two or more molecules are associated together. Where the same protein molecules are associated together, the complex is a homomultimer. An example of a homomultimer is a homodimer. Where at least one marker protein is associated with at least one non-marker protein, then the complex is a heteromultimer such as a heterodimer.

[0218] Reference to a "fragment" should be understood as a reference to a portion of the subject nucleic acid molecule or protein. This is particularly relevant with respect to screening for modulated RNA levels in stool samples since the subject RNA is likely to have been degraded or otherwise fragmented due to the environment of the gut. One may therefore actually be detecting fragments of the subject RNA molecule, which fragments are identified by virtue of the use of a suitably specific probe.

[0219] Although the preferred method is to detect the expression product or DNA changes of the neoplastic markers for the purpose of diagnosing neoplasia development or predisposition thereto, the detection of converse changes in the levels of said markers may be desired under certain circumstances, for example, to monitor the effectiveness of therapeutic or prophylactic treatment directed to modulating a neoplastic condition, such as adenoma or adenocarcinoma development. For example, where reduced expression of the subject markers indicates that an individual has developed a condition characterised by adenoma or adenocarcinoma development, for example, screening for an increase in the levels of these markers subsequently to the onset of a therapeutic regime may be utilised to indicate reversal or other form of improvement of the subject individual's condition. The method of the present disclosure is therefore useful as a one off test or as an on-going monitor of those individuals thought to be at risk of neoplasia development or as a monitor of the effectiveness of therapeutic or prophylactic treatment regimes directed to inhibiting or otherwise slowing neoplasia development.

[0220] Means of assessing the subject expressed neoplasm markers in a biological sample can be achieved by any suitable method, which would be well known to the person of skill in the art. To this end, it would be appreciated that to the extent that one is examining either a homogeneous cellular population (such as a tumour biopsy or a cellular population which has been enriched from a heterogeneous starting population) or a tissue section, one may utilise a wide range of techniques such as *in situ* hybridisation, assessment of expression profiles by microassays, immunoassays and the like (hereinafter described in more detail) to detect the absence of or downregulation of the level of expression of one or more markers of interest. However, to the extent that one is screening a heterogenous cellular population or a bodily fluid in which heterogeneous populations of cells are found, such as a blood sample, the absence of or reduction in level of expression of a particular marker may be undetectable due to the inherent expression of the marker by non-neoplastic cells which are present in the sample. That is, a decrease in the level of expression of a subgroup of cells may not be detectable. In this situation, a more appropriate mechanism of detecting a reduction in a neoplastic subpopulation of the expression levels of one or more markers of the present disclosure is via indirect means, such as the detection of epigenetic changes.

[0221] Methods of detecting changes to gene expression levels (in addition to the methylation analyses hereinbefore described in detail), particularly where the subject biological sample is not contaminated with high numbers of non-neoplastic cells, include but are not limited to:

1. (i) *In vivo* detection.
   Molecular Imaging may be used following administration of imaging probes or reagents capable of disclosing altered expression of the markers in the intestinal tissues.
   Molecular imaging (Moore et al., BBA, 1402:239-249, 1988; Weissleder et al., Nature Medicine 6:351-355, 2000) is the *in* vivo imaging of molecular expression that correlates with the macro-features currently visualized using "classical" diagnostic imaging techniques such as X-Ray, computed tomography (CT), MRI, Positron Emission Tomography (PET) or endoscopy.
2. (ii) Detection of downregulation of RNA expression in the cells by Fluorescent *In Situ* Hybridization (FISH), or in extracts from the cells by technologies such as Quantitative Reverse Transcriptase Polymerase Chain Reaction (QRTPCR) or Flow cytometric qualification of competitive RT-PCR products (Wedemeyer et al., Clinical Chemistry 48:9 1398-1405, 2002).
3. (iii) Assessment of expression profiles of RNA, for example by array technologies (Alon et al., Proc. Natl. Acad. Sci. USA: 96:6745-6750, June 1999).
   A "microarray" is a linear or multi-dimensional array of preferably discrete regions, each having a defined area, formed on the surface of a solid support. The density of the discrete regions on a microarray is determined by the total numbers of target polynucleotides to be detected on the surface of a single solid phase support. As used herein, a DNA microarray is an array of oligonucleotide probes placed onto a chip or other surfaces used to amplify or clone target polynucleotides. Since the position of each particular group of probes in the array is known, the identities of the target polynucleotides can be determined based on their binding to a particular position in the microarray.
   DNA microarray technology make it possible to conduct a large scale assay of a plurality of target nucleic acid molecules on a single solid phase support. U.S. Pat. No. 5,837,832 (Chee et al.) and related patent applications describe immobilizing an array of oligonucleotide probes for hybridization and detection of specific nucleic acid sequences in a sample. Target polynucleotides of interest isolated from a tissue of interest are hybridized to the DNA chip and the specific sequences detected based on the target polynucleotides' preference and degree of hybridization at discrete probe locations. One important use of arrays is in the analysis of differential gene expression, where the profile of expression of genes in different cells or tissues, often a tissue of interest and a control tissue, is compared and any differences in gene expression among the respective tissues are identified. Such information is useful for the identification of the types of genes expressed in a particular tissue type and diagnosis of conditions based on the expression profile.
4. (iv) Measurement of altered neoplastic marker protein levels in cell extracts, for example by immunoassay.
   Testing for proteinaceous neoplastic marker expression product in a biological sample can be performed by any one of a number of suitable methods which are well known to those skilled in the art. Examples of suitable methods include, but are not limited to, antibody screening of tissue sections, biopsy specimens or bodily fluid samples. To the extent that antibody based methods of diagnosis are used, the presence of the marker protein may be determined in a number of ways such as by Western blotting, ELISA or flow cytometry procedures. These, of course, include both single-site and two-site or "sandwich" assays of the non-competitive types, as well as in the traditional competitive binding assays. These assays also include direct binding of a labelled antibody to a target.
5. (v) Determining altered expression of protein neoplastic markers on the cell surface, for example by immunohistochemistry.
6. (vi) Determining altered protein expression based on any suitable functional test, enzymatic test or immunological test in addition to those detailed in points (iv) and (v) above.

[0222] A person of ordinary skill in the art could determine, as a matter of routine procedure, the appropriateness of applying a given method to a particular type of biological sample.

[0223] A related aspect of the present disclosure provides a molecular array, which array comprises a plurality of:

1. (i) nucleic acid molecules comprising a nucleotide sequence corresponding to any two or more of the neoplastic marker DNA hereinbefore

described or a sequence exhibiting at least 80% identity thereto or a functional derivative, fragment, variant or homologue of said nucleic acid molecule; or

2. (ii) nucleic acid molecules comprising a nucleotide sequence capable of hybridising to any one or more of the sequences of (i) under medium stringency conditions or a functional derivative, fragment, variant or homologue of said nucleic acid molecules; or
3. (iii) nucleic acid probes or oligonucleotides comprising a nucleotide sequence capable of hybridising to any two or more of the sequences of (i) under medium stringency conditions or a functional derivative, fragment, variant or homologue of said nucleic acid molecule; or
4. (iv) probes capable of binding to any two or more of the proteins encoded by the nucleic acid molecules of (i) or a derivative, fragment or, homologue thereof

wherein the level of expression of said marker genes of (i)-(iii) or proteins of (iv) is indicative of the neoplastic state of a cell or cellular subpopulation derived from the large intestine.

[0224] Preferably, said percent identity is at least 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99%.

[0225] "Hybridization" refers to the process by which a nucleic acid strand joins with a complementary strand through base pairing. Hybridization reactions can be sensitive and selective so that a particular sequence of interest can be identified even in samples in which it is present at low concentrations. Stringent conditions can be defined by, for example, the concentrations of salt or formamide in the prehybridization and hybridization solutions, or by the hybridization temperature, and are well known in the art. For example, stringency can be increased by reducing the concentration of salt, increasing the concentration of formamide, or raising the hybridization temperature, altering the time of hybridization, as described in detail, below. In alternative aspects, nucleic acids of the disclosure are defined by their ability to hybridize under various stringency conditions (e.g., high, medium, and low), as set forth herein.

[0226] Reference herein to a low stringency includes and encompasses from at least about 0 to at least about 15% v/v formamide and from at least about 1 M to at least about 2 M salt for hybridization, and at least about 1 M to at least about 2 M salt for washing conditions. Generally, low stringency is at from about 25-30°C to about 42°C. The temperature may be altered and higher temperatures used to replace formamide and/or to give alternative stringency conditions. Alternative stringency conditions may be applied where necessary, such as medium stringency, which includes and encompasses from at least about 16% v/v to at least about 30% v/v formamide and from at least about 0.5 M to at least about 0.9 M salt for hybridization, and at least about 0.5 M to at least about 0.9 M salt for washing conditions, or high stringency, which includes and encompasses from at least about 31% v/v to at least about 50% v/v formamide and from at least about 0.01 M to at least about 0.15 M salt for hybridization, and at least about 0.01 M to at least about 0.15 M salt for washing conditions. In general, washing is carried out $T_m = 69.3 + 0.41$ (G+C)% (Marmur and Doty, J. Mol. Biol. 5:109, 1962). However, the T_m of a duplex DNA decreases by 1°C with every increase of 1% in the number of mismatch base pairs (Bonner and Laskey, Eur. J. Biochem. 46:83, 1974). Formamide is optional in these hybridization conditions. Accordingly, particularly preferred levels of stringency are defined as follows: low stringency is 6 x SSC buffer, 0.1% w/v SDS at 25-42°C; a moderate stringency is 2 x SSC buffer, 0.1% w/v SDS at a temperature in the range 20°C to 65°C; high stringency is 0.1 x SSC buffer, 0.1% w/v SDS at a temperature of at least 65°C.

[0227] Where nucleic acids of the disclosure are defined by their ability to hybridize under high stringency, these conditions comprise about 50% formamide at about 37°C to 42°C. In one aspect, nucleic acids of the disclosure are defined by their ability to hybridize under reduced stringency comprising conditions in about 35% to 25% formamide at about 30°C to 35°C. Alternatively, nucleic acids of the disclosure are defined by their ability to hybridize under high stringency comprising conditions at 42°C in 50% formamide, 5X SSPE, 0.3% SDS, and a repetitive sequence blocking nucleic acid, such as cot-1 or salmon sperm DNA (e.g., 200 n/ml sheared and denatured salmon sperm DNA). In one aspect, nucleic acids of the disclosure are defined by their ability to hybridize under reduced stringency conditions comprising 35% formamide at a reduced temperature of 35°C.

[0228] Preferably, the subject probes are designed to bind to the nucleic acid or protein to which they are directed with a level of specificity which minimises the incidence of non-specific reactivity. However, it would be appreciated that it may not be possible to eliminate all potential cross-reactivity or non-specific reactivity, this being an inherent limitation of any probe based system.

[0229] In terms of the probes which are used to detect the subject proteins, they may take any suitable form including antibodies and aptamers.

[0230] A library or array of nucleic acid or protein probes provides rich and highly valuable information. Further, two or more arrays or profiles (information obtained from use of an array) of such sequences are useful tools for comparing a test set of results with a reference, such as another sample or stored calibrator. In using an array, individual probes typically are immobilized at separate locations and allowed to react for binding reactions. Primers associated with assembled sets of markers are useful for either preparing libraries of sequences or directly detecting markers from other biological samples.

[0231] A library (or array, when referring to physically separated nucleic acids corresponding to at least some sequences in a library) of gene markers exhibits highly desirable properties. These properties are associated with specific conditions, and may be characterized as regulatory profiles. A profile, as termed here refers to a set of members that provides diagnostic information of the tissue from which the markers were originally derived. A profile in many instances comprises a series of spots on an array made from deposited sequences.

[0232] A characteristic patient profile is generally prepared by use of an array. An array profile may be compared with one or more other array profiles or other reference profiles. The comparative results can provide rich information pertaining to disease states, developmental state, receptiveness to therapy and other information about the patient.

[0233] Another aspect of the present invention provides a diagnostic kit for assaying biological samples comprising one or more agents for detecting one or more neoplastic markers and reagents useful for facilitating the detection by said agents. Further means may also be included, for example, to receive a biological sample. The agent may be any suitable detecting molecule.

[0234] The present invention is further described by reference to the following non-limiting examples.

EXAMPLE 1

CAHM: Colorectal Adenocarcinoma HyperMethylated

Single-plex performance:

[0235]

- 74 normals: 0.8 pg hypermethylated/mL plasma (95% CI: 0.2; 1.4)
- 73 adenomas: 9.1 pg hypermethylated/mL plasma (95% CI: -8; 27)
- 73 cancers: 1788 pg hypermethylated/mL plasma (95% CI: 231; 3344).

[0236] The CAHM assay (threshold cut of 3pg/mL plasma) is 55% sensitive for colorectal cancer with a 93% specificity (Figure 1).

GRASP: General Receptor for Phosphoinositides 1-Associated Scaffold Protein.

Single plex performance:

[0237]

- 34 normals: 1.3 pg hypermethylated/mL plasma (95% CI: 0.2; 2.5)
- 33 adenomas: 0.1 pg hypermethylated/mL plasma (95% CI: -0.1; 0.4)
- 33 cancers: 670.8 pg hypermethylated/mL plasma (95% CI: -470.7; 1812)

[0238] The GRASP assay is 58% sensitive for colorectal cancer with a 100% specificity using a threshold cut of 20pg methylated/mL plasma (Figure 2).

IRF4: Interferon Regulatory Factor 4

Single plex performance:

[0239]

- 24 normals: 6 pg hypermethylated/mL plasma (95% CI: 2.9; 9.0)
- 23 adenomas: 3.7 pg hypermethylated/mL plasma (95% CI: -0.4; 8.0)
- 33 cancers: 5340 pg hypermethylated/mL plasma (95% CI: -5369; 16049)

[0240] The IRF4 assay is 57% sensitive for colorectal cancer with a 96% specificity using a threshold cut of 20pg methylated/mL plasma (Figure 3).

BCAT1: Branched chain amino acid transaminase 1, cytosolic

Single plex performance summary

[0241]

- 14 normals: 0 pg hypermethylated/mL plasma (95% CI: na)
- 13 adenomas: 0.4 pg hypermethylated/mL plasma (95% CI: -0.4; 1.3)
- 13 cancers: 4088 pg hypermethylated/mL plasma (95% CI: -4459; 10539)

[0242] The BCAT1 assay is 62% sensitive for colorectal cancer with a 100% specificity using a threshold cut of 3pg methylated/mL plasma (Figure 4).

IKZF1: IKAROS family zinc finger 1

Single plex performance summary

[0243]

- 14 normals: 0 pg hypermethylated/mL plasma (95% CI: na)
- 13 adenomas: 0 pg hypermethylated/mL plasma (95% CI: na)
- 13 cancers: 113 pg hypermethylated/mL plasma (95% CI: -43; 270)

[0244] The IKZF1 assay is 54% sensitive for colorectal cancer with a 100% specificity using a threshold cut of 3pg methylated/mL plasma (Figure 4).

[0245] The methylation levels of the five genes were measured in the same 14 normals, 13 adenomas and 13 cancers. The table below demonstrates the improvement in clinical utility when measuring the methylation in **TWO of the genes:**

(%sens;%spec)	CAHM>$_{6pg/mL}$	GRASP$_{>20pg/mL}$	IRF4$_{>20pg/mL}$	BCAT$_{>3pg/mL}$	IKZF1$_{>3pg/mL}$
CAHM>$_{6pg/mL}$	54% ; 100%	62% ; 100%	69% ; 100%	69% ; 100%	69% ; 100%
GRASP$_{>20pg/mL}$	-	54% ; 100%	69% ; 100%	77% ; 100%	77% ; 100%
IRF4$_{>20pg/mL}$	-	-	54% ; 100%	85% ; 100%	69% ; 100%
BCAT$_{>3pg/mL}$	-	-	-	62% ; 100%	77% ; 100%
IKZF1$_{>3pg/mL}$	-	-	-	-	54% ; 100%

[0246] Combining the methylation levels measured in **any three of the five genes** resulted in:

CAHM$_{6pg/mL}$ - GRASP$_{20pg/mL}$ - IRF4$_{20pg/mL}$:	77% sensitivity and 100% specificity
CAHM$_{6pg/mL}$ - GRASP$_{20pg/mL}$ - BCAT$_{3pg/mL}$:	77% sensitivity and 100% specificity
CAHM$_{6pg/mL}$ - GRASP$_{20pg/mL}$ - IKZF1$_{3pg/mL}$:	77% sensitivity and 100% specificity
CAHM$_{6pg/mL}$ - IKZF1$_{3pg/mL}$ - BCAT$_{3pg/mL}$:	77% sensitivity and 100% specificity
GRASP$_{20pg/mL}$ - IKZF1$_{3pg/mL}$ - BCAT$_{3pg/mL}$:	85% sensitivity and 100% specificity

[0247] Combining the methylation levels from all five genes results in a 92% sensitivity and 100% specificity:

Targeted amplicon sequences for GRASP, CAHM, IRF4, IKZF1 and BCAT1

[0248]

The wild-type DNA sequence of the CAHM MSP amplicon is located on Chromosome 6, plus strand; 163,834,393 ⇒ 163,834,455 (Hg19)
GAAGGAAGCA TTTCGAGCAC GACTGACGCT CCCCTTATTA TTTGCTAAGC

CGCTGCGCTC GGG

The wild-type DNA sequence of the GRASP MSP amplicon is located on Chromosome 12, plus strand; 52,400,886 ⇒ 52,400,973 (Hg19)
cggaagtcgc gcccgccgct ccggtcccga ccccgggacc ccctgccgca gccgccaccc ctgggccccc

agcggacgag ctgtacgc

The wild-type DNA sequence of the IKZF1 MSP amplicon is located on Chromosome 7, plus strand; 50,343,867 ⇒ 50,343,961 (Hg19)
gacgacgcac cctctccgtg tcccgctctg cgcccttctg cgcgccccgc tccctgtacc ggagcagcga tccgggaggc

ggccgagagg tg

The wild-type DNA sequence of the BCAT1 MSP amplicon is located on Chromosome 12, minus strand; 25,101,992 ⇒ 25,102,093 (Hg19)
gtcttcctgc tgatgcaatc CGctaggtcg cgagtctccg ccgcgagagg gccggtctgc aatccagccc gccacgtgta

ctcgccgccg cctcg

The wild-type DNA sequence of the IRF4 MSP amplicon is located on Chromosome 6, minus strand; 392,036 ⇒ 392,145 (Hg19)
tgggtgcctt ggacggcccc gcctcagcca ctcctggggc cccgacagtc cggttagctc atcccgtcca gcttgtggcg

accccgtcgc aggagcgcgg agggcaggcg

PCR protocols used to measure the methylation levels across GRASP, CAHM, IRF4, IKZF1 and BCAT1 in plasma specimens

Real-time PCR protocols GRASP, CAHM, IRF4, BCAT1, IKZF1

[0249]

	CAHM	GRASP	IRF4	BCAT1	IKZF1
FWD Primer	5'GAAGGAA GTATTTCGA GTACGATTG AC	5'CGGAAGT CGCGTTCGT C	5'TGGGTGT TTTGGACG GTTTC	5'GTTTTTTT GTTGATGTA ATTCGTTAG GTC	5'GACGACG TATTTTTTT CGTGTTTC
	200nM final	200nM final	400nM final	200 nM final	200 nM final
REV primer	5'CCCGAACG CAACGACTT AA	5'GCGTACA ACTCGTCCG CTAA	5'CGCCTAC CCTCCGCG	5'CAATACC CGAAACGA CGACG	5'GCGCACC TCTCGACCG
	200nM final	200nM final	400nM final	200nM final	200nM final
Probe	na	[HEX] TTCGATTTC GGGATTTTT TGTCGTAGT C [BHQ1]	[HEX] TCGTTTAGT TTGTGGCG ATTTCGTCG [BHQ1]	[HEX] TTCGTCGCG AGAGGGTC GGTT [BHQ]	na
		100nM final	200nM final	200nM final	
1x PCR	Platinum Taq DNA polymerase (Invitrogen)	Platinum Taq DNA polymerase (Invitrogen)	Platinum Taq DNA polymerase (Invitrogen)	Platinum Taq DNA polymerase (Invitrogen)	GoTaq Hot Start buffer. 1x buffer contains 2mM MgC12 (Promega)
Final $MgCL_2$ conc. [mM]	4.0	4.0	3.0	4.0	+1.0
dNTPs	0.2mM	0.2mM	0.2mM	0.2mM	-
SYBR	1/120,000	na	na	na	1/120,000
LC480 cycling conditions					
1x	95 °C; 2 min	95 °C; 2 min	95 °C; 2 min	95 °C; 2 min	95 °C; 2 min
3x	92 °C; 15 sec	92 °C; 15 sec			
	62 °C; 15 sec	64 °C; 15 sec		**50 cycles:**	**50 cycles:**
	72 °C; 20 sec	72 °C; 20 sec	**50 cycles:**	95 °C; 15 sec	95 °C; 15 sec
47x	82 °C; 15 sec	85 °C; 15 sec	95 °C; 10 sec	62 °C; 30 sec	62°C; 30 sec
	62 °C; 15 sec	64 °C; 15 sec	61 °C; 20 sec	72 °C; 30 sec	72 °C; 30 sec
	72 °C; 20 sec (w/quant)	72 °C; 20 sec (w/quant)	(w/quant)	(w/quant)	(w/quant)
melt curve analysis	95 °C; 5 sec				95 °C; 5 sec
	65 °C; 1 min				65 °C; 1 min
	97 °C	na	na	na	97 °C
	continuous 0.11deg/sec				continuous 0.11deg/sec
Correct Melt Temp (°C)	< 80 °C	na	na	na	82.9-83.2°C

TABLE 1

Gene	Genomic Strand	Current sub-region(s) of interest (genomic sequence)	Coordinates of sub-region(s)	Resulting bisulphite converted sequence (strands no longer complementary)	Oligonucleotide sequences for measurement of methylation levels
BCAT1	top strand	5'-cagtgccCGaggCGgCGgCGagtacaCGtggCGggctggattgcagacCGgcccctctCGCGgCGgagactCGCGacctagCGgattgcatcagcaggaagac (SEQ ID.NO. 1)	25,101,992 - 25,102,093	5'-tagtgttCGaggCGgCGgCGagtataCGtggCGggttggattgtagattCGgttttttCGCGgCGgagattCGCGatttagCGgattgtattagtaggaagat	
	minus strand	3'-gtcacggGCtccGCcGCcGCtcatgtGCaccGCccgacctaacgtctgGCcgggagaGCGCcGCctctgaGCGCtggatcGCctaacgtagtcgtccttctg		3'-gttatggGCtttGCtGCtGCttatgtGCattGCttgatttaatgttgGCtgggagaGCGCtGCtttgaGCGCtggattGCttaatgtagttgttttttg	5'gttttttttgttgatgtaattcgttaggtc 5'-caatacccgaaacgacgacg 5'-ttcgtcgcgagagggtcggtt 5'-tttttgttgatgtaattcgttaggtc 5'-attacaaaccgaccctctcg
	top strand	5'- agatcccaagggtCGtagcccctggcCGtgtggacCGggtctgCGgctgcagagCGCGgtccCGgctgcagcaagacctggggcagt (SEQ ID NO. 2)	25,101,909 - 25,101,995	This sequence is for measuring CpG methylation levels using methylation sensitive restriction enzymes (e.g. HbaII, HhaI (underlined)	5'-agatcccaagggtcgtagc 5'actgccccaggtcttgct
	minus strand	3'- tctagggttcccaGCatcggggaccgGCacacctgGCccagacGCcgacgtctcGCGCcaggGCcgacgtcgttctggaccccgtca			

Gene	Genomic Strand	Current sub-region(s) of interest (genomic sequence)	Coordinates of sub-region(s)	Resulting bisulphite converted sequence (strands no longer complementary)	Oligonucleotide sequences for measurement of methylation levels
IKZF1	top strand	5'-gaCGaCGcaccctctcCGtgtccCGctctgCGcccttctgCGCGcccCGctccctgtacCGgagcagCGatcCGgaggCGgcCGagaggtgCGc (SEQ ID NO. 3)	50,343,867-50,343,961	5'-gaCGaCGtatttttttCGtgtttCGtttgCGttttttgCGCGtttCGtttttgtatCGgagtagCGattCGgaggCGgtCGagaggtgCGt	5'-gacgacgtattttttcgtgtttc 5'gcgcacctctcgaccg 5'-tttgtatcggagtagcgattcgggag
	minus strand	3'-ctGCtGCgtgggagagGCacaggGCgagacGCgggaagacGCGCgggGCgagggacatgGCctcgtcGCtagGCcctccGCcgGCtctccacGCg		3'-ttGCtGCgtgggagagGCataggGCgagatGCgggaagatGCGCgggGCgagggatatgGCttgttGCtagGCtttttGCtgGCttttatGCg	
	top strand	5'- cCGgagttgCGgctgagaCGCGCGcCGCGCCGagcCGggggactCGgCGaCGgggCGgggaCGgaCGaCGcaccctctcCGtgtccCGctct (SEQ ID NO. 4)	50,343,804 - 50,343,895	This sequence is for measuring CpG methylation levels using methylation sensitive restriction enzymes (e.g. HbaII, HhaI (underlined)	5'-ggagttgcggctgagac 5'-agagcgggacacggaga
	minus strand	3'- gGCctcaacGCcgactctGCGCGCgGCGCGCtcgGCcccctgaGCcGCtGCcccGCccctGCcctGCtGCgtgggagagGCacaggGCgaga			
IRF4	top strand	5'- CGcctgcccctcCGCGctcctgCGaCGgggtCGccacaagctggaCGgatgagctaacCGactgtCGgggccccaggagtggctgaggCGgggcCGtccaaggcaccca (SEQ ID NO. 5)	392,036 - 392,145	5'-CGtttgttttttCGCGtttttgCGaCGgggtCGttataagttggaCGgatgagttaatCGattgtCGgggttttaggagtggttgaggCGgggtCGtttaaggtattta	5' - gtttttgcgacggggtc 5' - taaaaccccgacaatccg
	minus strand	3'-GCggacgggagGCGCgaggacGCtGCccaGCggtgttcgacctGCcctactcgattgGCtgacaGCcccggggtcctcaccgactccGCcccgGCaggttccgtgggt		3'-GCggatgggagGCGCgaggatGCtGCttaGCggtgtttgatttGCttattgattgGCtgataGCttggggtttttatgatttGCtttgGCaggtttgtgggt	5' - tgggtgttttggacggtttc 5' - tagttatttttggggtttcgatagttc 5' - cgcctaccctccgcg 5' - tcgtttagtttgtggcgatttcgtcg
GRASP	top strand	5'-caggaagctgcagcagaaggaggaggCGgCGgccacccCGgacccCGcCGccCGgactccCGactCGgaagtCGCGccCGcCGctcCGtccCGacccCGgacccccctgcCGcagcCGccaccccctgggcccccagCGgaCGagctgtaCGCGgCGctggaggactatcaccctgcCGagctgtacCGCGCGctCGcCGtgtcCGggggcaccctgcccCGcCGaaaggtgCGtccccCGccCGccttcaggatctgctcagcccctctcCGactccctacagggcctgctgactcCG (SEQ ID NO. 6)	52,400,821 - 52,401,051	5'-taggaagttgtagtagaaggaggaggCGgCGgttatttCGgatttCGtCGttCGgatttCGattCGgaagtCGCGttCGtCGtttCGtttCGatttCGgattttttgtCGtagtCGttattttgggtttttagCGgaCGagttgtaCGCGgCGttggaggattattatttgtCGagttgtatCGCGCGttCGtCGtgttCGgggggtattttgttttCGtCGaaaggtgCGttttCGttCGttttaggatttgtttagtttttttCGattttatagggtttgttgatttCG	5' -cggaagtcgcgttcgtc 5' -gcgtacaactcgtccgctaa 5' - ttcgatttcgggatttttgtcgtagtc 5' -cggattttcgattcggaagt
	minus strand	3'-gtccttcgacgtcgtcttcctcctccGCcGCcggtgggGCctgggGCgGCggGCctgaggGCtgaGCcttcaGCGCggGCgGCgagGCaggGCtgggGCcctgggggacgGCgtcgGCggtggggacccgggggtcGCctGCtcgacatGCGCcGCgacctcctgatagtgggacgGCtcgacatgGCGCGCgaGCgGCacagGCccccgtgggacgggGCgGCtttccacGCaggggGCggGCggaagtcctagacgagtcggggagagGCtgaggatgtcccggacgactgagGC		3'-gtttttgatgttgttttttttttttGCtGCtggtgggGCttgggGCgGCggGCttgaggGCtgaGCtttaGCGCggGCgGCgagGCtaggGCtgggGCttgggggatgGCgttgGCggtggggatttgggggttGCttGCttgatatGCGCtGCgatttttgatagtgggatgGCttgatatgGCGCGCgaGCgGCatagGCttttgtgggatgggGCgGCttttatGCaggggGCggGCggaagttttagatgagttggggagagGCtgaggatgttttggatgattgagGC	5' - ggtagggtgttttcggatac 5' - aacgaacgaactatacgcgac
	top strand	5'-gacagagacagcccccaggcaagttgaaggtcCGagagccccCGgtgggagaagCGggcCGgtggctgCGcCGCGtgCGtttctcactctgaggaagtgCGtggggagcCGctgactcCGatagcacaccccttcCGaggggactcccCGattcctgggctggggggcctgcCGcctggccccaCGtctgaCGtaCGgggCGCGagggccactgctccctggacttctgtCGgaacCGgaCGcagtgggaggggtCGcagg (SEQ ID NO. 7)	52,401,407 - 52,401,664	5'-gatagagatagttttaggtaagttgaaggttCGagagttttCGgtgggagaagCGggtCGgtggttgCGtCGCGtgCGttttttattttgaggaagtgCGtggggagtCGttgatttCGatagtatatttttttCGaggggatttttCGatttttgggttggggggtttgtCGtttggttttaCGtttgaCGtaCGgggCGCGagggttattgtttttggatttttgtCGgaatCGgaCGtagtgggaggggtCGtagg	
	minus strand	3'-ctgtctctgtcggggtccgttcaacttccagGCtctcggggGCcacccctcttcGCccgGCcaccgacGCgGCGCacGCaagagtgagactccttcacGCacccctcgGCgactgagGCctatcgtgtgggaagGCtcccctgaggGCtaaggacccgacccccggacgGCggaccggggtGCagactGCatGCcccGCGCtcccggtgacgagggacctgaagacaGCcttgGCctGCgtcaccctccccaGCgtcc		3'-ttgttttgttggggtttgttaattttagGCttttggggGCtatttttttttGCttgGCtattgatGCgGCGCatGCaagagtgagatttttatGCatttttgGCgattgagGCttattgtgtgggaagGCtttttgagggGCtaaggatttgatttttggatgGCggattggggtGCagattGCatGCtttGCGCttttggtgatgagggatttgaagataGCtttgGCttGCgttattttttttaGCgttt	5' -cggagttagcggtttttacg 5' -cgataaaaaaaaacgaaccga 5' -agagtgagaacgtacgcggc
	top strand	5'-gacagagacagcccccaggcaagttgaaggtcCGagagccccCGgtgggagaagCGggcCGgtggctgCGcCGCGtgCGtttctcactctgaggaagtgCGtggggagcCGctgactcCGatagcacaccccttcCGaggggactcccCGattcctgggctggggggcctgcCGcctggccccaCGtctgaCGtaCGgggCGCGagggccactgctccctggacttctgtCGgaacCGgaCGcagtgggaggggtCGcagg		This sequence is for measuring CpG methylation levels using methylation sensitive restriction enzymes (e.g. HbaII, HhaI (underlined)	5' -caagttgaaggtccgagagc 5' -cgcacttcctcagagtgaga
	minus strand	3'-ctgtctctgtcggggtccgttcaacttccagGCtctcggggGCcacccctcttcGCccgGCcaccgacGCgGCGCacGCaagagtgagactccttcacGCacccctcgGCgactgagGCctatcgtgtgggaagGCtcccctgaggGCtaaggacccgacccccggacgGCggaccggggtGCagactGCatGCcccGCGCtcccggtgacgagggacctgaagacaGCcttgGCctGCgtcaccctccccaGCgtcc			
		5'- atctgtaaaaatgttgacttctgcttttcagactaCGCGcac		5'-atttgtaaaaatgttgatttttgttttttagattaCGCGtat	5' - gaaggaagtattcgagtacgattgacc

Gene	Genomic Strand	Current sub-region(s) of interest (genomic sequence)	Coordinates of sub-region(s)	Resulting bisulphite converted sequence (strands no longer complementary)	Oligonucleotide sequences for measurement of methylation levels
CAHM	top strand	agcctctttatttcctactgCCgcttcattccctcaCGgaacactgaCGccatCGCGaaggaagcatttCGagcaCGactgaCGctccccttattatttgctaagcCGctgCCGctCGggtctggctaCGatttgctttcagaataaCGggaaggtgcaacaaga (SEQ ID NO. 8)	163,834,295 163,834,500	[illegible] tttattgCGgtttatttttaCGgaatattgaCGttatCGCGaaggaagtatttCGagtaCGattgaCGtttttattatttgttaagtCGttgCGttCGggtttggttaCGatttgttttagaataaCGggaaggtgtaataaga	5' - cccgaacgcaacgacttaa 5' - gcctctaaaaaaaacgatcttattacacc
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	minus strand	3'-cgGCacgacgaaaggtcggagagtcgtttagtGCttgtgGCtttcttcggtGCcGCcGCtGCcctccccGCaGCGCGCacgaagggaGCcGCtgtttcGCcctcgGCccGCGCgGCcgGCtcccGCggGCcGCgtctcaggGCgtctccGCctGCgGCGCcgtGCGCggaGCttttcggagttgagaataggaGCcgagaggGCggggtggagGCgggGCgtcggttctggGCGCgGCaccGCccggGCtGCcggttcctttcgggtggtcgggagGCtgGCac	163,834,621 163,834,906	tgGCatgatgaaaggttggagagttgtttagtGCttgtgGCtttttggtGCtGCtGCtGCttttGCaGCGCGCatgaagggaGCtGCtgtttGCtttgGCttGCGCgGCtgGCtttGCggGCtGCgttttaggGCgttttGCttGCgGCGCtgtGCGCggaGCttttggagtttgagaataggaGCtgagaggGCggggtggagGCgggGCgttggttttggGCGCgGCattGCttggGCtGCtggtttttgggtggttgggagGC tgGCat	5' -gtttttttcggcgataaagc 5' -cgcctctacgaaactctacg 5' -cgtcggtcgagggcgttc

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cacccctggg cccccagcgg acgagctgta cgcggcgctg gaggactatc accctgccga 180

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gcgtattttt cggtcgtttt tcggatcgtt gtttcggtat agggagcggg gcgcgtagaa 60

gggcgtagag cgggatacgg agagggtgcg tcgtt 95

<210> 39
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> IKZF1 oligonucleotide for measurement of methylation levels

<400> 39
ggagttgcgg ctgagac 17

<210> 40
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> IKZF1 oligonucleotide for measurement of methylation levels

<400> 40
agagcgggac acggaga 17

<210> 41
<211> 92
<212> DNA
<213> Homo sapiens

<400> 41
agagcgggac acggagaggg tgcgtcgtcc cgtccccgcc ccgtcgccga gtcccccggc 60

tcgcgcggcg cgcgtctcag ccgcaactcc gg 92

<210> 42
<211> 110
<212> DNA
<213> Artificial Sequence

<220>
<223> IRF4 resulting bisulphite converted sequence

<400> 42
cgtttgtttt tcgcgttttt gcgacggggt cgttataagt tggacgggat gagttaatcg 60

gattgtcggg gttttaggag tggttgaggc ggggtcgttt aaggtattta 110

<210> 43
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> IRF4 oligonucleotide for measurement of methylation levels

<400> 43
gttttgcga cggggtc 17

<210> 44
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> IRF4 oligonucleotide for measurement of methylation levels

<400> 44
taaaaccccg acaatccg 18

<210> 45
<211> 110
<212> DNA
<213> Homo sapiens

<400> 45
tgggtgcctt ggacggcccc gcctcagcca ctcctggggc cccgacagtc cggttagctc 60

atcccgtcca gcttgtggcg accccgtcgc aggagcgcgg agggcaggcg 110

<210> 46
<211> 110
<212> DNA
<213> Artificial Sequence

<220>
<223> IRF4 resulting bisulphite converted sequence

<400> 46
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atttcgttta gtttgtggcg atttcgtcgt aggagcgcgg agggtaggcg 110

<210> 47
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> IRF4 oligonucleotide for measurement of methylation levels

<400> 47
tagttatttt tggggtttcg atagttc 27

<210> 48
<211> 299
<212> DNA
<213> Artificial Sequence

<220>
<223> GRASP resulting bisulphite converted sequence

<400> 48

taggaagttg tagtagaagg aggaggcggc ggttatttcg gatttcgtcg ttcggatttt 60

cgattcggaa gtcgcgttcg tcgtttcggt ttcgatttcg ggatttttg tcgtagtcgt 120

tatttttggg tttttagcgg acgagttgta cgcggcgttg gaggattatt attttgtcga 180

gttgtatcgc gcgttcgtcg tgttcggggg tattttgttt cgtcgaaagg tgcgtttttc 240

gttcgttttt aggatttgtt tagtttttt tcgatttttt atagggtttg ttgatttcg 299

<210> 49
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> GRASP oligonucleotide for measurement of methylation levels

<400> 49
cggattttcg attcggaagt 20

<210> 50
<211> 298
<212> DNA
<213> Homo sapiens

<400> 50

cggagtcagc aggccctgta gggagtcgga gaggggctga gcagatcctg aaggcgggcg 60

ggggacgcac ctttcggcgg ggcagggtgc cccggacac ggcgagcgcg cggtacagct 120

cggcagggtg atagtcctcc agcgccgcgt acagctcgtc cgctgggggc ccaggggtgg 180

cggctgcggc agggggtccc ggggtcggga ccggagcggc gggcgcgact ccgagtcggg 240

agtccgggcg gcggggtccg gggtggccgc cgcctcctcc ttctgctgca gcttcctg 298

<210> 51
<211> 298
<212> DNA
<213> Artificial Sequence

<220>
<223> GRASP resulting bisulphite converted sequence

<400> 51

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ggggacgtat ttttcggcgg ggtagggtgt tttcggatac ggcgagcgcg cggtatagtt 120

cggtagggtg atagtttttt agcgtcgcgt atagttcgtt cgttgggggt ttaggggtgg 180

cggttgcggt agggggtttc ggggtcggga tcggagcggc gggcgcgatt tcgagtcggg 240

agttcgggcg gcggggttcg gggtggtcgt cgtttttttt ttttgttgta gtttttg 298

<210> 52
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> GRASP oligonucleotide for measurement of methylation levels

<400> 52
ggtagggtgt tttcggatac 20

<210> 53
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> GRASP oligonucleotide for measurement of methylation levels

<400> 53
aacgaacgaa ctatacgcga c 21

<210> 54
<211> 258
<212> DNA
<213> Artificial Sequence

<220>
<223> GRASP resulting bisulphite converted sequence

<400> 54
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gtggttgcgt cgcgtgcgtt tttattttga ggaagtgcgt ggggagtcgt tgatttcgga 120

tagtatattt tttcgagggg atttttcgat ttttgggttg ggggtttgtc gtttggtttt 180

acgtttgacg tacggggcgc gagggttatt gtttttttgga tttttgtcgg aatcggacgt 240

agtgggaggg gtcgtagg 258

<210> 55
<211> 258
<212> DNA
<213> Homo sapiens

<400> 55
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gccccgtacg tcagacgtgg ggccaggcgg caggccccca gcccaggaat cggggagtcc 120

cctcggaagg gtgtgctatc cggagtcagc ggctccccac gcacttcctc agagtgagaa 180

cgcacgcggc gcagccaccg gcccgcttct cccaccgggg gctctcggac cttcaacttg 240

cctggggctg tctctgtc 258

<210> 56
<211> 258
<212> DNA
<213> Artificial Sequence

<220>
<223> GRASP resulting bisulphite converted sequence

<400> 56
tttgcgattt tttttattgc gttcggtttc gatagaagtt tagggagtag tggttttcgc 60

gtttcgtacg ttagacgtgg ggttaggcgg taggttttta gtttaggaat cggggagttt 120

tttcggaagg gtgtgttatt cggagttagc ggtttttttac gtattttttt agagtgagaa 180

cgtacgcggc gtagttatcg gttcgttttt tttatcgggg gttttcggat ttttaatttg 240

tttggggttg tttttgtt 258

<210> 57
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> GRASP oligonucleotide for measurement of methylation levels

<400> 57
cggagttagc ggtttttttac g 21

<210> 58
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> GRASP oligonucleotide for measurement of methylation levels

<400> 58
cgataaaaaa aacgaaccga 20

<210> 59
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> GRASP oligonucleotide for measurement of methylation levels

<400> 59
agagtgagaa cgtacgcggc 20

<210> 60
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> GRASP oligonucleotide for measurement of methylation levels

<400> 60
caagttgaag gtccgagagc 20

<210> 61
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> GRASP oligonucleotide for measurement of methylation levels

<400> 61
cgcacttcct cagagtgaga 20

<210> 62
<211> 206
<212> DNA
<213> Artificial Sequence

<220>
<223> CAHM resulting bisulphite converted sequence

<400> 62
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tgcggtttta tttttttacg gaatattgac gttatcgcga aggaagtatt tcgagtacga      120

ttgacgtttt ttttattatt tgttaagtcg ttgcgttcgg gtttggttac gatttgtttt      180

tagaataacg ggaaggtgta ataaga                                           206
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<210> 63
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> CAHM oligonucleotide for measurement of methylation levels

<400> 63
gcctctaaaa aaacgatctt attacacc 28

<210> 64
<211> 206
<212> DNA
<213> Homo sapiens

<400> 64
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tcttgttgca ccttcccgtt attctgaaag caaatcgtag ccagacccga gcgcagcggc       60

ttagcaaata ataaggggag cgtcagtcgt gctcgaaatg cttccttcgc gatggcgtca      120

gtgttccgtg agggaatgaa gccgcagtag gaaataaaga ggctgtgcgc gtagtctgaa      180

aagcagaagt caacattttt acagat                                           206
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<210> 65
<211> 206
<212> DNA
<213> Artificial Sequence

<220>
<223> CAHM resulting bisulphite converted sequence

<400> 65
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ttttgttgta ttttttcgtt attttgaaag taaatcgtag ttagattcga gcgtagcggt       60

ttagtaaata ataaggggag cgttagtcgt gttcgaaatg tttttttcgc gatggcgtta      120

gtgtttcgtg agggaatgaa gtcgtagtag gaaataaaga ggttgtgcgc gtagtttgaa      180

aagtagaagt taatattttt atagat                                           206
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<210> 66
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> CAHM oligonucleotide for measurement of methylation levels

<400> 66
gaaacactaa cgccatcg 18

<210> 67
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> CAHM oligonucleotide for measurement of methylation levels

<400> 67
cgtagttaga ttcgagcgta g 21

<210> 68
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> CAHM oligonucleotide for measurement of methylation levels

<400> 68
aggggagcgt tagtcgtgtt cgaaa 25

<210> 69
<211> 285
<212> DNA
<213> Homo sapiens

<400> 69
cacggtcgga gggctggtgg gctttccttg gccgtcgggc ccgccacggc gcgggtcttg 60

gctgcggggc ggaggtgggg cgggagagcc gaggataaga gtttgaggct tttcgaggcg 120

cgtgccgcgg cgtccgcctc tgcgggactc tgcgccgggc gccctcggcc ggcgcgcccg 180

gctcccgctt tgtcgccgag ggaagcacgc gcgacgcccc tcccgtcgcc gccgtggctt 240

ctttcggtgt tcgtgatttg ctgagaggct ggaaagcagc acggc 285

<210> 70
<211> 285
<212> DNA
<213> Artificial Sequence

<220>
<223> CAHM resulting bisulphite converted sequence

<400> 7
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gctttttttg cagcgcgcat gaagggagct gctgttttgc ttttggcttg cgcggctggc 120

ttttgcgggc tgcgttttag ggcgtttttg cttgcggcgc tgtgcgcgga gctttttgga 180

gtttgagaat aggagctgag agggcggggt ggaggcgggg cgttggtttt gggcgcggca 240

ttgcttgggc tgctggtttt ttttgggtgg ttgggaggct ggcat 285

<210> 71
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> CAHM oligonucleotide for measurement of methylation levels

<400> 71
gtttttttcg gcgataaagc 20

<210> 72
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> CAHM oligonucleotide for measurement of methylation levels

<400> 72
cgcctctacg aaactctacg 20

<210> 73
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> CAHM oligonucleotide for measurement of methylation levels

<400> 73
cgtcggtcga gggcgttc 18

<210> 74
<211> 10924
<212> DNA
<213> Homo sapiens

<400> 74
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gtgctaatgc ttcacaatag agtcccatgt ttccccactg acaccccctc ggcccctcag 120

ctgatggcca cttggtggtg ccaaggcggg aggtgggagg agggagaaga aggcactaag 180

agagctacct cttagctcct ggcagtcctc aatccacccc ggccccccac ccaacaagca 240

tcctgccatc tggacttgtg caatcactga ggggcggaaa agcaccctct tccacccaca 300

cctcttgtag gggatggggg cctagaggac tgggggtggg gaggagaaca cagagtcaag 360

gagactagag aagaagactg agccaggcgc aagaactgag acaggcagga ggcagaaagt 420

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Patentkrav

1. Fremgangsmåde til screening for debut eller prædisponering for debut af eller overvågning af et tyktarmsneoplasma hos et individ, hvilken fremgangsmåde omfatter vurdering af methyleringsstatus for:
genregionen, der indbefatter 2 kb opstrøms for:
(2) IKZF1;
i kombination med en eller flere af følgende genregioner, der indbefatter 2 kb opstrøms for:
(1) BCAT1;
(3) IRF4;
(4) GRASP; og
(5) CAHM
i en biologisk prøve fra individet, hvor et højere methyleringsniveau i mindst én af DNA-regionerne i forhold til kontrolniveauer er indikation for et tyktarmsneoplasma eller prædisponering for debut af en tyktarmsneoplastisk tilstand.

2. Fremgangsmåde ifølge krav 1, hvor fremgangsmåden omfatter vurdering af methyleringsstatus for:
genregionen, der indbefatter 2 kb opstrøms for:
(2) IKZF1; og
(5) CAHM;
og eventuelt en eller flere af (1) BCAT1; (3) IRF4; og (4) GRASP;
i en biologisk prøve fra individet, hvor et højere methyleringsniveau i mindst én af DNA-regionerne i forhold til kontrolniveauer er indikation for et tyktarmsneoplasma eller prædisponering for debut af en tyktarmsneoplastisk tilstand.

3. Fremgangsmåde ifølge krav 1, hvor fremgangsmåden omfatter vurdering af methyleringsstatus for:
genregionen, der indbefatter 2 kb opstrøms for:
(2) IKZF1; og
(3) IRF4;
og eventuelt en eller flere af (1) BCAT1; (4) GRASP; og (5) CAHM;

i en biologisk prøve fra individet, hvor et højere methyleringsniveau i mindst én af DNA-regionerne i forhold til kontrolniveauer er indikation for et tyktarmsneoplasma eller prædisponering for debut af en tyktarmsneoplastisk tilstand.

4. Fremgangsmåde ifølge krav 1, hvor fremgangsmåden omfatter vurdering af methyleringsstatus for:
genregionen, der indbefatter 2 kb opstrøms for:
(2) IKZF1; og
(4) GRASP;
og eventuelt en eller flere af (1) BCAT1; (3) IRF4; og (5) CAHM;
i en biologisk prøve fra individet, hvor et højere methyleringsniveau i mindst én af DNA-regionerne i forhold til kontrolniveauer er indikation for et tyktarmsneoplasma eller prædisponering for debut af en tyktarmsneoplastisk tilstand.

5. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 4, hvor en hvilken som helst af DNA-regionerne fremviser et højere methyleringsniveau.

6. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 4, hvor hvilke som helst to eller flere af DNA-regionerne fremviser et højere methyleringsniveau.

7. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 6, hvor den neoplastiske celle er et adenom eller et adenokarcinom.

8. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 7, hvor kontrolniveauet er et ikke-neoplastisk niveau.

9. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 8, hvor neoplasien er en colorektal neoplasi.

10. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 9, hvor den biologiske prøve er en fækalprøve, et lavementudskyl, en kirurgisk resektion, en vævsbiopsi eller en

blodprøve.

11. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 10, hvor methyleringen vurderes i en eller flere kromosomale delregioner valgt blandt:
(1) BCAT-delregionerne chr12:25101992-25102093 (SEQ ID NO: 1 eller den tilsvarende minus-streng) og chr12:25101909-25101995 (SEQ ID NO: 2 eller den tilsvarende minus-streng);
(2) IKZF1-delregionerne: chr7:50343867-50343961 (SEQ ID NO: 3 eller den tilsvarende minus-streng) og chr7:50343804-5033895 (SEQ ID NO: 4 eller den tilsvarende minus-streng);
(3) IRF4-delregionerne chr6:392036-392145 (SEQ ID NO: 5 eller den tilsvarende minus-streng);
(4) GRASP-delregionerne: chr12:52399672-52399922, chr12:52400821-52401051 (SEQ ID NO: 6 eller den tilsvarende minus-streng), chr12:52401407-52401664 (SEQ ID NO: 7 eller den tilsvarende minus-streng), chr12:52400866-52400973 og chr12:52401107-52401664; og
(5) CAHM-delregionerne: chr6:163834295-163834500 (SEQ ID NO: 8 eller den tilsvarende minus-streng), chr6:163834621-163834906, chr6:163834393-163834455 og chr6:163834393-163834519.

12. Fremgangsmåde ifølge krav 11, hvor delregionen er valgt blandt SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7 eller SEQ ID NO: 8 eller de tilsvarende minus-strenge.

13. Fremgangsmåde ifølge krav 11 eller 12, hvilken fremgangsmåde omfatter vurdering af methyleringen af en eller flere cytosinrester valgt blandt:

(GRASP)			
chr12:52399713	chr12:52399731	chr12:52399749	chr12:52399783
chr12:52399796	chr12:52399808	chr12:52399823	chr12:52399835
chr12:52399891			
chr12:52400847	chr12:52400850	chr12:52400859	chr12:52400866

chr12:52400869	chr12:52400873	chr12:52400881	chr12:52400886
chr12:52400893	chr12:52400895	chr12:52400899	chr12:52400902
chr12:52400907	chr12:52400913	chr12:52400919	chr12:52400932
chr12:52400938	chr12:52400958	chr12:52400962	chr12:52400971
chr12:52400973	chr12:52400976	chr12:52400998	chr12:52401008
chr12:52401010	chr12:52401012	chr12:52401016	chr12:52401019
chr12:52401025	chr12:52401041	chr12:52401044	chr12:52401053
chr12:52401060	chr12:52401064	chr12:52401092	chr12:52401118
chr12:52401438	chr12:52401448	chr12:52401460	chr12:52401465
chr12:52401474	chr12:52401477	chr12:52401479	chr12:52401483
chr12:52401504	chr12:52401514	chr12:52401523	chr12:52401540
chr12:52401553	chr12:52401576	chr12:52401588	chr12:52401595
chr12:52401599	chr12:52401604	chr12:52401606	chr12:52401634
chr12:52401640	chr12:52401644	chr12:52401659	
chr12:52401160	chr12:52401165	chr12:52401174	chr12:52401177
chr12:52401179	chr12:52401183	chr12:52401204	chr12:52401215
chr12:52401223	chr12:52401240	chr12:52401253	chr12:52401288
chr12:52401295	chr12:52401299	chr12:52401304	chr12:52401334
chr12:52401340	chr12:52401344	chr12:52401359	
(CAHM)			
chr6:163834330	chr6:163834332	chr6:163834357	
chr6:163834373	chr6:163834384	chr6:163834390	
chr6:163834392	chr6:163834406	chr6:163834412	
chr6:163834419	chr6:163834443	chr6:163834448	
chr6:163834452	chr6:163834464	chr6:163834483	

chr6:163834653	chr6:163834660	chr6:163834672	
chr6:163834675	chr6:163834678	chr6:163834681	
chr6:163834815	chr6:163834824	chr6:163834835	
chr6:163834840	chr6:163834853	chr6:163834855	
chr6:163834858	chr6:163834863	chr6:163834869	
chr6:163834872			
(IKZF1)			
chr7:50343869	chr7:50343872	chr7:50343883	
chr7:50343889	chr7:50343890	chr7:50343897	
chr7:50343907	chr7:50343909	chr7:50343914	
chr7:50343934	chr7:50343939	chr7:50343950	
chr7:50343959	chr7:50343805	chr7:50343822	
chr7:50343824	chr7:50343826	chr7:50343829	
chr7:50343831	chr7:50343833	chr7:50343838	
chr7:50343847	chr7:50343850	chr7:50343858	
chr7:50343864	chr7:50343869	chr7:50343872	
chr7:50343890			
(IRF4)			
chr6:392036	chr6:392047	chr6:392049	
chr6:392057	chr6:392060	chr6:392066	
chr6:392080	chr6:392094	chr6:392102	
chr6:392131			

eller en tilsvarende cytosin i position n+1 på den modsatte DNA-streng.

14. Fremgangsmåde ifølge et hvilket som helst af kravene 1

til 13, hvor pattedyret er et menneske.

DRAWINGS

FIGURE 1

>hg19_refGene_NM_181711 range=chr12:52398748-52409671 5'pad=0 3'pad=0 strand=+ repeatMasking=none

GRASP resides on the plus strand, thus the top strand in the below is the representative 5'-3'- sequence of GRASP.

YELLOW: sub-regions of interest towards which three bisulphite conversion and methylation specific assays are given as examples of designs targeting both strands

GREEEN font: sub-region of interest given as an example of a methylation sensitive restriction enzymes (hhaI/HbaII) PCR amplicon

```
   1  CCCACCCCCCACAGATGCTGTCTGTCAGGAGCAGGCAACAGACGGTCCTGGGGTCCATCT
   1  GGGTGGGGGGTGTCTACGACAGACAGTCCTCGTCCGTTGTCTGCCAGGACCCCAGGTAGA

  61  GTGCTAATGCTTCACAATAGAGTCCCATGTTTCCCCACTGACACCCCCTCGGCCCCTCAG
  61  CACGATTACGAAGTGTTATCTCAGGGTACAAAGGGGTGACTGTGGGGGAGCCGGGGAGTC

 121  CTGATGGCCACTTGGTGGTGCCAAGGCGGGAGGTGGGAGGAGGGAGAAGAAGGCACTAAG
 121  GACTACCGGTGAACCACCACGGTTCCGCCCTCCACCCTCCTCCCTCTTCTTCCGTGATTC

 181  AGAGCTACCTCTTAGCTCCTGGCAGTCCTCAATCCACCCCGGCCCCCCACCCAACAAGCA
 181  TCTCGATGGAGAATCGAGGACCGTCAGGAGTTAGGTGGGGCCGGGGGGTGGGTTGTTCGT

 241  TCCTGCCATCTGGACTTGTGCAATCACTGAGGGGCGGAAAAGCACCCTCTTCCACCCACA
 241  AGGACGGTAGACCTGAACACGTTAGTGACTCCCCGCCTTTTCGTGGGAGAAGGTGGGTGT

 301  CCTCTTGTAGGGGATGGGGGCCTAGAGGACTGGGGGTGGGGAGGAGAACACAGAGTCAAG
 301  GGAGAACATCCCCTACCCCCGGATCTCCTGACCCCCACCCCTCCTCTTGTGTCTCAGTTC

 361  GAGACTAGAGAAGAAGACTGAGCCAGGCGCAAGAACTGAGACAGGCAGGAGGCAGAAAGT
 361  CTCTGATCTCTTCTTCTGACTCGGTCCGCGTTCTTGACTCTGTCCGTCCTCCGTCTTTCA

 421  CTTTCCTGGCCTCGCAGGTGGACGTGGCCATTGCCCCTCTGTGCTCCTTATGCCACGTGT
 421  GAAAGGACCGGAGCGTCCACCTGCACCGGTAACGGGGAGACACGAGGAATACGGTGCACA

 481  CTAACACAGCACATGTGCAAGGTACCACTCCCTACCAGGCCAAGAGCCTCTGTAACCCCA
 481  GATTGTGTCGTGTACACGTTCCATGGTGAGGGATGGTCCGGTTCTCGGAGACATTGGGGT

 541  GTGCCCAGCCAGTACCTGGCACACAGCAGGGCTTAAATGTTGGACAACATCACAGAGTGG
 541  CACGGGTCGGTCATGGACCGTGTGTCGTCCCGAATTTACAACCTGTTGTAGTGTCTCACC

 601  TTAGATTGCAGGCTCTGGAACCAGGCTGCCTGGCTTTGAATCTCAGCTCTGCCGCTGAGT
 601  AATCTAACGTCCGAGACCTTGGTCCGACGGACCGAAACTTAGAGTCGAGACGGCGACTCA

 661  GACTTAGGGCAAATTACTTATCTTCTCTGGGCCTCAGTTTCCTCATCTGTAAGGGAGGAT
 661  CTGAATCCCGTTTAATGAATAGAAGAGACCCGGAGTCAAAGGAGTAGACATTCCCTCCTA

 721  AATGGTGCTTATTTCGTAGGGTTGTTATGAAGACCAAGTGAGTTAATGCATGTATGTAAA
 721  TTACCACGAATAAAGCATCCCAACAATACTTCTGGTTCACTCAATTACGTACATACATTT

 781  AGGACACACAGAACAAACAGTGTGCATAGCACATGCTAAGTGCTCAATAAATGTTAACTG
 781  TCCTGTGTGTCTTGTTTGTCACACGTATCGTGTACGATTCACGAGTTATTTACAATTGAC

 841  TGAAGGCATAACAGATTTGGGAAGACTGGGGGAGGAGGGAGGGGACAGACAAGGGCACCG
 841  ACTTCCGTATTGTCTAAACCCTTCTGACCCCCTCCTCCCTCCCCTGTCTGTTCCCGTGGC

 901  CATTGCCGCCTCTGCTTCTTGGCCGATGGGTGTTGGGACATGGAGTCCCCAGCCTGTGCT
 901  GTAACGGCGGAGACGAAGAACCGGCTACCCACAACCCTGTACCTCAGGGGTCGGACACGA

 961  GCTGACGCCCTGTGGTGGCTAGCCGCTCTTTAGACACCAGACGCTGCCTTCCACTTCCTC
 961  CGACTGCGGGACACCACCGATCGGCGAGAAATCTGTGGTCTGCGACGGAAGGTGAAGGAG

1021  CTCTCACTTCTTATTCGGGCACCACTGACGACAGAGACTTCGGCTGGGCCATTCCCGCCT
1021  GAGAGTGAAGAATAAGCCCGTGGTGACTGCTGTCTCTGAAGCCGACCCGGTAAGGGCGGA
```

FIGURE 1 (cont'd)

```
1081  CTCCTACCGCCTGGCAGCCATGGTAACAGCCTGGGGATGGTCCCTAAGATGGGGTCAGA
1081  GAGGATGGCGGACCGTCGGTACCATTGTCGGACCCCTACCAGGGATTCTACCCCAGTCT

1141  GAACGGCTGAGCATGGCCATCCCCCCAGCCCTGAACTCCCACTCAGCCTGGGCTCATCCC
1141  CTTGCCGACTCGTACCGGTAGGGGGGTCGGGACTTGAGGGTGAGTCGGACCCGAGTAGGG

1201  AACCTCCTGAGTCAAGTCCACAGTAAGCGTCTGTCTCCTGGGAAGGGGGATCTGACCCCG
1201  TTGGAGGACTCAGTTCAGGTGTCATTCGCAGACAGAGGACCCTTCCCCCTAGACTGGGGC

1261  GCATCAGGAGCTGAGGAAAGGTGTTGCCAGCAGGGATCACTCAAGCCCCTTGGAGGGGAC
1261  CGTAGTCCTCGACTCCTTTCCACAACGGTCGTCCCTAGTGAGTTCGGGGAACCTCCCCTG

1321  AGGCCAGAACTAAGCCTACTGCTTTCAGGGTTTCCACCTCTTCCCTTCTTCCTAGACGTG
1321  TCCGGTCTTGATTCGGATGACGAAAGTCCCAAAGGTGGAGAAGGGAAGAAGGATCTGCAC

1381  CGAACAGGGGGCAGCCTCTTTCAGCTCTTCTGGGGCAGCTGCGTCAAGGGAAAATCCTGG
1381  GCTTGTCCCCCGTCGGAGAAAGTCGAGAAGACCCCGTCGACGCAGTTCCCTTTTAGGACC

1441  GCCCTCTCCCTCCCTGGGGGCTTCTGCGCAGTGAGTTCAGGGAGTCTCCTCCCTCCTCCA
1441  CGGGAGAGGGAGGGACCCCCGAAGACGCGTCACTCAAGTCCCTCAGAGGAGGGAGGAGGT

1501  TCGGGCCTCCACCCCTACTCCTGCGCAGCCCCGCTGCCGCTCTCCCTGCCCTGGAGTCTC
1501  AGCCCGGAGGTGGGGATGAGGACGCGTCGGGGCGACGGCGAGAGGGACGGGACCTCAGAG

1561  CTGCAGCCCCTTGGATCTCCGTGACTCTCCCTACCTCCCCGACTCCCCAGGCTTCTTACA
1561  GACGTCGGGGAACCTACAGGCACTGAGAGGGATGGAGGGGCTGAGGGGTCCGAAGAATGT

1621  GTGACCTCTTACCGTGCCCCACTCCATGAATCGCCAGAGCTATTCGTCCCTAAATTTCAA
1621  CACTGGAGAATGGCACGGGGTGAGGTACTTAGCGGTCTCGATAAGCAGGGATTTAAAGTT

1681  ACCTTGCGCAATGTCCCTTCACAGACCCCTCCAGGTATCACGCAGCCCCGAGCCCCGAGC
1681  TGGAACGCGTTACAGGGAAGTGTCTGGGGAGGTCCATAGTGCGTCGGGGCTCGGGGCTCG

1741  CCCGCCCCGGGGGCCTCATCCCGCCCCTTCGCGTCCGCGGCTCGTTTTCCCCCACTGAGC
1741  GGGCGGGGCCCCCGGAGTAGGGCGGGGAAGCGCAGGCGCCGAGCAAAAGGGGGTGACTCG

1801  GCCCAGCTCCCGCAGTTTCCCCGGCCGTCGAGCGCCGTGGGCGGGGCTCCAGGGCGGCGG
1801  CGGGTCGAGGGCGTCAAAGGGGCCGGCAGCTCGCGGCACCCGCCCCGAGGTCCCGCCGCC

1861  CGCCTCGCGGGGAGGGTCCTCCGTGCTGGGGGCGAGGCCACCCGAGGCAGCTCCCCGCCC
1861  GCGGAGCGCCCCTCCCAGGAGGCACGACCCCCGCTCCGGTGGGCTCCGTCGAGGGGCGGG

1921  GCCCCCAACCCCGCCCCGCTCTCGGAGCCTATAAAGGGAGGCGACCCGCGGCCCGCCCGG
1921  CGGGGGTTGGGGCGGGGCGAGAGCCTCGGATATTTCCCTCCGCTGGGCGCCGGGCGGGCC

1981  CTGGCATCCCCCAGCCGCCGCCAGCCCCGCCGAGGGGAGCCAGCGCCGTCTCTGAGGGGC
1981  GACCGTAGGGGGTCGGCGGCGGTCGGGGCGGCTCCCCTCGGTCGCGGCAGAGACTCCCCG

2041  GTCCGGCGCCGGAGCCATGACCCTCCGCCGACTCAGGAAGCTGCAGCAGAAGGAGGAGGC
2041  CAGGCCGCGGCCTCGGTACTGGGAGGCGGCTGAGTCCTTCGACGTCGTCTTCCTCCTCCG

2101  GGCGGCCACCCCGGACCCCGCCGCCCCGGACTCCCGACTCGGAAGTCGCCCCCGCCGCTCC
2101  CCGCCGGTGGGGCCTGGGGCGGCGGGCCTGAGGGCTGAGCCTTCAGCGCGGGCGGCGAGG

2161  GGTCCCGACCCCGGGACCCCCTGCCGCAGCCGCCACCCCTGGGCCCCCAGCGGACGAGCT
2161  CCAGGGCTGGGGCCCTGGGGGACGGCGTCGGCGGTGGGGACCCGGGGGTCGCCTGCTCGA

2221  GTACGCGGCGCTGGAGGACTATCACCCTGCCGAGCTGTACCGCGCGCTCGCCGTGTCCGG
2221  CATGCGCCGCGACCTCCTGATAGTGGGACGGCTCGACATGGCGCGCGAGCGGCACAGGCC

2281  GGGCACCCTGCCCCGCCGAAAGGTGCGTCCCCCGCCCGCCTTCAGGATCTGCTCAGCCCC
2281  CCCGTGGACGGGGCGGCTTTCCACGCAGGGGGCGGGCGGAAGTCCTAGACGAGTCGGGG

2341  TCTCCGACTCCCTACAGGGCCTGCTGACTCCGCAGTGCCCTCTCCTCGGCGTCCGCGGAG
2341  AGAGGCTGAGGGATGTCCCGGACGACTGAGGCGTCACGGGAGAGGAGCCGCAGGCGCCTC
```

FIGURE 1 (cont'd)

```
2401   TCCCCCACCTTCTTCCCCGGCCCCGCTGGGTGCCTCGACTCCCCCGTTCCCCGCTGCTGC
2401   AGGGGGTGGAAGAAGGGGCCGGGGCGACCCACGGAGCTGAGGGGGCAAGGGGCGACGACG

2461   GAAGGCCGTGGCCCTCGCCTGCACACCGCGCCCAGGCTCGGTGGCTCTTAACTCCGCGCC
2461   CTTCCGGCACCGGGAGCGGACGTGTGGCGCGGGTCCGAGCCACCGAGAATTGAGGCGCGG

2521   CCATGCACGCCCCCTCTCTCCCTCCTTGACTCCTCCCAGCACCCCCCTTCTCCTACCCGC
2521   GGTACGTGCGGGGGAGAGAGGGAGGAACTGAGGAGGGTCGTGGGGGGAAGAGGATGGGCG

2581   TCCATCTGGCTTTCTGCCCCCCATGCCCCGCCTCCCCGTGGCCAGGTGTCCTGGGTCCCC
2581   AGGTAGACCGAAAGACGGGGGGTACGGGGCGGAGGGGCACCGGTCCACAGGACCCAGGGG

2641   AGGAGCCCCTCGCCCGAGGGACAGAGACAGCCCCAGGCAAGTTGAAGGTCCGAGAGCCCC
2641   TCCTCGGGGAGCGGGCTCCCTGTCTCTGTCGGGGTCCGTTCAACTTCCAGGCTCTCGGGG

2701   CGGTGGCAGAAGCGGGCCGGTGGCTGCGCCGCGTGCGTTCTCACTCTGAGGAAGTGCGTG
2701   GCCACCCTCTTCGCCCGGCCACCGACGCGGCGCACGCAAGAGTGAGACTCCTTCACGCAC

2761   GGGAGCCGCTGACTCCGGATAGCACACCCTTCCGAGGGGACTCCCCGATTCCTGGGCTGG
2761   CCCTCGGCGACTGAGGCCTATCGTGTGGGAAGGCTCCCCTGAGGGGCTAAGGACCCGACC

2821   GGGCCTGCCGCCTGGCCCCACGTCTGACGTACGGGGCGCGAGGGCCACTGCTCCCTGGAC
2821   CCCGGACGGCGGACCGGGGTGCAGACTGCATGCCCCGCGCTCCCGGTGACGAGGGACCTG

2881   TTCTGTCGGAACCGGACGCAGTGGGAGGGGTCGCAGGGCGCCCGCGGGGCAGGAAGGATG
2881   AAGACAGCCTTGGCCTGCGTCACCCTCCCCAGCGTCCCGCGGGCGCCCCGTCCTTCCTAC

2941   CGGGCCGCGCCCACCTCTGAGTCCCCTCTGCCAGCCTCTTCCTCTGGCCCCAGGAGACCT
2941   GCCCGGCGCGGGTGGAGACTCAGGGGAGACGGTCGGAGAAGGAGACCGGGGTCCTCTGGA

3001   GAGGCTCAGAACCTACACAACACCAGGTTAAGAAGAGGGGCCTGGTGGCCTTTCCTCACC
3001   CTCCGAGTCTTGGATGTGTTGTGGTCCAATTCTTCTCCCCGGACCACCGGAAAGGAGTGG

3061   CAGCCGCCCTCCTTCGCCCCGGCCCCCAGCTAGCCCCCACACAATGAACAGCTTGTTGAG
3061   GTCGGCGGGAGGAAGCGGGGCCGGGGGTCGATCGGGGGTGTGTTACTTGTCGAACAACTC

3121   AATTTGCATTTTATGAAAATCATGTTGAAAGACAAAGGGGTCTCTCTGTGCTGCCCAGTC
3121   TTAAACGTAAAATACTTTTAGTACAACTTTCTGTTTCCCCAGAGAGACACGACGGGTCAG

3181   CTTCCTCCCTGGCCGTTTGGGAACTGTCCCCACCCCTGAGGCCAATCTGGTTCTGAACCT
3181   GAAGGAGGGACCGGCAAACCCTTGACAGGGGTGGGGACTCCGGTTAGACCAAGACTTGGA

3241   TCTCTTCCTTGCCTTGGGCAGCTTTGGGGCAGGCTTAGCAAAGCCACACAACAGAAAGGC
3241   AGAGAAGGAACGGAACCCGTCGAAACCCCCTCCCAATCGTTTCCGTGTCTTGTCTTTCCG

3301   CCTGGGCTGTGCAGGCTCCAAAGAAAAGGGCTGCTCTGGGACTGGACCTCCTCCCAGGAC
3301   GGACCCGACACGTCCGAGGTTTCTTTTCCCGACGAGACCCTGACCTGGAGGAGGGTCCTG

3361   CAAAAAGTTAGGGAGGGTGAGAGACTACTTTAGTTTATCAAGGACCCTGAAGAGACAGGA
3361   GTTTTTCAATCCCTCCCACTCTCTGATGAAATCAAATAGTTCCTGGGACTTCTCTGTCCT

3421   ACCTTCATCTCTCATCCTTCCTCCACACCCCCCACCACCACCCCTAAAGAACTCCCAGTC
3421   TGGAAGTAGAGAGTAGGAAGGAGGTGTGGGGGGTGGTGGTGGGGATTTCTTGAGGGTCAG

3481   TCGGTCCTTTAGTGAGACTTGCTGACAAGTTTGACATCTAAGATGTTTTGTCCCAGAAAG
3481   AGCCAGGAAATCACTCTGAACGACTGTTCAAACTGTAGATTCTACAAAACAGGGTCTTTC

3541   CACAAAATATATGGCAATGGAGAGAGAGACCCAGGTATAGCTGGGCACAGCTGGTCACCT
3541   GTGTTTTATATACCGTTACCTCTCTCTCTGGGTCCATATCGACCCGTGTCGACCAGTGGA

3601   GCAGCTGGGATCCACAACTGGTCCTTGAAACGGCCTGTACCTTAGGAGACCTGGCACCTC
3601   CGTCGACCCTAGGTGTTGACCAGGAACTTTGCCGGACATGGAATCCTCTGGACCGTGGAG

3661   TGACCCCACATTCTGGCTGGCATTGCCAGCCCTTCGGGACAGGCTCCCTGACCCCAGCCC
3661   ACTGGGGTGTAAGACCGACCCTAACGGTCGGGAAGCCCTGTCCCAGGGACTGGGGTCGGG
```

FIGURE 1 (cont'd)

```
3721  TCCCAAGCCACTGTCTGTAGCTGAGAAATTAGATGGAGAGACCCAACTGGCAGAAGGTCC
3721  AGGGTTCGGTGACAGACATCGACTCTTTAATCTACCTCTCTGGGTTGACCGTCTTCCAGG

3781  TCGGAGCACCTTGATAGGTGAGCCCAGGGGACACCTATCCTCTGAATCCCACTGGGGAAG
3781  AGCCTCGTGGAACTATCCACTCGGGTCCCCTGTGGATAGGAGACTTAGGGTGACCCCTTC

3841  AGCCCCTGCCTCAGCTTTGGGAGTCTGGATGGCCTGAGCCTCTACAGACATGGGCCCTAG
3841  TCGGGGACGGAGTCGAAACCCTCAGACCTACCGGACTCGGAGATGTCTGTACCCGGGATC

3901  GGGTGGAGACCATTTTAGAATAATGATCTCCCCACCTGCTGCCAGTGTGGAAACCAGCAA
3901  CCCACCTCTGGTAAAATCTTATTACTAGAGGGGTGGACGACGGTCACACCTTTGGTCGTT

3961  GGGCTTAGAGGTTCATGGATCTGGAACCCAGGAGGATGGTTGTGTCCCTGCAGTCCCAGG
3961  CCCGAATCTCCAAGTACCTAGACCTTGGGTCCTCCTACCAACACAGGGACGTCAGGGTCC

4021  TATGAAGGTAAGGCCTGTAGAGAAAGTTGAGGAGTGGTGCCAGTAGTGGCACTTGGCAAA
4021  ATACTTCCATTCCGGACATCTCTTTCAACTCCTCACCACGGTCATCACCGTGAACCGTTT

4081  TAGTTCCACCAGCACCAAAACAGGTGTGGATGTGGAGCTGGGAAGGGGCAGACAGGAAGT
4081  ATCAAGGTGGTCGTGGTTTTGTCCACACCTACACCTCGACCCTTCCCCGTCTGTCCTTCA

4141  GGGTCGCTGTGTCCAGGGTAACCTCTCAGTGTCTGCTCAAGGACAGTCCCGCCTTACCTG
4141  CCCAGCGACACAGGTCCCATTGGAGAGTCACAGACGAGTTCCTGTCAGGGCGGAATGGAC

4201  CTCCTTCTGACCATCTTACTGCCCAGGGCTCAGGATTCCGCTGGAAGAATCTCAGCCAGA
4201  GAGGAAGACTGGTAGAATGACGGGTCCCGAGTCCTAAGGCGACCTTCTTAGAGTCGGTCT

4261  GTCCTGAACAGCAGCGGTGAGTCACCAACACCCAGCCCCTGCCATGGTCCAAAGGGGTGA
4261  CAGGACTTGTCGTCGCCACTCAGTGGTTGTGGGTCGGGGACGGTACCAGGTTTCCCCACT

4321  GGTGCTGGGTTGGGGGGTGCCAGGACAGCATCTCAGCCTAGCGAGGGTAGTCATTCTCCT
4321  CCACGACCCAACCCCCCACGGTCCTGTCGTAGAGTCGGATCGCTCCCATCAGTAAGAGGA

4381  AGCCTTTAAACATGGCTCCCCCGCTGGGAGTGAGGGCAGGTGGGGGTGAGGGCTGTGTGA
4381  TCGGAAATTTGTACCGAGGGGGCGACCCTCACTCCCGTCCACCCCCACTCCCGACACACT

4441  AGGGGGTGGCAGAGAAAGGAGGTAGGGACTTTTGAGTCATTAGGTGCTCTTCAACACACC
4441  TCCCCCACCGTCTCTTTCCTCCATCCCTGAAAACTCAGTAATCCACGAGAAGTTGTGTGG

4501  CCCAGTCCCTGCCAGTTACCCCTCCCTGGGGAGATCTGGATGAACGGATGTGGGAGTTGG
4501  GGGTCAGGGACGGTCAATGGGGAGGGACCCCTCTAGACCTACTTGCCTACACCCTCAACC

4561  GAGGGGGTGTAGGCAAAGTCTATGGGGAACGTCCTAACCCAGGCCTCCTGGGCTCCCCTG
4561  CTCCCCCACATCCGTTTCAGATACCCCTTGCAGGATTGGGTCCGGAGGACCCGAGGGGAC

4621  AGCCCTCCTAGCCTTGGCAAACCCCACGGGCCCAGACCTTAGCCAGGCTGTGTCCAGCTG
4621  TCGGGAGGATCGGAACCGTTTGGGGTGCCCGGGTCTGGAATCGGTCCGACACAGGTCGAC

4681  CTTGGGGCTGGCTGCCCCTGCCTCCAGAATGTCAGTCCTCTTCTGGTCCCAGCCTGTGGC
4681  GAACCCCGACCGACGGGGACGGAGGTCTTACAGTCAGGAGAAGACCAGGGTCGGACACCG

4741  AGCCCTCTTAGGAGGGATCTGAGCGTGGGCAGAAGTAGGTGCTGACTCCAGGCCCTGGGA
4741  TCGGGAGAATCCTCCCTAGACTCGCACCCGTCTTCATCCACGACTGAGGTCCGGGACCCT

4801  CCCCACAGTTTCCCTTCTCTACTCATGTCCCATCCCTGATTTGGGCTTGACTTTCTCTAA
4801  GGGGTGTCAAAGGGAAGAGATGAGTACAGGGTAGGGACTAAACCCGAACTGAAAGAGATT

4861  AATGGATCAGCAAACTGACCTGCTAGCCAGATTGGCCTGTTTGGCCCTTGAGCTAATAAT
4861  TTACCTAGTCGTTTGACTGGACGATCGGTCTAACCGGACAAACCGGGAACTCGATTATTA

4921  TTTTAAAGAGTTGTAAAAATAAAAACAAATAACAATATATGACAGAGATCATAAGGGGCC
4921  AAAATTTCTCAACATTTTTATTTTTGTTTATTGTTATATACTGTCTCTAGTATTCCCCGG

4981  TGCAAAGAAAGCCTAAAGTATTTACCATTTGGCCCTTTGCAGAAAAAGTTTGCTGACCCT
4981  ACGTTTCTTTCGGATTTCATAAATGGTAAACCGGGAAACGTCTTTTTCAAACGACTGGGA
```

FIGURE 1 (cont'd)

```
5041  TCCAAAAACCCTAGAACATTGGGGTAGACGCGGAACTCCCAGCCACCCTGCTCCCTGCC
5041  AGGTTTTTGGGATCTTGTAACCCCATCTGCGCCTTGAGGGTCGGTGGGACGAGGGACGG

5101  CCAATAGTACAGAGAGGGGAAAGGCCTGCTGTTCAGAGTGAGAGGGGCTCGAGCTGGAGT
5101  GGTTATCATGTCTCTCCCCTTTCCGGACGACAAGTCTCACTCTCCCCGAGCTCGACCTCA

5161  GGGGAGGTGCTGCTCAGCATTTGGGGGAATCTCTGGGTCAGGCTGGAAGCGGAGAAGCCT
5161  CCCCTCCACGACGAGTCGTAAACCCCCTTAGAGACCCAGTCCGACCTTCGCCTCTTCGGA

5221  GGTCTCCAGGGCCTTTCCGAGGCTGAGCTACTTGAAGGGGCCTTTGGAGGCTGCTTTAAC
5221  CCAGAGGTCCCGGAAAGGCTCCGACTCGATGAACTTCCCCGGAAACCTCCGACGAAATTG

5281  TGTGCCTCTGGCTGGGCGGGAAGGAAGGGGGTGGGAGTGGGCAGAGGAAACTCTGGGCTC
5281  ACACGGAGACCGACCCGCCCTTCCTTCCCCCACCCTCACCCGTCTCCTTTGAGACCCGAG

5341  CCCCAGCAGGCGAGGATCTGGAGCAGCTCCAGACCATTGTGTCCAGCGGGCAGGCCTTCA
5341  GGGGTCGTCCGCTCCTAGACCTCGTCGAGGTCTGGTAACACAGGTCGCCCGTCCGGAAGT

5401  GTGCGGGAAGGGGCGGCCTCGAGGCTCCCCTCCCCCAGCCCCCACATCTGGTGGGCTGGC
5401  CACGCCCTTCCCCGCCGGAGCTCCGAGGGGAGGGGGTCGGGGGTGTAGACCACCCGACCG

5461  CCCAGCATAGCTGGGAGGAGCAGCTGTGGTCTTGCTGAGCCTCGTGACTGGCCTCTGGGG
5461  GGGTCGTATCGACCCTCCTCGTCGACACCAGAACGACTCGGAGCACTGACCGGAGACCCC

5521  GTGGGGCCAGTCCTCTCTCCAAAGCTGTGGAACAGAGGAGGCTCCAGGCTGTGGCTGAAT
5521  CACCCCGGTCAGGAGAGAGGTTTCGACACCTTGTCTCCTCCGAGGTCCGACACCGACTTA

5581  TTCGGGCCTTAGCTAGTCAGTAAGTGGTACTGTAGGGCTCACTGGAAAGCTGGGATGGGG
5581  AAGCCCGGAATCGATCAGTCATTCACCATGACATCCCGAGTGACCTTTCGACCCTACCCC

5641  CTAAAAAACTCAGCCGGCTCATCCTTCAGGGGACCGGCCCTTCTCTGTGCTTCCCTCCCA
5641  GATTTTTTGAGTCGGCCGAGTAGGAAGTCCCCTGGCCGGGAAGAGACACGAAGGGAGGGT

5701  CCACTAGAGGCTGGATTGGTTCTCTGTGGCTCCATGAGGCTGATTTCAATTGGGTATGGG
5701  GGTGATCTCCGACCTAACCAAGAGACACCGAGGTACTCCGACTAAAGTTAACCCATACCC

5761  AAAGACATTCCAATAATCTGTGATGAGACTGAGCTGTCACTGGAGACAGAGTCCTGCTGG
5761  TTTCTGTAAGGTTATTAGACACTACTCTGACTCGACAGTGACCTCTGTCTCAGGACGACC

5821  AATGTTCTAGACCAGTTGCCAATATCCAGGGAGGCCCAAGCTATGGGACTTCTACACCTT
5821  TTACAAGATCTGGTCAACGGTTATAGGTCCCTCCGGGTTCGATACCCTGAAGATGTGGAA

5881  TTAATCCTAATTGTCTTGACCCCTGTGTCTCTTGCAGGAAAGTGCTGACGTTGGAGAAGG
5881  AATTAGGATTAACAGAACTGGGGACACAGAGAACGTCCTTTCACGACTGCAACCTCTTCC

5941  AGGATAACCAGACCTTCGGCTTTGAGATCCAGGTGGGAGAAGCTGCACACAGGGGTCAGG
5941  TCCTATTGGTCTGGAAGCCGAAACTCTAGGTCCACCCTCTTCGACGTGTGTCCCCAGTCC

6001  GGGGTTGGATGACCAGCCTGAGGGATGAACGGACTTGTCCCAACCCTGGGCTGAGGGTCC
6001  CCCCAACCTACTGGTCGGACTCCCTACTTGCCTGAACAGGGTTGGGACCCGACTCCCAGG

6061  CCTTGTCCATTACAGACTTATGGCCTTCACCACCGGGAGGAGCAGCGTGTGGAAATGGTG
6061  GGAACAGGTAATGTCTGAATACCGGAAGTGGTGGCCCTCCTCGTCGCACACCTTTACCAC

6121  ACCTTTGTCTGCCGAGTTCATGAGTCTAGCCCTGCCCAGCTGGCTGGGCTCACACCAGGT
6121  TGGAAACAGACGGCTCAAGTACTCAGATCGGGACGGGTCGACCGACCCGAGTGTGGTCCA

6181  GGGGCCTGAGCCCAGGACACCCAGGTCTGGGAAGGGGATATGACCTTACTCCCAAGCAAA
6181  CCCCGGACTCGGGTCCTGTGGGTCCAGACCCTTCCCCTATACTGGAATGAGGGTTCGTTT

6241  GGGGGTGAGCAATCTCTCCTGAAATCAATTCCTCTTCCTTTTCCTTCTTTGAGAAGGCCA
6241  CCCCCACTCGTTAGAGAGGACTTTAGTTAAGGAGAAGGAAAAGGAAGAAACTCTTCCGGT

6301  GAAAGAAGAATGGATAGAATCTGGGCTTTGGATCTAGGCAAATTTGCCATGTACTGTGTG
6301  CTTTCTTCTTACCTATCTTAGACCCGAAACCTAGATCCGTTTAAACGGTACATGACACAC
```

FIGURE 1 (cont'd)

```
6361  ATCTTGCACAGCCCCATCTACAAAATGAGGGTAATAATGCATCCAAACATCACAGTGCGG
6361  TAGAACGTGTCGGGGTAGATGTTTTACTCCCATTATTACGTAGGTTTGTAGTGTCACGCC

6421  CAAGGGGATTCCCTGGGCACACTGCCAGGGCCTAATTAATGGTGGATGATGCTGCTGCTG
6421  GTTCCCCTAAGGGACCCGTGTGACGGTCCCGGATTAATTACCACCTACTACGACGACGAC

6481  CTCTGATTCCTCCCAGCAACCCTGGCAGTCAGCATGGGCAGGAGCCAGGGAAGAAGCAAC
6481  GAGACTAAGGAGGGTCGTTGGGACCGTCAGTCGTACCCGTCCTCGGTCCCTTCTTCGTTG

6541  ATTCCATTAAGTCTGTTTGATATTGGGGATCAGGCCAATCCTGCCCCAAAATGGGCCCAG
6541  TAAGGTAATTCAGACAAACTATAACCCCTAGTCCGGTTAGGACGGGGTTTTACCCGGGTC

6601  TGCTGAGGAACCGATGTTACTCCCTTTTAAAAAATTAGAAACTTTTTTTTTTTTTAAGAG
6601  ACGACTCCTTGGCTACAATGAGGGAAAATTTTTTAATCTTTGAAAAAAAAAAAAATTCTC

6661  ACAGGGCCTCAGTCTGTCACCCAGGCTAGAGTGCAGTGGCGTAATCATAACTCACTATAA
6661  TGTCCCGGAGTCAGACAGTGGGTCCGATCTCACGTCACCGCATTAGTATTGAGTGATATT

6721  CCTTGAACTCCTGGGCTCAAGCGATCCTCCTCTTGCCTCTGCCTCCCAAAGCAATATGTT
6721  GGAACTTGAGGACCCGAGTTCGCTAGGAGGAGAACGGAGACGGAGGGTTTCGTTATACAA

6781  ACTTCCTCTAACAAGGAAATTATGCTTCAGCAGGAGATCCCTGGATTGAGCAGATCTAGA
6781  TGAAGGAGATTGTTCCTTTAATACGAAGTCGTCCTCTAGGGACCTAACTCGTCTAGATCT

6841  GTCCCCAGGTTCCAGGAAGGGCAGCCTGAAACTGTATGAATCAATCCCCCCTCCACCATC
6841  CAGGGGTCCAAGGTCCTTCCCGTCGGACTTTGACATACTTAGTTAGGGGGGAGGTGGTAG

6901  TTTGCCCCTAAGCCCCTACCTCCTTCCCACTTACCAGCAGCCCGTGCTAGCTATCTTAGT
6901  AAACGGGGATTCGGGGATGGAGGAAGGGTGAATGGTCGTCGGGCACGATCGATAGAATCA

6961  CCATTTTCTGTTACCATAACAGAATACCTGATACTGGGTAATTATAAAGAAAAGAGGTTT
6961  GGTAAAAGACAATGGTATTGTCTTATGGACTATGACCCATTAATATTTCTTTTCTCCAAA

7021  ATTTAGCTCATGGTTCTGGAGGCTGGGAAGTTCAAGACTGGGTGGCCGCATCAGGTGAGG
7021  TAAATCGAGTACCAAGACCTCCGACCCTTCAAGTTCTGACCCACCGGCGTAGTCCACTCC

7081  GCCTCATGCTGCGTTCTGACATGATGGATGGCATCTCATGGCAGGAACGCCTGCAAGAGT
7081  CGGAGTACGACGCAAGACTGTACTACCTACCGTAGAGTACCGTCCTTGCGGACGTTCTCA

7141  GGTGAGTAGGCACACGCAAAAGAGACAAAACATGGGTGATCTTGCTTTATAGCAACCCAC
7141  CCACTCATCCGTGTGCGTTTTCTCTGTTTTGTACCCACTAGAACGAAATATCGTTGGGTG

7201  TCGCCAGGTAACTAAACCAGTCCTACCAGAGCAAGAACTCACTCCCCAAAAACAGCATGG
7201  AGCGGTCCATTGATTTGGTCAGGATGGTCTCGTTCTTGAGTGAGGGGTTTTTGTCGTACC

7261  ATCCCTTCACTGGGCAGATCCTTCATGGCCCAAATGCCACTTTTTTTGAGATGGAGTTTC
7261  TAGGGAAGTGACCCGTCTAGGAAGTACCGGGTTTACGGTGAAAAAAACTCTACCTCAAAG

7321  GCTCTTGTTGCCCAGGCTGGAGTGCAATGGCATGATCTCAGCTCACTGCAGCCTCTGCCT
7321  CGAGAACAACGGGTCCGACCTCACGTTACCGTACTAGAGTCGAGTGACGTCGGAGACGGA

7381  CCCAGATTCAAGCAATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACTGG
7381  GGGTCTAAGTTCGTTAAGAGGACGGAGTCGGAGGGCTCATCGACCCTAATGTCCGTGACC

7441  CCACCAAGCCCAGCTCATTTTTGTATTTTTAGTAGAGATGGGGTTTTGCCTTGTTGGCCA
7441  GGTGGTTCGGGTCGAGTAAAAACATAAAAATCATCTCTACCCCAAAACGGAACAACCGGT

7501  GGCTGGTCTCGAACTCCTGACCTCAGGTGATCCACCCGCCTCGGCCTCCCAAAGTGCTGG
7501  CCGACCAGAGCTTGAGGACTGGAGTCCACTAGGTGGGCGGAGCCGGAGGGTTTCACGACC

7561  GATTACAGGTGTGAGCCACGGCGCTCGGCCCCAAATGCCTCTTAAAGGTCCTACCATCTC
7561  CTAATGTCCACACTCGGTGCCGCGAGCCGGGGTTTACGGAGAATTTCCAGGATGGTAGAG

7621  TCAGCACTGTTACGTTGGGGATGAAGCCTCAACATGAGTTTTGGGGACAAACAATATTTA
7621  AGTCGTGACAATGCAACCCCTACTTCGGAGTTGTACTCAAAACCCCTGTTTGTTATAAAT
```

FIGURE 1 (cont'd)

```
7681  AATGGTAGCAGTAGCCAAGTGGTATACTACAACTTCTCAAAGTAGTTTCAAATCCACTCT
7681  TTACCATCGTCATCGGTTCACCATATGATGTTGAAGAGTTTCATCAAAGTTTAGGTGAGA

7741  CCCTCCCCATCATCCCTGAAGCATCCACAGCAGGGATCCATACCCCTTTTTACAGATAGG
7741  GGGAGGGGTAGTAGGGACTTCGTAGGTGTCGTCCCTAGGTATGGGGAAAAATGTCTATCC

7801  AATGGGGCCCTGACATGGGGCACACTGTGCTTGAGGTCAGGAAGCTCTCCAGTGGTGCAG
7801  TTACCCCGGGACTGTACCCCGTGTGACACGAACTCCAGTCCTTCGAGAGGTCACCACGTC

7861  GGTAGCAGAACTATCCCTCTGGGGGCCAGTCATTCCCTGTGCTTCTCTCCCACCACCAGA
7861  CCATCGTCTTGATAGGGAGACCCCCGGTCAGTAAGGGACACGAAGAGAGGGTGGTGGTCT

7921  GGCTGGACTGATTATCTGTGGATCCATGAGGCCATGCCATGCCTGGGGCCAGGGTCGGTT
7921  CCGACCTGACTAATAGACACCTAGGTACTCCGGTACGGTACGGACCCCGGTCCCAGCCAA

7981  CCCAGCTGGGTGCTGCTCACCTGCTCTTCCCTGAATTGACTGGGTCTTATGGCCAGCGTG
7981  GGGTCGACCCACGACGAGTGGACGAGAAGGGACTTAACTGACCCAGAATACCGGTCGCAC

8041  GACTGGACAGAAATAACCAAATCTGAGGGTAGCCCAGGGTCCTGGGTGGGCTTAGCTTTG
8041  CTGACCTGTCTTTATTGGTTTAGACTCCCATCGGGTCCCAGGACCCACCCGAATCGAAAC

8101  GGACAGAACTTCTTTTTTTTTTTTTTTTTTTTGAGACGGAGTCTCGCTCTGTCGCCCAGG
8101  CCTGTCTTGAAGAAAAAAAAAAAAAAAAAAAACTCTGCCTCAGAGCGAGACAGCGGGTCC

8161  CTGGAGTGCAGTGGCGCGATCTCGGCTCACTGCAAGCTCCGCCTCCCGGGTTCACGCCAT
8161  GACCTCACGTCACCGCGCTAGAGCCGAGTGACGTTCGAGGCGGAGGGCCCAAGTGCGGTA

8221  TCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCGCCTGCTACCACGCCCGGCTA
8221  AGAGGACGGAGTCGGAGGGCTCATCGACCCTGATGTCCGCGGACGATGGTGCGGGCCGAT

8281  ATTTTTTGTATTTTTAGTAGAGACGGGGTTTCACCGTGTTAGCCAGGATGGTCTCGATCT
8281  TAAAAAACATAAAAATCATCTCTGCCCCAAAGTGGCACAATCGGTCCTACCAGAGCTAGA

8341  CCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCC
8341  GGACTGGAGCACTAGGCGGGCGGAGCCGGAGGGTTTCACGACCCTAATGTCCGCACTCGG

8401  ACCGCGCCCGGCCGGACAGAACTTCTTGAGGGCAGAGTGAGGGTGTTGGGTGTGTGAGGT
8401  TGGCGCGGGCCGGCCTGTCTTGAAGAACTCCCGTCTCACTCCCACAACCCACACACTCCA

8461  CCCCACCCTTTGGCTGGGGTGCTGGGCGTGGACAACCTGGTAGTCACTACAGGCCCACAA
8461  GGGGTGGGAAACCGACCCCACGACCCGCACCTGTTGGACCATCAGTGATGTCCGGGTGTT

8521  GAATGGCTGTGGTTCTGTGTGTTTGGATCGAGTATGAGAGATGTCAGAGGAGATCTACAG
8521  CTTACCGACACCAAGACACACAAACCTAGCTCATACTCTCTACAGTCTCCTCTAGATGTC

8581  AGAACCATGAGGAGTTGGAGGAGGGAGTTCAGGAGTATTCCCTGGAGTTACTACCCACCC
8581  TCTTGGTACTCCTCAACCTCCTCCCTCAAGTCCTCATAAGGGACCTCAATGATGGGTGGG

8641  TTCTCCCCTTTCTGGCTAAGGTAGGAGGCTGGTATTCTAGCATGCCCCATGGAGCAAATC
8641  AAGAGGGGAAAGACCGATTCCATCCTCCGACCATAAGATCGTACGGGGTACCTCGTTTAG

8701  TAACCCCCTTGTCTGCCTGGCAGGGGACACCATCGCCAGCGTCAATGGCCTGAATGTGGA
8701  ATTGGGGGAACAGACGGACCGTCCCCTGTGGTAGCGGTCGCAGTTACCGGACTTACACCT

8761  AGGCATCCGGCATCGAGAGATTGTGGACATCATTAAGGCGTCAGGCAATGTTCTCAGGTA
8761  TCCGTAGGCCGTAGCTCTCTAACACCTGTAGTAATTCCGCAGTCCGTTACAAGAGTCCAT

8821  TGTCTGGGAGCCGAGGTGCCTGAATTCCTGAGCTCAGCCTCTTGGTATTTCCTCAGCCTG
8821  ACAGACCCTCGGCTCCACGGACTTAAGGACTCGAGTCGGAGAACCATAAAGGAGTCGGAC

8881  TGGCTCACTCAGGCTTTGATTCTCCAACCTCAGACTGGAAACTCTATATGGGACATCAAT
8881  ACCGAGTGAGTCCGAAACTAAGAGGTTGGAGTCTGACCTTTGAGATATACCCTGTAGTTA

8941  TCGGAAGGCAGAACTGGAGGCTCGTCTGCAGTACCTGAAGGTAGGGGAACCTAGATAACG
8941  AGCCTTCCGTCTTGACCTCCGAGCAGACGTCATGGACTTCCATCCCCTTGGATCTATTGC
```

FIGURE 1 (cont'd)

```
9001   TCCAGCCTCCACCCTCCTCTTCCCAAGCCTCTGCCCTGTGGGGGGTCACTTACAGCTGAA
9001   AGGTCGGAGGTGGGAGGAGAAGGGTTCGGAGACGGGACACCCCCCAGTGAATGTCGACTT

9061   TCTCCTGTAACTGAAGATTTCTTTTGTCTACTCCCTGATCCCTCGTCTGTACCCACGTCC
9061   AGAGGACATTGACTTCTAAAGAAAACAGATGAGGGACTAGGGAGCAGACATGGGTGCAGG

9121   TGCTAGTTTCCTGCTAGCTTGTGACAGTGGGGTGGGGACTGTCTCTTGCAGCAAACCCTG
9121   ACGATCAAAGGACGATCGAACACTGTCACCCCACCCCTGACAGAGAACGTCGTTTGGGAC

9181   TATGAGAAGTGGGGAGAGTACAGGTCCCTAATGGTGCAGGAGCAGCGGCTGGTGCATGGT
9181   ATACTCTTCACCCCTCTCATGTCCAGGGATTACCACGTCCTCGTCGCCGACCACGTACCA

9241   GAGTAGATCCCGGGGTGTGAGGGGCCACTTGTTCTGCTACAGACACCCCATCTGCGCTTC
9241   CTCATCTAGGGCCCCACACTCCCCGGTGAACAAGACGATGTCTGTGGGGTAGACGCGAAG

9301   CCCCTCAGAACTGGCGGGTTCTAGTAAAGAACGGTTTACTAGTAAACCTCCACAGTAAAG
9301   GGGGAGTCTTGACCGCCCAAGATCATTTCTTGCCAAATGATCATTTGGAGGTGTCATTTC

9361   CAAGGTTTGTTGAGCTACTACTACTTTGGGTACTGCCGCAGCCACATTTCTGGTTATTCT
9361   GTTCCAAACAACTCGATGATGATGAAACCCATGACGGCGTCGGTGTAAAGACCAATAAGA

9421   CACACTAGCCCTCTGCAGGTAAGTAACAGATAGTGTCATCTTCACTTTACAGAGGGGAAC
9421   GTGTGATCGGGAGACGTCCATTCATTGTCTATCACAGTAGAAGTGAAATGTCTCCCCTTG

9481   ACCAGGGCTCAAAGAGTTTGTGTCAATTATTTCCGAGGCCCGTTTGTGCTAAGCGGCCCC
9481   TGGTCCCGAGTTTCTCAAACACAGTTAATAAAGGCTCCGGGCAAACACGATTCGCCGGGG

9541   CATAAGGATCTGAGTGATAATTCCTGATTTGCGGGTGAGGGAAGTAGGGTCTCAGGTTTG
9541   GTATTCCTAGACTCACTATTAAGGACTAAACGCCCACTCCCTTCATCCCAGAGTCCAAAC

9601   TGCCTGGCCAGGGCCACAGAGATGGTCAGCAGGACGGAGCGGGGACGCCCCGCCCATGCC
9601   ACGGACCGGTCCCGGTGTCTCTACCAGTCGTCCTGCCTCGCCCCTGCGGGGCGGGTACGG

9661   CTCCCACCCTTTGCAGAGGCCACCACGGTCCAGGCCTGACCCGCCCCCTACCTCTCCCGT
9661   GAGGGTGGGAAACGTCTCCGGTGGTGCCAGGTCCGGACTGGGCGGGGGATGGAGAGGGCA

9721   CTCTGCGCAGGCCTGGTGGTGAAGGACCCCAGCATCTACGACACGCTGGAGTCGGTGCGC
9721   GAGACGCGTCCGGACCACCACTTCCTGGGGTCGTAGATGCTGTGCGACCTCAGCCACGCG

9781   TCCTGCCTCTACGGCGCGGGCCTGCTCCCGGGCTCGCTGCCCTTCGGGCCTCTGCTCGCC
9781   AGGACGGAGATGCCGCGCCCGGACGAGGGCCCGAGCGACGGGAAGCCCGGAGACGAGCGG

9841   GTGCCCGGGCGTCCCCGCGGAGGCGCCCGACGGGCCAGGGGCGACGCCGACGACGCCGTC
9841   CACGGGCCCGCAGGGGCGCCTCCGCGGGCTGCCCGGTCCCCGCTGCGGCTGCTGCGGCAG

9901   TACCACACGTGCTTCTTCGGGGACTCCGAGCCGCCGGCGCTGCCGCCCCCGCCGCCCCCG
9901   ATGGTGTGCACGAAGAAGCCCCTGAGGCTCGGCGGCCGCGACGGCGGGGGCGGCGGGGGC

9961   GCCCGCGCCTTCGGCCCGGGCCCCGCCGAGACCCCTGCCGTGGGGCCGGGCCCTGGGCCG
9961   CGGGCGCGGAAGCCGGGCCCGGGGCGGCTCTGGGGACGGCACCCCGGCCCGGGACCCGGC

10021  CGGGCCGCGCTGAGCCGCAGCGCCAGTGTGCGGTGCGCGGGCCCTGGCGGGGGCGGAGGC
10021  GCCCGGCGCGACTCGGCGTCGCGGTCACACGCCACGCGCCCGGGACCGCCCCCGCCTCCG

10081  GGGGGCGCGCCGGGCGCGCTCTGGACTGAGGCTCGCGAGCAGGCCCTATGCGGCCCCGGC
10081  CCCCCGCGCGGCCCGCGCGAGACCTGACTCCGAGCGCTCGTCCGGGATACGCCGGGGCCG

10141  CTGCGCAAAACCAAGTACCGCAGCTTCCGCCGGCGGCTGCTCAAGTTCATCCCCGGACTC
10141  GACGCGTTTTGGTTCATGGCGTCGAAGGCGGCCGCCGACGAGTTCAAGTAGGGGCCTGAG

10201  AACCGCTCCCTGGAGGAGGAGGAGAGCCAGCTGTAGGGGCGGGGGCGGGCAGGGAGGTAT
10201  TTGGCGAGGGACCTCCTCCTCCTCTCGGTCGACATCCCCGCCCCCGCCCGTCCCTCCATA

10261  TTATTTATTTATTCGCAACAGCCAGCGCTAAAAGAGGGGGAGGCCGAGCCAAGAGGACCC
10261  AATAAATAAATAAGCGTTGTCGGTCGCGATTTTCTCCCCCTCCGGCTCGGTTCTCCTGGG
```

FIGURE 1 (cont'd)

10321 CAGGAGCCCAGAGCAGCGGGAGAGGGTCCTTCCTAGCCTCGGCCCGCCGGGTCGGTTCCT
10321 GTCCTCGGGTCTCGTCGCCCTCTCCCAGGAAGGATCGGAGCCGGGCGGCCCAGCCAAGGA

10381 GGCTGGTGTCTGCTGAGGGAGTGGGGGGCCCAGCCCCTTCTCTTCTCCCCCGCCAAACCA
10381 CCGACCACAGACGACTCCCTCACCCCCCGGGTCGGGGAAGAGAAGAGGGGGCGGTTTGGT

10441 CAGTGGAGCTGGGGCAGGGGGAGAGCCAGGCAATCGGGGGCCAAAGATGGGGGTGCTCG
10441 GTCACCCTCGACCCCGTCCCCCTCTCGGTCCGTTAGCCCCCGGTTTCTACCCCCACGAGC

10501 CCTACAGTCTGCATCTGTAGTGCCTTGTGGGGTATCCAGGAACACCCTCCCAGCAGGGGA
10501 GGATGTCAGACGTAGACATCACGGAACACCCCATAGGTCCTTGTGGGAGGGTCGTCCCCT

10561 TGGGAACCCTGTCCCATGAAGCCCTCTCCTCAGCTTTACTTGCTCCCCCGCCCTTAGCCT
10561 ACCCTTGGGACAGGGTACTTCGGGAGAGGAGTCGAAATGAACGAGGGGGCGGGAATCGGA

10621 TGGGGAGAAATGGCCCGTGGTGGGCTGACCCCCCACCCTCCACACACACAGTTCCATGAC
10621 ACCCCTCTTTACCGGGCACCACCCGACTGGGGGGTGGGAGGTGTGTGTGTCAAGGTACTG

10681 CCAGCGGGCCCCCAGGGGCATCAGGTGCTGGTCCTCCTCCCTCCTGGCCTCGACCCCTAA
10681 GGTCGCCCGGGGGTCCCCGTAGTCCACGACCAGGAGGAGGGAGGACCGGAGCTGGGGATT

10741 GGGCTTCGCCCCTCCCAGGGGCCTGTAACTAAGTCGGGTCCTGCCAGGCAGGGGGCCTGT
10741 CCCGAAGCGGGGAGGGTCCCCGGACATTGATTCAGCCCAGGACGGTCCGTCCCCCGGACA

10801 GTTCTGTGCCCCTTGGGAGACAGGAACTGGCGAGTTCAGGTGGGGTGGGGACAGCACAGA
10801 CAAGACACGGGGAACCCTCTGTCCTTGACCGCTCAAGTCCACCCCACCCCTGTCGTGTCT

10861 CTGTTCCACCGTTGTGCATATTGTTGCTTCTGAACCACAAACTGTATAAATGGATGGTTT
10861 GACAAGGTGGCAACACGTATAACAACGAAGACTTGGTGTTTGACATATTTACCTACCAAA

10921 TTTG
10921 AAAC

FIGURE 2

>hg19_refGene_NR_037593 range=chr6:163834097-163836982 5'pad=0 3'pad=0 strand=- repeatMasking=none

CAHM resides on minus strand, thus the top strand in the below is the representative 5′- to 3′- sequence of CAHM

Yellow: sub-regions of interests towards which three bisulphite conversion and methylation specific assays are given as an example. Note this is also an example on assays running on opposite strands

```
   1  AGCATAATTTCGGTCTCCTACGGAATTTCTTTAAACTAACGAGCCCCACACTGACTTCCA
   1  TCGTATTAAAGCCAGAGGATGCCTTAAAGAAATTTGATTGCTCGGGGTGTGACTGAAGGT

  61  CTTAGTATTGAACAGCTGCACCAACTCCCCAACCACGAAACCCCGCTTTAGTCCTCACGG
  61  GAATCATAACTTGTCGACGTGGTTGAGGGGTTGGTGCTTTGGGGCGAAATCAGGAGTGCC

 121  GAGGGGAGAGCTCCCGAACGCGGGGCGGTGGGGGTCCGCGCAGAGCAGGCTCGGGAGGCC
 121  CTCCCCTCTCGAGGGCTTGCGCCCCGCCACCCCCAGGCGCGTCTCGTCCGAGCCCTCCGG

 181  GAGCGGAGGAGCGGGGCCCGCGCCGGGCACACGCGTCCTCCAGGCCGGCGGCGCGGCGTG
 181  CTCGCCTCCTCGCCCCGGGCGCGGCCCGTGTGCGCAGGAGGTCCGGCCGCCGCGCCGCAC

 241  GGCCTGCTCTCGGGAGGGCTCGGCGAGGACCACCGAGTCCGCGCAGCCCCCGCCGACCTC
 241  CCGGACGAGAGCCCTCCCGAGCCGCTCCTGGTGGCTCAGGCGCGTCGGGGGCGGCTGGAG

 301  TCGGAAATGTGACCGCCGAAGCTAGAGGGGCCCCAGGCCTCACCCCGCAGCCCTCCGCAA
 301  AGCCTTTACACTGGCGGCTTCGATCTCCCCGGCGTCCCGAGTGGGGCGTCGGGAGGCGTT

 361  CGCGCCAACTTGGACGCCAGCGGCGCGGGGTCCCGGCCGGGCAGGGGGCGTCCGGCACCG
 361  GCGCGGTTGAACCTGCGGTCGCCGCGCCCCAGGGCCGGCCCGTCCCCCGCAGGCCGTGGC

 421  GCGGGTCCACCCCGGCCCGCCCGCCCGCCGCAAGCCCGGCCCGGCACCTCCTTTGTGCGC
 421  CGCCCAGGTGGGGCCGGGCGGGCGGGCGGCGTTCGGGCCGGGCCGTGGAGGAAACACGCG

 481  CCTCCTGGCCTCCCAGTCCCCCCGGCGCTCGGTCCCGCCCGGCCGTGACCTTCCCGCCCT
 481  GGAGGACCGGAGGGTCAGGGGGGCCGCGAGCCAGGGCGGGCCGGCACTGGAAGGGCGGGA

 541  CCCCACCATCCCAAGCGGGGAAAGGGGCCGCCCCGGCGGGGGTCGGGCCGGGGCCGGGGC
 541  GGGGTGGTAGGGTTCGCCCCTTTCCCCGGCGGGGCCGCCCCCAGCCCGGCCCCGGCCCCG

 601  CCTGGAGACGCTCACCTTCGTCCAGCAGCCGCTCGAGGTGGTTGAAGATCCCGCAGAAGT
 601  GGACCTCTGCGAGTGGAAGCAGGTCGTCGGCGAGCTCCACCAACTTCTAGGGCGTCTTCA

 661  TGGGCAGGCTGCTCATGAGCTTCTTGTCGTTCATCAGCTGCATCAGGTAATCTGGGGTGG
 661  ACCCGTCCGACGAGTACTCGAAGAACAGCAAGTAGTCGACGTAGTCCATTAGACCCCACC

 721  GCTTCGGCTTCTCCTTCGTTTCCATTTCCCCGACCATATTCCAGGCTCCGCAGCTCACTC
 721  CGAAGCCGAAGAGGAAGCAAAGGTAAAGGGGCTGGTATAAGGTCCGAGGCGTCGAGTGAG

 781  CGCCCGCCGCCGCCGCCGCCGCCGCCGGAGAGGAGGGAGGGGCGGGGGCGAGCCCCGGCC
 781  GCGGGCGGCGGCGGCGGCGGCGGCGGCCTCTCCTCCCTCCCCGCCCCCGCTCGGGGCCGG

 841  GCGGGCCGCTCGGGACCCGGCGTCCCGCTCCGCGCCGGCTCCCGCTCTGGCTCCCGCGCC
 841  CGCCCGGCGAGCCCTGGGCCGCAGGGCGAGGCGCGGCCGAGGGCGAGACCGAGGGCGCGG

 901  GAGCCCCGGGGCGGCCGGCACCGCGCGCTCGCCCGCCCCCCGCAGGCACTTTCCGCCCGG
 901  CTCGGGGCCCCGCCGGCCGTGGCGCGCGAGCGGGCGGGGGGCGTCCGTGAAAGGCGGGCC

 961  GCCCGACGCGCTCCCAGCCGCCGCCGCTCTCGGCCGCCCGGCTCGGCGCGTCCCTCACGA
 961  CGGGCTGCGCGAGGGTCGGCGGCGGCGAGAGCCGGCGGGCCGAGCCGCGCAGGGAGTGCT

1021  GGCCGGCCGGCCGGCCCGGAGGCGGGTCTCGGCTGGCCCGACTGCGGGCGCCGGCGCGGGC
1021  CCGGCCGGCCGGCCGGGCCTCCGCCCAGAGCCGACCGGCTCACGCCCGCGGCCGCGCCCG

1081  TGCTGGCGCCGGACGAGGAGGAGCCGGGGCCGCCGCTCGCTCGGCTGGTCGAGCCCGCTC
1081  ACGACCGCGGCCTGCTCCTCCTCGGCCCCGGCGGCGAGCGAGCCGACCAGCTCGGGCGAG
```

FIGURE 2 (cont'd)

```
1141  AGCGCCGCCGCCGCCTGTGCCGCGGGCTCGGGGGGTCTCTCTGGGCTGGTCCCCGCCGCG
1141  TCGCGGCGGCGGCGGACACGGCGCCCGAGCCCCCCAGAGAGACCCGACCAGGGGCGGCGC

1201  GCGCCTCTGCCGCTGCCGCCGCGCTCCGACTGCGCTCCTCCTCTTCCTCCTCCTCCTTCT
1201  CGCGGAGACGGCGACGGCGGCGCGAGGCTGACGCGAGGAGGAGAAGGAGGAGGAGGAAGA

1261  CCTCCTCCTCCTCCTCACTCACTTGGCGGCGGAGTTCGCCTCAGTTCAGGCGGCGCTGCC
1261  GGAGGAGGAGGAGGAGTGAGTGAACCGCCGCCTCAAGCGGAGTCAAGTCCGCCGCGACGG

1321  AGCGGCGGCGGCAGCAGCGGCGGCGGCGGGGGGAGGGGCAGCGGCGCGGGGAGGGCCGGG
1321  TCGCCGCCGCCGTCGTCGCCGCCGCCGCCCCCCTCCCCGTCGCCGCGCCCCTCCCGGCCC

1381  GGCGGGCGGCGGGCGGGGCCGCGCAGGGCGGCCGTTAGCGGGTCCCGGCCGGCGCGCTCC
1381  CCGCCCGCCGCCCGCCCCGGCGCGTCCCGCCGGCAATCGCCCAGGGCCGGCCGCGCGAGG

1441  CGCTGCCTGCTGCCCGCCGCCCCGCGACCGGGGCAGCCGCCGGCGCCGCGCCCCCTCCTC
1441  GCGACGGACGACGGGCGGCGGGGCGCTGGCCCCGTCGGCGGCCGCGGCGCGGGGGAGGAG

1501  CCTGCCTCCCCGGCGGGGCGGGCGACGGGGGCAACGGGAGTGTGACGGACTGCGGCGCTC
1501  GGACGGAGGGGCCGCCCCGCCCGCTGCCCCCGTTGCCCTCACACTGCCTGACGCCGCGAG

1561  GGCGGGCCTGGGCGCAAGGACTGGGTCGCCGCCGTGCGGGGCGCCCGGGGCGGGTGGGTG
1561  CCGCCCGGACCCGCGTTCCTGACCCAGCGGCGGCACGCCCCGCGGGCCCCGCCCACCCAC

1621  TGGGCTGCGGGGCCGACGGCCGCGGGGGGGGCGCGGGGCTTTCCACGGCACGGGGCGGGT
1621  ACCCGACGCCCCGGCTGCCGGCGCCCCCCCCGCGCCCCGAAAGGTGCCGTGCCCCGCCCA

1681  GGGGCTGCGGGCGCGGTCGGGGCTGGCGCGGCAGGCGAGAGGAATTCCAGCGGGACGCGC
1681  CCCCGACGCCCGCGCCAGCCCCGACCGCGCCGTCCGCTCTCCTTAAGGTCGCCCTGCGCG

1741  CAGCGCTGCCTCCGCCTCGCCTCCCGTTACTATAGTTTTTTCAGAACCTCTTATCCACCC
1741  GTCGCGACGGAGGCGGAGCGGAGGGCAATGATATCAAAAAAGTCTTGGAGAATAGGTGGG

1801  CGCAGAAGAGAAATTTTTTTTTAACGTCCTGTTGCTTCACGGGGGACTTTCGGGGTGGGC
1801  GCGTCTTCTCTTTAAAAAAAAATTGCAGGACAACGAAGTGCCCCCTGAAAGCCCCACCCG

1861  ATCACGTGGCCCGACACGTAGCCGTGGGGCTCCAGAGCGCGTGCGCGCGTCGAGCCCGGT
1861  TAGTGCACCGGGCTGTGCATCGGCACCCCGAGGTCTCGCGCACGCGCGCAGCTCGGGCCA

1921  CGCCACGCCCCTTCCGAGGGTCGCTCCGCCCCCGTCGGGCCCCGCGAGCGCGCGGTGGGG
1921  GCGGTGCGGGGAAGGCTCCCAGCGAGGCGGGGGCAGCCCGGGGCGCTCGCGCGCCACCCC

1981  GAGGGGAGGGCCCCGGAGCGCGCCTGCGTGGGGCGGGGGCGGCAGCCGACTAGGGGCTGG
1981  CTCCCCTCCCGGGGCCTCGCGCGGACGCACCCCGCCCCCGCCGTCGGCTGATCCCCGACC

2041  GTCTGGCCGTTTAGGGCCGGGTCTTGGCCCGTCGCCCACGGTGCGGAGGGCTGGTGGGCT
2041  CAGACCGGCAAATCCCGGCCCAGAACCGGGCAGCGGGTGCCACGCCTCCCGACCACCCGA

2101  TTCCTTGGCCGTCGGGCCCGCCACGGCGCGGGTCTTGGCTGCGGGGCGGAGGTGGGGCGG
2101  AAGGAACCGGCAGCCCGGGCGGTGCCGCGCCCAGAACCGACGCCCCGCCTCCACCCCGCC

2161  GAGAGCCGAGGATAAGAGTTTGAGGCTTTTCGAGGCGCGTGCCGCGGCGTCCGCCTCTGC
2161  CTCTCGGCTCCTATTCTCAAACTCCGAAAAGCTCCGCGCACGGCGCCGCAGGCGGAGACG

2221  GGGACTCTGCGCCGGGCGCCCTCGGCCGGCGCGCCCGGCTCCCGCTTTGTCGCCGAGGGA
2221  CCCTGAGACGCGGCCCGCGGGAGCCGGCCGCGCGGGCCGAGGGCGAAACAGCGGCTCCCT

2281  AGCACGCGCGACGCCCCTCCCGTCGCCGCCGTGGCTTCTTTCGGTGTTCGTGATTTGCTG
2281  TCGTGCGCGCTGCGGGGAGGGCAGCGGCGGCACCGAAGAAAGCCACAAGCACTAAACGAC

2341  AGAGGCTGGAAAGCAGCACGGCGGAGAGGAGCCTTGCACTCGCCAGGCGGGAAGCCTGCG
2341  TCTCCGACCTTTCGTCGTGCCGCCTCTCCTCGGAACGTGAGCGGTCCGCCCTTCGGACGC

2401  CGGACACGCCGTGCGCACCCACGGGGCGGCGGGCGGGCGTGGGGGTCCGGGCCACGCGGG
2401  GCCTGTGCGGCACGCGTGGGTGCCCCGCCGCCCGCCCGCACCCCCAGGCCCGGTGCGCCC
```

FIGURE 2 (cont'd)

```
2461  CGACGCGCCTCTAGGGAAGCGATCTTGTTGCACCTTCCCGTTATTCTGAAAGCAAATCGT
2461  GCTGCGCGGAGATCCCTTCGCTAGAACAACGTGGAAGGGCAATAAGACTTTCGTTTAGCA

2521  AGCCAGACCCGAGCGCAGCGGCTTAGCAAATAATAAGGGGAGCGTCAGTCGTGCTCGAAA
2521  TCGGTCTGGGCTCGCGTCGCCGAATCGTTTATTATTCCCCTCGCAGTCAGCACGAGCTTT

2581  TGCTTCCTTCGCGATGGCGTCAGTGTTCCGTGAGGGAATGAAGCCGCAGTAGGAAATAAA
2581  ACGAAGGAAGCGCTACCGCAGTCACAAGGCACTCCCTTACTTCGGCGTCATCCTTTATTT


2641  GAGGCTGTGCGCGTAGTCTGAAAAGCAGAAGTCAACATTTTTACAGATGAAGAAAGAATA
2641  CTCCGACACGCGCATCAGACTTTTCGTCTTCAGTTGTAAAAATGTCTACTTCTTTCTTAT

2701  CGGAGGCAAGAGGTCTTTCTCTGCAGTTTGGTGGATTTCCAACATTTAGACTTGTTTGGA
2701  GCCTCCGTTCTCCAGAAAGAGACGTCAAACCACCTAAAGGTTGTAAATCTGAACAAACCT

2761  AGAATTTCCTCAGCTGCACCAATGAAGTCCTTGATCTATAGAAGTCGGCAGTCCCTAAAT
2761  TCTTAAAGGAGTCGACGTGGTTACTTCAGGAACTAGATATCTTCAGCCGTCAGGGATTTA

2821  CTACGTCTGCATTTTGTTGCAAATCCTTTATAACATTCCATTAAAATAATGCAGAGTTAT
2821  GATGCAGACGTAAAACAACGTTTAGGAAATATTGTAAGGTAATTTTATTACGTCTCAATA

2881  TTAATA
2881  AATTAT
```

FIGURE 3

>hg19_refGene_NM_001195286 range=chr6:389739-411443 5'pad=0 3'pad=0 strand=+ repeatMasking=none

The IRF4 gene resides on the plus strand. The top strand in the below is the representative 5′-3′ gene sequence of IRF4

Yellow: Sub-region of interest towards which a bisulphate conversion and methylation specfic assay is given as an example

```
   1  AGATTAGCAATTACATTTAAAAACAAGGTAGTGGTGTGAAGGCTCAGAGTTTCACACAAC
   1  TCTAATCGTTAATGTAAATTTTTGTTCCATCACCACACTTCCGAGTCTCAAAGTGTGTTG

  61  GACTGTTGTTCTGAACTAAAAGCAGAGGATGTGGATGAGTGAGGGGAGGGTATGTTGAAA
  61  CTGACAACAAGACTTGATTTTCGTCTCCTACACCTACTCACTCCCCTCCCATACAACTTT

 121  ATGACTAAACCCGGTGCAGAGGACACGTATACGAAAGTGCAAAAAGCTCTCATTTGCCAT
 121  TACTGATTTGGGCCACGTCTCCTGTGCATATGCTTTCACGTTTTTCGAGAGTAAACGGTA

 181  TTTTTGTCCTCAGCAAACTCCTCTCTGGTATGTTTGTGAACGTTTGAGGGAAAGGTAACA
 181  AAAAACAGGAGTCGTTTGAGGAGAGACCATACAAACACTTGCAAACTCCCTTTCCATTGT

 241  CTGATTAAAATATAATGCAACAAGAAGGCAACGATCTTTGCTTTGTTCACTGATGTGTTC
 241  GACTAATTTTATATTACGTTGTTCTTCCGTTGCTAGAAACGAAACAAGTGACTACACAAG

 301  CAAGTGCCTAGGACGGTTCCTGACAAGTAGCAGGTGCTCAAAATACATTTGTCAAGTGAA
 301  GTTCACGGATCCTGCCAAGGACTGTTCATCGTCCACGAGTTTTATGTAAACAGTTCACTT

 361  TAAATCTGTGAAAGGAAAGGAAGAAAAACAGGTTGTGACCAGAACTTTTTGTGAACAAAA
 361  ATTTAGACACTTTCCTTTCCTTCTTTTTGTCCAACACTGGTCTTGAAAAACACTTGTTTT

 421  CCCTGTTGTTTATTACATAGACTTTGGTAATGGAAAACTTACTTGGGTGAAATAAAAAAT
 421  GGGACAACAAATAATGTATCTGAAACCATTACCTTTTGAATGAACCCACTTTATTTTTTA

 481  GGCATCCTGTTAATTTCTGAGAACGTCTGTTGGTTTTAGGAAAAGCATACCTATCCATAC
 481  CCGTAGGACAATTAAAGACTCTTGCAGACAACCAAAATCCTTTTCGTATGGATAGGTATG

 541  CTCACTACCTGTTTTGCTCTAGCCTAAACATAGATTCTTCTTTGGTTAGGAGACATTGAC
 541  GAGTGATGGACAAAACGAGATCGGATTTGTATCTAAGAAGAAACCAATCCTCTGTAACTG

 601  CCAATATATAAGATTAAAACAAAAACTGAGAAATAAGTGAAATCAAAAGCTTTTCAAAAG
 601  GGTTATATATTCTAATTTTGTTTTTGACTCTTTATTCACTTTAGTTTTCGAAAAGTTTTC

 661  TTGCAGGTTGACCTACGGTGGTGGTGGTCTAAAATCATATAGAAACCAGAGATCTGATGG
 661  AACGTCCAACTGGATGCCACCACCACCAGATTTTAGTATATCTTTGGTCTCTAGACTACC

 721  TTTACCTGAAAATGCGAAGTAAATGCACATACTCAGCATCTCAGACGATCGAAAGCTCAA
 721  AAATGGACTTTTACGCTTCATTTACGTGTATGAGTCGTAGAGTCTGCTAGCTTTCGAGTT

 781  CGGGTGAAAGCTCAGGGGGTTAATTTTGCGATTAAGGACATCTTGGAAAAGTATGTAAAA
 781  GCCCACTTTCGAGTCCCCCAATTAAAACGCTAATTCCTGTAGAACCTTTTCATACATTTT

 841  TCCCTGGTCCACTTAAGTATTATTCCTATTTTGGGCTTTTATTTATTTATTTTGAGATGG
 841  AGGGACCAGGTGAATTCATAATAAGGATAAAACCCGAAAATAAATAAATAAAACTCTACC

 901  AGTCTTGCTCTGTCGCCCACCTCGGCTCACTGCAACTTCAGCCTCCCGGGTTCAAGCGAT
 901  TCAGAACGAGACAGCGGGTGGAGCCGAGTGACGTTGAAGTCGGAGGGCCCAAGTTCGCTA

 961  TCTCGTGGCTCGTCCTCTCAAGTAGCTGGGGCCACGCCCGGCTAATTTTTGTATTTTTAG
 961  AGAGCACCGAGCAGGAGAGTTCATCGACCCCGGTGCGGGCCGATTAAAAACATAAAAATC

1021  TAGAGATGGGGTTTCACCGTGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGGCGATC
1021  ATCTCTACCCCAAAGTGGCACAACCGGTCCGACCAGAGCTTGAGGACTGGAGTCCGCTAG

1081  CACCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCTTGAGCCACAGCGCCTGGCCTAT
1081  GTGGCGGAGCCGGAGGGTTTCACGACCCTAATGTCCGAACTCGGTGTCGCGGACCGGATA
```

FIGURE 3 (cont'd)

```
1141  TTTGGGCTTTTATACCCCACTGGTAAACTGCTTTCCTCCAGGTTGAGGTTAAAACGACAT
1141  AAACCCGAAAATATGGGGTGACCATTTGACGAAAGGAGGTCCAACTCCAATTTTGCTGTA

1201  CATTTTAAGGTGAACTGAAGTCTGGAAGTGATTAAGCACTTGGATCCTTAGGGAGCCTCT
1201  GTAAAATTCCACTTGACTTCAGACCTTCACTAATTCGTGAACCTAGGAATCCCTCGGAGA

1261  CCCCGCCCCCATCTCTTTCATGCTAAGATAATTAAAACTTCGGGGCCGGGGCATTGTCTG
1261  GGGGCGGGGGTAGAGAAAGTACGATTCTATTAATTTTGAAGCCCCGGCCCCGTAACAGAC

1321  AGTCACTTCAATTCACCAGCCTAATAGATGCAAAAGGATGTAAGCATGTCAGACACGCAG
1321  TCAGTGAAGTTAAGTGGTCGGATTATCTACGTTTTCCTACATTCGTACAGTCTGTGCGTC

1381  AGACAGTATTTGAATCAAGCTTAATAGCTCAAGGGAGCTGGGCCATTTCCTATTTTCTTT
1381  TCTGTCATAAACTTAGTTCGAATTATCGAGTTCCCTCGACCCGGTAAAGGATAAAAGAAA

1441  TTAGTGAGTGCGATGTTCTCTAAACACCGCGGAGAGGCAGGGTTCCCGGTGATGGCCTTG
1441  AATCACTCACGCTACAAGAGATTTGTGGCGCCTCTCCGTCCCAAGGGCCACTACCGGAAC

1501  CCGAGGGTGCTCCCGCAACCTCCACCTCCAGTTCTCTTTGGACCATTCCTCCGTCTTCCG
1501  GGCTCCCACGAGGGCGTTGGAGGTGGAGGTCAAGAGAAACCTGGTAAGGAGGCAGAAGGC

1561  TTACACGCTCTGCAAAGCGAAGTCCCCTTCGCACCAGATTCCCGCTACTACACGCCCCCC
1561  AATGTGCGAGACGTTTCGCTTCAGGGGAAGCGTGGTCTAAGGGCGATGATGTGCGGGGGG

1621  ATTTCCCGCCCTGGCCACATCGCTGCAGTTTAGTGATTGACTGGCCTCCTGAGGTCCTGG
1621  TAAAGGGCGGGACCGGTGTAGCGACGTCAAATCACTAACTGACCGGAGGACTCCAGGACC

1681  CGCAAAGGCGAGATTCGCATTTCGCACCTCGCCCTTCGCGGGAAACGGCCCCAGTGACAG
1681  GCGTTTCCGCTCTAAGCGTAAAGCGTGGAGCGGGAAGCGCCCTTTGCCGGGGTCACTGTC

1741  TCCCCGAAGCGGCGCGCGCCCGGCTGGAGGTGCGCTCTCCGGGCGCGGCGCGCGGAGGGT
1741  AGGGGCTTCGCCGCGCGCGGGCCGACCTCCACGCGAGAGGCCCGCGCCGCGCGCCTCCCA

1801  CGCCAAGGGCGCGGGAACCCCACCCCGGCCGCGGCAGCCCCCAGCCTTCACGCCGGCCCT
1801  GCGGTTCCCGCGCCCTTGGGGTGGGGCCGGCGCCGTCGGGGGTCGGAAGTGCGGCCGGGA

1861  GAGGCTCGCCCGCCCGGCCGGCCCCGGCTCTCGGCTTGCAAAGTCCCTCTCCCCAGTCCA
1861  CTCCGAGCGGGCGGGCCGGCCGGGGCCGAGAGCCGAACGTTTCAGGGAGAGGGGTCAGGT

1921  ACCCCCGGCCCCCACAGGCCTCGGCGCCCCGCCCCGCCCCAGGCCCCGCCCCAGAGAGTT
1921  TGGGGGCCGGGGGTGTCCGGAGCCGCGGGGCGGGGCGGGGTCCGGGGCGGGGTCTCTCAA

1981  CTATAAAGTTCCTCTTTCCCACCTCGCACTCTCAGTTTCACCGCTCGATCTTGGGACCCA
1981  GATATTTCAAGGAGAAAGGGTGGAGCGTGAGAGTCAAAGTGGCGAGCTAGAACCCTGGGT

2041  CCGCTGCCCTCAGCTCCGAGTCCAGGGCGAGGTAAGGGCTGGAGTCGGGCAGGAGGAGGG
2041  GGCGACGGGAGTCGAGGCTCAGGTCCCGCTCCATTCCCGACCTCAGCCCGTCCTCCTCCC

2101  GTGTGAGGCTGATACCAGAGAGGACCCGGAGCGCGAACCAGAGGTTCGACCTCCAGGGCA
2101  CACACTCCGACTATGGTCTCTCCTGGGCCTCGCGCTTGGTCTCCAAGCTGGAGGTCCCGT

2161  GCGCAGGGTACCCCGGCTTCGGAGCGGGAAGGGAGCGCGCCCCGTCCTGGAGCTCCGACT
2161  CGCGTCCCATGGGGCCGAAGCCTCGCCCTTCCCTCGCGCGGGGCAGGACCTCGAGGCTGA

2221  CCCACCCCATCTGCGCTGAGCCGGAGGCGCTGGTTTGGGCTCCAAGGCCCGCCTCCTTGG
2221  GGGTGGGGTAGACGCGACTCGGCCTCCGCGACCAAACCCGAGGTTCCGGGCGGAGGAACC

2281  CTCTGCCCGAGCCTCCCCGCCTGCCCTCCGCGCTCCTGCGACGGGTCGCCACAAGCTGG
2281  GAGACGGGCTCGGAGGGGCGGACGGGAGGCGCGAGGACGCTGCCCAGCGGTGTTCGACC

2341  ACGGGATGAGCTAACCGGACTGTCGGGGCCCCAGGAGTGGCTGAGGCGGGGCCGTCCAAG
2341  TGCCCTACTCGATTGGCCTGACAGCCCCGGGGTCCTCACCGACTCCGCCCCGGCAGGTTC

2401  GCACCCACACAAGACGGCACAACTGCCTGCGAGAAACAGGCCCGGCCCTGTGGACCCCAA
2401  CGTGGGTGTGTTCTGCCGTGTTGACGGACGCTCTTTGTCCGGGCCGGGACACCTGGGGTT
```

FIGURE 3 (cont'd)

```
2461  TCCGAGGCTCCTTCCCCTGCTCTTCGTTCCTAAGGGGCCCAAGCTCACGGCGGCCTCCGG
2461  AGGCTCCGAGGAAGGGGACGAGAAGCAAGGATTCCCCGGGTTCGAGTGCCGCCGGAGGCC

2521  CGCGGTGCTCACCCGCTGGCGCAGGAGGAGGAGGAGCTCCACATTTGGGTCGCTCCGAGC
2521  GCGCCACGAGTGGGCGACCGCGTCCTCCTCCTCCTCGAGGTGTAAACCCAGCGAGGCTCG

2581  CTTGCGTGCGGTGGCCTAGCCGGCCTGGCGCGGTCCCTGCCTCCCAGGCTCCGCAGCTGT
2581  GAACGCACGCCACCGGATCGGCCGGACCGCGCCAGGGACGGAGGGTCCGAGGCGTCGACA

2641  CGTCGCCCTCTCCCGCGCCCTCCCCGCCTCCGCTCTCCCGGGCCTGCTCCGGGGTCCGGC
2641  GCAGCGGGAGAGGGCGCGGGAGGGGCGGAGGCGAGAGGGCCCGGACGAGGCCCCAGGCCG

2701  GGACGCTCTGCGCGCGGAATCCCCCGTACTGGGGCTGCAGCCCCCGCGTCTGCGCCACTT
2701  CCTGCGAGACGCGCGCCTTAGGGGGCATGACCCCGACGTCGGGGGCGCAGACGCGGTGAA

2761  GTCGTTTGCAGAGCCCACTTAGTGCGCGCTAGCTGGGCAGGGATAGGGGTCCTATTCGGG
2761  CAGCAAACGTCTCGGGTGAATCACGCGCGATCGACCCGTCCCTATCCCCAGGATAAGCCC

2821  GCGAAGGGTCTGGATGCGAGCAGAGAAAGCGGAGGGTGGAGGAACCCGGGGCTGCGCCCC
2821  CGCTTCCCAGACCTACGCTCGTCTCTTTCGCCTCCCACCTCCTTGGGCCCCGACGCGGGG

2881  TGGAACGCCCGGCCGCAGGCGAGGTCCTCCGCGCGTGGAGGCCGCCAGGGGAGTGGAAAC
2881  ACCTTGCGGGCCGGCGTCCGCTCCAGGAGGCGCGCACCTCCGGCGGTCCCCTCACCTTTG

2941  TGACAGAGTCGCGGGGAAGGGGCGAGAAGCGGGTTGGGAGTGAGCGAAGGCAAGCGAGAG
2941  ACTGTCTCAGCGCCCCTTCCCCGCTCTTCGCCCAACCCTCACTCGCTTCCGTTCGCTCTC

3001  CTGCGAGTGAGTGCGGAAGGAGGGCCAGGAGGGGTGGCGGCTGGGTGGGGAGAGAGGGTG
3001  GACGCTCACTCACGCCTTCCTCCCGGTCCTCCCCACCGCCGACCCACCCCTCTCTCCCAC

3061  CAAGACGAGCGGCGCGTGTCGGGAGCCTTTGGGCTGCGGGTGCGTTACAGGAGAGCAGGC
3061  GTTCTGCTCGCCGCGCACAGCCCTCGGAAACCCGACGCCCACGCAATGTCCTCTCGTCCG

3121  GGGTAGGAGCCTTCGCGGGGGCCGAGCTCGGAAGGCGGACGGCTGTGCCCGCCCAGGGGA
3121  CCCATCCTCGGAAGCGCCCCCGGCTCGAGCCTTCCGCCTGCCGACACGGGCGGGTCCCCT

3181  TGCGCCCGGGCCGGCCGCGAAGGTGCCTTCTTCCGGGGGCCCGGACGACCCTGACACGGC
3181  ACGCGGGCCCGGCCGGCGCTTCCACGGAAGAAGGCCCCCGGGCCTGCTGGGACTGTGCCG

3241  ACGCGCGCGCTTCGCAGCCTCAAAGACTCCGGGGCCTCGTGGTCACTGGCGCAGGGGATC
3241  TGCGCGCGCGAAGCGTCGGAGTTTCTGAGGCCCCGGAGCACCAGTGACCGCGTCCCCTAG

3301  GGCGCGGGCTGCCCGGAGTGCGGTGCCTCGTGGCTGAAGGGCAGCTCTTCTCCCCGCAGT
3301  CCCCGCCCCACGGGCCTCACGCCACGGAGCACCGACTTCCCGTCGAGAAGAGGGGCGTCA

3361  GCAGAGCAGAGCGGGCGGAGGACCCCGGGCGCGGGCGCGGACGGCACGCGGGGCATGAAC
3361  CGTCTCGTCTCGCCCGCCTCCTGGGGCCCGCGCCCGCGCCTGCCGTGCGCCCCGTACTTG

3421  CTGGAGGGCGGCGGCCGAGGCGGAGAGTTCGGCATGAGCGCGGTGAGCTGCGGCAACGGG
3421  GACCTCCCGCCGCCGGCTCCGCCTCTCAAGCCGTACTCGCGCCACTCGACGCCGTTGCCC

3481  AAGCTCCGCCAGTGGCTGATCGACCAGATCGACAGCGGCAAGTACCCCGGGCTGGTGTGG
3481  TTCGAGGCGGTCACCGACTAGCTGGTCTAGCTGTCGCCGTTCATGGGGCCCGACCACACC

3541  GAGAACGAGGAGAAGAGCATCTTCCGCATCCCCTGGAAGCACGCGGGCAAGCAGGACTAC
3541  CTCTTGCTCCTCTTCTCGTAGAAGGCGTAGGGGACCTTCGTGCGCCCGTTCGTCCTGATG

3601  AACCGCGAGGAGGACGCCGCGCTCTTCAAGGTCTCCGGCCTCGGGAGCCGGCGGGGGCGC
3601  TTGGCGCTCCTCCTGCGGCGCGAGAAGTTCCAGAGGCCGGAGCCCTCGGCCGCCCCCGCG

3661  GCCGGGGAGGGCCCAGAGACAGAGCCCGGCGTCCCCGGCGCCGCCTCCGAGGCGAGCCCA
3661  CGGCCCCTCCCGGGTCTCTGTCTCGGGCCCCAGGGGCCGCGGCGGAGGCTCCGCTCGGGT

3721  GGGGACCGCGCGGGGCGGACGGGCGGGCGGCGGAGGCATCAGGTGGCGTCGCCGGAGCCG
3721  CCCCTGGCGCGCCCCGCCTGCCCGCCCGCCGCCTCCGTAGTCCACCGCAGCGGCCTCGGC
```

FIGURE 3 (cont'd)

3781 CAGGAGGAGGAAAGGAGGCCTCGGCTCTCAGCGGGACCGCGGGGGCCGGGAGCCGGGTCC
3781 GTCCTCCTCCTTTCCTCCGGAGCCGAGAGTCGCCCTGGCGCCCCCGGCCCTCGGCCCAGG

3841 TGGCGCGTGGAGGCTGCAGGGAAACCGCTGAAGGCCCGGCCGGCCCGGGGAAGGGCGG
3841 ACCCGCGCACCTCCGACGTCCCTTTGGCGACTTCCGGGCCGGCCCGGGCCCCTTCCCGCC

3901 CCAAAGGCTTGAGGGGTTTTGCGCGTTCGTCCGTGCGTTCTCGTTTCCACGCAAGCCTCC
3901 GGTTTCCGAACTCCCCAAAACGCGCAAGCAGGCACGCAAGAGCAAAGGTGCGTTCGGAGG

3961 CGCCCTTCCTCCGGGCTCCCGTCTGCCGCCTCCGTCCGTGGGTCCCCCTCGCCCTCTCCG
3961 GCGGGAAGGAGGCCCGAGGGCAGACGGCGGAGGCAGGCACCCAGGGGGAGCGGGAGAGGC

4021 TGCGTCCGCGCCTGTGCCGGCGGCTGTTTTCGTCTCTCACCGCGTCTCTGTTTCTCTTTT
4021 ACGCAGGCGCGGACACGGCCGCCGACAAAAGCAGAGAGTGGCGCAGAGACAAAGAGAAAA

4081 CGCTGCTTTTCTCTCTGAGTCTCTCTCTCTCCATGTTTTTCCTGAGGTCAGCCTCTCTTC
4081 GCGACGAAAAGAGAGACTCAGAGAGAGAGAGGTACAAAAAGGACTCCAGTCGGAGAGAAG

4141 TCGCTCCTGCTAGCTCTCTGCGGGTACTCCCACCTCTGTCTTTCTCTTTGTGTGTCTCTG
4141 AGCGAGGACGATCGAGAGACGCCCATGAGGGTGGAGACAGAAAGAGAAACACACAGAGAC

4201 TCTCTCTCTTTCCCCCATCGCAGTGGAACTCAGGGCCTCTGTCTAGAGCTGTCTCCCTTG
4201 AGAGAGAGAAAGGGGGTAGCGTCACCTTGAGTCCCGGAGACAGATCTCGACAGAGGGAAC

4261 CCCTTTGCGCGAGTGCACACACGTGTGTCGTTGTTACGATTGTTCTCCCCTAAGGCAGTT
4261 GGGAAACGCGCTCACGTGTGTGCACACAGCAACAATGCTAACAAGAGGGGATTCCGTCAA

4321 TACCCAGAGAACTACGTGTCTGGGCCCAGCCCCCACCTGTGGGCAGAGCAGGGGAAGGGG
4321 ATGGGTCTCTTGATGCACAGACCCGGGTCGGGGGTGGACACCCGTCTCGTCCCCTTCCCC

4381 ACTTCCTCCGGGAATTTGGTCTCAATTTGCTCTCAGAGTGCCTCAGCTGTGCTGCCATCC
4381 TGAAGGAGGCCCTTAAACCAGAGTTAAACGAGAGTCTCACGGAGTCGACACGACGGTAGG

4441 AGATGTCTCCTGTGGGTGACAGCTCACACCACAGCTGTCCTTAGTCCTAGGCAAGCTCAC
4441 TCTACAGAGGACACCCACTGTCGAGTGTGGTGTCGACAGGAATCAGGATCCGTTCGAGTG

4501 TCAGACACTGGGTGGGTAGAGCCCCCTCAAGGAACCTCCGCATCTCACTCTACCGGTTAT
4501 AGTCTGTGACCCACCCATCTCGGGGGAGTTCCTTGGAGGCGTAGAGTGAGATGGCCAATA

4561 AAATACCCAGAAAATGTGTCTTCAACTTGGCAGTGATAGGGTCCAAGATGGAAAATCATT
4561 TTTATGGGTCTTTTACACAGAAGTTGAACCGTCACTATCCCAGGTTCTACCTTTTAGTAA

4621 TTCCTAGAGCATAGCTGGGGTCTTTCAGTTTACGTTCTGAGCAACGGTGTAAATCTGAAG
4621 AAGGATCTCGTATCGACCCCAGAAAGTCAAATGCAAGACTCGTTGCCACATTTAGACTTC

4681 GACCTATGCGCCATTCTTTCTTTTAGAAATACAATTTCAAGATTCCTTATAAAATATCTG
4681 CTGGATACGCGGTAAGAAAGAAAATCTTTATGTTAAAGTTCTAAGGAATATTTTATAGAC

4741 TATTTTGGGTTTAGCATGGTGGCTCACACCTGTAATCCCAGCACTTTGGGAAGATGAGGT
4741 ATAAAACCCAAATCGTACCACCGAGTGTGGACATTAGGGTCGTGAAACCCTTCTACTCCA

4801 GGAAGGATGCCTATGCAACATAGTGAGACCCTGCCTCTGCAAAAAATAATAATTAAAAAA
4801 CCTTCCTACGGATACGTTGTATCACTCTGGGACGGAGACGTTTTTTATTATTAATTTTTT

4861 ATTAGCCAGGCATGGTGGTGAACACCTGTAGGCCGAGGGCCCAGCTACTCTAGAGGCTGA
4861 TAATCGGTCCGTACCACCACTTGTGGACATCCGGCTCCCGGGTCGATGAGATCTCCGACT

4921 GATAGGAGGACCCTAGAACTCAGGAGTTCGATGCTGCGGTGAGCTATCATCGTGCCACTG
4921 CTATCCTCCTGGGATCTTGAGTCCTCAAGCTACGACGCCACTCGATAGTAGCACGGTGAC

4981 TACTCTAGCCTGGGCAGCAGAGCAGGACTCTGATTCCAAAAAGAAAGCTAATAAACCAGA
4981 ATGAGATCGGACCCGTCGTCTCGTCCTGAGACTAAGGTTTTTCTTTCGATTATTTGGTCT

5041 CATGTATTTTGACTTTTCGTTCTCTTCATTCTTTCCCACCAGGCTTGGCACTGTTTAAA
5041 GTACATAAAACTGAAAAGCAAGAGAAGTAAGAAAGGGTGGTCCGAACCCGTGACAAATTT

FIGURE 3 (cont'd)

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5101  GGAAAGTTCCGAGAAGGCATCGACAAGCCGGACCCTCCCACCTGGAAGACGCGCCTGCGG
5101  CCTTTCAAGGCTCTTCCGTAGCTGTTCGGCCTGGGAGGGTGGACCTTCTGCGCGGACGCC

5161  TGCGCTTTGAACAAGAGCAATGACTTTGAGGAACTGGTTGAGCGGAGCCAGCTGGACATC
5161  ACGCGAAACTTGTTCTCGTTACTGAAACTCCTTGACCAACTCGCCTCGGTCGACCTGTAG

5221  TCAGACCCGTACAAAGTGTACAGGATTGTTCCTGAGGGAGCCAAAAAAGGTAGGGGCTCT
5221  AGTCTGGGCATGTTTCACATGTCCTAACAAGGACTCCCTCGGTTTTTTCCATCCCCGAGA

5281  CCTGAATTTGGGTCACCTAACAGAGGCAGCCAGATCCTTGAGGCACCTTAACTTCATTCT
5281  GGACTTAAACCCAGTGGATTGTCTCCGTCGGTCTAGGAACTCCGTGGAATTGAAGTAAGA

5341  GAGCATCACTTTCTAGCTTTCCTTTTGTATTGCCTGCCTGCCTGCCTTCTGCCTCACAGT
5341  CTCGTAGTGAAAGATCGAAAGGAAAACATAACGGACGGACGGACGGAAGACGGAGTGTCA

5401  GAAGCCCAGCCTCCTTGCCTGAGTTATGTGGGTCACAAGTTGAAATTCCTGTGGGGTTCA
5401  CTTCGGGTCGGAGGAACGGACTCAATACACCCAGTGTTCAACTTTAAGGACACCCCAAGT

5461  GCATAGGAGAATTAATCACACTGTATGCCTCAATGTATATGGGGGGGGGTGCATTGAATA
5461  CGTATCCTCTTAATTAGTGTGACATACGGAGTTACATATACCCCCCCCCACGTAACTTAT

5521  TGTGTTTTCCAGTTAGTCTTTCAAAAAAAAAAAGAAAAAAGAAAACTGGATAACTTGTTA
5521  ACACAAAAGGTCAATCAGAAAGTTTTTTTTTTTCTTTTTTCTTTTGACCTATTGAACAAT

5581  AAATTTACTTATCTAATAGTCTTTAGTGAGTGACTATTTTGCAGAAAAGGAGTAATGAGA
5581  TTTAAATGAATAGATTATCAGAAATCACTCACTGATAAAACGTCTTTTCCTCATTACTCT

5641  GGAATATCTCATCACTATGCATGGTAATAAAACTGTCAACTTTTAAAGTCTAACATGGTC
5641  CCTTATAGAGTAGTGATACGTACCATTATTTTGACAGTTGAAAATTTCAGATTGTACCAG

5701  AGCTGAGGTGTTTATTAAAAGTCAGATTCCTGGACCCCTCTTTTCAAGATTCTGACCAGT
5701  TCGACTCCACAAATAATTTTCAGTCTAAGGACCTGGGGAGAAAAGTTCTAAGACTGGTCA

5761  GTGTCTGGAAGAGAGCTCAGGAATCTGCATCTGGAACAAATCCTTCAGGTGACCTCACTT
5761  CACAGACCTTCTCTCGAGTCCTTAGACGTAGACCTTGTTTAGGAAGTCCACTGGAGTGAA

5821  GGGAAACATCTGGCTGGCGGGGTCCTTTATGTCACAAGGCACATTCGCATGCCATCTGTC
5821  CCCTTTGTAGACCGACCGCCCCAGGAAATACAGTGTTCCGTGTAAGCGTACGGTAGACAG

5881  ATGTATTTCTTTACCTCTCCTGTACAACTCAGACCTTGTAGAAAAAAATCAGTTTAATAG
5881  TACATAAAGAAATGGACAGGACATGTTGAGTCTGGAACATCTTTTTTTAGTCAAATTATC

5941  CATGAAAAAATAACTTCCCAAGGGAGTTGCTGAAAAATACCTTATTTGTCAACACCGTGT
5941  GTACTTTTTTATTGAAGGGTTCCCTCAACGACTTTTTATGGAATAAACAGTTGTGGCACA

6001  TATGCATTCTAAGAATTAAATGCTCAGGTATTTTTACAAGATTTGACATTTAGTTAGGTC
6001  ATACGTAAGATTCTTAATTTACGAGTCCATAAAAATGTTCTAAACTGTAAATCAATCCAG

6061  AGTTCCTGTTTTTACGTTGTGCCATTTCCCTTTTCCCCAAACATGTAGGAGCCAAGCAGC
6061  TCAAGGACAAAAATGCAACACGGTAAAGGGAAAAGGGGTTTGTACATCCTCGGTTCGTCG

6121  TCACCCTGGAGGACCCGCAGATGTCCATGAGCCACCCCTACACCATGACAACGCCTTACC
6121  AGTGGGACCTCCTGGGCGTCTACAGGTACTCGGTGGGGATGTGGTACTGTTGCGGAATGG

6181  CTTCGCTCCCAGCCCAGGTATGGTGGAGGGCACTGGGCTCCCTGAGGGCGAGGCTGTGTG
6181  GAAGCGAGGGTCGGGTCCATACCACCTCCCGTGACCCGAGGGACTCCCGCTCCGACACAC

6241  GGCCAGCTGCCCACATGGCCAGAGAACCACAGCAGCCCAGACAGCAGAACTTGCCATTTG
6241  CCGGTCGACGGGTGTACCGGTCTCTTGGTGTCGTCGGGTCTGTCGTCTTGAACGGTAAAC

6301  CTATGGCTGCTCCAACAGCCCAGAAAAACCCCAGGTCACTGAACGAATGTCTCACTTTCC
6301  GATACCGACGAGGTTGTCGGGTCTTTTTGGGGTCCAGTGACTTGCTTACAGAGTGAAAGG

6361  ACACGGTGCTGCCATTGGTGTGGATTTTAAGTTGGGGAGGGTCGGGCGTGTCCGCCTGTT
6361  TGTGCCACGACGGTAACCACACCTAAAATTCAACCCCTCCCAGCCCGCACAGGCGGACAA
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FIGURE 3 (cont'd)

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6421  GGAATATGCTTCTCAGGTCTTCTGGGAAACAGATGTTTTGTGGAAGTGGAAGATTTTGGA
6421  CCTTATACGAAGAGTCCAGAAGACCCTTTGTCTACAAAACACCTTCACCTTCTAAAACCT

6481  AGTAGTGCCTTATCATGTGAAACCACAGGGCAGCTGATCTCTTCAGGCTTTCTTGATGTG
6481  TCATCACGGAATAGTACACTTTGGTGTCCCGTCGACTAGAGAAGTCCGAAAGAACTACAC

6541  AATGACAGCTTTGTTTCATCCACTTTGGTGGGTAAAAGAAGGCAAATTCCCCTGTGGTAC
6541  TTACTGTCGAAACAAAGTAGGTGAAACCACCCATTTTCTTCCGTTTAAGGGGACACCATG

6601  TTTTGGTGCCAGGTTTAGCCATATGACGAAGCTTTACATAAAACAGTACAAGTATCTCCA
6601  AAAACCACGGTCCAAATCGGTATACTGCTTCGAAATGTATTTTGTCATGTTCATAGAGGT

6661  TTGTCCTTTATGATCCTCCATGAGTGTTTTCACTTAGTCTGATGAAGGGTTCACTCCAGT
6661  AACAGGAAATACTAGGAGGTACTCACAAAAGTGAATCAGACTACTTCCCAAGTGAGGTCA

6721  CTTTTCGGATGATAAAATGCTTCGGCTGTCAGTCTAATAAGGGATTCCCTGAGGAGTTTG
6721  GAAAAGCCTACTATTTTACGAAGCCGACAGTCAGATTATTCCCTAAGGGACTCCTCAAAC

6781  GAGGCTGTAAGAGCACCCCCCGTCTCAATGCCAGTGCTTCTTATCTCAGCCTCTCCTGCA
6781  CTCCGACATTCTCGTGGGGGGCAGAGTTACGGTCACGAAGAATAGAGTCGGAGAGGACGT

6841  CTCCTTTACCCCCGTCTCGATGCCAGTGCTTCCTATCTCAGCCTCTCCTGCACTCCTTTA
6841  GAGGAAATGGGGGCAGAGCTACGGTCACGAAGGATAGAGTCGGAGAGGACGTGAGGAAAT

6901  CCCCCGTCTCGATGCCAGTGCTTCCTATCTCAGCCTCTCCTGCACTCCTTTACCCCCGTC
6901  GGGGGCAGAGCTACGGTCACGAAGGATAGAGTCGGAGAGGACGTGAGGAAATGGGGGCAG

6961  TCGATGCCAGTGCTTCTTATCTCAGCCTCTCCTGCACTCCTTTACCCCCGTCTCAATGCC
6961  AGCTACGGTCACGAAGAATAGAGTCGGAGAGGACGTGAGGAAATGGGGGCAGAGTTACGG

7021  AGTGCTTCCTATCTCAGCCTCTCCTGCACTCCTTTAACCCCGTCTCGATGCCAGTGCTTC
7021  TCACGAAGGATAGAGTCGGAGAGGACGTGAGGAAATTGGGGCAGAGCTACGGTCACGAAG

7081  TTATCTCAGCCTCTCCTGCACTCCTTTACCCCCGTCTCAATGCCAGTGCTTCCTATCTCA
7081  AATAGAGTCGGAGAGGACGTGAGGAAATGGGGGCAGAGTTACGGTCACGAAGGATAGAGT

7141  GCCTCTCCTGCACTCCTTTACCCCCGTCTCAATGCCAGTGCTTCCTATCTCAGCCTCTCC
7141  CGGAGAGGACGTGAGGAAATGGGGGCAGAGTTACGGTCACGAAGGATAGAGTCGGAGAGG

7201  TGCACTCCTTTACCCCCGTCTCGATGCCAGTGCTTCTTATCTCAGCCTCTCCTGCACTCC
7201  ACGTGAGGAAATGGGGGCAGAGCTACGGTCACGAAGAATAGAGTCGGAGAGGACGTGAGG

7261  TTTACCCCCGTCTCGATGCCAGTGCTTCCTATCTCAGCCTCTCCTGCACTCCTTTACCCC
7261  AAATGGGGGCAGAGCTACGGTCACGAAGGATAGAGTCGGAGAGGACGTGAGGAAATGGGG

7321  CGTCTCAATGCCAGTGCTTCTTATCTCAGCCTCTCCTGCACTCCTTTAGCAGGTTCACAA
7321  GCAGAGTTACGGTCACGAAGAATAGAGTCGGAGAGGACGTGAGGAAATCGTCCAAGTGTT

7381  CTACATGATGCCACCCCTCGACCGAAGCTGGAGGGACTACGTCCCGGATCAGCCACACCC
7381  GATGTACTACGGTGGGGAGCTGGCTTCGACCTCCCTGATGCAGGGCCTAGTCGGTGTGGG

7441  GGAAATCCCGTACCAATGTCCCATGACGTTTGGACCCCGCGGCCACCACTGGCAAGGCCC
7441  CCTTTAGGGCATGGTTACAGGGTACTGCAAACCTGGGGCGCCGGTGGTGACCGTTCCGGG

7501  AGCTTGTGAAAATGGTAAGGAGGATACCAGTGCAGGAAATAGAAGAGCTAATTGCTAATG
7501  TCGAACACTTTTACCATTCCTCCTATGGTCACGTCCTTTATCTTCTCGATTAACGATTAC

7561  TGGCCATGGGCCATGGCGAATCCTGGTCTGTCCTGGGCAGCACCAAAGCTCTTTCCCCTT
7561  ACCGGTACCCGGTACCGCTTAGGACCAGACAGGACCCGTCGTGGTTTCGAGAAAGGGGAA

7621  CTTAGAGGCTGCGTGTGCAGCTCGGGGAGAGGGGGGTTTTCTCACTCCTGTGGGATGGTG
7621  GAATCTCCGACGCACACGTCGAGCCCCTCTCCCCCCAAAAGAGTGAGGACACCCTACCAC

7681  GCATCCCACAGCCAAGTTTACTCTCAGGATCCATGCTAGGCACTGCCCTTCGTGGGATCT
7681  CGTAGGGTGTCGGTTCAAATGAGAGTCCTAGGTACGATCCGTGACGGGAAGCACCCTAGA
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FIGURE 3 (cont'd)

7741 TATTTAAACACCACAGAGATCACTCCAGGCAGTGGAAAACAGCCCCCCACTTTTTATATA
7741 ATAAATTTGTGGTGTCTCTAGTGAGGTCCGTCACCTTTTGTCGGGGGGTGAAAAATATAT

7801 GAGAGGAGATTGTGGAAGCTCATAAATAATAAGTAGGGATGCTGGGAGATTATTGAGCTG
7801 CTCTCCTCTAACACCTTCGAGTATTTATTATTCATCCCTACGACCCTCTAATAACTCGAC

7861 GTATATTTCTCTCGAATAGTGGTGTGTTCATTGTTGCTATTGTTGGAATTAGAGGTGATA
7861 CATATAAAGAGAGCTTATCACCACACAAGTAACAACGATAACAACCTTAATCTCCACTAT

7921 CTAAAAAAGGAACGGAAAAATACCATGGCAAACACATAAAACGTCTCTACAGGTGCCTAC
7921 GATTTTTTCCTTGCCTTTTTATGGTACCGTTTGTGTATTTTGCAGAGATGTCCACGGATG

7981 CTACCACTGGGTCCCAGAAAGACTTGCTGATTGTGGATTAGATGTGGTCCCCTGCCCTCG
7981 GATGGTGACCCAGGGTCTTTCTGAACGACTAACACCTAATCTACACCAGGGGACGGGAGC

8041 GGAGTTCCCCAGACATCAAAATGAGCTCCCTCAGCAGAAGCTCTCATTAGCTGGGTGCAG
8041 CCTCAAGGGGTCTGTAGTTTTACTCGAGGGAGTCGTCTTCGAGAGTAATCGACCCACGTC

8101 GGAGAATCTAGCAATGCGGTAACTCAGGCCTTCAGGACTTTTGAGTTAGTTACTTAAATG
8101 CCTCTTAGATCGTTACGCCATTGAGTCCGGAAGTCCTGAAAACTCAATCAATGAATTTAC

8161 GAAGTCCTGAGACAGGTCAACACACTGAACCCTTTGGATGTTTTAGGAATATTTGTTCCT
8161 CTTCAGGACTCTGTCCAGTTGTGTGACTTGGGAAACCTACAAAATCCTTATAAACAAGGA

8221 TTGCAATTTGGCCTTTTTTTCCCCAGTCATGTTCAGGTTATCCTTGGCTGCAGGTAGTGA
8221 AACGTTAAACCGGAAAAAAAGGGGTCAGTACAAGTCCAATAGGAACCGACGTCCATCACT

8281 AGAGGTGTACCACTCTTTAATGTTTGTACTGAGTGGCATGTTCACAAAAAAGCTCAGAAT
8281 TCTCCACATGGTGAGAAATTACAAACATGACTCACCGTACAAGTGTTTTTTCGAGTCTTA

8341 TCAGTTGCATTGGCTTTTCAAGAGGGATTTGCAGCAAGGGCTGGTTTCCAATATGGTAGT
8341 AGTCAACGTAACCGAAAAGTTCTCCCTAAACGTCGTTCCCGACCAAAGGTTATACCATCA

8401 GGAGGAATTGGCTAACATAAAACTAGCTCCTGAAATTCAGACTTGCGTTTACTGCTCTGG
8401 CCTCCTTAACCGATTGTATTTTGATCGAGGACTTTAAGTCTGAACGCAAATGACGAGACC

8461 CTCTATGGAATTAGTAACCATGGGAAAGAGGCAATGCTTAGAACTGTGTAAAGTGATGGA
8461 GAGATACCTTAATCATTGGTACCCTTTCTCCGTTACGAATCTTGACACATTTCACTACCT

8521 GTAGGTAGAGACCTGTCTTGAAGCATCGGTAACAGTAAATGAAGCAGCAGCAAGATCAGG
8521 CATCCATCTCTGGACAGAACTTCGTAGCCATTGTCATTTACTTCGTCGTCGTTCTAGTCC

8581 TGTTCTGTGCCACATTCTTTTTCCATTCATGTTTCATACAACATTGTCTTCAGGAACATG
8581 ACAAGACACGGTGTAAGAAAAAGGTAAGTACAAAGTATGTTGTAACAGAAGTCCTTGTAC

8641 GTTCAGTGTTCTCCCAACCCACAAGAGACAAGCAAAATAAAAATGGACTAAATAATTTGC
8641 CAAGTCACAAGAGGGTTGGGTGTTCTCTGTTCGTTTTATTTTTACCTGATTTATTAAACG

8701 TAGTTTTTAATTGGGCTCTTTGGCACAGACTCAAGTAGACCTGAACTCTCAGCTCTGTTG
8701 ATCAAAAATTAACCCGAGAAACCGTGTCTGAGTTCATCTGGACTTGAGAGTCGAGACAAC

8761 TGAACCCGCTTTGTGAACAAGGACAAAGCATGTCATCTGTCTCTGAGCCTCAGTCTCCCT
8761 ACTTGGGCGAAACACTTGTTCCTGTTTCGTACAGTAGACAGAGACTCGGAGTCAGAGGGA

8821 GTTAGTCAGTTACAGAGAGAGCGCTCCAAGTTTCCTTCCAAAGCTGTGCACTGGCTCGTT
8821 CAATCAGTCAATGTCTCTCTCGCGAGGTTCAAAGGAAGGTTTCGACACGTGACCGAGCAA

8881 TCTCCATCAGCTTTGGTTTTCCAGTTGGTCTCCAGCTCATCTTTGCCTCACAAGAGCGTG
8881 AGAGGTAGTCGAAACCAAAAGGTCAACCAGAGGTCGAGTAGAAACGGAGTGTTCTCGCAC

8941 CCCTGCTAGTTGCTGGTGCTGGGAGTGGGTGGGAAGGTGATTGGGCGCCAGCCCCTTCCT
8941 GGGACGATCAACGACCACGACCCTCACCCACCCTTCCACTAACCCGCGGTCGGGGAAGGA

9001 TCCCAGGCTTCACACACACACCCCAGGAAGCCCCGCGGTGCGTCGGACTCTCTGTCTAGA
9001 AGGGTCCGAAGTGTGTGTGTGGGGTCCTTCGGGGCGCCACGCAGCCTGAGAGACAGATCT

FIGURE 3 (cont'd)

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 9061  CATCATCTGATTTTTATTTGCAAATGCAGGTTGCCAGGTGACAGGAACCTTTTATGCTTG
 9061  GTAGTAGACTAAAAATAAACGTTTACGTCCAACGGTCCACTGTCCTTGGAAAATACGAAC

 9121  TGCCCCACCTGAGTCCCAGGCTCCCGGAGTCCCCACAGAGCCAAGCATAAGGTCTGCCGA
 9121  ACGGGGTGGACTCAGGGTCCGAGGGCCTCAGGGGTGTCTCGGTTCGTATTCCAGACGGCT

 9181  AGCCTTGGCGTTCTCAGGTGAGTGCAGGGTTTGCTCCTGGAGGCACCGCAGGAGGCCAGC
 9181  TCGGAACCGCAAGAGTCCACTCACGTCCCAAACGAGGACCTCCGTGGCGTCCTCCGGTCG

 9241  CTCTGCTGCCAGCTCTGTCATCTTTGGGCAGATTCGATGGGACTTTAGACACTTGCTTTG
 9241  GAGACGACGGTCGAGACAGTAGAAACCCGTCTAAGCTACCCTGAAATCTGTGAACGAAAC

 9301  CTCCCTCTGGGGTCTGGAGTAGATGTAGACACATCCTGTGTGTGAGGTGACCAGGGTGAT
 9301  GAGGGAGACCCCAGACCTCATCTACATCTGTGTAGGACACACACTCCACTGGTCCCACTA

 9361  TTAGGAGCACCATTAGAAAACCTGACATCACTGCTTGTGGTTCTGCTGACCGTTTCAGCC
 9361  AATCCTCGTGGTAATCTTTTGGACTGTAGTGACGAACACCAAGACGACTGGCAAAGTCGG

 9421  ACTGGCTTGAATGGAGTCATTTTGGCTTCTTCACTGGCACCTCTCTGAATTTCTAGGAAT
 9421  TGACCGAACTTACCTCAGTAAAACCGAAGAAGTGACCGTGGAGAGACTTAAAGATCCTTA

 9481  GTGCCTTTACCTTTACCGAGGGCCCCTCTTCAGCCAACATTCTCACGATGTGGAATAATT
 9481  CACGGAAATGGAAATGGCTCCCGGGGAGAAGTCGGTTGTAAGAGTGCTACACCTTATTAA

 9541  GCTTGGAAGTGTAGAAGGGCTTCTCATTTTGAGAAGCTGATCATCCTTCCAGGTTGAGCC
 9541  CGAACCTTCACATCTTCCCGAAGAGTAAAACTCTTCGACTAGTAGGAAGGTCCAACTCGG

 9601  ACAAATAAGTCCTCCTCCTCTACTCCCTGGGGACATTAGTTCTGGTCCCTCATCTCTAAA
 9601  TGTTTATTCAGGAGGAGGAGATGAGGGACCCCTGTAATCAAGACCAGGGAGTAGAGATTT

 9661  ACATTGATGTGCCTAAGAGTAATACACATTTTGGTCTTCCTCTGAACTTTAATATAGCTT
 9661  TGTAACTACACGGATTCTCATTATGTGTAAAACCAGAAGGAGACTTGAAATTATATCGAA

 9721  GCAAACAAATATGGATTCAATCTGATTTTTAAAGTTTTATTTCTAAAAAAAAAAAAAAAA
 9721  CGTTTGTTTATACCTAAGTTAGACTAAAAATTTCAAAATAAAGATTTTTTTTTTTTTTTT

 9781  TCCCTGCACCATGGAGATCTTACCTACTATAAAGAAGGCACCTCTAGGCTTGGCAAGCAC
 9781  AGGGACGTGGTACCTCTAGAATGGATGATATTTCTTCCGTGGAGATCCGAACCGTTCGTG

 9841  ACGTGCTATATGTATATTTATTTTTCAGATAATATTTTGGATTGTTTTTAAATGGGATTT
 9841  TGCACGATATACATATAAATAAAAAGTCTATTATAAAACCTAACAAAAATTTACCCTAAA

 9901  GTTTTTATATTAAAACCAAATAGCTTAAGGTTTGGAATTCTCATCTTGCCCTCTGGCATC
 9901  CAAAAATATAATTTTGGTTTATCGAATTCCAAACCTTAAGAGTAGAACGGGAGACCGTAG

 9961  TTTAAAAATCAGTGATGAAAAATACTAACTAAATTCTGAAGGTTTCAGGGAGGCGAGAGT
 9961  AAATTTTTAGTCACTACTTTTTATGATTGATTTAAGACTTCCAAAGTCCCTCCGCTCTCA

10021  TGTGGCACTTTTGCTGCTCAGAGGGGAGCTGGAGTTTGACCTACCAGCTCTTTCTAGTTG
10021  ACACCGTGAAAACGACGAGTCTCCCCTCGACCTCAAACTGGATGGTCGAGAAAGATCAAC

10081  TGAATGAGGCTTGCACCTTTTTTTCTGAGGTGCTCGTGAGTAACTGAGGATGCCCTTTGG
10081  ACTTACTCCGAACGTGGAAAAAAAGACTCCACGAGCACTCATTGACTCCTACGGGAAACC

10141  GAGGAGGTGCTTCTGAGCAGGAAGGCTTGTGTTTGTTTTTAGAAACTTTCAAACCCTTGT
10141  CTCCTCCACGAAGACTCGTCCTTCCGAACACAAACAAAAATCTTTGAAAGTTTGGGAACA

10201  CTTGAACACCTAAGACTTGTGTGGGTGCCTGAAGAGTAGGAAATAAACAGCTATTTATAT
10201  GAACTTGTGGATTCTGAACACACCCACGGACTTCTCATCCTTTATTTGTCGATAAATATA

10261  CTCGGCAACCTCGTGATTTCTGATGACATTAAATGAAATGAAACCTGCCCCGAGAATCAC
10261  GAGCCGTTGGAGCACTAAAGACTACTGTAATTTACTTTACTTTGGACGGGGCTCTTAGTG

10321  CTCGAATGGCCAACACCCACTCTCTTTGGGGCGCACTGTCTGACTCGCTTTCAGACAGTG
10321  GAGCTTACCGGTTGTGGGTGAGAGAAACCCCGCGTGACAGACTGAGCGAAAGTCTGTCAC

10381  TGTTGAAGCAGAGAATTGAGACAGTGATGTGGGTTAAGTCTCAAAACCTGCTGTTGAGGA
10381  ACAACTTCGTCTCTTAACTCTGTCACTACACCCAATTCAGAGTTTTGGACGACAACTCCT
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FIGURE 3 (cont'd)

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10441  ATAAGATAGTTTTGTGGGTTTCTTTTTTTGGTATGCATGATACAGATTAATTATCAGCCA
10441  TATTCTATCAAAACACCCAAAGAAAAAAACCATACGTACTATGTCTAATTAATAGTCGGT

10501  TGAGCACATTTATTAGATAACTGTGATTCCCATTGATTTTGGGGTTCCATACAGTTACCA
10501  ACTCGTGTAAATAATCTATTGACACTAAGGGTAACTAAAACCCCAAGGTATGTCAATGGT

10561  GTGGCAGCTGCCTCCTGTCTGTGCCACTCCCCTGCGGTCTGGCTGAGGAGCTTGTGCAAA
10561  CACCGTCGACGGAGGACAGACACGGTGAGGGGACGCCAGACCGACTCCTCGAACACGTTT

10621  CCCAGCTTGGTTCTTTCAACTCATGGGCGATATTTTAAAGAGGCTTCTGAAATCAGCAAA
10621  GGGTCGAACCAAGAAAGTTGAGTACCCGCTATAAAATTTCTCCGAAGACTTTAGTCGTTT

10681  ACGTTTGTAAATGGATTCATCTTGTTTAAAGTTTCAGAGAGCGCAGTTTTAGAGTTCTTT
10681  TGCAAACATTTACCTAAGTAGAACAAATTTCAAAGTCTCTCGCGTCAAAATCTCAAGAAA

10741  TCAAACTTAAACACAAAGCCCAGTGGGAATTTCAGCAGACTTTACATGAACTTTTAGAGT
10741  AGTTTGAATTTGTGTTTCGGGTCACCCTTAAAGTCGTCTGAAATGTACTTGAAAATCTCA

10801  ATTTTTCTCATTAATTTCTTTCTTTTCACAAGAATTAATTTTGTGATAAAAACACCACAT
10801  TAAAAAGAGTAATTAAAGAAAGAAAAGTGTTCTTAATTAAAACACTATTTTTGTGGTGTA

10861  ATCCAGTGTGGAAAACTAATTTAAAAATCAGAAAAACAAAAATGGAAAATAAAAATATCA
10861  TAGGTCACACCTTTTGATTAAATTTTTAGTCTTTTTGTTTTTACCTTTTATTTTTATAGT

10921  CATTCTACCACCCAGAAATCACCATTAAGGCCTCAGTGCTTACCCTTTAATGTGTGTATG
10921  GTAAGATGGTGGGTCTTTAGTGGTAATTCCGGAGTCACGAATGGGAAATTACACACATAC

10981  TGAGTGTGTTTATATATAAATTATATAGACATAAATAATTAAGCACCTAATTCTATATAT
10981  ACTCACACAAATATATATTTAATATATCTGTATTTATTAATTCGTGGATTAAGATATATA

11041  AATTTATATATGTACACACACACACACACACACACACATTTGCTTTTTACCTAAATGATG
11041  TTAAATATATACATGTGTGTGTGTGTGTGTGTGTGTGTAAACGAAAAATGGATTTACTAC

11101  TCATGTTATTATTTTGGGGACGTTTCAGGTATGTGGACCGACTTGCTTCTTTCTGAAACA
11101  AGTACAATAATAAAACCCCTGCAAAGTCCATACACCTGGCTGAACGAAGAAAGACTTTGT

11161  CCGTTATATTTTTTGCTAGTATAAATTAAACTTAGGGTTCATTTCCTCCAAAGTAAAAAT
11161  GGCAATATAAAAAACGATCATATTTAATTTGAATCCCAAGTAAAGGAGGTTTCATTTTTA

11221  TGATTTGCTTAAAGATGAATTTTCATTCAGTGACACATGACTTAAATGACATCACCACTA
11221  ACTAAACGAATTTCTACTTAAAAGTAAGTCACTGTGTACTGAATTTACTGTAGTGGTGAT

11281  TCATCATCATAATTCACAAATAAGACTTAGCAAGTTCTTAATAGTGATGCTCTATAATAG
11281  AGTAGTAGTATTAAGTGTTTATTCTGAATCGTTCAAGAATTATCACTACGAGATATTATC

11341  GAATTCAACTTACATTTCCAGAAAATTAATGAAAGATACACTTGTTCCTTAAAAAAAGAG
11341  CTTAAGTTGAATGTAAAGGTCTTTTAATTACTTTCTATGTGAACAAGGAATTTTTTTCTC

11401  TCGGTGGCCACATACGTTTGTAATATGCTGGTTTAGACAGATTAAATGGGTTTCTTTCCA
11401  AGCCACCGGTGTATGCAAACATTATACGACCAAATCTGTCTAATTTACCCAAAGAAAGGT

11461  CGGGACTTCTCCAAGTGTTGACCGAGCTCATGCTGTCTGTGGATCTCTGGGGGAGACAAG
11461  GCCCTGAAGAGGTTCACAACTGGCTCGAGTACGACAGACACCTAGAGACCCCCTCTGTTC

11521  GGCACGCTGTGTTTCCCAGGCCTCCTTGACGCGGGAACCTTTTGTTCCCCCACGGGACAT
11521  CCGTGCGACACAAAGGGTCCGGAGGAACTGCGCCCTTGGAAAACAAGGGGGTGCCCTGTA

11581  GTGGGACACTAGAGTTCCACCACAGGTGCTTGGCTCTGTGGAGTCGTTGGCCTCGAGGTG
11581  CACCCTGTGATCTCAAGGTGGTGTCCACGAACCGAGACACCTCAGCAACCGGAGCTCCAC

11641  GTGTCCTTGGCCCCCAGCACTGACTCCGGAGCTCTGTGTTTGCAGACTGCCGGCTGCACA
11641  CACAGGAACCGGGGGTCGTGACTGAGGCCTCGAGACACAAACGTCTGACGGCCGACGTGT

11701  TCTGCCTGTACTACCGGGAAATCCTCGTGAAGGAGCTGACCACGTCCAGCCCCGAGGGCT
11701  AGACGGACATGATGGCCCTTTAGGAGCACTTCCTCGACTGGTGCAGGTCGGGGCTCCCGA
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FIGURE 3 (cont'd)

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11761  GCCGGATCTCCCATGGACATACGTATGACGCCAGCAACCTGGACCAGGTCCTGTTCCCCT
11761  CGGCCTAGAGGGTACCTGTATGCATACTGCGGTCGTTGGACCTGGTCCAGGACAAGGGGA

11821  ACCCAGAGGACAATGGCCAGAGGAAAAACATTGAGAAGCTGCTGAGCCACCTGGAGAGGG
11821  TGGGTCTCCTGTTACCGGTCTCCTTTTTGTAACTCTTCGACGACTCGGTGGACCTCTCCC

11881  GCGTGGTCCTCTGGATGGCCCCCGACGGGCTCTATGCGAAAAGACTGTGCCAGAGCAGGA
11881  CGCACCAGGAGACCTACCGGGGGCTGCCCGAGATACGCTTTTCTGACACGGTCTCGTCCT

11941  TCTACTGGGACGGGCCCCTGGCGCTGTGCAACGACCGGCCCAACAAACTGGAGAGAGACC
11941  AGATGACCCTGCCCGGGGACCGCGACACGTTGCTGGCCGGGTTGTTTGACCTCTCTCTGG

12001  AGACCTGCAAGCTCTTTGACACACAGCAGTTCTTGTCAGGTAAGGCACCTCGTTATCTGT
12001  TCTGGACGTTCGAGAAACTGTGTGTCGTCAAGAACAGTCCATTCCGTGGAGCAATAGACA

12061  TAGAATGGAGGTGGTGATGGCCTGCCTGCCACAGGGGTCAGAAACCACAGGGTCCCTCCC
12061  ATCTTACCTCCACCACTACCGGACGGACGGTGTCCCCAGTCTTTGGTGTCCCAGGGAGGG

12121  ACCCCAGGCTGAGGTCTTCCTCCTGTTGACTTCGGCGCCCACTGGGCTTGGGGCTTGACT
12121  TGGGGTCCGACTCCAGAAGGAGGACAACTGAAGCCGCGGGTGACCCGAACCCCGAACTGA

12181  CCAGTAGAGATCTTCTGTCTGGCTCTGTTGTGGGCAGAGAGTCCGGATCAGATGGTCCAG
12181  GGTCATCTCTAGAAGACAGACCGAGACAACACCCGTCTCTCAGGCCTAGTCTACCAGGTC

12241  GTGGACCATGGCTCAGGCTGTTCTCTTGCAATTCTGGTTTTCAGCAGTCGCCTCTTAAAA
12241  CACCTGGTACCGAGTCCGACAAGAGAACGTTAAGACCAAAAGTCGTCAGCGGAGAATTTT

12301  CAGTTCCATTTCATTGCACTATGATCTCGACAAATACGTCTGCTGATGTGGCGGCTCTTT
12301  GTCAAGGTAAAGTAACGTGATACTAGAGCTGTTTATGCAGACGACTACACCGCCGAGAAA

12361  TCAGGTTCCCAGAAAAATCATAAAGGTTGGAAGCATATTGTTAACATTCTTGGTTGTCAG
12361  AGTCCAAGGGTCTTTTTAGTATTTCCAACCTTCGTATAACAATTGTAAGAACCAACAGTC

12421  GTGTGTCACCCTCATGCAGATGCTGGCCCACGAGTGAGACGGAGGGTGGAGTGGACTGTA
12421  CACACAGTGGGAGTACGTCTACGACCGGGTGCTCACTCTGCCTCCCACCTCACCTGACAT

12481  CTGGTTTTGCACAGGAGAAGTTATAGGAGAGTGCTATAAGTTGGCTCTGTGATATGAACA
12481  GACCAAAACGTGTCCTCTTCAATATCCTCTCACGATATTCAACCGAGACACTATACTTGT

12541  TTTCTAAGCATATTTTTCAGAACCAGTGAGTTTTGTTTTTCTACCTTGGATTTCATGACA
12541  AAAGATTCGTATAAAAAGTCTTGGTCACTCAAAACAAAAAGATGGAACCTAAAGTACTGT

12601  ATTCAGCGAACCTCTGGCTGGCTTCTGTGAAGCCCCTCGCCCTGTCATGCTGGGCTTCCT
12601  TAAGTCGCTTGGAGACCGACCGAAGACACTTCGGGGAGCGGGACAGTACGACCCGAAGGA

12661  CACTGGCTTTGTGGGGCTGTCCAGGTGGAGGGAGCCTCCCGCGTGGGAGGGAGCTGCTCT
12661  GTGACCGAAACACCCCGACAGGTCCACCTCCCTCGGAGGGCGCACCCTCCCTCGACGAGA

12721  ACCCGCCACTCGCCACCCCACCGCCAACTCTTCCTCTGCCTTTTCCCAGTCCTGTCCCTT
12721  TGGGCGGTGAGCGGTGGGGTGGCGGTTGAGAAGGAGACGGAAAAGGGTCAGGACAGGGAA

12781  CCTGAGCCCCTTCAGAAACTCCTGTGTCTTTGATTTCTCATGTGCCTCCCCTTTTCTTGA
12781  GGACTCGGGGAAGTCTTTGAGGACACAGAAACTAAAGAGTACACGGAGGGGAAAAGAACT

12841  ATGTGCTTCTTCATTCAACTTATTTAAAATAAAAATATGACACGTCTGTGTGCTCTGGCA
12841  TACACGAAGAAGTAAGTTGAATAAATTTTATTTTTATACTGTGCAGACACACGAGACCGT

12901  CTGTTGACATGTGCTCGTACTTCTGGGTGTAAGTGACCCAAGTTTTTGTAAGCTCATCCA
12901  GACAACTGTACACGAGCATGAAGACCCACATTCACTGGGTTCAAAAACATTCGAGTAGGT

12961  GATTTTCTTTTGGTGCCCAAAGCAAATATGTCCCCAGATAACTAAGCTTCAGGCCAGGTG
12961  CTAAAAGAAAACCACGGGTTTCGTTTATACAGGGGTCTATTGATTCGAAGTCCGGTCCAC

13021  TGGTGGCCCATGCCTGTAATCCCAGCACTTTAGGAGGCTGAGGTGGGCAGATCACTTGAG
13021  ACCACCGGGTACGGACATTAGGGTCGTGAAATCCTCCGACTCCACCCGTCTAGTGAACTC

13081  GCCAGGAGTTCAAGACCAGCCTGGCCAACATGGCAAAACCCCGTCTCTACTAAAGATACA
13081  CGGTCCTCAAGTTCTGGTCGGACCGGTTGTACCGTTTTGGGGCAGAGATGATTTCTATGT
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FIGURE 3 (cont'd)

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13141  AAAATTAGCTGGGCGTGATGGTGGGCGCCTGTAATCCCAGCTACTCAGGAGGATGAGGCA
13141  TTTTAATCGACCCGCACTACCACCCGCGGACATTAGGGTCGATGAGTCCTCCTACTCCGT

13201  CAAGAATCGCTTGAACCTGTGGGAGGCGGAGGTTGCAGTGAGCTGAGATCGCACCACGGT
13201  GTTCTTAGCGAACTTGGACACCCTCCGCCTCCAACGTCACTCGACTCTAGCGTGGTGCCA

13261  GCTGCAGTTTGCAGGACAGAGCGAGACTCCATTGCCCCCCGCACCACAAAAAAATAACTA
13261  CGACGTCAAACGTCCTGTCTCGCTCTGAGGTAACGGGGGGCGTGGTGTTTTTTTATTGAT

13321  AGCTCACACAGAGGCTGACCATAGGAAGAGGGAGAACTGTGCTGGTTCCCCGAGGCGGCG
13321  TCGAGTGTGTCTCCGACTGGTATCCTTCTCCCTCTTGACACGACCAAGGGGCTCCGCCGC

13381  GCAAGTGAGGAAGTCACCTGGGGCTGGACACCTCTCATTCTAAGGGCAGAACCATCCCCA
13381  CGTTCACTCCTTCAGTGGACCCCGACCTGTGGAGAGTAAGATTCCCGTCTTGGTAGGGGT

13441  AGCCCTGGCCAGGGCGGTCCCATCCTTCTTGGGGTTGGGCATGGTGTTCATGGGGGACCA
13441  TCGGGACCGGTCCCGCCAGGGTAGGAAGAACCCCAACCCGTACCACAAGTACCCCCTGGT

13501  AGGAAATTGAAGGGCAACTGGGGGGACCCCCCCTCCCCTGTCAGCATCTCCTGTGTCTGC
13501  TCCTTTAACTTCCCGTTGACCCCCCTGGGGGGGAGGGGACAGTCGTAGAGGACACAGACG

13561  CTTGGGATCTGGAAGAGCTCACATGGGCCAGGAAGGCTAAGGCCCACTGGGCCTGGATTT
13561  GAACCCTAGACCTTCTCGAGTGTACCCGGTCCTTCCGATTCCGGGTGACCCGGACCTAAA

13621  CTGAAGACTCTGGACCTTGGTGCCAGTGGATTCAGAAGATACCACAAGGTGAGGGCTTTC
13621  GACTTCTGAGACCTGGAACCACGGTCACCTAAGTCTTCTATGGTGTTCCACTCCCGAAAG

13681  TAATGAAAGTGTCACAAGGAACTGGCACTGGCTTTTCTGAGTGCCTCTTGCTGGGCGTTT
13681  ATTACTTTCACAGTGTTCCTTGACCGTGACCGAAAAGACTCACGGAGAACGACCCGCAAA

13741  TTAGGGAGGTAGAGCCCCCGTGGTGACTAAGCTGGAAGGTGCACATTGAGTCACAGGTGC
13741  AATCCCTCCATCTCGGGGGCACCACTGATTCGACCTTCCACGTGTAACTCAGTGTCCACG

13801  ACTGCGTGAGAGACAGCACAGGCAGGGGGTGGACGCCTGTGAGTGTCCTGGGGCTGTAGA
13801  TGACGCACTCTCTGTCGTGTCCGTCCCCCACCTGCGGACACTCACAGGACCCCGACATCT

13861  CTTGCGCGACTAGAACTTACTATTAATCTGTGAGCAAGAGCTGGTCTTGGCTTTCATTCC
13861  GAACGCGCTGATCTTGAATGATAATTAGACACTCGTTCTCGACCAGAACCGAAAGTAAGG

13921  TTCCTCTGTAACCAAGGGCTGTGCTCTTTGCCCACTGCAGCCTCTCACCTCAAAGTGTTC
13921  AAGGAGACATTGGTTCCCGACACGAGAAACGGGTGACGTCGGAGAGTGGAGTTTCACAAG

13981  ACTGAGGTTCAAGGAGGATGCTGTGAACGTAAAAACTGCAGCTGTGCCAACCAGCTTCTG
13981  TGACTCCAAGTTCCTCCTACGACACTTGCATTTTTGACGTCGACACGGTTGGTCGAAGAC

14041  CATAATTAAGGATTCCCACCAAACACTCTCATGTTATCTAGGGTTGGAGCCATGCTTTCT
14041  GTATTAATTCCTAAGGGTGGTTTGTGAGAGTACAATAGATCCCAACCTCGGTACGAAAGA

14101  CAGAGAATTGTGCCAACTCGCCATTCTGATTAGCCTGTGTAGGTGTAGTCTCAGATCACG
14101  GTCTCTTAACACGGTTGAGCGGTAAGACTAATCGGACACATCCACATCAGAGTCTAGTGC

14161  GCAGTGTGAATGTATTTTACAGATTCTGACTAAGTCATTTGGGTTTGATTTGAATTCTGG
14161  CGTCACACTTACATAAAATGTCTAAGACTGATTCAGTAAACCCAAACTAAACTTAAGACC

14221  AAAAAAAAAAAAGCAGGAAGTCAAATAGTCCTGTAAGTTAGCTAGAAACTTCTGTTCAGT
14221  TTTTTTTTTTTTCGTCCTTCAGTTTATCAGGACATTCAATCGATCTTTGAAGACAAGTCA

14281  TGAAGAGAACAGTGGAGATCTTTGATATCTTCCTATTCAGGTCTGCACAGCACTAGGGAC
14281  ACTTCTCTTGTCACCTCTAGAAACTATAGAAGGATAAGTCCAGACGTGTCGTGATCCCTG

14341  AGCCCCCAGGGCCCGGCCCGAGGGTGTGTATCTGATAAGGACGCGTCTGTTCTGCAGAAG
14341  TCGGGGGTCCCGGGCCGGGCTCCCACACATAGACTATTCCTGCGCAGACAAGACGTCTTC

14401  CTGTAGCGGCTCCTGTGTCAACTCGTTTCTTTTGCGGGCGTGACATTTTATTGTAGCTAC
14401  GACATCGCCGAGGACACAGTTGAGCAAAGAAAACGCCCGCACTGTAAAATAACATCGATG
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FIGURE 3 (cont'd)

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14461  AGGCAGAAGATTTGTCTTGTGTACAGGGGAGGGAGCATGGGCTAAAGTCAGGGGATGGGC
14461  TCCGTCTTCTAAACAGAACACATGTCCCCTCCCTCGTACCCGATTTCAGTCCCCTACCCG

14521  ACTTGTCTTTCCAACAATGTTCCAGTCCGTTTTGTATCTTTTGGGTAGGTGTGGTGGCTT
14521  TGAACAGAAAGGTTGTTACAAGGTCAGGCAAAACATAGAAAACCCATCCACACCACCGAA

14581  CAGGATGTACATGTGTATATCCACAAGCGGGAGGCCAGGGGGGCTGCCCCACTCCTGTTC
14581  GTCCTACATGTACACATATAGGTGTTCGCCCTCCGGTCCCCCCGACGGGGTGAGGACAAG

14641  TCAAGTCAAGTTACTGTTCCATCCCTGGAGACAGGCAAGAAGTCTACTCAGAGTTACACA
14641  AGTTCAGTTCAATGACAAGGTAGGGACCTCTGTCCGTTCTTCAGATGAGTCTCAATGTGT

14701  GTTCAGGCATAGTGACAGTGGGACTCAGCTGCCGATGGCTGGTGCTCAGTCACCACGTTG
14701  CAAGTCCGTATCACTGTCACCCTGAGTCGACGGCTACCGACCACGAGTCAGTGGTGCAAC

14761  ACGTTACATATTTTCTGTGGTGCCTGAGTTACGTGGATGTCCGCAGTAGCACAGATACTG
14761  TGCAATGTATAAAAGACACCACGGACTCAATGCACCTACAGGCGTCATCGTGTCTATGAC

14821  GATTATGTGGGCTCTGTAGTGAGGGGATGAGGTTTTAAAATGATCCTGGGATGTCGAAAC
14821  CTAATACACCCGAGACATCACTCCCCTACTCCAAAATTTTACTAGGACCCTACAGCTTTG

14881  ATTCTGATTTTTTAAATGAAAACTTGTCCATGGCATAAATTGGTCTTTTGCCATTGCGTG
14881  TAAGACTAAAAAATTTACTTTTGAACAGGTACCGTATTTAACCAGAAAACGGTAACGCAC

14941  ACTACGTTTCTTGTTCTTTATCTCCCGACTTCACTGTGGTCTACTACCTTTTGAATCTTC
14941  TGATGCAAAGAACAAGAAATAGAGGGCTGAAGTGACACCAGATGATGGAAAACTTAGAAG

15001  GTGGGTCCAATGCTGCAAAGCAGTGTTCTTTAGCTGTCGACTAGTTCCTCTTGAAGAATC
15001  CACCCAGGTTACGACGTTTCGTCACAAGAAATCGACAGCTGATCAAGGAGAACTTCTTAG

15061  GAGGGAGACCGAGGGCCCTGGGGCGAAAGCACCCAAAGGAATGCATACATGCTATTTTGT
15061  CTCCCTCTGGCTCCCGGGACCCCGCTTTCGTGGGTTTCCTTACGTATGTACGATAAAACA

15121  ATCTGAGATGTTCACATCAAGAGCCCCACTCAGCGGAGTAAGAGTGCTCATTCCTCTTGC
15121  TAGACTCTACAAGTGTAGTTCTCGGGGTGAGTCGCCTCATTCTCACGAGTAAGGAGAACG

15181  AGTGTTCAGAATCACAGTAAGCTCTTGCTTCCTGTTTAACCTGGTGTGTTCGGTGATGAG
15181  TCACAAGTCTTAGTGTCATTCGAGAACGAAGGACAAATTGGACCACACAAGCCACTACTC

15241  GGTTTCTGAACATGGTCTCTTTCTTGTGGGCTTCTACAGAGCTGCAAGCGTTTGCTCACC
15241  CCAAAGACTTGTACCAGAGAAAGAACACCCGAAGATGTCTCGACGTTCGCAAACGAGTGG

15301  ACGGCCGCTCCCTGCCAAGATTCCAGGTGACTCTATGCTTTGGAGAGGAGTTTCCAGACC
15301  TGCCGGCGAGGGACGGTTCTAAGGTCCACTGAGATACGAAACCTCTCCTCAAAGGTCTGG

15361  CTCAGAGGCAAAGAAAGCTCATCACAGCTCACGTGAGTCCTCAGTTACACTCCTACCATA
15361  GAGTCTCCGTTTCTTTCGAGTAGTGTCGAGTGCACTCAGGAGTCAATGTGAGGATGGTAT

15421  GTGGCTTCCTGTTCTTTGTAAAGGCCAGAGTTTCATTTAGAAAAGTCCCAAATGAAAAGT
15421  CACCGAAGGACAAGAAACATTTCCGGTCTCAAAGTAAATCTTTTCAGGGTTTACTTTTCA

15481  AAATGTCAAATGACCTGGAAAAATAAGCGTAACCCTTAAACTAGTGAGGGAGGAAGCATG
15481  TTTACAGTTTACTGGACCTTTTTATTCGCATTGGGAATTTCATCACTCCCTCCTTCGTAC

15541  GTCCAACGAGCAGCACAGTCTGAGGACTCACGTGCTCCTCCCAGACTTGAGATCTGCTCA
15541  CAGGTTGCTCGTCGTGTCAGACTCCTGAGTGCACGAGGAGGGTCTGAACTCTAGACGAGT

15601  TCAAAGAACCAGGGAGGACAGCCTCAAAGGAGGCTGCCTCTTTCCCCATCTTTTTTATTT
15601  AGTTTCTTGGTCCCTCCTGTCGGAGTTTCCTCCGACGGAGAAAGGGGTAGAAAAAATAAA

15661  TTCAGGAAAGTTGTCGTATTTCCATTTTATAGGGATTGAAAAAGATTGATGGTTAAAGTT
15661  AAGTCCTTTCAACAGCATAAAGGTAAAATATCCCTAACTTTTTCTAACTACCAATTTCAA

15721  GCCCTTTAAAATTCTCCAGGTTAAGATTGCTGTAAGAATGCTATCTAGCTAGTGGATCTT
15721  CGGGAAATTTTAAGAGGTCCAATTCTAACGACATTCTTACGATAGATCGATCACCTAGAA

15781  CATTCAATGGAAAAGCTTTTCCCAAATGAGAAACTATCCATTCCCTGGAGGCATTTTGTA
15781  GTAAGTTACCTTTTCGAAAAGGGTTTACTCTTTGATAGGTAAGGGACCTCCGTAAAACAT
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FIGURE 3 (cont'd)

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15841  GGTCTCTGCAGCTGTGTCCTAGCACCTCTTTTATTTCTGGAATTTTAGAAATTATTTAAT
15841  CCAGAGACGTCGACACAGGATCGTGGAGAAAATAAAGACCTTAAAATCTTTAATAAATTA

15901  TATTGGGCATATGATATTTGAAAGAGGCTGAATCTTTCAAGGAATTCAAGCAAATCAGAC
15901  ATAACCCGTATACTATAAACTTTCTCCGACTTAGAAAGTTCCTTAAGTTCGTTTAGTCTG

15961  CCTCTCGTAATGTTCTCTAGCATAGCTCAAGATGGGTTCAACTGTGGCAAGTAACACTAA
15961  GGAGAGCATTACAAGAGATCGTATCGAGTTCTACCCAAGTTGACACCGTTCATTGTGATT

16021  AAGGGTAGGGTTAGGATTAGGGTTAGAGTTTTCTTTTTTATGAGAAAAGGTTTCCATAGA
16021  TTCCCATCCCAATCCTAATCCCAATCTCAAAAGAAAAAATACTCTTTTCCAAAGGTATCT

16081  TAACATGAAGCATTAATTTGCCATGGGAAACAGAATCTTGAACCCTTAAGACTTTTGAAT
16081  ATTGTACTTCGTAATTAAACGGTACCCTTTGTCTTAGAACTTGGGAATTCTGAAAACTTA

16141  TTGAAAACTTCACATTGCTACATACTTGCAAGCATTATTAACGGGCTTGCATGCTGAGCA
16141  AACTTTTGAAGTGTAACGATGTATGAACGTTCGTAATAATTGCCCGAACGTACGACTCGT

16201  ATACCAGGTAAAAGTTACACCCCCTAACATCAAAGTTCTCATCATGTTCTAGCTCTGATG
16201  TATGGTCCATTTTCAATGTGGGGGATTGTAGTTTCAAGAGTAGTACAAGATCGAGACTAC

16261  CTATTTCTCATTGAGAACTGAAATGAAACATGGTTTAATCTTGAACATACAACCCCCCTT
16261  GATAAAGAGTAACTCTTGACTTTACTTTGTACCAAATTAGAACTTGTATGTTGGGGGGAA

16321  CTTGATTTTAAAAACAAAGACCAGCCAACCAACCAGTATATAATCCCATAGACTCAGGAG
16321  GAACTAAAATTTTTGTTTCTGGTCGGTTGGTTGGTCATATATTAGGGTATCTGAGTCCTC

16381  TTTTCTCATGAGTTCTCTCCAGTGATTGACTTAATAATTGATATGATTGTTGAAATAATA
16381  AAAAGAGTACTCAAGAGAGGTCACTAACTGAATTATTAACTATACTAACAACTTTATTAT

16441  ACTGATACATTGTTAACAACAGGAATTGCTAAATGACTAAATAAACTTGGCATTGATAAG
16441  TGACTATGTAACAATTGTTGTCCTTAACGATTTACTGATTTATTTGAACCGTAACTATTC

16501  CAGCATTTAAGAAGTTGATGATCGGCCGGGCACAGTGGCTCACGCCTGTAATCCCGGCAC
16501  GTCGTAAATTCTTCAACTACTAGCCGGCCCGTGTCACCGAGTGCGGACATTAGGGCCGTG

16561  TTTGGGAGGCTGAGGCGGGCAGATCATGTGGTCAGGAGTTCGAGACCAGCCTGACCAACA
16561  AAACCCTCCGACTCCGCCCGTCTAGTACACCAGTCCTCAAGCTCTGGTCGGACTGGTTGT

16621  TGGTGAAACCCCCTCTCTACTAAAAATACAAAAATTAGCCGGGCGTGGTGGTGCGCACCT
16621  ACCACTTTGGGGGAGAGATGATTTTTATGTTTTTAATCGGCCCGCACCACCACGCGTGGA

16681  GTAATCCCAGCTACTCGGGAGGCTGAAGCAAGGGAGTCACTTGAACCCAGGAGTCAGAGC
16681  CATTAGGGTCGATGAGCCCTCCGACTTCGTTCCCTCAGTGAACTTGGGTCCTCAGTCTCG

16741  TTGCAGTGAGCCGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGTGAGACTCTGT
16741  AACGTCACTCGGCTCTAACGTGGTGACGTGAGGTCGGACCCACTGTCTCACTCTGAGACA

16801  CTCAAAAAAAAAACAAAAAAAGAAGTTGATGATCAGCTCAGCTATCACATCAATCCAGTT
16801  GAGTTTTTTTTTTGTTTTTTTCTTCAACTACTAGTCGAGTCGATAGTGTAGTTAGGTCAA

16861  TTAAAGTTGACATGGATGCAAGTCACTGTCCTCTAAGTCAGGGAAAGATGGATCCCCAGA
16861  AATTTCAACTGTACCTACGTTCAGTGACAGGAGATTCAGTCCCTTTCTACCTAGGGGTCT

16921  TGACCCCCTCATGCTGAAGACGAGGCTGCGTGGTCCATAAAATGAATAAACACACGTGTA
16921  ACTGGGGGAGTACGACTTCTGCTCCGACGCACCAGGTATTTTACTTATTTGTGTGCACAT

16981  CACCTATGAGTTCCACTTTTAAAAATTATTAATTTAATTCATTTCAGGTACTTAGGAGTT
16981  GTGGATACTCAAGGTGAAAATTTTTAATAATTAAATTAAGTAAAGTCCATGAATCCTCAA

17041  TAGCTTAAGTCGTCATATATAAAATACAGTCTCTAATATCATGATTGATGGAGAGCATTC
17041  ATCGAATTCAGCAGTATATATTTTATGTCAGAGATTATAGTACTAACTACCTCTCGTAAG

17101  AGCTTGCCTTAGATGCTGTAAATTCAGGAAAAGCTGAACATTAAGGCGTTTTTGTTTTTT
17101  TCGAACGGAATCTACGACATTTAAGTCCTTTTCGACTTGTAATTCCGCAAAAACAAAAAA
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FIGURE 3 (cont'd)

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17161  GGTGAGTGTGATCCACGCTAATAACCAGACAGTATAAATTTGAGGCCAGTTAGCTTCTCT
17161  CCACTCACACTAGGTGCGATTATTGGTCTGTCATATTTAAACTCCGGTCAATCGAAGAGA

17221  TTTTCCACAATAGTAGTTTTGTTGTTGTTTAACTTTACTTTTTATTTCTTTTACCTCTGG
17221  AAAAGGTGTTATCATCAAAACAACAACAAATTGAAATGAAAAATAAAGAAAATGGAGACC

17281  TTGAGAACTATACAGATTACCTAGAAATCAAATCATTCAGGATGAGCTCCTTGTTTCTTT
17281  AACTCTTGATATGTCTAATGGATCTTTAGTTTAGTAAGTCCTACTCGAGGAACAAAGAAA

17341  CAAACTGCAGTTGTGGAAAAACAAAATCATTGGCCTAAATTACCCTGCAGATTCCCTCAG
17341  GTTTGACGTCAACACCTTTTTGTTTTAGTAACCGGATTTAATGGGACGTCTAAGGGAGTC

17401  ACTTCCTTTTAATTTGATCACTTTACTTGATTTGATGCAGTTTTAGTTAAATGTACATTT
17401  TGAAGGAAAATTAAACTAGTGAAATGAACTAAACTACGTCAAAATCAATTTACATGTAAA

17461  TAAGTGGCAGTCGATTTGAAAGTAACATCTTTAACCCAGAATTAAGTCACTTTGGCTGTT
17461  ATTCACCGTCAGCTAAACTTTCATTGTAGAAATTGGGTCTTAATTCAGTGAAACCGACAA

17521  TTTTTACATGTTGATCTATGGAAGGACTAACCAAAAAATTGCTTCTTTAGATGGCTCCAA
17521  AAAAATGTACAACTAGATACCTTCCTGATTGGTTTTTTAACGAAGAAATCTACCGAGGTT

17581  ATATGAAATGTTTTGATGTGTTCTAGGATGTAACTTTGGGCTTTACGTTACTGTCTCCTT
17581  TATACTTTACAAAACTACACAAGATCCTACATTGAAACCCGAAATGCAATGACAGAGGAA

17641  AGAATCTGAGTGCTGTTTAATAGTGAGCCAGTTGCAGGATATCTCAGTAATGTCTTTTTA
17641  TCTTAGACTCACGACAAATTATCACTCGGTCAACGTCCTATAGAGTCATTACAGAAAAAT

17701  AAATCTCTTATTAAAGGTAGAACCTCTGCTAGCCAGACAACTATATTATTTTGCTCAACA
17701  TTTAGAGAATAATTTCCATCTTGGAGACGATCGGTCTGTTGATATAATAAAACGAGTTGT

17761  AAACAGTGGACATTTCCTGAGGGGCTACGATTTACCAGAACACATCAGCAATCCAGAAGA
17761  TTTGTCACCTGTAAAGGACTCCCCGATGCTAAATGGTCTTGTGTAGTCGTTAGGTCTTCT

17821  TTACCACAGATCTATCCGCCATTCCTCTATTCAAGAATGAAAAATGTCAAGATGAGTGGT
17821  AATGGTGTCTAGATAGGCGGTAAGGAGATAAGTTCTTACTTTTTACAGTTCTACTCACCA

17881  TTTCTTTTTCCTTTTTTTTTTTTTTTTTTTTTGATACGGGATACGGGTCTTGCTCTGTCT
17881  AAAGAAAAAGGAAAAAAAAAAAAAAAAAAACTATGCCCCTATGCCCCAGAACGAGACAGA

17941  CCCAGGCTGGAGTGCAGTGACACAATCTCAGCTCACTGTGACCTCCGCCTCCTGGGTTCA
17941  GGGTCCGACCTCACGTCACTGTGTTAGAGTCGAGTGACACTGGAGGCGGAGGACCCAAGT

18001  AGAGACTCTCCTGCCTCAGCCTCCCTGGTAGCTGGGATTACAGGTGTGAGCCACTGCACC
18001  TCTCTGAGAGGACGGAGTCGGAGGGACCATCGACCCTAATGTCCACACTCGGTGACGTGG

18061  CACCCAAGACAAGTGATTTTCATTGTAAATATTTGACTTTAGTGAAAGCGTCCAATTGAC
18061  GTGGGTTCTGTTCACTAAAAGTAACATTTATAAACTGAAATCACTTTCGCAGGTTAACTG

18121  TGCCCTCTTACTGTTTTGAGGAATTCAGAAGTGGAGATTTCAGTTCAGCGGTTGAGGAGA
18121  ACGGGAGAATGACAAAACTCCTTAAGTCTTCACCTCTAAAGTCAAGTCGCCAACTCCTCT

18181  ATTGCGGCGAGACAAGCATGGAAAATCAGTGACATCTGATTGGCAGATGAGCTTATTTCA
18181  TAACGCCGCTCTGTTCGTACCTTTTAGTCACTGTAGACTAACCGTCTACTCGAATAAAGT

18241  AAAGGAAGGGTGGCTTTGCATTTCTTGTGTTCTGTAGACTGCCATCATTGATGATCACTG
18241  TTTCCTTCCCACCGAAACGTAAAGAACACAAGACATCTGACGGTAGTAACTACTAGTGAC

18301  TGAAAATTGACCAAGTGATGTGTTTACATTTACTGAAATGCGCTCTTTAATTTGTTGTAG
18301  ACTTTTAACTGGTTCACTACACAAATGTAAATGACTTTACGCGAGAAATTAAACAACATC

18361  ATTAGGTCTTGCTGGAAGACAGAGAAAACTTGCCTTTCAGTATTGACACTGACTAGAGTG
18361  TAATCCAGAACGACCTTCTGTCTCTTTTGAACGGAAAGTCATAACTGTGACTGATCTCAC

18421  ATGACTGCTTGTAGGTATGTCTGTGCCATTTCTCAGGGAAGTAAGATGTAAATTGAAGAA
18421  TACTGACGAACATCCATACAGACACGGTAAAGAGTCCCTTCATTCTACATTTAACTTCTT

18481  GCCTCACACGTAAAAGAAATGTATTAATGTATGTAGGAGCTGCAGTTCTTGTGGAAGACA
18481  CGGAGTGTGCATTTTCTTTACATAATTACATACATCCTCGACGTCAAGAACACCTTCTGT
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FIGURE 3 (cont'd)

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18541  CTTGCTGAGTGAAGGAAATGAATCTTTGACTGAAGCCGTGCCTGTAGCCTTGGGGAGGCC
18541  GAACGACTCACTTCCTTTACTTAGAAACTGACTTCGGCACGGACATCGGAACCCCTCCGG

18601  CATCCCCCACCTGCCAGCGGTTTCCTGGTGTGGGTCCCTCTGCCCCGCCCTCCTTCCCAT
18601  GTAGGGGGTGGACGGTCGCCAAAGGACCACACCCAGGGAGACGGGGCGGGAGGAAGGGTA

18661  TGGCTTTCTCTCCTTGGCCTTTCCTGGAAGCCAGTTAGTAAACTTCCTATTTTCTTGAGT
18661  ACCGAAAGAGAGGAACCGGAAAGGACCTTCGGTCAATCATTTGAAGGATAAAAGAACTCA

18721  CAAAAAACATGAGCGCTACTCTTGGATGGGACATTTTTGTCTGTCCTACAATCTAGTAAT
18721  GTTTTTTGTACTCGCGATGAGAACCTACCCTGTAAAAACAGACAGGATGTTAGATCATTA

18781  GTCTAAGTAATGGTTAAGTTTTCTTGTTTCTGCATCTTTTTGACCCTCATTCTTTAGAGA
18781  CAGATTCATTACCAATTCAAAAGAACAAAGACGTAGAAAAACTGGGAGTAAGAAATCTCT

18841  TGCTAAAATTCTTCGCATAAAGAAGAAGAAATTAAGGAACATAAATCTTAATACTTGAAC
18841  ACGATTTTAAGAAGCGTATTTCTTCTTCTTTAATTCCTTGTATTTAGAATTATGAACTTG

18901  TGTTGCCCTTCTGTCCAAGTACTTAACTATCTGTTCCCTTCCTCTGTGCCACGCTCCTCT
18901  ACAACGGGAAGACAGGTTCATGAATTGATAGACAAGGGAAGGAGACACGGTGCGAGGAGA

18961  GTTTGTTTGGCTGTCCAGCGATCAGCCATGGCGACACTAAAGGAGGAGGAGCCGGGGACT
18961  CAAACAAACCGACAGGTCGCTAGTCGGTACCGCTGTGATTTCCTCCTCCTCGGCCCCTGA

19021  CCCAGGCTGGAGAGCACTGCCAGGACCCACCACTGGAAGCAGGATGGAGCTGACTACGGA
19021  GGGTCCGACCTCTCGTGACGGTCCTGGGTGGTGACCTTCGTCCTACCTCGACTGATGCCT

19081  ACTGCACACTCAGTGGGCTGTTTCTGCTTATTTCATCTGTTCTATGCTTCCTCGTCCCAA
19081  TGACGTGTGAGTCACCCGACAAAGACGAATAAAGTAGACAAGATACGAAGGAGCACGGTT

19141  TTATAGTTTGACAGGGCCTTAAAATTACTTGGCTTTTTCCAAATGCTTCTATTTATAGAA
19141  AATATCAAACTGTCCCGGAATTTTAATGAACCGAAAAAGGTTTACGAAGATAAATATCTT

19201  TCCCAAAGACCTCCACTTGCTTAAGTATACCTATCACTTACATTTTTGTGGTTTTGAGAA
19201  AGGGTTTCTGGAGGTGAACGAATTCATATGGATAGTGAATGTAAAAACACCAAAACTCTT

19261  AGTACAGCAGTAGACTGGGGCGTCACCTCCAGGCCGTTTCTCATACTACAGGATATTTAC
19261  TCATGTCGTCATCTGACCCCGCAGTGGAGGTCCGGCAAAGAGTATGATGTCCTATAAATG

19321  TATTACTCCCAGGATCAGCAGAAGATTGCGTAGCTCTCAAATGTGTGTTCCTGCTTTTCT
19321  ATAATGAGGGTCCTAGTCGTCTTCTAACGCATCGAGAGTTTACACACAAGGACGAAAAGA

19381  AATGGATATTTTAAATTCATTCAACAAGCACCTAGTAAGTGCCTGCTGTATCCCTACATT
19381  TTACCTATAAAATTTAAGTAAGTTGTTCGTGGATCATTCACGGACGACATAGGGATGTAA

19441  ACACAGTTCAGCCTTTATCAAGCTTAGTGAGCAGTGAGCACTGAAACATTATTTTTAAT
19441  TGTGTCAAGTCGGAAATAGTTCGAATCACTCGTCACTCGTGACTTTGTAATAAAAATTA

19501  GTTTAAAAAGTTTCTAATATTAAAGTCAGAATATTAATACAATTAATATTAATATTAACT
19501  CAAATTTTTCAAAGATTATAATTTCAGTCTTATAATTATGTTAATTATAATTATAATTGA

19561  ACAGAAAAGACAAACAGTAGAGAACAGCAAAAAAATAAAAAGGATCTCCTTTTTTCCCAG
19561  TGTCTTTTCTGTTTGTCATCTCTTGTCGTTTTTTTATTTTTCCTAGAGGAAAAAAGGGTC

19621  CCCAAATTCTCCTCTCTAAAAGTGTCCACAAGAAGGGGTGTTTATTCTTCCAACACATTT
19621  GGGTTTAAGAGGAGAGATTTTCACAGGTGTTCTTCCCCACAAATAAGAAGGTTGTGTAAA

19681  CACTTTTCTGTAAATATACATAAACTTAAAAAGAAAACCTCATGGAGTCATCTTGCACAC
19681  GTGAAAAGACATTTATATGTATTTGAATTTTTCTTTTGGAGTACCTCAGTAGAACGTGTG

19741  ACTTTCATGCAGTGCTCTTTGTAGCTAACAGTGAAGATTTACCTCGTTCTGCTCAGAGGC
19741  TGAAAGTACGTCACGAGAAACATCGATTGTCACTTCTAAATGGAGCAAGACGAGTCTCCG

19801  CTTGCTGTGGAGCTCCACTGCCATGTACCCAGTAGGGTTTGACATTTCATTAGCCATGCA
19801  GAACGACACCTCGAGGTGACGGTACATGGGTCATCCCAAACTGTAAAGTAATCGGTACGT
```

FIGURE 3 (cont'd)

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19861  ACATGGATATGTATTGGGCAGCAGACTGTGTTTCGTGAACTGCAGTGATGTATACATCTT
19861  TGTACCTATACATAACCCGTCGTCTGACACAAAGCACTTGACGTCACTACATATGTAGAA

19921  ATAGATGCAAAGTATTTTGGGGTATATTATCCTAAGGGAAGATAAAGATGATATTAAGAA
19921  TATCTACGTTTCATAAAACCCCATATAATAGGATTCCCTTCTATTTCTACTATAATTCTT

19981  CTGCTGTTTCACGGGGCCCTTACCTGTGACCCTCTTTGCTGAAGAATATTTAACCCCACA
19981  GACGACAAAGTGCCCCGGGAATGGACACTGGGAGAAACGACTTCTTATAAATTGGGGTGT

20041  CAGCACTTCAAAGAAGCTGTCTTGGAAGTCTGTCTCAGGAGCACCCTGTCTTCTTAATTC
20041  GTCGTGAAGTTTCTTCGACAGAACCTTCAGACAGAGTCCTCGTGGGACAGAAGAATTAAG

20101  TCCAAGCGGATGCTCCATTTCAATTGCTTTGTGACTTCTTCTTCTTTGTTTTTTTAAATA
20101  AGGTTCGCCTACGAGGTAAAGTTAACGAAACACTGAAGAAGAAGAAACAAAAAAATTTAT

20161  TTATGCTGCTTTAACAGTGGAGCTGAATTTTCTGGAAAATGCTTCTTGGCTGGGGCCACT
20161  AATACGACGAAATTGTCACCTCGACTTAAAAGACCTTTTACGAAGAACCGACCCCGGTGA

20221  ACCTCCTTTCCTATCTTTACATCTATGTGTATGTTCACTTTTTAAAATTCTGAGTCATCC
20221  TGGAGGAAAGGATAGAAATGTAGATACACATACAACTGAAAAATTTTAAGACTCACTAGG

20281  AGGGTATGACCTAGGGAATGAACTAGCTATGAAATACTCAGGGTTAGGAATCCTAGCACT
20281  TCCCATACTGGATCCCTTACTTGATCGATACTTTATGAGTCCCAATCCTTAGGATCGTGA

20341  TGTCTCAGGACTCTGAAAAGGAACGGCTTCCTCATTCCTTGTCTTGATAAAGTGGAATTG
20341  ACAGAGTCCTGAGACTTTTCCTTGCCGAAGGAGTAAGGAACAGAACTATTTCACCTTAAC

20401  GCAAACTAGAATTTAGTTTGTACTCAGTGGACAGTGCTGTTGAAGATTTGAGGACTTGTT
20401  CGTTTGATCTTAAATCAAACATGAGTCACCTGTCACGACAACTTCTAAACTCCTGAACAA

20461  AAAGAGCACTGGGTCATATGGAAAAAATGTATGTGTCTCCCAGGTGCATTTCTTGGTTTA
20461  TTTCTCGTGACCCAGTATACCTTTTTTACATACACAGAGGGTCCACGTAAAGAACCAAAT

20521  TGTCTTGTTCTTGAGATTTTGTATATTTAGGAAAACCTCAAGCAGTAATTAATATCTCCT
20521  ACAGAACAAGAACTCTAAAACATATAAATCCTTTTGGAGTTCGTCATTAATTATAGAGGA

20581  GGAACACTATAGAGAACCAAGTGACCGACTCATTTACAACTGAAACCTAGGAAGCCCCTG
20581  CCTTGTGATATCTCTTGGTTCACTGGCTGAGTAAATGTTGACTTTGGATCCTTCGGGGAC

20641  AGTCCTGAGCGAAAACAGGAGAGTTAGTCGCCCTACAGAAAACCCAGCTAGACTATTGGG
20641  TCAGGACTCGCTTTTGTCCTCTCAATCAGCGGGATGTCTTTTGGGTCGATCTGATAACCC

20701  TATGAACTAAAAAGAGACTGTGCCATGGTGAGAAAAATGTAAAATCCTACAGTGAAATGA
20701  ATACTTGATTTTTCTCTGACACGGTACCACTCTTTTTACATTTTAGGATGTCACTTTACT

20761  GCAGCCCTTACAGTATTGTTACCACCAAGGGCAGGTAGGTATTAGTGTTTGAAAAAGCTG
20761  CGTCGGGAATGTCATAACAATGGTGGTTCCCGTCCATCCATAATCACAAACTTTTTCGAC

20821  GTCTTTGAGCCAGGGCATAAATACAGCTAGCCCCAGGGGTGGAACAACTCTGGGAGTCTT
20821  CAGAAACTCGCTCCCGTATTTATGTCGATCGGGGTCCCCACCTTGTTGAGACCCTCAGAA

20881  GGGTACTCGCACCTCTTGGCTTTGTTGATGCTCCGCCAGGAAGGCCACTTGTGTGTGCGT
20881  CCCATGAGCGTGGAGAACCGAAACAACTACGAGGCGGTCCTTCCGGTGAACACACACGCA

20941  GTCAGTTACTTTTTTAGTAACAATTCAGATCCAGTGTAAACTTCCGTTCATTGCTCTCCA
20941  CAGTCAATGAAAAAATCATTGTTAAGTCTAGGTCACATTTGAAGGCAAGTAACGAGAGGT

21001  GTCACATGCCCCCACTTCCCCACAGGTGAAAGTTTTTCTGAAAGTGTTGGGATTGGTTAA
21001  CAGTGTACGGGGGTGAAGGGGTGTCCACTTTCAAAAAGACTTTCACAACCCTAACCAATT

21061  GGTCTTTATTTGTATTACGTATCTCCCGAAGTCCTCTGTGGCCAGCTGCATCTGTCTGAA
21061  CCAGAAATAAACATAATGCATAGAGGGCTTCAGGAGACACCGGTCGACGTAGACAGACTT

21121  TGGTGCGTGAAGGCTCTCAGACCTTACACACCATTTTGTAAGTTATGTTTTACATGCCCC
21121  ACCACGCACTTCCGAGAGTCTGGAATGTGTGGTAAAACATTCAATACAAAATGTACGGGG

21181  GTTTTTGAGACTGATCTCGATGCAGGTGGATCTCCTTGAGATCCTGATAGCCTGTTACAG
21181  CAAAAACTCTGACTAGAGCTACGTCCACCTAGAGGAACTCTAGGACTATCGGACAATGTC
```

FIGURE 3 (cont'd)

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21241  GAATGAAGTAAAGGTCAGTTTTTTTTTTGTATTGATTTTCACAGCTTTGAGGAACATGCAT
21241  CTTACTTCATTTCCAGTCAAAAAAAAAACATAACTAAAAGTGTCGAAACTCCTTGTACCTA

21301  AAGAAATGTAGCTGAAGTAGAGGGGACGTGAGAGAAGCGCCAGGCCGCCAGGCCAACCCT
21301  TTCTTTACATCGACTTCATCTCCCCTGCACTCTCTTCCCGGTCCGGCCGTCCGGTTGGGA

21361  CCTCCAATGGAAATTCCCGTGTTGCTTCAAACTGAGACAGATGGGACTTAACAGGCAATG
21361  GGAGGTTACCTTTAAGGGCACAACGAAGTTTGACTCTGTCTACCCTGAATTGTCCGTTAC

21421  GGGTCCACTTCCCCCTCTTCAGCATCCCCCGTACCCCACTTTCTGCTGAAAGAACTGCCA
21421  CCCAGGTGAAGGGGGAGAAGTCGTAGGGGGCATGGGGTGAAAGACGACTTTCTTGACGGT

21481  GCAGGTAGGACCCCAGAGGCCCCCAAATGAAAGCTTGAATTTCCCCTACTGGCTCTGCGT
21481  CGTCCATCCTGGGGTCTCCGGGGGTTTACTTTCGAACTTAAAGGGGATGACCGAGACGCA

21541  TTTGCTGAGATCTGTAGGAAAGGATGCTTCACAAACTGAGGTAGATAATGCTATGCTGTC
21541  AAACGACTCTAGACATCCTTTCCTACGAAGTGTTTGACTCCATCTATTACGATACGACAG

21601  GTTGGTATACATCATGAATTTTTATGTAAATTGCTCTGCAAAGCAAATTGATATGTTTGA
21601  CAACCATATGTAGTACTTAAAAATACATTTAACGAGACGTTTCGTTTAACTATACAAACT

21661  TAAATTTATGTTTTTAGGTAAATAAAAACTTTTAAAAATTTGTTA
21661  ATTTAAATACAAAAATCCATTTATTTTTGAAAATTTTTAAACAAT
```

FIGURE 4

>hg19_refGene_NM_001178092 range=chr12:24962958-25102393

The BCAT1 gene resides on the minus strand, thus the top strand in the below is the representative 5′- to 3′- sequence of BCAT1

YELLOW: Sub-region of interest towards which a bisulphite conversion and methylation specific assay IS GIVEN AS AN EXAMPLE

Green: Sub-region of interest where a methylation specific restriction enzyme (HHaI/HBAII) amplicon is given as an example

```
   1  AGTAGGGAGGTGGGCAGGAGCCAGTGATGACGGAATGGCAATCACATTTGACCTCTGATC
   1  TCATCCCTCCACCCGTCCTCGGTCACTACTGCCTTACCGTTAGTGTAAACTGGAGACTAG

  61  TGTTTATTTCCTCCTCCTTGACGTCTCCATATAAATGTTACACGGGCATCCCCACACTCG
  61  ACAAATAAAGGAGGAGGAACTGCAGAGGTATATTTACAATGTGCCCGTAGGGGTGTGAGC

 121  GATACGCACCCACAGTGGCTGATTCGGGGGTAACCGTGTCATTTGCTTGCAACACTGGCA
 121  CTATGCGTGGGTGTCACCGACTAAGCCCCCATTGGCACAGTAAACGAACGTTGTGACCGT

 181  CCTCTGCCCTGCACCCCGGGAGTGAGCAGTGAGTGAGGCTCGGGTCTGGGCGCTGGCTCC
 181  GGAGACGGGACGTGGGGCCCTCACTCGTCACTCACTCCGAGCCCAGACCCGCGACCGAGG

 241  GAATCTTCGGGCTGGGAGAGACTCCACCATCTGGGGCCGGCCTGGCGGAGCAGCCTTAGT
 241  CTTAGAAGCCCGACCCTCTCTGAGGTGGTAGACCCCGGCCGGACCGCCTCGTCGGAATCA

 301  GTCTTCCTGCTGATGCAATCCGCTAGGTCGCGAGTCTCCGCCGCGAGAGGGCCGGTCTGC
 301  CAGAAGGACGACTACGTTAGGCGATCCAGCGCTCAGAGGCGGCGCTCTCCCGGCCAGACG

 361  AATCCAGCCCGCCACGTGTACTCGCCGCCGCCTCGGGCACTGCCCCAGGTCTTGCTGCAG
 361  TTAGGTCGGGCGGTGCACATGAGCGGCGGCGGAGCCCGTGACGGGGTCCAGAACGACGTC

 421  CCGGGACCGCGCTCTGCAGCCGCAGACCCGGTCCACACGGCCAGGGGCTACGACCCTTGG
 421  GGCCCTGGCGCGAGACGTCGGCGTCTGGGCCAGGTGTGCCGGTCCCCGATGCTGGGAACC

 481  GATCTGCCCTCCGCTCAGCTCGAGCTTCCCTCGTGGCCGACGGAACAATGAAGGTAACTA
 481  CTAGACGGGAGGCGAGTCGAGCTCGAAGGGAGCACCGGCTGCCTTGTTACTTCCATTGAT

 541  CTTATGGTTTTGTCCGTGTTTTACAAAAATGTGTGCGTGAATCGAACCGGCGATTTCTCC
 541  GAATACCAAAACAGGCACAAAATGTTTTTACACACGCACTTAGCTTGGCCGCTAAAGAGG

 601  AAGAAACATAGTTGGCAGGGAGGGGAGGAAGGCGAGACAACCATGGCTTATATCCCCCGC
 601  TTCTTTGTATCAACCGTCCCTCCCCTCCTTCCGCTCTGTTGGTACCGAATATAGGGGGCG

 661  AAACGTCTCAGTATCTTCTTTATCAATCGTAGTTTGCGGGGACCGTGCATTCTGTTCAGA
 661  TTTGCAGAGTCATAGAAGAAATAGTTAGCATCAAACGCCCCTGGCACGTAAGACAAGTCT

 721  TTTCGGTTTAACCTCCACTCGCAGGACGTGCCTTCTCGGACTTTTTCACATTCGCTTTTG
 721  AAAGCCAAATTGGAGGTGAGCGTCCTGCACGGAAGAGCCTGAAAAAGTGTAAGCGAAAAC

 781  GGAACGGAGGTGAAAGTCTGCTACAGCTCCCTCCCCTGCTTGTGAAGTTTGGAAAGGAAG
 781  CCTTGCCTCCACTTTCAGACGATGTCGAGGGAGGGGACGAACACTTCAAACCTTTCCTTC

 841  TGAGGGCTTCTCTCAGTTTCTCCTATGCACAGGAGGTGGGGAATTTTGGAGAGGAGGTCT
 841  ACTCCCGAAGAGAGTCAAAGAGGATACGTGTCCTCCACCCCTTAAAACCTCTCCTCCAGA

 901  GGGGATGTCCCGGGCTGTAAATGCGCTTTCCTGCAGCGTGTGTTCCTGATGCAGGAGGGA
 901  CCCCTACAGGGCCCGACATTTACGCGAAAGGACGTCGCACACAAGGACTACGTCCTCCCT

 961  GCGGCTGGAAGAGTTGACCCGGGTGGAGAGGGGAGGGAGAACGATCTTTTCACTGTTAAA
 961  CGCCGACCTTCTCAACTGGGCCCACCTCTCCCCTCCCTCTTGCTACAAAAGTGACAATTT

1021  AGCAGAAGGCCCCTCTTATTTTGTTTCTTGTGGAAATTAAAGCTTCTAGGAGTTACAAAT
1021  TCGTCTTCCGGGGAGAATAAAACAAAGAACACCTTTAATTTCGAAGATCCTCAATGTTTA

1081  GATAGACGCCTAAGGGCATTCATTTGTTAAACCAGTGAGCACCCTAATGGCTCTGATCTT
1081  CTATCTGCGGATTCCCGTAAGTAAACAATTTGGTCACTCGTGGGATTACCGAGACTAGAA
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FIGURE 4 (cont'd)

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1141   GCTAATCAAGGATAATTAGCCTAGCTGCCTATTATTTCTGACTATTTAGGTGTAGGGATG
1141   CGATTAGTTCCTATTAATCGGATCGACGGATAATAAAGACTGATAAATCCACATCCCTAC

1201   TACACCGTTGAGTGTTTTGTTTTCCTAGTTTCACACACTGGAAAACTGCAATCGCATATA
1201   ATGTGGCAACTCACAAAACAAAAGGATCAAAGTGTGTGACCTTTTGACGTTAGCGTATAT

1261   AAACCCGAAGAGCAACTTTTTCCAAGGAAAGTGAAGGATGGGCAGATATTCTTGCCATCT
1261   TTTGGGCTTCTCGTTGAAAAAGGTTCCTTTCACTTCCTACCCGTCTATAAGAACGGTAGA

1321   AACATTTTGGAATTGAGATGACCATAATGCAATCTGAACTTCTGGTAGGAATAAAGCCTC
1321   TTGTAAAACCTTAACTCTACTGGTATTACGTTAGACTTGAAGACCATCCTTATTTCGGAG

1381   GTTTCAGAGTTTCTAAGGAGGGAGATGAAGCGTGGTTCTCAACTGCTCTTATCTACAACC
1381   CAAAGTCTCAAAGATTCCTCCCTCTACTTCGCACCAAGAGTTGACGAGAATAGATGTTGG

1441   CATCCCAGACCATAGTTTCACTTAGAAGAAATAATATGTAAATAGCGCCTTTGTTGCCAA
1441   GTAGGGTCTGGTATCAAAGTGAATCTTCTTTATTATACATTTATCGCGGAAACAACGGTT

1501   ACAAAAACTTTCACTACAATTAAACAGTAACCGAGTGGAAACTATGCGTTTTTGTATTCA
1501   TGTTTTTGAAAGTGATGTTAATTTGTCATTGGCTCACCTTTGATACGCAAAAACATAAGT

1561   ACAGAGATCACACAACTTTTCTTCTATAGTTAGAGGTTCTATTTCTGGCTTCCTCATGCT
1561   TGTCTCTAGTGTGTTGAAAAGAAGATATCAATCTCCAAGATAAAGACCGAAGGAGTACGA

1621   TGTTTCATTTCAGATGAAAAACACACTTTAGTTGATTATAGCTTTAGTAAGTAAAAGGAG
1621   ACAAAGTAAAGTCTACTTTTTGTGTGAAATCAACTAATATCGAAATCATTCATTTTCCTC

1681   AAAACTAAGAATGAACAGTCTTGCTTTTCCAGCTTTTTCCTGTCCATGTGCAGTTGTGGT
1681   TTTTGATTCTTACTTGTCAGAACGAAAAGGTCGAAAAAGGACAGGTACACGTCAACACCA

1741   TAATTACGCGTTTTTGTAGGTCCAAAAACCCCTGTCCCTTCCACAAGATACTTTTATAAC
1741   ATTAATGCGCAAAAACATCCAGGTTTTTGGGGACAGGGAAGGTGTTCTATGAAAATATTG

1801   ATGGGGAACTAGGTAAGATATCTACAAGTAGTCTCTTTTCTGTTTCCTGATATTTCCTAA
1801   TACCCCTTGATCCATTCTATAGATGTTCATCAGAGAAAAGACAAAGGACTATAAAGGATT

1861   GATTAAGAAAGAAATGATTGTATTCTAGGTATGATCGAAGAAGTATGGAAGGTTCCATTA
1861   CTAATTCTTTCTTTACTAACATAAGATCCATACTAGCTTCTTCATACCTTCCAAGGTAAT

1921   AGTTAGTTTTATCACAATATTTCAAACATCTTTCCACTTATCTCTTAAATATGTATTGCT
1921   TCAATCAAAATAGTGTTATAAAGTTTGTAGAAAGGTGAATAGAGAATTTATACATAACGA

1981   ATCACAAGCTTGATTTTTTAAAAAAATGTTATTTGCACATGGCATCTTGATTGCCTTTGT
1981   TAGTGTTCGAACTAAAAAATTTTTTTACAATAAACGTGTACCGTAGAACTAACGGAAACA

2041   CCTCAGCAAATTCTCCGGGCTTAAGTCATGCATGAGCTTGTATTTTAAGACAGACACATG
2041   GGAGTCGTTTAAGAGGCCCGAATTCAGTACGTACTCGAACATAAAATTCTGTCTGTGTAC

2101   CAGAATGGGCAACTTGGATAAGAAACATAGGATATACACTGAGTAGCATGTGTACAAAAA
2101   GTCTTACCCGTTGAACCTATTCTTTGTATCCTATATGTGACTCATCGTACACATGTTTTT

2161   TGGTAAGTGAGTATTATGACTTAATAAATTTAGATGGGGATTTAAAAATGATACACATGT
2161   ACCATTCACTCATAATACTGAATTATTTAAATCTACCCCTAAATTTTTACTATGTGTACA

2221   AAATGGGATTGGAGGCAAGGGAAGTCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
2221   TTTACCCTAACCTCCGTTCCCTTCAGGCACACACACACACACACACACACACACACACAC

2281   TGTGTGTGTGTGGAGGGAAGACGGGAGGCCTAGTGGGGAGAGAGGTTTTACATTCCAGAC
2281   ACACACACACACCTCCCTTCTGCCCTCCGGATCACCCCTCTCTCCAAAATGTAAGGTCTG

2341   ACAGGATGTGGCCCCTCAGGCTAGGCTCAGAGATGTAAAGCTAGTTAAGCTGGCCTAACA
2341   TGTCCTACACCGGGGAGTCCGATCCGAGTCTCTACATTTCGATCAATTCGACCGGATTGT

2401   AAAGGGTGGTGGTTAGAAAAAGGAAAAAAAGAGGTGGGGGTTGGGGAGGAAAAGAATTTA
2401   TTTCCCACCACCAATCTTTTTCCTTTTTTTCTCCACCCCCAACCCCTCCTTTTCTTAAAT
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FIGURE 4 (cont'd)

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2461   ATGCTGGCCAATATTTTCATCTGATAAGTTTCAGTAATGAGTAATTTCACTGGATTTCAG
2461   TACGACCGGTTATAAAAGTAGACTATTCAAAGTCATTACTCATTAAAGTGACCTAAAGTC

2521   AACTACAGAGAGAAAAGGGGAAAAATATTTTTCCTTTTTTACGCAAGAATTTCTCTTGCT
2521   TTGATGTCTCTCTTTTCCCCTTTTTATAAAAAGGAAAAAATGCGTTCTTAAAGAGAACGA

2581   TTTCAGCTCATTAGAACCAGATCTAATTATTTGAAATGAGTTTAAAACCTTATTATGAAA
2581   AAAGTCGAGTAATCTTGGTCTAGATTAATAAACTTTACTCAAATTTTGGAATAATACTTT

2641   GGAAGTTGAAAACATTCGATCACAATTGAGTTTTGTACTATGGACTAAAACCAAGATGTG
2641   CCTTCAACTTTTGTAAGCTAGTGTTAACTCAAAACATGATACCTGATTTTGGTTCTACAC

2701   CTTTCTGTCAGTAGCTGTGCAACTCCCTGAAAAAAGAAAAATAGCGCAGAGCGATCTGAG
2701   GAAAGACAGTCATCGACACGTTGAGGGACTTTTTTCTTTTTATCGCGTCTCGCTAGACTC

2761   CTTTGTGAAGGCTACACAATTTATCAGGCCCAGAGAGATAGGAGTGTGAGACTTCAGTCA
2761   GAAACACTTCCGATGTGTTAAATAGTCCGGGTCTCTCTATCCTCACACTCTGAAGTCAGT

2821   CGTCCCCCCGTACGCATGCGCAGGAGTAATTATTTAAAGACATTTTGTTCCTGACTAACT
2821   GCAGGGGGGCATGCGTACGCGTCCTCATTAATAAATTTCTGTAAAACAAGGACTGATTGA

2881   GCCTCACTCATTATGTTCCTGGAATTTGTGATACAAAAAAACAATGTTTAGCCTATCAAT
2881   CGGAGTGAGTAATACAAGGACCTTAAACACTATGTTTTTTTGTTACAAATCGGATAGTTA

2941   AGTTTATATAGTTTATGTTATTTTAATATAAATTCTTCTCAACTTAGAAACTGCCTCTTT
2941   TCAAATATATCAAATACAATAAAATTATATTTAAGAAGAGTTGAATCTTTGACGGAGAAA

3001   TTTCTTTTAAAAACCCACTTGTAACTGCTGTATATATTCAGGGCAACTTGATTTGGTGTT
3001   AAAGAAAATTTTTGGGTGAACATTGACGACATATATAAGTCCCGTTGAACTAAACCACAA

3061   TCGTTGGTTGCAGTCCTCAAATTTGACCTCAATATACTCTCTACTTATATAAATTTTGTC
3061   AGCAACCAACGTCAGGAGTTTAAACTGGAGTTATATGAGAGATGAATATATTTAAAACAG

3121   TCAGTTTTGTCCGTAGGCTGACATTCCAATTGTTTTCCTAATTATATATTTTGTTCCTTA
3121   AGTCAAAACAGGCATCCGACTGTAAGGTTAACAAAAGGATTAATATATAAAACAAGGAAT

3181   TTTCTCATGTCTAGAAATAAAGCTAGGGAAGTAAACAGCTGGAAAACTGATAGTGGTGTT
3181   AAAGAGTACAGATCTTTATTTCGATCCCTTCATTTGTCGACCTTTTGACTATCACCACAA

3241   ATTAACCTAACTGAGAGGGCTGGGCTTATGAGTAAATTATTCCTGTGCATAAATGAAAGA
3241   TAATTGGATTGACTCTCCCGACCCGAATACTCATTTAATAAGGACACGTATTTACTTTCT

3301   TTGTTTCTAAATGGCAGCTATGTTGAGCCTTTGTATTAGTTACATCTTTTGGGGTTTCAG
3301   AACAAAGATTTACCGTCGATACAACTCGGAAACATAATCAATGTAGAAAACCCCAAAGTC

3361   GTTGCCAGCTTCTTTAAATGGCCTCTTCTCAACTGGTATAGGAAGTTGGAAAATAAAGAA
3361   CAACGGTCGAAGAAATTTACCGGAGAAGAGTTGACCATATCCTTCAACCTTTTATTTCTT

3421   CTTTCTTTATTTCCCTTTAGTGTTGGTAACCACAGTTTCTTTAAATAACAGATGCCCACC
3421   GAAAGAAATAAAGGGAAATCACAACCATTGGTGTCAAAGAAATTTATTGTCTACGGGTGG

3481   CCAGGGAAACCCAGTGGCATGATCAGCCTTATGCTCAGGAAGGTTTGGTTGCTATACTGG
3481   GGTCCCTTTGGGTCACCGTACTAGTCGGAATACGAGTCCTTCCAAACCAACGATATGACC

3541   AGAGTGAGAATCTGGGACCTTCCATGATAGACATAATTGTGCCAGCTATCCTCTACTTTC
3541   TCTCACTCTTAGACCCTGGAAGGTACTATCTGTATTAACACGGTCGATAGGAGATGAAAG

3601   TATATGATGCTATCATTCTTTTTTCTTTTCTTTTTTTTGACAGAATCTCACTGTGTTGTT
3601   ATATACTACGATAGTAAGAAAAAAGAAAAGAAAAAAAACTGTCTTAGAGTGACACAACAA

3661   CAGGCTGGAGTGCCGCAGAGTGATCTCTACTCACTGCAACCTCTGCCTCCTAGGTTCAAG
3661   GTCCGACCTCACGGCGTCTCACTAGAGATGAGTGACGTTGGAGACGGAGGATCCAAGTTC

3721   CAATTCTTGTGCCTCAGCCTCCTGAGAAGCTGGGATTACCACCATGCCCAGCTAATTTTC
3721   GTTAAGAACACGGAGTCGGAGGACTCTTCGACCCTAATGGTGGTACGGGTCGATTAAAAG
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FIGURE 4 (cont'd)

```
3781  GTATTTTTTTGTAAAGACGGAGTTTTGCCATGTTGGCCAGGCTGGTCTGGAACTCCTGGC
3781  CATAAAAAAACATTTCTGCCTCAAAACGGTACAACCGGTCCGACCAGACCTTGAGGACCG

3841  CTCAAGCGATCTGCCCATCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGTGCTATCA
3841  GAGTTCGCTAGACGGGTAGAGCCGGAGGGTTTCACGACCCTAATGTCCGTACACGATAGT

3901  TTCTTTTTGAGCACAGGAGGAAACTATGGCTGATCTGCTCATTTTACTGTCAAAAATATA
3901  AAGAAAAACTCGTGTCCTCCTTTGATACCGACTAGACGAGTAAAATGACAGTTTTTATAT

3961  GGCAGCTTTTGTATTGTAACATTATCCCCTTAACAGCTGTCCAACTGGTCTATACATTTC
3961  CCGTCGAAAACATAACATTGTAATAGGGGAATTGTCGACAGGTTGACCAGATATGTAAAG

4021  ACCTAACATATGGTAAATGTTCCTACTGTTGGCCTTTCCTGAGCCTCTGTCCATTCAACT
4021  TGGATTGTATACCATTTACAAGGATGACAACCGGAAAGGACTCGGAGACAGGTAAGTTGA

4081  AAGGCCACTCCAATGGCATTGTATGCAGTTCAGCCAAGAAATAAATGTGAGGTGCAACTC
4081  TTCCGGTGACGTTACCCTAACATACGTCAAGTCGGTTCTTTATTTACACTCCACGTTGAG

4141  ACATTTTTTAAATGTTTCAAAATTAAGCATTTAGGTGCTTTTATTCATAAACATGACTTT
4141  TGTAAAAAATTTACAAAGTTTTAATTCGTAAATCCACGAAAATAAGTATTTGTACTGAAA

4201  GCAAATATTGGTAAACAGTTTCATCATAAGACCTTGTCAGTGACTCACAATGTCAATGGT
4201  CGTTTATAACCATTTGTCAAAGTAGTATTCTGGAACAGTCACTGAGTGTTACAGTTACCA

4261  GAACGCAAAGGAGAATCTGTCTTTTCTGGAACACCAGGTTCAGGTATCAGTTTCAACTAT
4261  CTTGCGTTTCCTCTTAGACAGAAAAGACCTTGTGGTCCAAGTCCATAGTCAAAGTTGATA

4321  GCTTATAATTTGTGCTCTAAAGTCCACAAAGCTAAATTATCTTTCCCCTAAAAATTGAGT
4321  CGAATATTAAACACGAGATTTCAGGTGTTTCGATTTAATAGAAAGGGGATTTTTAACTCA

4381  ACTCATATCCTTAAAATAGCTTGGAAATTAGATTACCTTATGAATACAGCATAGCATGTC
4381  TGAGTATAGGAATTTTATCGAACCTTTAATCTAATGGAATACTTATGTCGTATCGTACAG

4441  ACATAAACGTTTTTCTACTGTTATACCTTTTTGGTGGGAAAGACTATTTTGCAAAACATT
4441  TGTATTTGCAAAAAGATGACAATATGGAAAAACCACCCTTTCTGATAAAACGTTTTGTAA

4501  TTTCTTGTGTTCAGTAATTAATGGGAAAAACAAACTCTAAAAGAAAGAGACAGTTATGTC
4501  AAAGAACACAAGTCATTAATTACCCTTTTTGTTTGAGATTTTCTTTCTCTGTCAATACAG

4561  CCAAAAATACAGGAAAATGGAAGAATGGAAACAGGGAAGACCAATAAAGAAAAAAATAGA
4561  GGTTTTTATGTCCTTTTACCTTCTTACCTTTGTCCCTTCTGGTTATTTCTTTTTTTATCT

4621  GGAAATTACAAGTAATAAACTGAAGTCATACTGAAAAACATATGGCTCTTTCTTATTGAA
4621  CCTTTAATGTTCATTATTTGACTTCAGTATGACTTTTTGTATACCGAGAAAGAATAACTT

4681  AGTTGTGAAATACTTGCAAAACTCAGCTAGTTCCATTAAGAATAGTCTTTAATCTAAAAA
4681  TCAACACTTTATGAACGTTTTGAGTCGATCAAGGTAATTCTTATCAGAAATTAGATTTTT

4741  GAACAAATTCATTTGTCAGTTCTTTATTTCGGTGTGTAGATTTGAATGTTTCATCAATTG
4741  CTTGTTTAAGTAAACAGTCAAGAAATAAAGCCACACATCTAAACTTACAAAGTAGTTAAC

4801  CATTTACGGTTTATCCCTCAGTGTGAGAACTGTTTTTGCTGTTTTGACTATAAATGGATA
4801  GTAAATGCCAAATAGGGAGTCACACTCTTGACAAAAACGACAAAACTGATATTTACCTAT

4861  TCTGCTTTAGGAAGACTTAGGAAGCCTGGGACATAGGATTACAGATCAAATTCTATTTGA
4861  AGACGAAATCCTTCTGAATCCTTCGGACCCTGTATCCTAATGTCTAGTTTAAGATAAACT

4921  CTCCATAGAAGTTGAGACGGAAGGAGCACCTGTTGGGATATTCTAGACCAAACATTCCAC
4921  GAGGTATCTTCAACTCTGCCTTCCTCGTGGACAACCCTATAAGATCTGGTTTGTAAGGTG

4981  AGCTGTCTCTTAACGTGACTGACAAAGAGACACAGTTGAGACGAAGTTTGGGTATATCCT
4981  TCGACAGAGAATTGCACTGACTGTTTCTCTGTGTCAACTCTGCTTCAAACCCATATAGGA

5041  GGGATGAGGCCAAGGGTGGATTTGCACAGGATGGTCACAGGGCAGTTGTTAGCATTCCAC
5041  CCCTACTCCGGTTCCCACCTAAACGTGTCCTACCAGTGTCCCGTCAACAATCGTAAGGTG
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FIGURE 4 (cont'd)

```
5101  CACTACATAAAAGGGTGATTTTGCCAAGTGCATTTCATTTCATTTCAGTTGATTTAGATA
5101  GTCATGTATTTTCCCACTAAAACGGTTCACGTAAAGTAAAGTAAAGTCAACTAAATCTAT

5161  CCAAGTTATATTGTTTTGACTTTAGGACTAGATGTGAGTTCAGGAATTTGAAATCATAAT
5161  GGTTCAATATAACAAAACTGAAATCCTGATCTACACTCAAGTCCTTAAACTTTAGTATTA

5221  AAATGTTTCCTTGAACTTTGAAGATAAAAGGTAGAGTTAAAAGACAGCTGCGAAGTCTAC
5221  TTTACAAAGGAACTTGAAACTTCTATTTTCCATCTCAATTTTCTGTCGACGCTTCAGATG

5281  ATGGGGAAGCATAATACATGACTCAGGGTTCCATGGTTTTCAGTGTCGGTGAGTGCTCTG
5281  TACCCCTTCGTATTATGTACTGAGTCCCAAGGTACCAAAAGTCACAGCCACTCACGAGAC

5341  TACACTTATAAGAATAGTGCTGGTGTTTATAGAAGAAACACATGCAGGTTTGAGGCAAGA
5341  ATGTGAATATTCTTATCACGACCACAAATATCTTCTTTGTGTACGTCCAAACTCCGTTCT

5401  CTTCCTTGCTTAATTGGTGCTTTTGCTTTCCATTTTCTAAATGCCATGCAAACTACTTTT
5401  GAAGGAACGAATTAACCACGAAAACGAAAGGTAAAAGATTTACGGTACGTTTGATGAAAA

5461  TTTTTTTTCTTTTGTTCAGACGGAGTCTTGCTCTGTCACCCAGGCTGGAGTACAGTGCTG
5461  AAAAAAAAGAAAACAACTCTGCCTCAGAACGAGACAGTGGGTCCGACCTCATGTCACCAC

5521  CGATCTCGGCTCACTGCAAGCTCCGCCTCCTGGGTTCACGCCATTCTCCTGCCTCAGCTT
5521  GCTAGAGCCGAGTGACGTTCGAGGCGGAGGACCCAAGTGCGGTAAGAGGACGGAGTCGAA

5581  CCTGAGTAGCTGGGACTACAGGCGCCCGCCACCACGCCCGGCTAATTTTTTGTATTTTTT
5581  GGACTCATCGACCCTGATGTCCGCGGGCGGTGGTGCGGGCCGATTAAAAAACATAAAAAA

5641  GTAGAGACGGGGTTTCACCATGTTAGCCAGGAAGGTCTTGATCTCCTGACCTCGTGATCT
5641  CATCTCTGCCCCAAAGTGGTACAATCGGTCCTTCCAGAACTAGAGGACTGGAGCACTAGA

5701  GCCCGCCTCGGCCACCCAAGGTGCTGGGATTACAGGCGTGAGCCACCGCTCCCGGCCTCA
5701  CGGGCGGAGCCGGTGGGTTCCACGACCCTAATGTCCGCACTCGGTGGCGAGGGCCGGAGT

5761  AACTACTTTAACTGAAAACATTCTTCTAAGGAAAGCATCAGAAAACTTACTAGAATTGCT
5761  TTGATGAAATTGACTTTTGTAAGAAGATTCCTTTCGTAGTCTTTTGAATGATCTTAACGA

5821  TAAGAATAAATAAATAATACAAATAAAAGAGCAAAATGAGAAAGTAGACAGACTCCTAGT
5821  ATTCTTATTTATTTATTATGTTTATTTTCTCGTTTTACTCTTTCATCTGTCTGAGGATCA

5881  CTATTGTGCTATTGATCTCTCCAGGTTCTAGGCTTTCTTGGGTCTGACACCACTTTGTAA
5881  GATAACACGATAACTAGAGAGGTCCAAGATCCGAAAGAACCCAGACTGTGGTGAAACATT

5941  ATTTTTTTTTTTTTTTTTTTTTTTTTCCAGATAGGGTCTCATTCTGTCACCTAGGCTGGA
5941  TAAAAAAAAAAAAAAAAAAAAAAAAAGGTCTATCCCAGAGTAAGACAGTGGATCCGACCT

6001  GTGCAGTGGTACAATCATGGCTCACTTCAGCTTCAACCTCCTGGGCTCAAGTGATCTTCC
6001  CACGTCACCATGTTAGTACCGAGTGAAGTCGAAGTTGGAGGACCCGAGTTCACTAGAAGG

6061  TGCCTCAGCTCCCTGAGTAGCTGGGACCACAGGCATGTGCCACCACGCCCGGTGAATTTT
6061  ACGGAGTCGAGGGACTCATCGACCCTGGTGTCCGTACACGGTGGTGCGGGCCACTTAAAA

6121  TGTATTTTTTGTAGAGATGGGGTTTCTCCATGTTGCACTGGCTGGTCTTGAACTCCTGGG
6121  ACATAAAAAACATCTCTACCCCAAAGAGGTACAACGTGACCGACCAGAACTTGAGGACCC

6181  CTCCAGTGATCCACCCACCTTGGCCTCCAAAGTGCTGGGATTACAGGCATCCGTCACTGC
6181  GAGGTCACTAGGTGGGTGGAACCGGAGGTTTCACGACCCTAATGTCCGTAGGCAGTGACG

6241  ACTGGGCCAGTTTGTAAATCTTATGAAAAGTATGGCCAATCTTTTGCAAAATGTGCAAAC
6241  TGACCCGGTCAAACATTTAGAATACTTTTCATACCGGTTAGAAAACGTTTTACACGTTTG

6301  ACATATAGACACAAAGTTTTATATCTAAATTATTGGTTATTAAAGCCAGGACAATAGAGT
6301  TGTATATCTGTGTTTCAAAATATAGATTTAATAACCAATAATTTCGGTCCTGTTATCTCA

6361  GCATATAGCATGGAAGACAGGTAGAAAAGACTGAAATGGTTTAGTTATTCAGAGCAGTGG
6361  CGTATATCGTACCTTCTGTCCATCTTTTCTGACTTTACCAAATCAATAAGTCTCGTCACC
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FIGURE 4 (cont'd)

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6421  AGGGCTATTGGCTCTTGCCTTTGCAGTCAGCTGAGATATGAAACTATATAAGCAGAAGCT
6421  TCCCGATAACCGAGAACGGAAACGTCAGTCGACTCTATACTTTGATATATTCGTCTTCGA

6481  TCACGCTGCCATTTGAATATTGAAAATCTCCACTTTTAGTTCAAGAGATAAACAACCAAT
6481  AGTGCGACGGTAAACTTATAACTTTTAGAGGTGAAAATCAAGTTCTCTATTTGTTGGTTA

6541  GGTTTGTTTGTTCACAGCACATAAGTTATCACTTTCTTCTCTGTTTCATCCCATCAAGAT
6541  CCAAACAAACAAGTGTCGTGTATTCAATAGTGAAAGAAGAGACAAAGTAGGGTAGTTCTA

6601  CTAAGGTGTATAGTTACAGAATAGAACTCGGTTCATACCATATGCACCCTAATTTCTTCG
6601  GATTCCACATATCAATGTCTTATCTTGAGCCAAGTATGGTATACGTGGGATTAAAGAAGC

6661  ATCTTCAACTAGTTTGGAAGTGTGTGTGGGTGTTTTCTTAGCCAAGGTTAATATGCAATT
6661  TAGAAGTTGATCAAACCTTCACACACACCCACAAAAGAATCGGTTCCAATTATACGTTAA

6721  TCTTAGTGCAGTGTAGGAGTTTGGGTGCCTAGCCTTCCTACTTCCCACTTAGATAACTT
6721  AGAATCACCTCACATCCTCAAACCCCACGGATCGGAAGGATGAAGGGTGAATCTATTGAA

6781  CCCCTACCTGTTGTACCTGTCAAAGGAGAAGGCCAGTATGGCCATGTTCTTTGCAGGTGA
6781  GGGGATGGACAACATGGACAGTTTCCTCTTCCGGTCATACCGGTACAAGAAACGTCCACT

6841  CTCCACCTTAGCCACAGCTGATTGTAACAAGGGTGTATATTTGGCCCAAGTCCAGCCATC
6841  GAGGTGGAATCGGTGTCGACTAACATTGTTCCCACATATAAACCGGGTTCAGGTCGGTAG

6901  TTTTTTTTTTTTTTTTGAGGCGGAGTCTTGTTCTGTCACCCACGCTGGAGTGCAGTGGTG
6901  AAAAAAAAAAAAAAAACTCCGCCTCAGAACAAGACAGTGGGTGCGACCTCACGTCACCAC

6961  TGATTTTGGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGCAATTCTCCTGCCTCAGCCT
6961  ACTAAAACCGAGTGACGTTGGAGACGGAGGGCCCAAGTTCGTTAAGAGGACGGAGTCGGA

7021  CCTGAGTAGCTGGGATTACAGACACCCACGACCACGCTTGGCTTTGTATTTTTGTATTTT
7021  GGACTCATCGACCCTAATGTCTGTGGGTGCTGGTGCGAACCGAAACATAAAAACATAAAA

7081  TAGTAGAGACGGGGTTTCTCCATGTTGGCCAGGCTGGTCTAGAACTCTTGACCTCAACTG
7081  ATCATCTCTGCCCCAAAGAGGTACAACCGGTCCGACCAGATCTTGAGAACTGGAGTTCAC

7141  ATCCGCCCGCCTTGGCCTCCCAAACTACTGGGATTACATGCCCAGCCAGCCATCTTTTAC
7141  TAGGCGGGCGGAACCGGAGGGTTTGATGACCCTAATGTACGGGTCGGTCGGTAGAAAATG

7201  TTCTTTCTTATTCTCTTATTCCACATATTCAAGCAGGTACCACGTCCTGTGGACTCTGTC
7201  AAGAAAGAATAAGAGAATAAGGTGTATAAGTTCGTCCATGGTGCAGGACACCTGAGACAG

7261  TTCTCTGAATCTATAGGTTCTCTCTTTCCCATTGCCCTGCATACTGGTTTATGCTCTCAT
7261  AAGAGACTTAGATATCCAAGAGAGAAAGGGTAACGGGACGTATGACCAAATACGAGAGTA

7321  TACTTCTCGCTTGAATTATTCCAAAAGTCTCCCAACTGGTCTGAAGCTTAATTTTCATTA
7321  ATGAAGAGCGAACTTAATAAGGTTTTCAGAGGGTTGACCAGACTTCGAATTAAAAGTAAT

7381  TGTGCTGTTCGATGTCATTCCACCACGCAAAATCTATGGCTTCTCCATTGTCTCCTGAGT
7381  ACACGACAAGCTACAGTAAGGTGGTGCGTTTTAGATACCGAAGAGGTAACAGAGGACTCA

7441  TTAGTTTAGTGCATGAGACCGTTTAAAATCTACCTACACCTCTTCTATGTGCATGCATTT
7441  AATCAAATCACGTACTCTGGCAAATTTTAGATGGATGTGGAGAAGATACACGTACGTAAA

7501  CTCTAGTCATAAGAGAGGATTTGATCTATCTCAAAATGTGTTCTTATATTTGCATTTACT
7501  GAGATCAGTATTCTCTCCTAAACTAGATAGAGTTTTACACAAGAATATAAACGTAAATGA

7561  GGTTTTTAACTCCCTCCATCCTATCTATAATTTGCACCATGTTGCTCACCATGCAGCCCA
7561  CCAAAAATTGAGGGAGGTAGGATAGATATTAAACGTGGTACAACGAGTGGTACGTCGGGT

7621  CTCCCCAGACACCTTGTGAGAACAGTGATCATGTTTTTGCAGTGGAATGAACATGGGCGA
7621  GAGGGGTCTGTGGAACACTCTTGTCACTAGTACAAAAACGTCACCTTACTTGTACCCGCT

7681  AAGGTGGGAAGGTATGCATAGATTTACATTTTGAAGTCAGGAAATAAGATACTGATCAAT
7681  TTCCACCCTTCCATACGTATCTAAATGTAAAACTTCAGTCCTTTATTCTATGACTAGTTA
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FIGURE 4 (cont'd)

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7741  GCTTTAATTCGACTGTGCTTTTTACCTTTTCCTCTGTTGTAGCATGAACCTTGCCCCAAA
7741  CGAAATTAAGCTGACACGAAAAATGGAAAAGGAGACAACATCGTACTTGGAACGGGGTTT

7801  AAGATATTGATCATATGCTGCAACTCCTCTGCACTTACCTTTTCTTCTACCATGGCAGGA
7801  TTCTATAACTAGTATACGACGTTGAGGAGACGTGAATGGAAAAGAAGATGGTACCGTCCT

7861  ACCTTGCACCATTGTTGGTGCTTTACAGATATTGGTTGAGTTAAATCGAGAGCCTATTTC
7861  TGGAACGTGGTAACAACCACGAAATGTCTATAACCAACTCAATTTAGCTCTCGGATAAAG

7921  TGGACTTTCAAGATTCAGATTAATTGATTCTGTTTTATACTTCTCTGTTTTTGAATGGCA
7921  ACCTGAAAGTTCTAAGTCTAATTAACTAAGACAAAATATGAAGAGACAAAAACTTACCGT

7981  CATACATCTTTCCACACTTGGATTTCTTTGAAGTTAAAGCTTTAATTGACTTCCAAAAGA
7981  GTATGTAGAAAGGTGTGAACCTAAAGAAACTTCAATTTCGAAATTAACTGAAGGTTTTCT

8041  CAGAGGATTATAAAAACACAGAGAACAGTAAAGTATTTACACGGTCTTAATGCCTATTGC
8041  GTCTCCTAATATTTTTGTGTCTCTTGTCATTTCATAAATGTGCCAGAATTACGGATAACG

8101  CAAACACATATAGCTGCTATTAATGCCTATTGCCAGACTCATATAGCTGCAAACTCATGT
8101  GTTTGTGTATATCGACGATAATTACGGATAACGGTCTGAGTATATCGACGTTTGAGTACA

8161  AGCTTAATGCCCATTGCCAAACTCATATAGCTGCTATATATGTCTACTGGAAAACTCACA
8161  TCGAATTACGGGTAACGGTTTGAGTATATCGACGATATATACAGATGACCTTTTGAGTGT

8221  TAGCTGGTTGATTTTAAATTGATTGTAGGAAAATTCATACAAAAAGATGCTACATAGGAA
8221  ATCGACCAACTAAAATTTAACTAACATCCTTTTAAGTATGTTTTTCTACGATGTATCCTT

8281  TATAAACTGAACACCACAAAAATCGTAATGAACAAACTCAGTAATGCCAGCCTGTTCAAT
8281  ATATTTGACTTGTGGTGTTTTTAGCATTACTTGTTTGAGTCATTACGGTCGGACAAGTTA

8341  CACTAGTTTTCAGATTAAGGCAGTATGCAAAGGGAAACATCCTTGGAATGGTCTTAGAAT
8341  GTGATCAAAAGTCTAATTCCGTCATACGTTTCCCTTTGTAGGAACCTTACCAGAATCTTA

8401  ATAGAACAAAGTCATGTGTTTGGGAATCTTAACCAATTCCAATACTGTTCAACATGTTTT
8401  TATCTTGTTTCAGTACACAAACCCTTAGAATTGGTTAAGGTTATGACAAGTTGTACAAAA

8461  TCTTTGTTGCAAACAATGCAGTTTTTAAGCAAACTAATGAATGCATACCCTGACAAACAA
8461  AGAAACAACGTTTGTTACGTCAAAAATTCGTTTGATTACTTACGTATGGGACTGTTTGTT

8521  ATCCAACAAAAGAGGTACTTAGAGCAGTGTTCATTGAATCCTAGAATTTTGAAAGAAAAA
8521  TAGGTTGTTTTCTCCATGAATCTCGTCACAAGTAACTTAGGATCTTAAAACTTTCTTTTT

8581  ATCTATTAGGTCATTTTGGGCTTTTACTTCTGCTGAAGAAGGATTGTTCTTTTGAGTTTA
8581  TAGATAATCCAGTAAAACCCGAAAATGAAGACGACTTCTTCCTAACAAGAAAACTCAAAT

8641  TTTTTCTAGCTTTCAGTTCTATTCCATTTAAATGCCTCGAGAAATAGGACTTCTCAAATT
8641  AAAAAGATCGAAAGTCAAGATAAGGTAAATTTACGGAGCTCTTTATCCTGAAGAGTTTAA

8701  CCCTGTGGAGAGTTCTGGCACCTACTATATTCACTTTTGAAAGTCTCCTGATAACTGATT
8701  GGGACACCTCTCAAGACCGTGGATGATATAAGTGAAAACTTTCAGAGGACTATTGACTAA

8761  TCCTTTTTCTTTTGGTTATACACATCAACTATTCATGGTTGGCTCTGCTGATAGTTTTCC
8761  AGGAAAAAGAAAACCAATATGTGTAGTTGATAAGTACCAACCGAGACGACTATCAAAAGG

8821  ATGATTCTTTATGCTTATTTAAAAGAAATCATATAACATTAATCATATAACATATAACCA
8821  TACTAAGAAATACGAATAAATTTTCTTTAGTATATTGTAATTAGTATATTGTATATTGGT

8881  TTACTTGGTTATAAAGCATGATATTAACTAAACTGGCTTTTAAAAATTCAATAACATTAG
8881  AATGAACCAATATTTCGTACTATAATTGATTTGACCGAAAATTTTTAAGTTATTGTAATC

8941  AGCAAATATTTTATTAATATTGTCAGTAGTTCCATGAATATATAGATGTAGGATGTCAAT
8941  TCGTTTATAAAATAATTATAACAGTCATCAAGGTACTTATATATCTACATCCTACAGTTA

9001  AAAGTTTATGCCCCTTAATAACTGAGTGTGTTAATGTTGTATTTGCTGGTTAACTGGCAC
9001  TTTCAAATACGGGGAATTATTGACTCACACAATTACAACATAAACGACCAATTGACCGTG
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FIGURE 4 (cont'd)

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 9061  CTTCCCTCCTTTTGATCAATGTTCTTAGAACAGTATGTACAGGAGTACTTTAGTCTACCA
 9061  GAAGGGAGGAAAACTAGTTACAAGAATCTTGTCATACATGTCCTCATGAAATCAGATGGT

 9121  CTTGATATTCAAGGACAACACTTCGAAGCTTGAAATGAGGGATTGTTTTAACCATATTAA
 9121  GAACTATAAGTTCCTGTTGTGAAGCTTCGAACTTTACTCCCTAACAAAATTGGTATAATT

 9181  CGTAACTGCATAGTTTGCAATAGATTTAATGATTCAACATCATTGTTAATATTTAGTTTA
 9181  GCATTGACGTATCAAACGTTATCTAAATTACTAAGTTGTAGTAACAATTATAAATCAAAT

 9241  ATTAAAAGTGCCTTATATTAACTTGTACACATGTGAAATGACTTATCAACAAGATTATTT
 9241  TAATTTTCACGGAATATAATTGAACATGTGTACACTTTACTGAATAGTTGTTCTAATAAA

 9301  ATTGCAGCATTGTTTGTGATTACAAAGAGTGGAAGTCATTTGCATAGTCATTAGGCGTAA
 9301  TAACGTCGTAACAAACACTAATGTTTCTCACCTTCAGTAAACGTATCAGTAATCCGCATT

 9361  AAAATAATGACATTAAAAGAAAACAATTGAGGAAAGAACCAGTAAGCTCTCAGGTAGAGA
 9361  TTTTATTACTGTAATTTTCTTTTGTTAACTCCTTTCTTGGTCATTCGAGAGTCCATCTCT

 9421  TAAAAAGAAAGTTACCGTGAGCCTTTTCACTGTATATATTTATATATTTGATTTTTGACA
 9421  ATTTTTCTTTCAATGGCACTCGGAAAAGTGACATATATAAATATATAAACTAAAAACTGT

 9481  CGTGAGTTTATTATAATCAAGATTGAATGAAAAAAATTGAAGCCTTTTAATGAAATTAGC
 9481  GCACTCAAATAATATTAGTTCTAACTTACTTTTTTTAACTTCGGAAAATTACTTTAATCG

 9541  TTGACACCAGAGTCATTATCAAGAAAATCTGAAATACTGGTACCTATGCACATTTGATTT
 9541  AACTGTGGTCTCAGTAATAGTTCTTTTAGACTTTATGACCATGGATACGTGTAAACTAAA

 9601  TATTATTTTTAGTTTTATTATTTTTTGAGACAGAGTCTTGCTCTGTCGCCCAGACTGGAG
 9601  ATAATAAAAATCAAAATAATAAAAAACTCTGTCTCAGAACGAGACAGCGGGTCTGACCTC

 9661  TGAAGTGGTGTGATCTCAGCTCACTGCAATCTCCAGCCTCCCAGGTTCAAGCGATTCTCC
 9661  ACTTCACCACACTAGAGTCGAGTGACGTTAGAGGTCGGAGGGTCCAAGTTCGCTAAGAGG

 9721  TCAGCCTCCCGAGTAGCTGGGATTACAGATGCCTGCCACCATGCTTGGCTAGTTTTTGTA
 9721  AGTCGGAGGGCTCATCGACCCTAATGTCTACGGACGGTGGTACGAACCGATCAAAAACAT

 9781  TTTTTAGTAGTGACGGAGTTTTGCCATGCTGGCCAGGCTGATCTCAAACTCCTGACCTCA
 9781  AAAAATCATCACTGCCTCAAAACGGTACGACCGGTCCGACTAGAGTTTGAGGACTGGAGT

 9841  GGTGGTCCACCTGCCTCAGCCTCCCAAAGTGTTGGGATTACAGGCGTGAGCCACTGCACC
 9841  CCACCAGGTGGACGGAGTCGGAGGGTTTCACAACCCTAATGTCCGCACTCGGTGACGTGG

 9901  CGGCCATTTAAGCAAATTTTAGTTAAGACCAGTAACATATTTTTGACAGTATTTCCGAAG
 9901  GCCGGTAAATTCGTTTAAAATCAATTCTGGTCATTGTATAAAAACTGTCATAAAGGCTTC

 9961  TGTTGTATTTAATTTAACTAATTGAAAATTATCTATTAAGAAAGCAAGTTAAATGTAATG
 9961  ACAACATAAATTAAATTGATTAACTTTTAATAGATAATTCTTTCGTTCAATTTACATTAC

10021  TGTATACTTCATAGTATACACATTATAATGATTCATAGTAACCATTATATGAAGAGTGTC
10021  ACATATGAAGTATCATATGTGTAATATTACTAAGTATCATTGGTAATATACTTCTCACAG

10081  TAAACTTTTCTTCAAATCTACCATTTATATAGTACAATAATGACCAGCAAACAATGGCTA
10081  ATTTGAAAAGAAGTTTAGATGGTAAATATATCATGTTATTACTGGTCGTTTGTTACCGAT

10141  AGTTTTACTTAATTAGACATTTGTGTAGCTCCTACCAAGGCTACCAGACTTTGTACCCAG
10141  TCAAAATGAATTAATCTGTAAACACATCGAGGATGGTTCCGATGGTCTGAAACATGGGTC

10201  TAACAGGAAAACAGAAATAATTCAAGCATTATTCTCACTCTTGAGAAACAATTCTATTTA
10201  ATTGTCCTTTTGTCTTTATTAAGTTCGTAATAAGAGTGAGAACTCTTTGTTAAGATAAAT

10261  GGGAGATATACATAAAAAGCAAAGGTGGCTGGGTGCAGTGGCTCATGCCTGTAATCCCAG
10261  CCCTCTATATGTATTTTTCGTTTCCACCGACCCACGTCACCGAGTACGGACATTAGGGTC

10321  CACTTTGGGAGGCCAAGGCAGGCAGATCACTTGAGGCCAGGAGTTCGAGACTAGCCTGAC
10321  GTGAAACCCTCCGGTTCCGTCCGTCTAGTGAACTCCGGTCCTCAAGCTCTGATCGGACTG
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FIGURE 4 (cont'd)

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10381  CAACATGGTGAAACCCTGTTTCTACTAAACATACAAAAATTAGCTGGGTGTGGTGGCATG
10381  GTTGTACCACTTTGGGACAAAGATGATTTGTATGTTTTTAATCGACCCACACCACCGTAC

10441  CACCTGCAATCCCAGCTACTGGGCAGGCTGAGGCAGATAATTGCTTGAACCTGGGAGGTG
10441  GTGGACGTTAGGGTCGATGACCCGTCCGACTCCGTCTATTAACGAACTTGGACCCTCCAC

10501  GAGGCTACAGTGAGCTGAGATTGCACCACTGTACTCCAGCCTGGGTGACAGAGCGAGACT
10501  CTCCGATGTCACTCGACTCTAACGTGGTGACATGAGGTCGGACCCACTGTCTCGCTCTGA

10561  CCATCTCAATGAATAAATAAATAAATAAATAAATAGCAAAGGCAATAATGTGCATATAGT
10561  GGTAGAGTTACTTATTTATTTATTTATTTATTTATCGTTTCCGTTATTACACGTATATCA

10621  AGGTGCTACAGTAGAAGTCTGCACAAGGTTCTGTGTATGTGGAAAAGACAAGTCAGAAAA
10621  TCCACGATGTCATCTTCAGACGTGTTCCAAGACACATACACCTTTTCTGTTCAGTCTTTT

10681  ATTAGGAAAGGCTTTATTGGGAGGTGACATTTAAGCAGAATCACGAAAGAAGACCTGATG
10681  TAATCCTTTCCGAAATAACCCTCCACTGTAAATTCGTCTTAGTGCTTTCTTCTGGACTAC

10741  AACATGGGGGTAAGAGCACTTGTACACAACCCCATACTCCTGGGCTCAGACTCACTTGCT
10741  TTGTACCCCCATTCTCGTGAACATGTGTTGGGGTATGAGGACCCGAGTCTGAGTGAACGA

10801  CATTCCCTAATCATAGAAGACCTTGAGGAAAAGCATGCTGGGGTTCCCTTCCAGCCCACT
10801  GTAAGGGATTAGTATCTTCTGGAACTCCTTTTCGTACGACCCCAAGGGAAGGTCGGGTGA

10861  GGTAAATACAGAGAGGCCTAAGCACCCAACATCCCCCAGGGAATACACCACTGGGACTTA
10861  CCATTTATGTCTCTCCGGATTCGTGGGTTGTAGGGGGTCCCTTATGTGGTGACCCTGAAT

10921  AAGCATTGGCAACCCAGCACCCAGTTAAATTCCCCTTGTCACTGTTTCCACATTGTCCCC
10921  TTCGTAACCGTTGGGTCGTGGGTCAATTTAAGGGGAACAGTGACAAAGGTGTAACAGGGG

10981  ATCACCTTCACTCTCTTGATGCTCTGCATTTTCTCTCTTAACTCGACCCACAGTAGACCC
10981  TAGTGGAAGTGAGAGAACTACGAGACGTAAAAGAGAGAATTGAGCTGGGTGTCATCTGGG

11041  TCCCACTCAAATCTGCCCCCAATAACCTTTGCAACCAATATTACCGCACTACACTTTATC
11041  AGGGTGAGTTTAGACGGGGGTTATTGGAAACGTTGGTTATAATGGCGTGATGTGAAATAG

11101  TTCCCTAAGGGTTTCCTGCTCCTCCTGGTCTTAGGTGAGGTCATTTCTCTGCCAGCCTTT
11101  AAGGGATTCCCAAAGGACGAGGAGGACCAGAATCCACTCCAGTAAAGAGACGGTCGGAAA

11161  AAAGTGGAAGCTGCTCATTTTCTCTGTCCCTCATCCAGGGCTGGAGTGGGACTGATGCCC
11161  TTTCACCTTCGACGAGTAAAAGAGACAGGGAGTAGGTCCCGACCTCACCCTGACTACGGG

11221  TTCACCCTGCCCAGTACTGTTTCCACATGAGACTCCTTGCATAGCATCTGCTCTCTGCTA
11221  AAGTGGGACGGGTCATGACAAAGGTGTACTCTGAGGAACGTATCGTAGACGAGAGACGAT

11281  CTCAGACCAGGAGTCTGTGCTCTCTCTTCCTCTAACCATCATTGGAAGACACCCCAGTCC
11281  GAGTCTGGTCCTCAGACACGAGAGAGAAGGAGATTGGTAGTAACCTTCTGTGGGGTCAGG

11341  CTCTGGCCCCATTATCCACTGTAGATTTTAGCACTTACCTCCTCTCTTCCCTCCCATGTG
11341  GAGACCGGGGTAATAGGTGACATCTAAAATCGTGAATGGAGGAGAGAAGGGAGGGTACAC

11401  CTGTTTTCCCATTTATTTTAAGGTGCATGTGGATGGCCCATTCCCCTTCCTGGCATCTTA
11401  GACAAAAGGGTAAATAAAATTCCACGTACACCTACCGGGTAAGGGGAAGGACCGTAGAAT

11461  ATCCCTTTAATTTCTCATTTCCATTAATTTGCTACATTCCTCATATGCCAGCTACCCCTA
11461  TAGGGAAATTAAAGAGTAAAGGTAATTAAACGATGTAAGGAGTATACGGTCGATGGGGAT

11521  TGGCCATATCCCAGACCTTTGAATCACACACCAAATTCCATCAAGTCCTATGAGTCATTT
11521  ACCGGTATAGGGTCTGGAAACTTAGTGTGTGGTTTAAGGTAGTTCAGGATACTCAGTAAA

11581  TTGGTCCAAGACCTATCTTACATCTATGCAGTGCTATCTATTTTAACAACCATGTGCCCA
11581  AACCAGGTTCTGGATAGAATGTAGATACGTCACGATAGATAAAATTGTTGGTACACGGGT

11641  GTTTAGGCCACTGTCTTCTCTTCACTGAATATATGTGTTCCTGTTTTTTCTCATCCCCAT
11641  CAAATCCGGTGACAGAAGAGAAGTGACTTATATACACAAGGACAAAAAAGAGTAGGGGTA
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FIGURE 4 (cont'd)

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11701   TTGTTTCCCAGACACAATTTGTTCTCCAGAGCAGAGTGATCACATCAGTCACCTGCTATA
11701   AACAAAGGGTCTGTGTTAAACAAGAGGTCTCGTCTCACTAGTGTAGTCAGTGGACGATAT

11761   AAAACTCCTCAACCCGGTGGGGCATGGTGACTCACAGCCCCAGCACTGTAATCCCAGCAC
11761   TTTTGAGGAGTTGGGCCACCCCGTACCACTGAGTGTCGGGGTCGTGACATTAGGGTCGTG

11821   TTTGGGAGGCTGAGGTGGGAGGATCACTTGAGCACAGGAGGAGCTGAAGTGATCTGTGAT
11821   AAACCCTCCGACTCCACCCTCCTAGTGAACTCGTGTCCTCCTCGACTTCACTAGACACTA

11881   CACGTCACTGCACTCCAGCCTGGGCTACAGAGTGACACCCTATCTCAAAAACAAGCAAAC
11881   GTGCAGTGACGTGAGGTCGGACCCGATGTCTCACTGTGGGATAGAGTTTTTGTTCGTTTG

11941   AAACAAACAAACAAAAACCAACAAAAAATTTTTATTAAGCAAAAAACCTCTTCAACCTC
11941   TTTGTTTGTTTGTTTTTGGTTGTTTTTTAAAAATAATTCGTTTTTTGGAGAAGTTGGAG

12001   TTCCTGTTATGTTTTGAATAAAAGCTAAAGTCCCCACCATGCTCCAGAAGTTCCCAAGGG
12001   AAGGACAATACAAAACTTATTTTCGATTTCAGGGGTGGTACGAGGTCTTCAAGGGTTCCC

12061   ATCTGGTCCTTCTCATCTTTACAGCCTCATCTTGTTTTGCCGTTTCCACCTCCCTCATCC
12061   TAGACCAGGAAGAGTAGAAATGTCGGAGTAGAACAAAACGGCAAAGGTGGAGGGAGTAGG

12121   CCCAAACTCTTTTTCTTCAGGGCCTTTGCACTTGCTGATGCCTCTGCCTGGAAGGTCTTC
12121   GGGTTTGAGAAAAAGAAGTCCCGGAAACGTGAACGACTACGGAGACGGACCTTCCAGAAG

12181   TTCTGATTCCCCATCCAGGGGTGCCTTATCACCCTGCCCTGCCAACCTCAGATTGGATGC
12181   AAGACTAAGGGGTAGGTCCCCACGGAATAGTGGGACGGGACGGTTGGAGTCTAACCTACG

12241   TACTTCCTCAAAGAGACCCTTGGGACTCCCATGTTTCCCAGGCTTTCAGTGCCCTCATCT
12241   ATGAAGGAGTTTCTCTGGGAACCCTGAGGGTACAAAGGGTCCGAAAGTCACGGGAGTAGA

12301   CAACTTGTAATGATTGTATTGGGGTGATTATTTGTATGACTTTGGGATTGATATCTGACT
12301   GTTGAACATTACTAACATAACCCCACTAATAAACATACTGAAACCCTAACTATAGACTGA

12361   CTTCCACTAGACCATACATTTCTTGAGAGCAGAGAGCATATCCAGTTTTTTTACCACTGT
12361   GAAGGTGATCTGGTATGTAAAGAACTCTCGTCTCTCGTATAGGTCAAAAAAATGGTGACA

12421   GCAACCATATGTCGTCCAATGCTTGGCCCATAATAGGGGGTTGGTGAATGTGGTAGGCTG
12421   CGTTGGTATACAGCAGGTTACGAACCGGGTATTATCCCCCAACCACTTACACCATCCGAC

12481   AGTCATAGCCCCCAAGGATGCCCATAGCCTCATCCCCAGAAGCTTTCATGGTAAAAGGGA
12481   TCAGTATCGGGGGTTCCTACGGGTATCGGAGTAGGGGTCTTCGAAAGTACCATTTTCCCT

12541   TTTTGCAGATTGTGATTAAGTTATGGATCTTGAGATGGAGAGATTATCCTTGATTATCTA
12541   AAAACGTCTAACACTAATTCAATACCTAGAACTCTACCTCTCTAATAGGAACTAATAGAT

12601   AATAGGTCCAATATAATCAGTAGCGTCTTTATAAGAGAGAGGCAGAGGGTCAAAAGCAGA
12601   TTATCCAGGTTATATTAGTCATCGCAGAAATATTCTCTCTCCGTCTCCCAGTTTTCGTCT

12661   ATCAGAGAAGGAGATGCCACAGTGGAAGCAAAGGGGTGTGTGTGTATGTGTGTGTGTATG
12661   TAGTCTCTTCCTCTACGGTGTCACCTTCGTTTCCCCACACACACATACACACACACATAC

12721   TGTGTGTGTGTGTGTGAGAGAGAGAGATTGAGATTTAAAGAGCTCCATTACTTGATCTGA
12721   ACACACACACACACACTCTCTCTCTCTAACTCTAAATTTCTCGAGGTAATGAACTAGACT

12781   GGATAAGGATGAGCCAAAGAATGCAGGTGGCTTGTAGAAGCTGGAGAAGCCAAGAAAACA
12781   CCTATTCCTACTCGGTTTCTTACGTCCACCGAACATCTTCGACCTCTTCGGTTCTTTTGT

12841   TTCTCACTCTAGAGCCTCCAGAAGGAATGCAGCTCTGCTGACACCTTGATTTGGAACTTC
12841   AAGAGTGAGATCTCGGAGGTCTTCCTTACGTCGAGACGACTGTGGAACTAAACCTTGAAG

12901   CAGAACCATAAGATAATAATTTTGTGTAGTTTTGAGGCTGGGCTCATGCCTGTAATTCCA
12901   GTCTTGGTATTCTATTATTAAAACACATCAAAACTCCGACCCGAGTACGGACATTAAGGT

12961   GCACTTTGGGAGGCCAAGGTGGGTGGATCACTTGAGGTCAGGAGTTTGAGACTAGCCTGG
12961   CGTGAAACCCTCCGGTTCCACCCACCTAGTGAACTCCAGTCCTCAAACTCTGATCGGACC
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FIGURE 4 (cont'd)

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13021  CCAACATGGTGAAACCCTGTATGTACTAAATATACAAAAATTAGCCAGGTGTGGTGGTGC
13021  GGTTGTACCACTTTGGGACATACATGATTTATATGTTTTTAATCGGTCCACACCACCACG

13081  ACGCCTATAGACCCAACTACTTGGGAAGCTGGGGCAGGAGAATCACTTGAACCCGGGAGG
13081  TGCGGATATCTGGGTTGATGAACCCTTCGACCCCGTCCTCTTAGTGAACTTGGGCCCTCC

13141  TAGAGATTGCAGTAAGCTAAGATTGTGCCACTGCACTCCAGCCTGGGCTACAGCGTGAGA
13141  ATCTCTAACGTCATTCGATTCTAACACGGTGACGTGAGGTCGGACCCGATGTCGCACTCT

13201  CTTCGTCAGAAAAAAAGAATAATTTTGTATAATTTCAGGCCACAAAGTCTGCAGTCATCT
13201  GAAGCAGTCTTTTTTTCTTATTAAAACATATTAAAGTCCGGTGTTTCAGACGTCAGTAGA

13261  GTTACAACAGCAGTAGTACACGAATACAGATTTTGGTACCTGGAAATGGTGTGCTACTGT
13261  CAATGTTGTCGTCATCATGTGCTTATGTCTAAAACCATGGACCTTTACCACACGATGACA

13321  AACAGATACCTAAACAATGTGGAAGTGGCTTTTGAATTGGGTGTTGGGCAGCATGTGGAA
13321  TTGTCTATGGATTTGTTACACCTTCACCGAAAACTTAACCCACAACCCGTCGTACACCTT

13381  GAATTTTGAGAAGCATGATAGGAAAAGCCTAGCTTGCCTTAGAAAGACTGTTAGTAGAAG
13381  CTTAAAACTCTTCGTACTATCCTTTTCGGATCGAACGGAATCTTTCTGACAATCATCTTC

13441  TAGGGATGTTAAAGGCGCTGCTGGTGAGGACTTGGAAGTGAAGAGCATGGTAAAGAAAAT
13441  ATCCCTACAATTTCCGCGACGACCACTCCTGAACCTTCACTTCTCGTACCATTTCTTTTA

13501  GTGTTTCATTTTAGAGAATATCAAAGTCATTGTAGAAGGTTGGCAGAAGTGTAGGTTTTC
13501  CACAAAGTAAAATCTCTTATAGTTTCAGTAACATCTTCCAACCGTCTTCACATCCAAAAG

13561  ATAATGTGTTGTTGGTGAGGGCTGAGAAAGAAATGAGGACCATGTTTAGGGAAACTGGAG
13561  TATTACACAACAACCACTCCCGACTCTTTCTTTACTCCTGGTACAAATCCCTTTGACCTC

13621  GAAAAAGATCCTTGTCATACAGTGGAATGAAACTGTGGAATTGTGTCTTACAGTTATATG
13621  CTTTTTCTAGGAACAGTATGTCACCTTACTTTGACACCTTAACACAGAATGTCAATATAC

13681  GGAAGCAGAATTTGTTTGAACTTGGATATTTGGCTTAGCTTTCCAAGTAAAGTATTGAAG
13681  CCTTCGTCTTAAACAAACTTGAACCTATAAACCGAATCGAAAGGTTCATTTCATAACTTC

13741  GTGTAGCCTGGTTTTCTCTTGCTGTTTTATAGTAAAATGCCCGAGAAAAAGGGATAAATT
13741  CACATCGGACCAAAAGAGAACGACAAAATATCATTTTACGGGCTCTTTTTCCCTATTTAA

13801  GAGGTAGGAACTGTTAAGAAAAAGGAACAAAGACATGATGACTTGGGAAATTCTCAGGAT
13801  CTCCATCCTTGACAATTCTTTTTCCTTGTTTCTGTACTACTGAACCCTTTAAGAGTCCTA

13861  ACCTGGTTTGTAAAAGATGCTAGAATTAGAAGATTCATTGTCAGGAAAGTGTGCTCTGGA
13861  TGGACCAAACATTTTCTACGATCTTAATCTTCTAAGTAACAGTCCTTTCACACGAGACCT

13921  GAGGAAGCCAAGGGTGAGTTCCTTGTGGCGTAGGTTAGGGGCTGTGGCAGGGATGCAGGG
13921  CTCCTTCGGTTCCCACTCAAGGAACACCGCATCCAATCCCCGACACCGTCCCTACGTCCC

13981  AAGAGATGATGGTGACTTGGACTAGGGGTCTGACGGGGTATGGGAAAATAGAGAGGAATG
13981  TTCTCTACTACCACTGAACCTGATCCCCAGACTGCCCCATACCCTTTTATCTCTCCTTAC

14041  AGTTGATTCTGTTGGGACTTTGTATTGAGTTCCTTGATTCCATAAGTGGAAACACATGTA
14041  TCAACTAAGACAACCCTGAAACATAACTCAAGGAACTAAGGTATTCACCTTTGTGTACAT

14101  GAGCTCTCTTTCCTGGCCACCTAAGCTCTCTGACCATATCCCTGACTCTCTCCAGAATGC
14101  CTCGAGAGAAAGGACCGGTGGATTCGAGAGACTGGTATAGGGACTGAGAGAGGTCTTACG

14161  CTTGGCTTCATGTCCACGTGAGGACAAATCATATTTTTCTGCATTTTGCGTGCTGGATTC
14161  GAACCGAAGTACAGGTGCACTCCTGTTTAGTATAAAAAGACGTAAAACGCACGACCTAAG

14221  CTCTCTGGACTAAAGATCCAATGAGAGGTGGTTTCTAGCTTTCTGCTCTTTCCCACAACA
14221  GAGAGACCTGATTTCTAGGTTACTCTCCACCAAAGATCGAAAGACGAGAAAGGGTGTTGT

14281  CTCCGTCAGTGAGTCTTCTGGATGTCCTATAGGCAACTCACTGGATCCACTTGGTCTGTG
14281  GAGGCAGTCACTCAGAAGACCTACAGGATATCCGTTGAGTGACCTAGGTGAACCAGACAC
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FIGURE 4 (cont'd)

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14341  GAAGAATCACTACCACATCCATTTCACCTTGGGCACAGACTAGAAGGTGAGGCAGTCATG
14341  CTTCTTAGTGATGGTGTAGGTAAAGTGGAACCCGTGTCTGATCTTCCACTCCGTCAGTAC

14401  TCCTGCAGTCACTGGGTAGCTTACAAGTGCTAATACAGCAATAGCTTAATTAGAGAGAGA
14401  AGGACGTCAGTGACCCATCGAATGTTCACGATTATGTCGTTATCGAATTAATCTCTCTCT

14461  GAGAAGAAGAAGAATGTTATGGAGCCTGTTTCTAGAGAGGAAACCACAATATCTTGATCA
14461  CTCTTCTTCTTCTTACAATACCTCGGACAAAGATCTCTCCTTTGGTGTTATAGAACTAGT

14521  AGAGACCCTAAAACTGGAAGAACCAGAGCAGCTGGTATCAAAATGTGGAAAAAACTGAGA
14521  TCTCTGGGATTTTGACCTTCTTGGTCTCGTCGACCATAGTTTTACACCTTTTTTGACTCT

14581  TGTGGCAAGTGGTACAACTGATAGCCAAGGAGGAAAAATTTGTATCCCCCTGTAATCCCA
14581  ACACCGTTCACCATGTTGACTATCGGTTCCTCCTTTTTAAACATAGGGGGACATTAGGGT

14641  GCACTTTGGGAGGCTGAAACAGGTGGATCACCTGAGGTCAGGAGTTCGAGACCAGCCTGG
14641  CGTGAAACCCTCCGACTTTGTCCACCTAGTGGACTCCAGTCCTCAAGCTCTGGTCGGACC

14701  CCAATATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCGTGGTGGTGT
14701  GGTTATACCACTTTGGGACAGAGATGATTTTTATGTTTTTAATCGACCCGCACCACCACA

14761  GCACCTATAGTCCCAGCTACTTGGGAGGCTGAGGCAGGAAAATTGCTTGAACCTGGGAGC
14761  CGTGGATATCAGGGTCGATGAACCCTCCGACTCCGTCCTTTTAACGAACTTGGACCCTCG

14821  AGAGGTTGCAGTGAGCCAAGATCGCACCACTGCACTCCAGCCTGGGTGACAAGAGTTAAA
14821  TCTCCAACGTCACTCGGTTCTAGCGTGGTGACGTGAGGTCGGACCCACTGTTCTCAATTT

14881  CTCTGTCTCAAAAAAATAAAAAGAAAAGTTTGTACCCTCTTCTTTTCTCTTGCCTCAGGA
14881  GAGACAGAGTTTTTTTATTTTTCTTTTCAAACATGGGAGAAGAAAAGAGAACGGAGTCCT

14941  TAACTGAGATTCTTATAATGCATTTATTGAACAAATATTTGAGGAGTACTCATTATGTAA
14941  ATTGACTCTAAGAATATTACGTAAATAACTTGTTTATAAACTCCTCATGAGTAATACATT

15001  GCATCAGACACTGCTCAAGGTCTTGAGGCTGTGAGGGTGTATTAGTCCGTTTTCACACTG
15001  CGTAGTCTGTGACGAGTTCCAGAACTCCGACACTCCCACATAATCAGGCAAAAGTGTGAC

15061  CTATAAAGAACTACCTGAGACTGGGTGATTTATAAAGAAAAGAGGTTTAACTGAATTACA
15061  GATATTTCTTGATGGACTCTGACCCACTAAATATTTCTTTTCTCCAAATTGACTTAATGT

15121  GTTCATCATGGCCAGAAAGGCCTCAGGAAACTTACAATCATGGCAGAAGGTGAAGAGGAA
15121  CAAGTAGTACCGGTCTTTCCGGAGTCCTTTGAATGTTAGTACCGTCTTCCACTTCTCCTT

15181  GCAAGGCACATCTTACATGGTGGCAGGAGACACAGTGAGAAGGGAGAAGTGCCACACTTT
15181  CGTTCCGTGTAGAATGTACCACCGTCCTCTGTGTCACTCTTCCCTCTTCACGGTGTGAAA

15241  TAAACCATCAGATCTTATGATGATATAGGAGTTAAGAAGAAATCACTTAGGTAGATAGTG
15241  ATTTGGTAGTCTAGAATACTACTATATCCTCAATTCTTCTTTAGTGAATCCATCTATCAC

15301  AGGGTACGGGAGTCCTTGGTAAGGCTTTTCTTTTAAATGAAAAGCAGCCCCACACATAGA
15301  TCCCATGCCCTCAGGAACCATTCCGAAAAGAAAATTTACTTTTCGTCGGGGTGTGTATCT

15361  CAAGCAAGCTGGGAGCTTGCACGGGTGAATGCCGGCAGAAACTAGGAACCAGACACGTTA
15361  GTTCGTTCGACCCTCGAACGTGCCCACTTACGGCCGTCTTTGATCCTTGGTCTGTGCAAT

15421  AGATGGCGGCTCCATTTTCCCTTCTCTGCCAGCCAAGTGTACAGTAAGGAGCAGACAAGC
15421  TCTACCGCCGAGGTAAAAGGGAAGAGACGGTCGGTTCACATGTCATTCCTCGTCTGTTCG

15481  TGGTGCCGGCCAAGAGGAGAATTCATGTGCATAATAAGATTAGGGTGGGGTGACCAGCCT
15481  ACCACGGCCGGTTCTCCTCTTAAGTACACGTATTATTCTAATCCCACCCCACTGGTCGGA

15541  TCCCAGTGCGCTATGTGAACATCATACCTGATTGAACCAATCTGTGAGCCCTATGTAAAT
15541  AGGGTCACGCGATACACTTGTAGTATGGACTAACTTGGTTAGACACTCGGGATACATTTA

15601  CAGACACCACCTCCTCAAGCCTGACTATAAAATCTGGTGCATTCGCCACCCGCCGGTGTT
15601  GTCTGTGGTGGAGGAGTTCGGACTGATATTTTAGACCACGTAAGCGGTGGGCGGCCACAA
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FIGURE 4 (cont'd)

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15661  TCCTCTCAGAAGTCCCCTCTCTCTCATTAGAGAGAGGGCTGTTTTCCTTTCTCCTTCTTC
15661  AGGAGAGTCTTCAGGGGAGAGAGAGTAATCTCTCTCCCGACAAAAGGAAAGAGGAAGAAG

15721  TGCCTATTAACCTGTGCTCCTAAACTCCCTGTGTGTGTCTGTTCTGAATTTTCCCGGCAT
15721  ACGGATAATTGGACACGAGGATTTGAGGGACACACACAGACAAGACTTAAAAGGGCCGTA

15781  GAGAGGATGAACCTGGGGTATATACCCCAGAAAACATAGCCACTTAAGTGAGAACTCACT
15781  CTCTCCTACTTGGACCCCATATATGGGGTCTTTTGTATCGGTGAATTCACTCTTGAGTGA

15841  CACTATTCACCCCCAAGATCCAATCACCTTCGACCAGGTTCCTCCCCTGGCGTGAGGGGA
15841  GTGATAAGTGGGGGTTCTAGGTTAGTGGAAGCTGGTCCAAGGAGGGGACCGCACTCCCCT

15901  TTAAAATTCCACATGAGGTTTGAGTAGGGACACAGAGCCAAACCAAACCATATCAGAGGG
15901  AATTTTAAGGTGTACTCCAAACTCATCCCTGTGTCTCGGTTTGGTTTGGTATAGTCTCCC

15961  TGAAGAGCAGGTAAAGTTGCAGCTCTCCTGCAACTTGCAGGGAAAGGCCATATAACACAT
15961  ACTTCTCGTCCATTTCAACGTCGAGAGGACGTTGAACGTCCCTTTCCGGTATATTGTGTA

16021  GGTTATGAGCACAAACTGGGACTGGACTGCAGGTGTGTGAGCCCCAGCTTTGCTATTGAG
16021  CCAATACTCGTGTTTGACCCTGACCTGACGTCCACACACTCGGGGTCGAAACGATAACTC

16081  TGACCACCAGCAAGTTATTAAACTGTGCCTCAGTTTTTTTCTTTATGAAATGGTGGTATT
16081  ACTGGTGGTCGTTCAATAATTTGACACGGAGTCAAAAAAACAAATACTTTACCACCATAA

16141  AGTACAACCCACCTCTCATGGATGATGTGAGGATTAAATAAAATAACATGTTGCCAGGCA
16141  TCATGTTGGGTGGAGAGTACCTACTACACTCCTAATTTATTTTATTGTACAACGGTCCGT

16201  CAGTGGTGCACACCTGTAATCTCGGCACATTGGGAGGCTGAGGCCCGAGGGTTACTTGAG
16201  GTCACCACGTGTGGACATTAGAGCCGTGTAACCCTCCGACTCCGGGCTCCCAATGAACTC

16261  GTTAGAAGCCTGAGACCTGCCTGGCCAACATAGCGAAACCTCATCTCTGCTTAAAATACA
16261  CAATCTTCGGACTCTGGACGGACCGGTTGTATCGCTTTGGAGTAGAGACGAATTTTATGT

16321  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGCCAGGCGTGGTGGCTCATGCTTGTAATC
16321  TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCGGTCCGCACCACCGAGTACGAACATTAG

16381  CCAGCACTTTGGGAGGCCGAGGCGGGTGGATCACAAGGTCAGGAGTTTGAGACCAGCCTG
16381  GGTCGTGAAACCCTCCGGCTCCGCCCACCTAGTGTTCCAGTCCTCAAACTCTGGTCGGAC

16441  GCCAATATGGTGAATCCCCGTCTCTACTAAAAATACAAAAATTAGCCAAGTGTGGTGGTG
16441  CGGTTATACCACTTAGGGGCAGAGATGATTTTTATGTTTTTAATCGGTTCACACCACCAC

16501  GGCACCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAG
16501  CCGTGGACATCAGGGTCGATGAGCCCTCCGACTCCGTCCTCTTAGTGAACTTGGACCCTC

16561  GCAGAAGTTGCAGTGAGCCGAGGTTGCGCCACTGCACTCCAGCCTGGGCGACGGAGCGAG
16561  CGTCTTCAACGTCACTCGGCTCCAACGCGGTGACGTGAGGTCGGACCCGCTGCCTCGCTC

16621  ACTCCATCTCAAAACAAAACAAAAAAACCAAAAAAATTAACCAGGCATGGTGGCACACAC
16621  TGAGGTAGAGTTTTGTTTTGTTTTTTTGGTTTTTTTAATTGGTCCGTACCACCGTGTGTG

16681  CTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATCACTTGAACCCAGGAGGTGGA
16681  GACATTAGGGTCGATGAGTCCTCCGACTCCGTCCTCTTAGTGAACTTGGGTCCTCCACCT

16741  GGTTGCAGTGAGTTAAGATTGTGCCACTGCACTCCAGCCTGTGCGATAGAAGGAGACAGT
16741  CCAACGTCACTCAATTCTAACACGGTGACGTGAGGTCGGACACGCTATCTTCCTCTGTCA

16801  CTGCAACAAAGATCCAAAAACAAATATAAAGCACTTATAACAGGGTCTGGTCTGAAATAA
16801  GACGTTGTTTCTAGGTTTTTGTTTATATTTCGTGAATATTGTCCCAGACCAGACTTTATT

16861  GTACTATGTAAGTACTGTAAGTATTAACTAATATTATTACAATTTATCCTCATATAGTAA
16861  CATGATACATTCATGACATTCATAATTGATTATAATAATGTTAAATAGGAGTATATCATT

16921  CATATCAAATATTTTCAGTCAGTGATGCAATATGAATAAAATGAAATGATGCAGTAGTGA
16921  GTATAGTTTATAAAAGTCAGTCACTACGTTATACTTATTTTACTTTACTACGTCATCACT
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FIGURE 4 (cont'd)

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16981   CACAACTGAGAGAAAGCTGGTACAAATTTATACTGACTGGTCAGGGAAAGCTTCACAGAA
16981   GTCTTGACTCTCTTTCGACCATGTTTAAATATGACTGACCAGTCCCTTTCGAAGTGTCTT

17041   AAGGTGAACTTTCAGCTGACACCTGAGTACCATGGTCTGGAGGTAAGAGTGTCCCATGCA
17041   TTCCACTTGAAAGTCGACTGTGGACTCATGGTACCAGACCTCCATTCTCACAGGGTACGT

17101   TATGGAACAGCAAATGAAACTTCCCAGAGCATAATCTGAGAGGGGAGATTTCAGGAGTGG
17101   ATACCTTGTCGTTTACTTTGAAGGGTCTCGTATTAGACTCTCCCCTCTAAAGTCCTCACC

17161   AGCCACATCATTGAAGTTCCTTAGTCCTGGTAAGTGTGGATTTTATTCTAAGTGTGGTGA
17161   TCGGTGTAGTAACTTCAAGGAATCAGGACCATTCACACCTAAAATAAGATTCACACCACT

17221   AATGCCCCTGAGAGGTTTTGAGTAGTAGATGGAATTCCATTTTTAAAAGTCACTGGTGAG
17221   TTACGGGGACTCTCCAAAACTCATCATCTACCTTAAGGTAAAAATTTTCAGTGACCACTC

17281   TCAAGTAGTGTACTATGGTTACATTTTTTTCCCCTTATACCTCATTTTGTTTTTCCTGCA
17281   AGTTCATCACATGATACCAATGTAAAAAAAGGGGAATATGGAGTAAAACAAAAAGGACGT

17341   GTTAATTCTTGCATTATTTCCTTTTATTTACTTACCTTACTATATATTTATTATGAATTC
17341   CAATTAAGAACGTAATAAAGGAAAATAAATGAATGGAATGATATATAAATAATACTTAAG

17401   TTTCCAATTCCCAACTTCCTGACAGCCTCTCAATGTAATTTTACTTAGGTTAAATGTATC
17401   AAAGGTTAAGGGTTGAAGGACTGTCGGAGAGTTACATTAAAATGAATCCAATTTACATAG

17461   TGACAGTTCATTTTCTTTTTTGTCTCTGTACTCTTTCTGCTACCATTCTCATTCTTGCAC
17461   ACTGTCAAGTAAAAGAAAAAACAGAGACATGAGAAAGACGATGGTAAGAGTAAGAACGTG

17521   TAATTTGTGCTGGTTTCTCTCTGAGCCAGCTGCACAGCTGCCTGCCTAAGACTTCCTCTT
17521   ATTAAACACGACCAAAGAGAGACTCGGTCGACGTGTCGACGGACGGATTCTGAAGGAGAA

17581   GGCATCTTTTACCCTCTCTCTGTGTTACATCCCCGGTTTTCTGAATCGTGTGGCGTTCTC
17581   CCGTAGAAAATGGGAGAGAGACACAATGTAGGGGCCAAAAGACTTAGCACACCGCAAGAG

17641   CTTTTTACTTTACTTCCTCATTTGTGTTGCACGTATGCTCTAGTTGTTTTTAGATAAAGA
17641   GAAAAATGAAATGAAGGAGTAAACACAACGTGCATACGAGATCAACAAAAATCTATTTCT

17701   GTGCATCAGAGGTAGATGTTTTGATTCCTTACATGCCTGACTTTTTGTTCTACTTTTGCT
17701   CACGTAGTCTCCATCTACAAAACTAAGGAATGTACGGACTGAAAAACAAGATGAAAACGA

17761   CTAGGTTAATACTTGATTTTGAATAATATCCTAGGTTAGAAATGATTTTTCGTCAGAATT
17761   GATCCAATTATGAACTAAAACTTATTATAGGATCCAATCTTTACTAAAAAGCAGTCTTAA

17821   TTAAGGGAATTGCTTTTCTGTTGTCTAGTTTCCTGTGTTACTGATAGGAAGTCCAAAGGG
17821   AATTCCCTTAACGAAAAGACAACAGATCAAAGGACACAATGACTATCCTTCAGGTTTCCC

17881   GCTCGTATTTCAGGTCCTTTTTATGTGTAACCTGTTTTTTGTTCCTTGAGGTATTCAGGG
17881   CGAGCATAAAGTCCAGGAAAAATACACATTGGACAAAAAACAAGGAACTCCATAAGTCCC

17941   TCTCTTTTTATTGCTAATTTGGGGAGCTTTATCATAACATGGGTCCTTAGTCATTCATCC
17941   AGAGAAAAATAACGATTAAACCCCTCGAAATAGTATTGTACCCAGGAATCAGTAAGTAGG

18001   TAGAAAATTTTCCTTTCCTATATCTTTGATGATTTCGTCTCCTCTGCTTTCCCTCTTTTC
18001   ATCTTTTAAAAGGAAAGGATATAGAAACTACTAAAGCAGAGGAGACGAAAGGGAGAAAAG

18061   TCATTCTTAAACTTCTATTTGTTTGACATTAGACCTCCTTGTTTGATCTTCTAATTTAAT
18061   AGTAAGAATTTGAAGATAAACAAACTGTAATCTGGAGGAACAAACTAGAAGATTAAATTA

18121   TTTTCTCTCCTAGTGTCCAATTTTTGAGGTGGGAGAAAGATCTCATCAATGTTATCTTTC
18121   AAAAGAGAGGATCACAGGTTAAAAACTCCACCCTCTTTCTAGAGTAGTTACAATAGAAAG

18181   AGCCTTTCCCCTGAATTTTAAAATTTTACTCTTCATATTTCTTCTGATTAATCCTTTAAA
18181   TCGGAAAGGGGACTTAAAATTTTAAAATGAGAAGTATAAAGAAGACTAATTAGGAAATTT

18241   AAAATAGCATCCTGGGCCAGGTGCAGTGGCTCACACCTGTAATCCCAGCACTTTGGAAGG
18241   TTTTATCGTAGGACCCGGTCCACGTCACCGAGTGTGGACATTAGGGTCGTGAAACCTTCC
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FIGURE 4 (cont'd)

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18301   CTGAGCGGGGAGTGGATCACCTGAGGTCAGGAGCTCAAGACCAGTCTGGCCAACATGATG
18301   GACTCGCCCCTCACCTAGTGGACTCCAGTCCTCGAGTTCTGGTCAGACCGGTTGTACTAC

18361   AAACCCTGTCTCTACTAAAAATACAAAAACTTAGCCAGGCGTGGTGGTGGGCTCCTGTAG
18361   TTTGGGACAGAGATGATTTTTATGTTTTTGAATCGGTCCGCACCACCACCCGAGGACATC

18421   TCCCAGCTACTTGGGAGGCTGAGACAGGAGAATCACCAGAACCTGGGAGGTGGAGGTTGT
18421   AGGGTCGATGAACCCTCCGACTCTGTCCTCTTAGTGGTCTTGGACCCTCCACCTCCAACA

18481   AGTGAGCTGAGATTGTGTGCCATTGTACTCCAACCTGGGTGACAGAGCAAGACTCTATCT
18481   TCACTCGACTCTAACACACGGTAACATGAGGTTGGACCCACTGTCTCGTTCTGAGATAGA

18541   CAAAAAAAAAAAAAAAAAAAAAAGGGCCCTGTTCCACTGAGGCTTCAGTGCGGAGCATGG
18541   GTTTTTTTTTTTTTTTTTTTTTTCCCGGGACAAGGTGACTCCGAAGTCACGCCTCGTACC

18601   AGGGATACTACCTCCAAATTCCAAACACGTTTGACACATCTAAAGAACCTTCTAAAGGAT
18601   TCCCTATGATGGAGGTTTAAGGTTTGTGCAAACTGTGTAGATTTCTTGGAAGATTTCCTA

18661   GACTAAACTAATTCTGCAAGCTTTAGCCTCTAACTTATCTCCAATTTATATTTAATAGAA
18661   CTGATTTGATTAAGACGTTCGAAATCGGAGATTGAATAGAGGTTAAATATAAATTATCTT

18721   GGCTGGAAATTGAACAGAAAGGAAATAAGATTATTTGGAAATAAAAAATTGTCAGCCAAG
18721   CCGACCTTTAACTTGTCTTTCCTTTATTCTAATAAACCTTTATTTTTTAACAGTCGGTTC

18781   CAAGGAGAGCTTGGCATTTCTGGAAACTTCTTTACCCTGGAAGAGGTAAAAAAGTGATTC
18781   GTTCCTCTCGAACCGTAAAGACCTTTGAAGAAATGGGACCTTCTCCATTTTTTCACTAAG

18841   TCCCATTCCCCCAACAGGGCATTCACTAAAAATTAAGTGAGAAATGCTTTGCCTAGAGGA
18841   AGGGTAAGGGGGTTGTCCCGTAAGTGATTTTTAATTCACTCTTTACGAAACGGATCTCCT

18901   TCTGTAGCTTGCGAACACTTGACTTGTGCCACTGGTGTACGGAACATAGCAGTGTCAGCT
18901   AGACATCGAACGCTTGTGAACTGAACACGGTGACCACATGCCTTGTATCGTCACAGTCGA

18961   CTGCCCTGGGACAGTCAAGGCTGGCTGGTGCTGCCTGTGGTTAGAGTCAAGAGAGGGGTC
18961   GACGGGACCCTGTCAGTTCCGACCGACCACGACGGACACCAATCTCAGTTCTCTCCCCAG

19021   TTCAGTGGGTGCAGTTTGCAGTTCCAGAGTTTAGTAGAGCAAAGACGTCATGAACTATGT
19021   AAGTCACCCACGTCAAACGTCAAGGTCTCAAATCATCTCGTTTCTGCAGTACTTGATACA

19081   GAACTCTGAGGAAAGGTGTCATAGAAACACCTCAAAAGGACACTGTCTAAGAAGGCTACT
19081   CTTGAGACTCCTTTCCACAGTATCTTTGTGGAGTTTTCCTGTGACAGATTCTTCCGATGA

19141   TGCTGGGGCAAGGAGACCCCAGGGGTCAGAGGCTGTGTAGGGAATAATGCCAGAGCTGGG
19141   ACGACCCCGTTCCTCTGGGGTCCCCAGTCTCCGACACATCCCTTATTACGGTCTCGACCC

19201   GTTGAAGGAGAATCCTTAGAGGTGAGACAGAATGTGCATCATTGCAGTGGGGCTGTGCAA
19201   CAACTTCCTCTTAGGAATCTCCACTCTGTCTTACACGTAGTAACGTCACCCCGACACGTT

19261   GGCAGTGGTCTCCACAGGAGGTGAGGACAAGGGGGAGGGGAGGTTGTGAAGAATCCGTAA
19261   CCGTCACCAGAGGTGTCCTCCACTCCTGTTCCCCCTCCCCTCCAACACTTCTTAGGCATT

19321   GTGACCATGATGCAATAGAAAGCCAGAATTTGGGCATTTGCCATAGGAGAGGGCCCCCAG
19321   CACTGGTACTACGTTATCTTTCGGTCTTAAACCCGTAAACGGTATCCTCTCCCGGGGGTC

19381   TGCCAGATTATAATGGTCACAGACAAATGAGATTTTTAACCATTTCCTCTAATTCATGGT
19381   ACGGTCTAATATTACCAGTGTCTGTTTACTCTAAAAATTGGTAAAGGAGATTAAGTACCA

19441   CCACACTTAACCCCGTGGGTCCTGGAAACAGCAGCTGGAGAATGGAGAGGAAAGTGATGT
19441   GGTGTGAATTGGGGCACCCAGGACCTTTGTCGTCGACCTCTTACCTCTCCTTTCACTACA

19501   GGGAGAGAGAAAACTTTCTTTACCCTTTTCATAACTGAGTTTATGAAGTAAACTGACAGT
19501   CCCTCTCTCTTTTGAAAGAAATGGCAAAACTATTGACTCAAATACTTCATTTGACTGTCA

19561   AGAAAGATAAATAGGAGAAAAGACATAAATTTATTTTGTGCGTACACATGGGAGTCCCAT
19561   TCTTTCTATTTATCCTCTTTTCTGTATTTAAATAAAACACGCATGTGTACCCTCAGGGTA
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FIGURE 4 (cont'd)

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19621  AAAATATGAGACTCAAAGAAAGGCCAGATGATTGAAGTTTATATAGTATTCCTGAGCTAC
19621  TTTTATACTCTGAGTTTCTTTCCGGTCTACTAACTTCAAATATATCATAAGGACTCGATG

19681  AGAAAAGGAATCAGGGCTTGGGGCTTATTGAGGGGAGGTGGTGACAGGTTATAAGAGGGT
19681  TCTTTTCCTTAGTCCCGAACCCCGAATAACTCCCCTCCACCACTGTCCAATATTCTCCCA

19741  GAGGAGAGGAAGTGTATAGCAAGCATAGGTTGTCTTGTTATGCAGATAAAAAGTCTCTCA
19741  CTCCTCTCCTTCACATATCGTTCGTATCCAACAGAACAATACGTCTATTTTTCAGAGAGT

19801  GGTGATAAAAGTTGTCTCAGAGTCCCCCATCAGAAGAATAGGTAATAGCCTGTGACAAGG
19801  CCACTATTTTCAACAGAGTCTCAGGGGGTAGTCTTCTTATCCATTATCGGACACTGTTCC

19861  TCTACCTGTCCAATCTTCTCCCTGGTGATAAAATCTTCCCTGGTTGATGAGATTCTTATC
19861  AGATGGACAGGTTAGAAGAGGGACCACTATTTTAGAAGGGACCAACTACTCTAAGAATAG

19921  AAAGTTTTTTTCTTTATAGATATAAATTTTGTTTACAAAAAGACAGTTTTTCAGAGCTAC
19921  TTTCAAAAAAAGAAATATCTATATTTAAAACAAATGTTTTTCTGTCAAAAAGTCTCGATG

19981  TCCTGTGTCTACAGTGTCTCAGAATAACTAACTGGAAATACATCAAATAAGCATATCCTG
19981  AGGACACAGATGTCACAGAGTCTTATTGATTGACCTTTATGTAGTTTATTCGTATAGGAC

20041  ATGTGGCATATTCTGGTCATATTTTGGGATGGTGCGTCCTGAGCTCCAATGCTGAAAAAA
20041  TACACCGTATAAGACCAGTATAAAACCCTACCACGCAGGACTCGAGGTTACGACTTTTTT

20101  CAGGAACCCCATTTCTGTTGGATGTGCCAACCTAAAATAATCAAAAGGGTCAGAATCTAG
20101  GTCCTTGGGGTAAAGACAACCTACACGGTTGGATTTTATTAGTTTTCCCAGTCTTAGATC

20161  TTTAAAGATACTTTATTCAAGTGCAAAGTTTAAGGACAGTGCTAGGGAAACACGGATCCC
20161  AAATTTCTATGAAATAAGTTCACGTTTCAAATTCCTGTCACGATCCCTTTGTGCCTAGGG

20221  AAAGAATGGAAGTCAGCGTTCTGAACTTTAGAAGTTTGGGATTGTTTATAGAGAGAGAGT
20221  TTTCTTACCTTCAGTCGCAAGACTTGAAATCTTCAAACCCTAACAAATATCTCTCTCTCA

20281  TTAGGGAAGCTTAACAGAATTTCAACATCTTTCTGTGTAAGGCTTAATGCCTAGTTACAA
20281  AATCCCTTCGAATTGTCTTAAAGTTGTAGAAAGACACATTCCGAATTACGGATCAATGTT

20341  TGATCTGATTAGTCAAGGTGGTCACTTTCATTTGAGAAAGGCATATTTAACATTTCACGG
20341  ACTAGACTAATCAGTTCCACCAGTGAAAGTAAACTCTTTCCGTATAAATTGTAAAGTGCC

20401  GCTGGGAGCGGTGGTTCATGCCTGTAATCTCAGCACTTTGGGAGGCCGAGGCGGGCAGAT
20401  CGACCCTCGCCACCAAGTACGGACATTAGAGTCGTGAAACCCTCCGGCTCCGCCCGTCTA

20461  CATCTGAGGTCAGGAGTTCGAGGCCAGCCTGGCCAATATGGGGAAACCCCTTCTCTACTA
20461  GTAGACTCCAGTCCTCAAGCTCCGGTCGGACCGGTTATACCCCTTTGGGGAAGAGATGAT

20521  AAAATACAATACAATAAAATAAAATAAAATAAAAAAAATTAGCCGGGCATGGTGCACGTG
20521  TTTTATGTTATGTTATTTTATTTTATTTTATTTTTTTTAATCGGCCCGTACCACGTGCAC

20581  CCTGTAATCCCAGCTACTTGGGAAGCTGAGGCAGGAGAATTGCTTGAACCTGGGAGGCAG
20581  GGACATTAGGGTCGATGAACCCTTCGACTCCGTCCTCTTAACGAACTTGGACCCTCCGTC

20641  AGGTTGTGGTGAGCTGAGATTGCACCATTGCACTCCAGCCTGGGCAACAAGAATGAAACT
20641  TCCAACACCACTCGACTCTAACGTGGTAACGTGAGGTCGGACCCGTTGTTCTTACTTTGA

20701  CCATCTCAAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAAACATT
20701  GGTAGAGTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTTGTAA

20761  TCACACTGAAGGTGTAACAGTCATGGGTTTGTATTTTCGTTTTTCTTGGTTTTTTTTTTT
20761  AGTGTGACTTCCACATTGTCAGTACCCAAACATAAAAGCAAAAAGAACCAAAAAAAAAAA

20821  TTTTTTTGAGACTGTCTCGCTCTGTATTGCAGGCTGGCATGGCACAATCACAGCTCGCTG
20821  AAAAAAACTCTGACAGAGCGAGACATAACGTCCGACCGTACCGTGTTAGTGTCGAGCGAC

20881  CAGCTTCGATTTTGTGGGCTCAAGTGATCCTACCACCTCAGTCTCCCGACTAGCTGGGAC
20881  GTCGAAGCTAAAACACCCGAGTTCACTAGGATGGTGGAGTCAGAGGGCTGATCGACCCTG
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FIGURE 4 (cont'd)

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20941  CACAGTCATGTGCCACCACACCCGGCTAATTTATTTTTTATTTCTTATAGAGACCAGATC
20941  GTGTCAGTACACGGTGGTGTGGGCCGATTAAATAAAAAATAAAGAATATCTCTGGTCTAG

21001  CCCCTTTTGCCCAGGCTGGTCTCAAACTCCTGGACTCAAACAATTCTCCTGCCTCAGCCT
21001  GGGGAAAACGGGTCCGACCAGAGTTTGAGGACCTGAGTTTGTTAAGAGGACGGAGTCGGA

21061  CCCAAAGTGCCTGGATTACAGGCATGGGCTACTGTGCTCATCCCATGGGGTCTTTTGTGC
21061  GGGTTTCACGGACCTAATGTCCGTACCCGATGACACGAGTAGGGTACCCCAGAAAACACG

21121  CAACTGGTGTGAGTTAGGTACAGGACAATAAAGGAGGCAGTTAATCCATTAATCCATAAC
21121  GTTGACCACACTCAATCCATGTCCTGTTATTTCCTCCGTCAATTAGGTAATTAGGTATTG

21181  AAAGATCAGTGAAGGGGGAAGGTCTGGTCTCTGGTCTCTCCTAGTCATTTACAGAACTAG
21181  TTTCTAGTCACTTCCCCCTTCCAGACCAGAGACCAGAGAGGATCAGTAAATGTCTTGATC

21241  AACGATGAGAAGAGAGTGAATCTATAACCTAAGAAGCAGAATTGCAAACATGCTATGTGA
21241  TTGCTACTCTTCTCTCACTTAGATATTGGATTCTTCGTCTTAACGTTTGTACGATACACT

21301  CTCAGTTTCCAGTACTTAACTTCTCCCTTGGCATAATAAATAATTTTAGAGAGTTTTAAG
21301  GAGTCAAAGGTCATGAATTGAAGAGGGAACCGTATTATTTATTAAAATCTCTCAAAATTC

21361  AATTTTGTTTTCTTTTACAGATGTTAACAACCTCAGCTTGCTGGGGGCTGGTGGTGGTGG
21361  TTAAAACAAAAGAAAATGTCTACAATTGTTGGAGTCGAACGACCCCCGACCACCACCACC

21421  CTGCTCAGACAGTAAAGCATTGAATGCAATGTGAGGTCAAAGTTTTATTACAGATCATAC
21421  GACGAGTCTGTCATTTCGTAACTTACGTTACACTCCAGTTTCAAAATAATGTCTAGTATG

21481  CGGTCTTTTAAGTACTTGCAGCAAGATTTTCCTAATACTTAAAAGTGACTGGAAACTCAA
21481  GCCAGAAAATTCATGAACGTCGTTCTAAAAGGATTATGAATTTTCACTGACCTTTGAGTT

21541  TAGGATCAGTGTGATCTTCTCCAGATAGGGATGGTAGATTTTTGAAAGTGGGTGTGAAGG
21541  ATCCTAGTCACACTAGAAGAGGTCTATCCCTACCATCTAAAAACTTTCACCCACACTTCC

21601  GCAGTAATGAGAGAAAAATAAAACTATTTCTGGTTGTACTCTCCCAAGTCAAGGTCATTC
21601  CGTCATTACTCTCTTTTTATTTTGATAAAGACCAACATGAGAGGGTTCAGTTCCAGTAAG

21661  AATGAATGGTTATATAGATTTGCATCAAAAGTCCCTGTTTTCAGCCTCACCTTTGGAAAC
21661  TTACTTACCAATATATCTAAACGTAGTTTTCAGGGACAAAAGTCGGAGTGGAAACCTTTG

21721  ACCTGGATTCTCTATTCTGAGACTTTCTGAGATGAGGGAAAGGTGGCTTCTCATCAGTAT
21721  TGGACCTAAGAGATAAGACTCTGAAAGACTCTACTCCCTTTCCACCGAAGAGTAGTCATA

21781  CTCCTTCTTTGTGCAATACAGTTTCAGTTCTTTCTAATCTACAGAGTTAGTTCCTTCTCT
21781  GAGGAAGAAACACGTTATGTCAAAGTCAAGAAAGATTAGATGTCTCAATCAAGGAAGAGA

21841  ACTGTCAGCTTTCTACCTTCCAAAATGTGTTAATGTCACTCATTATCATGTTTCCCATTC
21841  TGACAGTCGAAAGATGGAAGGTTTTACACAATTACAGTGAGTAATAGTACAAAGGGTAAG

21901  TCTTTCCCTTATGGTTTAAACTTTAAAAGACAATGGTATTTGTTTAAGTGAATATCTAAA
21901  AGAAAGGGAATACCAAATTTGAAATTTTCTGTTACCATAAACAAATTCACTTATAGATTT

21961  AAGATGTGGAGAAAGATTCATGTGTTCAGTCTACCATGTTTAATTGGAGTCACTGGTAGA
21961  TTCTACACCTCTTTCTAAGTACACAAGTCAGATGGTACAAATTAACCTCAGTGACCATCT

22021  TTTTTAAGGAAAAATAACATTCTAGGTTTTTCCAGTATTGCTATGTAGCTTGTCTATGTA
22021  AAAAATTCCTTTTTATTGTAAGATCCAAAAAGGTCATAACGATACATCGAACAGATACAT

22081  GATCACCTTGCATTCTTCTGTTTCTCTCTTATAACTTGATTTTTTTCTTTTCTTTTCTTT
22081  CTAGTGGAACGTAAGAAGACAAAGAGAGAATATTGAACTAAAAAAAGAAAAGAAAAGAAA

22141  TCTTTTTTTTTCGAGACAGAGTCTCACTTTGTCACCCAGGCTGGAGTACAGTGGCACAAT
22141  AGAAAAAAAAAGCTCTGTCTCAGAGTGAAACAGTGGGTCCGACCTCATGTCACCGTGTTA

22201  CTCGTCTCATTGCTGCCTCCATCTCCTGGGTTCAAGTGATTCTCCCACCTCACCTTCCCA
22201  GAGCAGAGTAACGACGGAGGTAGAGGACCCAAGTTCACTAAGAGGGTGGAGTGGAAGGGT
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FIGURE 4 (cont'd)

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22261   AATAGCCGGGATTACAGACATCTTATAACTTGATTTTTACTCATTTCATTATCATCCAAG
22261   TTATCGGCCCTAATGTCTGTAGAATATTGAACTAAAAATGAGTAAAGTAATAGTAGGTTC

22321   AGATGAAATTTAACTCAAAGCAAATGACTATTGTTTCAAATACAAATCTTAATCAGGGAG
22321   TCTACTTTAAATTGAGTTTCGTTTACTGATAACAAAGTTTATGTTTAGAATTAGTCCCTC

22381   AAAAGATTATAACTTATAGTTGAACTGGGGTTTGGAGATTATATGTGTTTTTTAAAATTA
22381   TTTTCTAATATTGAATATCAACTTGACCCCAAACCTCTAATATACACAAAAAATTTTAAT

22441   TTCTGTCCCACATGTAACATACAAGTGAGGATTTTAAAAATTTGTCTGCAGTTTTTTTTT
22441   AAGACAGGGTGTACATTGTATGTTCACTCCTAAAATTTTTAAACAGACGTCAAAAAAAAA

22501   TTTTAATTGATCATTCTTGGGTGTTTCTCGCAGAGGGGGATTTGGCAGGGTCATAGGACA
22501   AAAATTAACTAGTAAGAACCCACAAAGAGCGTCTCCCCCTAAACCGTCCCAGTATCCTGT

22561   ATAGTGGAGGGAAGGTCAGCAGATAAACGAGTGAACAAAGGTCTCTGGTTTTCCTAGGCA
22561   TATCACCTCCCTTCCAGTCGTCTATTTGCTCACTTGTTTCCAGAGACCAAAAGGATCCGT

22621   GAGGACCCTGCGGCCTTCCGCAGTGTTTGTGTCCCTGGGTACTTGAGATTAGGGAGTGGT
22621   CTCCTGGGACGCCGGAAGGCGTCACAAACACAGGGACCCATGAACTCTAATCCCTCACCA

22681   GATGACTCTTAAAGAGCATGCTGCCTTCAAGCATCTGTTTAACAAAGCACATCTTGCACC
22681   CTACTGAGAATTTCTCGTACGACGGAAGTTCGTAGACAAATTGTTTCGTGTAGAACGTGG

22741   GCCCTTAATCCATTTAACCCTCAGTGGCACACAGCACATGTTTCAGAGAGCACCGGCTTGG
22741   CGGGAATTAGGTAAATTGGGACTCACCTGTGTCGTGTACAAAGTCTCTCGTGGCCCAACC

22801   GGGTAAGGTCATAGATCAACAGCATCCCAAGGCAGAAGAATTTTTCTTAGTACAGAACAA
22801   CCCATTCCAGTATCTAGTTGTCGTAGGGTTCCGTCTTCTTAAAAAGAATCATGTCTTGTT

22861   AATGGAGTCTCCTATGTCTACTTCTTTCTACACAGACACAGCAACAATCTGATTTCTCTA
22861   TTACCTCAGAGGATACAGATGAAGAAAGATGTGTCTGTGTCGTTGTTAGACTAAAGAGAT

22921   TCTTTTCCCCACATTTCCCCCTTTTCTATTCCACAAAACCGCCATTGTCATCATGGCCCG
22921   AGAAAAGGGGTGTAAAGGGGGAAAAGATAAGGTGTTTTGGCGGTAACAGTAGTACCGGGC

22981   TTCTCAATGAGCTGTTGGGTACACCTCCCAGACGGGGTGGCGGCCGGGCAGAGGGGCTCC
22981   AAGAGTTACTCGACAACCCATGTGGAGGGTCTGCCCCACCGCCGGCCCGTCTCCCCGAGG

23041   TCACTTCCCAGAAGGGGTGGCCTGGCAGAGGCACCCCCAACCTCCCTCCCGGACGGGGCG
23041   AGTGAAGGGTCTTCCCCACCGGACCGTCTCCGTGGGGGTTGGAGGGAGGGCCTGCCCCGC

23101   GCTGGCCAGGCGGGGGCTGCCCCCAACTTCCCAGACGGGGTGGCTGCTGGGCGGAGGGGC
23101   CGACCGGTCCGCCCCCGACGGGGGTTGAAGGGTCTGCCCCACCGACGACCCGCCTCCCCG

23161   TCTTTACTTCTCAGATGGGGCGGCTGCCGGGTGGAGGGGCTCCTCACTTCTCAGACGGGG
23161   AGAAATGAAGAGTCTACCCCGCCGACGGCCCACCTCCCCGAGGAGTGAAGAGTCTGCCCC

23221   CGGCCGGGCAGAGGCGCTCCTCACCTCCCAGACGGGGCAGCAGGGCAGAGGCGCTCCCCA
23221   GCCGGCCCGTCTCCGCGAGGAGTGGAGGGTCTGCCCCGTCGTCCCGTCTCCGCGAGGGGT

23281   CATCTCAGACGATGGGCGGCCGGGCAGAGACGCTCCTCACTTCCTAGACGGGATGGCAGC
23281   GTAGAGTCTGCTACCCGCCGGCCCGTCTCTGCGAGGAGTGAAGGATCTGCCCTACCGTCG

23341   CGGGAAGAGGCGCTCCTCACTTCCCAGACTGGGCAGCCAGGCAGAGGGGCTCCTCACATC
23341   GCCCTTCTCCGCGAGGAGTGAAGGGTCTGACCCGTCGGTCCGTCTCCCCGAGGAGTGTAG

23401   CCAGACGATGGGCAGCCAGGCAGAGAAGCTCCTCACTTCCCAGATGGGGTGGCGGCCGGG
23401   GGTCTGCTACCCGTCGGTCCGTCTCTTCGAGGAGTGAAGGGTCTACCCCACCGCCGGCCC

23461   CAGAGGCTGCAATCTCGGCACTTTGGGAGGCCAAGGCAGGCGGCTGGGAGGTGGAGGTTG
23461   GTCTCCGACGTTAGAGCCGTGAAACCCTCCGGTTCCGTCCGCCGACCCTCCACCTCCAAC

23521   TAGCGAGCCGAGATCACGCCACTACACTCCAGCTTGGGCAACATTGAGCACTGAGTGAAC
23521   ATCGCTCGGCTCTAGTGCGGTGATGTGAGGTCGAACCCGTTGTAACTCGTGACTCACTTG
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FIGURE 4 (cont'd)

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23581  GAGACTCCGTCTGCAATCCCGGCACCTCGGGAGGCCGAGGCTGGCAGATCACTCCCGGTT
23581  CTCTGAGGCAGACGTTAGGGCCGTGGAGCCCTCCGGCTCCGACCGTCTAGTGAGGGCCAA

23641  AGGAGCTGGAGACCAGCCCGGCCAACACAGCGAAACCCCGTCTCCACCAAAAAAATACGA
23641  TCCTCGACCTCTGGTCGGGCCGGTTGTGTCGCTTTGGGGCAGAGGTGGTTTTTTTATGCT

23701  AAACCAGTCAGGCATGGTGGCGCGCGCCTGCAATCACAGGCACTCGGCAGGCTGAGGCAG
23701  TTTGGTCAGTCCGTACCACCGCGCGCGGACGTTAGTGTCCGTGAGCCGTCCGACTCCGTC

23761  GACAATCAGGCAGGGAGGTTGCAGTGAGCAGAGATGGCAGCAGTACAGTCCAGCTTCGGC
23761  CTGTTAGTCCGTCCCTCCAACGTCACTCGTCTCTACCGTCGTCATGTCAGGTCGAAGCCG

23821  TTGGCATCAGAGGGAGACCGTGGAAAGAGAGGGAGAGGGAGACCGTGGGGAGAGGGAGAG
23821  AACCGTAGTCTCCCTCTGGCACCTTTCTCTCCCTCTCCCTCTGGCACCCCTCTCCCTCTC

23881  GGGGAGGGGGAGCTGCAATTTTTTATTTAGCAATTTCCAAACCTATTGTGTTAGGCAGGG
23881  CCCCTCCCCCTCGACGTTAAAAAATAAATCGTTAAAGGTTTGGATAACACAATCCGTCCC

23941  TTCTCCAGGGAAACAGAACCAATAGGGCATATCTATATCTATATTTATATCTTTATCTAT
23941  AAGAGGTCCCTTTGTCTTGGTTATCCCGTATAGATATAGATATAAATATAGAAATAGATA

24001  ATCTATATCTATAATCTTTCTATCTATCTATCAAGAGATCGAGAGAGAGAGATTTATTTT
24001  TAGATATAGATATTAGAAAGATAGATAGATAGTTCTCTAGCTCTCTCTCTCTAAATAAAA

24061  AAGGAATTGGTTCATGTGATTGTGGGAGCTGGCAAGTCTGAAATCCATAGGGCAAGTTGG
24061  TTCCTTAACCAAGTACACTAACACCCTCGACCGTTCAGACTTTAGGTATCCCGTTCAACC

24121  TCAGCTGGAAATTCTGGTAAGAGTTGATGTTGCAGTCGTGAGTCTGAAATTTGCAGGGCA
24121  AGTCGACCTTTAAGACCATTCTCAACTACAACGTCAGCACTCAGACTTTAAACGTCCCGT

24181  GGTCAGGTACAGTATCTATTGCAATTGCAGTCCTGAGGCCAAATTCCTTCTTCAGGAAAC
24181  CCAGTCCATGTCATAGATAACGTTAACGTCAGGACTCCGGTTTAAGGAAGAAGTCCTTTG

24241  CTCCGTCTTTTTTGCTGTTAAGGCCTTCAACTAATTGGATGAAGCCCTCCCACATTGAGG
24241  GAGGCAGAAAAAACGACAATTCCGGAAGTTGATTAACCTACTTCGGGAGGGTGTAACTCC

24301  GCAATCTGCTTTACTCAAAGTCTGCTGATTTAAATGCTAATCACATCTAAAAAATACTTT
24301  CGTTAGACGAAATGAGTTTCAGACGACTAAATTTACCATTAGTGTAGATTTTTTATGAAA

24361  CACAGCAACATTTGAACTTGTCTTGTCTAAGCAATTGGGCACTATAGCTTAGCCAAGCAG
24361  GTGTCGTTGTAAACTTGAACACAACAGATTCGTTAACCCGTGATATCGAATCGGTTCGTC

24421  ACACATGAAATTAACCATCACTCTGTAGAGATGAAAGAACTACTGTTTCAAAAAACAACT
24421  TGTGTACTTTAATTGGTAGTGAGACATCTCTACTTTCTTGATGACAAAGTTTTTTGTTGA

24481  GTTTTTGAATCCGTCATTTATCAACGGATTCACCCAATGGTTAACCTTTCTATATGCTTT
24481  CAAAAACTTAGGCAGTAAATAGTTGCCTAAGTGGGTTACCAATTGGAAAGATATACGAAA

24541  CTCTTTCTCCCAAGTACTGAATCATATGAAAATAAATTATGGTTGTGATATTTCCTATCT
24541  GAGAAAGAGGGTTCATGACTTAGTATACTTTTATTTAATACCAACACTATAAAGGATAGA

24601  AAATACTTCATATGGGACATTCTCCTACATAGCACACCTAAGAAGATTAGTATTAATTCA
24601  TTTATGAAGTATACCCTGTAAGAGGATGTATCGTGTGGATTCTTCTAATCATAATTAAGT

24661  GAGAGATCATGTCATATCTGGTTCATATATAATTTTCCCTAGCTGACCTCAAAATGTGTT
24661  CTCTCTAGTACAGTATAGACCAAGTATATATTAAAAGGGATCGACTGGAGTTTTACACAA

24721  TGTTTTGTTTACATATTACTCTTTATAGTTATGTTTCTTTTAATACGGATCAATATTTGT
24721  ACAAAACAAATGTATAATGAGAAATATCAATACAAAGAAAATTATGCCTAGTTATAAACA

24781  GTGTTTTTGCTGCTATTTTTTTTAATGACATTGTTTTGAATAATTCAGGCTCATTGGCTA
24781  CACAAAAACGACGATAAAAAAAATTACTGTAACAAAACTTATTAAGTCCGAGTAACCGAT

24841  TTTCACATCCTGAATTTCTCTAATTTTATCTTTATGATTAGAGCCAGGCTCTAATTCTTG
24841  AAAGTGTAGGACTTAAAGAGATTAAAATAGAAATACTAATCTCGGTCCGAGATTAAGAAC
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FIGURE 4 (cont'd)

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24901  GCAAGAATAACACTGAAGTGAGGTTGTGTACTCCTAATTGCCCTGCATCAAAGACACATG
24901  CGTTCTTATTGTGACTTCACTCCAACACATGAGGATTAACGGGACGTAGTTTCTGTGTAC

24961  ATATGCATTGGTTCCTGCATTAGTCATGTTAAGTTTGATTAGCTGGTGAAGGTGGTCGCC
24961  TATACGTAACCAAGGACGTAATCAGTACAATTCAAACTAATCGACCACTTCCACCAGCGG

25021  ACCATTTCTCACTCTTGTAAAGGGACATTTTCTCCTTTTAAATTAATATGTAATTTGTGG
25021  TGGTAAAGAGTGAGAACATTTCCCTGTAAAAGAGGAAAATTTAATTATACATTAAACACC

25081  CACAAGACTTTGAGACTGTGTAAATATCCCATTCTCTGACAACCTTTCTTCTGATGACTT
25081  GTGTTCTGAAACTCTGACACATTTATAGGGTAAGAGACTGTTGGAAAGAAGACTACTGAA

25141  TAGCATTAACTGATCTAATTATATCATTCTTGGCATTGAGTAGCATTCTTGTGTAAAGAA
25141  ATCGTAATTGACTAGATTAATATAGTAAGAACCGTAACTCATCGTAAGAACACATTTCTT

25201  GGGGTTCTCTTTCTCTCCCTCCTCTCATTATAATTTGTTACTGTTATTTTCTTACAAGTT
25201  CCCCAAGAGAAAGAGAGGGAGGAGAGTAATATTAAACAATGACAATAAAAGAATGTTCAA

25261  ACTAAGAATTACTCAAAGGCAGTATTTTTCAATAAATCATTGGTAATTTATGGTCTTCTC
25261  TGATTCTTAATGAGTTTCCGTCATAAAAAGTTATTTAGTAACCATTAAATACCAGAAGAG

25321  ACTCTAGAAAAGGGAGGATGGGTCAGAAAGCTGAGGGGAAAAAAAGGGAGGAAACGAGAA
25321  TGAGATCTTTTCCCTCCTACCCAGTCTTTCGACTCCCCTTTTTTTCCCTCCTTTGCTCTT

25381  TGTATATTATCGACATAATCGGTTGAAAATGTCTAGTGCTGTAATTATGCCATCATGCAG
25381  ACATATAATAGCTGTATTAGCCAACTTTTACAGATCACGACATTAATACGGTAGTACGTC

25441  ATTAAAAAGCCACCTGTGAAAAATCAACTTGTATTGTTTTGTTTTGTTTGATTTTTAATA
25441  TAATTTTTCGGTGGACACTTTTTAGTTGAACATAACAAAACAAAACAAACTAAAAATTAT

25501  AATCCTTATAGTGTATGAATAAAAATTAAATTAATTGATCAGTATCTTCACTAATGGCAG
25501  TTAGGAATATCACATACTTATTTTTAATTTAATTAACTAGTCATAGAAGTGATTACCGTC

25561  AGAAGGGGATGGACTGAGCAGATTCTGCTTTTCACTCTGATATTTGTTAATTGCCCTGTG
25561  TCTTCCCCTACCTGACTCGTCTAAGACGAAAAGTGAGACTATAAACAATTAACGGGACAC

25621  TGGTCTGAAGACCTGGGTTCTAGTACCAGCTCTCCCTCTGCAGACAGGTGTGTTACTTTG
25621  ACCAGACTTCTGGACCCAAGATCATGGTCGAGAGGGAGACGTCTGTCCACACAATGAAAC

25681  GTCAAGGCAATCAATCTTCTTGATACTCAGTTTGGTTCTCTCTGATTTGAGCATAAGAAA
25681  CAGTTCCGTTAGTTAGAAGAACTATGAGTCAAACCAAGAGAGACTAAACTCGTATTCTTT

25741  TATACTTGAAGGCCGGGCATGGTGGCTTATGCCTGTAATTCCAGCACTATGGGAAGCCGA
25741  ATATGAACTTCCGGCCCGTACCACCGAATACGGACATTAAGGTCGTGATACCCTTCGGCT

25801  GGTGGGAGGATCGCTTGGGCTCAGGAGTTTGAGACCAGGCTGGGCAACATGGCAAAACCT
25801  CCACCCTCCTAGCGAACCCGAGTCCTCAAACTCTGGTCCGACCCGTTGTACCGTTTTGGA

25861  CAACTCTACAAAAAACAAACAAAAAATTAGCCAGGCATGGTGGTGCACGCCTGTAGTCCC
25861  GTTGAGATGTTTTTTGTTTGTTTTTTAATCGGTCCGTACCACCACGTGCGGACATCAGGG

25921  AGCTACTCAGGAGGTTGAGGCAGGAGAATCCTGGGAGGCAGAGGTTGCAGTGATCTGAGA
25921  TCGATGAGTCCTCCAACTCCGTCCTCTTAGGACCCTCCGTCTCCAACGTCACTAGACTCT

25981  TTGTGCCACTGCACTCCAGCCTGGGAGCCTGGGTGACAGAGAGAGACCCTGTCTAAAATA
25981  AACACGGTGACGTGAGGTCGGACCCTCGGACCCACTGTCTCTCTCTGGGACAGATTTTAT

26041  TATATATACACACACTTGAATGCTTCATGTCCCTTGCTCAGTGACAGCCCCGTCCTCTGC
26041  ATATATATGTGTGTGAACTTACGAAGTACAGGGAACGAGTCACTGTCGGGGCAGGAGACG

26101  TTCTGCACAGTTGACCAAGGCTTCTCAGTCTACTCCTGTGTAGAAAAGAATTAAAGCAGG
26101  AAGACGTGTCAACTGGTTCCGAAGAGTCAGATGAGGACACATCTTTTCTTAATTTCGTCC

26161  CCTGAGGCTGCTAGTCTTAGAAAGGCTTGCAAAGTTGGCCCTTGTCTGGTGTCTGGGAAC
26161  GGACTCCGACGATCAGAATCTTTCCGAACGTTTCAACCGGGAACAGACCACAGACCCTTG
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FIGURE 4 (cont'd)

26221 TTGAATTTCTGGAGGGTTCTCACCATTCCCTGAAAAGAATGGCTCACGATGCCTAAAATA
26221 AACTTAAAGACCTCCCAAGAGTGGTAAGGGACTTTTCTTACCGAGTGCTACGGATTTTAT

26281 TTTGTACAAACAATGAAGTTTCTGCTGAACATCTGCTTCCTTCTGGGAGTCTGGAATTTT
26281 AAACATGTTTGTTACTTCAAAGACGACTTGTAGACGAAGGAAGACCCTCAGACCTTAAAA

26341 AGGATGTGCTAGGTAGGGGTGTTTACATGACAGCCCCACATAAAAACCTTGGGCACTGAG
26341 TCCTACACGATCCATCCCCACAAATGTACTGTCGGGGTGTATTTTTGGAACCCGTGACTC

26401 TGTCTAATGAGATTCCCTAGTAAGTAATATTTTACACATATTATCACAACTCATTGCTGG
26401 ACAGATTACTCTAAGGGATCATTCATTATAAAATGTGTATAATAGTGTTGAGTAACGACC

26461 AGGAGTTAAGTGCATCCTGTGTGACTCCACTGGGAGAGGACTCTGGGAAGCACATGTCTG
26461 TCCTCAATTCACGTAGGACACACTGAGGTGACCCTCTCCTGAGACCCTTCGTGTACAGAC

26521 ATTTCCTTTGTCCCATGTGCCTTTTCCTTTTGCTGATTTTTGCCTTGTAAATTTTTTTTT
26521 TAAAGGAAACAGGGTACACGGAAAAGGAAAACGACTAAAAACGGAACATTTAAAAAAAAA

26581 TTTTTTTTGAGAGACAGAGTCTTACTCTGTTGCCCAGACTGGAGTTCAGTGGCCCCATGT
26581 AAAAAAAACTCTCTGTCTCAGAATGAGACAACGGGTCTGACCTCAAGTCACCGGGGTACA

26641 CGGCTCACTGCAGCCTCTGCCTCCTGGATTCAAGCAATTCTCCTGCCTCAGCCTCCCGAG
26641 GCCGAGTGACGTCGGAGACGGAGGACCTAAGTTCGTTAAGAGGACGGAGTCGGAGGGCTC

26701 TAGCTGGGACTACAGGCGCGCGCTGCCACACCGGCTAATTTTTGTATTTTTAGTAGAGAC
26701 ATCGACCCTGATGTCCGCGCGCGACGGTGTGGCCGATTAAAAACATAAAAATCATCTCTG

26761 GGGGTTTCACCATGTTGGCCAGGATGGTCTTGATCTCCTGACCTCGTGATCCGCCTGCCT
26761 CCCCAAAGTGGTACAACCGGTCCTACCAGAACTAGAGGACTGGAGCACTAGGCGGACGGA

26821 CGGCCTCCCAAAGTGCTGGAATTATAGGCCTGGGCCACTGTGCCTGGCCATAATTTTTAT
26821 GCCGGAGGGTTTCACGACCTTAATATCCGGACCCGGTGACACGGACCGGTATTAAAAATA

26881 CCTGTAATAAATTATAGTCGAAAGTATTGAGTCCTGTGAATCAACTTAGAGAATCACCAA
26881 GGACATTATTTAATATCAGCTTTCATAACTCAGGACACTTAGTTGAATCTCTTAGTGGTT

26941 ACTGCTTCCAATTTTCTCATATGTAAAATGGGTTGCTATAATAATGATGATATCTACCTT
26941 TGACGAAGGTTAAAAGAGTATACATTTTACCCAACGATATTATTACTACTATAGATGGAA

27001 ATAGGGTTGTTTTAAGTATGAAAAATATGGTGAAATATGTGTGAAACTAGGGGCCGGATG
27001 TATCCCAACAAAATTCATACTTTTTATACCACTTTATACACACTTTGATCCCCGGCCTAC

27061 TAGGATGAGTCATACAGTGGGTGGTTATTATTACGGATCATATTAACTCTTCAGGTAAAA
27061 ATCCTACTCAGTATGTCACCCACCAATAATAATGCCTAGTATAATTGAGAAGTCCATTTT

27121 ACCATCTTGTAGCTGGGCAAGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGGGACTGA
27121 TGGTAGAACATCGACCCGTTCCACCGTGTACGGACATCAGGGTCGATGAACCCCCTGACT

27181 GGCAGGTGGATCGCTTGAGCCTAGGAGTTCAAGGCTGTAGTACGCTATGATCACGTCTAT
27181 CCGTCCACCTAGCGAACTCGGATCCTCAAGTTCCGACATCATGCGATACTAGTGCAGATA

27241 CAATAGCCACTGGACTCCAGCCTGGACAATGTAATGAGAGTCTGTCTCAAAAAAAAGGAA
27241 GTTATCGGTGACCTGAGGTCGGACCTGTTACATTACTCTCAGACAGAGTTTTTTTTCCTT

27301 CAATCTTGTGTTTGCGTGTGTGCTCATGTCTTTGTTGGAATAATACTGACACAGTCACTC
27301 GTTAGAACACAAACGCACACACGAGTACAGAAACAACCTTATTATGACTGTGTCAGTGAG

27361 AAATTAACTCTCAAATCTTTGATTATTCATTTGATGGGAACAACAGGTTTATGTGCCAGC
27361 TTTAATTGAGAGTTTAGAAACTAATAAGTAAACTACCCTTGTTGTCCAAATACACGGTCG

27421 TTATCAGGACCCCTAGTTCTTTCATTAAAGTGTGTATGTGTGTGTGTATGTGTGTATGTG
27421 AATAGTCCTGGGGATCAAGAAAGTAATTTCACACATACACACACACATACACACATACAC

27481 TGCACATGTGTGCTAGTTTTCTTATCTAACGACGAAGTCCTTTGGGAGGTTTACTTTTTC
27481 ACGTGTACACACGATCAAAAGAATAGATTGCTGCTTCAGGAAACCCTCCAAATGAAAAAG

FIGURE 4 (cont'd)

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27541   ATTACTATTTTTTTCATGCTTTCCTTTGATGTGCACCTGGCAATTTATAGAGCCAATGTG
27541   TAATGATAAAAAAAGTACGAAAGGAAACTACACGTGGACCGTTAAATATCTCGGTTACAC

27601   TACTACATATTCTGCTGCAGAAAATGACAGAGGTGAGGAAGGAGCAGGAAGCAGATTTAG
27601   ATGATGTATAAGACGACGTCTTTTACTGTCTCCACTCCTTCCTCGTCCTTCGTCTAAATC

27661   AAAGGAATGTTACAGTTTATCAAGTTGTGACTAATGGAAGCTATTAAAACAAAAGGTACC
27661   TTTCCTTACAATGTCAAATAGTTCAACACTGATTACCTTCGATAATTTTGTTTTCCATGG

27721   AACCCATCTTAAATATTCACTGCCTCTACAACTATTTTTCTATAACTGTTGTTCCTTGTC
27721   TTGGGTAGAATTTATAAGTGACGGAGATGTTGATAAAAAGATATTGACAACAAGGAACAG

27781   AGCTCTGGGGTGGAGGGAATATTCCTGAATGTTTTATTAAGTAATTCAAAGATCTTCCTA
27781   TCGAGACCCCACCTCCCTTATAAGGACTTACAAAATAATTCATTAAGTTTCTAGAAGGAT

27841   GGTATGTGTATCAAAGATCCTATGATGTATCTGTCTTGTAAATTGAGACTGGCATATATT
27841   CCATACACATAGTTTCTAGGATACTACATAGACAGAACATTTAACTCTGACCGTATATAA

27901   GGGCTTACATTACTGGGAAAAATGTATGTCATCATCATTGGTGAAAAAGAGTTTCCATAG
27901   CCCGAATGTAATGACCCTTTTTACATACAGTAGTAGTAACCACTTTTTCTCAAAGGTATC

27961   CAGTTTTTTCTAAGTAGAGAGATAAATGAATCAGACTTTTGGAGGAGGTATGTTTTAACT
27961   GTCAAAAAAGATTCATCTCTCTATTTACTTAGTCTGAAAACCTCCTCCATACAAAATTGA

28021   CACTGGAGGATCACACCAAGTCTGAACATCTAAGGAACCCTAGTGGAAAACTGGTTTTCC
28021   GTGACCTCCTAGTGTGGTTCAGACTTGTAGATTCCTTGGGATCACCTTTTGACCAAAAGG

28081   TGTATGCTGCTCTAGCGATCTGAGGAAAGGCCTAAAAAAAGCCAGTGTCCCTGTGATATT
28081   ACATACGACGAGATCGCTAGACTCCTTTCCGGATTTTTTTCGGTCACAGGGACACTATAA

28141   GTGAAATACATATATGTGGTCTTTGTTCCTGTTTCCTGGCATACAAGTACTAAAAATCCT
28141   CACTTTATGTATATACACCAGAAACAAGGACAAAGGACCGTATGTTCATGATTTTTAGGA

28201   TGGAATCTCCAAAGTGCTGTCTTTTTGTATATTAGTGTTGACTGATAGCTTCAGAGTGGG
28201   ACCTTAGAGGTTTCACGACAGAAAAACATATAATCACAACTGACTATCGAAGTCTCACCC

28261   GCTGGTCAAGTTGATCACCAATGGCCAGTGGTTTAATCAGTCATGCCTATGTAATGAAGC
28261   CGACCAGTTCAACTAGTGGTTACCGGTCACCAAATTAGTCAGTACGGATACATTACTTCG

28321   CTCCATGAAAATCCAAAGGGAATGGACTGGGGAGCTTCTAAGAAGTGTTTTTTACCTTCC
28321   GAGGTACTTTTAGGTTTCCCTTACCTGACCCCTCGAAGATTCTTCACAAAAAATGGAAGG

28381   CGTGAGCCTCCTGTGCTGAACACGTGGAGGGTCACGGGAAGGTAAGCAAAAATTCATTCA
28381   GCACTCGGAGGACACGACTTGTGCACCTCCCAGTGCCCTTCCATTCGTTTTTAAGTAAGT

28441   CATGCTGGGAGGGTGGCACATCCCAACTCCACGAGGACAAAGCTCCTGTGCTCAGAACC
28441   GTACGACCCTCCCACCGTGTAGGGTTGAGGTGCTCCTGTTTCGAGGACACGAGTCTTGG

28501   CTTCCAGACTTGGACCTTGTATCTCTTCATTGGCTTTTATTTGTATTTTAAAAAATATCC
28501   GAAGGTCTGAACCTGGAACATAGAGAAGTAACCGAAAATAAACATAAAATTTTTTATAGG

28561   TGAGTGATAAACTGGTAGATGTAAGTGTCTTCCTCAGTTCTGTGAACCACGCTAGCAAAT
28561   ACTCACTATTTGACCATCTACATTCACAGAAGGAGTCAAGACACTTGGTGCGATCGTTTA

28621   TAATCAAACCGGAAGAGGGGTCATGGCAACCCCAACTTGAAACCTGTTGGTCAGCAGTT
28621   ATTAGTTTGGCCTTCTCCCCAGTACCGTTGGGGTTGAACTTTGGACAACCAGTCGTCAA

28681   CCAGAGACCTGAACTTATGACTGGTTGGAAGGACGGGGTGCTCTTGTGGGACTGAGCCCT
28681   GGTCTCTGGACTTGAATACTGACCAACCTTCCTGCCCCACGAGAACACCCTGACTCGGGA

28741   CAACTTGTGGATCTGATGCTATCTCTGGGTAGACAGTGTTGGAGCTGAATTGGAGGACAC
28741   GTTGAACACCTAGACTACGATAGAGACCCATCTGTCACAACCTCGACTTAACCTCCTGTG

28801   CTAGCTTGTGTCCACTGCAGAACTGATTGCTTGCTTCCTGCTGGGGAGAAATCCCTATAT
28801   GATCGAACACAGGTGACGTCTTGACTAACGAACGAAGGACGACCCCTCTTTAGGGATATA
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FIGURE 4 (cont'd)

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28861  ATTTTGGGGTCCAGAAGTCTTCCGTGTTGATTGTTTTTGTGTGAGAGCAGAGGAAAAATG
28861  TAAAACCCCAGGTCTTCAGAAGGCACAACTAACAAAAACACACTCTCGTCTCCTTTTTAC

28921  GTTTGAGAGTTTTTCGGGAAACAGCCCCTCTTAGTATAGTGGTAGAAACACTCCAAAAAT
28921  CAAACTCTCAAAAAGCCCTTTGTCGGGGAGAATCATATCACCATCTTTGTGAGGTTTTTA

28981  AAAATATGCTACCCCAAAAATAAAAAATGAAAATAAAAATAAAAATCTGGAGTGGTCAGT
28981  TTTTATACGATGGGGTTTTTATTTTTTACTTTTATTTTTATTTTTAGACCTCACCAGTCA

29041  TTGCCAAGAGGATTTATGGAGCATCTAAGGTCAAGCATTACTTCTCAGCCCTGCAGCAGG
29041  AACGGTTCTCCTAAATACCTCGTAGATTCCAGTTCGTAATGAAGAGTCGGGACGTCGTCC

29101  CCTCTAATTAAGCCATGCCACAGAGTGCGGTTTGCAGAGAGGTGGAGTTCCTGTGGATTC
29101  GGAGATTAATTCGGTACGGTGTCTCACGCCAAACGTCTCTCCACCTCAAGGACACCTAAG

29161  ATTCTTCTCTCTAAAATTATAAATAACGCAGCTTCCAAACATGCCATATTACCTCACAAG
29161  TAAGAAGAGAGATTTTAATATTTATTGCGTCGAAGGTTTGTACGGTATAATGGAGTGTTC

29221  GTCTAAAGACTCAATATGAATCTTCAACTTAACAATTATAACTGACACAGATTGAGATCT
29221  CAGATTTCTGAGTTATACTTAGAAGTTGAATTGTTAATATTGACTGTGTCTAACTCTAGA

29281  TCCTGGATGCTGAAATAGGCTTTACATGATTTATCTCATTTAGTTCTCATAAAACTCTAT
29281  AGGACCTACGACTTTATCCGAAATGTACTAAATAGAGTAAATCAAGAGTATTTTGAGATA

29341  TATTAATATTATTTTACAGATAGAGAAATGGAAGCACAGAGAGGGTAAGTGTATTAGTCC
29341  ATAATTATAATAAAATGTCTATCTCTTTACCTTCGTGTCTCTCCCATTCACATAATCAGG

29401  ATTTTTATGCTGCTAATAAAGACATACCCAAGACAGGGTAATTTATACAGAAAAAGAGGT
29401  TAAAAATACGACGATTATTTCTGTATGGGTTCTGTCCCATTAAATATGTCTTTTTCTCCA

29461  TTAATGGACTCACATTTCCACATGGCTGGGAGGCCTCACAATCATGGCAGAAGGCAAAAG
29461  AATTACCTGAGTGTAAAGGTGTACCGACCCTCCGGAGTGTTAGTACCGTCTTCCGTTTTC

29521  GCACTTCTTACCTGGTGGTGGCAAGACAGAAAATGAGAACCAAGCGAAAGGGGTTTCCCC
29521  CGTGAAGAATGGACCACCACCGTTCTGTCTTTTACTCTTGGTTCGCTTTCCCCAAAGGGG

29581  TTATAAAACCATCAGGTAACATGAGACAATTATTCACTACCACAGAAACTATATGGGGGA
29581  AATATTTTGGTAGTCCATTGTACTCTGTTAATAAGTGATGGTGTCTTTGATATACCCCCT

29641  AACCGCCCCCATGATTCAGTTATCTTCCATTGGGTCCCTCCCACAACACGTGGAGCTACA
29641  TTGGCGGGGGTACTAAGTCAATAGAAGGTAACCCAGGGAGGGTGTTGTGCACCTCGATGT

29701  ATTCAAGATGAGATTTGTGTGGAGACATAGCTAACCCATATCAGTAAGTAATTAGACAAA
29701  TAAGTTCTACTCTAAACACACCTCTGTATCGATTGGGTATAGTCATTCATTAATCTGTTT

29761  CCTTGCAAAGCTAGTAAGTGGTATTGCTGGAATTAAATCTGCCAATGTCACTCCAGAGTC
29761  GGAACGTTTCGATCATTCACCATAACGACCTTAATTTAGACGGTTACAGTGAGGTCTCAG

29821  TATGTGATTTACTGGTATATTATAGGGTCTACCTATAAGCTTGATAACCTTATGTTAGAA
29821  ATACACTAAATGACCATATAATATCCCAGATGGATATTCGAACTATTGGAATACAATCTT

29881  CAAATAACCATGACATATTCTGTTCAGTAGTTTGCATTTCCTTTTGACTCCTACAGGGGA
29881  GTTTATTGGTACTGTATAAGACAAGTCATCAAACGTAAAGGAAAACTGAGGATGTCCCCT

29941  GGAGGCCGAGGTTCAGGGACATTAAAGTGGGGTTTAGAGACATTAGGTGGTTTACCCAAG
29941  CCTCCGGCTCCAAGTCCCTGTAATTTCACCCCAAATCTCTGTAATCCACCAAATGGGTTC

30001  CTTTATCTACTAGATACTAGATAATTGTCTATCTGACAATAAAGCTAGAACTTACACCCA
30001  GAAATAGATGATCTATGATCTATTAACAGATAGACTGTTATTTCGATCTTGAATGTGGGT

30061  GCTGGACAATGGAGCTACAGCTTAAAACAAAATCTTCTAATGAGCTCAGAACTCATGGCT
30061  CGACCTGTTACCTCGATGTCGAATTTTGTTTTAGAAGATTACTCGAGTCTTGAGTACCGA

30121  TAATAAGATTTGGGAAAAGTCCTGCGGACATTTCACTGTCTATCCAGAAATGCGAGGAAG
30121  ATTATTCTAAACCCTTTTCAGGACGCCTGTAAAGTGACAGATAGGTCTTTACGCTCCTTC
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FIGURE 4 (cont'd)

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30181  TTAGGAGAAAAGGCAAAGTATCTCATAGACAGATAAAGGCAGTTCAGTAAGTAGCCTGAA
30181  AATCCTCTTTTCCGTTTCATAGAGTATCTGTCTATTTCCGTCAAGTCATTCATCGGACTT

30241  TAAATAGCCATATTTAAAATCTAATTTGGTTCTTTTGTGCCTAACACAATTGACTTTATG
30241  ATTTATCGGTATAAATTTTAGATTAAACCAAGAAAACACGGATTGTGTTAACTGAAATAC

30301  CTGGTATCTATTTTCTGCTCTGTCTCTCTTTCTGTCTCTACTTATGTGTGTATGCATGTG
30301  GACCATAGATAAAAGACGAGACAGAGAGAAAGACAGAGATGAATACACACATACGTACAC

30361  TTATAAAATATATCAGCCCATTGATCAATTTTTAATTTAAGCAAAAACATGGTAGATTAA
30361  AATATTTTATATAGTCGGGTAACTAGTTAAAAATTAAATTCGTTTTTGTACCATCTAATT

30421  TATATTCAATCAATTTATTGAGTAGATATTTATCGAGGCTCACACATTTATCTGACTGTG
30421  ATATAAGTTAGTTAAATAACTCATCTATAAATAGCTCCGAGTGTGTAAATAGACTGACAC

30481  TACTAAGCACTGGAAACCCAAAGAGAATGAAGTCACTGCCTAGACAGTTGGAGGCTGACA
30481  ATGATTCGTGACCTTTGGGTTTCTCTTACTTCAGTGACGGATCTGTCAACCTCCGACTGT

30541  CATAAACAAGCAGGGTAATAATCAAGTGTCATAACTAGTCTATTACATGCAATGTTAAAC
30541  GTATTTGTTCGTCCCATTATTAGTTCACAGTATTGATCAGATAATGTACGTTACAATTTG

30601  TAGCATCTCTACCATGCAAAACTTGTGCTCTTGGGGATACAGGAAGACTTTCCAGAGAAG
30601  ATCGTAGAGATGGTACGTTTTGAACACGAGAACCCCTATGTCCTTCTGAAAGGTCTCTTC

30661  TACACAGGACAGGAATGTGTTAGGAAACCAGTCAGTTCCCAGGTCCTCGATCAGGTCACA
30661  ATGTGTCCTGTCCTTACACAATCCTTTGGTCAGTCAAGGGTCCAGGAGCTAGTCCAGTGT

30721  GTGACTTGCGATTCTATTTTGAACATAGGTCTTAAATCTTTATTTTGATAGCAAGGGTTT
30721  CACTGAACGCTAAGATAAAACTTGTATCCAGAATTTAGAAATAAAACTATCGTTCCCAAA

30781  TAAACTTTTGATATATGATATACTTCTGAAAATCAAATTTCATATTCTAAAATTAAGTAT
30781  ATTTGAAAACTATATACTATATGAAGACTTTTAGTTTAAAGTATAAGATTTTAATTCATA

30841  TTTTGCCCTTAACTAACTTGAACATAATACTATAATACATTAACATATATTATTAATAAT
30841  AAAACGGGAATTGATTGAACTTGTATTATGATATTATGTAATTGTATATAATAATTATTA

30901  AAATAGGACCCCTGGAAGTCCAAGAGAGACATGAGGCTTATTTGGTATGTTAAAATCATA
30901  TTTATCCTGGGGACCTTCAGGTTCTCTCTGTACTCCGAATAAACCATACAATTTTAGTAT

30961  CAGGAAGTGTTGTTAAATAAGAAATGGTGTTACACTTTCTTTGAGTTATATTTATATGGA
30961  GTCCTTCACAACAATTTATTCTTTACCACAATGTGAAAGAAACTCAATATAAATATACCT

31021  TATGTTGTTAATATGTGTTCCAACATTGTATGAGATTCCTAAAAATCTGATATGGACATC
31021  ATACAACAATTATACACAAGGTTGTAACATACTCTAAGGATTTTTAGACTATACCTGTAG

31081  CAGTGTGGTTGTTGGGTCCTCTATGAGCCTAGGGAGCACTGGCCGGTTACCTTGCATCCA
31081  GTCACACCAACAACCCAGGAGATACTCGGATCCCTCGTGACCGGCCAATGGAACGTAGGT

31141  TTCATGTCAGCGTTGGTAGTGTCAGGCACCCGATGGTTCTTAGAAGAGTACTTAGCTCTA
31141  AAGTACAGTCGCAACCATCACAGTCCGTGGGCTACCAAGAATCTTCTCATGAATCGAGAT

31201  CTCTGCAGTGTCTGAAGTTGCTGGATATATACCTGCTGTATAAACTGCTGACTAGGGCGC
31201  GAGACGTCACAGACTTCAACGACCTATATATGGACGACATATTTGACGACTGATCCCGCG

31261  TGCAGTTTACTTACTGTCTTCTCATGGGGACCTTCCCCTTCAACTCTTTCCTCTTGGGTT
31261  ACGTCAAATGAATGACAGAAGAGTACCCCTGGAAGGGGAAGTTGAGAAAGGAGAACCCAA

31321  TCACATCTTGGGTGGGGAGTTTCATCCTAGTAGTTTGCCTGAGAATACAGGTGAACCCAC
31321  AGTGTAGAACCCACCCCTCAAAGTAGGATCATCAAACGGACTCTTATGTCCACTTGGGTG

31381  AGAACAAAGTGGACTTCGAAAGCATCTCCTTGGAGTGAGACTTTGCTTCTTTCTCTTTGC
31381  TCTTGTTTCACCTGAAGCTTTCGTAGAGGAACCTCACTCTGAAACGAAGAAAGAGAAACG

31441  TAGCACCATCTTGTACCTTATCGTCATGAACTTTGTTGGCTGAATCATTCCCATTTACTT
31441  ATCGTGGTAGAACATGGAATAGCAGTACTTGAAACAACCGACTTAGTAAGGGTAAATGAA

31501  AATTGAAGAGTAAGAGACTGGAACAATGCTCACTTTGATTTTCCTGGATAAGAGTTAAGA
31501  TTAACTTCTCATTCTCTGACCTTGTTACGAGTGAAACTAAAAGGACCTATTCTCAATTCT
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FIGURE 4 (cont'd)

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31561  GTTCTTGAGATGGCAGCTTGTTTGACACATGAATTTTCTTCAAATTTGTGCTTACTACCA
31561  CAAGAACTCTACCGTCGAACAAACTGTGTACTTAAAAGAAGTTTAAACACGAATGATGGT

31621  ACTGATTTGGTGTGGAGGAGAGCCCAGAGAAGTTCCCTCTCTCTGTCAGAACAACTTTGT
31621  TGACTAAACCACACCTCCTCTCGGGTCTCTTCAAGGGAGAGAGACAGTCTTGTTGAAACA

31681  AACATTTATTAACCTGACTTCTGCCTTCAATTAACTGTAACCTTTTGCCTTCCAAATTAA
31681  TTGTAAATAATTGGACTGAAGACGGAAGTTAATTGACATTGGAAAACGGAAGGTTTAATT

31741  AAAGTTCCACATTACTCCAAAAATAAAAAGTGAAAATAAAAATAAAAGGCTGATATGTCA
31741  TTTCAAGGTGTAATGAGGTTTTTATTTTTCACTTTTATTTTTATTTTCCGACTATACAGT

31801  TGGTATATGCAGTAAATTGCTTTATTCTGATTTTTTTTTCTAAAAGCCTTTTGCAAATCC
31801  ACCATATACGTCATTTAACGAAATAAGACTAAAAAAAAAGATTTTCGGAAAACGTTTAGG

31861  TGAAGTGCTGTGTATTCAAGGAAATTCATGAAAGGGACCTTGACAAGTAGTCTTAAATAC
31861  ACTTCACGACACATAAGTTCCTTTAAGTACTTTCCCTGGAACTGTTCATCAGAATTTATG

31921  AGGTTTCTGATAACTTTGGAGATCACACCTTTGGACTAGGTAAAAACATCCAAAACTCGT
31921  TCCAAAGACTATTGAAACCTCTAGTGTGGAAACCTGATCCATTTTTGTAGGTTTTGAGCA

31981  CTGGGCGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCAGGCGGATC
31981  GACCCGCGTCACCGAGTGCGGACATTAGGGTCGTGAAACCCTCCGGTTCCGTCCGCCTAG

32041  ACGAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAACCCCATCTCTACTAAAA
32041  TGCTCCAGTCCTCTAGCTCTGGTAGGACCGATTGTGCCACTTTGGGGTAGAGATGATTTT

32101  ACACAAAAACAAAATTAGCCGGGCGTGGTGGCGGGCGCCTGTAGTTCCAGCTACCCGGCA
32101  TGTGTTTTTGTTTTAATCGGCCCGCACCACCGCCCGCGGACATCAAGGTCGATGGGCCGT

32161  GGCTGAGGCGGAAGAATGGCGCGAAGCGGCAAGACGGAGCTTGCAGTGAGCCGAGATCGC
32161  CCGACTCCGCCTTCTTACCGCGCTTCGCCGTTCTGCCTCGAACGTCACTCGGCTCTAGCG

32221  GCCACTGCACTCCAGCCTCAAAAAAAAAAAAAAAAAAAAAAAAAGTCCAAAGCTCTAATG
32221  CGGTGACGTGAGGTCGGAGTTTTTTTTTTTTTTTTTTTTTTTTTCAGGTTTCGAGATTAC

32281  AAAAACTGATGCATTCATGCAGATTGCTAACCCAACATCAAGGAGAACGAGAATTACATG
32281  TTTTTGACTACGTAAGTACGTCTAACGATTGGGTTGTAGTTCCTCTTGCTCTTAATGTAC

32341  GGACTGAGTGAATGAAGGATTGAAATTACTATTTTAAAGGGTTTTTGTTTGAAACATTAC
32341  CCTGACTCACTTACTTCCTAACTTTAATGATAAAATTTCCCAAAAACAAACTTTGTAATG

32401  TGATTTTTTTTATGTTTTGTTTTCCAGACTCAAGAAAATATTTTTTTTCTTTTGAGCTAT
32401  ACTAAAAAAAATACAAAACAAAAGGTCTGAGTTCTTTTATAAAAAAAAGAAAACTCGATA

32461  TTATAGCTTACAGCATTGGGGTAAAGTATACTTCTGTGAGCAAAATGGAAACATTTACCT
32461  AATATCGAATGTCGTAACCCCATTTCATATGAAGACACTCGTTTTACCTTTGTAAATGGA

32521  TTCTTTCTACCTGAATTCTTCAGAATTTGGAAACTATTCATTAGTGTTCTTATTTTCTGG
32521  AAGAAAGATGGACTTAAGAAGTCTTAAACCTTTGATAAGTAATCACAAGAATAAAAGACC

32581  CAATATAGTTATTTGCATAAGTTCAATAAGAACCTATTTTCGGCTGTGCATGGTGGCTCA
32581  GTTATATCAATAAACGTATTCAAGTTATTCTTGGATAAAAGCCGACACGTACCACCGAGT

32641  TGCCTGTAATCCCAGCACCTTGGGAGGGCGAGGCCGGTGGATCACAAGGTCAGGAGTTTG
32641  ACGGACATTAGGGTCGTGGAACCCTCCCGCTCCGGCCACCTAGTGTTCCAGTCCTCAAAC

32701  AGAACAGCCTGGCCAAGATGGTGAAACCCCGTCTCTACTAAAACTACAAAGATTAACCAG
32701  TCTTGTCGGACCGGTTCTACCACTTTGGGGCAGAGATGATTTTGATGTTTCTAATTGGTC

32761  GCGCGGTGGCAGGCGCCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATAGCTT
32761  CGCGCCACCGTCCGCGGACATTAGGGTCGATGAGCCCTCCGACTCCGTCCTCTTATCGAA

32821  GAACCTTGGGTGGCAGAGGTTGCAGTGAGCCGAGATCGCACCACTGCGCTCCAGCCTAGG
32821  CTTGGAACCCACCGTCTCCAACGTCACTCGGCTCTAGCGTGGTGACGCGAGGTCGGATCC
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FIGURE 4 (cont'd)

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32881  GGACAAGAGCGAGACTCTATCTCAAAACAAACAAACAAAAAAACAAAAAGCAAACAAACA
32881  CCTGTTCTCGCTCTGAGATAGAGTTTTGTTTGTTTGTTTTTTTGTTTTTCGTTTGTTTGT

32941  AAAAAAGAGCTTATTTTCTTTTGTAACTGGACACATGGAAACAGTGGTTATTTTACCAAG
32941  TTTTTTCTCGAATAAAAGAAAACATTGACCTGTGTACCTTTGTCACCAATAAAATGGTTC

33001  GCTTTGACTGGAATGTCTTTTTTTTGAGTGCAACCGGACTGCTTCGAGGGATTGAGGTTG
33001  CGAAACTGACCTTACAGAAAAAAAACTCACGTTGGCCTGACGAAGCTCCCTAACTCCAAC

33061  ACTTTATACAGCCAGTAGACTTGGAAAAAGACACACCTGGTACCTTGCCCACACAATTCC
33061  TGAAATATGTCGGTCATCTGAACCTTTTTCTGTGTGGACCATGGAACGGGTGTGTTAAGG

33121  TTTATAGCGTTTCTAACTTTGCAATAAGTAAAGAATGTCACTTTCTGACAGGCCCAGGGA
33121  AAATATCGCAAAGATTGAAACGTTATTCATTTCTTACAGTGAAAGACTGTCCGGGTCCCT

33181  CCTCAAGATATTTTGGAGACGTTGAAAAGAGAGCAATTCACCCAATTCATACAGGTTTTA
33181  GGAGTTCTATAAAACCTCTGCAACTTTTCTCTCGTTAAGTGGGTTAAGTATGTCCAAAAT

33241  CAGGCACAGTCTGATGGCGAATCTTTGGCTTGGCTTCATTGCTTCAAGAGTTTGTTTTTT
33241  GTCCGTGTCAGACTACCGCTTAGAAACCGAACCGAAGTAACGAAGTTCTCAAACAAAAAA

33301  TGACACGGAATCTCACTCTGTCACCCATTCTGGAGTGCAGTGGTGAGATCTTGGCTCACT
33301  ACTGTGCCTTAGAGTGAGACAGTGGGTAAGACCTCACGTCACCACTCTAGAACCGAGTGA

33361  GAAACCTCTGCTTCCTGGATTCAAGTGATTCTCCTGCTTCAGCCTCCCGAGTAGCTGGGA
33361  CTTTGGAGACGAAGGACCTAAGTTCACTAAGAGGACGAAGTCGGAGGGCTCATCGACCCT

33421  TTACAGGCATGTGTTGCTACTCCCAGCTAATTTTTTGTATTTTTGGTAGAGATGAGGTTT
33421  AATGTCCGTACACAACGATGAGGGTCGATTAAAAAACATAAAAACCATCTCTACTCCAAA

33481  CACCATGTTGCCCAGGGTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCC
33481  GTGGTACAACGGGTCCCACCAGAACTTGAGGACTGGAGTCCACTAGGTGGGTGGAGTCGG

33541  TCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGTGCCCAGCCCTTGAGAGGTTTCAAA
33541  AGGGTTTCACGACCCTAATGTCCGCACTCGGTGACACGGGTCGGGAACTCTCCAAAGTTT

33601  AGTCTTAATCTGAGATTCCTTATGAAAAAATTCCAACAAAGCCAACTTAAGAGCCATCCC
33601  TCAGAATTAGACTCTAAGGAATACTTTTTTAAGGTTGTTTCGGTTGAATTCTCGGTAGGG

33661  TGTAGAAAATATATCTATTTAAATATCGTCTGTTTTATGCCACAATGTTTGTTTTGCGTT
33661  ACATCTTTTATATAGATAAATTTATAGCAGACAAAATACGGTGTTACAAACAAAACGCAA

33721  GCAAGCCGTTATCTCCTAGGCATGGGTAATCCACTTTGAGAGGAAAATCCAGACATCATT
33721  CGTTCGGCAATAGAGGATCCGTACCCATTAGGTGAAACTCTCCTTTTAGGTCTGTAGTAA

33781  GTGCCTAATTTGCTGCCACCTGTGTCTGTGCTGGATCTTACCAGGGTTAGCTTTATTTTC
33781  CACGGATTAAACGACGGTGGACACAGACACGACCTAGAATGGTCCCAATCGAAATAAAAG

33841  TTTCAACTGGCAAAATTCTGATAAAGCATGTAGCTTCACGGTAGAGCAAAAAGTGTAACT
33841  AAAGTTGACCGTTTTAAGACTATTTCGTACATCGAAGTGCCATCTCGTTTTTCACATTGA

33901  TAATTGAAAGTCATGACTTTCAGGAGTCTAATGATGCTAATATATTTTCTTCTAGAGAGG
33901  ATTAACTTTCAGTACTGAAAGTCCTCAGATTACTACGATTATATAAAAGAAGATCTCTCC

33961  TGTCTTTATTGTATGTAATTCCCTGAAGAAATGTAAAGATTTATCTAATTCCTATTGCTC
33961  ACAGAAATAACATACATTAAGGGACTTCTTTACATTTCTAAATAGATTAAGGATAACGAG

34021  TGACAGGCGTGCTCAATAGAAGCATTGAAGTAAAATAAAAATAACCTTTTTAATCTGTGT
34021  ACTGTCCGCACGAGTTATCTTCGTAACTTCATTTTATTTTTATTGGAAAAATTAGACACA

34081  ATTTCTCTTGCCCACCAAGATATTTAATTTTTTTCTTGATCTTTGCTTTTCTTTATGTGA
34081  TAAAGAGAACGGGTGGTTCTATAAATTAAAAAAAGAACTAGAAACGAAAACAAATACACT

34141  AGATATTTATGTCTATATCATTTCTGTATATATCACAGAAAAGTTTTCACTTGCTTGACA
34141  TCTATAAATACAGATATAGTAAAGACATATATAGTGTCTTTTCAAAAGTGAACGAACTGT

34201  TTTTATTCTACAATGATTTTTAGTTTAAGTTTAAAGAATGGCTACATTCAGATTTATTTT
34201  AAAATAAGATGTTACTAAAAATCAAATTCAAATTTCTTACCGATGTAAGTCTAAATAAAA
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FIGURE 4 (cont'd)

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34261   CACAACTATAGTCCTGCTAAACTGCCTTTGTTGAAAACTCAGTTTTTATAATAAATAAAA
34261   GTGTTGATATCAGGACGATTTGACGGAAACAACTTTTGAGTCAAAAATATTATTTATTTT

34321   AATATCAAAGCAAAAAAAAAAGAGCCTTCATGATAAATCACCATTCTTACTGCACTTTAA
34321   TTATAGTTTCGTTTTTTTTTTCTCGGAAGTACTATTTAGTGGTAAGAATGACGTGAAATT

34381   GCAGATAATCATGCCAGAGACTAAACTGACTTTGCAAATAAATTAGTTTTATTATTATTA
34381   CGTCTATTAGTACGGTCTCTGATTTGACTGAAACGTTTATTTAATCAAAATAATAATAAT

34441   TCTTTGTGGGTAAAAGTTGGGATGACTGTAGAAGAGAAAATTATATTTCAGAAGAAAATT
34441   AGAAACACCCATTTTCAACCCTACTGACATCTTCTCTTTTAATATAAAGTCTTCTTTTAA

34501   ATACCATACTTGTTATTAGATTCTAGTCTTGATAATTGTTTTTTTGAGTTTTTGTTATTT
34501   TATGGTATGAACAATAATCTAAGATCAGAACTATTAACAAAAAAACTCAAAAACAATAAA

34561   GCCTACAATTTGGGCTGAATCCTGAATTCCTTCCTGGGTACAAGTCTCCAAACTAATGTT
34561   CGGATGTTAAACCCGACTTAGGACTTAAGGAAGGACCCATGTTCAGAGGTTTGATTACAA

34621   TCCTAATTTTTCTACCATTTTTCTGTCTTGGAATCACCAAGCCCTGCAGGCTTTAGCTAG
34621   AGGATTAAAAAGATGGTAAAAAGACAGAACCTTAGTGGTTCGGGACGTCCGAAATCGATC

34681   ACAACTTGATATAAACTTTGGAAGAAATAATGACAGCAACTTAATATATGAGCAGTGTTC
34681   TGTTGAACTATATTTGAAACCTTCTTTATTACTGTCGTTGAATTATATACTCGTCACAAG

34741   ATGTCAGCTGATGTATGGATTACTCAGAAGGTTTACTTGAACACCTGATTCAAACTATAA
34741   TACAGTCGACTACATACCTAATGAGTCTTCCAAATGAACTTGTGGACTAAGTTTGATATT

34801   TCCAGAAATATCTGTAAGATTGCCACTGCAATCTGAAGCTACTTCAGAGACTCTAGGAAA
34801   AGGTCTTTATAGACATTCTAACGGTGACGTTAGACTTCGATGAAGTCTCTGAGATCCTTT

34861   ATTAGTTTATAGACAACTCCAGATGTTAATCTTTGTTTTTCTTTTGTTTTCATGGAAATG
34861   TAATCAAATATCTGTTGAGGTCTACAATTAGAAACAAAAAGAAAACAAAAGTACCTTTAC

34921   CCTTTTATTAAACATCTGATTGCTTGATTCATAGAGGCCTGACTTTGGTGGAAGCAACAC
34921   GGAAAATAATTTGTAGACTAACGAACTAAGTATCTCCGGACTGAAACCACCTTCGTTGTG

34981   CACTGCCTGAAATGAGATATAACTGTTAACCGTTTAATTGGAGCGGCCTGTTCTCACGAC
34981   GTGACGGACTTTACTCTATATTGACAATTGGCAAATTAACCTCGCCGGACAAGAGTGCTG

35041   TGCAAGACTAGTTCAATGGCTTATAAAATAATCCACCCGCTGGGCACAGTAGTTCACACC
35041   ACGTTCTGATCAAGTTACCGAATATTTTATTAGGTGGGCGACCCGTGTCATCAAGTGTGG

35101   TGTAATCTCAGCACTTTGGGAGGCTGAGGTGGGCAAATTGCTTGAGCTCAGGAGTTCGAG
35101   ACATTAGAGTCGTGAAACCCTCCGACTCCACCCGTTTAACGAACTCGAGTCCTCAAGCTC

35161   ACCAGCCAGAGCAACATGGTGAAACCCTGTCTCTACCAAAAATATAAAAAATTAGCCGGG
35161   TGGTCGGTCTCGTTGTACCACTTTGGGACAGAGATGGTTTTTATATTTTTTAATCGGCCC

35221   CATAGTAGCATGTGCCTGTGGTCCCAGCTCCTCGGGAGGTGGATGTGGGAGGATTGCCTG
35221   GTATCATCGTACACGGACACCAGGGTCGAGGAGCCCTCCACCTACACCCTCCTAACGGAC

35281   AGCCTGGGAGGCAGAGCTTGCAGTGAGCTGAGATTATGACACTGCACTCTAGCCTGGGCA
35281   TCGGACCCTCCGTCTCGAACGTCACTCGACTCTAATACTGTGACGTGAGATCGGACCCGT

35341   ATACAGTGAGACCCCATCTCAAAAAAAAAAAAAAAAGATAATCTACCAACCCAATTTCTC
35341   TATGTCACTCTGGGGTAGAGTTTTTTTTTTTTTTTTCTATTAGATGGTTGGGTTAAAGAG

35401   AACTGGGGAATGTTGGGCTCCTGCTCTCCTGTCTCTGACCTTTCATTCTCCCTTGAGGCT
35401   TTGACCCCTTACAACCCGAGGACGAGAGGACAGAGACTGGAAAGTAAGAGGGAACTCCGA

35461   AGCCATCAAGACTACAACCCCTCTTCCCCAAAGTGGGCCATAGAAACAAAACCCCTTTTC
35461   TCGGTAGTTCTGATGTTGGGGAGAAGGGGTTTCACCCGGTATCTTTGTTTTGGGGAAAAG

35521   CCCAAAGCCAACCATAAAACCTAAAAATAGTACTCTAACTTCCACCACCCCCAGCCTGTC
35521   GGGTTTCGGTTGGTATTTTGGATTTTTATCATGAGATTGAAGGTGGTGGGGGTCGGACAG
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FIGURE 4 (cont'd)

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35581  TGTGTAAGGCCATAAAGAAATTATCTGACTCACTTTGTTTGACTGAAGGTTATAAGACCC
35581  ACACATTCCGGTATTTCTTTAATAGACTGAGTGAAACAAACTGACTTCCAATATTCTGGG

35641  CCATTCCAGAGAGGGTCCAGCACCACACCCAGAAGGAAGAAATGCATGCTCAGAGAGGCA
35641  GGTAAGGTCTCTCCCAGGTCGTGGTGTGGGTCTTCCTTCTTTACGTACGAGTCTCTCCGT

35701  AGAAGGGTCCAGACAGACAGGCTGTGCTGGATTTCCCTGCTCAGTCTATTAGCATTAGAC
35701  TCTTCCCAGGTCTGTCTGTCCGACACGACCTAAAGGGACGAGTCAGATAATCGTAATCTG

35761  CATACCTTTTTTGTCCAATCATATTTCTACGTGGCTCTCCATACTTTGTTTAACCTAACC
35761  GTATGGAAAAAACAGGTTAGTATAAAGATGCACCGAGAGGTATGAAACAAATTGGATTGG

35821  TAAGGGGGCTCAGGGTTTTGGCCTGGGCATTGTCTGTTGGGGAATAGAGTGAGTCATCCC
35821  ATTCCCCCGAGTCCCAAAACCGGACCCGTAACAGACAACCCCTTATCTCACTCAGTAGGG

35881  CAGCTCATGGGTTTGCATCCAGTTCTTGTTGTAAAAGGCCCAAAGCCTGTTGGATGGCAA
35881  GTCGAGTACCCAAACGTAGGTCAAGAACAACATTTTCCGGGTTTCGGACAACCTACCGTT

35941  CCCTGAGCCATCGTGGAAGGGGGGTTCCAGTTTCACAAATAGATACTCAGACAGCCAAAC
35941  GGGACTCGGTAGCACCTTCCCCCCAAGGTCAAAGTGTTTATCTATGAGTCTGTCGGTTTG

36001  TACCATCTACTTGGTGCCAACGTTTGCACTGTGGTCAAAGACTTACCTAGCACAGACTGA
36001  ATGGTAGATGAACCACGGTTGCAAACGTGACACCAGTTTCTGAATGGATCGTGTCTGACT

36061  ACAAATCTTCCCATCTGTCACATAAATGTCCCCAAGCAATGTTGAAGCACATGCCAGGAT
36061  TGTTTAGAAGGGTAGACAGTGTATTTACAGGGGTTCGTTACAACTTCGTGTACGGTCCTA

36121  CGGCCTTGCTAGGTCCTGCTTGGTAGATAAGCAAATGGCTTCCTTGTGGTGTTTTTATTC
36121  GCCGGAACGATCCAGGACGAACCATCTATTCGTTTACCGAAGGAACACCACAAAAATAAG

36181  TATTTTGTCTCATTAACACTACAACTTTGTGTTATCTACTTGATAATCTGTAATTGTAAA
36181  ATAAAACAGAGTAATTGTGATGTTGAAACACAATAGATGAACTATTAGACATTAACATTT

36241  TACATACAGGATTATGTAATTTGTGTAAATACATAATGACAGACTTCTGAAAACTGGTAT
36241  ATGTATGTCCTAATACATTAAACACATTTATGTATTACTGTCTGAAGACTTTTGACCATA

36301  TTTTTACTTGGTGTCCATTTGAAGCTGTTTTAGGTTCTGTGGCACATGAACCAATGGCAT
36301  AAAAATGAACCACAGGTAAACTTCGACAAAATCCAAGACACCGTGTACTTGGTTACCGTA

36361  TTAAAAAGCATACTCTCCTTGCTCTTAAAAAAACAAACAAAACAAAACAAAAACTGTCCA
36361  AATTTTTCGTATGAGAGGAACGAGAATTTTTTTGTTTGTTTTGTTTTGTTTTTGACAGGT

36421  TTAAAATTTTTGTATTTTTGTAAAGACAGGGTTTCACCATAAAAATGGACAGTTTCCCTT
36421  AATTTTAAAAACATAAAAACATTTCTGTCCCAAAGTGGTATTTTTACCTGTCAAAGGGAA

36481  ATATCTTTGGGTCTTCGTTCTGTAGGCTCTCGTGTCACATAAAATTATGATCAAATAAAT
36481  TATAGAAACCCAGAAGCAAGACATCCGAGAGCACAGTGTATTTTAATACTAGTTTATTTA

36541  TTGTATGACTTTTCTCCTATTAATCTGCCCCTTGTCAATGATTTTGAGCAACCTTCTGAA
36541  AACATACTGAAAAGAGGATAATTAGACGGGGAACAGTTACTAAAACTCGTTGGAAGACTT

36601  GAAAGTGATGGGGAAGTATTCCCTTTGCTGCCACAAGGTATATATCAGATAAGTCAGTCT
36601  CTTTCACTACCCCTTCATAAGGGAAACGACGGTGTTCCATATATAGTCTATTCAGTCAGA

36661  ATTTTCTTGAACATATATCACATTCATAGGAAAAACACTTTTTCCAAAAGATTACTGTCT
36661  TAAAAGAACTTGTATATAGTGTAAGTATCCTTTTTGTGAAAAAGGTTTTCTAATGACAGA

36721  TCCCAAATACCCACGTTCTCCATTTTTTTTTTTTTTTTTTTAGAGATGGGTCTCACTGTG
36721  AGGGTTTATGGGTGCAAGAGGTAAAAAAAAAAAAAAAAAAATCTCTACCCAGAGTGACAC

36781  TTGTCCAGGCTAGTCTCAAGCTTCTGGACTCAAGCAATCCTCTCACCTCAGCTTCCCAAA
36781  AACAGGTCCGATCAGAGTTCGAAGACCTGAGTTCGTTAGGAGAGTGGAGTCGAAGGGTTT

36841  GTGCTGTGATTACAGACATAAGCCATCACGCCCGGCCCCATTTTCTCCTTTGGGTGTATG
36841  CACGACACTAATGTCTGTATTCGGTAGTGCGGGCCGGGGTAAAAGAGGAAACCCACATAC

36901  TATATTGCTCATTGTCAGGCATCAACCATTTCTCTTCTCTGAGATGGAGTCTCACTCTGT
36901  ATATAACGAGTAACAGTCCGTAGTTGGTAAAGAGAAGAGACTCTACCTCAGAGTGAGACA
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FIGURE 4 (cont'd)

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36961  CACCCAGGCTGGAGTGCAGTGGCGCAATCTTGGCTCACTGCAAGCTCTGCCTCCCTGGTT
36961  GTGGGTCCGACCTCACGTCACCGCGTTAGAACCGAGTGACGTTCGAGACGGAGGGACCAA

37021  CACGCCATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGTGCCCACCACTACG
37021  GTGCGGTAAGAGGACGGAGTCGGAGGGCTCATCGACCCTGATGTCCACGGGTGGTGATGC

37081  CCCGGCTAATTTTTTTGTATTTCTTTTTTGGTAGAGACGGGGTTTCACCGTGTTAGACAG
37081  GGGCCGATTAAAAAAACATAAAGAAAAAACCATCTCTGCCCCAAAGTGGCACAATCTGTC

37141  GATGGTCTCAATCTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGAT
37141  CTACCAGAGTTAGAGGACTGGAGCACTAGGCGGGCGGAGCCGGAGGGTTTCACGACCCTA

37201  TACAGGTGTGAGCCACTGCGCCCAGCCCTCTTCTAATTTTTTATATTTATCATGTATTTA
37201  ATGTCCACACTCGGTGACGCGGGTCGGGAGAAGATTAAAAAATATAAATAGTACATAAAT

37261  CTAGAACTGGTTTATTTTCGTGAGCATATGTTGTGGATTCTACTATAAATAATGCACTTA
37261  GATCTTGACCAAATAAAAGCACTCGTATACAACACCTAAGATGATATTTATTACGTGAAT

37321  ATAATCATTAATAAAACTTAAATCCTTTCCGTCTTGATTGTGGCCTTTTCTTTTTGCTAT
37321  TATTAGTAATTATTTTGAATTTAGGAAAGGCAGAACTAACACCGGAAAAGAAAAACGATA

37381  TAATTTCCTCAGCATAGGTTAACCTGAACTCTTAAAAGCTATTTAGGTACTGGTATAAAA
37381  ATTAAAGGAGTCGTATCCAATTGGACTTGAGAATTTTCGATAAATCCATGACCATATTTT

37441  CAAAATTTTCTCCAAAGCAATCCAGTATATAATATCTGGATTTTAAAAAAGCAGCCTCAT
37441  GTTTTAAAAGAGGTTTCGTTAGGTCATATATTATAGACCTAAAATTTTTTCGTCGGAGTA

37501  TTAATTAGGATTAATTTCTCCTTTCAGAAGTTAAGTGATTCTGTTTCTGTAAAACGCAAA
37501  AATTAATCCTAATTAAAGAGGAAAGTCTTCAATTCACTAAGACAAAGACATTTTGCGTTT

37561  ATTATAAGCTTAATTGTTTTCCACACAGGAAATGAAATTCCTAATCTTTTTATCCAGAAT
37561  TAATATTCGAATTAACAAAAGGTGTGTCCTTTACTTTAAGGATTAGAAAAATAGGTCTTA

37621  CTTCATGTGTTTGTCTCTCTGTCCATCTGTCACTCCTTTTTAAGGTACCTGGAGATGACC
37621  GAAGTACACAAACAGAGAGACAGGTAGACAGTGAGGAAAAATTCCATGGACCTCTACTGG

37681  TAGAGGCTTGCCACGCTTAGGGTTTCCTCCCTGTGCAGAAGAAGATGGGAAGTGCAAATG
37681  ATCTCCGAACGGTGCGAATCCCAAAGGAGGGACACGTCTTCTTCTACCCTTCACGTTTAC

37741  AGGACGAGGGGTGGGGAGGGAAGAGGGAGTCAGGTGATTCAGCAAGTGCAGGAGCCCACA
37741  TCCTGCTCCCCACCCCTCCCTTCTCCCTCAGTCCACTAAGTCGTTCACGTCCTCGGGTGT

37801  GACTAAGCTCAGGAATTTGCACTTTGTCTGCTCGCAGAGTGAGTTTCATCGTGGTGTGTA
37801  CTGATTCGAGTCCTTAAACGTGAAACAGACGAGCGTCTCACTCAAAGTAGCACCACACAT

37861  TATATTGAGATATGCAACAGACTCCACTGGAATGTCAGAAGAACTTATGTTTATTTTTCC
37861  ATATAACTCTATACGTTGTCTGAGGTGACCTTACAGTCTTCTTGAATACAAATAAAAAGG

37921  TCTAACATGTGGGAAAGATTAAACTGTATTTGTATTTAACTCACATAGATTGGCACGTGC
37921  AGATTGTACACCCTTTCTAATTTGACATAAACATAAATTGAGTGTATCTAACCGTGCACG

37981  TCATTCTGTGTGTCACCCTGCCACGCTGTCACAAACTTCGAGCAGGGTCCTGAGGGGAGA
37981  AGTAAGACACACAGTGGGACGGTGCGACAGTGTTTGAAGCTCGTCCCAGGACTCCCCTCT

38041  GGAGGGCATAGCTCCTGCTCCCAGGGGGTTGCCTGTGTAGCCCTGCGCATTCATTCTCTT
38041  CCTCCCGTATCGAGGACGAGGGTCCCCCAACGGACACATCGGGACGCGTAAGTAAGAGAA

38101  CCAGAGGGTTGTGATTTGTGGCGGTCTGTGTGAGCCTGGTTAAGGAGAGTTACAGATTAT
38101  GGTCTCCCAACACTAAACACCGCCAGACACACTCGGACCAATTCCTCTCAATGTCTAATA

38161  GTCATCTGGTGTTAACTGATAATCTTTGCAAAAGGGACATTGGCTTTAAGAGATGTCTGC
38161  CAGTAGACCACAATTGACTATTAGAAACGTTTTCCCTGTAACCGAAATTCTCTACAGACG

38221  AAAAAAAACTCTAAACAAACATAAATAAAAATTTAAAAGGATAAAGCCAGAATAATAATG
38221  TTTTTTTTGAGATTTGTTTGTATTTATTTTTAAATTTTCCTATTTCGGTCTTATTATTAC
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FIGURE 4 (cont'd)

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38281   AAAATATTAGTAATGTAAAACAAGGAAATGTGTCATGTTTTTCATGATAACTAATATTTT
38281   TTTTATAATCATTACATTTTGTTCCTTTACACAGTACAAAAAGTACTATTGATTATAAAA

38341   TTCAATTTTTTTTTTTTTTTAAGACAGTCTCACTCTGTCACCAGGCTGGAGTCAGTAGTG
38341   AAGTTAAAAAAAAAAAAAAATTCTGTCAGAGTGAGACAGTGGTCCGACCTCAGTCATCAC

38401   CGATCTTGGCTCACTGCAACCTCCACCTCCCAGGTTCACACAATTCTCATGTCTCAGCCT
38401   GCTAGAACCGAGTGACGTTGGAGGTGGAGGGTCCAAGTGTGTTAAGAGTACAGAGTCGGA

38461   CCTGAGTAGCTGGGTTTACAGGCACTCGCCACCATGCCCAGCTAATTTTTGTATTTTTAG
38461   GGACTCATCGACCCAAATGTCCGTGAGCGGTGGTACGGGTCGATTAAAAACATAAAAATC

38521   TAAAGACAGGGTTTTACCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTCAGGTGATC
38521   ATTTCTGTCCCAAAATGGTACAACCGGTCCGACCAGAGTTTGAGGACTGGAGTCCACTAG

38581   GGCCGCCTTGGCCTCCCAAAGTGCTGGGATTACAGGCGTGTGCCACTGTGCCTGGCCCCA
38581   CCGGCGGAACCGGAGGGTTTCACGACCCTAATGTCCGCACACGGTGACACGGACCGGGGT

38641   GTTCTTATTATAAGTTCTCCATTAACCATATCATGAGATTAAAAAAACAACAATGATTTC
38641   CAAGAATAATATTCAAGAGGTAATTGGTATAGTACTCTAATTTTTTTGTTGTTACTAAAG

38701   ATCGGAACTGACAAATAGTGGGTGACACAATTTTGATCATCAAGAAGACTTTAAAAGAAG
38701   TAGCCTTGACTGTTTATCACCCACTGTGTTAAAACTAGTAGTTCTTCTGAAATTTTCTTC

38761   GATTTGTATCACTGTCATTACTGATTACTTGGCCCTTGTGTATACTGGGCCTTTAGCTAG
38761   CTAAACATAGTGACAGTAATGACTAATGAACCGGGAACACATATGACCCGGAAATCGATC

38821   GGCTGGTACAATAAAATAACCATAGTTAGAAAGATATTTTAAAGGATTACTTATTTCATG
38821   CCGACCATGTTATTTTATTGGTATCAATCTTTCTATAAAATTTCCTAATGAATAAAGTAC

38881   TTTATCTCACCCTTTTATCCCTATTTTTGGGCATGATTTATTATTATTAGGTTTTTAAAT
38881   AAATAGAGTGGGAAAATAGGGATAAAAACCCGTACTAAATAATAATAATCCAAAAATTTA

38941   AAATAATGAAATAAGCATGTTAGGTTTGCATGCTGCTTTGGTTAACATTGCTATATAACC
38941   TTTATTACTTTATTCGTACAATCCAAACGTACGACGAAACCAATTGTAACGATATATTGG

39001   AACCACCCCAAACTTTGTGGCCTTAAAACAATAATTTATTTATTTATTTATTTATTTATT
39001   TTGGTGGGGTTTGAAACACCGGAATTTTGTTATTAAATAAATAAATAAATAAATAAATAA

39061   TATTTATTTATTTATTTATTTTTGAGACAGAGTCTCGCTATGTCACCCAGGCTGGAGTGC
39061   ATAAATAAATAAATAAATAAAAACTCTGTCTCAGAGCGATACAGTGGGTCCGACCTCACG

39121   AGCGGCATGATCTCGGCTCACTGCAACCTCCACCTCCTGGGTTCAAGTGATCCTCCTGCC
39121   TCGCCGTACTAGAGCCGAGTGACGTTGGAGGTGGAGGACCCAAGTTCACTAGGAGGACGG

39181   TCAGCCTCCCGTAGAGCTGGGATTACAGGCACCCGCCATCAAGCCCAGCTAATTTTTCCT
39181   AGTCGGAGGGCATCTCGACCCTAATGTCCGTGGGCGGTAGTTCGGGTCGATTAAAAAGGA

39241   TTATTTTTAGTAGAGACGGGGTTTCACCATGTTGGCCAGGTTGGTCTCGAACTCCTGATC
39241   AATAAAAATCATCTCTGCCCCAAAGTGGTACAACCGGTCCAACCAGAGCTTGAGGACTAG

39301   TCAGGTGATATGCCTGCTTTGGCCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACTGT
39301   AGTCCACTATACGGACGAAACCGGAGGGTTTCACGACCCTAATGTCCACACTCGGTGACA

39361   GCATGGCCAACAATAATTTATTTTTATCTCTCATGGTCTCTAGATTGCCTGGGCCCGGCT
39361   CGTACCGGTTGTTATTAAATAAAAATAGAGAGTACCAGAGATCTAACGGACCCGGGCCGA

39421   GAGCAGTCTGAGTCAGCCTTATGGTCTCTCATGTGTTTTTAATCAGTCATGAGGGGCCGG
39421   CTCGTCAGACTCAGTCGGAATACCAGAGAGTACACAAAAATTAGTCAGTACTCCCCGGCC

39481   CATCATCTGAAGGCTTGACTGGGCTGGATGTTTAAGACAGCCACTCACAGGGCTGACAGT
39481   GTAGTAGACTTCCGAACTGACCCGACCTACAAATTCTGTCGGTGAGTGTCCCGACTGTCA

39541   GATGCTGGATGTTGCACTGTTGACTAATGAGCCTGCACGTGGCTCCTCCATGTGATTTGG
39541   CTACGACCTACAACGTGACAACTGATTACTCGGACGTGCACCGAGGAGGTACACTAAACC
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FIGURE 4 (cont'd)

39601 GCTATTTATAGCTGGGGTGACTGGGTTCTAGGTGGGGTAGTTCCAAGATCCTTCCAAGAG
39601 CGATAAATATCGACCCCACTGACCCAAGATCCACCCCATCAAGGTTCTAGGAAGGTTCTC

39661 GAAGAAAGCAGAAACTGCCTGGCCAGTTAGTGTATATGCTTAGTCTTAGAACAGTGTCAC
39661 CTTCTTTCGTCTTTGACGGACCGGTCAATCACATATACGAATCAGAATCTTGTCACAGTG

39721 TTCCATATTTCTCCATAGTCCATTAATCAAAGCAGTTACAGGAAGCAGACAGACAGGAAG
39721 AAGGTATAAAGAGGTATCAGGTAATTAGTTTCGTCAATGTCCTTCGTCTGTCTGTCCTTC

39781 GGAAAACACAATGCAACAGAAGGAGAGATTGAAGTGTTGGCAGCTGCAAGCCAAGAAACA
39781 CCTTTTGTGTTACGTTGTCTTCCTCTCTAACTTCACAACCGTCGACGTTCGGTTCTTTGT

39841 CCTGGGTTACCAGAAGCTAGAAGAAGAAAGGTAGGATTCTCCCCTACAGGTTCCAAAGGA
39841 GGACCCAATGGTCTTCGATCTTCTTCTTTCCATCCTAAGAGGGGATGTCCAAGGTTTCCT

39901 AGCTGGGCCTGTCCACACCTCACCTCTGGAACTATGAGACAATCACTTTCTGTGGGTTTA
39901 TCGACCCGGACAGGTGTGGAGTGGAGACCTTGATACTCTGTTAGTGAAAGACACCCAAAT

39961 AGCTACCCAGTTTGTGGCACTTTGTTACTACCGTCCTAGGCAAATGATACAGTAACTACA
39961 TCGATGGGTCAAACACCGTGAAACAATGATGGCAGGATCCGTTTACTATGTCATTGATGT

40021 TACACAGTACATAGAATTGCTCATTTTACTTCGTTGAATGGGACTTGGCATTGAATAAGC
40021 ATGTGTCATGTATCTTAACGAGTAAAATGAAGCAACTTACCCTGAACCGTAACTTATTCG

40081 CCAAATGAGAATTCTTTTGTCAAGATTTTTTTATGGCTCACTTTTCCAGAGACGTGACAT
40081 GGTTTACTCTTAAGAAAACAGTTCTAAAAAAATACCGAGTGAAAAGGTCTCTGCACTGTA

40141 GGCAGGAGTAAGGGGAGGGTTTGGCAGGTAGGAATTATACTCATCTGTCATTGTCTTCCC
40141 CCGTCCTCATTCCCCTCCCAAACCGTCCATCCTTAATATGAGTAGACAGTAACAGAAGGG

40201 AATACCAACCAGGAAGCATGTAAATAATAGCTGTGCAGTTTGTTTTCTGAACCAAACTGG
40201 TTATGGTTGGTCCTTCGTACATTTATTATCGACACGTCAAACAAAAGACTTGGTTTGACC

40261 GCCTTATTTTTTTTAAAGAAACTTTATTAAACAAACAAAAACCTAGAAACACTAGATGTA
40261 CGGAATAAAAAAAATTTCTTTGAAATAATTTGTTTGTTTTTGGATCTTTGTGATCTACAT

40321 TATTTTTAAGGTTTCTCTCACATAATATCCTAATCATCAGTATACCGTAATCCAAGGGCT
40321 ATAAAAATTCCAAAGAGAGTGTATTATAGGATTAGTAGTCATATGGCATTAGGTTCCCGA

40381 ACATATAACTGAAAAATAAATGGGTCTTAAAAAAATTAAAACATGGTATATAACACTAGC
40381 TGTATATTGACTTTTTATTTACCCAGAATTTTTTTAATTTTGTACCATATATTGTGATCG

40441 TAACATGTACTGAGCAGTTACTAAGTGCTAAGTACTGCTAAGTCCTTTATAGATATCTTC
40441 ATTGTACATGACTCGTCAATGATTCACGATTCATGACGATTCAGGAAATATCTATAGAAG

40501 ATGTTGAGTGTCGTCACTGCCCATTACTTACTCTGAGTTTAAATATGAGACTCAAAAGAG
40501 TACAACTCACAGCAGTGACGGGTAATGAATGAGACTCAAATTTATACTCTGAGTTTTCTC

40561 GTTAGTAATTTGCCAAAAGTCATAGGGCTTATAAGTGATAGAACCAGGATAACGAATCTC
40561 CAATCATTAAACGGTTTTCAGTATCCCGAATATTCACTATCTTGGTCCTATTGCTTAGAG

40621 AACCAAGGGACTTCAATGCCCAAACCGGTGCTCAGACTGTAGCCCCATGTAGTTAGCTAT
40621 TTGGTTCCCTGAAGTTACGGGTTTGGCCACGAGTCTGACATCGGGGTACATCAATCGATA

40681 TTACATTTGAAAAAATTTTTAATGTTTATTATTTTTTTTAAGACAGGGTCTTGCTCTGTC
40681 AATGTAAACTTTTTTAAAAATTACAAATAATAAAAAAAATTCTGTCCCAGAACGAGACAG

40741 ACCTAGGCTGGAGTGGAGTGGTGTGATCTTGGCTCACTGCAACCTCCACCTCCTGGGCTC
40741 TGGATCCGACCTCACCTCACCACACTAGAACCGAGTGACGTTGGAGGTGGAGGACCCGAG

40801 AAGTGATCCTCTCATCTCAGCCTCCCAAGTAGCTGGGACCACAGGTGTATGGCACCACGC
40801 TTCACTAGGAGAGTAGAGTCGGAGGGTTCATCGACCCTGGTGTCCACATACCGTGGTGCG

40861 CCAACTAATTTGTTGTGTTCTTGGTAGAGGTGAGTTTCACCATGTTGCCCAGGCTGGTCT
40861 GGTTGATTAAACAACACAAGAACCATCTCCACTCAAAGTGGTACAACGGGTCCGACCAGA

FIGURE 4 (cont'd)

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40921  TGAACTCCTGAGCTCAAGTGACCTCCCCACTTGCCTCACCCTCCTAAAGTGGCGGGCATTA
40921  ACTTGAGGACTCGAGTTCACTGGACGGGTGAACGGAGTGGCAGGATTTCACCCCCCTAAT

40981  CAGGTGTGAGCCACCATGCCCGGCCCAGCTATTTACATTTAAATATAAATTAAAATGAAA
40981  GTCCACACTCGGTGGTACGGGCCGGGTCGATAAATGTAAATTTATATTTAATTTTACTTT

41041  CAAGATTAAAAATTCGGTTTCTCAATCACACTAACCACACTTGAAGTGCTCAGTAGCTAC
41041  GTTCTAATTTTTAAGCCAAAGAGTTAGTGTGATTGGTGTGAACTTCACGAGTCATCGATG

41101  ATGTGGCTTAGTGGCTACCTGGCAGATATAGAACGTTTCCATCAGCACAGAAACTTCTAC
41101  TACACCGAATCACCGATGGACCGTCTATATCTTGCAAAGGTAGTCGTGTCTTTCAAGATG

41161  TGGAAAGCATTGATCCAATCTCTTTGAACAGTCACAATGCATATAAAGTCCTTATTATGA
41161  ACCTTTCGTAACTAGGTTAGAGAAACTTGTCAGTGTTACGTATATTTCAGGAATAATACT

41221  CTGTACAAGGGAAGACAACGAGTAGAGGAAGGCAGAAAATAGGAAAAAAGGAAGAAGAAA
41221  GACATGTTCCCTTCTGTTGCTCATCTCCTTCCGTCTTTTATCCTTTTTTCCTTCTTCTTT

41281  GATTTAGGGTGAGGGAGAGCAGTTCTATGAAGAAAAGAAGCTCATATCTAGGAGTGGAGT
41281  CTAAATCCCACTCCCTCTCGTCAAGATACTTCTTTTCTTCGAGTATAGATCCTCACCTCA

41341  GGACCCTGAGAACATGTTAGTCTATTATATTCTAAACTTTGGCAGTTAAAATTCCAAAGT
41341  CCTGGGACTCTTGTACAATCAGATAATATAAGATTTGAAACCGTCAATTTTAAGGTTTCA

41401  ATATTAAGTACATGCTTTCTAAAATATTAGAGAGCTGCAGTTCAACAGATTTTTAACTCT
41401  TATAATTCATGTACGAAAGATTTTATAATCTCTCGACGTCAAGTTGTCTAAAAATTGAGA

41461  CCACAGCATGTCCCGCACTGGGTGAGGTGGGATGGCTAGGTGAATAATATAGGCATTGTC
41461  GGTGTCGTACAGGCCGTGACCCACTCCACCCTACCGATCCACTTATTATATCCGTAACAG

41521  ATGTGTGTTCGTGTGAAGAGACCACCAAACAGGCTTTGTGTGAGCAATAAAGCTTTTTAA
41521  TACACACAAGCACACTTCTCTGGTGGTTTGTCCGAAACACACTCGTTATTTCGAAAAATT

41581  TCACCTGGGTACAGGCGGGCCGAGTCTGAAAAGAGAGTCAGCAAAGGGTGGTGGGATTAT
41581  AGTGGACCCATGTCCGCCCGGCTCAGACTTTTCTCTCAGTCGTTTCCCACCACCCTAATA

41641  AATTAGTTCTTAGAGGTTTGGGATAGGCGGTGGAGTAGGAACAATTTTTTGTGGGCAGGG
41641  TTAATCAAGAATCTCCAAACCCTATCCGCCACCTCATCCTTGTTAAAAAACACCCGTCCC

41701  GATGGATCTTACAAAGTACATTCTCAAGGGCGAGGAGAATATTACAAAGTACCTTAAGGG
41701  CTACCTAGAATGTTTCATGTAAGAGTTCCCGCTCCTCTTATAATGTTTCATGGAATTCCC

41761  CAGGGAAGGATATTACAAAGTACCTTCTCAAGGGTGGGGAGGGTGTATCATACAAAGTGC
41761  GTCCCTTCCTATAATGTTTCATGGAAGAGTTCCCACCCCTCCCACATAGTATGTTTCACG

41821  ATTCACAAGGGTGGGGAAATATCACAAAGTACATTATCGCAAGGGCAGGGAGGGTGTATT
41821  TAAGTGTTCCCACCCCTTTATAGTGTTTCATGTAATAGCGTTCCCGTCCCTCCCACATAA

41881  GTCACAAAGTCAATTGATCGGTTAGGGTGGGGCAGGAACAAATCACAACAGTGGAATGTC
41881  CAGTGTTTCAGTTAACTAGCCAATCCCACCCCGTCCTTGTTTAGTGTTGTCACCTTACAG

41941  ATCAGTTAAGGCAGGAACCTGCTATTTTCACTTTTGTTGATCTTCAGTTGCTTCAGGCCA
41941  TAGTCAATTCCGTCCTTGGACGATAAAAGTGAAAACAACTAGAAGTCAACGAAGTCCGGT

42001  TCTGGATGTATACGTGCAGGTCACAGGGGATATGATGGATTAGCTTGGGCTCAGAGGCCT
42001  AGACCTACATATGCACGTCCAGTGTCCCCTATACTACCTAATCGAACCCGAGTCTCCGGA

42061  GACAGACATGAACTTCCCATCATAAAATTAGAAGAGCATTAATCAAATGATTAGAATAAA
42061  CTGTCTGTACTTGAAGGGTAGTATTTTAATCTTCTCGTAATTAGTTTACTAATCTTATTT

42121  ATATTACCATTATTTTGAAATGGCAAGCATTGTATGTAAATAAACAGCAGAGGAACCCAC
42121  TATAATGGTAATAAAACTTTACCGTTCGTAACATACATTTATTTGTCGTCTCCTTGGGTG

42181  TGTAGCCTAGACAGGGTTCAGAGACGTTCCTGCCAAGGACATGGCACAGGGACTGAACAA
42181  ACATCGGATCTGTCCCAAGTCTCTGCAAGGACGGTTCCTGTACCGTGTCCCTGACTTGTT

42241  GGAAGGATGACAGTGCCTGGCAAAGGCAGGGAATGTTACAGGTATTTGGGCACCTGTGAG
42241  CCTTCCTACTGTCACGGACCGTTTCCGTCCCTTACAATGTCCATAAACCCGTGGACACTC
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FIGURE 4 (cont'd)

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42301  AAGGCCTGATGTCCGAAAGGACTGAAATAAATTAAATCTGTGGGGGCAGAGAGAAACAAA
42301  TTCCGGACTACAGGCTTTCCTGACTTTATTTAATTTACACACCCCCCTCTCTCTTTCTTT

42361  GAGCCTAGCAAAAGGTGAGCTGGAGAGTCAGAGGCAGAAGGCAGAATCTGGGATGGGCTG
42361  CTCGGATCGTTTTCCACTCGACCTCTCAGTCTCCGTCTTCCGTCTTAGACCCTACCCGAC

42421  GGAGCTTGCCAATCATTTTGTCAAATGGGTGATGTGAAGCCTTGAAGGTTTTTTGACCAA
42421  CCTCGAACGGTTAGTAAAACAGTTTACCCACTACACTTCGGAACTTCCAAAAAACTGGTT

42481  GAGGAGATGTCTTCAGATTTGCGTTTGAGACATTTTCACTGGTTGTCATGCTAAGAATGG
42481  CTCCTCTACAGAAGTCTAAACGCAAACTCTGTAAAAGTGACCAACAGTACGATTCTTACC

42541  CTTAAAGAGAAGCAAGGCTGGGGTCAGAGGAGCTGCTTGGAAGCTGTTTGGTACTAGGAT
42541  GAATTTCTCTTCGTTCCGACCCCAGTCTCCTCGACGAACCTTCGACAAACCATGATCCTA

42601  GCGGATAACATGGTTGGAGAAATGGCAACTGTCAGGGTATTTGGAGCAAGAATGGATAGA
42601  CGCCTATTGTACCAACCTCTTTACCGTTGACAGTCCCATAAACCTCGTTCTTACCTATCT

42661  CATTGGTGATCATCACTTGGATGCATTTGAGGGACAACTGCTATGTTTCTACTAGAGCAA
42661  GTAACCACTAGTAGTGAACCTACGTAAACTCCCTGTTGACGATACAAAGATGATCTCGTT

42721  CTACATAGAGCAGGAGTAAGCAACTTACAGTCCACAGACCACATTTGCTCTGTCCCGTTT
42721  GATGTATCTCGTCCTCATTCGTTGAATGTCAGGTGTCTGGTGTAAACGAGACAGGGCAAA

42781  TTCAAATACAGTTTAATGGAAACAGAGCCATGCCCGTTCTTTCACCTATTCTGCATGGCT
42781  AAGTTTATGTCAAATTACCTTTGTCTCGGTACGGGCAAGAAAGTGGATAAGACGTACCGA

42841  GACATCAGGCATGGTTCTAAGTAATATACATAAGTTTCATATATTAATGCTCATCTATCC
42841  CTGTAGTCCGTACCAAGATTCATTATATGTATTCAAAGTATATAATTACGAGTAGATAGG

42901  CAGTTGACAAACATGAAGTGTTGCTATTGTCTCATTTTACAGCGGAGAAAACTGACATAG
42901  GTCAACTGTTTGTACTTCACAACGATAACAGAGTAAAATGTCGCCTCTTTTGACTGTATC

42961  AGATTCTCTTTCGCACCCATAGCTTCAGTTACCACCTCTATGCCAATGATTCAATAATAC
42961  TCTAAGAGAAAGCGTGGGTATCGAAGTCAATGGTGGAGATACGGTTACTAAGTTATTATG

43021  CTCTAATCCAGACCTCTTCTCTGAGCTTCAGACAGGCAGATCTCTCACAGCCAGTCTTGG
43021  GAGATTAGGTCTGGAGAAGAGACTCGAAGTCTGTCCGTCTAGAGAGTGTCGGTCAGAACC

43081  AGACACTTCAGAAATCATAGGTCCCAAACCAGACTCCTCCTCATCCCCTCAAACACATTC
43081  TCTGTGAAGTCTTTAGTATCCAGGGTTTGGTCTGAGGAGGAGTAGGGGAGTTTGTGTAAG

43141  TTTTTCAACATTCCTTTTTTCTTAGTGAACATCACCAAATAGATAACCAAGTCAGATCCA
43141  AAAAAGTTGTAAGGAAAAAAGAATCACTTGTAGTGGTTTATCTATTCGTTCAGTCTAGGT

43201  AGGAGGCCTCCTTGGCACTTCTCTCATCCTTGTCCCACCTTATATCATCTATTTTTCTTT
43201  TCCTCCGGAGGAACCGTGAAGAGAGTAGGAACAGGGTGGAATATAGTAGATAAAAAGAAA

43261  TTCTTTTTTTTTGAGATGGTGTCTCACTGTGTCACCCAGGCAAGTGCAGTGGTGTGATCC
43261  AAGAAAAAAAAACTCTACCACAGAGTGACACAGTGGGTCCGTTCACGTCACCACACTAGG

43321  TGGCCCACTGCAGCCTCAACCTCACCAAGTTCAGGTAATCCTCTCACCTTAATCCCGTGA
43321  ACCGGGTGACGTCGGAGTTGGAGTGGTTCAAGTCCATTAGGAGAGTGGAATTAGGGCACT

43381  GTAGCTGGGACTACAGGCACATGCCACCGAGCCCGGCTAATTTTTGTATTTTTACCAGAG
43381  CATCGACCCTGATGTCCGTGTACGGTGGCTCGGGCCGATTAAAAACATAAAAATGGTCTC

43441  ACAGGGTTTTGCCATGTTGCCCAGGCTGCCACCTTATCTCCATTCTTGCTGAAATCTGGC
43441  TGTCCCAAAACGGTACAACGGGTCCGACGGTGGAATAGAGGTAAGAACGACTTTAGACCG

43501  TGTTTCTCTCCACTTCTATTACCAACCACCAGCCAAATCTGACTTATTAAAAGGATCATC
43501  ACAAAGAGAGGTGAAGATAATGGTTGGTGGTCGGTTTAGACTGAATAATTTTCCTAGTAG

43561  TCGTATGTGGGTTCTGTAATAGCTTCTTCAAAATCCATTCCTCTCCACCCAGACCCTCTT
43561  AGCATACACCCAAGACATTATCGAAGAAGTTTTAGGTAAGGAGAGGTGGGTCTGGGAGAA
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FIGURE 4 (cont'd)

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43621  CCAATCTCCAAACTGCAGCCAATACCTTCAATTCTGTCACCGCTCCTGCATACTCCACCT
43621  GGTTAGAGGTTTGACGTCGGTTATGGAAGTTAAGACAGTGGCGAGGACGTATGAGGTGGA

43681  AATCCTTAACCTTTCAATGGTTTCTCTTGCCCCTAGGTTAAGCTAAATTGAAAACTGCTA
43681  TTAGGAATTGGAAAGTTACCAAAGAGAACGGGGATCCAATTCGATTTAACTTTTGACGAT

43741  AAGCTACAGCTTCTTAGTGTAACTAGTAAGTACAGTGACTACTATGTCTGGTTTACTTCA
43741  TTCGATGTCGAAGAATCACATTGATCATTCATGTCACTGATGATACAGACCAAATGAAGT

43801  GCTGTTGCTGACTAATAGCACTTCTTGAATGAAGAAATTATATTACCGTACTGTAGGGAA
43801  CGACAACGACTGATTATCGTGAAGAACTTACTTCTTTAATATAATGGCATGACATCCCTT

43861  AAATTTGTACTTCAATGGAAAACTGAATTATTTAGAGCAAACCTTTAAGGTTATCTGATT
43861  TTTAAACATGAAGTTACCTTTTGACTTAATAAATCTCGTTTGGAAATTCCAATAGACTAA

43921  CTGATTCCATGGCCCCTTTCATTGGCTCTTACATTGTTTCATTGTTTTTGAGTTATTTTA
43921  GACTAAGGTACCGGGGAAAGTAACCGAGAATGTAACAAAGTAACAAAAACTCAATAAAAT

43981  CAGATGACTGATAGAAATGCAAAATAATTATTGCATGCAGTCATGCAAGTAAAATCTGAA
43981  GTCTACTGACTATCTTTACGTTTTATTAATAACGTACGTCAGTACGTTCATTTTAGACTT

44041  GGTCAGGGTTCAATTAACTTCTCTCCCCTACTGTGGAAGAAGCCAATTTCATTTGCATAT
44041  CCAGTCCCAAGTTAATTGAAGAGAGGGGATGACACCTTCTTCGGTTAAAGTAAACGTATA

44101  TCATTTCAATATTTCTGACCTATAAACATGCCTGTTCTTTGAACCAGTTTTTATATCTGC
44101  AGTAAAGTTATAAAGACTGGATATTTGTACGGACAAGAAACTTGGTCAAAAATATAGACG

44161  CTGGTAACTTCATTAAATGATTTAAATAAACTCTATAATTTAGTTTATTTTATACCTGTA
44161  GACCATTGAAGTAATTTACTAAATTTATTTGAGATATTAAATCAAATAAAATATGGACAT

44221  TGACAGTCAGGCTTTTACCTTATTTTTGCTTTTTAAAATTATTCTTTAGCTCTCCCTAAG
44221  ACTGTCAGTCCGAAAATGGAATAAAAACGAAAAATTTTAATAAGAAATCGAGAGGGATTC

44281  GCACTACTTGGCTGGCCCTTTGGCTACTCACTAGCCCAAGCTCCATCCTCTTCTGTCTAC
44281  CGTGATGAACCGACCGGGAAACCGATGAGTGATCGGGTTCGAGGTAGGAGAAGACAGATG

44341  CGCAGCCCCAGGCTCTCTTTTGGCCCTTTGTTCCAGCCCTCCTCAGAGAAGTTCTTTTGT
44341  GCGTCGGGGTCCGAGAGAAAACCGGGAAACAAGGTCGGGAGGAGTCTCTTCAAGAAAACA

44401  CCTGGAACTCACTTTCATACCAGGTGCTCTTCATCCCTTCTTCCTTTAGTAAATTTCTTT
44401  GGACCTTGAGTGAAAGTATGGTCCACGAGAAGTAGGGAAGAAGGAAATCATTTAAAGAAA

44461  AATCTTTCAGATTTCTGCTCAAGGATCACTTGCTGAAAGCCTTTCCAGGCCTTTCTGAGT
44461  TTAGAAAGTCTAAAGACGAGTTCCTAGTGAACGACTTTCGGAAAGGTCCGGAAAGACTCA

44521  CAATACAATCCATTATTAGAGGCTCTTAGAGCACAGGCAGCACTTGTTATAATTTTACAT
44521  GTTATGTTAGGTAATAATCTCCGAGAATCTCGTGTCCGTCGTGAACAATATTAAAATGTA

44581  CTGTCTGTGGGATTCCTTAACACTTTCTAACACAATTAACACTTTTCTCTCTGGCTGGGG
44581  GACAGACACCCTAAGGAATTGTGAAAGATTGTGTTAATTGTGAAAAGAGAGACCGACCCC

44641  GCAATGCATGATAACAGGATGATGGTATGCTCTCAACCCTCCCCCAGCAACTAGCCCAGT
44641  CGTTACGTACTATTGTCCTACTACCATACGAGAGTTGGGAGGGGGTCGTTGATCGGGTCA

44701  GCTTCGAACATGGTGGATAGATACACCGTTTTTATTTTAGACAGATTTTTGAGTAGCAAG
44701  CGAAGCTTGTACCACCTATCTATGTGGCAAAAATAAAATCTGTCTAAAAACTCATCGTTC

44761  TACCTACTGCTCAGCAGACAGATGGACTGAAAAAATATATTTGGCAGTCATCAGCACATA
44761  ATGGATGACGAGTCGTCTGTCTACCTGACTTTTTTATATAAACCGTCAGTAGTCGTGTAT

44821  GGTGCAGCCATGAAAATGCACGAGAAGCAAAACCATTGGCAGGAACAAAATGAAGGCTAT
44821  CCACGTCGGTACTTTTACGTGCTCTTCGTTTTGGTAACCGTCCTTGTTTTACTTCCGATA

44881  TAGAGACCTTATTTAGGTGGAATAATTGGACAGAAGCCCTTAATGGGGAGGAAATAGAAG
44881  ATCTCTGGAATAAATCCACCTTATTAACCTGTCTTCGGGAATTACCCCTCCTTTATCTTC

44941  CAGTTAATACAGATGGAGGCCGGGCGCCGTGGCTCACGCCTGTAATCCTAGCACTTTGGG
44941  GTCAATTATGTCTACCTCCGGCCCGCGGCACCGAGTGCGGACATTAGGATCGTGAAACCC
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FIGURE 4 (cont'd)

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45001  AGGCTGAGATAGGTGGGTGGCTTGAGTCCAGGAGTTTGAGAGCAGCCTGGGCAACATAGC
45001  TCCGACTCTATCCACCCACCGAACTCAGGTCCTCAAACTCTCGTCGGACCCGTTGTATCG

45061  AAAACCCGGTCTCTACAAAAAATACAAAAATTAGCCCGGCGTGGTGGCGCAGGCCTGTAG
45061  TTTTGGGCCAGAGATGTTTTTTATGTTTTTAATCGGGCCGCACCACCGCGTCCGGACATC

45121  TCCCGGCTACTGGGGAGGCTGAGATGGGAGAATTGCTTGAACCGGGGAGGCGGATGTTGC
45121  AGGGCCGATGACCCCTCCGACTCTACCCTCTTAACGAACTTGGCCCCTCCGCCTACAACG

45181  AATTAGACGAGATCGCGCCACTGCACTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCA
45181  TTAATCTGCTCTAGCGCGGTGACGTGAGGTCGGACCCGCTGTCTCGCTCTGAGGCAGAGT

45241  AAACAACAAGGACAAAACTTATCTTATAAGCGACCCTGGACTTCCAGGGACACTCGCCGC
45241  TTTGTTGTTCCTGTTTTGAATAGAATATTCGCTGGGACCTGAAGGTCCCTGTGAGCGGCG

45301  TCTATGGTGGTACGTGACCTGCCTGGACTCTGTGGTCTTTGGAGCTTGGGACCCCACCCC
45301  AGATACCACCATGCACTGGACGGACCTGAGACACCAGAAACCTCGAACCCTGGGGTGGGG

45361  AGCGTAAGAGGCCTTTCTGTGCCTTGTATAAAGGAGAGGAAAAGTGTAGGTTTTCTGAGT
45361  TCGCATTCTCCGGAAAGACACGGAACATATTTCCTCTCCTTTTCACATCCAAAAGACTCA

45421  TGATAAGATTAGAGCTACAGTATATTATCAGTAGCGTTGTATGAAACCATTTAAAAAACC
45421  ACTATTCTAATCTCGATGTCATATAATAGTCATCGCAACATACTTTGGTAAATTTTTTGG

45481  AAACCGGATTTAACCGCTTTCACCCAGAATAAACTGCCCTCCCCCTCTTTCCAAGATCAA
45481  TTTGGCCTAAATTGGCGAAAGTGGGTCTTATTTGACGGGAGGGGGAGAAAGGTTCTAGTT

45541  GTCAGCCCCAGTTACCACTTCCTATTAATTTAAAAACCAGGAAGGCTCATAATTTAGGCT
45541  CAGTCGGGGTCAATGGTGAAGGATAATTAAATTTTTGGTCCTTCCGAGTATTAAATCCGA

45601  GACGTTGCCCCAGGCGAACACTGCATATAAGACAATAGCTATTCCAATCCTCCTTTCCCT
45601  CTGCAACGGGGTCCGCTTGTGACGTATATTCTGTTATCGATAAGGTTAGGAGGAAAGGGA

45661  TTCTAAACCGAATAGTACTTCTAACATCACTTTTCCAGTCCTCTTTCTAAATATTGCGAT
45661  AAGATTTGGCTTATCATGAAGATTGTAGTGAAAAGGTCAGGAGAAAGATTTATAACGCTA

45721  CACGAGCCTACATCGGAAAACTATGAAAACAGTATGATTGGAGCTCTTGATGGTCTGCTT
45721  GTGCTCGGATGTAGCCTTTTGATACTTTTGTCATACTAACCTCGAGAACTACCAGACGAA

45781  TGCCTGAAAACGATGAAAGGCATTGAGATCTTTGGGCAGAAATGGCCCTTAGGGAATGCG
45781  ACGGACTTTTGCTACTTTCCGTAACTCTAGAAACCCGTCTTTACCGGGAATCCCTTACGC

45841  AGCCTGGTAGCCCCATAACACCCCGAGTTACAAATTCGGTTTGGGTAGGTGGCGCAGGGA
45841  TCGGACCATCGGGGTATTGTGGGGCTCAATGTTTAAGCCAAACCCATCCACCGCGTCCCT

45901  AATCTAAAAGCTGGATTCACGTTCTCCCCCTTCAGTTTGCACATAGCGGTCAGTGGCAGA
45901  TTAGATTTTCGACCTAAGTGCAAGAGGGGGAAGTCAAACGTGTATCGCCAGTCACCGTCT

45961  CAAGAGCAGACGCACAAATGTCAATCCCCGCCCGCAAACTCTCGAGGGCAGAAACTGCTT
45961  GTTCTCGTCTGCGTGTTTACAGTTAGGGGCGGGCGTTTGAGAGCTCCCGTCTTTGACGAA

46021  TTTGTCAGTTGGATTTGGAGTCGGTGGAAAAGCTGCCCTAATGTAGTTTCTCCGAGGTTT
46021  AAACAGTCAACCTAAACCTCAGCCACCTTTTCGACGGGATTACATCAAAGAGGCTCCAAA

46081  CCTTAGCCTTGACCGAGGGGCGCTTCCCGGCCATTCACCTAGAGGTTGTTTAATAAACAA
46081  GGAATCGGAACTGGCTCCCCGCGAAGGGCCGGTAAGTGGATCTCCAACAAATTATTTGTT

46141  GGATGCTCGCGAAATATCTGCGCTTGGAAAGGCGCTCGTTCGTGGCGCGCATTCTCGGGC
46141  CCTACGAGCGCTTTATAGACGCGAACCTTTCCGCGAGCAAGCACCGCGCGTAAGAGCCCG

46201  CTCCGCAAGCGACCCCGGTGACAGGGACAACCGCTTCGGTTTTAGCGACTGCAGACAGAC
46201  GAGGCGTTCGCTGGGGCCACTGTCCCTGTTGGCGAAGCCAAAATCGCTGACGTCTGTCTG

46261  TGGGACGAGACGGTTGGAGGCTCCTCCCCAAGGGATGCTGGAGGGGTTGCGTCGTACCCT
46261  ACCCTGCTCTGCCAACCTCCGAGGAGGGGTTCCCTACGACCTCCCCAACGCAGCATGGGA
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FIGURE 4 (cont’d)

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46321  GCGCCTGGCCCTGGCGCGCGGCCCCAGGTCGTGGTACCCAGCGCCCTATGGGCCGTGCGC
46321  CGCGGACCGGGACCGCGCGCCGGGGTCCAGCACCATGGGTCGCGGGATACCCGGCACGCG

46381  CGGGGCTTGGCCACACCGCCTGCTTTCGCTTCCAGCCGCGCGCTCCGTGCCACTGCCGCT
46381  GCCCCGAACCGGTGTGGCGGACGAAAGCGAAGGTCGGCGCGCGAGGCACGGTGACGGCGA

46441  CTCTGCAGCCCCGCGTCCCCGCAGCCTCCCCATGGCCAGCCCGCTTCGCTCCGCTGCGGC
46441  GAGACGTCGGGGCGCAGGGGCGTCGGAGGGGTACCGGTCGGGCGAAGCGAGGCGACGCCG

46501  CCTTGCCCGCCAGGTACCTCGAACCCGGGCGTTTGCGGAAGGGGGGAGGATTGGAACCCG
46501  GGAACGGGCGGTCCATGGAGCTTGGGCCCGCAAACGCCTTCCCCCCTCCTAACCTTGGGC

46561  GGTCTCGGTAGCTCGCGGGCCTGGCCGGGCGCCTTGTCGCCGTTTCCTGCACCATCCTCC
46561  CCAGAGCCATCGAGCGCCCGGACCGGCCCGCGGAACAGCGGCAAAGGACGTGGTAGGAGG

46621  TTCGCCTTGCCCTCCATTCCGCCTCCAGCGAGGCGTCTTCCCTTCCCCGCATCCCTGCCC
46621  AAGCGGAACGGGAGGTAAGGCGGAGGTCGCTCCGCAGAAGGGAAGGGGCGTAGGGACGGG

46681  GAAATCTGGAGTCCCAGCCTGCAATCTCCACCTCTTCGAGGTTCCCGCTGCCCAGGTCTA
46681  CTTTAGACCTCAGGGTCGGACGTTAGAGGTGGAGAAGCTCCAAGGGCGACGGGTCCAGAT

46741  GCACCCTCATGGGTAACCCGCTCCGGAGCGTGGCGAGGACCGCCACGGGGGACGTGAGGG
46741  CGTGGGAGTACCCATTGGGCGAGGCCTCGCACCGCTCCTGGCGGTGCCCCCTGCACTCCC

46801  TAGCTATGGACTCGCTCTGAGGGAGGAGGCGGGAGCTGAATCTCTGGGCTGCCAGAACCC
46801  ATCGATACCTGAGCGAGACTCCCTCCTCCGCCCTCGACTTAGAGACCCGACGGTCTTGGG

46861  ACAGCCACATCCTACGTGACTCTGCCACCCCAAAATATTTTGACCGCAGCCTTCTGCCTC
46861  TGTCGGTGTAGGATGCACTGAGACGGTGGGGTTTTATAAAACTGGCGTCGGAAGACGGAG

46921  CTTGGATCTCTTCCTTCCCCACCCCCACCCCCGTAGTTATTTAGCAGATTACGCATTAAA
46921  GAACCTAGAGAAGGAAGGGGTGGGGGTGGGGGCATCAATAAATCGTCTAATGCGTAATTT

46981  ACAAATGTCTGCAGGTTTTCCCAATTAGTCCCGCTTCCCTGTGTCTTTATCTTTTAAATT
46981  TGTTTACAGACGTCCAAAAGGGTTAATCAGGGCGAAGGGACACAGAAATAGAAAATTTAA

47041  GCCCACTAATACCATGAGGTTTAAGGTGTGGGGTGGATGCTGCGGCATCGGAGGACCCTG
47041  CGGGTGATTATGGTACTCCAAATTCCACACCCCACCTACGACGCCGTAGCCTCCTGGGAC

47101  CTGGTGGAGGAAATGGTTCACGCCCGTCCCCGTTCCCTTTGCAGGCTTGCTATTGTGCGT
47101  GACCACCTCCTTTACCAAGTGCGGGCAGGGGCAAGGGAAACGTCCGAACGATAACACGCA

47161  CTGTGATTGACAAGACCACGAGGCTGAGCGCGCCCTGGAGATTTTTCTATAAATGGCTTA
47161  GACACTAACTGTTCTGGTGCTCCGACTCGCGCGGGACCTCTAAAAAGATATTTACCGAAT

47221  ACACCCCAGTCTAGACTATTTGCTCGGATATAAGGGAGACAATTGTTTTTTTGTTCTTTG
47221  TGTGGGGTCAGATCTGATAAACGAGCCTATATTCCCTCTGTTAACAAAAAAACAAGAAAC

47281  CCGGCGAACCCTGGCTCTGTAGGGCTGACCTGGAATTTAACCAGTCTTCCCTGAGCCGGC
47281  GGCCGCTTGGGACCGAGACATCCCGACTGGACCTTAAATTGGTCAGAAGGGACTCGGCCG

47341  GGAGGAGGACAAAAACCGCCGCGACCCCGGCAGGGTGGGAAGTGCAGGGCAGCGCTCCCA
47341  CCTCCTCCTGTTTTTGGCGGCGCTGGGGCCGTCCCACCCTTCACGTCCCGTCGCGAGGGT

47401  AGACACGCTTGTTGGAGGTTCGGGCCTGGGTGCTTGGTTGTCTGAGCCTCCTTTTTTGTG
47401  TCTGTGCGAACAACCTCCAAGCCCGGACCCACGAACCAACAGACTCGGAGGAAAAAACAC

47461  TTTGCCTGGGTCCTGGAGAGGAGCGCACGGTATCATGGTGAGCGTCACGTAGGTTACCCC
47461  AAACGGACCCAGGACCTCTCCTCGCGTGCCATAGTACCACTCGCAGTGCATCCAATGGGG

47521  GGGTCCCGCTTACCCACCTGCATTTACTTAATGGTGGTTTAATTCTTCTTTAAGGATTGC
47521  CCCAGGGCGAATGGGTGGACGTAAATGAATTACCACCAAATTAAGAAGAAATTCCTAACG

47581  AGTAACGGATGCTCCGCAGAGTGTACCGGAGAAGGAGGATCAAAAGAGGTGGTGGGGACT
47581  TCATTGCCTACGAGGCGTCTCACATGGCCTCTTCCTCCTAGTTTTCTCCACCACCCCTGA

47641  TTTAAGGTAAGTTGCTTGCCAGAGGCTTAGTGTCTAAAGCAACGTTCAACTGAATAAATC
47641  AAATTCCATTCAACGAACGGTCTCCGAATCACAGATTTCGTTGCAAGTTGACTTATTTAG
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FIGURE 4 (cont'd)

47701 CATTTCTTCTTGAGATTCGGGGAAATTTTCACTGTGTGGGTTACCCACTTCCTAGGTTGT
47701 GTAAAGAACAACTCTAAGCCCCTTTAAAAGTGACACACCCAATGGGTCAAGGATCCAACA

47761 GTTGCCAGACTTTTAAAATTCCACTCTTAGAGGAAAAAAAGCCATTTAGAGAGTGACAGT
47761 CAACGGTCTGAAAATTTTAAGGTGAGAATCTCCTTTTTTTCGGTAAATCTCTCACTGTCA

47821 ACATTCATCACAACAAAAATTATCTAGCAGCTAATTGCTGATTTTATTTTGAGTCATATA
47821 TGTAAGTAGTGTTGTTTTTAATAGATCGTCGATTAACGACTAAAATAAAACTCAGTATAT

47881 TTTTTCTTGAAAAATAGTCAATGCGTAAATATTAAACTAGTTGTTTATCAGATTCCATAA
47881 AAAAAGAACTTTTTATCAGTTACGCATTTATAATTTGATCAACAAATAGTCTAAGGTATT

47941 TACGTACAAACCTTCAGTCTACTTGTAGAAAAAGTTAAACTGTGATTTTTCTCTTTCAGT
47941 ATGCATGTTTGGAAGTCAGATGAACATCTTTTTCAATTTGACACTAAAAAGAGAAAGTCA

48001 AGCACATAACACTCTACAGTGAAAGTGTTGCATTTTCTTCTTTTCTATCTGAATTGCGGG
48001 TCGTGTATTGTGAGATGTCACTTTCACAACGTAAAAGAAGAAAAGATAGACTTAACGCCC

48061 GTTTATATAGTAAATAGCTCATACTTCAAACAGTGAGAAACAAAGCACGTTGAAAACTGT
48061 CAAATATATCATTTATCGAGTATGAAGTTTGTCACTCTTTGTTTCGTGCAACTTTTGACA

48121 ACAAATACAAATGTAAGATGTAATATTATTTTTTCTATAAGTCTATCTCCTACCCTCCCT
48121 TGTTTATGTTTACATTCTACATTATAATAAAAAAGATATTCAGATAGAGGATGGGAGGGA

48181 CCTCGTGGAGGTTTTAGCTTCTTCTTTTTATGCCTAGTGCTGCTCTTCTGCCTGTTTGAG
48181 GGAGCACCTCCAAAATCGAAGAAGAAAAATACGGATCACGACGAGAAGACGGACAAACTC

48241 TCACTGTCAATTGTCATCAGACAATTGACACAGAGTGTCCTAATGATCTCACATCCTGGC
48241 AGTGACAGTTAACAGTAGTCTGTTAACTGTGTCTCACAGGATTACTAGAGTGTAGGACCG

48301 GGTTCAGAGAGGGAAGGAAACTTGACTCATCAGTTTCTCACACATTGAGCTCTCTCACAG
48301 CCAAGTCTCTCCCTTCCTTTGAACTGAGTAGTCAAAGAGTGTGTAACTCGAGAGAGTGTC

48361 TGTGCTGGAGACTGTGCCATGCATTGGACATCCAAAGGTGAATTCAAGATTAGGTCTCTA
48361 ACACGACCTCTGACACGGTACGTAACCTGTAGGTTTCCACTTAAGTTCTAATCCAGAGAT

48421 CTTGCAAGGAATTTTTATTTTATTTTTCTTTTTCCTTCTCTTGCTGTCATCTTAGCAAGG
48421 GAACGTTCCTTAAAAATAAAATAAAAAGAAAAAGGAAGAGAACGACAGTAGAATCGTTCC

48481 ATTTTTTAAAAAGCAAAATTAGAATATTGCAATTTCTTTTCTGTTTTTTGAGACAGGGTC
48481 TAAAAAATTTTTCGTTTTAATCTTATAACGTTAAAGAAAAGACAAAAAACTCTGTCCCAG

48541 TCGCTCTGTCACCCAGGCTGGAGTGCAGTGGCACGATCTCAGCTCACTGCAATCTCTGCC
48541 AGCGAGACAGTGGGTCCGACCTCACGTCACCGTGCTAGAGTCGAGTGACGTTAGAGACGG

48601 TCCCAGGTTCAAGTGATTCTCCTGCCTCAGCCTCCTGAGTAGCTGAGATTACAGGCATGT
48601 AGGGTCCAAGTTCACTAAGAGGACGGAGTCGGAGGACTCATCGACTCTAATGTCCGTACA

48661 GCCATCACGCCCAGCTAATTTTGTATTTTTAGTAGAGATGGGGTTATCACCATGTTAGCC
48661 CGGTAGTGCGGGTCGATTAAAACATAAAAATCATCTCTACCCCAATAGTGGTACAATCGG

48721 AGGCTGGTCTCGAACTCCTGGCCTCATGCAATCCACCTCCCAAAGTGCTGGGATTGCAGG
48721 TCCGACCAGAGCTTGAGGACCGGAGTACGTTAGGTGGAGGGTTTCACGACCCTAACGTCC

48781 CGTGAGCCACCAAGCCTAGCCTGAAGAATTCTTTGCAAAGAAAAATATCAACTCAAATTT
48781 GCACTCGGTGGTTCGGATCGGACTTCTTAAGAAACGTTTCTTTTTATAGTTGAGTTTAAA

48841 AAATAATCTTTTCCTTTCTTTTTCTTTTTTTTGAGACAGAGTCTTGTTCTGTTGCCCAGA
48841 TTTATTAGAAAAGGAAAGAAAAAGAAAAAAAACTCTGTCTCAGAACAAGACAACGGGTCT

48901 CTGAAGTGCAGTGGCACCATCAATTAGGTATCACTTTCAGCCTTGATCTCTCAGACTCAA
48901 GACTTCACGTCACCGTGGTAGTTAATCCATAGTGAAAGTCGGAACTAGAGAGTCTGAGTT

48961 GTGATCCTCTTAGCCTCTCAAGTACCTGAGACTATCGGCTTGCATGCCATCAGGCCCAAC
48961 CACTAGGAGAATCGGAGAGTTCATGGACTCTGATAGCCGAACGTACGGTAGTCCGGGTTG

FIGURE 4 (cont'd)

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49021  TAATTTCGTCATTTTTTGTAGAGATGGGATCTCCCTGTGTTGCCCAGACTGATCTCCAAC
49021  ATTAAAGCAGTAAAAAACATCTCTACCCTAGAGGGACACAACGGGTCTGACTAGAGGTTG

49081  TCCTGGGCTTGTGCAACCCTCCCACCTCGGCCTCCCAAAATGCTGGGTCACAGGCATAAG
49081  AGGACCCGAACACGTTGGGAGGGTGGAGCCGGAGGGTTTTACGACCCAGTGTCCGTATTC

49141  CCACAATGCCTGGCCATAAATAATCTTTTTTATTTGTTAATTTAGATTTCTGTATATTAG
49141  GGTGTTACGGACCGGTATTTATTAGAAAAAATAAACAATTAAATCTAAAGACATATAATC

49201  GTTTTATTTAGGGGAATTGCCTGTTTACACTCATGTATTTACACATCAAAACATGAGTTA
49201  CAAAATAAATCCCCTTAACGGACAAATGTGAGTACATAAATGTGTAGTTTTGTACTCAAT

49261  TGGTGGATGTATTCACAGCACATATGTAATAAGGCATGTGTAAAAATGATATTGATAATT
49261  ACCACCTACATAAGTGTCGTGTATACATTATTCCGTACACATTTTTACTATAACTATTAA

49321  TAGGGAATAAAAATGGTAGATTTTATAGACCATCTTTGTTTTTGATATACTTTTCTCTGT
49321  ATCCCTTATTTTTACCATCTAAAATATCTGGTAGAAACAAAAACTATATGAAAAGAGACA

49381  CTCAAAAAACAAAAACAAAAACAAACAAACAAACAAAATATATATATATAGCCTACATTG
49381  GAGTTTTTTGTTTTTGTTTTTGTTTGTTTGTTTGTTTTATATATATATATCGGATGTAAC

49441  TTGTTAACTATAATCACCCTACTCTGCTATGAACAGTAGACTTTATCGCTTCTATCTAAC
49441  AACAATTGATATTAGTGGGATGAGACGATACTTGTCATCTGAAATAGCGAAGATAGATTG

49501  TGTATGTTTGTACTCATTAACCAACCTCTCTTCCTCCACCTACACCCTTCCCACCCCCTG
49501  ACATACAAACATGAGTAATTGGTTGGAGAGAAGGAGGTGGATGTGGGAAGGGTGGGGGAC

49561  CCATCTTCTGATATCTATCATTCTATGAGTACTCTCTTCCTCCATGAGATCAACTTTTTT
49561  GGTAGAAGACTATAGATAGTAAGATACTCATGAGAGAAGGAGGTACTCTAGTTGAAAAAA

49621  TTTTAGCTCTCACGTATGAGTGAGAACATGCAATATTTGTTTTTCTGGGTTTTTTTTTTT
49621  AAAATCGAGAGTGCATACTCACTCTTGTACGTTATAAACAAAAAGACCCAAAAAAAAAAA

49681  TTCTGTGTTTGGCTTATTTCGCTTACCATAATGACTTCCAGTTCCATCCATGTTGCTACA
49681  AAGACACAAACCGAATAAAGCGAATGGTATTACTGAAGGTCAAGGTAGGTACAACGATGT

49741  AATGACACGATTTTACTCTTTTTTAATGGCTGAGTAGTATTCCATTGTGTATATGCACCA
49741  TTACTGTGCTAAAATGAGAAAAAATTACCGACTCATCATAAGGTAACACATATACGTGGT

49801  CATTTTATTTGTTCATTGATGGACACTTAGGTGATTCCATGTCTTGACTATTGTGAATAG
49801  GTAAAATAAACAAGTAACTACCTGTGAATCCACTAAGGTACAGAACTGATAACACTTATC

49861  TGCTGTAATAAACATGGGACTGCAGATATCCCTTTGATATACTGATTTCCTTTCCTTTGG
49861  ACGACATTATTTGTACCCTGACGTCTATAGGGAAACTATATGACTAAAGGAAAGGAAACC

49921  AAAATACCCAGTAGTAGGATTGTTGGTTTATATGGTCATTCTACTTTTAGTTTTTTTTTT
49921  TTTTATGGGTCATCATCCTAACAACCAAATATACCAGTAAGATGAAAATCAAAAAAAAAA

49981  GGAAAGCTTCATACCATTTTCCACAGTACATAAACTAATTTACATTCTTACCAACACTGT
49981  CCTTTCGAAGTATGGTAAAAGGTGTCATGTATTTGATTAAATGTAAGAATGGTTGTGACA

50041  ATAAGCGTTCTCTTTTCTCTGTATCCTCATCAGCATCTGTTATTTTTTGTCTTTCTAATA
50041  TATTCGCAAGAGAAAAGAGACATAGGAGTAGTCGTAGACAATAAAAAACAGAAAGATTAT

50101  ATAACCATTCTAACTGTGGTTGCTTTTGACATATTTCTCTACCTTTTTGTTAATCTACAT
50101  TATTGGTAAGATTGACACCAACGAAAACTGTATAAAGAGATGGAAAAACAATTAGATGTA

50161  CATTTATAACATTTCATATGGCCTTTTGGGTCTCTCTTGGGTAGTTTTCGTATTTCTTCT
50161  GTAAATATTGTAAAGTATACCGGAAAACCCAGAGAGAACCCATCAAAAGCATAAAGAAGA

50221  CCCCTCCCCATTTATGATGCAGTCATATTACATGAGGATGCAGTTTTGCAGCAGGGCCTA
50221  GGGGAGGGGTAAATACTACGTCAGTATAATGTACTCCTACGTCAAAACGTCGTCCCGGAT

50281  GCAATGAGATACGTTGTTACACATCCTGGCGAATCTTTCTGTGGACTCTAGGATCCTCTT
50281  CGTTACTCTATGCAACAATGTGTAGGACCGCTTAGAAAGACACCTGAGATCCTAGGAGAA

50341  CATTTGCAAGAGGTCAGCCATCTATTTCTTCCAATTCCTCCAGCTTCACATATCTCCACA
50341  GTAAACGTTCTCCAGTCGGTAGATAAAGAAGGTTAAGGAGGTCGAAGTGTATAGAGGTGT
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FIGURE 4 (cont'd)

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50401  GAATGCAACACTGCAAATCTGCACTTCTCTTCATGATCCTCTTTATTAGATTTTAAAACA
50401  CTTACGTTGTGACGTTTAGACGTCAAGAGAAGTACTAGGAGAAATAATCTAAAATTTTCT

50461  GTATCTCCAAAAGATGAACATAGTGCCTAAGGCTTTCCAAATGGAGTAAGAATAATGCAC
50461  CATAGAGGTTTTCTACTTGTATCACGGATTCCGAAAGGTTTACCTCATTCTTATTACGTG

50521  AAGAACCTAGAATAAAGTTATTAAATGTCTGATACAGTTGTAATACAGACTTGATTTTTG
50521  TTCTTGGATCTTATTTCAATAATTTACAGACTATGTCAACATTATGTCTGAACTAAAAAC

50581  AAAAATGTGGCCAATGAAGAGAAGAGCAAATGTGCTATACGATGGTGAGCAAAAGGTGTT
50581  TTTTTACACCGGTTACTTCTCTTCTCGTTTACACGATATGCTACCACTCGTTTTCCACAA

50641  GACAGGCCTGGCATGGTGACTCACCCCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGG
50641  CTGTCCGGACCGTACCACTGAGTGGGGACATTAGGGTCGTGAAACCCTCCGACTCCACCC

50701  TGGATCATTTGAGGTCAGGAGTTTGAGACTAGCCTGGCCAACATGGTGAAACCCTGTTTG
50701  ACCTAGTAAACTCCAGTCCTCAAACTCTGATCGGACCGGTTGTACCACTTTGGGACAAAC

50761  TATTAAAAATACAAAAATTAGCCAGGTGCGATGACACATGCCTGTAATCCCAGCTACCTG
50761  ATAATTTTTATGTTTTTAATCGGTCCACGCTACTGTGTACGGACATTAGGGTCGATGGAC

50821  GGAGGCTGAGGCTTGAGACTTGCTTGAACCGGGGAGGCGGAGGTTGCAGCGAGCCGAGAT
50821  CCTCCGACTCCGAACTCTGAACGAACTTGGCCCCTCCGCCTCCAACGTCGCTCGGCTCTA

50881  TCTGCCACTGCACTCCAGCCTGGGCAACAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAG
50881  ACACGGTGACGTGAGGTCGGACCCGTTGTCTCGTTTTTTTTTTTTTTTTTTTTTTTTTTC

50941  TGTTGACTGAACCCTGGCTGAAACAGTTTTCAGGTGCTTTCAACAAATTTACACTTCCCT
50941  ACAACTGACTTGGGACCGACTTTGTCAAAAGTCCACGAAAGTTGTTTAAATGTGAAGGGA

51001  GCCCTGAGCCTCCCTATTTCAGAACAAATGATTACCCAACTGCAAACTTTGAATTAGGAA
51001  CGGGACTCGGAGGGATAAAGTCTTGTTTACTAATGGGTTGACGTTTGAAACTTAATCCTT

51061  GTTGTTTTTAATATGCCCTGTTTTTCTCAATATTTCTTGCCATTTCACAATCAGTTATTG
51061  CAACAAAAATTATACGGGACAAAAAGAGTTATAAAGAACGGTAAAGTGTTAGTCAATAAC

51121  TGGCATTCCAATTCTTCCACAAACATATGATGTGAAACATCCTGACTTCGATGTCATCAG
51121  ACCGTAAGGTTAAGAAGGTGTTTGTATACTACACTTTGTAGGACTGAAGCTACAGTAGTC

51181  GGAATGTGGAGCATTGGAAAGAGACAGATTAATTATGCAGAAGAAAGTATCATTTGACAA
51181  CCTTACACCTCGTAACCTTTCTCTGTCTAATTAATACGTCTTCTTTCATAGTAAACTGTT

51241  AATATTATTTTTATTTATCTTTGGAAAGGAAATCTAGAAAAAGAAAATACTTTTTAAAGA
51241  TTATAATAAAAATAAATAGAAACCTTTCCTTTAGATCTTTTTCTTTTATGAAAAATTTCT

51301  ACACTGATAAAAATTGTTTATAAAATTTGTTTCCTTTAGGAAACAAATCGTTCCCTTAAA
51301  TGTGACTATTTTTAACAAATATTTTAAACAAAGGAAATCCTTTGTTTAGCAAGGGAATTT

51361  ACTACATTTCATATCTGCCCCAAACGAGTCACATGTCTTCAGCTAATATTGCTTGTTTAC
51361  TGATGTAAAGTATAGACGGGGTTTGCTCAGTGTACAGAAGTCGATTATAACGAACAAATG

51421  GTTTGAACTTTATTCAATTCTATCACCTAGTAATTTAGTATTCTTAGGTAATTTCTCTTT
51421  CAAACTTGAAATAAGTTAAGATAGTGGATCATTAAATCATAAGAATCCATTAAAGAGAAA

51481  GAGCTCAGGTTAAAAGTTGTTATTTTTAGTTTTCAGAGTTGCAGAATTTTTTTTTCAAGT
51481  CTCGAGTCCAATTTTCAACAATAAAAATCAAAAGTCTCAACGTCTTAAAAAAAAAGTTCA

51541  AGAGAAAAGTTCATGATGAGATTCTGAAGCCACCTAATCGTATATTACTTTGAAAAACTG
51541  TCTCTTTTCAAGTACTACTCTAAGACTTCGGTGGATTAGCATATAATGAAACTTTTTGAC

51601  GATATATGCCGGGCGCGGTAGCTCACACCTGTAATCCCAGCACTTTCAGAGGCCGAGGTG
51601  CTATATACGGCCCGCGCCATCGAGTGTGGACATTAGGGTCGTGAAAGTCTCCGGCTCCAC

51661  GGTGGGTCACCTGAGGTCAGGAGTTCGAGACCAGCCTGGTCAACATGGTGAAACCCCATC
51661  CCACCCAGTGGACTCCAGTCCTCAAGCTCTGGTCGGACCAGTTGTACCACTTTGGGGTAG
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FIGURE 4 (cont'd)

51721 TCTACCAAAAATACAAAACTTAGCCGGGTGTTGTGGCACATGCCTGTAGTCCCAGCTACT
51721 AGATGGTTTTTATGTTTTGAATCGGCCCACAACACCGTGTACGGACATCAGGGTCGATGA

51781 CAGGAGGCTGAAGCAGGAGAATCACTTGAACCTGGGAGGCGGAGGTTGCAGTGAGCCCAG
51781 GTCCTCCGACTTCGTCCTCTTAGTGAACTTGGACCCTCCGCCTCCAACGTCACTCGGGTC

51841 ATCACATCACTGCTCTTCCGCCTGGGTGACAGAGTGAGACTCCATCTAAAAGAAAAAGCA
51841 TAGTGTAGTGACGAGAAGGCGGACCCACTGTCTCACTCTGAGGTAGATTTTCTTTTTCGT

51901 AAACAAAACAAAACTGGATACAGGGCAGTGCTTAGGTACAAATCAGAAAGTTAGAGGTTG
51901 TTTGTTTTGTTTTGACCTATGTCCCGTCACGAATCCATGTTTAGTCTTTCAATCTCCAAC

51961 CTATTCATATCATTAAGAAATAATGTGTCTTACGAAAGAATGTAGCAGTTTACTGAAATA
51961 GATAAGTATAGTAATTCTTTATTACACAGAATGCTTTCTTACATCGTCAAATGACTTTAT

52021 GAAGTCATACCTAGAAATGTAATAATTTATCTTTAATTGTCAGAAATTTAACTGATATTA
52021 CTTCAGTATGGATCTTTACATTATTAAATAGAAATTAACAGTCTTTAAATTGACTATAAT

52081 TGAAGTTCTAATTATAAGAACACTTATTTGAGGTTAAAAATTACCTTATTCTATCCCTGC
52081 ACTTCAAGATTAATATTCTTGTGAATAAACTCCAATTTTTAATGGAATAAGATAGGGACG

52141 TTTGCCGCTAATTTGATCTCTCTGGATTAGTGGGTTATTGTGGGTCCTATGGGTATTTTA
52141 AAACGGCGATTAAACTAGAGAGACCTAATCACCCAATAACACCCAGGATACCCATAAAAT

52201 AGGAGAGGTCTCAGAAAACTAAAAATTATATATACTGGATCATAATCATTCTTGTCACCC
52201 TCCTCTCCAGAGTCTTTTGATTTTTAATATATATGACCTAGTATTAGTAAGAACAGTGGG

52261 ACTCTCATCTTTCTGTTTTTGTTTTGTGTTTTACTACCCTTCCCCTTTTACTAAGTAGTC
52261 TGAGAGTAGAAAGACAAAAACAAAACACAAAATGATGGGAAGGGGAAAATGATTCATCAG

52321 TTAGTAGAAGAAAATTTGCATTAAGTTTGTCGTACTGTATTGATATGGCTCCAAATGTTT
52321 AATCATCTTCTTTTAAACGTAATTCAAACAGCATGACATAACTATACCGAGGTTTACAAA

52381 CTTAGCCCAGGGTCCTCCCCATTCACTGATAAAAGCTAACTAAGGTAAATCACAGGTGTT
52381 GAATCGGGTCCCAGGAGGGGTAAGTGACTATTTTCGATTGATTCCATTTAGTGTCCACAA

52441 TATTGTGCAAGAATACTGTGAAACTATTCATGTAATAAAAAGTTTGTGTTAGAATTTCAC
52441 ATAACACGTTCTTATGACACTTTGATAAGTACATTATTTTTCAAACACAATCTTAAAGTG

52501 TCTCTTTAAATCCTGGACATCTTCTGTGAGTGTATCTGAAAGCAGCCAGACATCTTCAGT
52501 AGAGAAATTTAGGACCTGTAGAAGACACTCACATAGACTTTCGTCGGTCTGTAGAAGTCA

52561 ATTTAAGAAACCCTTTACTATTCTGTGTGCTAGGCACTGTGTTAGCTTTGGAATTCAACT
52561 TAAATTCTTTGGGAAATGATAAGACACACGATCCGTGACACAATCGAAACCTTAAGTTGA

52621 GTGAATACTCTAGCCAGACTTCTTGTCTAAATAGTCCAGAATAGGGGTTGCTAAACTTTC
52621 CACTTATGAGATCGGTCTGAAGAACAGATTTATCAGGTCTTATCCCCAACGATTTGAAAG

52681 TTTCTTTTTTTTTGAGATGGAGTTCCACTCTTATTGCCCAGGCTGGAGTGCACTGGTGTG
52681 AAAGAAAAAAAAACTCTACCTCAAGGTGAGAATAACGGGTCCGACCTCACGTGACCACAC

52741 TCTCTGCTGACTGCAACCTCTGCCTCCCAGGTTCAAGCAGTTCTCCTGCCTCAGCCTCCC
52741 AGAGACGACTGACGTTGGAGACGGAGGGTCCAAGTTCGTCAAGAGGACGGAGTCGGAGGG

52801 AAGTAGCTGGGATTACAGGCGCCCACCACTACACTCAGTTAATTTTTGTATTTTTAGTAG
52801 TTCATCGACCCTAATGTCCGCGGGTGGTGATGTGAGTCAATTAAAAACATAAAAATCATC

52861 AGACAGGGTTGTGCTGTTTGCCAGGTTGATCTCAAACTCCTGACCTTTGGTGATCCACCC
52861 TCTGTCCCAACACGACAAACGGTCCAACTAGAGTTTGAGGACTGGAAACCACTAGGTGGG

52921 GCCTCGGCCTCCCAAAGTGTTGGGATTCAGGGTGTGCCACTGTGCCCGGCCTGCTAAACT
52921 CGGAGCCGGAGGGTTTCACAACCCTAAGTCCCACACGGTGACACGGGCCGGACGATTTGA

52981 TTCTTAAATGGCTAGATGATAAATATTTTAGGCTTGAGGGCCATCAGGTTTCTGTTACAA
52981 AAGAATTTACCGATCTACTATTTATAAAATCCGAACTCCCGGTAGTCCAAAGACAATGTT

53041 CTAGTTGGCTGTGCTGCCACTGAAGATACAAGAATGGCGTGACTATGTTCCAATAACATT
53041 GATCAACCGACACGACGGTGACTTCTATGTTCTTACCGCACTGATACAAGGTTATTGTAA

FIGURE 4 (cont'd)

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53101   TTAATTTCAAAACAGGCCAGCTGGCTGCATTTGGTCTGCAAGTAAAGTCTGCCTGACCCC
53101   AATTAAAGTTTTGTCCGGTCGACCGACGTAAACCAGACGTTCATTTCAGACGGACTGGGG

53161   CTACCTAGTCCAGAGGACAACGGGAGAGAAAAGGGATTCAAAGATAAAAATAATTTAGCT
53161   GATGGATCAGGTCTCCTGTTGCCCTCTCTTTTCCCTAAGTTTCTATTTTTATTAAATCGA

53221   GGAATATATTTCTTTAAATAAACTTATTATACTTAGTAAAAAGTCTTAAATTAACGTTTT
53221   CCTTATATAAAGAAATTTATTTGAATAATATGAATCATTTTTCAGAATTTAATTGCAAAA

53281   TACTTGAATTAAATAGTGGTAAAACAGGCTGGGCACAGTGGCTCATGCCTGTAATCTTAG
53281   ATGAACTTAATTTATCACCATTTTGTCCGACCCGTGTCACCGAGTACGGACATTAGAATC

53341   AACTTTGGGAGGTCGAGGCAGGCAGATTGCTTAAGCCCAGGAGTTCGAGACCAGCCTGGG
53341   TTGAAACCCTCCAGCTCCGTCCGTCTAACGAATTCGGGTCCTCAAGCTCTGGTCGGACCC

53401   CAACATAGTGAGTCCCTATCTCTAAAAAAAATACAAAATAATAATAATAATGGTAGAACA
53401   GTTGTATCACTCAGGGATAGAGATTTTTTTTATGTTTTATTATTATTATTACCATCTTGT

53461   AAGTCAATTTTTTATTGAAACTTGGCATTTTATTGGCATATTACAAAGTAGCATTACTAG
53461   TTCAGTTAAAAAATAACTTTGAACCGTAAAATAACCGTATAATGTTTCATCGTAATGATC

53521   ACTAGCCTGAACATTACAGTAATATTCTGTCCTTAATGCCTTTTGTGTCACTGTAATATG
53521   TGATCGGACTTGTAATGTCATTATAAGACAGGAATTACGGAAAACACAGTGACATTATAC

53581   AGCTTTCTGTTTGTTTTGGAATATGTTTTCAGCCTGAATATTATTCTAAAAATACAATTT
53581   TCGAAAGACAAACAAAACCTTATACAAAAGTCGGACTTATAATAAGATTTTTATGTTAAA

53641   ACTATCATTCATAATATATCAAATGACTCACGTAGCTGCAAGGCAGTGAATTAAACAGAA
53641   TGATAGTAAGTATTATATAGTTTACTGAGTGCATCGACGTTCCGTCACTTAATTTGTCTT

53701   TTAGATCATTTTAAAAATAATGATAAGAGCTGATGATGTAAAGTGAAGGTCTGTATTTAA
53701   AATCTAGTAAAATTTTTATTACTATTCTCGACTACTACATTTCACTTCCAGACATAAATT

53761   TTTGGGAGGGAAAAGACTTTTTTTGTATATTCAAAGAGATGGAGTTTGACATCCCTTCAC
53761   AAACCCTCCCTTTTCTGAAAAAAACATATAAGTTTCTCTACCTCAAACTGTAGGGAAGTG

53821   AACCTGTTACAGGTTGAACTTGCCCCTGTTTTTTTAACTGATCAAAAAGTTCCTTCTCTT
53821   TTGGACAATGTCCAACTTGAACGGGGACAAAAAAATTGACTAGTTTTTCAAGGAAGAGAA

53881   GTGTTTCTTTTTTTCTTCTCTTTTCTCTTCTTTTCTTTTCTTTTTTTTTTTTCTGAGACA
53881   CACAAAGAAAAAAAGAAGAGAAAAGAGAAGAAAAGAAAAGAAAAAAAAAAAAGACTCTGT

53941   GAGTCTTGCTCTGTCTCCCAGGCTGGAGTGCAGTGGTGCGATCTTGACTCTCTGCAACCT
53941   CTCAGAACGAGACAGAGGGTCCGACCTCACGTCACCACGCTAGAACTGAGAGACGTTGGA

54001   CCGCCTCCCGGGTTCAAGTGATTTTCCTGCCTCAGCCTCCTGAGTAGCTGCGACTACAGG
54001   GGCGGAGGGCCCAAGTTCACTAAAAGGACGGAGTCGGAGGACTCATCGACGCTGATGTCC

54061   TGCATGCCACCACGCCTGGCTAATTTTTAGTATTTTTAGTAGAGACGGGGTTTCACCATG
54061   ACGTACGGTGGTGCGGACCGATTAAAAATCATAAAAATCATCTCTGCCCCAAAGTGGTAC

54121   TTAGCTAGGATGGTCTCAATCTCCAAACCTTGTGATCTGCATGCCTCGGCTTCCCAAAGT
54121   AATCGATCCTACCAGAGTTAGAGGTTTGGAACACTAGACGTACGGAGCCGAAGGGTTTCA

54181   GCTGGTCTCCTGTGTTTTTGTCAGCATTCCACAGATGCTATAAAGTTAGTGGTGGTATCG
54181   CGACCAGAGGACACAAAAACAGTCGTAAGGTGTCTACGATATTTCAATCACCACCATAGC

54241   CATGCAATTTGTACGCTTAATGTTTGGCCATTTGCAGTGGGCAAACTGGCTATGTCGGGA
54241   GTACGTTAAACATGCGAATTACAAACCGGTAAACGTCACCCGTTTGACCGATACAGCCCT

54301   GCTGGTGAGATGCTGCTTGTGGGGAGTTGTTTCCTATTACTCTGATTTATCTTTGTTTAA
54301   CGACCACTCTACGACGAACACCCCTCAACAAAGGATAATGAGACTAAATAGAAACAAATT

54361   ATAAGAGTTCCTTTGTTCACTGTTTCCTCCACACAGAACAGAGGATTTATATCTTAGTGT
54361   TATTCTCAAGGAAACAAGTGACAAAGGAGGTGTGTCTTGTCTCCTAAATATAGAATCACA
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FIGURE 4 (cont'd)

54421 TCATTCTCAACTTTCCTGTTTTCAAAGAGGAAAACATTTGCTTCACTTTGCTCATTTCTT
54421 AGTAAGAGTTGAAAGGACAAAAGTTTCTCCTTTTGTAAACGAAGTGAAACGAGTAAAGAA

54481 CTCCAGTGCACCCAGAGGATTTTGAAGGCTTATGCCAACAATTCTTTGGGGCAGTTGGAG
54481 GAGGTCACGTGGGTCTCCTAAAACTTCCGAATACGGTTGTTAAGAAACCCCGTCAACCTC

54541 TGTAACCATTGCTAAATAGCAGTTCAGTACTTAATGACATTCATTTTAGTTTAACAAATC
54541 ACATTGGTAACGATTTATCGTCAAGTCATGAATTACTGTAAGTAAAATCAAATTGTTTAG

54601 ATTGTGAGTGTTGCCATTTTTTATTAGGGAAAACATCTCTTTCATCTTTCCCAAATACTC
54601 TAACACTCACAACGGTAAAAAATAATCCCTTTTGTAGAGAAAGTAGAAAGGGTTTATGAG

54661 AACATGAGTCCTATGGTGAGAGTGAAAAAGGGTTGTATTCTTTTTTTGCATCATCTTACC
54661 TTGTACTCAGGATACCACTCTCACTTTTTCCCAACATAAGAAAAAAACGTAGTAGAATGG

54721 CCATCTGCTATTTTGTCCCTCTTCTATATATCACTGAAATTTGGTTCTGATATTCTATTA
54721 GGTAGACGATAAAACAGGGAGAAGATATATAGTGACTTTAAACCAAGACTATAAGATAAT

54781 GGCAGTGTACATTGCAGAGATTATGAATAACTGGCCGAATTCTGAATGCAGGCATGATTT
54781 CCGTCACATGTAACGTCTCTAATACTTATTGACCGGCTTAAGACTTACGTCCGTACTAAA

54841 GTTCAGCTCAGAGTGTTAAATTTCTGTGTTAGCTGCTAACCTTTAAAAGTCAATTGATTT
54841 CAAGTCGAGTCTCACAATTTAAAGACACAATCGACGATTGGAAATTTTCAGTTAACTAAA

54901 CCTTTTTTTTTTTCCCCTCTGTATAATCTAGCCAGCGAATGCTCAGTAGCTTTTCTGTAA
54901 GGAAAAAAAAAAAGGGGAGACATATTAGATCGGTCGCTTACGAGTCATCGAAAAGACATT

54961 ATAGTGATGATTTTTCTTCCCCAGGCTAAAGACCTAATAGTCACACCAGCTACCATTTTA
54961 TATCACTACTAAAAAGAAGGGGTCCGATTTCTGGATTATCAGTGTGGTCGATGGTAAAAT

55021 AAGGAAAAACCAGACCCCAATAATCTGGTTTTTGGAACTGTGTTCACGGATCATATGCTG
55021 TTCCTTTTTGGTCTGGGGTTATTAGACCAAAAACCTTGACACAAGTGCCTAGTATACGAC

55081 ACGGTGGAGTGGTCCTCAGAGTTTGGATGGGAGAAACCTCATATCAAGCCTCTTCAGAAC
55081 TGCCACCTCACCAGGAGTCTCAAACCTACCCTCTTTGGAGTATAGTTCGGAGAAGTCTTG

55141 CTGTCATTGCACCCTGGCTCATCAGCTTTGCACTATGCAGTGGAAGTAAGTACATGGGAA
55141 GACAGTAACGTGGGACCGAGTAGTCGAAACGTGATACGTCACCTTCATTCATGTACCCTT

55201 TTAAAGAGAGTGACATGCTTGCACTTCACTGTGGGTACTAAGTAGCTTCTCCTGCTAAAA
55201 AATTTCTCTCACTGTACGAACGTGAAGTGACACCCATGATTCATCGAAGAGGACGATTTT

55261 TAGCTCTTGGGCAGTATGGGCTTTATCATATTTACCAGAGGAAGCCGAAAATGTCTTTAA
55261 ATCGAGAACCCGTCATACCCGAAATAGTATAAATGGTCTCCTTCGGCTTTTACAGAAATT

55321 AAGTTTTCCTATAGACAGTTGGATTGAAGATAAATCTTAGCAGCTAATTTTTCAGATAAT
55321 TTCAAAAGGATATCTGTCAACCTAACTTCTATTTAGAATCGTCGATTAAAAAGTCTATTA

55381 CTTGCATTTTCTGTGACGTCAATAAAAAAATTATTTAAAGCAAATAGAAAGGACAGCTGG
55381 GAACGTAAAAGACACTGCAGTTATTTTTTTAATAAATTTCGTTTATCTTTCCTGTCGACC

55441 TGGGAAAATTGGCAATTAAAAAGCCAGCACTGTTGATAATTTAATAAGTCACCTTTCTTC
55441 ACCCTTTTAACCGTTAATTTTTCGGTCGTGACAACTATTAAATTATTCAGTGGAAAGAAG

55501 TTAGATCTTCTAATAATTGAGAAAGGGTCATTGAGAACAATATTATGATTTGATTTTAAT
55501 AATCTAGAAGATTATTAACTCTTTCCCAGTAACTCTTGTTATAATACTAAACTAAAATTA

55561 GCTAACTCCACATTTTTATGACCAGTAATAATGTCTAGTTATGCATGTTAAGGGACATGT
55561 CGATTGAGGTGTAAAAATACTGGTCATTATTACAGATCAATACGTACAATTCCCTGTACA

55621 AATTAAATGTCCTCCTTCAGCCATGAGTTGAAATAATTTTAAGCATAAAATGTTTAAAGA
55621 TTAATTTACAGGAGGAAGTCGGTACTCAACTTTATTAAAATTCGTATTTTACAAATTTCT

55681 ATTCTTTCTCTGGTCCTTTTCAGGGTGCACAATTAACCAGATGCACAGTATACTTCCCAT
55681 TAAGAAAGAGACCAGGAAAAGTCCCACGTGTTAATTGGTCTACGTGTCATATGAAGGGTA

55741 TGTCTTGATTCTCATTGTATTTTACTTTTGAATGATTTGGACATCTTTCCCAGAATAATA
55741 ACAGAACTAAGAGTAACATAAAATGAAAACTTACTAAACCTGTAGAAAGGGTCTTATTAT

FIGURE 4 (cont'd)

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55801  GGGGTGCTGGAAATAATAATAGTCTTCCTATTAAGTGCTAAAATATGGTAATAGTAAAAT
55801  CCCCACGACCTTTATTATTATCAGAAGGATAATTCACGATTTTATACCATTATCATTTTA

55861  ATTAATAGATTAATGATAAAATAACAACTTTTGTTTACTGAATTCCTGCAATACGTTCTG
55861  TAATTATCTAATTACTATTTTATTGTTGAAAACAAATGACTTAAGGACGTTATGCAAGAC

55921  TATTATGTTCCATATATGAATCATCTCATTTAATTACCTTAAGTGAGAAGGCATGTGATT
55921  ATAATACAAGGTATATACTTAGTAGAGTAAATTAATGGAATTCACTCTTCCGTACACTAA

55981  AAGCATTCAGGCTTTGAAGTCAGACATCCTGGGCTCAAATTCGGTCTCATTTGCTCCATA
55981  TTCGTAAGTCCGAAACTTCAGTCTGTAGGACCCGAGTTTAAGCCAGAGTAAACGAGGTAT

56041  GGAACCTTTATGACTTGAGGAATTTAATCATTTGTGCTTTAATTTCTTTATCTATAAAAT
56041  CCTTGGAAATACTGAACTCCTTAAATTAGTAAACACGAAATTAAAGAAATAGATATTTTA

56101  TGGGGTAGTTATAATATCTATCTTACAGTGATCTCATAAGTATAAAATAAAGTAATTTAT
56101  ACCCCATCAATATTATAGATAGAATGTCACTAGAGTATTCATATTTTATTTCATTAAATA

56161  CTAAGCATATAGAGTCATATCTGGTGCATAGCGAGAGCCCAGTTGTTAGCAATAATAATT
56161  GATTCGTATATCTCAGTATAGACCACGTATCGCTCTCGGGTCAACAATCGTTATTATTAA

56221  AACTCTTGAAGCAGTGGTCTCATCCATTATAAAAGGAGGCTCAGAAGAGTTGTTTCTTGA
56221  TTGAGAACTTCGTCACCAGAGTAGGTAATATTTTCCTCCGAGTCTTCTCAACAAAGAACT

56281  CTAATATTACACAGCAGTAAGGGTGGAGCTAAGGTTCCAATGAGAAGCTTCTTTCTGTTA
56281  GATTATAATGTGTCGTCATTCCCACCTCGATTCCAAGGTTACTCTTCGAAGAAAGACAAT

56341  TATAGCCCCTACATGTATACACCAAAATTACTAGGATGCTTTTGCAATTAACTCCTTCAA
56341  ATATCGGGGATGTACATATGTGGTTTTAATGATCCTACGAAAACGTTAATTGAGGAAGTT

56401  AATTATAAATTCATATAATTTTGGAAAGATATTCACTGTCCATATGTATCCACAAAATGT
56401  TTAATATTTAAGTATATTAAAACCTTTCTATAAGTGACAGGTATACATAGGTGTTTTACA

56461  TGAATTTAGGAATCTAAGTTTCTGTTCCCAGCTCTTCCTGTTATGTCAATTTGAATGAGT
56461  ACTTAAATCCTTAGATTCAAAGACAAGGGTCGAGAAGGACAATACAGTTAAACTTACTCA

56521  TCTTTCATTATTTGCCACAAGCCCTCACCATGTCATAAGGTATAATAAAGAACAGGTGAA
56521  AGAAAGTAATAAACGGTGTTCGGGAGTGGTACAGTATTCCATATTATTTCTTGTCCACTT

56581  ATGAAGTGCTTTTATTTATTTATTTTTCAGACAGATTCTTGCTCTGTCACCCAGGCTGGA
56581  TACTTCACGAAAATAAATAAATAAAAAGTCTGTCTAAGAACGAGACAGTGGGTCCGACCT

56641  GTGCAGTGGCACGATCGTGGCTCACTGCAGCCTCAAACTCCTGGGCTCAAGCAAACCTCG
56641  CACGTCACCGTGCTAGCACCGAGTGACGTCGGAGTTTGAGGACCCGAGTTCGTTTGGAGC

56701  TACCTCAGCCTCCTGAGTAGCTGGGACCACAGACACATGTCACCATGTCTGGCTAATTTT
56701  ATGGAGTCGGAGGACTCATCGACCCTGGTGTCTGTGTACAGTGGTACAGACCGATTAAAA

56761  TACATATTTTGTTGAGACTGGGTTTTGCCATGTTGCCCAGGCTGGTCTCAAACTCCTGGG
56761  ATGTATAAAACAACTCTGACCCAAAACGGTACAACGGGTCCGACCAGAGTTTGAGGACCC

56821  CTCAAGCAATCCTCTTGCCTTGGCTTCTTCAAGTGCTGGGATGACAGCCATGAGCCACTG
56821  GAGTTCGTTAGGAGAACGGAACCGAAGAAGTTCACGACCCTACTGTCGGTACTCGGTGAC

56881  CTCCTGGCTATGTGCTTTTAAATTTGAAAGGAATAATATGCCCAAGCCCAGGTCACTGGT
56881  GAGGACCGATACACGAAAATTTAAACTTTCCTTATTATACGGGTTCGGGTCCAGTGACCA

56941  TCTCAAACTTAATGTGCATCAGAATCAGCTGGCTACATCTCCAGAGTTTCTCATTTCTAA
56941  AGAGTTTGAATTACACGTAGTCTTAGTCGACCGATGTAGAGGTCTCAAAGAGTAAAGATT

57001  CAAGTGTCCAGATCATGTTAATTTTGTCGCTCCAGGGACCACATTTTGGGAATTGCTGGC
57001  GTTCACAGGTCTAGTACAATTAAAACAGCGAGGTCCCTGGTGTAAAACCCTTAACGACCG

57061  CTATGGGAAGTAAATGAGAAATGATTTAATGTCATTTTTGGAAGTTAAAAAAGATTTTGG
57061  GATACCCTTCATTTACTCTTTACTAAATTACAGTAAAAACCTTCAATTTTTTCTAAAACC
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FIGURE 4 (cont'd)

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57121  TGGTCACTGGTTTTTGAAAACTCTTTGAAGGCTGGGTGGGGTGGTTCACATCTGTAATTT
57121  ACCAGTGACCAAAAACTTTTGAGAAACTTCCGACCCACCCCACCAAGTGTAGACATTAAA

57181  CAGCAGTTTCGGGGAGATGGGGTTCTTGGGAAATGAGCCCTCCACCCATGGGATCTGATG
57181  GTCGTCAAAGCCCCTCTACCCCAAGAACCCTTTACTCGGGAGGTGGGTACCCTAGACTAC

57241  CTATTTCCACGTAGATAATGTCAGAGTCGTTCAAACCAGAGTGACTCCATCCTGAATAGG
57241  GATAAAGGTGCATCTATTACAGTCTCAGCAAGTTTGGTCTCACTGAGGTAGGACTTATCC

57301  GGCTGGGTAAAATAAGGCTGAGACCTACTGGGCTGCAACATGATGAGACCCTGACTCTAT
57301  CCGACCCATTTTATTCCGACTCTGGATGACCCGACGTTGTACTACTCTGGGACTGAGATA

57361  TGAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAAAACGGCCAGGCGAGGTGGCT
57361  ACTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTTTGCCGGTCCGCTCCACCGA

57421  CACGCCTGTAATACCAGCACTTTGGGAGGCCAAGGCGGGCGGATCACGAGGTCAGGAGAT
57421  GTGCGGACATTATGGTCGTGAAACCCTCCGGTTCCGCCCGCCTAGTGCTCCAGTCCTCTA

57481  CGAGACCATCCTGGCTAACATGGTGAAACCCCATCTCTACTAAAAATAGAAAAAAAAAAA
57481  GCTCTGGTAGGACCGATTGTACCACTTTGGGGTAGAGATGATTTTTATCTTTTTTTTTTT

57541  AAAATTAGCCGGGCGTGGTGGCAGGCGCCTGTAGTCCAAGCTACTTAGGAGGCTGAGGCA
57541  TTTTAATCGGCCCGCACCACCGTCCGCGGACATCAGGTTCGATGAATCCTCCGACTCCGT

57601  GGAAAATGACGTGAACCCAGGAGGCGGAGTTTGCAGTGAGCCGAGATCACGCCGCTGCAC
57601  CCTTTTACTGCACTTGGGTCCTCCGCCTCAAACGTCACTCGGCTCTAGTGCGGCGACGTG

57661  TCCACACTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAAAAAACAAAAACCTCTTTGG
57661  AGGTGTGACCCACTGTCTCGTTCTGAGGTAGAGTTTTTTTTTTTTGTTTTTGGAGAAACC

57721  CCATCTATTTAGATGAGTTGGAATGCTACTTTGATTGGTTTTGCCAATTTAGATTTTTGT
57721  GGTAGATAAATCTACTCAACCTTACGATGAAACTAACCAAAACGGTTAAATCTAAAAACA

57781  AATTAGGGTAGTTTAAAAAAACTCTCAAATTACTGTTATCCTTTGTTAAAAACCAAAATC
57781  TTAATCCCATCAAATTTTTTTGAGAGTTTAATGACAATAGGAAACAATTTTTGGTTTTAG

57841  TTTTATTATTAGTCTTCTGCTTACAATATAAGTAAAATAAATGTTTTGTATTAATAACTG
57841  AAAATAATAATCAGAAGACGAATGTTATATTCATTTTATTTACAAAACATAATTATTGAC

57901  GATTGTATATTGCATGGTTACCACTATGTAACAAAATTAATAGCTTAAAATTACAAGCGT
57901  CTAACATATAACGTACCAATGGTGATACATTGTTTTAATTATCGAATTTTAATGTTCGCA

57961  CATTTTAAAATTATTTTTCATGTTTCTGGGGTTGACTAGGATGGCTAAGTGGTTTTTGCT
57961  GTAAAATTTTAATAAAAAGTACAAAGACCCCAACTGATCCTACCGATTCACCAAAAACGA

58021  TGGGGTCCGTCACACGGTTGCTGTCAGTGGCTGGGGTTAGAGTCAGCTCACAGGCTTCCT
58021  ACCCCAGGCAGTGTGCCAACGACAGTCACCGACCCCAATCTCAGTCGAGTGTCCGAAGGA

58081  AACTCATATGGTGCTGGAGGGAGTGTCTCTTAGCATGCTAATGCTTCATAATTTGTGTAT
58081  TTGAGTATACCACGACCTCCCTCACAGAGAATCGTACGATTACGAAGTATTAAACACATA

58141  AATGAACAGTGAGGATGACCAGAGGTCACTTTCATTGCCATCTGGGCTGCAAAACTCAAG
58141  TTACTTGTCACTCCTACTGGTCTCCAGTGAAAGTAACGGTAGACCCGACGTTTTGAGTTC

58201  GAGTTGAAGGCTCTTCCGGCATTACTTGTTCTCCATGTGGTCTCCTCAGGATGGCAGTCA
58201  CTCAACTTCCGAGAAGGCCGTAATGAACAAGAGGTACACCAGAGGAGTCCTACCGTCAGT

58261  CAGAGTAGGCAGCCTTCTTATGTGCTGACCTAGGGCCCAAAATCTGTATGTGTCAGTTGA
58261  GTCTCATCCGTCGGAAGAATACACGACTGGATCCCGGGTTTTAGACATACACAGTCAACT

58321  CTGAGCCCAGATGGAAGCTCTATTGCTGTTTACGCCCTAGCCTCAAAACTACTCTTTCAA
58321  GACTCGGGTCTACCTTCGAGATAACGACAAATGCGGGATCGGAGTTTTGATGAGAAAGTT

58381  GAAAAATTCTCCAACCGAGTTTTTCCTCTACTCTCACACCACCACAACAATAGTCAACAT
58381  CTTTTTAAGAGGTTGGCTCAAAAAGGAGATGAGAGTGTGGTGGTGTTGTTATCAGTTGTA

58441  AGGAGACTTCTATGATCAAAGGTGTAGGGATTTCTCCCCACCACCAAGCAGTGAACCCCA
58441  TCCTCTGAAGATACTAGTTTCCACATCCCTAAAGAGGGGTGGTGGTTCGTCACTTGGGGT
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FIGURE 4 (cont'd)

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58501  GCTGGGTGTCCTCCAATTCAATTCTCACACTGTTATTACGGGAAAGGTGTCCCAATCCAG
58501  CGACCCACAGGAGGTTAAGTTAAGAGTGTGACAATAATGCCCTTTCCACAGGGTTAGGTC

58561  TCCCCAAGAGGTTCTTGGATGTTGCACAAGAAAGAATTTGGGGAGAGTCCACAAAGTAAA
58561  AGGGGTTCTCCAAGAACCTACAACGTGTTCTTTCTTAAACCCCTCTCAGGTGTTTCATTT

58621  ATAAAATTTATTAAGAAAGTAAAGGAAAAAAAGAATGGCTACTCCGTAGACAGAGGAGCT
58621  TATTTTAAATAATTCTTTCATTTCCTTTTTTTCTTACCGATGAGGCATCTGTCTCCTCGA

58681  CCGAGGGCTGCTGGTTGGCTATTTTAATGGTTATTTCTTGATCATTTGCTAAAGAAGGGG
58681  GGCTCCCGACGACCAACCGATAAAATTACCAATAAAGAACTAGTAAACGATTTCTTCCCC

58741  TAGATTATTCATAAATTTTCCAGAAAAGGGATGGGCAATTCCTGCAACTGAGGGTTCCTC
58741  ATCTAATAAGTATTTAAAAGGTCTTTTCCCTACCCGTTAAGGACCTTGACTCCCAAGGAG

58801  CCCTTTTTAGACCTTGTAGGTTAACTTCCCACCATTGCCATGGCCTCTGTAAATTGTCGT
58801  GGGAAAAATCTGGAACATCCAATTGAAGGGTGGTAACGGTACCGGAGACATTTAACAGCA

58861  GACACTGGTAGGAGTGTCTGTTAGCATGCTAATGCATTATAATTAGCTTATAATGAGCAG
58861  CTGTGACCATCCTCACAGACAATCGTACGATTACGTAATATTAATCGAATATTACTCGTC

58921  CGAGGACGGCCAGACATCCCTTTCATTGCCATATGGGATTTGGCAGGTTTTGGCTGGCTT
58921  GCTCCTGCCGGTCTGTAGGGAAAGTAACGGTATACCCTAAACCGTCCAAAACCGACCGAA

58981  CTTTACCACATCTTGTTTTATCAGTGGGGTCTTTGTAACCTGTATGTTGTGCCGACCTCC
58981  GAAATGGTGTAGAACAAAATAGTCACCCCAGAAACATTGGACATACAACACGGCTGGAGG

59041  TATCTCATCCTGTGACCTAGAATACTAACCTCCTGAGAATGCAGCCCAGTAGGTTTCAGC
59041  ATAGAGTAGGACACTGGATCTTATGATTGGAGGACTCTTACGTCGGGTCATCCAAAGTCG

59101  CTTATTTTACCCAGCCCCTAATCAGGATGGAGTCGCTCTGGTCCAAACACCTCTGACATT
59101  GAATAAAATGGGTCGGGGATTAGTCCTACCTCAGCGAGACCAGGTTTGTGGAGACTGTAA

59161  ATCCACCTGGAAATAGTGTCAGATCCCATGGGTTAAGGGCTCATTCCCCAAGACCCTAAC
59161  TAGGTGGACCTTTATCACAGTCTAGGGTACCCAATTCCCGAGTAAGGGGTTCTGGGATTG

59221  CACCCTCACCTGGCCCAGACACAAGTCACAAGTCCTGTCCTCTGGAATGTCTGACTGAGA
59221  GTGGGAGTGGACCGGGTCTGTGTTCAGTGTTCAGGACAGGAGACCTTACAGACTGACTCT

59281  GGCATCAAGTTGGAGTTCCCATGACCCCCTCTTCTGGTTTGATTAATTTACTGGAGCAGC
59281  CCGTAGTTCAACCTCAAGGGTACTGGGGGAGAAGACCAAACTAATTAAATGACCTCGTCG

59341  TCACAAAACTCAGGGAAACACTTAGGTTTAGTGGTTTATTATAAAGGATACTGCAAAGTG
59341  AGTGTTTTGAGTCCCTTTGTGAATCCAAATCACCAAATAATATTTCCTATGACGTTTCAC

59401  TATAGATGAAGCGATGTGTAGGGTGAGGTATCGGGGGATAGAGTGCAGGGCTTCCATGCC
59401  ATATCTACTTCGCTACACATCCCACTCCATAGCCCCCTATCTCACGTCCCGAAGGTACGG

59461  CTCCCGGGGTGTGCCACCCTTTAGGAACCTTCATGTGTTCTGCTATCCGGAAGCTCACTG
59461  GAGGGCCCCACACGGTGGGAAATCCTTGGAAGTACACAAGACGATAGGCCTTCGAGTGAC

59521  AACTCATTCTTTTGGGTTTTTATGGAAGCTTCACGTCAATATTCCTTCCCCTGGGGTATG
59521  TTGAGTAAGAAAACCCAAAAATACCTTCGAAGTGCAGTTATAAGGAAGGGGACCCCATAC

59581  AGGCAGGACCTTCACCGGAGAGGGTCTTTTATTTTATTTCATTATTTTTAAAATATAAGA
59581  TCCGTCCTGGAAGTGGCCTCTCCCAGAAAATAAAATAAAGTAATAAAAATTTTATATTCT

59641  TGGGGTCTTGCTATGTAGCCTAGGGTGGTATTGAATTCCTGGGCCCAAGTAAGCCTCCCG
59641  ACCCCAGAACGATACATCGGATCCCACCATAACTTAAGGACCCGGGTTCATTCGGAGGGC

59701  CCTCTGCCTCCGAAAGTGCTGGGACTACAGGCATGAGCCACCCAGCCCCTTTGGAGAGGA
59701  GGAGACGGAGGCTTTCACGACCCTGATGTCCGTACTCGGTGGGTCGGGGAAACCTCTCCT

59761  TCTTAAGACTCACAGTTAGAAAGGAGGGCAGGAGAAGGTCAGAGAGATTCTGCTTCCTGC
59761  AGAATTCTGAGTGTCAATCTTTCCTCCCGTCCTCTTCCAGTCTCTCTAAGACGAAGGACG
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FIGURE 4 (cont'd)

59821 CCCTGAGGCCTAACACACCCAGCATTATAACAAAAGACTGTAACAAGGGCTATGGGAGTT
59821 GGGACTCCGGATTGTGTGGGTCGTAATATTGTTTTCTGACATTGTTCCCGATACCCTCAA

59881 ACCAGCCAGGAACTGTAAATCACACAGTATTATTTCTGCCTTACTCTTATCAGTCATGAT
59881 TGGTCGGTCCTTGACATTTAGTGTGTCATAATAAAGACGGAATGAGAATAGTCAGTACTA

59941 GGTTACAAAGGCCTGTCCAAGTTCAAAAGGAGGAAAAAAGCACTCCACTTCTTGATGAGG
59941 CCAATGTTTCCGGACAGGTTCAAGTTTTCCTCCTTTTTTCGTGAGGTGAAGAACTACTCC

60001 AAGGTCAGGGTTCTGGAAGAGCATGGGGGACTGGAAATATTGTTCGGCCATTTCATGGAA
60001 TTCCAGTCCCAAGACCTTCTCGTACCCCCTGACCTTTATAACAAGCCGGTAAAGTACCTT

60061 AATACAGTCTGTAATAGACATCAGTGATAAATGGGGAGATATGGTGGATGTATTGTTTTC
60061 TTATGTCAGACATTATCTGTAGTCACTATTTACCCCTCTATACCACCTACATAACAAAAG

60121 CTCTGAGTGCCAAATTGGGTTCTAAGATTTCACAGGCCAGATATTATTGAAGTGGCTACG
60121 GAGACTCACGGTTTAACCCAAGATTCTAAAGTGTCCGGTCTATAATAACTTCACCGATGC

60181 TTGTCTGGGGTATATACCTTGGGGTTCGTCATTTTGTGCCAGGAAAATTTAGGACAAGGA
60181 AACAGACCCCATATATGGAACCCCAAGCAGTAAAACACGGTCCTTTTAAATCCTGTTCCT

60241 CTCACACGAGGAGTTTAGGAGTGGAGGTTTAATAGGCAGAAGAGAAACAGAAACAGTTCT
60241 GAGTGTGCTCCTCAAATCCTCACCTCCAAATTATCCGTCTTCTCTTTGTCTTTGTCAAGA

60301 TTCTGTAGGGAGAGAGGGATCTTCGAGGGAAAAGACCATCCAGCAGCAGATGAGCTGGAT
60301 AAGACATCCCTCTCTCCCTAGAAGCTCCCTTTTCTGGTAGGTCGTCGTCTACTCGACCTA

60361 TTTATAGTCAGGTTTGAGGAGGAAGTGTCTGATTTACTTAGGGCTAACAGGTTGGTTTGA
60361 AAATATCAGTCCAAACTCCTCCTTCACAGACTAAATGAATCCCGATTGTCCAACCAAACT

60421 TCAGGTATGACGTTTACATAGCACACCGGGAAGTCTGGTTGCCCCACCCTAATCCTTTTA
60421 AGTCCATACTGCAAATGTATCGTGTGGCCCTTCAGACCAACGGGGTGGGATTAGGAAAAT

60481 TGCAAATGGACTTTCCTAGTTGATTGGAGCTATCTTGTCTGCTCCTTACTGTACAGGTGG
60481 ACGTTTACCTGAAAGGATCAACTAACCTCGATAGAACAGACGAGGAATGACATGTCCACC

60541 CTGACAAAGAGAAGGGAAGATGGAGCCGCCATCTTGAACATGATTGACGCAGCTGTGGAT
60541 GACTGTTTCTCTTCCCTTCTACCTCGGCGGTAGAACTTGTACTAACTGCGTCGACACCTA

60601 ATCTATGTCTGCAGCTTGATTTTACAGGCTGCTCTTCTTTAGAAAGGGGCTGCTTTTCAT
60601 TAGATACAGACGTCGAACTAAAATGTCCGACGAGAAGAAATCTTTCCCCGACGAAAAGTA

60661 TAAAACAAAAACCTTACTGAGGACTCTTGTACCCTCACTATCTGCAGGTGATTTCTTAAC
60661 ATTTTGTTTTTGGAATGACTCCTGAGAACATGGGAGTGATAGACGTCCACTAAAGAATTG

60721 TCCTGTATCATTATTATAGTGTCATAGGAATCTAGGAAGTGTGATTGCCTTCTGGAGAGA
60721 AGGACATAGTAATAATATCACAGTATCCTTAGATCCTTCACACTAACGGAAGACCTCTCT

60781 ACTTCAGGGTCCCTGGATTTTCTCACTAATCATATTCATTTCATTCCCTGTTTACCTGTT
60781 TGAAGTCCCAGGGACCTAAAAGAGTGATTAGTATAAGTAAAGTAAGGGACAAATGGACAA

60841 TAATAAATCTTGAGTGCCTACTATGTGCCCAGGGCTCTGCAAGGTGCCTGGAATAGGATG
60841 ATTATTTACAACTCACGGATGATACACGGGTCCCGACACGTTCCACGGACCTTATCCTAC

60901 GCAAGCAAACCAACCATGACCTTGCTCTCAAAGAATTGTTTTCTTTCTTTCTTTTTTTTC
60901 CGTTCGTTTGGTTGGTACTGGAACGAGAGTTTCTTAACAAAAGAAAGAAAGAAAAAAAAG

60961 TGAGACAAGGTCTTGCTCTGTCGCCCAGGCTGGAGTGCAGTGGCCTGATCTCAGCTCACT
60961 ACTCTGTTCCAGAACGAGACAGCGGGTCCGACCTCACGTCACCGGACTAGAGTCGAGTGA

61021 GCAACTTCCACCTCCTGGCTTCAACAGATTCTCCTCCCTCAGCCTCCCAGGTAGCTGGGA
61021 CGTTGAAGGTGGAGGACCGAAGTTGTCTAAGAGGAGGGAGTCGGAGGGTCCATCGACCCT

61081 TTATAGGTGCCCACCACCATGCCCGGCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTC
61081 AATATCCACGGGTGGTGGTACGGGCCGATTAAAAACATAAAAATCATCTCTGTCCCAAAG

61141 ATCATGTTGGCCAGGCTAGTCTCAAACTCCTGACCTCAAGTGATCCGCCTGCCTCAGTGC
61141 TAGTACAACCGGTCCGATCAGAGTTTGAGGACTGGAGTTCACTAGGCGGACGGAGTCACG

FIGURE 4 (cont'd)

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61201   CGAGATTACAGGCATGAGCCACTGCACCTGGCCTGTTTTCTGTCTTTTTTTTTTAACCCC
61201   GCTCTAATGTCCGTACTCGGTGACGTGGACCGGACAAAAGACAGAAAAAAAAAAATTGGGG

61261   CACATGGAAAGTTAGGCAGGGATTTAATTTCAAAGAGTTTCTTCCCAAATATTGTGGTGA
61261   GTGTACCTTTCAATCCGTCCCTAAATTAAAGTTTCTCAAAGAAGGGTTTATAACACCACT

61321   AACATCTAGTCCATTTATGTTTCAGGCTTTTTCATAGATATTACTGTTTCTCTTAGACTG
61321   TTGTAGATCAGGTAAATACAAAGTCCGAAAAAGTATCTATAATGACAAAGAGAATCTGAC

61381   ACAGACTTAGGACATCACATGATTGAATGTCAACCTGACTTTTAAGTTCAATAATAGTTT
61381   TGTCTGAATCCTGTAGTGTACTAACTTACAGTTGGACTGAAAATTCAAGTTATTATCAAA

61441   CATTTTTTAAATGCAAAATTAAATAGGAGTAATATCCTTGAACATGTTTCTCCTTCACTC
61441   GTAAAAAATTTACGTTTTAATTTATCCTCATTATAGGAACTTGTACAAAGAGGAAGTGAG

61501   ATCGGACCTATTGAGTCTAGAATCCATTTTATTTTGAGAGCTCCAACTACATGTGGTTTC
61501   TAGCCTGGATAACTCAGATCTTAGGTAAAATAAAACTCTCGAGGTTGATGTACACCAAAG

61561   TGTTAATATCTGAAAGTAATTTTTAATATCTGAAAGTTTCAAATAGTGATAATATTTGAA
61561   ACAATTATAGACTTTCATTAAAAATTATAGACTTTCAAAGTTTATCACTATTATAAACTT

61621   GGTTTCAAATAGTGGAGGAGAGACGCAAACTGCGAGTAGGGAACGCGGATTGAAGGAAAT
61621   CCAAAGTTTATCACCTCCTCTCTGCGTTTGACGCTCATCCCTTGCGCCTAACTTCCTTTA

61681   GAAAAGTTGATAATAGGCACTTCATTTTCAGATTATAACAAATATTTAGTGAAATAAAGC
61681   CTTTTCAACTATTATCCGTGAAGTAAAAGTCTAATATTGTTTATAAATCACTTTATTTCG

61741   ATAATTTTAAAAAATGGATAAGACATGTATGTACTATTTAATGTGTACTAATAAATGAAT
61741   TATTAAAATTTTTTACCTATTCTGTACATACATGATAAATTACACATGATTATTTACTTA

61801   GCTCATATTTGCCATCCAGATAAAGAAATAGAACAGTTGAACATCACAGAAGCCCTCGCG
61801   CGAGTATAAACGGTAGGTCTATTTCTTTATCTTGTCAACTTGTAGTGTCTTCGGGAGCGC

61861   TGTCCCATTCAGATCACAAACTCTATCTTTCTACTGGTAACCATTATTCTTACTTTTGTG
61861   ACAGGGTAAGTCTAGTGTTTGAGATAGAAAGATGACCATTGGTAATAAGAATGAAAACAC

61921   ATAACCTTTCTTTGCTTTCCTTTATGGAGTGTGTAGATTCTTAACACTATAGTTTTGCCT
61921   TATTGGAAAGAAACGAAAGGAAATACCTCACACATCTAAGAATTGTGATATCAAAACGGA

61981   CTTTTTGAACTTCATGTAAATGAAAAAATGTATATATTTTGTGTTTGTGTGCATGTGTGT
61981   GAAAAACTTGAAGTACATTTACTTTTTTACATATATAAAACACAAACACACGTACACACA

62041   GTGTGTGCTTGCACACGTGTGAATACCCCTTATTGTTTGAGCTTAGTATTATGTAAGATC
62041   CACACACGAACGTGTGCACACTTATGGGGAATAACAAACTCGAATCATAATACATTCTAG

62101   TAACCAGGAAGGACCAACCTAACATTTGTGGGGCCTGGGACCTAAGTATAGACAGAGATG
62101   ATTGGTCCTTCCTGGTTGGATTGTAAACACCCCGGACCCTGGATTCATATCTGTCTCTAC

62161   ACATGGTCCACTCCATATCTGTTCCCATCCCAGTTCTGCCCTGTGCTACAAGGGGTCTTC
62161   TGTACCAGGTGAGGTATAGACAAGGGTAGGGTCAAGACGGGACACGATGTTCCCCAGAAG

62221   CAGACACTGCATAGGTACCCATACCACCTGCAGGCAGATGACCTTTGCCTGTCCTTTGGA
62221   GTCTGTGACGTATCCATGGGTATGGTGGACGTCCGTCTACTGGAAACGGACAGGAAACCT

62281   GTTAGGCCTGGGTACCCTACTAGTGGTGTCTGCTCTTGGGATGATAAACCCGAGGGGCTT
62281   CAATCCGGACCCATGGGATGATCACCACAGACGAGAACCCTACTATTTGGGCTCCCCGAA

62341   ATCAGCTTTATATATATATATATATATATATATATATATATTTTTTTTTTTTTTTTTTTTAG
62341   TAGTCGAAATATATATATATATATATATATATATATATATAAAAAAAAAAAAAAAAAAAATC

62401   CTAGCATCTCTCTCGTTCTTCCAGGCTGGAGAGCAGTGGTGTGATCTTGGCTCACTGTAA
62401   GATCGTAGAGAGAGCAAGAAGGTCCGACCTCTCGTCACCACACTAGAACCGAGTGACATT

62461   TCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGAGATTAC
62461   AGAGGTGGAGGACCCAAGTTCGCTAAGAGGACGGAGTCGGAGGGTTCATCGACTCTAATG
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FIGURE 4 (cont'd)

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62521  AGGCACGTGCCACTATGCCTGGCTAATTTTTGTATTTTTAGTAGAGACTGGGTTTCACCA
62521  TCCGTGCACGGTGATACGGACCGATTAAAAACATAAAAATCATCTCTGACCCAAAGTGGT

62581  TGTTGGCATGTGAGCCACTATGCCCGGCCTCTTTTTTTTTTTTTTTTTAAGAGACAGGGTC
62581  ACAACCGTACACTCGGTGATACGGGCCGGAGAAAAAAAAAAAAAAAAATTCTCTGTCCCAG

62641  TTACTATGTTGCCCAGGCTGGTGTTGAACTCCTGGCCTCAATAGATCCTCTGTCCTTGGT
62641  AATGATACAACGGGTCCGACCACAACTTGAGGACCGGAGTTATCTAGGAGACAGGAACCA

62701  CTCCCAAAGTGCTGGCTCAGTCATTATGTTCTTTACTGCCATCCATTGCAGTATAAAAAG
62701  GAGGGTTTCACGACCGAGTCAGTAATACAAGAAATGACGGTAGGTAACGTCATATTTTTC

62761  AATAACAGTTTTCCCTCAGAATATTCTTGGTGAAACAGTAACAATTATTAATTTTATTAA
62761  TTATTGTCAAAAGGGAGTCTTATAAGAACCACTTTGTCATTGTTAATAATTAAAATAATT

62821  ATCTTGGCTCTTGAGCAAATGTCATTTTAATATTCTGTGTGATAAAATAGCAATGTCACA
62821  TAGAACCGAGAACTCGTTTACAGTAAAATTATAAGACACACTATTTTATCGTTACAGTGT

62881  TAAAGTGCTTTTACATACTTAAGTACTATGGTTGTCTGAAGAAAAAGGAGTTGTGTGATT
62881  ATTTCACGAAAATGTATGAATTCATGATACCAACAGACTTCTTTTTCCTCAACACACTAA

62941  GTCTTGAGTTTGTAAGTGGAACTACTTTTTTCATCGAGCACCGTTTTTACTTGAAATAAC
62941  CAGAACTCAAACATTCACCTTGATGAAAAAAGTAGCTCGTGGCAAAAATGAACTTTATTG

63001  AAAGTATGAATATGAATGCAGATTTGGCCATTTGGCAGATTTTTATTTATTTATTTGAGA
63001  TTTCATACTTATACTTACGTCTAAACCGGTAAACCGTCTAAAAATAAATAAATAAACTCT

63061  CAAGGTCTTGCTGTGTCACCCAGACTGGGGTGCAGCTCACTGCAGCCTTTACCTCCTGGG
63061  GTTCCAGAACGACACAGTGGGTCTGACCCCACGTCGAGTGACGTCGGAAATGGAGGACCC

63121  CTCAAGTGATCCTCCTGCCTCAGCCTCCTTAGTTGCTGGGACCACAGGTGTGCAGCACCA
63121  GAGTTCACTAGGAGGACGGAGTCGGAGGAATCAACGACCCTGGTGTCCACACGTCGTGGT

63181  TGCTCAGCTAATTTTTAAATTTTTTGTGGAGACAAGGTCTGACCATGTTGCCCAGGCTGG
63181  ACGAGTCGATTAAAAATTTAAAAAACACCTCTGTTCCAGACTGGTACAACGGGTCCGACC

63241  TCTCGAACTCCTGGGCTCCAGCAATCCTCTCGCTTCAGCTTCTCAAAGTGCTGGAATTAC
63241  AGAGCTTGAGGACCCGAGGTCGTTAGGAGAGCGAAGTCGAAGAGTTTCACGACCTTAATG

63301  AGGCGTGAGCCACGGTTCCCAGCTCGCCTTTTCATATGTTTATTGGGTTGCTAAATATGT
63301  TCCGCACTCGGTGCCAAGGGTCGAGCGGAAAAGTATACAAATAACCCAACGATTTATACA

63361  TCTTATTTGAAGTGCCCACTTGTTCAAGTTTTTTGTTCACTTTTTTATTGCTGTCTTTAT
63361  AGAATAAACTTCACGGGTGAACAAGTTCAAAAAACAAGTGAAAAAATAACGACAGAAATA

63421  AATTTTTTGATGACAAGAAATATGTTTAAATTAAAGGCAGTTTTGTCAATCTGCCTTATG
63421  TTAAAAAACTACTGTTCTTTATACAAATTTAATTTCCGTCAAAACAGTTAGACGGAATAC

63481  TTTGGAATTTGTTGTGTCTTTAAAGACTCTTTTCCTGCCCTTATATTATAAAGATATCTT
63481  AAACCTTAAACAACACAGAAATTTCTGAGAAAAGGACGGGAATATAATATTTCTATAGAA

63541  ATAGTATTGATATTGTCATTCACAGTTAGGTCTTTAATCCTAGAAGTTGATTTTTGTATG
63541  TATCATAACTATAACAGTAAGTGTCAATCCAGAAATTAGGATCTTCAACTAAAAACATAC

63601  AAGTAAGGGCCCAATTTATTTTTTTCCACCTATGTATACCCAGTTTTCCCAGCACCATTT
63601  TTCATTCCCGGGTTAAATAAAAAAAGGTGGATACATATGGGTCAAAAGGGTCGTGGTAAA

63661  AAACGGGCGGTACTTTCCCCTCTGATATGTCATGATGACACCTTTGTCATGTACACATGA
63661  TTTGCCCGCCATGAAAGGGGAGACTATACAGTACTACTGTGGAAACAGTACATGTGTACT

63721  GTTTGCTTCTGGATCTCTATTTGTGTTCAGTTGTTTTACTTGTCTGCATAAATGCCACAG
63721  CAAACGAAGACCTAGAGATAAACACAAGTCAACAAAATGAACAGACGTATTTACGGTGTC

63781  TCTTGGTTTCTCAGTCATTATAATGAGCCTTGCCTGCTAGGAAGGGTCCTTCTACTTTGT
63781  AGAACCAAAGAGTCAGTAATATTACTCGGAACGGACGATCCTTCCCAGGAAGATCAAACA
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FIGURE 4 (cont'd)

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63841   TCTCCAAGAGTGCCTTGGATATTCTTGGTCATTTTCTTTCCATATAATTTTTAGATTTGG
63841   AGAGGTTCTCACGGAACCTATAAGAACCAGTAAAAGAAAGGTATATTAAAAATCTAAACC

63901   TTTATCAAGTCGATAAACTTTTGTCATGCAGTTTTTTAAAAGAAAATAAAGTGCCCTAAT
63901   AAATAGTTCAGCTATTTGAAAACAGTACGTCAAAAAATTTTCTTTTATTTCACGGGATTA

63961   GTGATTTTTTTTAATTTGGATTACATTGAATACATAAATCAGTTTGGGGAAAATCAACAT
63961   CACTAAAAAAAATTAAACCTAATGTAACTTATGTATTTAGTCAAACCCCTTTTAGTTGTA

64021   CTTTATAATATTGAGGCTTTTTATCCATGAGCATGAAATTGCTTTCTACATTAATAACTT
64021   GAAATATTATAACTCCGAAAAATAGGTACTCGTACTTTAACGAAAGATGTAATTATTGAA

64081   GGTAAAGTTTTATATTTTCCTTATGGATCTTTCACTTCTTTTGTTAGATTTTTCTCCACC
64081   CCATTTCAAAATATAAAAGGAATACCTAGAAAGTGAAGAAAACAATCTAAAAAGAGGTGG

64141   TAAGTACTGTATCTTTTAATTCTACTGTAAATAGTGTTTTTATTTTTTAACTGCTGCTAT
64141   ATTCATGACATAGAAAATTAAGATGACATTTATCACAAAAATAAAAAATTGACGACGATA

64201   TACATAGGAATATAATTTTGCATCTGGCCAGCTTGCCTAAACAGATGATTTCAAAATATT
64201   ATGTATCCTTATATTAAAACGTAGACCGGTCGAACGGATTTGTCTACTAAAGTTTTATAA

64261   ATCTGTCAGATTTTCTGTGTTCTCTATCTCTGTAATCATATCATCTATGTTTTATGATCT
64261   TAGACAGTCTAAAAGACACAAGAGATAGAGACATTAGTATAGTAGATACAAAATACTAGA

64321   ATGACAGTTATATTTTTTCATCTCCAAGCTGATATTTTAAATTTCATTATTCTTGCTTTA
64321   TACTGTCAATATAAAAAAGTAGAGGTTCGACTATAAAATTTAAAGTAATAAGAACGAAAT

64381   TACTGGTTGTACATATTCAGTTAGAGTGATTGCAGTAGGCAATTTGCGATGTTCCCAATT
64381   ATGACCAACATGTATAAGTCAATCTCACTAACGTCATCCGTTAAACGCTACAAGGGTTAA

64441   TGATAAGGAAAGCTTTTACATTTTACCATTAAGTATAACGTTTGCGAGCTTATTATAGCT
64441   ACTATTCCTTTCGAAAATGTAAAATGGTAATTCATATTGCAAACGCTCGAATAATATCGA

64501   ATCCTTTGTCACTTAGGGAAGTTATCTTTGTTTTTTAGTTATCTAGGAAACTAAAAAATC
64501   TAGGAAACAGTGAATCCCTTCAATAGAAACAAAAAATCAATAGATCCTTTGATTTTTTAG

64561   AGAAAAGTTAGTTTGATTTTATCAGATACATCTGCTACATCTAATGAGATGATCATATAG
64561   TCTTTTCAATCAAACTAAAATAGTCTATGTAGACGATGTAGATTACTCTACTAGTATATC

64621   TTTTTTTCCTCCCATAAACTGTGAATATAATGAATCACATTAATTGATTTTTTTAAATGT
64621   AAAAAAAGGAGGGTATTTGACACTTATATTACTTAGTGTAATTAACTAAAAAAATTTACA

64681   TAAACCAATCTCCATTTCTGGGATAAATTCAACTTAGTCATGTTGTATTAGCCTTTTGTA
64681   ATTTGGTTAGAGGTAAAGACCCTATTTAAGTTGAATCAGTACAACATAATCGGAAAACAT

64741   TATCTTATATCTATAATACTGAATGAGATTATCATACTCTTTACATGTATTTGAAGCCAT
64741   ATAGAATATAGATATTATGACTTACTCTAATAGTATGAGAAATGTACATAAACTTCGGTA

64801   GTCATTAAGTGCATACAATTTTTATTAAATTTTTAATTGACAAATAATTGTATTTATTTA
64801   CAGTAATTCACGTATGTTAAAAATAATTTAAAAATTAACTGTTTATTAACATAAATAAAT

64861   TGGGGTACGATGTAGTGTTTTGATATATGTTTACATTGTAGAGTGACTAAATCAAGCTAA
64861   ACCCCATGCTACATCACAAAACTATATACAAATGTAACATCTCACTGATTTAGTTCGATT

64921   TTAGCATACTCATCACTGAACATATTTATCATTTCTTGTGGTGAGAACATTTGAAATTTA
64921   AATCGTATGAGTAGTGACTTGTATAAATAGTAAAGAACACCACTCTTGTAAACTTTAAAT

64981   ATCTCTTAGCAATTTTGAAATATATGATACATTATTATTAACTACAGTCACCATGCTGTG
64981   TAGAGAATCGTTAAAACTTTATATACTATGTAATAATAATTGATGTCAGTGGTACGACAC

65041   CGATAGGTCTCAAAAACTTATTCCTCCTAATTGAAATTTTGTTCCCTTTGACCAACATCT
65041   GCTATCCAGAGTTTTTGAATAAGGAGGATTAACTTTAAAACAAGGGAAACTGGTTGTAGA

65101   TCCAATTCCCCAACCCCTAGCCTCCTCTGGTAACCACCATTCTACTCTCTACTTCCATTA
65101   AGGTTAAGGGGTTGGGGATCGGAGGAGACCATTGGTGGTAAGATGAGAGATGAAGGTAAT
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FIGURE 4 (cont'd)

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65161  GTTTGACTTTTTCAGTCCACATATGAGTGAAATCGTGCAGTATTTGTCTTTCTGTACTTG
65161  CAAACTGAAAAAGTCAGGTGTATACTCACTTTAGCACGTCATAAACAGAAAGACATGAAC

65221  TCTTGTTTCACTTAGCATAATGTCCAACGGGTTCCCCATGTCATTGTAAATGATGGAATT
65221  AGAACAAAGTGAATCGTATTACAGGTTGCCCAAGGGGTACAGTAACATTTACTACCTTAA

65281  TTCTTTTTTATAGCTAAATAACATTCCATCATGTATACATACCACATTTTCTTTATCGAT
65281  AAGAAAAAATATCGATTTATTGTAAGGTAGTACATATGTATGGTGTAAAAGAAATAGCTA

65341  TCATCTGTTGATGGACAGTTAGGTTGCTTCTGTATCCTGGCTATTGTGAATAATGCTACA
65341  AGTAGACAACTACCTGTCAATCCAACGAAGACATAGGACCGATAACACTTATTACGATGT

65401  ATAAACATGAGAGCACAGATACCTCATGCTGATTTCAATTCCTTTGGATAAGGGTCCCCA
65401  TATTTGTACTCTCGTGTCTATGGAGTACGACTAAAGTTAAGGAAACCTATTCCCAGGGGT

65461  AACCCCAGGCTATGGAACAGCAGTGGTATGTGTGGCCTGTTAGGTACTGGATCGCACTGT
65461  TTGGGGTCCGATACCTTGTCGTCACCATACACACCGGACAATCCATGACCTAGCGTGACA

65521  AGGAGGTGAGCAGCTGCGAGTGAGCATTACCACCTGAGCTCCATCTCATCTCAGATCAGT
65521  TCCTCCACTCGTCGACGCTCACTCGTAATGGTGGACTCGAGGTAGAGTAGAGTCTAGTCA

65581  GGCAGCATTAGGTTCTCATAGGAGTGTGAACCCTATTGTGAACTGTGCATTGCAGGAATC
65581  CCGTCGTAATCCAAGAGTATCCTCACACTTGGGATAACACTTGACACGTAACGTCCTTAG

65641  TAGGTGGTGCACTTTTTATGAGAATCTAATGCTTGATGATCTGAGGTAGAATGATTGCAC
65641  ATCCACCACGTGAAAAATACTCTTAGATTACGAACTACTAGACTCCATCTTACTAACGTG

65701  TCTGCAAGACTCCCCACGCTCATCCCTGTGGAAAAATTATCTTCCACAAAACTGGTCCCT
65701  AGACGTTCTGAGGGGTGCGAGTAGGGACACCTTTTTAATAGAAGGTGTTTTGACCAGGGA

65761  GGTGCCAAAAAGGTTGGGGACTGCTGCTTTTGGATATATACCCAGAAGTGGGATTGCTGA
65761  CCACGGTTTTTCCAACCCCTGACGACGAAAACCTATATATGGGTCTTCACCCTAACGACT

65821  AGCATATGGTAGTTTAATTTTAATTTTAATTTAATTTAGTTTAATTAATTTATTTTTAGC
65821  TCGTATACCATCAAATTAAAATTAAAATTAAATTAAATCAAATTAATTAAATAAAAATCG

65881  ACCTAGGCTGGAATGCAGCAGTGCAATCATAGCTCACTGCAGCTTCCAATTCCTGACCTC
65881  TGGATCCGACCTTACGTCGTCACGTTAGTATCGAGTGACGTCGAAGGTTAAGGACTGGAG

65941  AAGCCATCCTCCCAACTCAGCCTCCCAAATTTCTGGAACTACAGGAATGAGCCATCTCAC
65941  TTCGGTAGGAGGGTTGAGTCGGAGGGTTTAAAGACCTTGATGTCCTTACTCGGTAGAGTG

66001  TCAGCCCTATTTTTAGTGTTGGGAAGAATCTCAAAAAGTAATGACTGTACTAATTTACAC
66001  AGTCGGGATAAAAATCACAACCCTTCTTAGAGTTTTTCATTACTGACATGATTAAATGTG

66061  CGCTACCCTCAGTATACAAGGGTTCCATATCCTCACTAATACTTATCTTTTATCTTTTTG
66061  GCGATGGGAGTCATATGTTCCCAAGGTATAGGAGTGATTATGAATAGAAAATAGAAAAAC

66121  ATAGTAGCCATTCTAAGTATGTATAGTTTTAAAATTATGAAGTTTAAATTGAACCTTAGG
66121  TATCATCGGTAAGATTCATACATATCAAAATTTTAATACTTCAAATTTAACTTGGAATCC

66181  AAGTTGCTACTCTGTCACCAGGCTGGAGTGCAGCAGCGTGATCTTGGTTCACCACAATCT
66181  TTCAACGATGAGACAGTGGTCCGACCTCACGTCGTCGCACTAGAACCAAGTGGTGTTAGA

66241  CCGCCTCCTGGGTTTAAGCAATTCTCCTGGCTCAGCCTCCCAAGTAGCTGGGACTACAGG
66241  GGCGGAGGACCCAAATTCGTTAAGAGGACCGAGTCGGAGGGTTCATCGACCCTGATGTCC

66301  CACATGGTACCATGCCTGGCTCATTTTTATATTTTTGGTAGAGATGGGTTTCACCATGTT
66301  GTGTACCATGGTACGGACCGAGTAAAAATATAAAAACCATCTCTACCCAAAGTGGTACAA

66361  GTCCAGGCTGGTCTCGAACTCCTGACCTCAAGTGATCCAACAGCCTTGGCCTCCCAACGT
66361  CAGGTCCGACCAGAGCTTGAGGACTGGAGTTCACTAGGTTGTCGGAACCGGAGGGTTGCA

66421  GTTGGGATTACAGACGTGAGCCATCACACCCAGCCTTGAAGTTGCCTTTTTTATCTTCAG
66421  CAACCCTAATGTCTGCACTCGGTAGTGTGGGTCGGAACTTCAACGGAAAAAATAGAAGTC

66481  TAGTGCTTCTTGGCTTAAATTCTTTTGTTTTATAAATAGTAATGGAAGCTTGCCAGTTTT
66481  ATCACGAAGAACCGAATTTAAGAAAACAAAATATTTATCATTACCTTCGAACGGTCAAAA
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FIGURE 4 (cont'd)

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66541  ATTTTAGAAACTATTTGCAGGCCACGTCCAGTGGCTCATGCCTGTAATCCCAGCACTTTG
66541  TAAAATCTTTGATAAACGTCCGGTGCAGGTCACCGAGTACGGACATTAGGGTCGTGAAAC

66601  GGAGGCCGAGGCAGGCACATCACTTGAGCCCAGGAGTTCGAGACCAGCCTAGGCAACATG
66601  CCTCCGGCTCCGTCCGTGTAGTGAACTCGGGTCCTCAAGCTCTGGTCGGATCCGTTGTAC

66661  GCAAAACCTCGTCTCTACAAAAAATACAAAAAATTAACTTGGGCGTGGTGGTGCGCGCCT
66661  CGTTTTGGAGCAGAGATGTTTTTTATGTTTTTTAATTGAACCCGCACCACCACGCGCGGA

66721  GTAGTCCCAGCTACTCTGGAGGCTGAGGTGGGAGGATTGCTTGAACCCAGGGGGTAGAGG
66721  CATCAGGGTCGATGAGACCTCCGACTCCACCCTCCTAACGAACTTGGGTCCCCCATCTCC

66781  TTGCAGTGAGCCAAGATCTTGCCACTGAACTTCATTCAGCCTGGGTGACAGAGAAAAACA
66781  AACGTCACTCGGTTCTAGAACGGTGACTTGAAGTAAGTCGGACCCACTGTCTCTTTTTGT

66841  ACTCTGTCTCAAAAAAAAAAAATAAATAATAAAAAATAAAGTATTTGCATGATATATCTT
66841  TGAGACAGAGTTTTTTTTTTTTATTTATTATTTTTTATTTCATAAACGTACTATATAGAA

66901  TTTCTGTCTTTTTGATTCAGATATTGTCAGCTGAGTCCAATCTAACAAACTTATATTTTA
66901  AAAGACAGAAAAACTAAGTCTATAACAGTCGACTCAGGTTAGATTGTTTGAATATAAAAT

66961  ACCGAAGCTTTAGTACTGTTATATTTAATAAACTAATAATATATTTGCACTTAAATACAA
66961  TGGCTTCGAAATCATGACAATATAAATTATTTGATTATTATATAAACGTGAATTTATGTT

67021  CATCTAATTTTATGCTTTTTAATTATACATGATTTGTATTTCTTTTTTTCCCATGTAAGT
67021  GTAGATTAAAATACGAAAAATTAATATGTACTAAACATAAAGAAAAAAAGGGTACATTCA

67081  TTTTAGGGTATACATCTTTAAAGGCCTTACTTTTCATTATCGTTCAGTTTAACTTATTTT
67081  AAAATCCCATATGTAGAAATTTCCGGAATGAAAAGTAATAGCAAGTCAAATTGAATAAAA

67141  CTAATTTCCATTTTTCTTCTGTGACCTATGGTTTAGTTAGTGGTGGATTTATTTTCCAAA
67141  GATTAAAGGTAAAAAGAAGACACTGGATACCAAATCAATCACCACCTAAATAAAAGGTTT

67201  ATATGGATGGTGTCCAGTCAAACTTTTGGTATTGATTTCTGGCTTATCTTGTGTTTGGAA
67201  TATACCTACCACAGGTCAGTTTGAAAACCATAACTAAAGACCGAATAGAACACAAACCTT

67261  AATATGTGAATTCTACAGCTGGTCTGTGTAAGAGTTCTCTGTATCAGTTAGGGAAGTTTG
67261  TTATACACTTAAGATGTCGACCAGACACATTCTCAAGAGACATAGTCAATCCCTTCAAAC

67321  TTCTTCCTGTTGTTCATATCTTGCATATCTTTACTAAGGTTTAGCCTGTTTGTTCTATAA
67321  AAGAAGGACAACAAGTATAGAACGTATAGAAATGATTCCAAATCGGACAAACAAGATATT

67381  ATTACTTAGAGAAGCTGTGTTAAATTTTCCCACTAAAATTATTGATTTTTGTCTTTCTCT
67381  TAATGAATCTCTTCGACACAATTTAAAAGGGTGATTTTAATAACTAAAAACAGAAAGAGA

67441  GTATTTATCAGTATGTATCTACTGAAGTCTTTTCAAATCCCTGATCAGTGGTTTGTTCAG
67441  CATAAATAGTCATACATAGATGACTTCAGAAAAGTTTAGGGACTAGTCACCAAACAAGTC

67501  GACAGCACTTTGATTGAGGGAGGTGACGTGGCTTAACATAGTATGGTCTTGAGCTGCCTG
67501  CTGTCGTGAAACTAACTCCCTCCACTGCACCGAATTGTATCATACCAGAACTCGACGGAC

67561  GTTTCTGTGATTTAGGGACTGAACCAGCTCTGGTCACATCTGGATTATCTACTATCCAGC
67561  CAAAGACACTAAATCCCTGACTTGGTCGAGACCAGTGTAGACCTAATAGATGATAGGTCG

67621  ATTCAAATGAACCAGATTACATGAAAGGATATGGGGGTACTCTTTGGGGGCCACGGTGCC
67621  TAAGTTTACTTGGTCTAATGTACTTTCCTATACCCCCATGAGAAACCCCCGGTGCCACGG

67681  ACAAGGCCTTTGGTTTCGATCTCCATTGCCTAGGGAATTAACCTGTGCTGTGTGATTCTA
67681  TGTTCCGGAAACCAAAGCTAGAGGTAACGGATCCCTTAATTGGACACGACACACTAAGAT

67741  GATGTTTTCTTCCTGCTCCCTTAAATAACACCTAAATGTGTTATTCAGCAGTGTGGCTCC
67741  CTACAAAAGAAGGACGAGGGAATTTATTGTGGATTTACACAATAAGTCGTCACACCGAGG

67801  TGCTAAGCAGAGGAGAACTCGGAATTCCTACCAAATTCTGATAATAAAATAACTTTCCTC
67801  ACGATTCGTCTCCTCTTGAGCCTTAAGGATGGTTTAAGACTATTATTTTATTGAAAGGAG
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FIGURE 4 (cont'd)

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67861   CACCTCAACCATTGTTTTTACCAGTCCTGTCAACTGTTAGCTTTCCTGGATTTAATGATC
67861   GTGGAGTTGGTAACAAAAATGGTCAGGACAGTTGACAATCGAAAGGACCTAAATTACTAG

67921   TCAAGTTGAGGTCAATGTCAACAGCTTTATGGGATGAATAAGATGAACGCCCATAGGAAA
67921   AGTTCAACTCCAGTTACAGTTGTCGAAATACCCTACTTATTCTACTTGCGGGTATCCTTT

67981   GTCAGTCTCTTGAACACGGGTTGTTTTCTTTTGGTTACCCTCTAAGATTTTTTCTCTTTG
67981   CAGTCAGAGAACTTGTGCCCAACAAAAGAAAACCAATGGGAGATTCTAAAAAAGAGAAAC

68041   ATCTCCAGTTATTTGAAGGATTGAAGGCATTTCGAGGAGTAGATAATAAAATTCGACTGT
68041   TAGAGGTCAATAAACTTCCTAACTTCCGTAAAGCTCCTCATCTATTATTTTAAGCTGACA

68101   TTCAGCCAAACCTCAACATGGATAGAATGTATCGCTCTGCTGTGAGGGCAACTCTGCCGG
68101   AAGTCGGTTTGGAGTTGTACCTATCTTACATAGCGAGACGACACTCCCGTTGAGACGGCC

68161   TATGTAAGTGTAGGAGTTTCTTTTGTGTTTCTTTTAATGTAACGGGTCACGGTGTTGACC
68161   ATACATTCACATCCTCAAAGAAAACACAAAGAAAATTACATTGCCCAGTGCCACAACTGG

68221   ACCAAATAAATAATTTCTGAATAGTTAGATAAATATTCAGTACAAACCATATGAACATTA
68221   TGGTTTATTTATTAAAGACTTATCAATCTATTTATAAGTCATGTTTGGTATACTTGTAAT

68281   ACATTATTTCTGATCTACTTTAGTTAGGTAAAAATACAAGAAAATGGCCGGGCACGGTGG
68281   TGTAATAAAGACTAGATGAAATCAATCCATTTTTATGTTCTTTTACCGGCCCGTGCCACC

68341   TTCACTCCTATAATCCCAGCACTCTGGGAGACTGAGGTGGGTGGATCACTTGAAACCAGG
68341   AAGTGAGGATATTAGGGTCGTGAGACCCTCTGACTCCACCCACCTAGTGAACTTTGGTCC

68401   AATTGGAGACAAGCCTGGCCAACATGGTGAAACACCATCTCTGCAAAAAATACAAAAATT
68401   TTAACCTCTGTTCGGACCGGTTGTACCACTTTGTGGTAGAGACGTTTTTTATGTTTTTAA

68461   AGCCGGGTTTGGTGGCACATGCCTGTGGTCCCATCGGTGTGGCTGAGGCATGAGAATTGC
68461   TCGGCCCAAACCACCGTGTACGGACACCAGGGTAGCCACACCGACTCCGTACTCTTAACG

68521   TTGAACCTGGCAGGTGGAGGCTGCAGTGAGCCAAGATAATCACATCACTGCCCTCCAGCC
68521   AACTTGGACCGTCCACCTCCGACGTCACTCGGTTCTATTAGTGTAGTGACGGGAGGTCGG

68581   TAAGCCGCAAAGTGAGACTCTGTAAAAAAAAAAAACAAAAAACAAAAAACCCAAGAAAAT
68581   ATTCGGCGTTTCACTCTGAGACATTTTTTTTTTTTGTTTTTTGTTTTTTGGGTTCTTTTA

68641   AATATCATTTGGCAATTCCACAATTTTTTAAAATCAGTGTCTGTGGGGGATTCATATGCA
68641   TTATAGTAAACCGTTAAGGTGTTAAAAAATTTTAGTCACAGACACCCCCTAAGTATACGT

68701   AGTGAGAGATGAAAGAGTAAGGAAGAAAAATGTATCTCAACCTAAAATAATATTTGAAGA
68701   TCACTCTCTACTTTCTCATTCCTTCTTTTTACATAGAGTTGGATTTTATTATAAACTTCT

68761   CCACATGAAATTAATATTGAAAATGGAAAATATGGTGTGCAGCACAGGTATTTTGCGGAT
68761   GGTGTACTTTAATTATAACTTTTACCTTTTATACCACACGTCGTGTCCATAAAACGCCTA

68821   ATTTTGCCTAATTGCTTTAGATGCTAGCAAGATATAGTAACTTAATTATTTTGATATTTT
68821   TAAAACGGATTAACGAAATCTACGATCGTTCTATATCATTGAATTAATAAAACTATAAAA

68881   ATCTTAAGTAATGTTTTGAGATAAAAAGATATCAAAATGGTTTCTCATGGCCATTGAATC
68881   TAGAATTCATTACAAAACTCTATTTTTCTATAGTTTTACCAAAGAGTACCGGTAACTTAG

68941   GTGGCTGTCACAATGTTTCTTATGGAGCAGAAATCATTGTAAGATGGGTTAGATTTTTTT
68941   CACCGACAGTGTTACAAAGAATACCTCGTCTTTAGTAACATTCTACCCAATCTAAAAAAA

69001   TTTGAGAGAGAGTCTCACTCTGTCACCCAAGCTATAGTGCAGTGGCACAATCTTGGCTCA
69001   AAACTCTCTCTCAGAGTGAGACAGTGGGTTCGATATCACGTCACCGTGTTAGAACCGAGT

69061   CTACAACCTCCACCTCCGGGGTTCAAGTGATTCTTGTGCCTCAGCCTCCTTAGTATCTGG
69061   GATGTTGGAGGTGGAGGCCCCAAGTTCACTAAGAACACGGAGTCGGAGGAATCATAGACC

69121   GATTACAAGTGCACGCAGCCATGCCCAGCTTAATTTTTTTAAAAATTATTTTTAGTGGAG
69121   CTAATGTTCACGTGCGTCGGTACGGGTCGAATTAAAAAAATTTTTAATAAAAATCACCTC
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FIGURE 4 (cont'd)

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69181  ACATGATTTCACCATGTTAGCCAGGCTGGACTTGAACTTCTGGCCTCAAGTGATCTGCCT
69181  TGTACTAAAGTGGTACAATCGGTCCGACCTGAACTTGAAGACCGGAGTTCACTAGACGGA

69241  GCCTCAGCCTCCCAAAGTTCTGGGATTACAGGCATGAGCCACCGTGCCCAGCTTCAGGGA
69241  CGGAGTCGGAGGGTTTCAAGACCCTAATGTCCGTACTCGGTGGCACGGGTCGAAGTCCCT

69301  TTTAGCCCAACCTATGCATTCAGGAAGCCTGAGGACGGCTAAATCCAAGTGTTCTTCATT
69301  AAATCGGGTTGGATACGTAAGTCCTTCGGACTCCTGCCGATTTAGGTTCACAAGAAGTAA

69361  CCTCTGCCTATTTTTGTAACCCGCATTTCACCCATCTCCTTTGGAGGCCATAATATAGTA
69361  GGAGACGGATAAAAACATTGGGCGTAAAGTGGGTAGAGGAAACCTCCGGTATTATATCAT

69421  GCAGAGGGGAAATTAAGGTAAATTCTTTGGACTAGGGCATAGTTTCGCTCTTCTTCTCAT
69421  CGTCTCCCCTTTAATTCCATTTAAGAAACCTGATCCCGTATCAAAGCGAGAAGAAGAGTA

69481  TACAGCTAGATCACTGGGGAAAAGTCTTTAAAATGGGGCTGGAAGGAAAGGGAAGTAATA
69481  ATGTCGATCTAGTGACCCCTTTTCAGAAATTTTACCCCGACCTTCCTTTCCCTTCATTAT

69541  TTTGTTAGACATCAATTTTGCTACCAAACTGTGTTATGTAGTTTCACATTCCTTATCTGT
69541  AAACAATCTGTAGTTAAAACGATGGTTTGACACAATACATCAAAGTGTAAGGAATAGACA

69601  GTAATCACAGCAGTAAGGCGTTGCTAAGAAGATTATTTGTTGTACAGTTTATTAGTGCCT
69601  CATTAGTGTCGTCATTCCGCAACGATTCTTCTAATAAACAACATGTCAAATAATCACGGA

69661  TTGTACAGAGAAGAAAACTTGAGTCCAGAGAGATTAAATGACTTGTCTGAAGTCACAAAG
69661  AACATGTCTCTTCTTTTGAACTCAGGTCTCTCTAATTTACTGAACAGACTTCAGTGTTTC

69721  AGCAAAAGGACAGGGCAAGAAATTAGATCCAGGTGTTTTTATTCCTGGTCAAGTTCTCTT
69721  TCGTTTTCCTGTCCCGTTCTTTAATCTAGGTCCACAAAAATAAGGACCAGTTCAAGAGAA

69781  CTCACTGAATTCTGTCTCTAGACAGCAATACCAGGGGCTGAGGCAGGTGCTACAGGGTTC
69781  GAGTGACTTAAGACAGAGATCTGTCGTTATGGTCCCCGACTCCGTCCACGATGTCCCAAG

69841  ACCTATATGATTGGCAGTCCCAATTTCTATAACATTACTACATTATTATTGCTGTTACAG
69841  TGGATATACTAACCGTCAGGGTTAAAGATATTGTAATGATGTAATAATAACGACAATGTC

69901  GTCAATATTTAAATAGACAAATTCTGACTTCATGAGCTTTACTCAGATGCTTATGACTGA
69901  CAGTTATAAATTTATCTGTTTAAGACTGAAGTACTCGAAATGAGTCTACGAATACTGACT

69961  CTCATTTCTACCTTAGGTGACCCATCACATCTCTGAAAGTATGTTTCTCTACTTTGCAAG
69961  GAGTAAAGATGGAATCCACTGGGTAGTGTAGAGACTTTCATACAAAGAGATGAAACGTTC

70021  TGAGCAGAGACTAAATTATTTTATGAAGTATCACCCATCTAGTAGATGTAATTTTTTTTT
70021  ACTCGTCTCTGATTTAATAAAATACTTCATAGTGGGTAGATCATCTACATTAAAAAAAAA

70081  CTTTAGAAATAAAGTGCTCTTTGCTTTTGCCCATTTTCCTATTGGGTTATCTATCTCTTC
70081  GAAATCTTTATTTCACGAGAAACGAAAACGGGTAAAAGGATAACCCAATAGATAGAGAAG

70141  ATTGACTTTGGGGATATCCAAATATATATACCAGTTAAAATTCTTTGTTGATCATGCTAC
70141  TAACTGAAACCCCTATAGGTTTATATATATGGTCAATTTTAAGAAACAACTAGTACGATG

70201  CAATAACTTCACCCAGTTTGTTGCTTTACATCTTTTGAAGAACGGAAGTCTTTAAGTTTC
70201  GTTATTGAAGTGGGTCAAACAACGAAATGTAGAAAACTTCTTGCCTTCAGAAATTCAAAG

70261  AAATAGTCACATTTTATCCATTTTTTTCCTTCATGATTTGTGTTTTACATCTCCTACTTA
70261  TTTATCAGTGTAAAATAGGTAAAAAAAGGAAGTACTAAACACAAAATGTAGAGGATGAAT

70321  AGAATCCTTTCCTACCTTAAGGTCACAGAGATATTTTGTACTTTTTAAATAAAGTCTTAG
70321  TCTTAGGAAAGGATGGAATTCCAGTGTCTCTATAAAACATGAAAAATTTATTTCAGAATC

70381  TATTTTGTCACATTTAAGTATATCATCTAATTAGAATTGATTGGGGGGTATGGTAAGATG
70381  ATAAAACAGTGTAAATTCATATAGTAGATTAATCTTAACTAACCCCCCATACCATTCTAC

70441  TAGGATCTAATCTTATCTTTCACATGTGGATAGCTCGTCATCCCATCACAATTTTTGGG
70441  ATCCCTAGATTAGAATAGAAAGTGTACACCTATCGAGCAGTAGGCTAGTGTTAAAAACCC
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FIGURE 4 (cont'd)

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70501   GGGAAAATCAGAAAAAATTGTTTGGTTTTATTATTACTTTAAAATTTTTTTTATTGGTAC
70501   CCCTTTTAGTCTTTTTTAACAAACCAAAATAATAATGAAATTTTAAAAAAAATAACCATG

70561   CATAAATTATACATATTTATGAGGTACACTGATGTTTTCATGCATGCATATAATGTGTAA
70561   GTATTTAATATGTATAAATACTCCATGTGACTACAAAAGTACGTACGTATATTACACATT

70621   TGATTAGGACAAATAAGAAAGAAATAAATAAAAATTAGGATAATTAGGATATCCATCACC
70621   ACTAATCCTGTTTATTCTTTCTTTATTTATTTTTAATCCTATTAATCCTATAGGTAGTGG

70681   TCAAACATTTCTTATTTTTTTGTGTTGGGATTATTAATTTTTTAACAGTTTAAATGCTTC
70681   AGTTTGTAAAGAATAAAAAAACACAACCCTAATAATTAAAAAATTGTCAAATTTACGAAG

70741   AGTGAGGATCATTTATTATTGCCACATTGTGAGAAAATTCTGTCATTTATTATGTTTTTC
70741   TCACTCCTAGTAAATAATAACGGTGTAACACTCTTTTAAGACAGTAAATAATACAAAAAG

70801   ATTCTTTCAGGTATTTGACAAAGAAGAGCTCTTAGAGTGTATTCAACAGCTTGTGAAATT
70801   TAAGAAAGTCCATAAACTGTTTCTTCTCGAGAATCTCACATAAGTTGTCGAACACTTTAA

70861   GGATCAAGAATGGGTCCCATATTCAACATCTGCTAGTCTGTATATTCGTCCTACATTCAT
70861   CCTAGTTCTTACCCAGGGTATAAGTTGTAGACGATCAGACATATAAGCAGGATGTAAGTA

70921   TGGAACTGAGGTGCAAACTGACTCTTTATTTTGGGGTACTTTGCTGGCCAAGTTATTATT
70921   ACCTTGACTCCACGTTTGACTGAGAAATAAAACCCCATGAAACGACCCGTTCAATAATAA

70981   GTTTATTGTTGTTTGAAACTTCTAGCATATAGTTTGCAGTAGCCCCCCAGTAGCATCATT
70981   CAAATAACAACAAACTTTGAAGATCGTATATCAAACGTCATCGGGGGGTCATCGTAGTAA

71041   AATGACTTCTTCCTTCTGATTGTCAAGATTAGAGGTAGCAAACATTTTCTGTGAAGCGCC
71041   TTACTGAAGAAGGAAGACTAACAGTTCTAATCTCCATCGTTTGTAAAAGACACTTCGCGG

71101   AATCAGTAAATATTTTTTGGCTTTGTGGCCATATAGTTTCTAATAAGAAATTAGATCCCT
71101   TTAGTCATTTATAAAAAACCGAAACACCGGTATATCAAAGATTATTCTTTAATCTAGGGA

71161   ACCTCTTACCATACCCCAAAATCAATTATAATTCGATTATATACTTAAATGTGACAAAAT
71161   TGGAGAATGGTATGGGGTTTTAGTTAATATTAAGCTAATATATGAATTTACACTGTTTTA

71221   ACTAAGACGTTTATTAAGAAATACAAAATATCTCTGTGACCTTAGGTAGGAAATGATTTT
71221   TGATTCTGCAAATAATTCTTTATGTTTTATAGAGACACTGGAATCCATCCTTTACTAAAA

71281   TTTTTTTTGAGGTCTCTCTCTGGTTTTTTTTTTTTGCCCACGTTGTCGCTTAGGCTGGGG
71281   AAAAAAAACTCCAGAGACAGACCAAAAAAAAAAAACGGGTGCAACAGCGAATCCGACCCC

71341   TGCAGTGATGCAATCACGGCTGACTGCAGCTTTGACCTCCTGGGCTCAAGTGATCCTCCT
71341   ACGTCACTACGTTAGTGCCGACTGACGTCGAAACTGGAGGACCCGAGTTCACTAGGAGGA

71401   GCCTCAGCTTCCCAAGTAGCTAGTACTACAGGCATGTGCTACCATGCCTAGCTAATTTTT
71401   CGGAGTCGAAGGGTTCATCGATCATGATGTCCGTACACGATGGTACGGATCGATTAAAAA

71461   AAATTTTTTGTAGAGATGATGTCTCACTCTGTTGTCCTGGCTGGTCTCAAACTCCTGGCC
71461   TTTAAAAAACATCTCTACTACAGAGTGAGACAACAGGACCGACCAGAGTTTGAGGACCGG

71521   TCTAGCAATCCTCCCACCTTGGCCTCCCAAAGTCCTGGGATTACAGGCATGAGCCACTTC
71521   AGATCGTTAGGAGGGTGGAACCGGAGGGTTTCAGGACCCTAATGTCCGTACTCGGTGAAG

71581   ACCTGACCGGAGAGGATTCTTAAACTCTGCCATTTTAGTACTAAAGCAGCCATAGACAGC
71581   TGGACTGGCCTCTCCTAAGAATTTGAGACGGTAAAATCATGATTTCGTCGGTATCTGTCG

71641   ACATAAATGAGTAAATGCAGTGCTGTTTGCCTTGCCCAATTAAGACTAGTCATTATTTTC
71641   TGTATTTACTCATTTACGTCACGACAAACGGAACGGGTTAATTCTGATCAGTAATAAAAG

71701   TAAGTTTACAAGTGCAGTGCCTCCCATTGTGGCAGTACTTCTCTGAGGTAGAAATGGTTT
71701   ATTCAAATGTTCACGTCACGGAGGGTAACACCGTCATGAAGAGACTCCATCTTTACCAAA

71761   TAAAATTTAGGGGACGGAGAGCTGCTAATTTTCATTTTCATGAGGTCTTGGGATTACTTG
71761   ATTTTAAATCCCCTCCCTCTCGACGATTAAAAGTAAAAGTACTCCAGAACCCTAATGAAC

71821   GCATGGAGTGAGAATGGAGGTTCCCCTTCCCACATAGAAAAATGGTGAAAATAAAGTTCA
71821   CGTACCTCACTCTTACCTCCAAGGGGAAGGGTGTATCTTTTTACCACTTTTATTTCAAGT
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FIGURE 4 (cont'd)

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71881  CAGTGGGAGTTAAGGAAGGAAATTGAAGAGCTGGGATGGTAGGTTTAAATAACATGACCT
71881  GTCACCCTCAATTCCTTCCTTTAACTTCTCGACCCTACCATCCAAATTTATTGTACTGGA

71941  TATGATTTCCTGGTGGGTCACAGTCTCTTGGTTGGGTGCCCTTGTGAATAAAGGCATGGA
71941  ATACTAAAGGACCACCCAGTGTCAGAGAACCAACCCACGGGAACACTTATTTCCGTACCT

72001  TTGGGCATGCCTGGAGGGGCCAAGGCCTTTTGAGCGGACGAGTATGTTTATATGAAGACC
72001  AACCCGTACGGACCTCCCCGGTTCCGGAAAACTCGCCTGCTCATACAAATATACTTCTGG

72061  CTGTCACCTGTCTCTGGTATCTGCTAGGCAGCTGTGGCTTGAGAGTGTGATATTGAGGGA
72061  GACAGTGGACAGAGACCATAGACGATCCGTCGACACCGAACTCTCACACTATAACTCCCT

72121  TAATTGATGGAAGGAGATTGAATGTGGCTGGCAGGTAAAGAGATAGGGAACATATGGAGA
72121  ATTAACTACCTTCCTCTAACTTACACCGACCGTCCATTTCTCTATCCCTTGTATACCTCT

72181  TATTTAGAATAAGAGAGTGTGAGATAGAGCGCTTTTGCTATAGCCTAGCCATTCTGTTCT
72181  ATAAATCTTATTCTCTCACACTCTATCTCGCGAAAACGATATCGGATCGGTAAGACAAGA

72241  CTACTAAGTGTTGCGGGGTTACCAGGTTTTCTACTAGGCTGTATGAATGCAAAAGGTAGA
72241  GATGATTCACAACGCCCCAATGGTCCAAAAGATGATCCGACATACTTACGTTTTCCATCT

72301  GAGATATATAGGGCCATGGAATAAATACCGAAGTGTTTTCTTTGGTATCCTTGATACCTT
72301  CTCTATATATCCCGGTACCTTATTTATGGCTTCACAAAAGAAACCATAGGAACTATGGAA

72361  TCGAAAGCCGTGTAAGGATCTAGATAATGAATTTCGTGAATTGCAGTCTCTCTGACAAGT
72361  AGCTTTCGGCACATTCCTAGATCTATTACTTAAAGCACTTAACGTCAGAGAGACTGTTCA

72421  TTTAAAGAATAGGAACAATTTTAAAAAGTCATCTACTTCCATAAGTTTTTTGACATTTTA
72421  AAATTTCTTATCCTTGTTAAAATTTTTCAGTAGATGAAGGTATTCAAAAAACTGTAAAAT

72481  AGATAATTGAATTTTTTTTTTTCAGCTTTTAAGTTCCAGGGTACATGTGCAGGTAGGTGT
72481  TCTATTAACTTAAAAAAAAAAAGTCGAAAATTCAAGGTCCCATGTACACGTCCATCCACA

72541  GTTATATAGGTAAATGTAAGCCATGGTGGTTTGCTGTACAAATCAACCCATCACCTAGGT
72541  CAATATATCCATTTACATTCGGTACCACCAAACGACATGTTTAGTTGGGTAGTGGATCCA

72601  ATTAAGCCCAGCATCCATTAGCTATTCTTCCTGATGCTCTTCCTCCTCCCGCCCCTTCCG
72601  TAATTCGGGTCGTAGGTAATCGATAAGAAGGACTACGAGAAGGAGGAGGGCGGGGAAGGC

72661  ACAGACCCTAGTATGTGCTGCTCCCTGCATGTGCCCATGTGTTCTCATTGTTCAGCTCCC
72661  TGTCTGGGATCATACACGACGAGGGACGTACACGGGTACACAAGAGTAACAAGTCGAGGG

72721  ACTTATAAGAGAACATGCAGTGTTTGGTTTTCTTTTAATATTATTTTTAACTTTATGATA
72721  TGAATATTCTCTTGTACGTCACAAACCAAAAGAAAATTATAATAAAAATTGAAATACTAT

72781  GGAAGGAGTACTTTTTAAAGTTGGTTGAAACATTGTTACTGATCTCAAAGCACTACCTTC
72781  CCTTCCTCATGAAAAATTTCAACCAACTTTGTAACAATGACTAGAGTTTCGTGATGGAAG

72841  CAGTTATTCTGAGATACTTTTTCAGTCTAAGATCTGATACTCCTATTCCTGGTTTGTTGA
72841  GTCAATAAGACTCTATGAAAAAGTCAGATTCTAGACTATGAGGATAAGGACCAAACAACT

72901  GAGTTTTTGTCATGAATGGATGTTGGATTTTGTCAATTGCTTTTTTTGAATCTCTTGACA
72901  CTCAAAAACAGTACTTACCTACAACCTAAAACAGTTAACGAAAAAAACTTAGAGAACTGT

72961  TGATTATGTGGTTTTGTACTTTATTACATTATTAATGAATGAATTATATCAATTTATTTT
72961  ACTAATACACCAAAACATGAAATAATGTAATAATTACTTACTTAATATAGTTAAATAAAA

73021  TGGATGTTAAATCAACCTTATTTTCCTAAGCTAAATCCTACTTGGTCATTGTGAATAATC
73021  ACCTACAATTTAGTTGGAATAAAAGGATTCGATTTAGGATGAACCAGTAACACTTATTAG

73081  CATTTTTTTATCTTGCTATATTCAGTTTGCTAATATTTTAAGAATTTTTGTTTCACTGTT
73081  GTAAAAAAATAGAACGATATAAGTCAAACGATTATAAAATTCTTAAAAACAAAGTGACAA

73141  CATGAAATATATTGATCTAGTTTTCATTTTTCTTTTCTTTCTTTTTTTTTTTTTTTTTTA
73141  GTACTTTATATAACTAGATCAAAAGTAAAAAGAAAAGAAAGAAAAAAAAAAAAAAAAAAT
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FIGURE 4 (cont'd)

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73201   CATCTCCCTCCTCTTCCTCTTGATCTAGTTTTCTAATACAGCTGCACTCCAACTTACGAT
73201   GTAGAGGGAGGAGAAGGAGAACTAGATCAAAAGATTATGTCGACGTGAGGTTGAATGCTA

73261   GGTCCTACTTAGGAGTTTTTGACTGTATGATGTTTGAAAACAATATGAGTTTAGTAGAAA
73261   CCAGGATGAATCCTCAAAAACTGACATACTACAAACTTTTGTTATACTCAAATCATCTTT

73321   CTTACTTTGAGTACACATACCATTCTGTTTTTTTGCTTTTAGTACAGTATTCAATAAATT
73321   GAATGAAACTCATGTGTATGGTAAGACAAAAAAACGAAAATCATGTCATAAGTTATTTAA

73381   ATGTGAGATAACCAATACTTTATTATAAAATAATACACTTTTAGATGATTCTGCCCTACC
73381   TACACTCTATTGGTTATGAAATAATATTTTATTATGTGAAAATCTACTAAGACGGGATGG

73441   ATAGGCTAATGTAATTGTTCTGAGCACATTTAAGATAGGATAAGCTAAGATACGATGGAT
73441   TATCCGATTACATTAACAAGACTCGTGTAAATTCTATCCTATTCGATTCTATGCTACCTA

73501   GTTTGGTAGGTTAGGTATATTAAATGCATTTTCACCTTAAGGATATTTTCAACTTAGGAT
73501   CAAACCATCCAATCCATATAATTTACGTAAAAGTGGAATTCCTATAAAAGTTGAATCCTA

73561   GAGTTTATTGAGTTGTAACCCCATCACAAGTTGAGGAACATCTATGTATCTAATTCCATG
73561   CTCAAATAACTCAACATTGGGGTAGTGTTCAACTCCTTGTAGATACATAGATTAAGGTAC

73621   ATTCAGTAAATTCTTTAGACTGCCAAAATCCTGTAATCTAGAGTTAGACAAGATCTTAAA
73621   TAAGTCATTTAAGAAATCTGACGGTTTTAGGACATTAGATCTCAATCTGTTCTAGAATTT

73681   TCAGGTTTTGTGGTCCATCTTGTAGTCATGATCATTCTCACTATTAGGGAATTCTTAACT
73681   AGTCCAAAACACCAGGTAGAACATCAGTACTAGTAAGAGTGATAATCCCTTAAGAATTGA

73741   TTTTGCATTTGAATCACCGAGGTGTTATTTAAAATACACATATGGAATCCAAGCTCCAGA
73741   AAAACGTAAACTTAGTGGCTCCACAATAAATTTTATGTGTATACCTTAGGTTCGAGGTCT

73801   GACTCTGAGTAGATCTGGTGAGTGATTGTGATGCCTGCCCACATTCAAGAACCTTAGTAC
73801   CTGAGACTCATCTAGACCACTCACTAACACTACGGACGGGTGTAAGTTCTTGGAATCATG

73861   AAAAGCCCTGCTGAATGGTTCTCTTTCACTATACACTCTATCAACTTATGTACTTGATCA
73861   TTTTCGGGACGACTTACCAAGAGAAAGTGATATGTGAGATAGTTGAATACATGAACTAGT

73921   CACTTTGGACCTCAAAATCAATAATTTTTAAAAATCTACTTCCTAAGTTGTGAGGTACGA
73921   GTGAAACCTGGAGTTTTAGTTATTAAAAATTTTTAGATGAAGGATTCAACACTCCATGCT

73981   ATTGAAGGAAATAATGAATACTATTTGGGGAGTCAACATTATTTATTAACGAATACCATT
73981   TAACTTCCTTTATTACTTATGATAAACCCCTCAGTTGTAATAAATAATTGCTTATGGTAA

74041   TGGGGAGCCGACATTATTTATATTTGGTTGGTATATTTGTATCAACTATCATTTTCTAAT
74041   ACCCCTCGGCTGTAATAAATATAAACCAACCAAATAAACATAGTTGATAGTAAAAGATTA

74101   TAATGGTATAGGCAGAATAAACCATCACTTGTGATTCAGAAAGGAACATGATACAAATAA
74101   ATTACCATATCCGTCTTATTTGGTAGTGAACACTAAGTCTTTCCTTGTACTATGTTTATT

74161   CATCCAATAATGTATATGGATTTAAATAGATCTGCCCCCTACAGATGTTACGCAATTCAT
74161   GTAGGTTATTACATATACCTAAATTTATCTAGACGGGGGATGTCTACAATGCGTTAAGTA

74221   GTTGGTAATGATCATTCATTAGGTTTTCGTGGTGGCTACATTTGATATGTGAAGTACTGG
74221   CAACCATTACTAGTAAGTAATCCAAAAGCACCACCGATGTAAACTATACACTTCATGACC

74281   CTGGAAGACTGGTGCCAGTAGCTTCAGGTTTGCTGGGATTCTTTCATCAGAGATGACTAG
74281   GACCTTCTGACCACGGTCATCGAAGTCCAAACGACCCTAAGAAAGTAGTCTCTACTGATC

74341   CTTTACTTATCTTTTTATGTTGCATGTTTCTATGATGGGCCTATCCTGTCATTGTCTTCA
74341   GAAATGAATAGAAAAATACAACGTACAAAGATACTACCCGGATAGGACAGTAACAGAAGT

74401   TAGTATAATTGCAAGCTCAACTCTGTCAGTTATGTGATTTTTTTTTTTTTTTGGTCCTG
74401   ATCATATTAACGTTCGAGTTGAGACAGTCAATACACTAAAAAAAAAAAAAAACCAGGAC

74461   TCTTGCTTTTGGCTGACTTCTATATGTTTTTATTTCATGTCCTTTTCATAGTTAGATTAA
74461   AGAACGAAAACCGACTGAAGATATACAAAAATAAAGTACAGGAAAAGTATCAATCTAATT

74521   CTGGGTCTTATGTCCAACAGATATTTTCATTTCTTTGAATGAATAAATCTATGTTAGGCT
74521   GACCCAGAATACAGGTTCTCTATAAAACTAAAGAAACTTACTTATTTAGATACAATCCGA
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FIGURE 4 (cont'd)

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74581  ACTGTATTACGTTTTATACACACCTAGTTGATCACTTGTGTCCAGTCTCTATTCCCTGGT
74581  TGACATAATCCAAAATATCTGTGGATCAACTAGTGAACACAGGTCAGAGATAAGGGACCA

74641  ATGGTAGTTGCTGTGTTTATAGAACATTGAGGATTCTACAATGGACACATTGGTGTTGGG
74641  TACCATCAACGACACAAATATCTTGTAACTCCTAAGATGTTACCTGTGTAACCACAACCC

74701  CCCCAGCCCAGACCCAAATCGAAATTTCTAGAGCCAGGATCAGAGACTCTGCATTCAACA
74701  GGGGTCGGGTCTGGGTTTAGCTTTAAAGATCTCGGTCCTAGTCTCTGAGACGTAAGTTGT

74761  AACTCTCCAGAGATTTCATAACCACTTTTAAAGGACTCACCATCCCAAACCTTGTTAAGG
74761  TTGAGAGGTCTCTAAAGTATTGGTGAAAATTTCCTGAGTGGTAGGGTTTGGAACAATTCC

74821  AATGAAATATATGTCTGCCAGTAATTTCAGTGCTTTAAGTCATTGAAAGCTGAACTTTTA
74821  TTACTTTATATACAGACGGTCATTAAAGTCACGAAATTCAGTAACTTTCGACTTGAAAAT

74881  ATGGCACCAAAGTGGAAATATTTATATAATTGAAAGCTAAACTTCATCCTAATGGCAGTG
74881  TACCGTGGTTTCACCTTTATAAATATATTAACTTTCGATTTGAAGTAGGATTACCGTCAC

74941  TTGAGTTCACTTCCATAGGCCCTGATATAACAGTCTAATATTATTGTTTTTCACATAAAA
74941  AACTCAAGTGAAGGTATCCGGGACTATATTGTCAGATTATAATAACAAAAAGTGTATTTT

75001  TAAGATTCAGTCACTGCCATATAATTAGGGAGTGGCTCTGCTATTGGATGGACTTAAAAT
75001  ATTCTAAGTCAGTGACGGTATATTAATCCCTCACCGAGACGATAACCTACCTGAATTTTA

75061  ATTTCATTATGTTTGCCAAGCTCTGTCTCTTTACATGTTTTATAATTAACTGATCCTTCA
75061  TAAAGTAATACAAACGGTTCGAGACAGAGAAATGTACAAAATATTAATTGACTAGGAAGT

75121  TTTTTATTTTGTTTTATTTTATTTTTGAGATAGAGTCTCGCTTGGTTGCCCAGGCTGGAG
75121  AAAAATAAAACAAAATAAAATAAAAACTCTATCTCAGAGCGAACCAACGGGTCCGACCTC

75181  TGCAATGGTGCAATCTTGGCTCATTGCAACCTCTGCTTCCCAGGTTCAAGTGATTCTCCT
75181  ACGTTACCACGTTAGAACCGAGTAACGTTGGAGACGAAGGGTCCAAGTTCACTAAGAGGA

75241  GCCTCAGCCTCCTGATTAGCGGGGACTACAGGTGCGTGCCACCATGCCCAGCTAATTTTT
75241  CGGAGTCGGAGGACTAATCGCCCCTGATGTCCACGCACGGTGGTACGGGTCGATTAAAAA

75301  GTACTTTTAGTAGAGACGGGGTTTCACCATGTTGGCCAGGCTGGTCCCAAACTCCTGACC
75301  CATGAAAATCATCTCTGCCCCAAAGTGGTACAACCGGTCCGACCAGGGTTTGAGGACTGG

75361  TCAGGTGTTCTGCCCACCTCGGCCTCCCAAAGTGCTGGATTACAGGCATGAGCCACCATG
75361  AGTCCACAAGACGGGTGGAGCCGGAGGGTTTCACGACCTAATGTCCGTACTCGGTGGTAC

75421  CCCGGCCTCCTTCATTTTTAATAATCTTCATAGATACATACTTGTTGTACTAATGTTTTT
75421  GGGCCGGAGGAAGTAAAAATTATTAGAAGTATCTATGTATGAACAACATGATTACAAAAA

75481  GTGCAGTTCCTCATGATAAATAATTAAATCAATTACTAAAATCCTTATAGATTTATGATG
75481  CACGTCAAGCAGTACTATTTATTAATTTAGTTAATGATTTTAGGAATATCTAAATACTAC

75541  ATAATAAATGGAAGTGTGTATTATTGAAACATGTTTAATTAACTGTTCATATATAACCAG
75541  TATTATTTACCTTCACACATAATAACTTTGTACAAATTAATTGACAAGTATATATTGGTC

75601  TGAGTAGGGATTGGCAATTAAAAATACCAGGCTACCAGTGCATGGAAATTTGAAGAAAAC
75601  ACTCATCCCTAACCGTTAATTTTTATGGTCCGATGGTCACGTACCTTTAAACTTCTTTTG

75661  AACAACCTGAAATTCAGAATACTCCAAAATCTGAAACTTTTTGAGCACTGACATGACTAA
75661  TTGTTGGACTTTAAGTCTTATGAGGTTTTAGACTTTGAAAAACTCGTGACTGTACTGATT

75721  AAATGCTCATTGGAGCATTTCAGATTTCATTTTTTCAGATTAGGGATGCTGAATTGGTAA
75721  TTTACGAGTAACCTCGTAAAGTCTAAAGTAAAAAAGTCTAATCCCTACGACTTAACCATT

75781  GCATAATGCAGATTAATCCAAAATCTGAAAAAAATCCTAAATCAAAAACAGTTTTGGTCA
75781  CGTATTACGTCTAATTAGGTTTTAGACTTTTTTTAGGATTTAGTTTTTGTCAAAACCAGT

75841  GAAGCTTTGTGGATAAGGGATAGTCCAAGCTTTTTGGACTGAAGCTTTTTGGATAAGGTA
75841  CTTCGAAACACCTATTCCCTATCAGGTTCGAAAAACCTGACTTCGAAAAACCTATTCCAT
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FIGURE 4 (cont'd)

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75901  TAGCCTATAATACATAAATACATAATACAGGATAATCACTGACCTGAATGTATAGGATCA
75901  ATCGGATATTATGTATTTATGTATTATGTCCTATTAGTGACTGGACTTACATATCCTAGT

75961  GTATGGTACACAAATATTTAAATCCATGTACTTTGTTGGATATTATGTTATATAAACTTC
75961  CATACCATGTGTTTATAAATTTAGGTACATGAAACAACCTATAATACAATATATTTGAAG

76021  TTGTAAAAAGTTTAGAGAGTAAAATCATTCACATTACCAAAAGATTTCTCATATTTATAA
76021  AACATTTTTCAAATCTCTCATTTTAGTAAGTGTAATGGTTTTCTAAAGAGTATAAATATT

76081  AAAGGATTATAGCAGCATTTTAATCAGTATCTCCTAAAGTATTTATTTATGGGTTGTTAA
76081  TTTCCTAATATCGTCGTAAAATTAGTCATAGAGGATTTCATAAATAAATACCCAACAATT

76141  ATCTAAAAGAGAAACTACAGTCTGGAGGGCTCTAAACTACTGCTGATTACATATCAGTTG
76141  TAGATTTTCTCTTTGATGTCAGACCTCCCGAGATTTGATGACGACTAATGTATAGTCAAC

76201  GGAATTAAGAGAAAATCTCAGATCATAATATTTAAATAAAAACATTTACATGAATGATTT
76201  CCTTAATTCTCTTTTAGAGTCTAGTATTATAAATTTATTTTTGTAAATGTACTTACTAAA

76261  CTAAGTTTTCACTTTACTAGACAAGAAACTAAAATTATATGACTGTCATGTTCAATATTG
76261  GATTCAAAAGTGAAATGATCTGTTCTTTGATTTTAATATACTGACAGTACAAGTTATAAC

76321  GATACTTAACAACACTACATCCAAGGAAGCCAGGTTTTGCTGATTTTAACCTCGTCCTGT
76321  CTATGAATTGTTGTGATGTAGGTTCCTTCGGTCCAAAACGACTAAAATTGGAGCAGGACA

76381  TGAGTAACTCCATGCAGGTACAGTGGTACAAACACATGTGGACACACAGACCCAGACCTT
76381  ACTCATTGAGGTACGTCCATGTCACCATGTTTGTGTACACCTGTGTGTCTGGGTCTGGAA

76441  TATTTCCTCGGGGATTCTGGTAAGTGTAGAGGTGTCTTGACCATAGTCAATAGCAGAAAT
76441  ATAAAGGAGCCCCTAAGACCATTCACATCTCCACAGAACTGGTATCAGTTATCGTCTTTA

76501  ATGCACAACCACAAGCTCTGAAATTCCATTTGATTGTTGCTCTTAGCCTTCCACTTTTTA
76501  TACGTGTTGGTGTTCGAGACTTTAAGGTAAACTAACAACGAGAATCGGAAGGTGAAAAAT

76561  GGCATATGTCAGTCCCATTTCATCCCACCCACTCTCTCCATTTGGGAGGTGGTAGAGTGA
76561  CCGTATACAGTCAGGGTAAAGTAGGGTGGGTGAGAGAGGTAAACCCTCCACCATCTCACT

76621  GACAATACTGAACTATACCAGGGCTGAGAATAAGTGTCTTTGAAAAGGGTCGAATCTGTG
76621  CTGTTATGACTTGATATGGTCCCGACTCTTATTCACAGAAACTTTTCCCAGCTTAGACAC

76681  ATGCTAGAGACAGCCCTGGAAACTGTCAGGAGTTAGCCCAACCAGGACTGTGACCAGATC
76681  TACGATCTCTGTCGGGACCTTTGACAGTCCTCAATCGGGTTGGTCCTGACACTGGTCTAG

76741  CCAGGCTGTCCACCACAGATTTGCAGGCTACCTGCAGATGTGACTTTTTCAAATGTACTC
76741  GGTCCGACAGGTGGTGTCTAAACGTCCGATGGACGTCTACACTGAAAAAGTTTACATGAG

76801  AAAGACAAGCTGACTTTGGCTAATGCAGAAATTAATTAATTCCTCTTTTTCAGTAAACTT
76801  TTTCTGTTCGACTGAAACCGATTACGTCTTTAATTAATTAAGGAGAAAAAGTCATTTGAA

76861  TATCCTCCTACACTTAGATTGTCTGTAAGTACATCTCTGGAGTTGAGCTCAACTAGAAAG
76861  ATAGGAGGATGTGAATCTAACAGACATTCATGTAGAGACCTCAACTCGAGTTGATCTTTC

76921  AAGCTGTCTGCATTTAGTTAATACCAGCATTGGATGCACACAATATAATTTGAATAATGT
76921  TTCGACAGACGTAAATCAATTATGGTCGTAACCTACGTGTGTTATATTAAACTTATTACA

76981  AGAGCAACATTTTAATGATCTCTCATAAGCAGTTTCCCCATTTGCAACTTCCTGGGAAAT
76981  TCTCGTTGTAAAATTACTAGAGAGTATTCGTCAAAGGGGTAAACGTTGAAGGACCCTTTA

77041  CTTACATTATGAAATGTTCATTAGAACTCCCATTTTAAAACCCTGCTGCCATTTTGTGAG
77041  GAATGTAATACTTTACAAGTAATCTTGAGGGTAAAATTTTGGGACGACGGTAAAACACTC

77101  TGGGCAGAAGAAAGGCTGGAGATGAGATTTGTCTGTCTCAAATGATTCACTCCTTCATTT
77101  ACCCGTCTTCTTTCCGACCTCTACTCTAAACAGACAGAGTTTACTAAGTGAGGAAGTAAA

77161  CTGGTTCACTCCACAGGGAGCTTAAGGACATGTGCGTTTCATAGACATGCCTTTCTTTTC
77161  GACCAAGTGAGGTGTCCCTCGAATTCCTGTACACGCAAAGTATCTGTACGGAAAGAAAAG

77221  CTTTTATCACCTTGTTAAATCTTAAGATTGAACATACAATTCAGCCTGTAATCATATCAA
77221  GAAAATAGTGGAACAATTTAGAATTCTAACTTGTATGTTAAGTCGGACATTAGTATAGTT
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FIGURE 4 (cont'd)

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77281  TTCCCATGAAAAATATTTTCCTTATTCACTCCCTCTATTTGTGCTTATACATCTGATCAT
77281  AAGGGTACTTTTTATAAAAGGAATAAGTGACGGAGATAAACACGAATATGTAGACTAGTA

77341  CTTTTTCCTTTACTTTACAATTAGTTTCTATGAACAGAAGAATCTGAAAGATTTAAAGAC
77341  GAAAAAGGAAATGAAATGTTAATCAAAGATACTTGTCTTCTTAGACTTTCTAAATTTCTG

77401  TACTTAGCACAGCAGCAATTTATAAATCATTAATTTGGGTACTGTCTATACATTTAATGT
77401  ATCAATCGTGTCGTCGTTAAATATTTAGTAATTAAACCCATGACAGATATGTAAATTACA

77461  GTTCTTTTTCATAGTCCTATGTGAAATACATATACATATATATATATTCCACTGTTTATA
77461  CAAGAAAAAGTATCAGGATACACTTTATGTATATGTATATATATATAAGGTGACAAATAT

77521  AACAATATTCAGTTTTATTTGCATAACTCAATATATTTTATATTAACAGCTCCGTTTTTA
77521  TTGTTATAAGTCAAAATAAACGTATTGAGTTATATAAAATATAATTGTCGAGGCAAAAAT

77581  GTGTCTTAAGACATCGAGTCTGTTTTTAGAGATACAGTCTATTTGCCTTGATTTTAGCCT
77581  CACAGAATTCTGTAGCTCAGACAAAAATCTCTATGTCAGATAAACGGAACTAAAATCGGA

77641  GTTATAATCAGCTTATTATTATCTGGCCACTCTTACCAGTGAGTATCATCTTGAGGCTGT
77641  CAATATTAGTCGAATAATAATAGACCGGTGAGAATGGTCACTCATAGTAGAACTCCGACA

77701  TCTTGCTCATTTCAACTTGTCACAGGGGATGTTTTTTACTCTTTGGAGTTTAGGTACACC
77701  AGAACGAGTAAAGTTGAACAGTGTCCCCTACAAAAAATGAGAAACCTCAAATCCATGTGG

77761  AGCTTATTAATTATGCTCCTGATTCATGGTACTTCCATCATGGGGCATATAAGGTCCCTG
77761  TCCAATAATTAATACGAGGACTAAGTACCATGAAGGTAGTACCCCGTATATTCCAGGGAC

77821  TCTTTGTTTTATTCCCTTCTATCTTCATTCACCACTCTCATTTCCTCTCTCTCCACTAGA
77821  AGAAACAAAATAAGGGAAGATAGAAGTAAGTGGTGAGAGTAAAGGAGAGAGAGGTGATCT

77881  AATAATTCTCAGGAATCAAATTAATATTATTCTGGCTTATATGTGTTTTTAAAAATCTCA
77881  TTATTAAGAGTCCTTAGTTTAATTATAATAAGACCGAATATACACAAAAATTTTTAGAGT

77941  TCGCTTTTTTATACATGTAATTTTAATTTATGTAAGAGACTTTGTCCTACAGATTTCATTG
77941  AGCGAAAAAATATGTACATTAAAATTAAATACATTCTCTGAAACAGGATGTCTAAAGTAAC

78001  TGTTTCTTCTCTTTTTCGCCCAGCACTGTGTGTTCCATTTCTATCCAGTCTACTATGTGT
78001  ACAAAGAAGAGAAAAAGCGGGTCGTGACACACAAGGTAAAGATAGGTCAGATGATACACA

78061  ACATCAAGTCCATCATTTCTAACTGTTGCATAGTTCATGATGCGAGGCATCTTCCACATT
78061  TGTAGTTCAGGTAGTAAAGATTGACAACGTATCAAGTACTACGCTCCGTAGAAGGTGTAA

78121  GTATCCCAATTCCCTAACTGGAATCCCAGTTCCCTGCTACCTCACACAATGCTCCAGTGA
78121  CATAGGGTTAAGGGATTGACCTTAGGGTCAAGGGACGATGGAGTGTGTTACGAGGTCACT

78181  ACAGCTGGAAAATCATACAACCCAAGGAATTATTGAAAGTGATTATATCCCAGCAAAAGG
78181  TGTCGACCTTTTAGTATGTTGGGTTCCTTAATAACTTTCACTAATATAGGGTCGTTTTCC

78241  CCCAGGCCCATCTTACACTTCCACCCCAAGAAGGTACTGCTACTTTTCGGGAATGGCCTG
78241  GGGTCCGGGTAGAATGTGAAGGTGGGGTTCTTCCATGACGATGAAAAGCCCTTACCGGAC

78301  GTCTCCTTGGCGAAATTGGCATTTGATCTGTTCTCATCACTGTCGTCTGGCATCAGAAGT
78301  CAGAGGAACCGCTTTAACCGTAAACTAGACAAGAGTAGTGACAGCAGACCGTAGTCTTCA

78361  GACCCCACTTGTCAGGCACTGTACTCAGTGCTTTCCATGCACTAACTCTGATAACAATCT
78361  CTGGGGTGAACAGTCCGTGACATGAGTCACGAAAGGTACGTGATTGAGACTATTGTTAGA

78421  TTTTTTTTTCTTTTTTTGAGACAGAGTCTTGCTCTGTTGCCCAGGCTGGAGTGCAGTTGT
78421  AAAAAAAAAGAAAAAAACTCTGTCTCAGAACGAGACAACGGGTCCGACCTCACGTCAACA

78481  GTGATCTCAGCTCACTGCAACCTCCACCTCCCAAATTCAAGCGATTCTCCTGCCTCAGCC
78481  CACTAGAGTCGAGTGACGTTGGAGGTGGAGGGTTTAAGTTCGCTAAGAGGACGGAGTCGG

78541  TCCCCAGTAGCTGGGACTACAGGCGTGCACCACTACACCTGGCTAATTTTTGTATTTTTA
78541  AGGGGTCATCGACCCTGATGTCCGCACGTGGTGATGTGGACCGATTAAAAACATAAAAAT
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FIGURE 4 (cont'd)

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78601  GTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTTGAAATCCTGACCTCAGGTGAT
78601  CATCTCTACCCCAAAGTGGTACAACCGGTCCGACCAGAACTTTAGGACTGGAGTCCACTA

78661  CCACTTGACCTCCCAAAGTGCTGGAATTGCAGGCAAGAGCCACTGAGCTTGGCCTGATAA
78661  GGTGAACTGGAGGGTTTCACGACCTTAACGTCCGTTCTCGGTGACTCGAACCGGACTATT

78721  CAATCTTGTGAGCAGGTGCTTATGCAGTATTTTAGGGATGTGAAAGTAAGGTCCAAAGCG
78721  GTTAGAACACTCGTCCACGAATACGTCATAAAATCCCTACACTTTCATTCCAGGTTTCGC

78781  GTGAAATAAGAGCCTGTATTCTCTTAACCTCCATCCCGCAACATCTTTTATGTGTCAGTC
78781  CACTTTATTCTCGGACATAAGAGAATTGGAGGTAGGGCGTTGTAGAAAATACACAGTCAG

78841  CCTGCACTAAGTCTAGGGATACTGTGCTGAGCAAAAACTATCTTCTTGCTTTCACAGAGC
78841  GGACGTGATTCAGATCCCTATGACACGACTCGTTTTTGATAGAAGAACGAAAGTGTCTCG

78901  TCAGTGTCTGGCAGGGGGTCAGACTTTCATAATATAAACCCACTAAATGAGTGCATATTG
78901  AGTCACAGACCGTCCCCCAGTCTGAAAGTATTATATTTGGGTGATTTACTCACGTATAAC

78961  ATGGCGGTCACTGCTGTGAAGAAGTGGGAATGGTTAGCATGGAAACATAGCCCCAATGGG
78961  TACCGCCAGTGACGACACTTCTTCACCCTTACCAATCGTACCTTTGTATCGGGGTTACCC

79021  GGCGACTAAGTTCTTTCCCATCTCATTCTACTATGTCTACTTTCATCTCTACTTTTTTCT
79021  CCGCTGATTCAAGAAAGGGTAGAGTAAGATGATACAGATGAAAGTAGAGATGAAAAAAGA

79081  TTTCTGAGCTATCAGCTTTCTTGCTCTCAACTATATTTGATGTATTTAACCAGATTTTAT
79081  AAAGACTCGATAGTCGAAAGAACGAGAGTTGATATAAACTACATAAATTGGTCTAAAATA

79141  ATATTGTATTATGTATTTTATAACATGTATATATATCATATAACATACACATATACATAC
79141  TATAACATAATACATAAAATATTGTACATATATATAGTATATTGTATGTGTATATGTATG

79201  ATACACACAGCCAATTAAGTCTCAAGTTCAATTACAATGCTTCTAAGTTTAGGACTATTC
79201  TATGTGTGTCGGTTAATTCAGAGTTCAAGTTAATGTTACGAAGATTCAAATCCTGATAAG

79261  ATTTTCATTTTGGCAGAGAAATTATCTGGTAAAAAATTCAAGTAGAACCAAAGGTATACA
79261  TAAAAGTAAAACCGTCTCTTTAATAGACCATTTTTTAAGTTCATCTTGGTTTCCATATGT

79321  ATAGATGGGAAGTTTCCTTTTCACTCTCACACTCTCATTTCCATCCAGGGTTCTACAATT
79321  TATCTACCCTTCAAAGGAAAAGTGAGAGTGTGAGAGTAAAGGTAGGTCCCAAGATGTTAA

79381  CATCTCCTTCCAAGCAATTCCTATTGCCAGCTTTTCTTATACCCTTTCAGAAATACACAC
79381  GTAGAGGAAGGTTCGTTAAGGATAACGGTCGAAAAGAATATGGGAAAGTCTTTATGTGTG

79441  ACACACACACACACATATATACACACACACACACACACCTTACATGTGTTTGTACATTA
79441  TGTGTGTGTGTGTGTATATATGTGTGTGTGTGTGTGTGGGAATGTACACAAACATGTAAT

79501  TCTCTCTTTTTACAAAATTGGCAGTGATTCTTTGTCCTGTTTCTGCCACTACTCAAAAAT
79501  AGAGAGAAAAATGTTTTAACCGTCACTAAGAAACAGGACAAAGACGGTGATGAGTTTTTA

79561  TTTAAAACAAATTACACACCTATAAACATACAATTTAAAGAAAAGAGTGAAAGTGAAAAT
79561  AAATTTTGTTTAATGTGTGGATATTTGTATGTTAAATTTCTTTTCTCACTTTCACTTTTA

79621  CTAAGGACCCAGCACATGGTTAAGATGAGAGCATGATGGGTTCAATGGAAAGCCTTTGTG
79621  GATTCCTGGGTCGTGTACCAATTCTACTCTCGTACTACCCAAGTTACCTTTCGGAAACAC

79681  TACCTTTCTCCTTTGCCTCCGTTCCCTCTCCAATAGAGTCAACCACGTTGGAGGTTATAG
79681  ATGGAAAGAGGAAACGGAGGCAAGGGAGAGGTTATCTCAGTTGGTGCAACCTCCAATATC

79741  CACTTCCTTCTTTATGTCCCCCCATCTCCCATCTGGTATGGTATTCTCTTTTACTGCAGA
79741  GTGAAGGAAGAAATACAGGGGGGTAGAGGGTAGACCATACCATAAGAGAAAATGACGTCT

79801  TGGACATTTTGGCAGACATATGTAGTTGCTTCTCTTTGGTATTTACCTAGGAGTTGAAGT
79801  ACCTGTAAAACCGTCTGTATACATCAACGAAGAGAAACCATAAATGGATCCTCAACTTCA

79861  GCTGGGTCACAGGGTGTATGTATATTTCACTTTAGTAGATACTGCTGTTGTAGGACTTTC
79861  CGACCCAGTGTCCCACATACATATAAAGTGAAATCATCTATGACGACAACATCCTGAAAG

79921  TCCTTAGTTTAGCTAAAGATGGGGTCCTTGTCCCAAGGCCATGAAAAATTAGGCTCGCAG
79921  AGGAATCAAATCGATTTCTACCCCAGGAACAGGGTTCCGGTACTTTTTAATCCGAGCGTC
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FIGURE 4 (cont'd)

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79981  ACAATTTGAAAGGTGAGAATAATGGAACTTATTGGGAAAAAAGGGAAACAGGGACTCCCC
79981  TGTTAAACTTTCCACTCTTATTACCTTGAATAACCCTTTTTTCCCTTTGTCCCTGAGGGG

80041  ACAAAGCCAGGGTCCTGCTAGCATGCTTCCTGCCTTGCAGATTGAATCCCAGGTACCACC
80041  TGTTTCGGTCCCAGGACGATCGTACGAAGGACGGAACGTCTAACTTAGGGTCCATGGTGG

80101  CAGGAAGAGGAGGGGCCAGGCTCCTCCCCACTGTGAATGGTGTGACCGTCTGTGGCTCCC
80101  GTCCTTCTCCTCCCCGGTCCGAGGAGGGGTGACACTTACCACACTGGCAGACACCGAGGG

80161  CAGTGTGCACTCCTCCCAGTGTGCAGGCCGGTTGGAGTTTCTCTGGGGTCTTCTTCCCAC
80161  GTCACACGTGAGGAGGGTCACACGTCCGGCCAACCTCAAAGAGACCCCAGAAGAAGGGTG

80221  TTGGCTGTCTCACTGCCAAACTCCCAAAGTGCTTATACCAGTTTACTCTCCCATCAGTGG
80221  AACCGACAGAGTGACGGTTTGAGGGTTTCACGAATATGGTCAAATGAGAGGGTAGTCACC

80281  TGTATGTATTTGCTTCATTTCTTTGCCAATACTGATACTGTCTTATTAACTTTCCTCATT
80281  ACATACATAAACGAAGTAAAGAAACGGTTATGACTATGACAGAATAATTGAAAGGAGTAA

80341  CTAATGTATACAGTCTTGTGTTATTTGTGGTTTAATTTCCCTGAGAACCAATTATGTTGA
80341  GATTACATATGTCAGAACACAATAAACACCAAATTAAAGGGACTCTTGGTTAATACAACT

80401  GTACCTTTTCATAGGTTTACCAGCTACAGAAGTCCTCTTGTGAAGTGCCTTTGCAAGTCT
80401  CATGGAAAAGTATCCAAATGGTCGATGTCTTCAGGAGAACACTTCACGGAAACGTTCAGA

80461  TTTGTCTTTTTAATTTTTTGCATCTTTGTATATTCTAGGTATAAATCCTTTGATACATAT
80461  AAACAGAAAAATTAAAAAACGTAGAAACATATAAGATCCATATTTAGGAAACTATGTATA

80521  ATCACAAATAACTTCCTAGTCTATGGCAAATCCTATGTTGGATAAACGTACTGCAAATAG
80521  TAGTGTTTATTGAAGGATCAGATACCGTTTAGGATACAACCTATTTGCATGACGTTTATC

80581  TTTCGCAGTCTGTGGCTAGCTTCTGTGTCTGTGTCTTGCTTTGTCACTTTCTTAGTGATA
80581  AAAGCGTCAGACACCGATCGAAGACACAGACACAGAACGAAACAGTGAAAGAATCACTAT

80641  TCTTTTGATGAACAGAAGTACTTAGTTTTAAAGTAGTTAAAGTTTTCTTTATGTTTTATA
80641  AGAAAACTACTTGTCTTCATGAATCAAAATTTCATCAATTTCAAAAGAAATACAAAATAT

80701  CTTTTTATGCATTTTAAAGAAATTTTTTGTTACTCCAAGGTCATACAGGTTAAATAAATT
80701  GAAAAATACGTAAAATTTCTTTAAAAAACAATGAGGTTCCAGTATGTCCAATTTATTTAA

80761  CTTACTCCAAGAACATTCTTTTAAAGTTTTGCTTTTTTTCATTTAAATGAAATCCATATG
80761  GAATGAGGTTCTTGTAAGAAAATTTCAAAACGAAAAAAAGTAAATTTACTTTAGGTATAC

80821  AAAGTGAACTTTGTTATCAAGTAACATATACAATTTCTTTTATTTTTCTGCACGGAGACC
80821  TTTCACTTGAAACAATAGTTCATTGTATATGTTAAAGAAAATAAAAAGACGTGCCTCTGG

80881  AAGTTGTCCCATCACCATTTATTGAGTGGTCTATCCTTTCCTCACTGATTACAGTGCCAG
80881  TTCAACAGGGTAGTGGTAAATAACTCACCAGATAGGAAAGGAGTGACTAATGTCACGGTC

80941  TTTTGATATGTCATGTTTCCATAGATGAAGAATATTTTGGGGCTCTCTATCTGTACCTTC
80941  AAAACTATACAGTACAAAGGTATCTACTTCTTATAAAACCCCGAGAGATAGACATGGAAG

81001  CTTTTTAAAAAATATAAATAGTGGTGATACTATGAACAATTTTGTTTGTATTATTGTTTT
81001  GAAAAATTTTTTATATTTATCACCACTATGATACTTGTTAAAACAAACATAATAACAAAA

81061  TTGCACTTAAAATTTGTCTTGGAGATCTTTTCATTTTGGCACATACGGATACACCCCTAT
81061  AACGTGAATTTTAAACAGAACCTCTAGAAAAGTAAAACCGTGTATGCCTATGTGGGGATA

81121  TTTTTTTTCCATTTTCCTAGATGTGGGGTATCCATTGGACATATGTACCGTACTGAATTT
81121  AAAAAAAAGGTAAAAGGATCTACACCCCATAGGTAACCTGTATACATGGCATGACTTAAA

81181  AATATAGAATGTCATAAATTACAAGATGTAACATTATTTTATACACTGAGATGGAGAATC
81181  TTATATCTTACAGTATTTAATGTTCTACATTGTAATAAAATATGTGACTCTACCTCTTAG

81241  AAACTGCAACGCAGTACTTCCCTGATCATCCTGAGTGATTCATGAGTTAGTTATACTAGC
81241  TTTGACGTTGCGTCATGAAGGGACTAGTAGGACTCACTAAGTACTCAATCAATATGATCG
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FIGURE 4 (cont'd)

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81301  CTCTTATTTCTTTGAGGTGTACGTTTTCTGAGGGAATCTGCCATTTCTCCTGCCATGAGT
81301  GAGAATAAAGAAACTCCACATGCAAAAGACTCCCTTAGACGGTAAAGAGGACGGTACTCA

81361  TGCATTGCTTGGCTCGTGATAGGCATTTTTATTTTTGCATGTAATTTTGTAACAAATGCT
81361  ACGTAACGAACCGAGCACTATCCGTAAAAATAAAAACGTACATTAAAACATTGTTTACGA

81421  AACACTGCTTTATCTTCTTTTTGTTTTTGTTTATTGAGACGGAGTCTTGCTCTGTTTCCC
81421  TTGTGACGAAATAGAAGAAAAACAAAAACAAATAACTCTGCCTCAGAACGAGACAAAGGG

81481  AGGCTGGAGTGCAGTGGTGCAATCTCGGCTCACTGCAACCTCTGTCTCCCAGGTTCAAGC
81481  TCCGACCTCACGTCACCACGTTAGAGCCGAGTGACGTTGGAGACAGAGGGTCCAAGTTCG

81541  GATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCATGTGCCACCATGCTCGG
81541  CTAAGAGGACGGAGTCGGAGGACTCATCGACCCTAATGTCCGTACACGGTGGTACGAGCC

81601  CTACTTTTTGTATTTTTTGTAGAGATGGGGTTTCACCATGTTGGTCAGGCTTGTCTTGAA
81601  GATGAAAAACATAAAAAACATCTCTACCCCAAAGTGGTACAACCAGTCCGAACAGAACTT

81661  CTCCTGACCTCAGGTGATCTGCCCCACTCAGCCTCCCAAAGTGCTGGGATTACAGGTGTG
81661  GAGGACTGGAGTCCACTAGACGGGGTGAGTCGGAGGGTTTCACGACCCTAATGTCCACAC

81721  AGCCACCAGCCAGCTTTATCTTTTTAAAGGTTTCTTCCTATTGTGGGTTTCATTAGAGGG
81721  TCGGTGGTCGGTCGAAATAGAAAAATTTCCAAAGAAGGATAACACCCAAAGTAATCTCCC

81781  CTTGGTTGTTGCTTTGCAAGAAAACATTGACTTGCTTTTGTTTAATAGTCTTATAAATAT
81781  GAACCAACAACGAAACGTTCTTTTGTAACTGAACGAAAACAAATTATCAGAATATTTATA

81841  TTGTTTCACTAACATCAAATACATGCCATGCTCCTGCTTTTGAGCTTTTCTGTGCAGTAA
81841  AACAAAGTGATTGTAGTTTATGTACGGTACGAGGACGAAAACTCGAAAAGACACGTCATT

81901  CTTTTCTTCTCAGTGCTAAATCATAAGTTTTTAAAGACATTTAACATGGCACACTCAACA
81901  GAAAAGAAGAGTCACGATTTAGTATTCAAAAATTTCTGTAAATTGTACCGTGTGAGTTGT

81961  TGTGTCACCAATGCCCATAGCCACTGGAAGTATCATCAGTGTCAACAGCTATGACGTTTG
81961  ACACAGTGGTTACGGGTATCGGTGACCTTCATAGTAGTCACAGTTGTCGATACTGCAAAC

82021  GCAATGACAGCTTTGCCATAACTGCTGCTTAGCCAATAACAATTGTGGAATGCTGAGTCC
82021  CGTTACTGTCGAAACGGTATTGACGACGAATCGGTTATTGTTAACACCTTACGACTCAGG

82081  AGATCTCAAACATGTTAAAGGTAAAAAAAAAAAAAAAAAAAAGATATTTTCGAGTCTGTA
82081  TCTAGAGTTTGTACAATTTCCATTTTTTTTTTTTTTTTTTTTCTATAAAAGCTCAGACAT

82141  AAACATGGTAGCGTATCCGGAATTGGTGGGTTCTTGGTCTCACTGACTTCAAGAATGAAG
82141  TTTGTACCATCGCATAGGCCTTAACCACCCAAGAACCAGAGTGACTGAAGTTCTTACTTC

82201  CCATGGACCCTCGCGGTAAGTGTTACAGTTCTTAAAGGTGTCGTGTCTGGAGTTTGTTCC
82201  GGTACCTGGGAGCGCCATTCACAATGTCAAGAATTTCCACAGCACAGACCTCAAACAAGG

82261  TTCTGATGTTCAGATGTGTTCGGAGTTTCTTCCTTCTGGTAGGTTCGTGGTCTCGTTGGC
82261  AAGACTACAAGTCTACACAAGCCTCAAAGAAGGAAGACCATCCAAGCACCAGAGCAACCG

82321  TCAGGAGTGAAGCTGCGGACCTTTGCGGTGAGTGTTGCAGCTCTTAAGGCGGCATGTCTG
82321  AGTCCTCACTTCGACGCCTGGAAACGCCACTCACAACGTCGAGAATTCCGCCGTACAGAC

82381  GAGTTGTTCGTTCCTTGCGGTGGGTTCGTGGTCTCGCTGGCTTCAGGAGTGAAGCTGCAG
82381  CTCAACAAGCAAGGAACGCCACCCAAGCACCAGAGCGACCGAAGTCCTCACTTCGACGTC

82441  ACCTTCCCAGTGAGTGTTACAGCTCATAAAGGCAGTGTGGACCCAAACAGTGAGCACCAG
82441  TGGAAGGGTCACTCACAATGTCGAGTATTTCCGTCACACCTGGGTTTGTCACTCGTGGTC

82501  CAAGATTTACTGCAAAGAGCGAGAGAACAAAGCTTCCACAGTATGGAAGGGGACCCCAGC
82501  GTTCTAAATGACGTTTCTCGCTCTCTTGTTTCGAAGGTGTCATACCTTCCCCTGGGGTCG

82561  AGGTTGCCACTGCTGGCTCAGGCAGCCTGCTTTTATTCTCTTATCTGGCCCCACCCACAT
82561  TCCAACGGTGACGACCGAGTCCGTCGGACGAAAATAAGAGAATAGACCGGGGTGGGTGTA

82621  CCTGCTGATTGGTCCATTTTACAGAGAGCTGATTGGTCTGTTTTGTCAGGGTGCTGATTG
82621  GGACGACTAACCAGGTAAAATGTCTCTCGACTAACCAGACAAAACAGTCCCACGACTAAC
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FIGURE 4 (cont'd)

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82681  CTGCATTTACAATCCCTGAGCTAGACACAAAAGTTCTCCACCTCCCCACTGCATTAGCTA
82681  CACGTAAATGTTAGGGACTCGATCTGTGTTTTCAAGAGGTGGAGGGGTGACCTAATCGAT

82741  GATAAAGAGTGTTGATTGATGTATTTACAAACCCTGAGCTAGACACAGAGTGCTGACTGG
82741  CTATTTCTCACAACTAACTACATAAATGTTTGGGACTCGATCTGTGTCTCACGACTGACC

82801  TGCATTTACAAACCTTGAGCTAGATACAGAGCGCCGATTGGTGTATTTACAATCTCTTAG
82801  ACGTAAATGTTTGGAACTCGATCTATGTCTCGCGGCTAACCACATAAATGTTAGAGAATC

82861  CCAGACGTAAAGATTCTCCAAGTCCCCACTAGACTCAGGAGCCCAGCTGGCTTCACCCAG
82861  GGTCTGCATTTCTAAGAGGTTCAGGGGTGATCTGAGTCCTCGGGTCGACCGAAGTGGGTC

82921  TGTATCTTGCACCAGGGCTGCAGGTGGAGCTGCCTGCCAGTCCCGCGCCGTGCACCCGCA
82921  ACATAGAACGTGGTCCCGACGTCCACCTCGACGGACGGTCAGGGCGCGGCACGTGGGCGT

82981  CTCCTCAGCCCTCGGGCTGTTGATGGGACCAGGCACTGTGGAGTGGGGGTGGCACTCGTC
82981  GAGGAGTCGGGAGCCCGACAACTACCCTGGTCCGTGACACCTCACCCCCACCGTGAGCAG

83041  AGGGAGACTCAGGCCGCACAGGATCCCACAGCGGTGGCGGGGGCGGGAGGCTCAGGCAT
83041  TCCCTCTGAGTCCGGCGTGTCCTAGGGTGTCGCCACCGCCCCCGCCCTCCGAGTCCGTA

83101  GGCAGGCTGCAGGTCCCGAGCCCTGCCCTGCAGGGAGGCAGCTAAGGCCTGGCGAGAAAT
83101  CCGTCCGACGTCCAGGGCTCGGGACGGGACGTCCCTCCGTCGATTCCGGACCGCTCTTTA

83161  CTGGCCCGGCGAGAAATCTAGCGCGGCGCCGGTGGGCCAGCACTGCTGGGGGACCCGGTG
83161  GACCGGGCCGCTCTTTAGATCGCGCCGCGGCCACCCGGTCGTGACGACCCCCTGGGCCAC

83221  CACCCTCCGCAGCTGCTGGCCTGGGTGCTAAGCCCCTCACTGCCCGGGGCTGGCAGGGCC
83221  GTGGGAGGCGTCGACGACCGGACCCACGATTCGGGGAGTGACGGGCCCCGACCGTCCCGG

83281  AGCCGGTCGCTCCGAATGTGGGGCCTGCCAAGCCCACTCCCACCCGGAACTCCAGCTGGC
83281  TCGGCCAGCGAGGCTTACACCCCGGACGGTTCGGGTGAGGGTGGGCCTTGAGGTCGACCG

83341  CCACAAGCACCATGCGCAGCCCGGGTTCCCGCCCATGCCTCTCCCTCCACACCTCCCTGC
83341  GGTGTTCGTGGTACGCGTCGGGCCCAAGGGCGGGTACGGAGAGGGAGGTGTGGAGGGACG

83401  AAACTGAGGGAGCCAGCTCCGGCCTTGGCCAGCCCAGAGAATGGCTCCCACAGTGCAGCG
83401  TTTGACTCCCTCGGTCGAGGCCGGAACCGGTCGGGTCTCTTACCGAGGGTGTCACGTCGC

83461  GCAGGCTGAAGGGCTCCTCAAGCGCGGTCAGAATGGGCGCCGAGGCCGAGGAGGCACCGA
83461  CGTCCGACTTCCCGAGGAGTTCGCGCCAGTCTTACCCGCGGCTCCGGCTCCTCCGTGGCT

83521  GAGCGAGTGAGGGCTGGGAGGGCTGCCAGCACTGTCATCTCTCAGTAGCATAATTTATAT
83521  CTCGCTCACTCCCGACCCTCCCGACGGTCGTGACAGTAGAGAGTCATCGTATTAAATATA

83581  AACCAGTCTCTTGTTGATTAACCATTATATTATTGATACAACAAATATAAGAACTGTTAC
83581  TTGGTCAGAGAACAACTAATTGGTAATATAATAACTATGTTGTTTATATTCTTGACAATG

83641  TAGTAAATTGAGTAAAGCAGGAAAATTAAATTTGGTCTCTTACTGATCAACCATTATTAG
83641  ATCATTTAACTCATTTCGTCCTTTTAATTTAAACCAGAGAATGACTAGTTGGTAATAATC

83701  ATTGTTGATAACAACGGTTATAATGTTCATCAACCGTTATATTGTTGATACAATTATATT
83701  TAACAACTATTGTTGCCAATATTACAACTAGTTGGCAATATAACAACTATGTTAATATAA

83761  TGATGTATTTAACCAGATTTTATATATTATATTCTATATTTTATAACATGTATATGTATC
83761  ACTACATAAATTGGTCTAAAATATATAATATAAGATATAAAATATTGTACATATACATAG

83821  ATATAACATACACATATACATACACACACACAGCCAATATAATTTCACTCTCAGTTTCTT
83821  TATATTGTATGTGTATATGTATGTGTGTGTGTCGGTTATATTAAAGTGAGAGTCAAAGAA

83881  GTTAATCAACTATTATATTGTTGATACAACAAATATAAGAACTGTTACTAGTAAATTGAA
83881  CAATTAGTTGATAATATAACAACTATGTTGTTTATATTCTTGACAATGATCATTTAACTT

83941  TAAAGCAGGAAAATTACATTTGGGAGCCTTAAAGATGTAGGTTTTCTTCAAGAAATTTAT
83941  ATTTCGTCCTTTTAATGTAAACCCTCGGAATTTCTACATCCAAAAGAAGTTCTTTAAATA
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FIGURE 4 (cont'd)

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84001   GTTATAGTTATATCCCCTGTTGCATGTGAAGACATACATTCAAGGATACTTACTGCAGCT
84001   CAATATCAATATAGGGGACAACGTACACTTCTGTATGTAAGTTCCTATGAATGACGTCGA

84061   CACACAATTTGCTGATAGGTTGGATGTGGGTGTGAGAGAAGAGATGCTGTTTTCCTTTTG
84061   GTGTGTTAAACGACTATCCAACCTACACCCACACTCTCTTCTCTACGACAAAAGGAAAAC

84121   GGCGATGGCAACTGGATAGTAATCAGTTACTAAGATGGAGAAGAATGAGAAAGAAGTCTT
84121   CCGCTACCGTTGACCTATCATTAGTCAATGATTCTACCTCTTCTTACTCTTTCTTCAGAA

84181   TTTTTGTTTGTTTGTTGGAGTGATATGGGTAGAATAAAGAGTTAAAACAGTCATGCATGT
84181   AAAAACAAACAAACAACCTCACTATACCCATCTTATTTCTCAATTTTGTCAGTACGTACA

84241   AGGTACTATAGATGTGAAAGTCTATTATTCAGGGGAGAGTTTGGAATTTAAGGGATAGAT
84241   TCCATGATATCTACACTTTCAGATAATAAGTCCCCTCTCAAACCTTAAATTCCCTATCTA

84301   TCTTGTCTTTAAGCATAAAAATGCCTTTGAAGGTGAGAAACTAGATTACATCTTTAAGGG
84301   AGAACAGAAATTCGTATTTTTACGGAAACTTCCACTCTTTGATCTAATGTAGAAATTCCC

84361   GAGAACTGTAGATAGAGATGAAAAGAAGGCAAGGACTAACCCCTGGGGCAGGTCAGCATT
84361   CTCTTGACATCTATCTCTACTTTTCTTCCGTTCCTGATTGGGGACCCCGTCCAGTCGTAA

84421   TAGAAGAAAGGGAGTTTGTAAAATGCTAAGCTGTCTGAGAAGTAGCAGCCTGCAAGGTAG
84421   ATCTTCTTTCCCTCAAACATTTTACGATTCGACAGACTCTTCATCGTCGGACGTTCCATC

84481   AAAGAAAAACAAGAGAGGTTTAGTGGACTGGAAACCAAGTGAACCTGGAAACCACAAGCA
84481   TTTCTTTTTGTTCTCTCCAAATCACCTGACCTTTGGTTCACTTGGACCTTTGGTGTTCGT

84541   GCTGTGGCAAATCCTGCCACAGTGAGATGAGGCCTGAGAACTGAGTATTGGATTTGTCAA
84541   CGACACCGTTTAGGACGGTGTCACTCTACTCCGGACTCTTGACTCATAACCTAAACAGTT

84601   TGTGGAAGGCCTTGGTGATCTTGATAAGCATGTGTTAGTAGGGTGGTGGGGTTGCAGTGT
84601   ACACCTTCCGGAACCACTAGAACTATTCGTACACAATCATCCCACCACCCCAACGTCACA

84661   TTGGGATTTGAGAGAGAATGAGAGAATGGGTAGCTGTGATGCTGAATATGTATAAATGTC
84661   AACCCTAAACTCTCTCTTACTCTCTTACCCATCGACACTACGACTTATACATATTTACAG

84721   AGGAGGAATTCTGCTGCACAGTGGGACAGAGAATGGACGCCTCCCTGGAATGGGATAGAT
84721   TCCTCCTTAAGACGACGTGTCACCCTGTCTCTTACCTGCGGAGGGACCTTACCCTATCTA

84781   GCTAAAGGGAGTGTGTGTCTTAGTTGGGAGATATTATGGCATATCTCTAAGCTAATAGTA
84781   CGATTTCCCTCACACACAGAATCAACCCTCTATAATACCGTATAGAGATTCGATTATCAT

84841   ATTAGCCAGAAGGAAGGGAAAACTGATAGTTAAAATGTTCAAAAGATTTCTCACATTCCT
84841   TAATCGGTCTTCCTTCCCTTTTGACTATCAATTTTACAAGTTTTCTAAAGAGTGTAAGGA

84901   ATCATAGTTCTCCTTCTAAGGGTGACCACGTAAGCAGGCAGGGACATGTGACTAAGTAGA
84901   TAGTATCAAGAGGAAGATTCCCACTGGTGCATTCGTCCGTCCCTGTACACTGATTCATCT

84961   GCAGCATCCAACCCCCACCTTGCACGGTCACACACATACTGCTCCATTGACACCATAGTG
84961   CGTCGTAGGTTGGGGGTGGAACGTGCCAGTGTGTGTATGACGAGGTAACTGTGGTATCAC

85021   TCTTGGTGTGAGCTCTTCATTACTTGACTCAATATCTTCTTCCTCATCTTCTCAGCTGGG
85021   AGAACCACACTCGAGAAGTAATGAACTGAGTTATAGAAGAAGGAGTAGAAGAGTCGACCC

85081   GTTGTTGGGTATATCTTCATTGCAGATATTAGCATCCTTTGTGGTCTTCTTTGTCTTTCT
85081   CAACAACCCATATAGAAGTAACGTCTATAATCGTAGGAAACACCAGAAGAAACAGAAAGA

85141   ATTCTAGGGCCAGCACAGTGGGAGGCCTAGTCAACTGAGCCAAACTGGATATAACCACAA
85141   TAAGATCCCGGTCGTGTCACCCTCCGGATCAGTTGACTCGGTTTGACCTATATTGGTGTT

85201   GGTCAAAGGCAGGAGCCAGTGAGGAGATCTTGGTTTTGAGGTCATTCCTGGTGCGATAAT
85201   CCAGTTTCCGTCCTCGGTCACTCCTCTAGAACCAAAACTCCAGTAAGGACCACGCTATTA

85261   AACCATCCTGTAGCATTTTCTTGTCACTTAGAGAAGGCATTAGCAAACTTTTTTTGTAAT
85261   TTGGTAGGACATCGTAAAAGAACAGTGAATCTCTTCCGTAATCGTTTGAAAAAAACATTA

85321   GGTCTTAATAGTAAATATTTTTGACTTTGTAGGCTATATAGCTACTCACCTCTGCTTTTA
85321   CCAGAATTATCATTTATAAAAACTGAAACATCCGATATATCGATGAGTGGAGACGAAAAT
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FIGURE 4 (cont'd)

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85381  TAGTACAAAAGCAGCCATAGACAATTCATAAATAAATCAACATGTTCCAATAAAAGCAAT
85381  ATCATGTTTTCGTCGGTATCTGTTAAGTATTTATTTACTTGTACAAGGTTATTTTCGTTA

85441  AAAAACAGGCAGCAGTCTGAAGTTTGTCGACTCCTGATTTGGAATCATTCCAGAAAGTGA
85441  TTTTTGTCCGTCGTCAGACTTCAAACAGCTGAGGACTAAACCTTAGTAAGGTCTTTCACT

85501  AATAAAAGCATGCCTTCTTTTTTTTTTTTCAGACAAGGTCCTGCTCTGTCACCCAGGCTG
85501  TTATTTTCGTACCGAAGAAAAAAAAAAAACTCTGTTCCAGGACGAGACAGTGGGTCCGAC

85561  GAGTACAGTGGTGTCATCATAGCTCACTACAGCTTTGACCTGCTGGGCTCAAGTAATCCT
85561  CTCATGTCACCACAGTAGTATCGAGTGATGTCGAAACTGGACGACCCGAGTTCATTAGGA

85621  CCCACCTCAGCCTCCTGAGTGTCTAGGATTACAGGCATGTGACATCACACCTGGCTGATT
85621  GGGTGGAGTCGGAGGACTCACAGATCCTAATGTCCGTACACTGTAGTGTGGACCGACTAA

85681  TTTAAATTTTTTGTATTGATGGGGTCTTGCTATGTTGCCAAGGCTCACCTCAAACTCCTG
85681  AAATTTAAAAAACATAACTACCCCAGAACGATACAACGGTTCCGAGTGGAGTTTGAGGAC

85741  GTCTCAAGTGATTCTCCTGCCCCAGGATTCCCAAAGTGCTGGAATTAAAGGTGGGGGCCA
85741  CAGAGTTCACTAAGAGGACGGGGTCCTAAGGGTTTCACGACCTTAATTTCCACCCCCGGT

85801  CTGTGCCCAGCCAAAGCATGGCCTTTCTAAGGGTGACTCACTGTAGCACCTCCTGAGTAC
85801  GACACGGGTCGGTTTCGTACCGGAAAGATTCCCACTGAGTGACATCGTGGAGGACTCATG

85861  TTTCCTATCAAGTATCCTGGACCACTTTTTAAATAATTCATTCTAAAATCCATATTTAGG
85861  AAAGGATAGTTCATAGGACCTGGTGAAAAATTTATTAAGTAAGATTTTAGGTATAAATCC

85921  ATTGATTCCAAATTTGCCAACCTGTATTTCCCAAATAACTGGCATGATAATTCTTGTCTT
85921  TAACTAAGGTTTAAACGGTTGGACATAAAGGGTTTATTGACCGTACTATTAAGAACAGAA

85981  TTTCCCAAATGCTCATTTTCCACTCTTCAAACGTTGAGTGTTGACTGAAGTTCTGTGGTC
85981  AAAGGGTTTACGAGTAAAAGGTGAGAAGTTTGCAACTCACAACTGACTTCAAGACACCAG

86041  ATGTTTACAGTCATTTTTATGCTCTTTGTATTGTACATATGGAATGTATTTACCATTTCT
86041  TACAAATGTCAGTAAAAATACGAGAAACATAACATGTATACCTTACATAAATGGTAAAGA

86101  GTTAGCAATGATTTCTTGCAAAAACAATAACACTTGCTAGTTTTGCGTGCTTAAAAATAT
86101  CAATCGTTACTAAAGAACGTTTTTGTTATTGTGAACGATCAAAACGCACGAATTTTTATA

86161  CGAGCCCTGGCGCTCTCTACATATTATCTAATGTAATCCTTATATTAACCCTGTGAGTAG
86161  GCTCGGGACCGCGAGAGATGTATAATAGATTACATTAGGAATATAATTGGGACACTCATC

86221  TCATTATCACTTCTTTTACACAGGAGGAAGTTAGAGAAGAGTGTTAAGTGTTCTTTTAGT
86221  AGTAATAGTGAAGAAAATGTGTCCTCCTTCAATCTCTTCTCACAATTCACAAGAAAATCA

86281  CTTTTCCACTTTGTCTTTAGTTTTCTCTTAGCTGTTCTTTTAAATTCTAAGGTCATTCTT
86281  GAAAAGGTGAAACAGAAATCAAAAGAGAATCGACAAGAAAATTTAAGATTCCAGTAAGAA

86341  ATCTAAAAACTTAAAAGAGTTGATCAGCCTTTTTATCAAGTGTTAAATTTATACCATCTT
86341  TAGATTTTTGAATTTTCTCAACTAGTCGGAAAAATAGTTCACAATTTAAATATGGTAGAA

86401  TTTTCTTTGAACAGGGCTGGCAAATAAACCTGGATTTATCCCTTAGCCCTGTTACAGCAA
86401  AAAAGAAACTTGTCCCGACCGTTTATTTGGACCTAAATAGGGAATCGGGACAATGTCGTT

86461  GTCTCAGAAAATTTGGACTTCAGCTTCCCCAGTGATACATTTTCAAATGCCTATGTATGG
86461  CAGAGTCTTTTAAACCTGAAGTCGAAGGGGTCACTATGTAAAAGTTTACGGATACATACC

86521  ATTGCCCATTAGTTTATTGGCTAGAACTAAAGGAAATCAGGCAAGAGACAAAGGACATTT
86521  TAACGGGTAATCAAATAACCGATCTTGATTTCCTTTAGTCCGTTCTCTGTTTCCTGTAAA

86581  TCTCTAGGGTGTCAGTCAATGCAAAATGTTAGGACTAGCATCAGATTTTTTTTTTTTTAC
86581  AGAGATCCCACAGTCAGTTACGTTTTACAATCCTGATCGTAGTCTAAAAAAAAAAAAATG

86641  AAATGAAAATAATTGAAGTGTGGTAGAAGTTCCTCTAGTTCTGGCAGTCCTAAATATTGT
86641  TTTACTTTTATTAACTTCACACCATCTTCAAGGAGATCAAGACCGTCAGGATTTATAACA
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FIGURE 4 (cont'd)

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86701  TAACTGAAGAATGATGGGGCTCATAAATTTGGAAAGGAGAGAGAGGGGAAAAGAGAACGG
86701  ATTGACTTCTTACTACCCCGAGTATTTAAACCTTTCCTCTCTCTCCCCTTTTCTCTTGCC

86761  GAATTTATGCTGAGCAGGGTGGCTAAGTATATATATTCAACAGGCTATAGGAGGAGCTAT
86761  CTTAAATACGACTCGTCCCACCGATTCATATATATAAGTTGTCCGATATCCTCCTCGATA

86821  TAGTATTCACCAAGGGGTGGCACACACATACATAGTAGGCTAACGTGTATCCAGCATGCA
86821  ATCATAAGTGCTTCCCCACCGTGTGTGTATGTATCATCCGATTGCACATACGTCGTACGT

86881  TCACAAGTCACTTTGGGGTGGAGCCTTAACATTTAATGTATTACAGTTAGGGCCTATACA
86881  AGTGTTCAGTGAAACCCCACCTCGGAATTGTAAATTACATAATGTCAATCCCGGATATGT

86941  TCAAAAGGTGAAGCAGAGGACACGAAAGCCCTCTGTGTTCAGCCTCTGTAGACTGGCCAG
86941  AGTTTTCCACTTCGTCTCCTGTGCTTTCGGGAGACACAAGTCGGAGACATCTGACCGGTC

87001  AACCACTCTGTGGTCAGAGGTCTCTTATCAGGAAAGAATTCTTGTTGTTGTGTTGAAACT
87001  TTGGTGAGACACCAGTCTCCAGAGAATAGTCCTTTCTTAAGAACAACAACACAACTTTGA

87061  GCAAAAGGGAGGGGCAGTGTCAGGCAGGTGGTTGATACCAGTCTTTCAGAAGCACTGGTT
87061  CGTTTTCCCTCCCCGTCACAGTCCGTCCACCAACTATGGTCAGAAAGTCTTCGTGACCAA

87121  TCTGTTTAACTTTTAGAGAAGAAAGCTTAATTGGAGTGTTACTGGAAAGGGATACCAGTC
87121  AGACAAATTGAAAATCTCTTCTTTCGAATTAACCTCACAATGACCTTTCCCTATGGTCAG

87181  TAGACCACAAGAGAGGATTCTTGGATCTCACACAAGAAAGAATTCAGGGTGAGTCCACAG
87181  ATCTGGTGTTCTCTCCTAAGAACCTAGAGTGTGTTCTTTCTTAAGTCCCACTCAGGTGTC

87241  AGTAAGATCAAATCAAGTTTATTAGAGAAGTAGAGAAAGAAAAGAATGGCTGCTCCATAA
87241  TCATTCTAGTTTAGTTCAAATAATCTCTTCATCTCTTTCTTTTCTTACCGACGAGGTATT

87301  GCAGAGCAGCACTGAAGGCTTCTGGTTGGCTATTTTTATGGTTATTTCTTGATTATATGC
87301  CGTCTCGTCGTGACTTCCGAAGACCAACCGATAAAAATACCAATAAAGAACTAATATACG

87361  TAAGCAAGGGGTGGATTATTCATGAATTTTCCTGGAAAGGGGTGGGGAATTCCCAGAACT
87361  ATTCGTTCCCCACCTAATAAGTACTTAAAAGGACCTTTCCCCACCCCTTAAGGGTCTTGA

87421  GAGGGTTTCTCTTTCTTTTAGACCATATAGGGTAAGTTCTGGATGTTGCCATGGCATTTG
87421  CTCCCAAAGAGAAAGAAAATCTGGTATATCCCATTCAAGACCTACAACGGTACCGTAAAC

87481  TAAACTGCCATGGCACTGGTGGCAATGTCTTTTAGCATGCTAATGCATTATAAATAGCCT
87481  ATTTGACGGTACCGTGACCACCCTTACAGAAAATCGTACGATTACGTAATATTTATCGGA

87541  AAGATAAGCTGTGAGGATGACCAGAGGTCAATTTCCTCACCATCTTAGTTTTGGCTGGCT
87541  TTCTATTCGACACTCCTACTGGTCTCCAGTTAAAGGAGTGGTAGAATCAAAACCGACCGA

87601  TCTTTACTGCTTCCTGTTTTTTCAGTGGGTTCTTTGTGACCTGTATCTGTCTTGTAATGT
87601  AGAAATGACGAAGGACAAAAAAGTCACCCAAGAAACACTGGACATAGACAGAACATTACA

87661  CCTATCTCATCCTGTAACTAAGAATGCCTGACCTCTTAGGAATGGAGCACAGGTGGTCTC
87661  GGATAGAGTAGGACATTGATTCTTACGGACTGGAGAATCCTTACCTCGTGTCCACCAGAG

87721  AGCTCATTTTATCTATCCCCTATTCAAGATGGAGTTGCTCTGGTTTAAATAGTTCTGACA
87721  TCGAGTAAAATAGATAGGGGATAAGTTCTACCTCAACGAGACCAAATTTATCAAGACTGT

87781  TATTTTCCCCAATACCCCCAAAGGGACCCTTAATCCCAAAATTTGCAGACAGATGAAGAT
87781  ATAAAAGGGGTTATGGGGGTTTCCCTGGGAATTAGGGTTTTAAACGTCTGTCTACTTCTA

87841  CCATCTTCTGTAGCTTCTTCTGGCTGAATACAGGTGATGATATTTTTGCGTAACTATTCA
87841  GGTAGAAGACATCGAAGAAGACCGACTTATGTCCACTACTATAAAAACGCATTGATAAGT

87901  GGGTAGAGAGGAGCTCAGTGAGAAAGCATCAGTATGGTGAAGGCCATTCCTAACTCCCGA
87901  CCCATCTCTCCTCGAGTCACTCTTTCGTAGTCATACCACTTCCGGTAAGGATTGAGGGCT

87961  GTTCTCACAAAAGGTGATATCTGGAAGATTAATAAGTGTTCAATTTAAGAAAACGTTGAG
87961  CAAGAGTGTTTTCCACTATAGACCTTCTAATTATTCACAAGTTAAATTCTTTTGCAACTC

88021  TAGTCTTATCCTGCATTGCTACACAAAGAGTACCACAGCAATATATTCTACAACAGTAAA
88021  ATCAGAATAGGACGTAACGATGTGTTTCTCATGGTGTCGTTATATAAGATGTTGTCATTT
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FIGURE 4 (cont'd)

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88081  GCAAAATAAGTATAATTATCCCAACTAAACTAAATAACAAGCCTTTCCATCAACTAGCCA
88081  CGTTTTATTCATATTAATAGGGTTGATTTGATTTATTGTTCGGAAAGGTACTTGATCCGT

88141  GTTGTTGGAACCAAGCTTATATGGGGTTGCTAGCCAATTCCAACACATGTTCAGAATTAA
88141  CAACAACCTTGGTTCGAATATACCCCAACGATCGGTTAAGGTTGTGTACAAGTCTTAATT

88201  AATACTGATCCAGATATTTATGTTACCCTTCTGTTTCTTCTGAGCAGCAGCTAGAGATCA
88201  TTATGACTAGGTCTATAAATACAATGGGAAGACAAAGAAGACTCGTCGTCGATCTCTAGT

88261  CTGGTTGGTTCATAGGAACAAACAGGGTCAATCTAAATGGCAGAAAAAACTCGAAACAAT
88261  GACCAACCAAGTATCCTTGTTTGTCCCAGTTAGATTTACCGTCTTTTTTGAGCTTTGTTA

88321  GAATGGGACTAGAGTTGAATAACAAGTATACCATAGTTTCTGAAACATAATTTTTCTCTC
88321  CTTACCCTGATCTCAACTTATTGTTCATATGGTATCAAAGACTTTGTATTAAAAAGAGAG

88381  TCCAGTCTCCCATTTCTATTGAAAACAAATCATGGTAGGACTGATTTGTTTGCACAGTAA
88381  AGGTCAGAGGCTAAAGATAACTTTTGTTTAGTACCATCCTGACTAAACAAACGTGTCATT

88441  GCTTTAGTCTTATTATGCTTGGCCTGGTTATTTGTATAAAGCATAGCAATAATAATTATT
88441  CGAAATCAGAATAATACGAACCGGACCAATAAACATATTTCGTATCGTTATTATTAATAA

88501  TGCCACGTAGGCTTTTTAAAAATTGACTTTGATGTAACTTTGTTCCATAAGAAATCTCAG
88501  ACGGTGCATCCGAAAAATTTTTAACTGAAACTACATTGAAACAAGGTATTCTTTAGAGTC

88561  ATTAGACTTTCTAAAGCCTTGAGCTGAGACACAGATTTATCTGTGCCTGCAAATACTTGT
88561  TAATCTGAAAGATTTCGGAACTCGACTCTGTGTCTAAATAGACACGGACGTTTATGAACA

88621  ATGAGTTGTGTGAATTCTCCTTTTGAGATCCCAAGATAACTGGAGCTCCTAGGCCTGTCA
88621  TACTCAACACACTTAAGAGGAAAACTCTAGGGTTCTATTGACCTCGAGGATCCGGACAGT

88681  GAAAGTGACATTCTTTACTTACCACAGGTCAGGAACCCTGTAAAGGAATTGAATAGACAA
88681  CTTTCACTGTAAGAAATGAATGGTGTCCAGTCCTTGGGACATTTCCTTAACTTATCTGTT

88741  GGTATGAGGCCAGCTTTTCCCAGAGGCTTTCATCAGTTCTGTAAGTCAACTTTGATTCCT
88741  CCATACTCCGGTCGAAAAGCGTCTCCGAAAGTAGTCAAGACATTCAGTTGAAACTAAGGA

88801  TAAAGCAATCTGTTTATATTTGAAAGAATGCCATTCCAGTCAAAGCCCTGGTAAAACAGG
88801  ATTTCGTTAGACAAATATAAACTTTCTTACGGTAAGGTCAGTTTCGGGACCATTTTGTCC

88861  CAGTGTCTCTAATTGTGTCCTGTTACAAAGGAAAACAGATTTTTATTGCACATATGCAAA
88861  GTCACAGAGATTAACACAGGACAATGTTTCCTTTTGTCTAAAAATAACGTGTATACGTTT

88921  TTACTATGCTGCCATAAGTTAAGAATACTCACAAATAGTTTTCAAATTCTTGAGAAATCA
88921  AATGATACGACGGTATTCAATTCTTATGAGTGTTTATCAAAAGTTTAAGAACTCTTTAGT

88981  GGTAGAAAGAAATATGCTCCAAAGTTTTCTCATAGGAGTATAATTTACTCAATTTTTAAC
88981  CCATCTTTCTTTATACGAGGTTTCAAAAGAGTATCCTCATATTAAATGAGTTAAAAATTG

89041  AACTGTAAATAGCTCAAAAAAAAAGGTTTCTTGACTCTGAAAAATGAAACAAAGCATCAG
89041  TTGACATTTATCGAGTTTTTTTTTCCAAAGAACTGAGACTTTTTACTTTGTTTCCTAGTC

89101  CAACATTTTAAGCAAAAAGTCACTAGAAGGTTATTTTGTTCTTTTATTAGTTTAGTCCAT
89101  GTTGTAAAATTCGTTTTTCAGTGATCTTCCAATAAAACAAGAAAATAATCAAATCAGGTA

89161  GCTGTTAATTCCTGTTTGCTCAATATTTATGAACATATTGGTTTCCCAAGGGAGACTCTT
89161  CGACAATTAAGGACAAACGAGTTATAAATACTTGTATAACCAAAGGGTTCCCTCTGAGAA

89221  GAAAGTTTTTTTCCTCTCTATCTTAATGGCACACTTTACAAAATTTTTCAGAAACCTGCA
89221  CTTTCAAAAAAAGGAGAGATAGAATTACCGTGTGAAATGTTTTAAAAAGTCTTTGGACGT

89281  TTTAAGAGCCCTCTATCTGATTATAAACCATCTTTTAAAGAGGATCAAAACAAGACAACA
89281  AAATTCTCGGGAGATAGACTAATATTTGGTAGAAAATTTCTCCTAGTTTTGTTCTGTTGT

89341  ATTTTCTGTGGATAACATAAAGTCTTAGGAAAGCCGTGGTTAAAGACACAATTGACTAGA
89341  TAAAAGACACCTATTGTATTTCAGAATCCTTTCGGCACCAATTTCTGTGTTAACTGATCT
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FIGURE 4 (cont'd)

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89401   AATTTTGGTTACTTCTGTGGCATACAACAATTTTACATAACAGTTATAATTATTACTGAT
89401   TTAAAACCAATGAAGACACCGTATGTTGTTAAAATGTATTGTCAATATTAATAATGACTA

89461   AACATAAACTAAGTCATATCAGAATTTAGGAGTTTCCCATAATTTTGGAGCACATACCAA
89461   TTGTATTTGATTCAGTATAGTCTTAAATCCTCAAAGGGTATTAAAACCTCGTGTATGGTT

89521   TAACATATTTATACAAATACAACTCAAAGAAAGCTAAACACCATTTCATATTTGACAGTG
89521   ATTGTATAAATATGTTTATGTTGAGTTTCTTTCGATTTGTGGTAAAGTATAAACTGTCAC

89581   CTTCCTGTATGATTTTAATATACCAAGTAAGCCAAATATGTCATTTTTGGACTTAAGGGG
89581   GAAGGACATACTAAAATTATATGGTTCATTCGGTTTATACAGTAAAAACCTGAATTCCCC

89641   ACCTCATATCTAAAGTATTGACCAGATCAGGAAAAGGCATAATATAGAATTTGATTTTGG
89641   TGGAGTATAGATTTCATAACTGGTCTAGTCCTTTTCCGTATTATATCTTAAACTAAAACC

89701   AAAGTTTGTCAAATATCAAAGATTTAAAACACTTGATATTATAAAATCGAATCCCAGGTC
89701   TTTCAAACAGTTTATAGTTTCTAAATTTTGTGAACTATAATATTTTAGCTTAGGGTCCAG

89761   ACTGTAAAGTCATTTATTTAGCCAAAATGATAATACAAAGATTTTCCAAAAGCAAAATCC
89761   TGACATTTCAGTAAATAAATCGGTTTTACTATTATGTTTCTAAAAGGTTTTCGTTTTAGG

89821   TTTTTTTTTTTTTTTTTTTTTGAGACGAGTCTGGCTCTGTCGCCCAGCTGGAGTTCAGTG
89821   AAAAAAAAAAAAAAAAAAAAACTCTGCTCAGACCGAGACAGCGGGTCGACCTCAAGTCAC

89881   GCGCCATCTCGGCTCACTGCAAGCTCCGTCTCCCGGGTTCACACCATTCTCCTGCCTCAG
89881   CGCGGTAGAGCCGAGTGACGTTCGAGGCAGAGGGCCCAAGTGTGGTAAGAGGACGGAGTC

89941   CCTCCGGGGTAGCTGGGACTACAGGCACCCGCCACTACGCTTGGCTAATTTTTTTGTGTT
89941   GGAGGCCCCATCGACCCTGATGTCCGTGGGCGGTGATGCGAACCGATTAAAAAAACACAA

90001   TTTAGTAGAGACGGGGTTTCACCATGTTAGCCAGGATGGTCTCCATCTTCTGACCTCGTG
90001   AAATCATCTCTGCCCCAAAGTGGTACAATCGGTCCTACCAGAGGTAGAAGACTGGAGCAC

90061   ATCCACCCGCCTCAGCCTCCCAAAGTGCTGGTATTACAGGCGTGAGCCACTGCGCCCAGC
90061   TAGGTGGGCGGAGTCGGAGGGTTTCACGACCATAATGTCCGCACTCGGTGACGCGGGTCG

90121   AAGCAAAATCCTTTACTCATTGATAGAGGGAAGACAGCTTTCCAAACAATGTCTCACTTT
90121   TTCGTTTTAGGAAATGAGTAACTATCTCCCTTCTGTCGAAAGGTTTGTTACAGAGTGAAA

90181   TTCTTCTTTATTTTGTTGTTTATTCAAAAGGCAAACAAAAATCTTCCATGATCTTTTAAT
90181   AAGAAGAAATAAAACAACAAATAAGTTTTCCGTTTGTTTTTAGAAGGTACTAGAAAATTA

90241   ATTACATGAAAATTTTGTTCAAGAGAGAAAGCCAAATTTCATCTTTGCATTAATGAATGT
90241   TAATGTACTTTTAAAACAAGTTCTCTCTTTCGGTTTAAAGTAGAAACGTAATTACTTACA

90301   CAAATCCAATTCTTAAGAAAACCTTGTAGACAAATTATTCAATCTTAATCAATTTTACCA
90301   GTTTAGGTTAAGAATTCTTTTGGAACATCTGTTTAATAAGTTAGAATTAGTTAAAATGGT

90361   TGAGATAAGATTCTCATAAACCTTTTGTAGTCCTTTACAATTTTTTTTTGTTGTTGTTAA
90361   ACTCTATTCTAAGAGTATTTGGAAAACATCAGGAAATGTTAAAAAAAAACAACAACAATT

90421   AGAGCAGATTAATGCTCTAAGAAAACCCTGTTGTGCTTTTATTCCAATCTTCTATTTATG
90421   TCTCGTCTAATTACGAGATTCTTTTGGGACAACACGAAAATAAGGTTACAAGATAAATAC

90481   GAAAAACTGAATAATACCCTTTAACTTTAGCTAATATTTTAACACACAGAATTTCTTTTA
90481   CTTTTTGACTTATTATGGGAAATTGAAATCGATTATAAAATTGTGTGTCTTAAAGAAAAT

90541   CAAGATTAATTTTCACTGACCTCCCACAACTTACTCAAACCTTTAGCTTTATCCTATGTA
90541   GTTCTAATTAAAAGTGACTGGAGGGTGTTGAATGAGTTTGGAAATCGAAATAGGATACAT

90601   ACTTAAAACAGTCTTTTAACTCTGTAAACTAGGCAATAAGACCACATTCCCATGCCTTCT
90601   TGAATTTTGTCAGAAAATTGAGACATTTGATCCGTTATTCTGGTGTAAGGGTACGGAAGA

90661   TATAATCTTTTACCAAAAACACATTCTATTTTCCTTACACGCCTTGCAGGTAACACTGTT
90661   ATATTAGAAAATGGTTTTTGTGTAAGATAAAAGGAATGTGCGGAACGTCCATTGTGACAA

90721   TCTCTGGTAGCCTCAATTACATGTGCTACAATGTTAACTCTTAGCAACTTTTATATTTGG
90721   AGAGACCATCGGAGTTAATGTACACGATGTTACAATTGAGAATCGTTGAAAATATAAACC
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FIGURE 4 (cont'd)

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90781  TGAAAAGTCTGATAAATAAGTGGTTTTAATTATGTACCAGGTGTGGAGCCTAGGACGCCA
90781  ACTTTTCAGACTATTTATTCACCAAAATTAATACATGGTCCACACCTCGGATCCTGCGGT

90841  GACAGAAGTGCAGATAAGGTCTGAGTCTTTCCAGCATAGCTAGGGGGCATGGCCAACTCC
90841  CTGTCTTCACGTCTATTCCAGACTCAGAAAGGTCGTATCGATCCCCCGTACCGGTTGAGG

90901  ACATGTCCCCAGGCCCTACCTAGAATCTAATGGCTCCAAAGCAGGTGAGTTGAACAATTA
90901  TGTACAGGGGTCCGGGATGGATCTTAGATTACCGAGGTTTCGTCCACTCAACTTGTTAAT

90961  TCAAGTTAAAGAAGCAGTTTATGGCATTGAAGCATTCAGCAAATCTAATTTAATCTGACC
90961  AGTTCAATTTCTTCGTCAAATACCGTAACTTCGTAAGTCGTTTAGATTAAATTAGACTGG

91021  TAATTTAGACCAGATGTCTAAATTTTGAAGACATTTTTATTTTACCAATATATTTGATTC
91021  ATTAAATCTGGTCTACAGATTTAAAACTTCTGTAAAAATAAAATGGTTATATAAACTAAG

91081  TCTTTATTTCCCAAAGATTATTAAAGTCCCATGAATTAAAAGGTGTTAAAGTTTTTATTT
91081  AGAAATAAAGGGTTTCTAATAATTTCAGGGTACTTAATTTTCCACAATTTCAAAAATAAA

91141  TTCTGACAAAATATTCAATTTAAGTGCTTATTTTTCAAGCCAATTAATTAGAGCTCTTTT
91141  AAGACTGTTTTATAAGTTAAATTCACGAATAAAAAGTTCGGTTAATTAATCTCGAGAAAA

91201  CTATGCATATCACACATACAACACACAAAAATACACAGACAGAAGACCCAGTAGCTGTTA
91201  GATACGTATAGTGTGTATGTTGTGTGTTTTTATGTGTCTGTCTTCTGGGTCATCGACAAT

91261  ATTTTTTCATTTGCCAGCTTTTAAGAATCTTAATTGGATTACTGGCTTCAGGGTGGAGCA
91261  TAAAAAAGTAAACGGTCGAAAATTCTTAGAATTAACCTAATGACCGAAGTCCCACCTCGT

91321  ACGTGTGGGGACAGAGCCGGGAAAACATGCAGTTTCTGGGGCCTAATAAACAGGTGCAGT
91321  TGCACACCCCTGTCTCGGCCCTTTTGTACGTCAAAGACCCCGGATTATTTGTCCACGTCA

91381  TAGAAGGCAAAACAGATTCCCCAAAATTACAGATCTCATTTTTATATTGGATTCTGGATC
91381  ATCTTCCGTTTTGTCTAAGGGGTTTTAATGTCTAGAGTAAAAATATAACCTAAGACCTAG

91441  CCAAAAAGAGGGAATCAGCCCATCCCCTCTGGGAGTTTTGGAAGGTGTAGAAGAATGTTT
91441  GGTTTTTCTCCCTTAGTCGGGTAGGGGAGACCCTCAAAACCTTCCACATCTTCTTACAAA

91501  CCATACCTTCTAGGTGGCCAAGAGCATGCTTCTCTGATCCAAACGTGCACAGAGTGGGGT
91501  GGTATGGAAGATCCACCGGTTCTCGTACGAAGAGACTAGGTTTGCACGTGTCTCACCCCA

91561  ATTCCCCTATAACTGCTATTAGCCTTCCCTTAAAGCATATTTCCTGCCTAGTTATTACAC
91561  TAAGGGGATATTGACGATAATCGGAAGGGAATTTCGTATAAAGGACGGATCAATAATGTG

91621  ACCAAGGTTAAAAGCTCTCCCATAATGCAAAGTAATTTCTGATACCCCTACAAGTAAAAA
91621  TGGTTCCAATTTTCGAGAGGGTATTACGTTTCATTAAAGACTATGGGGATGTTCATTTTT

91681  ACATTAGGTAACACAATGCAAATCAGAGCAATGCCTTGGATTTTGAGAGGGATTTGCTTG
91681  TGTAATCCATTGTGTTACGTTTAGTCTCGTTACGGAACCTAAAACTCTCCCTAAACGAAC

91741  CCTTCAATTCCTGGGGTTCCATGAGGAAAACAGATTTTTCCCAAAATGGAGCCTGTGGTG
91741  GGAAGTTAAGGACCCCAAGGTACTCCTTTTGTCTAAAAAGGGTTTTACCTCGGACACCAC

91801  CTCCCTCAGTTTTTTCTAAGGAAGCCCAGGCTGTTAGAAATGATCTTAGGTCCTCTCAAT
91801  GAGGGAGTCAAAAAAGATTCCTTCGGGTCCGACAATCTTTACTAGAATCCAGGAGAGTTA

91861  GTGGGCATCAAGAGTGGCAAGAAAACAAAATGAGAAAAACAATTCAGTTGACTGAGAAGA
91861  CACCCGTAGTTCTCACCGTTCTTTTGTTTTACTCTTTTTGTTAAGTCAACTGACTCTTCT

91921  AAAAACTTTTATCTAGAAAAAAATCAATATAAAACCTGCCAGATAGATAGATAGATAGAT
91921  TTTTTGAAAATAGATCTTTTTTTAGTTATATTTTGGACGGTCTATCTATCTATCTATCTA

91981  AATCTTGGACATCACTTTTAATTAAGCTGACTTTTAACCAAATCTCTTATTATCAGACTC
91981  TTAGAACCTGTAGTGAAAATTAATTCGACTGAAAATTGGTTTAGAGAATAATAGTCTGAG

92041  TAGCCAGGACAAACAGCTAATATTTCTGGCTTTTGAACTTTACCAAAAGTAACCTCCCAG
92041  ATCGGTCCTGTTTGTCGATTATAAAGACCGAAAACTTGAAATGGTTTTCATTGGAGGGTC
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FIGURE 4 (cont'd)

92101 GTGAAACCAATAAGCCTTAACTAAGGTTATGATTTAACCACAGGTGTGGGAGGTATTTTC
92101 CACTTTGGTTATTCGGAATTGATTCCAATACTAAATTGGTGTCCACACCCTCCATAAAAG

92161 AAAGAGGTGGTAAGCAGTTTTTACAAGATCTGGAACCTCCAAACATAGCTCAGAGAAAGG
92161 TTTCTCCACCATTCGTCAAAAATGTTCTAGACCTTGGAGGTTTGTATCGAGTCTCTTTCC

92221 AAGATTCAAGACAGGGAGTCAGAAGTTGTTCATGAGGGGAAGATAATTAATAAATGGCAA
92221 TTCTAAGTTCTGTCCCTCAGTCTTCAACAAGTACTCCCCTTCTATTAATTATTTACCGTT

92281 AGGTCACATAGATATCAAACCAGAAAGGACTCATTCCCGAAGCTAGGAATTGAATCCAGG
92281 TCCAGTGTATCTATAGTTTGGTCTTTCCTGAGTAAGGGCTTCGATCCTTAACTTAGGTCC

92341 CCACCACTGTGAAATAGCAAAGCCTTAGTTACTGAGCTGCAGTACTGCACAGTCTCCATT
92341 GGTGGTGACACTTTATCGTTTCGGAATCAATGACTCGACGTCATGACGTGTCAGAGGTAA

92401 GCTCCTCCGAGAAGGAGCCTAGAGCAGCCAATTTTGAGCTTGCAAAGGCTTTTAACTGCT
92401 CGAGGAGGCTCTTCCTCGGATCTCGTCGGTTAAAACTCGAACGTTTCCGAAAATTGACGA

92461 CAAGATAATTTTTAGGACTAATTGACAGGAACCCCAAAATTCACACCCTCTGGATGGCAG
92461 GTTCTATTAAAAATCCTGATTAACTGTCCTTGGGGTTTTAAGTGTGGGAGACCTACCGTC

92521 AGATCAGGAGAAAGTACCCCCACGTGGTTACAAGGTCAAGCTTTCAAGGACATAAAACAA
92521 TCTAGTCCTCTTTCATGGGGGTGCACCAATGTTCCAGTTCGAAAGTTCCTGTATTTTGTT

92581 GACGAGAGGGAAACTTCATCCAGTTTTTGTTTCAGGGACCTGCAGAAAAGTTTGTAACTG
92581 CTGCTCTCCCTTTGAAGTAGGTCAAAAACAAAGTCCCTGGACGTCTTTTCAAACATTGAC

92641 ACCAGTTTGCGGGCCAGCTTGAAGACCAGATTTGTAGGATTCCTAGGCCTGCATTCTATC
92641 TGGTCAAACGCCCGGTCGAACTTCTGGTCTAAACATCCTAAGGATCCGGACGTAAGATAG

92701 CTGTGGCTAGCTAGGGCTGCCATAATAGAATATTACAGACTAGGCAGCTTCAACCACAGG
92701 GACACCGATCGATCCCGACGGTATTATCTTATAATGTCTGATCCGTCGAAGTTGGTGTCC

92761 TGTTTATTTTCTCACTGCTCCAAAGTCTAGAAGTCCAAGATGAGGGTGCCTGTAAAGCTG
92761 ACAAATAAAAGAGTGACGAGGTTTCAGATCTTCAGGTTCTACTCCCACGGACATTTCGAC

92821 ATTTCTGGTAAGAGCTCTCCTGGCTTGTAGATGGCCACCTTCTCCCTATGTCCTCTCTGG
92821 TAAAGACCATTCTCGAGAGGACCGAACATCTACCGGTGGAAGAGGGATACAGGAGAGACC

92881 GCCTTTCCTCTATCTGGCCAAGGGAGCTATCTCTGGTGTCTTTTCCTCTTCTTATAAGGA
92881 CGGAAAGGAGATAGACCGGTTCCCTCGATAGAGACCACAGAAAAGGAGAAGAATATTCCT

92941 CAGCAGGCCTATGGATTAAGGCCTCACTTTCATGTCTTCATTTAAGTTTAATTACCTCTT
92941 GTCGTCCGGATACCTAATTCCGGAGTGAAAGTACAGAAGTAAATTCAAATTAATGGAGAA

93001 TAAAGGCCCGATGTCCAAATACAGTCACACCGTGGGTTAGGATTTCAACATAGGAATTTT
93001 ATTTCCGGGCTACAGGTTTATGTCAGTGTGGCACCCAATCCTAAAGTTGTATCCTTAAAA

93061 AGGGACACAATTCAACCCATAATAGGAGGGCATTGGAAGGAGAGTGTTCCAGGCAGAGGA
93061 TCCCTGTGTTAAGTTGGGTATTATCCTCCCGTAACCTTCCTCTCACAAGGTCCGTCTCCT

93121 AGTAGTGCAGTAGAGCATATGGAAGTAGGAAAGTGAGGAGCAATGGAAGGGGTTCAGTAT
93121 TCATCACGTCATCTCGTATACCTTCATCCTTTCACTCCTCGTTACCTTCCCCAAGTCATA

93181 GGTTTGAGCGTGGGGTGTGTAGAGGGTGAAGGCTATTTCACCCAGTGCAGTAAGCTCTAT
93181 CCAAACTCGCACCCCACACATCTCCCACTTCCGATAAAGTGGGTCACGTCATTCGAGATA

93241 CATCCACACCGGGGTTTTACAGTGGGAGAAAGGAGGGTGTTTATTTGCAGGTCAAGAAGC
93241 GTAGGTGTGGCCCCAAAATGTCACCCTCTTTCCTCCCACAAATAAACGTCCAGTTCTTCG

93301 AAACAGAATCAGGGAGCTCATGCTTAAGACCTGAACTCCACAGTGGCTTACATGTAAGGT
93301 TTTGTCTTAGTCCCTCGAGTACGAATTCTGGACTTGAGGTGTCACCGAATGTACATTCCA

93361 GCAGAGGTTACAGGCAAAGGCATCAATCAACACATGGAAGCCATATATTGGTTTGGCCTA
93361 CGTCTCCAATGTCCGTTTCCGTAGTTAGTTGTGTACCTTCGGTATATAACCAAACCGGAT

93421 AAAAGGTGGGATATCCTGAAGTAGGGGCTTACAGGTTACAGGTAAATCCAAATATTTTCT
93421 TTTTCCACCCTATAGGACTTCATCCCCGAATGTCCAATGTCCATTTAGGTTTATAAAAGA

FIGURE 4 (cont'd)

93481 GATTTGCACATTCTTTAAGGAAGGGGATATTTGTCTAAAGATGGGATCAGCAGGCCAGGT
93481 CTAAACGTGTAACAAATTCCTTCCCCTATAAACAGATTTCTACCCTAGTCGTCCGGTCCA

93541 GTGGTGGCTCATGCTTGTAACCTCAGCACTTTGAAAGGCTGAAGAAGGAGGGTAACTTGA
93541 CACCACCGAGTACGAACATTGGAGTCGTGAAACTTTCCGACTTCTTCCTCCCATTGAACT

93601 GGCCAGGATTTCAAGACCAGCCTAGTCAACATGGCAAGACTCTGTCTCTAAAAAAAATAA
93601 CCGGTCCTAAAGTTCTGGTCGGATCAGTTGTACCGTTCTGAGACAGAGATTTTTTTTATT

93661 AAAAGAAAAAAAGAAAAAGAAAAAAAATAAAGATGGAATCAGCAGAAAGGAATGTTAGGT
93661 TTTTCTTTTTTTCTTTTTCTTTTTTTTATTTCTACCTTAGTCGTCTTTCCTTACAATCCA

93721 CTGGCCCATGGGCGGACTTCCTCCAGACTTCTCAGAAAGAAATTTAAGACAAAGAATGGT
93721 GACCGGGTACCCGCCTGAAGGAGGTCTGAAGAGTCTTTCTTTAAATTCTGTTTCTTACCA

93781 GCCAGGCGTGCTAGTTCACGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGAGGGTGGAT
93781 CGGTCCGCACCATCAAGTGCGGACATTAGGGTCGTGAAACCCTCCGACTCCTCCCACCTA

93841 CACTTGAGGTCAGGGATTTGAGACCAGCCTGGCCAACATGGTGAAACCCCATCTCTACTA
93841 GTGAACTCCAGTCCCTAAACTCTGGTCGGACCGGTTGTACCACTTTGGGGTAGAGATGAT

93901 AAAATACAAAAACTAGCCGGGTGTGGTGGTGCACGCCTGTAATCCCAGCTCCTCAGGAGG
93901 TTTTATGTTTTTGATCGGCCCACACCACCACGTGCGGACATTAGGGTCGAGGAGTCCTCC

93961 CTGAGGCAGGAGAATCGCTTGAACCTGGGAGGTGGAGGTTGCAGTGAGCCAAGATTGCGC
93961 GACTCCGTCCTCTTAGCGAACTTGGACCCTCCACCTCCAACGTCACTCGGTTCTAACGCG

94021 CACTGCACTCCACCCTGGGCAAGAGAGCGAGACTTGAGACTCCATCTAAAAAAACAAAAT
94021 GTGACGTGAGGTGGGACCCGTTCTCTCGCTCTGAACTCTGAGGTAGATTTTTTTGTTTTA

94081 GGAAAACAAACAATGGTGATAATTCAGTCCTCAATTCCTTTTCTTTTTTTTTTCTTTCTT
94081 CCTTTTGTTTCTTACCACTATTAAGTCAGGAGTTAAGGAAAAGAAAAAAAAAAGAAAGAA

94141 TTTTTTTTTTTTTAACTGCTCCTGCGGAGCAGGGCTACCTCATAGCCAGTATGTCCAGAG
94141 AAAAAAAAAAAAATTGACGAGGACGCCTCGTCCCGATGGAGTATCGGTCATACAGGTCTC

94201 TTGTCTCAGTTCCCTCGTTATCTGTGGTCTGGAGGATCCATATGATGGTGATCCAGGTTC
94201 AACAGAGTCAAGGGAGCAATAGACACCAGACCTCCTAGGTATACTACCACTAGGTCCAAG

94261 TGAAAAACAACTCTGGAACATCTGTTAAGATGTTATCTTTAGTTTCTATAGGAAACCAAA
94261 ACTTTTTGTTGAGACCTTGTAGACAATTCTACAATAGAAATCAAAGATATCCTTTGGTTT

94321 CATCTTCTGACTCTGACCTCCTTGGTGATTATTTTAAGCTACTGTTTCCCTTTTTGCTTA
94321 GTAGAAGACTGAGACTGGAGGAACCACTAATAAAATTCGATGACAAAGGGAAAAACGAAT

94381 TCGAGTTGCTCATTTACTTCTCAAGGCTAGCAGGATGACTGGACTTTCTCTTGAAGGAAC
94381 AGCTCAACGAGTAAATGAAGAGTTCCGATCGTCCTACTGACCTGAAAGAGAACTTCCTTG

94441 TCAAGCTGTTCCTTTATTTTTATGCTCAGGGGCGGGGGGCACTCAGCAGGTCCCTAAGAG
94441 AGTTCGACAAGGAAATAAAAATACGAGTCCCCGCCCCCCGTGAGTCGTCCAGGGATTCTC

94501 GTATCCCCGCTGTGTCTCACTATGGGTGAAGGCTCAGCGGGAAGAAAGCTAGATACCAGT
94501 CATAGGGGCGACACAGAGTGATACCCACTTCCGAGTCGCCCTTCTTTCGATCTATGGTCA

94561 TGGAACTCTCTTAAAGTAAGGAGATCTTGGGTACTTTATTAATATTTTTTTCAAGCTTTG
94561 ACCTTGAGAGAATTTCATTCCTCTAGAACCCATGAAATAATTATAAAAAAAGTTCGAAAC

94621 GTAAAGTATGAAATAACTCTGGATTAAGAGGAGAAGAACTAGAACTTAATAACCATGACA
94621 CATTTCATACTTTATTGAGACCTAATTCTCCTCTTCTTGATCTTGAATTATTGGTACTGT

94681 TTTGGGCAAATTGTTTGAAGCCTCAGTTTCCTCAACCTAAAAATAGGAATTATAACTTTT
94681 AAACCCGTTTAACAAACTTCGGAGTCAAAGGAGTTGGATTTTTATCCTTAATATTGAAAA

94741 TGAATTGTTCTGTTGTATGAGATAATGACAGTGAAATATTTTGGAGCCAAAAAGCAATGC
94741 ACTTAACAAGACAACATACTCTATTACTGTCACTTTATAAAACCTCGGTTTTTCGTTACG

FIGURE 4 (cont'd)

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94801  ATACTATTGGGGGTTATTATTATTTTTTGATCTTTCAGCAAGCCAGCTATAGTAGCTTTT
94801  TATGATAACCCCCAATAATAATAAAAAACTAGAAAGTCGTTCGGTCGATATCATCGAAAA

94861  CCTATATAAACACAGTATGAATTCAGTGCCCTCGCTTTCCTGACCCTCACAGCATTCAAG
94861  GGATATATTTGTGTCATACTTAAGTCACGGGAGCGAAAGGACTGGGAGTGTCGTAAGTTC

94921  CCCTGTATGGACCGCTGAGCTCTCCCTTGAAGCACCCCTTAGTCCAGTATTCTTTACTAT
94921  GGGACATACCTGGCGACTCGAGAGGGAACTTCGTGGGGAATCAGGTCATAAGAAATGATA

94981  TTTCCCCTTTAACAATTTAAACTTCTTTCAAAACAACTGGCAGTAGTTTTTTAAAAAAGA
94981  AAAGGGGAAATTGTTAAATTTGAAGAAAGTTTTGTTGACCGTCATCAAAAAATTTTTTCT

95041  AAACAGGCTACTCTTCAAATTAAAAAAAAAATTGTCTTGCTTTAGGAAAAATGTTCTTCT
95041  TTTGTCCGATGAGAAGTTTAATTTTTTTTTTAACAGAACGAAATCCTTTTTACAAGAAGA

95101  GTCTTTTCCAATTATCTTATTTCTTCTGCCTCTCATCTGCCTTGCCTAGGCAGAATTATT
95101  CAGAAAAGGTTAATAGAATAAAGAAGACGGAGAGTAGACGGAACGGATCCGTCTTAATAA

95161  CTCAAGCCTGCACATGCTGCTGTGCCTCTCTGGCTTCTAGGCCAAAACATAGGCTAATAG
95161  GAGTTCGGACGTGTACGACGACACGGAGAGACCGAAGATCCGGTTTTGTATCCGATTATC

95221  TACTCTTCTCAGCTCACTGAGCTCTTTCCTGCCGTCATTCAAATCACCTCTGAAATCCTG
95221  ATGAGAAGAGTCGAGTGACTCGAGAAAGGACGGCAGTAAGTTTAGTGGAGACTTTAGGAC

95281  CCTTTTGATAAAGTAATTTCTGACTGATCAGAGGAAAGTGATGATTTTCTCTGTGACATG
95281  GGAAAACTATTTCATTAAAGACTGACTAGTCTCCTTTCACTACTAAAAGAGACACTGTAC

95341  TCTTTTTATTTTCCATCACACTCAGTGTCTTGTCCTTCTATGCAACATATCCATGTATTT
95341  AGAAAAATAAAAGGTAGTGTGAGTCACAGAACAGGAAGATACGTTGTATAGGTACATAAA

95401  AAAAACCCTTGTATATGTATTTGCCATGTATTTGTGAGGTATAGCTCGTGAAGTAAAAAA
95401  TTTTTGGGAACATATACATAAACGGTACATAAACACTCCATATCGAGCACTTCATTTTTT

95461  AGTCTTTATTTTTTTAAACACATCATCATTTCAGCTTCAAAGTCAATGTGGTCTCTTGAG
95461  TCAGAAATAAAAAAATTTGTGTAGTAGTAAAGTCGAAGTTTCAGTTACACCAGAGAACTC

95521  AAGTTAAATATGCTGCATTTGAAATTTTATGTTTCTCATTTTTCATGTTTTTTTTTAAAG
95521  TTCAATTTATACGACGTAAACTTTAAAATACAAAGAGTAAAAAGTACAAAAAAAAATTTC

95581  CCCCTTTTAATTCCTCATGTATTTGAATATTCCAGGAAGCTAGTAGAGTAAAAAGCCAAA
95581  GGGGAAAATTAAGGAGTACATAAACTTATAAGGTCCTTCGATCATCTCATTTTTCGGTTT

95641  GTGTTAAAGTGTTTATAAGGAATGTGACTCATCGAAATTGACTCACACAATTCATCAGCT
95641  CACAATTTCACAAATATTCCTTACACTGAGTAGCTTTAACTGAGTGTGTTAAGTAGTCGA

95701  ATTGTCATCCATATGTTCTCATTATTTATGTGGCTTTTGCTTTATTTAATCAGATGACTG
95701  TAACAGTAGGTATACAAGAGTAATAAATACACCGAAAACGAAATAAATTAGTCTACTGAC

95761  AACTTATCATCGTGGGATTTTGCTTGTAGTTGTTTAATATTATATAATAAAATACTCTTG
95761  TTGAATAGTAGCACCCTAAAACGAACATCAACAAATTATAATATATTATTTTATGAGAAC

95821  TGTGAAACAAGTTAATTGACTTTTTTTAATTAAAAAAAATTTATGTGAGAGTCAGGAGTT
95821  ACACTTTGTTCAATTAACTGAAAAAAATTAATTTTTTTTAAATACACTCTCAGTCCTCAA

95881  ACATGTGCAAGTTTGTTACATGGGTATATGTTGTGATACAAAGATTTTAGCTTCTAAGGA
95881  TGTACACGTTCAAACAATGTACCCATATACAACACTATGTTTCTAAAATCGAAGATTCCT

95941  TCTCATTGCCCAAGTAGTGAACGTAGTACACTATAGGTAGTATTTCTAAACACTTTTCCC
95941  AGAGTAACGGGTTCATCACTTGCATCATGTGATATCCATCATAAAGATTTGTGAAAAGGG

96001  CTCCCCCTCTTTTGGAATCCCTAGTGTTTATTGTTCCCATCTTTGTGTCTATATGTACCT
96001  GAGGGGGAGAAAACCTTAGGGATCACAAATAACAAGGGTAGAAACACAGATATACATGGA

96061  AATGCTTAGCTCTCACTTATAAGTGCGGACGTGTGATATTTTGGTTTTCTGTTTCTGTGT
96061  TTACGAATCGAGAGTGAATATTCACGCCTGCACACTATAAAACCAAAAGACAAAGACACA

96121  TAATTCATTTAGGATAGAGAGACTCCAGCTGCAGCTGTGTTGCTACAAATGACATGAGTT
96121  ATTAAGTAAATCCTATCTCTCTGAGGTCGACGTCGACACAACGATGTTTACTGTACTCAA
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FIGURE 4 (cont'd)

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96181  CATTCTTTTTTATGGCTGCATAGTATTCCATGGTTTATATGTATCACATTTTCTTTATTC
96181  GTAAGAAAAAATACCGACGTATCATAAGGTACCAAATATACATAGTGTAAAAGAAATAAG

96241  AGTCCACCATTGATGGTCACCTGGGTTGATTCCATGTCTTTGTTGTTGTGGACAGGGCTG
96241  TCAGGTGGTAACTACCAGTGGACCCAACTAAGGTACAGAAACAACAACACCTGTCCCGAC

96301  TGATAAACATATGAGTGCAGTTACCTTTTTTTGTATAACAGTTCATAATAAAATACTCTT
96301  ACTATTTGTATACTCACGTCAATGGAAAAAAACATATTGTCAAGTATTATTTTATGAGAA

96361  AACAGTAGCACAGAATTTAGATTGCTTTTCAGGCTAGAAGGGATAATTGAAACATAGAAA
96361  TTGTCATCGTGTCTTAAATCTAACGAAAAGTCCGATCTTCCCTATTAACTTTGTATCTTT

96421  AAAATAATGACTCCTAAGCATAGAAACAGACCCAATCATAAAGCTCTCTTCCTCTCTTTC
96421  TTTTATTACTGAGGATTCGTATCTTTGTCTGGGTTAGTATTTCGAGAGAAGGAGAGAAAG

96481  TGCCTAGTGTTAGATCTTATTCATTGTCTTAAAGCACTGTGACCATTTTCAGTGAAATCA
96481  ACGGATCACAATCTAGAATAAGTAACAGAATTTCGTGACACTGGTAAAAGTCACTTTAGT

96541  CAGTTTTATTCATGAAAAGACAATGAATTGGTGTAAGTAATCATTTGAGGATGAAGGTGA
96541  GTCAAAATAAGTACTTTTCTGTTACTTAACCACATTCATTAGTAAACTCCTACTTCCACT

96601  CTAGTCTGTGATCAACACCAGTACTTGAAGTACTTGTAAAACATGAATTGACCTTGGTTA
96601  GATCAGACACTAGTTGTGGTCATGAACTTCATGAACATTTTGTACTTAACTGGAACCAAT

96661  AATTGCAGAAAATAAAGTATTAGTATACATAAACACATTTTCTCTCAGCATTGAAAAGTT
96661  TTAACGTCTTTTATTTCATAATCATATGTATTTGTGTAAAAGAGAGTCGTAACTTTTCAA

96721  ATAGTCTATAATTTACCTGCTTGCTAAGAATAAAAATATTACTTAGAGGTTTATCAAGAC
96721  TATCAGATATTAAATGGACGAACGATTCTTATTTTTATAATGAATCTCCAAATAGTTCTG

96781  CTTTTTTCTACAAATGGATTTAATGTACAGAATTATTCCATTTTCTATCTGTGCTCTGTA
96781  GAAAAAAGATGTTTACCTAAATTACATGTCTTAATAAGGTAAAAGATAGACACGAGACAT

96841  TACTACCACCTAGTGGAATAAAATGCAAATTTACCTGTCAAAATCAGGAGAAGAAAATGA
96841  ATGATGGTGGATCACCTTATTTTACGTTTAAATGGACAGTTTTAGTCCTCTTCTTTTACT

96901  ACCAGGGGAAATTTATTTCAGGAAAAAATTTTCATAACACGTTATTGTTACTTCTTTTAG
96901  TGGTCCCCTTTAAATAAAGTCCTTTTTTAAAAGTATTGTGCAATAACAATGAAGAAAATC

96961  TATAATGTAGTTTGCATAAAATACATTAGTTTGGAGTGAAAAAAGTCCCAGCCATTTTTG
96961  ATATTACATCAAACGTATTTTATGTAATCAAACCTCACTTTTTTCAGGGTCGGTAAAAAC

97021  TGATAGCTATTAAAATGCTATTAGTTTGTCCACAAATAAGCTATTCTATTCAGAAACTTA
97021  ACTATCGATAATTTTACGATAATCAAACAGGTGTTTATTCGATAAGATAAGTCTTTGAAT

97081  GAAGCTAGGTAAATTATTGAGATGATGCCAGCATATTATATCTCTAAATTATGTTAAGAA
97081  CTTCGATCCATTTAATAACTCTACTACGGTCGTATAATATAGAGATTTAATACAATTCTT

97141  GCTTCTCTAAATTCCTCATCACTAGGGTGTATTAGTCCATTTTCACACTGCTATAAAGAA
97141  CGAAGAGATTTAAGGAGTAGTGATCCCACATAATCAGGTAAAAGTGTGACGATATTTCTT

97201  CTACCTGAGACTGGGTAATTTATGAAGAAAAGAGGTTTAATTGACTCACAGTTCTGCAGG
97201  GATGGACTCTGACCCATTAAATACTTCTTTTCTCCAAATTAACTGAGTGTCAAGACGTCC

97261  CTTAACAGGAAGCATGACTGGGAGACCTCAGGAAACATACAGTGGAAGAAGGTGAAAGGG
97261  GAATTGTCCTTCGTACTGACCCTCTGGAGTCCTTTGTATGTCACCTTCTTCCACTTTCCC

97321  AAGCAAGGACCTTCTCATGGCAGCAGGAGAGGGAGAGCACAGGGGAAGTGCCACACACTT
97321  TTCGTTCCTGGAAGAGTACCGTCGTCCTCTCCCTCTCGTGTCCCCTTCACGGTGTGTGAA

97381  TTAAACCATCAGATCTCAGGAGAACTCACTCACTCTCACAAGCACAGCAGGGAGGAAATT
97381  AATTTGGTAGTCTAGAGTCCTCTTGAGTGAGTGAGAGTGTTCGTGTCGTCCCTCCTTTAA

97441  CACCCCCACGATCCTATCATCTCACACTGGGCCCCTCCTCCAATTTGACATGAGATATGG
97441  GTGGGGGTGCTAGGATAGTAGAGTGTGACCCGGGGAGGAGGTTAAACTGTACTCTATACC
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FIGURE 4 (cont'd)

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97501  GCAGGGACACAAATCCAAACCGTATCATAGGATTTGTTAAAAAAATCTAACATGTTCTGC
97501  CGTCCCTGTGTTTAGGTTTGGCATAGTATCCTAAACAATTTTTTTAGATTGTACAAGACG

97561  TTCAAGGCACCCATGAAATGAAGGTGTCATTTCTTAACTGAGAGGTTAAATAAAAGTGCA
97561  AAGTTCCGTGGGTACTTTACTTCCACAGTAAAGAATTGACTCTCCAATTTATTTTCACGT

97621  GAGATAAGATGGTTAAGTTTTATCGTAGCTGGGAAGAAAAGCGGGTGTGTGTATTATGCT
97621  CTCTATTCTACCAATTCAAAATAGCATCGACCCTTCTTTTCGCCCACACACATAATACGA

97681  TAGGTTTTTCCTCCCAAACAATGAAACCCAAAAAGGCAAATGAAGCTTTAAGGCGCTTTA
97681  ATCCAAAAAGGAGGGTTTGTTACTTTGGGTTTTTCCGTTTACTTCGAAATTCCGCGAAAT

97741  TCCTTTACTGGTAGGATGGTCCTCCTTTAATCTTCAGTCTCTGTTAAAGAACAAACACAA
97741  AGGAAATGACCATCCTACCAGGAGGAAATTAGAAGTCAGAGACAATTTCTTGTTTGTGTT

97801  GCTAACAATCAAAACCTGTTGTTGCTTGCTGACGGATTTCTCTAACATAGTCTTCCATCA
97801  CGATTGTTAGTTTTGGACAACAACGAACGACTGCCTAAAGAGATTGTATCAGAAGGTAGT

97861  ACCATCATAGGTTTGTTGTGGCCACCCAGGCCCTTTGGTCGTCATGTTCCCATGGAATGC
97861  TGGTAGTATCCAAACAACACCGGTGGGTCCGGGAAACCAGCAGTACAAGGGTACCTTACG

97921  TAATGAAATTACCTTCCCATTTCCTAAGGTGACATGCCTTTCAGATGGCATTGGTGTGTG
97921  ATTACTTTAATGGAAGGGTAAAGGATTCCACTGTACGGAAAGTCTACCGTAACCACACAC

97981  CTTGTGTAAACACATTTTTTTGTGCTCATGAATATTTTACCTGCCTGATTTTGGTGATCT
97981  GAACACATTTGTGTAAAAAAACACGAGTACTTATAAAATGGACGGACTAAAACCACTAGA

98041  GAGTGTTGAGCAGTGGGTGAGGGATGGTGGGGCAATGGGTAGTAAGGGGAAGTTTAATTG
98041  CTCACAACTCGTCACCCACTCCCTACCACCCCGTTACCCATCATTCCCCTTCAAATTAAC

98101  AAGTTCAGATAAAAATATCCCTCCAGAAACATTACAAAGCCACAAAATCAGCTGAAGTTG
98101  TTCAAGTCTATTTTTATAGGGAGGTCTTTGTAATGTTTCGGTGTTTTAGTCGACTTCAAC

98161  AGTCTTCTATTGTAAAGATTCTCTTTCTTCTCCTGACAGATCCCCATTCCTATCCAGGTA
98161  TCAGAAGATAACATTTCTAAGAGAAAGAAGAGGACTGTCTAGGGGTAAGGATAGGTCCAT

98221  GACCAGGCTCTAGTGAAGATTGGACACAAGTGGTTTATATCCCGAAGCTCTTAACCTAAG
98221  CTGGTCCGAGATCACTTCTAACCTGTGTTCACCAAATATAGGGCTTCGAGAATTGGATTC

98281  AGTCCTGCCTTGTTTTTTTACTTCATGTGGTCTTATATTGCTGAGGATAGCCCAGTGATC
98281  TCAGGACGGAACAAAAAAATGAAGTACACCAGAATATAACGACTCCTATCGGGTCACTAG

98341  ATTTCTACCTTAATATGTAGCCTTCAAAACGTTGGGTCTCTCAGTTTTCTTCCTTAATAA
98341  TAAAGATGGAATTATACATCGGAAGTTTTGCAACCCAGAGAGTCAAAAGAAGGAATTATT

98401  ACAATGAACCCTAATTATTTATAACTGCTCTTGTGATGGAGGAATTGGCATGATTTTGCA
98401  TGTTACTTGGGATTAATAAATATTGACGAGAACACTACCTCCTTAACCGTACTAAAACGT

98461  TTGTGGGCTTCTGGCTTTACAGTGTTTGTGGGAAAGATGGTCTTCTATCTTTGTTATTTA
98461  AACACCCGAAGACCGAAATGTCACAAACACCCTTTCTACCAGAAGATAGAAACAATAAAT

98521  TAAGTCATTCATTCCCTGTTTTTTTGAAGATATTGTTAAATAAAAAAACTTCAGCTGAAT
98521  ATTCAGTAAGTAAGGGACAAAAAAACTTCTATAACAATTTATTTTTTTGAAGTCGACTTA

98581  TAAATTTAAAAGTTTTTAATTGAGCAAAGAACCATTCTCAATTCGGGCAGCCTTCCCATC
98581  ATTTAAATTTTCAAAAATTAACTCGTTTCTTGGTAAGAGTTAAGCCCGTCGGAAGGGTAG

98641  CAGAGTAGTCCCTGTGACTTCAGTGCAGCCACATGGTGGAAGAGGATTTATGGACAGAGG
98641  GTCTCATCAGGGACACTGAAGTCACGTCGGTGTACCACCTTCTCCTAAATACCTGTCTCC

98701  AAGGAAAGTGACATACAGGAAACAGAAAAGAGATTCAGAAACAGCTGAATTGGTTATAAC
98701  TTCCTTTCACTGTATGTCCTTTGTCTTTTCTCTAAGTCTTTGTCGACTTAACCAATATTG

98761  TCAGCGTTTGCCTTATTTGAACATGGTTTGAACAGTTGGCCACGTTTGATTGGCCAAAAC
98761  AGTCGCAAACGGAATAAACTTGTACCAAACTTGTCAACCGGTGCAAACTAACCGGTTTTG
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FIGURE 4 (cont'd)

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 98821  TCAGTAATTGGCACAAGAGTAGGCTACCATCTGTTTATAATGTCCACTTAGGTTATAGTT
 98821  AGTCATTAACCGTGTTCTCATCCGATGGTAGACAAATATTACAGGTGAATCCAATATCAA

 98881  CATGATGTGCAAAGAAACCTTTAAGCTGAGCTTAAAATGTAATGAGGCAGCTGTAGGCTA
 98881  GTACTACACGTTTCTTTGGAAATTCGACTCGAATTTTACATTACTCCGTCGACATCCGAT

 98941  AACTTGATTTAACAGTACTTATCCCTCTGTTGAAATTGCACTCTTGCTACCTGCTAGTTG
 98941  TTGAACTAAATTGTCATGAATAGGGAGACAACTTTAACGTGAGAACGATGGACGATCAAC

 99001  ATGTGGGCAGGTGTGCTAATGACACATTCGCCTGCACCTACCACCTGCTGAAGACCCTGC
 99001  TACACCCGTCCACACGATTACTGTGTAAGCGGACGTGGATGGTGGACGACTTCTGGGACG

 99061  CATGTCCTGAAGCAGTCACTTAGGCTATGAAACACAAGGATGAGTTAGAGAAGTAAATAT
 99061  GTACAGGACTTCGTCAGTGAATCCGATACTTTGTCTTCCTACTCAATCTCTTCATTTATA

 99121  TATATTTTACCCCCCAAAGCCTAAAACCATGTCTAGGTTCTCCCCTTTCTCAATTCCCAA
 99121  ATATAAAATGGGGGGTTTCGGATTTTGGTACAGATCCAAGAGGGGAAAGAGTTAAGGGTT

 99181  TCATGCAACCTTGAAAGGTGTTATATAGATAGTTGTTAGAAATATGTCTGTCCTCCAAAA
 99181  AGTACGTTGGAACTTTCCACAATATATCTATCAACAATCTTTATACAGACAGGAGGTTTT

 99241  CCCTACTAACACGCAAAAATGGACAAATCTAGCTTTTTTGCTAAAATCCTAACAACTCAG
 99241  GGGATGATTGTGCGTTTTTACCTGTTTAGATCGAAAAAACGATTTTAGGATTGTTGAGTC

 99301  AAAGCAAAGCAAAATGAAATGTATGTACTCCATTCTCAGGATTTCCTTCTTAAAAACCAC
 99301  TTTCGTTTCGTTTTACTTTACATACATGAGGTAAGAGTCCTAAAGGAAGAATTTTTGGTG

 99361  TAGGCTTTGTGTAACTCAATTTTAAAAGTATGGTAATAGCTCCTGTAATTCGATGGCTTC
 99361  ATCCGAAACACATTGAGTTAAAATTTTCATACCATTATCGAGGACATTAAGCTACCGAAG

 99421  TTCTGGGAGACAGATATAAATCTATTCTAGACTTTAAGACTGGTGTCCACATTTTAAGTT
 99421  AAGACCCTCTGTCTATATTTAGATAAGATCTGAAATTCTGACCACAGGTGTAAAATTCAA

 99481  ACAGTTGTATGTACTTCTACTTTGTTGCAGCCTTCTCTTGGAGTCAAGAAGCCTACCAAA
 99481  TGTCAACATACATGAAGATGAAACAACGTCGGAAGAGAACCTCAGTTCTTCGGATGGTTT

 99541  GCCCTGCTCTTTGTACTCTTGAGCCCAGTGGGACCTTATTTTTCAAGTGGAACCTTTAAT
 99541  CGGGACGAGAAACATGAGAACTCGGGTCACCCTGGAATAAAAAGTTCACCTTGGAAATTA

 99601  CCAGTGTCCCTGTGGGCCAATCCCAAGTATGTAAGAGCCTGGAAAGGTGGAACTGGGGAC
 99601  GGTCACAGGGACACCCGGTTAGGGTTCATACATTCTCGGACCTTTCCACCTTGACCCCTG

 99661  TGCAAGATGGGAGGGTAAGTAAATCTGTGTCTCTGTCTAAAGGAAAGACACCTTCATGAC
 99661  ACGTTCTACCCTCCCATTCATTTAGACACAGAGACAGATTTCCTTTCTGTGGAAGTACTG

 99721  CATTTAGTTAGTGCCATTTCACTTCAGTATGAACACATATAATACTTTTCAAACTTTAAT
 99721  GTAAATCAATCACGGTAAAGTGAAGTCATACTTGTGTATATTATGAAAAGTTTGAAATTA

 99781  GCTCATTGTGTTTCATGGTTAATTTTCAGTTTAATCTTTCAGCAAGCCAGCTGTAGTAGC
 99781  CGAGTAACACAAAGTACCAATTAAAAGTCAAATTAGAAAGTCGTTCGGTCGACATCATCG

 99841  TTTTCCTATATAAACGCAGTATGAATTCAGTGCCCTCGCTTTTAGATGTGCTAGTTTAAA
 99841  AAAAGGATATATTTGCGTCATACTTAAGTCACGGGAGCGAAAATCTACACGATCAAATTT

 99901  GGATAGCCCATGGCCCTTTGTAAGGGAGAAACACTGGATATGATATCTAGGGAAGAACTG
 99901  CCTATCGGGTACCGGGAAACATTCCCTCTTTGTGACCTATACTATAGATCCCTTCTTGAC

 99961  AAGTAAGAAACTACAACAAGCATCACATCGGTGCTTTGGATAAACTTCCCCTGGCGCTG
 99961  TTCATTCTTTGATGTTGTTCGTAGTGTAGCCACGAAACCTATTTGAAGGGGACCCGCGAC

100021  GTCTCTGGCTGCAGGCTGACGGCTGCCATTAAAAAGCATCTGGTCCTGGCACCCAGGCTC
100021  CAGAGACCGACGTCCGACTGCCGACCGTAATTTTTCGTAGACCAGGACCCTGGGTCCGAG

100081  TCAGTTGGCTCCAGGGAGTCATGTCTGGGGAAGGTGCCCGCTTCACTGAAGTGCTGTCTT
100081  AGTCAACCGAGGTCCCTCAGTACAGACCCCTTCCACGGGCGAAGTGACTTCACGACAGAA
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FIGURE 4 (cont'd)

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100141  CATTGCCACAGATTGTGGCCACACCTGCTGCCAACTGGCTGCGGGACAGCCCTGCTTTGG
100141  GTAACGGTGTCTAACACCGGTGTGGACGACGGTTGACCGACGCCCTGTCGGGACGAAACC

100201  CTCTGTCAGGCCAGTCTCATAGGCCATATGTAGCTGGCAGGAAATAAAAGAGCATTTGAA
100201  GAGACAGTCCGGTCAGAGTATCCGGTATACATCGACCGTCCTTTATTTTCTCGTAAACTT

100261  AAGTGTTGGACGATTTCAGGGGTGGACTTGGCCATGAGTTGGGAATGCCCCTATGGGTGA
100261  TTCACAACCTGCTAAAGTCCCCACCTGAACCGGTACTCAACCCTTACGGGGATACCCACT

100321  ACGAGAATAACTGGTTTAAGCAGCATGGGTTCTTGCTTTGCATGTATCAAATGGTGCTGT
100321  TGCTCTTATTGACCAAATTCGTCGTACCCAAGAACGAAACGTACATAGTTTACCACGACA

100381  TTGCATACTCAGGGCAGCAGCTGTCCTAGAAGGTGACTCCATGGCAGTCTTGTGGGCCCT
100381  AACGTATGAGTCCCGTCGTCGACAGGATCTTCCACTGAGGTACCGTCAGAACACCCGGGA

100441  GGTAGGACATTTAGGTCCAGGAGGCAGGGGAGAGTCACATGACGTGCTGCTGGGGTATTA
100441  CCATCCTGTAAATCCAGGTCCTCCGTCCCCTCTCAGTGTACTGCACGACGACCCCATAAT

100501  GAGGCAATGACCACTGGCTTTGACCCCTCTGTAGTCTTGCTGTATTTCCTTTTTCTTTTC
100501  CTCCGTTACTGGTGACCGAAACTGGGGAGACATCAGAACGACATAAAGGAAAAAGAAAAG

100561  TCTCCTCACCTACCCAAATTAAAAAAGAACGGTTATAAAAGTCATCCCCACTGGCAACTT
100561  AGAGGAGTGGATGGGTTTAATTTTTTCTTGCCAATATTTTCAGTAGGGGTGACCGTTGAA

100621  TAGCAACTGCATTCCCTCAATGGGTAGAGAAATCCAAATGGAGTGCATTAAAACTAGGAA
100621  ATCGTTGACGTAAGGGAGTTACCCATCTCTTTAGGTTTACCTCACGTAATTTTGATCCTT

100681  CTCTATTCTCCTTCTGGCTTAGAGCACACCTTCCTGTGTCCTAGGCTAGCCAGGTTCAAA
100681  GAGATAAGAGGAAGACCGAATCTCGTGTGGAAGGACACAGGATCCGATCGGTCCAAGTTT

100741  ACTCCTTTTTTTGACTCTTGATTTCTTTTTTTACTGGTTCAAACTTCTTCGCAGAGCATG
100741  TGAGGAAAAAAACTGAGAACTAAAGAAAAAAATGACCAAGTTTGAAGAAGCGTCTCGTAC

100801  TGCCTATGTACCACTGCATACCATATATATACCATATATAGAGAGTAAATAAACAGTCTT
100801  ACGGATACATGGTGACGTATGGTATATATATGGTATATATCTCTCATTTATTTGTCAGAA

100861  GATGAAAAGTAATAAGGAAAAAGTTTCCCTGTTTAAAATATTGCTTTCTAGCTCCCCGAC
100861  CTACTTTTCATTATTCCTTTTTCAAAGGGACAAATTTTATAACGAAAGATCGAGGGGCTG

100921  CTGTTTAGGAAAAAGATAACCTGGGGACACAGAAATTGCAGGGCAATCTTTATTAACCGG
100921  GACAAATCCTTTTTCTATTGGACCCCTGTGTCTTTAACGTCCCGTTAGAAATAATTGGCC

100981  TATTTGGGCAGGTTGTAATTTATTTTGTAAACAATGATTTAATGCACTATTGCAGAATAC
100981  ATAAACCCGTCCAACATTAAATAAAACATTTGTTACTAAATTACGTGATAACGTCTTATG

101041  ATGATCACTGTAGGCCAGTTAAAAATTAATGTTTTCAGTACCACACAGAGTGAACCCTAA
101041  TACTAGTGACATCCGGTCAATTTTTAATTACAAAAGTCATGGTGTGTCTCACTTGGGATT

101101  TGTAAACTGTGGACTTGTGGACCACACTAATGCAAGATGATAATAAGAAGAAAAACTGAG
101101  ACATTTGACACCTGAACACCTGGTGTGATTACGTTCTACTATTATTCTTCTTTTTGACTC

101161  AGGGTGTTCGGGAAGGGGTATAATAGGGGAATTCTGTTACCTTTTGCTCAATTTCTCTGT
101161  TCCCACAAGCCCTTCCCCATATTATCCCCTTAAGACAATGGAAAACGAGTTAAAGAGACA

101221  GAATCTAAAAGTACTCTAAAATAATAAAATCTATTATAAAAATATTTGATTCATTAGGCT
101221  CTTAGATTTTCATGAGATTTTATTATTTTAGATAATATTTTTATAAACTAAGTAATCCGA

101281  CAGGTGGACTATGATCCATGGAAATTGACTTGAAATCTCTTAGGAAAGGAAGAGACCGGA
101281  GTCCACCTGATACTAGGTACCTTTAACTGAACTTTAGAGAATCCTTTCCTTCTCTGGCCT

101341  GAAGAAAGTATTGAACTCATAAATTAAAAATGGCAAGAGGGAAGGTGGTAACCAAAAGGA
101341  CTTCTTTCATAACTTGAGTATTTAATTTTTACCGTTCTCCCTTCCACCATTGGTTTTCCT

101401  TGGGCATTTAACCTATATGCCTATCACTTCCAAAAAGTTCTAGGGCCGTCTCCTCCTATG
101401  ACCCGTAAATTGGATATACGGATAGTGAAGGTTTTTCAAGATCCCGGCAGAGGAGGATAC

101461  CTTCTGACCTGGAGAGGTACAAGGGGAACAAAATATTCCGCATTTAATATTATCCTGTTG
101461  GAAGACTGGACCTCTCCATGTTCCCCTTGTTTTATAAGGCGTAAATTATAATAGGACAAC
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FIGURE 4 (cont'd)

101521 AGTTGGCAAAGACATTTGGAGTCAACTTTAGTTTTGTGTATTATTACATCTGTAAACCTA
101521 TCAACCGTTTCTGTAAACCTCAGTTGAAATCAAAACACATAATAATGTAGACATTTGGAT

101581 ATTAAGTCAACAGTTACCCTTGACACCTGTAGTCAACTGGTATTATTAAATAACTATTGA
101581 TAATTCAGTTGTCAATGGGAACTGTGGACATCAGTTGACCATAATAATTTATTGATAACT

101641 GTCTCATAAAGTCAAGAACTTTCTGCTTTCTATCTAAGTGAATCTAGGGCAGAGACTGAG
101641 CAGAGTATTTCAGTTCTTGAAAGACGAAAGATAGATTCACTTAGATCCCGTCTCTGACTC

101701 CATCAGGATTCTTTAGCATGCAGCCAAGCTTGAGAAGCACTGAGCTAGAGAAAGGTCTTG
101701 GTAGTCCTAAGAAATCGTACGTCGGTTCGAACTCTTCGTGACTCGATCTCTTTCCAGAAC

101761 CACTGTAGAAACAGCTTTAGTTCCAGGTGATTCCTTGGTTAATTTGGCAGGAATAAGGCT
101761 GTGACATCTTTGTCGAAATCAAGGTCCACTAAGGAACCAATTAAACCCTCCTTATTCCGA

101821 TTCTGTCACTCTCTCTCTCTTTCTCTCTTTTTCTCTCTCTCTTGCACATGCACACGTGCA
101821 AAGACAGTGAGAGAGAGAGAAAGAGAGAAAAAGAGAGAGAGAACGTGTACGTGTGCACGT

101881 CACACACACACAAATTATCTCTCTTAGTTTTTTCTTTTTTCCTTGCATTCTGATTCTGCA
101881 GTGTGTGTGTGTTTAATAGAGAGAATCAAAAAAGAAAAAAGGAACGTAAGACTAAGACGT

101941 TTTAAGAGTACAAGCTTTGAAGTCAGAAAGACCTGGCTTAAAAACCTAACTGTCATAATG
101941 AAATTCTCATGTTCGAAACTTCAGTCTTTCTGGACCGAATTTTTGGATTGACAGTATTAC

102001 GTGCGTAAATGTCGTTATAGATTTGTCCAAACCCATAGAATGTACACCAGGAATGAACAC
102001 CACGCATTTACAGCAATATCTAAACAGGTTTGGGTATCTTACATGTGGTCCTTACTTGTG

102061 TAATGAAAACTCTAGACTTCAGGTGATAATGGTATGTCAATGTGGTTCATTAATTTCAGC
102061 ATTACTTTTGAGATCTGAAGTCCACTATTACCATACAGTTACACCAAGTAATTAAAGTCG

102121 AAATGTACCACTCTGGTGTGAGGCATTGGTAATGGTAGAAACTATTCATTTGGATGGGGA
102121 TTTACATGGTGAGACCACACTCCGTAACCATTACCATCTTTGATAAGTAAACCTACCCCT

102181 GAAAGGGATATGGGAAATCTTTGTACTTGCCTTTCAGTTTTGGTGGGAACCTAAAACTGC
102181 CTTTCCCTATACCCTTTAGAAACATGAACGGAAAGTCAAAACCACCCTTGGATTTTGACG

102241 TCTGAAAAAAACCTGAAGTCTTTAAAAACAAACCAACCTAATTGCCTTGGGCATGTTACT
102241 AGACTTTTTTTGGACTTCAGAAATTTTTGTTTGGTTGGATTAACGGAACCCGTACAATGA

102301 TAACTGCTCTATGTATCAGTTTCCTCATTTTTAAAGTTGAGGCAATAATACCTTGCACAG
102301 ATTGACGAGATACATAGTCAAAGGAGTAAAAATTTCAACTCCGTTATTATGGAACGTGTC

102361 ATTAAGTGAGATAATAGAAAGTGCCTAGGATAGTACTTGGCATATAGAAAGCTCTCAGCA
102361 TAATTCACTCTATTATCTTTCACGGATCCTATCATGAACCGTATATCTTTCGAGAGTCGT

102421 AATGCAGTATGATAACCTAATGGTTAAAAGCTTGGGTTTAGGAGTCAAATGTCTGGGAGT
102421 TTACGTCATACTATTGGATTACCAATTTTCGAACCCAAATCCTCAGTTTACAGACCCTCA

102481 TACACACTTAACTATCTGTGAGATCTTCTACAACTGAATCCTCTCTCCAAGTCTTCCAAT
102481 ATGTGTGAATTGATAGACACTCTAGAAGATGTTGACTTAGGAGAGAGGTTCAGAAGGTTA

102541 GAACAATAAAGTCTAGGGTTGTTTTTAGATGACTCAATGAAATAATGTAGTTAAGTACTT
102541 CTTGTTATTTCAGATCCCAACAAAAATCTACTGAGTTACTTTATTACATCAATTCATGAA

102601 AGCACCCAGTCTGGCAGGTATGGGTTGCATATCTCTTATCTGAAATGCTTGGGACCAGAT
102601 TCGTGGGTCAGACCGTCCATACCCAACGTATAGAGAATAGACTTTACGAACCCTGGTCTA

102661 GTGTTTTGGATTTCAAATTTTGGAGTATTTCTCTTTGGGCATCCCTAATCCAAAAAATTC
102661 CACAAAACCTAAAGTTTAAAACCTCATAAAGAGAAACCCGTAGGGATTAGGTTTTTTAAG

102721 GAAATCCAAATTGAGCATCATGTTGGCACCGAAAAAGTTTTAGATTTTAGAGCATTTCAA
102721 CTTTAGGTTTAACTCGTAGTACAACCGTGGCTTTTTCAAAATCTAAAATCTCGTAAAGTT

102781 AGTTTTAAATTAGGGATCCTCAACCTGTAGTAAACTCTCACAGTCACTGATGTTGTGAGG
102781 TCAAAATTTAATCCCTAGGAGTTGGACATCATTTGAGAGTGTCAGTGACTACAACACTCC

FIGURE 4 (cont'd)

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102841  TTTTCTCACTTTCTCATTTCATTTCCTGGACTCTCTTTATCTTAGAAGAAATCAGTTAAA
102841  AAAAGAGTGAAAGAGTAAAGTAAAGGACCTGAGAGAAATAGAATCTTCTTTAGTCAATTT

102901  TTTTACATAATAGAATTTATTCTTTTGGAGGGATGTATTTAATATGTCTATTCTCCCAGA
102901  AAAATGTATTATCTTAAATAAGAAAACCTCCCTACATAAATTATACAGATAAGAGGGTCT

102961  TAACCTATTTAAAACCATATTGAAATGTTTCTATGTCAACAGCTTTCTTACTTTTTCATT
102961  ATTGGATAAATTTTGGTATAACTTTACAAAGATACAGTTGTCGAAAGAATGAAAAAGTAA

103021  TTTCTGTTTCCTCCAAGAACATGTTTCTCTTATGAATATTGGCAGCACATGGGCGGGAAC
103021  AAAGACAAAGGAGGTTCTTGTACAAAGAGAATACTTATAACCGTCGTGTACCCGCCCTTG

103081  CCAACTATATTACCATGGTATCAGTTATCCTGTGGACATTAATAATACAGCTTACACCTG
103081  GGTTGATATAATGGTACCATAGTCAATAGGACACCTGTAATTATTATGTCGAATGTGGAC

103141  TGAGAGAACTCTGGGAAAATTAAAACTTGTTTGGGGGAATAAAGACCATCTACAGAATAT
103141  ACTCTCTTGAGACCCTTTTAATTTTGAACAAACCCCCTTATTTCTGGTAGATGTCTTATA

103201  AATAATACATCAATCAATCAATTAAAACTTAAACATAAAAAACCCTTTTCTTTTCAGTGC
103201  TTATTATGTAGTTAGTTAGTTAATTTTGAATTTGTATTTTTTGGGAAAAGAAAAGTCACG

103261  ATTGAAATAGTCACTGTCTTTAATCCTCTTTCCTTGCTCAGTGCTTCATGAAGCTGAGGA
103261  TAACTTTATCAGTGACAGAAATTAGGAGAAAGGAACGAGTCACGAAGTACTTCGACTCCT

103321  GCCATGGTTTTAATTCAGCTACACTTTCAGAAATGTGTATGCATTTGTATTTAGAAGCTT
103321  CGGTACCAAAATTAAGTCGATGTGAAAGTCTTTACACATACGTAAACATAAATCTTCGAA

103381  CTTTGAAAGGCTAAATATTCATCCTGTAAGAATTCTCTATGTGTTTTTTAATACAGTCTA
103381  GAAACTTTCCGATTTATAAGTAGGACATTCTTAAGAGATACACAAAAAATTATGTCAGAT

103441  AAGGGCATTTTGTATATGAAAAAATAATTTATTTTCAGGTAGGGTAAAACTTCACTGCTT
103441  TTCCCGTAAAACATATACTTTTTTATTAAATAAAAGTCCATCCCATTTTGAAGTGACGAA

103501  CACTACTTCGTAGTTGTGTCTACGAATGAGAAAAAATTCAAATAAAATAGTTATTATTAT
103501  GTGATGAAGCATCAACACAGATGCTTACTCTTTTTTAAGTTTATTTTATCAATAATAATA

103561  TAGTTTTTAGAGATGCAGTCTTGCTGTGTTGCCCAGGCTGGTCTGGGACTTCTGGCCTCA
103561  ATCAAAAATCTCTACGTCAGAACGACACAACGGGTCCGACCAGACCCTGAAGACCGGAGT

103621  AGCCATCCTCCTGCCTCGGTGTCCTGAGTCACTGGGATTACAGGCATGAGCCACCACACC
103621  TCGGTAGGAGGACGGAGCCACAGGACTCAGTGACCCTAATGTCCGTACTCGGTGGTGTGG

103681  CCACTGAAATAGTTATTTTTTAAAAAACTTAATTTCATTAGGATGTAACAGTCTCATGTA
103681  GGTGACTTTATCAATAAAAAATTTTTTGAATTAAAGTAATCCTACATTGTCAGAGTACAT

103741  ACTCATCCTTTGGCTTTTATTGTTATTATTTATTTTTTCCAAGCAACCCAATGAGATATA
103741  TGAGTAGGAAACCGAAAATAACAATAATAAATAAAAAAGGTTCGTTGGGTTACTCTATAT

103801  TAAAGCAGATATTTTTATCTGCCAGATAATTAAATGAGGGAAAAATAAGGACTAACTTGC
103801  ATTTCGTCTATAAAAATAGACGGTCTATTAATTTACTCCCTTTTTATTCCTGATTGAACG

103861  TTAAGTTCACATATACCAAATAGTGGAAATGCAAGAGCTGTCCTCAGGTCTGTTAACAAC
103861  AATTCAAGTGTATATGGTTTATCACCTTTACGTTCTCGACAGGAGTCCAGACAATTGTTG

103921  AAACCTGTGGTCTTTCTACCAGACGTCCCCTGCAATCTGGTTTATACTCATTATTAAAAA
103921  TTTGGACACCAGAAAGATGGTCTGCAGGGGACGTTAGACCAAATATGAGTAATAATTTTT

103981  GCATTTGTAATTTAACTCAGTTATCTATTTACTATCAGTTATGAATAAGGATTATTTGAC
103981  CGTAAACATTAAATTGAGTCAATAGATAAATGATAGTCAATACTTATTCCTAATAAACTG

104041  TTTTTATGGTCATTAAACAATAGCTTCCTATCTGTTGTCTTTGTCTTTTTAATTTTTATT
104041  AAAAATACCAGTAATTTGTTATCGAAGGATAGACAACAGAAACAGAAAAATTAAAAATAA

104101  TATTTTATTGTTTTTTTAATAGCTTCCTATCTGTATACCAGACTTGCTTCATCTCCACAT
104101  ATAAAATAACAAAAAAATTATCGAAGGATAGACATATGGTCTGAACGAAGTAGAGGTGTA

104161  TGACCAAGAATTTATATTTTGTCATCTGTATTTAGAAGCATATGTTTTAAGCGTCTTTTA
104161  ACTGGTTCTTAAATATAAAACAGTAGACATAAATCTTCGTATACAAAATTCGCAGAAAAT
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FIGURE 4 (cont'd)

104221 ATGGCTCTTTTTTTTTTTTTGCTGGCAGGCCACAGTCTCGCTCTGTCTCCTAGGCTGGAG
104221 TACCGAGAAAAAAAAAAAAACGACCCTCCCCTGTCAGAGCGAGACAGAGGATCCGACCTC

104281 TGCAGTGGCACCATCTCAGCTCACTGCAACCTCCGCCTCCCTGGTGTGAGTGGTGCTCCT
104281 ACGTCACCGTGGTAGAGTCGAGTGACGTTGGAGGCGGAGGGACCACACTCACCACGAGGA

104341 GCCTCAGCCTCCCGAGTAGGTGGGATTACAGGCGTGGTCCACCAAACCCAGCTAGTTTTT
104341 CGGAGTCGGAGGGCTCATCCACCCTAATGTCCGCACCAGGTGGTTTGGGTCGATCAAAAA

104401 TATATTTTTGGTAGAGACAGGGTTTCACCATGTTAGCCAGGCTGGTCTGGAACTCCTGAC
104401 ATATAAAAACCATCTCTGTCCCAAAGTGGTACAATCGGTCCGACCAGACCTTGAGGACTG

104461 CTCAAGTAACTTGCCCACCTCAGCCTCCCAAAGTGCTGAGATTACAGGTATGAGCCACTG
104461 GAGTTCATTGAACGGGTGGAGTCGGAGGGTTTCACGACTCTAATGTCCATACTCGGTGAC

104521 TGCCTGGCCCTTTTAAGGACTCTTTTTTTTTTTTTTTTTTTTTTTGAGACAGTCTCACTC
104521 ACGGACCGGGAAAATTCCTGAGAAAAAAAAAAAAAAAAAAAAAAACTCTGTCAGAGTGAG

104581 TGTCGCTCAGACTGGAGTGCAGTGGCGCGATCTCGGCTCACTGCAAGCTCCACCTCCCGG
104581 ACAGCGAGTCTGACCTCACGTCACCGCGCTAGAGCCGAGTGACGTTCGAGGTGGAGGGCC

104641 GTTCACGCCATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCGCCAGCCACC
104641 CAAGTGCGGTAAGAGGACGGAGTCGGAGGGCTCATCGACCCTGATGTCCGCGGTCGGTGG

104701 ACGCCCGGATAATTTTTAGTATTTTTAGTAGAGACGAGGTTTCACCGTGTTAGCCAGGAT
104701 TGCGGGCCTATTAAAAATCATAAAAATCATCTCTGCTCCAAAGTGGCACAATCGGTCCTA

104761 GGTCTCAATCTCCTGACCTCATGATCCGGCCGTCTCGCCTCCCAAAGTGCTGGGATTACA
104761 CCAGAGTTAGAGGACTGGAGTACTAGGCCGGCAGAGCGGAGGGTTTCACGACCCTAATGT

104821 GGCGTGAGCCACCGCGCCTGGCCCTTTTAAGGACTCTTAACATTACCTTGGTGTGAGTCA
104821 CCGCACTCGGTGGCGCGGACCGGGAAAATTCCTGAGAATTGTAATGGAACCACACTCAGT

104881 ACCTCATCGTGCTCCAATGGCAATCACCATAGTATGATGTCTATTTTCCACAGCTTACTG
104881 TGGAGTAGCACGAGGTTACCGTTAGTGGTATCATACTACAGATAAAAGGTGTCGAATGAC

104941 GAATATTTCAGCTATTAGTCAATATTCTTTCAGTTGCAAGTCAGAAAACCAACTTGAAAT
104941 CTTATAAAGTCGATAATCAGTTATAAGAAAGTCAACGTTCAGTCTTTTGGTTGAACTTTA

105001 TATTATTTATTTATTTATTTATTTTTTTGAGACGGAATTTTGCTCTTGTTGCCCAGGCTG
105001 ATAATAAATAAATAAATAAATAAAAAAACTCTGCCTTAAAACGAGAACAACGGGTCCGAC

105061 GAGTGCCATGGCACAATCTCGGCTCACTGCAACCTCCGCCTCCCGAGTTCAAGCAATTCT
105061 CTCACGGTACCGTGTTAGAGCCGAGTGACGTTGGAGGCGGAGGGCTCAAGTTCGTTAAGA

105121 CCTGCCTCAGCCTCCAGAGTAGCTGGGATTACAGGCATGGGCCACCACTCCCGGCTAATT
105121 GGACGGAGTCGGAGGTCTCATCGACCCTAATGTCCGTACCCGGTGGTGAGGGCCGATTAA

105181 TTTTTGTTATTTTTAGTAGAGACGGGGTTTCTCCATGTTGGTCAGGATGGTCTCAAACTC
105181 AAAAACAATAAAAATCATCTCTGCCCCAAAGAGGTACAACCAGTCCTACCAGAGTTTGAG

105241 CCAACCTCAGGTCATCTGCCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCATGAGC
105241 GGTTGGAGTCCAGTAGACGGGTGGAGTCGGAGGGTTTCACGACCCTAATGTCCGTACTCG

105301 CACCGTGCCCGGCCTGGAAATGATCTTAAGCAGACAAGGGCTTATGAAACTAGGATGCTA
105301 GTGGCACGGGCCGGACCTTTACTAGAATTCGTCTGTTCCCGAATACTTTGATCCTACGAT

105361 GGGGCTAAAGCAATTATTTCCAAGTTTCTTGTGTCCTTTGCACATCCCCCTTTTTCTTCC
105361 CCCCGATTTCGTTAATAAAGGTTCAAAGAACACAGGAAACGTGTAGGGGGAAAAAGAAGG

105421 CTTCTTCCTCTGCCTCTGGTCAGAGCTTCTGGCTCCATGTTGGCCTAGGGCTCTCCCACT
105421 GAAGAAGGAGACGGAGACCAGTCTCGAAGACCGAGGTACAACCGGATCCCGAGAGGGTGA

105481 TCAGCCGCTTTCTTCTGTGAAGTGTGGTGATCATGGACACAGCCGACCCCAGTTTTACAG
105481 AGTCGGCGAAAGAAGACACTTCACACCACTAGTACCTGTGTCGGCTGGGGTCAAAATGTC

FIGURE 4 (cont'd)

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105541  CATACCAAGTAAGCAACCCCAGAAGGGAGAAAATGCCTGTATTTCAGGTTATAGACATTA
105541  GTATGGTTCATTCGTTGGGGTCTTCCCTCTTTTACGGACATAAAGTCCAATATCTGTAAT

105601  AAATGAGTGAATGCACCCAAAAAAGGAATCATGTGACTGTCTTAGGTTATATGCCCACCC
105601  TTTACTCACTTACGTGGGTTTTTTCCTTAGTACACTGACAGAATCCAATATACGGGTGGG

105661  TTTAACTCAGCTGCAGCAGGGCAAGATGCTATATTGTCATCAGTTGTGGTAGGGCAAGAT
105661  AAATTGAGTCGACGTCGTCCCGTTCTACGATATAACAGTAGTCAACACCATCCCGTTCTA

105721  GCTATATTATCAGTCCAAGCAGAATGACATAGCTCTATAGAAAGACTATGTTTTTATAAG
105721  CGATATAATAGTCAGGTTCGTCTTACTGTATCGAGATATCTTTCTGATACAAAAATATTC

105781  AGTATGGAATATAGTGCAGATGAAAACAGTAGATATACACTAACATGTGGCTCTAATGTT
105781  TCATACCTTATATCACGTCTACTTTTGTCATCTATATGTGATTGTACACCGAGATTACAA

105841  TAATTTTTATTTTTTTTGAGACAGAGTCTCACTGTGTCACCCAGGCTGGAGTGCAGTGGT
105841  ATTAAAAATAAAAAAAACTCTGTCTCAGAGTGACACAGTGGGTCCGACCTCACGTCACCA

105901  GCTATCTTGGCTCACTGCAACTTTTGCCTCCCGAGTTAAGATGATTCTCCTCCCTCAGCC
105901  CGATAGAACCGAGTGACGTTGAAAACGGAGGGCTCAATTCTACTAAGAGGAGGGAGTCGG

105961  TCCCTAGCAGCTGAGATTATAGGCACCCGCCACCACGCCCAGCTAATTCTTGTATTTTCA
105961  AGGGATCGTCGACTCTAATATCCGTGGGCGGTGGTGCGGGTCGATTAAGAACATAAAAGT

106021  GTAGAGACATGGTTTCACCATGTTGGCCGGGCTGGTCTCGAACTCCTGACCTCAGTGATC
106021  CATCTCTGTACCAAAGTGGTACAACCGGCCCGACCAGAGCTTGAGGACTGGAGTCACTAG

106081  CGCCCATCTTAGGCTCCTAAAGTGCTAGGATTACAGACATAAGCCACCGCGCCTGGCCTC
106081  GCGGGTAGAATCCGAGGATTTCACGATCCTAATGTCTGTATTCGGTGGCGCGGACCGGAG

106141  ATGCTCAACTTTTATTTAGACAACAGTACAAATTGTAATTTTACCCAGATGTAAAAGAGT
106141  TACGAGTTGAAAATAAATCTGTTGTCATGTTTAACATTAAAATGGGTCTACATTTTCTCA

106201  CTAAGAGACCTAAATAGATATTTTGTGGTAGATTACATTAATGTAATGTAATGTAATGTA
106201  GATTCTCTGGATTTATCTATAAAACACCATCTAATGTAATTACATTACATTACATTACAT

106261  GGAGTTTTACATTACTACATTTGTAGTTGTTTTAGTTGTTTTTCATTGTTTGTTTCTGTG
106261  CCTCAAAATGTAATGATGTAAACATCAACAAAATCAACAAAAAGTAACAAACAAAGACAC

106321  TATTTCTGGGGATTTCATGGTGCAACAGGAGGACTAGAGTTTATTCCCGATCCCTGACTG
106321  ATAAAGACCCCTAAAGTACCACGTTGTCCTCCTGATCTCAAATAAGGGCTAGGGACTGAC

106381  TCTTACGGCAGTACTTCTCAGACCTACTGAGTTATACAACCAGGGGTGTAGGGAGGCAAG
106381  AGAATGCCGTCATGAAGAGTCTGGATGACTCAATATGTTGGTCCCCACATCCCTCCGTTC

106441  CAGTCATCACATTTATTTGAGGACTCTCATGTTTTGTCTAAAATATTCATCCTTATTTTA
106441  GTCAGTAGTGTAAATAAACTCCTGAGAGTACAAAACAGATTTTATAAGTAGGAATAAAAT

106501  TAATATACTCCATAATTTTCCCATATAAGTTTAGATAAAAGATGATACCTTAAAAGTATT
106501  ATTATATGAGGTATTAAAAGGGTATATTCAAATCTATTTTCTACTATGGAATTTTCATAA

106561  ATAACACTAAATTGTCATTCCGGGAAAATGTGCTGTGTTCCTTTCATTTTAAATAATCTG
106561  TATTGTGATTTAACAGTAAGGCCCTTTTACACGACACAAGGAAAGTAAAATTTATTAGAC

106621  AGATGAATGGTGCAGGCTGAGAAAAATAGGCTTTTGAAATACTTTTTGGTCAACATCGAG
106621  TCTACTTACCACGTCCGACTCTTTTTATCCGAAAACTTTATGAAAAACCAGTTGTAGCTC

106681  ACTTTTAACATTTGTCCTATCTTTTAGGGGAATTTAGACATTGGGCATTATGTATTCCTT
106681  TGAAAATTGTAAACAGGATAGAAAATCCCCTTAAATCTGTAACCCGTAATACATAAGGAA

106741  GGATACATTAAAAGGTGTTAGATAAGAGCGCTCACACTTGCTGCTCTTCTATTGCAACTT
106741  CCTATGTAATTTTCCACAATCTATTCTCGCGAGTGTGAACGACGAGAAGATAACGTTGAA

106801  GACAGAAGTTACTTCTCTAAACCTTAGTTTCTCATCTGAACAATGGAAATAATGATAGTG
106801  CTGTCTTCAATGAAGAGATTTGGAATCAAAGAGTAGACTTGTTACCTTTATTACTATCAC

106861  TCTATCTCATAGTATTGCTGTGACATTTAAATCAAATAATTCATCTAAAATTGCTTCGTC
106861  AGATAGAGTATCATAACCACACTCTAAATTTACTTTATTAAGTACATTTTAACGAACCAC
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FIGURE 4 (cont'd)

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106921  TGTGGAAACATAGTAACTTTTAACTGTTCTCATTAACTTGGCTATTTACCTGTGTTCTTC
106921  ACACCTTTGTATCATTGAAAATTGACAAGAGTAATTGAACCGATAAATGGACACAAGAAG

106981  TATCATTACATTTCAAGTTAAAATTTCAAGGTTTCACGTTGTTCTCTCTCCAATGAATGC
106981  ATAGTAATGTAAAGTTCAATTTTAAAGTTCCAAAGTGCAACAAGAGAGAGGTTACTTACG

107041  AGTTAAATCACTTAGATTTTCTAATGAGTTTTCCTTTAATGTTATGCAGTTGACTAGAGA
107041  TCAATTTAGTGAATCTAAAAGATTACTCAAAAGGAAATTACAATACGTCAACTGATCTCT

107101  GTGTATATATATTAAGAACATAATACCTTCACTATGTCCACATGTGAATTAAGAGCTTGA
107101  CACATATATATAATTCTTGTATTATGGAAGTGATACAGGTGTACACTTAATTCTCGAACT

107161  GGCTATCAGAGGGTAGAAGATGAGGGAGTGGGGATGAAGTATGTTTGTAACCTGTGTATT
107161  CCGATAGTCTCCCATCTTCTACTCCCTCACCCCTACTTCATACAAACATTGGACACATAA

107221  TTCTCTTTCTTAAAGGAATTACGGCTCATCTCTTTTTGCCCAATGTGAAGCAGTAGATAA
107221  AAGAGAAAGAATTTCCTTAATGCCGAGTAGAGAAAAACGGGTTACACTTCGTCATCTATT

107281  TGGGTGTCAGCAGGTCCTGTGGCTCTATGGAGAGGACCATCAGATCACTGAAGTGGGAAC
107281  ACCCACAGTCGTCCAGGACACCGAGATACCTCTCCTGGTAGTCTAGTGACTTCACCCTTG

107341  TATGAATCTTTTTCTTTACTGGATAAATGAAGATGGAGGTAATCCACTCAGATTTCACTG
107341  ATACTTAGAAAAAGAAATGACCTATTTACTTCTACCTCCATTAGGTGAGTCTAAAGTGAC

107401  TGTGCATTTCTCAGTCATTTTCAACAGGACCAGAAAGACAAGAGCTAGAAACTTAGTACA
107401  ACACGTAAAGAGTCAGTAAAAGTTGTCCTGGTCTTTCTGTTCTCGATCTTTGAATCATGT

107461  AGGGAGTAAGTAGCACAGTTCCAAAGGCTAAGTAAGGACTACTGTGCTTTTGCTGCCCAA
107461  TCCCTCATTCATCGTGTCAAGGTTTCCGATTCATTCCTGATGACACGAAAACGACGGGTT

107521  ATAGACACAAGTTTCTTTTTTTTCTTTCTTTCTTTTTTAAAGAGGTGGAGTCTCACTATG
107521  TATCTGTGTTCAAAGAAAAAAAAGAAAGAAAGAAAAAATTTCTCCACCTCAGAGTGATAC

107581  TCACCCAGGCTGCAGTGCAATGGTGTGATCTCAGCTCACTGCACCCTGGTTCAAGCAATT
107581  AGTGGGTCCGACGTCACGTTACCACACTAGAGTCGAGTGACGTGGGACCAAGTTCGTTAA

107641  CTCCTGCCTCAGCCTCCCGAGTAGCTGGGATTGCAGGAGCCTGCCACCATGCCCAGCTAA
107641  GAGGACGGAGTCGGAGGGCTCATCGACCCTAACGTCCTCGGACGGTGGTACGGGTCGATT

107701  TTTTTGTATTTTTTTTTTAGTAGAGATAGGGTTTCACCATGTTGGTCAGGCTGGTCTTG
107701  AAAAACATAAAAAAAAAATCATCTCTATCCCAAAGTGGTACAACCAGTCCGACCAGAAC

107761  AACTCCTGACCTCAGGTGATCCACCGGCCTTGGCCTCCCAAAGTGCTGGGATTACAGGTG
107761  TTGAGGACTGGAGTCCACTAGGTGGCCGGAACCGGAGGGTTTCACGACCCTAATGTCCAC

107821  TGAGCCACTGCACCCGGCCGAGTTTCGATTTAAAGAAGCTCTAGAGGTTTTTTGTTTTTC
107821  ACTCGGTGACGTGGGCCGGCTCAAAGCTAAATTTCTTCGAGATCTCCAAAAAACAAAAAG

107881  GTTTTTTGTTTTTCTGGCTCTAGATGTACTGATTATTGAGATACTGAGATGTCACATTAA
107881  CAAAAAACAAAAAGACCGAGATCTACATGACTAATAACTCTATGACTCTACAGTGTAATT

107941  GGGATTTAAGTTACCATGATTGGAAGATTTGCTTCCTTATCCCTTCTGCAGTTCCCCAAC
107941  CCCTAAATTCAATGGTACTAACCTTCTAAACGAAGGAATAGGGAAGACGTCAAGGGGTTG

108001  AATTTTCCTATCTGAACACCTTGCATTGAGACACAGGTCTCAGATCAGGTCAATGGTCAT
108001  TTAAAAGGATAGACTTGTGGAACGTAACTCTGTGTCCAGAGTCTAGTCCAGTTACCAGTA

108061  TCACCATATACCGTATATAAAATGCTAGAGTAATAAATGCAGTGTACTGATTCTACTGGA
108061  AGTGGTATATGGCATATATTTTACGATCTCATTATTTACGTCACATGACTAAGATGACCT

108121  AGGATTTTGTGTACTCTCTGGCTGTAATTGTTTTAACAATTGTTGCCTTTTCTACATATT
108121  TCCTAAAACACATGAGAGACCGACATTAACAAAATTGTTAACAACGGAAAAGATGTATAA

108181  TTGAAAATGTATCACAATCTCTCCAAATTTACTCTAGAACTCAATCTGATTAAAGAGCAC
108181  AACTTTTACATAGTGTTAGAGAGGTTTAAATGAGATCTTGAGTTAGACTAATTTCTCGTG
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FIGURE 4 (cont'd)

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108241  CATTTTAAAAGATAAATCAATGTATCTTGGGATTGTAACTAGATCCTGGTTCATTCAAGA
108241  GTAAAATTTTCTATTTAGTTACATAGAACCCTAACATTGATCTAGGACCAAGTAAGTTCT

108301  CAATTTCATATATCCACTATAGATATCAATATTTCTCTATTATCTTTAATATCCTGAGTA
108301  GTTAAAGTATATAGGTGATATCTATAGTTATAAAGAGATAATAGAAATTATAGGACTCAT

108361  CTCATTACTTTTCTTTGCTGTTTTTTTTTATTAGTTGGCAGAGACCATAGGGGTTCAGTG
108361  GAGTAATGAAAAGAAACGACAAAAAAAAATAATCAACCGTCTCTGGTATCCCCAAGTCAC

108421  AAGTGTTGGCAACGTGTATGATATTGAATTAAATGGCCAACGGTGGGAGAAAAACAGGCA
108421  TTCACAACCGTTGCACATACTATAACTTAATTTACCGGTTGCCACCCTCTTTTTGTCCGT

108481  TTTATTTCTATTAGAATTTTGATAATCATACCAAATTTAGAAGCGTATTTTTAGACTTGT
108481  AAATAAAGATAATCTTAAAACTATTAGTATGGTTTAAATCTTCGCATAAAAATCTGAACA

108541  TTACATTCTTAGGTTGTTCATTTCACAGTAGTAATTATAGAGACTAGAAATATAAATGAT
108541  AATGTAAGAATCCAACAAGTAAAGTGTCATCATTAATATCTCTGATCTTTATATTTACTA

108601  GTTTCCAAATACTTATGAAGTCTCAGTGTTAGTAGTTTCAATTAAATTTTTTAAAATGCA
108601  CAAAGGTTTATGAATACTTCAGAGTCACAATCATCAAAGTTAATTTAAAAAATTTTACGT

108661  GTTTATATTTGAAAGTAGCTACAGTAGCCTCTCTTGCTCTAATGTTATTTGGCTACAAAA
108661  CAAATATAAACTTTCATCGATGTCATCGGAGAGAACGAGATTACAATAAACCGATGTTTT

108721  AGAGGAAAATGGTAATTTAGATGTGGCTGAATTCAGAGCTAAGTACTAATTTTAGTGTTA
108721  TCTCCTTTTACCATTAAATCTACACCGACTTAAGTCTCGATTCATGATTAAAATCACAAT

108781  GTTGCAGACACTAACAAGATGAGTCTTATACTGCAGTCAGAGCTAGAATAAACAGAAGAT
108781  CAACGTCTCTGATTGTTCTACTCAGAATATGACGTCAGTCTCCATCTTATTTGTCTTCTA

108841  ATGGTGAGTAAGCCTTGTCCTGGGCTTGGCCATTGGTAGTCCTTGGCATATGAAAAACCA
108841  TACCACTCATTCGGAACAGGACCCGAACCGGTAACCATCAGGAACCGTATACTTTTTGGT

108901  GATACAGATCATTCTCATCCTTCCATTCCTGCTGTTTGTACTTGGCACTGTTTGAAAATA
108901  CTATGTCTAGTAAGAGTAGGAAGGTAAGGACGACAAACATGAACCGTGACAAACTTTTAT

108961  AAATTTATACAGGAATATTTATGATTTATAAATTTGAGTTACTGTATGTGACATATAACA
108961  TTTAAATATGTCCTTATAAATACTAAATATTTAAACTCAATGACATACACTGTATATTGT

109021  AAAGCTACACTTGGAAGATTGTAGCCAGTGTTGACCTCTGCACTTAGAAGATAATAGGCC
109021  TTTCGATGTGAACCTTCTAACATCGGTCACAACTGGAGACGTGAATCTTCTATTATCCGG

109081  GATTCAACCCTTCTTCCCATCTGCCCACTCTTACCCCCACCCCAAACTCCACCAAAAAAC
109081  CTAAGTTGGGAAGAAGGGTAGACGGGTGAGAATGGGGGTGGGGTTTGAGGTGGTTTTTTG

109141  CACACAGCTCAAAACAAAAACAGTTACATCATTCAGAGGTGGTACCATCATTATTTTTAT
109141  GTGTGTCGAGTTTTGTTTTTGTCAATGTAGTAAGTCTCCACCATGGTAGTAATAAAAATA

109201  CGATGGAGATGTCAGAATTTAAGTACACTCTGAATCAGAGCTACATGATTTAACCAGAA
109201  CCTACCTCTACAGTCTTAAATTCATGTGAGACTTAGTCTCGATGTACTAAATTGGTCTT

109261  ACACCAGAAACTGTCCTGGTGGAAAATTGTTCTTTATCCAAACAATAATCATGAAACATT
109261  TGTGGTCTTTGACAGGACCACCTTTTAACAAGAAATAGGTTTGTTATTAGTACTTTGTAA

109321  TCCACCATGGCTTTTAAAGGTCAGAATAGAAATGAGTGAGTTTGTCTTCTGCCTCTTGCA
109321  AGGTGGTACCGAAAATTTCCAGTCTTATCTTTACTCACTCAAACAGAAGACGGAGAACGT

109381  AAATATACAAGACCTTAAGACTGTTAGTTACTATTCAGATTATGGTTGCCTGGGATAACT
109381  TTTATATGTTCTGGAATTCTGACAATCAATGATAAGTCTAATACCAACGGACCCTATTGA

109441  TTAGTTTTAATATACTCCTTCACTTTGGGGATGTTCATCTAACAGAACAAATAAAATTCA
109441  AATCAAAATTATATGAGGAAGTGAAACCCCTACAAGTAGATTGTCTTGTTTATTTTAAGT

109501  GAATAAGGAGAAAGGAAATAGAATATATATTTGAAGTAAATAGAATGTTAGGAAAAACCT
109501  CTTATTCCTCTTTCCTTTATCTTATATATAAACTTCATTTATCTTACAATCCTTTTTGGA

109561  TTGCCCTAAAAAAAAAGACATGCAATTCTGAAGTAACTTTGATTTATATCATATGATTTT
109561  AACCCGATTTTTTTTTCTGTACGTTAAGACTTCATTGAAACTAAATATAGTATACTAAAA
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FIGURE 4 (cont'd)

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109621  AAGAAAATACAATGAACAAACGAGTTGAAAATCAGCACAATACTGATTTTCACAAACGTT
109621  TTCTTTTATGTTACTTGTTTGCTCAACTTTTAGTCGTGTTATGACTAAAAGTGTTTGCAA

109681  ACCGATAGGAGGTATAAACAGAGTTCTTTCGGTAATAGCCTGCCGTCTTTTCATGAGCGC
109681  TGGCTATCCTCCATATTTGTCTCAAGAAAGCCATTATCGGACGGCAGAAAAGTACTCGCG

109741  CCACACACACTGCTCCTGTTGGTTGAGATGGCTGGTGCAGGAAGGTGGATGGGGTGGTGG
109741  GGTGTGTGTGACGAGGACAACCAACTCTACCGACCACGTCCTTCCACCTACCCCACCACC

109801  ATAGTGTGTGTTCAAAGCACAGTGCTGTGCACAGTCACTATGTGTGGCACTCAGCTTGTA
109801  TATCACACACAAGTTTCGTGTCACGACACGTGTCAGTGATACACACCGTGAGTCGAACAT

109861  ACTCATGGGAGTTTTGATTTCAGTAACAGCACCCATGGTGGCAAGATCACACATCATCAC
109861  TGAGTACCCTCAAAACTAAAGTCATTGTCGTGGGTACCACCGTTCTAGTGTGTAGTAGTG

109921  TCTGTTGATGAGTAATTTAACCCATACGCTTGCTATTCACCATTTGAACAAAGCATTGTA
109921  AGACAACTACTCATTAAATTGGGTATGCGAACGATAAGTGGTAAACTTGTTTCGTAACAT

109981  TCATATCCTGGACCCTGGAGATACCCTGAAAAATAAGACCCAGGCCTTGTGGTTGAGTTC
109981  AGTATAGGACCTGGGACCTCTATGGGACTTTTTATTCTGGGTCCGGAACACCAACTCAAG

110041  ACAGTCACTTTGGGAAAACAACCACAGCAGTGAATCTCGGTATTGCTCAGGCCACATCAT
110041  TGTCAGTGAAACCCTTTTGTTGGTGTCGTCACTTAGAGCCATAACGAGTCCGGTGTAGTA

110101  GAGTCTTCTCGGACACGTCAGGCGTGTATACGGACTCGACTTGGAGCACTCTTCCTCAGA
110101  CTCAGAAGAGCCTGTGCAGTCCGCACATATGCCTGAGCTGAACCTCGTGAGAAGGAGTCT

110161  TGTCTGTACCGCTTGCTCTTTGACATCCTCCAAATCTTTGCTTACAAATCCCATTCTCAG
110161  ACAGACATGGCGAACGAGAAACTGTAGGAGGTTTAGAAACGAATGTTTAGGGTAAGAGTC

110221  TCTGGCTTTCCTTGAGCTCTTAATCAAAATCATAAACTCCATTTCCCATTTCTCCTCAGC
110221  AGACCGAAAGGAACTCGAGAATTAGTTTTAGTATTTGAGGTAAAGGGTAAAGAGGAGTCG

110281  ATTCCAGCATTCTCCATTGCTTTTCCTTCTTTGTTTCCCCCTGTGTAGTCTAACATACTA
110281  TAAGGTCGTAAGAGGTAACGAAAAGGAAGAAACAAAGGGGGACACATCAGATTGTATGAT

110341  TCAACACAATAAATGTTTACCTGTGTCTATTAGAAAGTAAGCAGGGAGATATGTCAGTTT
110341  AGTTGTGTTATTTACAAATGGACACAGATAATCTTTCATTCGTCCCTCTATACAGTCAAA

110401  TGTTCACTGCTGTATTCATAGAGCTTAAAACGGTAAACAGCACTCAATATGTATTTGTAG
110401  ACAAGTGACGACATAAGTATCTCGAATTTTGCCATTTGTCGTGAGTTATACATAAACATC

110461  AATAAATGGCTAATTGTGCTGATGGTGTTTAGGGCACTTATGCAGACCTACATTCCTGGT
110461  TTATTTACCGATTAACACGACTACCACAAATCCCGTGAATACGTCTGGATGTAAGGACCA

110521  TTCCATTAGTGTTTGACTTTGGCAAGTCACAGATGAATCCTGCTGTTATTGCTTCTAAAT
110521  AAGGTAATCACAAACTGAAACCGTTCAGTGTCTACTTAGGACGACAATAACGAAGATTTA

110581  TCCTCATCTCCTAAAAATGACTTCTTTGTCAAAAACAAGCTGCATTTGTAGGTTCTGTTT
110581  AGGAGTAGAGGATTTTTACTGAAGAAACAGTTTTTGTTCGACGTAAACATCCAAGACAAA

110641  TCCTCATGTTGGGCAATCTGGAGTGATTTCTGGCTCTTGTAAGTATGTTTGTGGTTGCAG
110641  AGGAGTACAACCCGTTAGACCTCACTAAAGACCGAGAACATTCATACAAACACCAACGTC

110701  AGGAAAATGAATATTTCTCACCCAAATGTTGTCATGTCATCATCTCTGTCTGGCAACCAG
110701  TCCTTTTACTTATAAAGAGTGGGTTTACAACAGTACAGTAGTAGAGACAGACCGTTGGTC

110761  AGAAGCAGATGTTCTGTTCCTTGACCTCAGGCTAGTGGTTACAGTTCTGGGTGTTAAACA
110761  TCTTCGTCTACAAGACAAGGAACTGGAGTCCGATCACCAATGTCAAGACCCACAATTTGT

110821  TGTTTCACAAAACAGCACTTGCACATGCGGGGCTGCTGTTTTCATTTAACTTCATGTAGT
110821  ACAAAGTGTTTTGTCGTGAACGTGTACGCCCCGACGACAAAAGTAAATTGAAGTACATCA

110881  CTCAGGGCTCAGCAAGCTTTAGGAAAGGTCCGGTTTGGGGGCACTGGAAGTGTGTGTGTG
110881  GAGTCCCGAGTCGTTCGAAATCCTTTCCAGGCCAAACCCCCGTGACCTTCACACACACAC
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FIGURE 4 (cont'd)

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110941   TGTGTACATATATATACACACACAAATAGATCCATACATTTATGTATCTAGTTGGCTAGC
110941   ACACATGTATATATATGTGTGTGTTTATCTAGGTATGTAAATACATAGATCAACCGATCG

111001   TATTGCAAAACACATGTTTATTTTGAGATCATCAACACTTCTAAACATGACAAAGAGTAG
111001   ATAACGTTTTGTGTACAAATAAAACTCTAGTAGTTGTGAAGATTTGTACTGTTTCTCATC

111061   CCCTAAGAACATTGCCAAGAACAAATTTTCTCCTTTCCAGAAAGCAATTTTCAGCAGATG
111061   GGGATTCTTGTAACGGTTCTTGTTTAAAAGAGGAAAGGTCTTTCGTTAAAAGTCGTCTAC

111121   ATTTTCAGAAACAAAATTCAAAAAAGCCATACTGCTGTATCCTAGCAAAGATAACTTATT
111121   TAAAAGTCTTTGTTTTAAGTTTTTTCGGTATGACGACATAGGATCGTTTCTATTGAATAA

111181   CGTTTATTTTTTACTCAAAAACATTTATTATATACACTCTGGGCTAGGCACAATGCCCAG
111181   GCAAATAAAAAATGAGTTTTTGTAAATAATATATGTGAGACCCGATCCGTGTTACGGGTC

111241   TTTTGAGGATAGAAGGATGAAGATAGAGTTTGGTATTCCAGATAGAGCTTGATTGTTGGG
111241   AAAACTCCTATCTTCCTACTTCTATCTCAAACCATAAGGTCTATCTCGAACTAACAACCC

111301   CATGTCTGATGTAACCCCAGTGGAGTGGGCGAGCCTAGAACCACCATGTATTGAGGGAGA
111301   GTACAGACTACATTGGGGTCACCTCACCCGCTCGGATCTTGGTGGTACATAACTCCCTCT

111361   GGGTGGTGGCCTCAGTGTCAGGACTCACTAGATTCAGACTCCTGGGTGTCAGAAGTGGGG
111361   CCCACCACCGGAGTCACAGTCCTGAGTGATCTAAGTCTGAGGACCCACAGTCTTCACCCC

111421   AGGAAAGGGAGATGCTGAGTGCCAGAGGGTACTGTAAGGAGAGCTTGTGCAGCTGATGGA
111421   TCCTTTCCCTCTACGACTCACGGTCTCCCATGACATTCCTCTCGAACACGTCGACTACCT

111481   TCATGCATGATGCCTGTGAACAATTGTCCTACTAGACCTCACAGTAGTTAGGGATGTCTG
111481   AGTACGTACTACGGACACTTGTTAACAGGATGATCTGGAGTGTCATCAATCCCTACAGAC

111541   CAGTCATCTCACAGTAGAGCAGTAGCTCAGCTTTGGAGTTTTGTTTCTTGAATGTCTTCT
111541   GTCAGTAGAGTGTCATCTCGTCATCGAGTCGAAACCTCAAAACAAAGAACTTACAGAAGA

111601   TTTTTAACCGTACACGTGCTTGAGCTCACTCTGATAAGCCCATTACATTTGAATCTCAGA
111601   AAAAATTGGCATGTGCACGAACTCGAGTGAGACTATTCGGGTAATGTAAACTTAGAGTCT

111661   GAGCAAAGGCAGCATCTCCATACTTGTTGCTGATGCTCCACCAGGTTTGAAAATCACTAA
111661   CTCGTTTCCGTCGTAGAGGTATGAACAACGACTACGAGGTGGTCCAAACTTTTAGTGATT

111721   AGATAGACTCTTAGGCTGGGTGCGGTGGCTCACATCTGTAATCTCAGCACTTTGGGAGGC
111721   TCTATCTGAGAATCCGACCCACGCCACCGAGTGTAGACATTAGAGTCGTGAAACCCTCCG

111781   CGAAGTGGGCAGATCATCTGAGCTCAGGAGTTCGAGACCAGCCTGACCAACATGGTGAAA
111781   GCTTCACCCGTCTAGTAGACTCGAGTCCTCAAGCTCTGGTCGGACTGGTTGTACCACTTT

111841   CCCCGTCTCTACTAAAAATACAAAAATTAGCCAGGCGTGGTGGCGCGTACCTGTAATCCC
111841   GGGGCAGAGATGATTTTTATGTTTTTAATCGGTCCGCACCACCGCGCATGGACATTAGGG

111901   AGCTACTCAGGAGGCTGAGGCAGGAGAATCACTTGACCCTGGGAGGCAGAGGGTGCAGTG
111901   TCGATGAGTCCTCCGACTCCGTCCTCTTAGTGAACTGGGACCCTCCGTCTCCCACGTCAC

111961   AGCTGAGATGGTGCCACTGCACTCCAGCCTGGGTAACCTAAAAAAAAAAAAAAAAAAAAA
111961   TCGACTCTACCACGGTGACGTGAGGTCGGACCCATTGGATTTTTTTTTTTTTTTTTTTTT

112021   AAATTAGACTTTCCAAGGGCAGCGTGGAAGCAGTGACCAGCCTGAGTAGGCACGCACACT
112021   TTTAATCTGAAAGGTTCCCGTCGCACCTTCGTCACTGGTCGGACTCATCCGTGCGTGTGA

112081   TCTTGGGGATAGCCTCCTCCATAGCATTCTTAGAAGGTTTGGTAATGACCAGTTTTTCTG
112081   AGAACCCCTATCGGAGGAGGTATCGTAAGAATCTTCCAAACCATTACTGGTCAAAAAGAC

112141   AGTAAGACCCTATCTACATTATTCTAATTAGTAACCACCTTTCATCTGCTAAGGTAAATT
112141   TCATTCTGGGATAGATGTAATAAGATTAATCATTGGTGGAAAGTAGACGATTCCATTTAA

112201   TTCACTTCAGAATATTCCTCTTAAGACCATGCAATAACTCTTACTGTTTGTTGGTGGAAA
112201   AAGTGAAGTCTTATAAGGAGAATTCTGGTACGTTATTGAGAATGACAAACAACCACCTTT
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FIGURE 4 (cont’d)

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112261   ACCATCTCATTATTTTACTGGTTAAGGGTAAACTGAAGATGATTAGATAACTTTCCTTCC
112261   TGGTAGAGTAATAAAATGACCAATTCCCATTTGACTTCTACTAATCTATTGAAAGGAAGG

112321   TTCCCTCCCCCCTTCCTCCCTTCCTTCTCTTTCTTCCTTCCTTTCTCCCTCCCTCCCTCC
112321   AAGGGAGGGGGGAAGGAGGGAAGGAAGAGAAAGAAGGAAGGAAAGAGGGAGGGAGGGAGG

112381   CTCTCTCTTTCTTTCCTTCTCTCTTTCTTTTCTTTTCTTTTTTCTTTCTTTCTTTCTTTT
112381   GAGAGAGAAAGAAAGGAAGAGAGAAAGAAAAGAAAAGAAAAAAGAAAGAAAGAAAGAAAA

112441   TTCTTTCTTCCTTCCTTCGTTCCTTCCTCCCTCCCTCCCTCTCTCTCTTTCTTTCTTTCT
112441   AAGAAAGAAGGAAGGAAGCAAGGAAGGAGGGAGGGAGGGAGAGAGAGAAAGAAAGAAAGA

112501   CTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTCTCTTTCTT
112501   GAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAGAGAAAGAA

112561   TTCTTTCTTTCTTTCTTTCTCTTTCTCTTTCCTTCCTTCCTTCCTTTCTTTCTCTCTCTC
112561   AAGAAAGAAAGAAAGAAAGAGAAAGAGAAAGGAAGGAAGGAAGGAAAGAAAGAGAGAGAG

112621   TCCTTCCTTCCTTCCTTCTTTCCTTCCTTCCTTCTTTCCTTCCTTCCTTCTTTCTTCTTT
112621   AGGAAGGAAGGAAGGAAGAAAGGAAGGAAGGAAGAAAGGAAGGAAGGAAGAAAGAAGAAA

112681   TTTTAAATAAGGGTCTACCTGAAGTGTGAACTGATTTGGGAAATTTGATCATGCAGAACA
112681   AAAATTTATTCCCAGATGGACTTCACACTTGACTAAACCCTTTAAACTAGTACGTCTTGT

112741   GTAAAATTTTCTTTATGTTTGTTGCTAGCAAAATTGTGATGGTTTTTTAAAAAAATGGCT
112741   CATTTTAAAAGAAATACAAACAACGATCGTTTTAACACTACCAAAAAATTTTTTTACCGA

112801   ATTGATAATAAGGCATGCCTAATGTAGTGAAAGTTTGAAAATGTCCCAATTTCTGATTGA
112801   TAACTATTATTCCGTACGGATTACATCACTTTCAAACTTTTACAGGGTTAAAGACTAACT

112861   CAGAAGAAGAACTGGCAACTCCTCCACTAGATGGCATCATTCTTCCAGGAGTGACAAGGC
112861   GTCTTCTTCTTGACCGTTGAGGAGGTGATCTACCGTAGTAAGAAGGTCCTCACTGTTCCG

112921   GGTGCATTCTGGACCTGGCACATCAGTGGGTGGGTGCCTTTGATATGAACAACTTTTGTA
112921   CCACGTAAGACCTGGACCGTGTAGTCACCCACCCACGGAAACTATACTTGTTGAAAACAT

112981   AGCCTGAAATAAAAAATAATCAAAATAAGCCCAGCCTAGTCTTGAAATAATATCCTGTGG
112981   TCGGACTTTATTTTTTATTAGTTTTATTCGGGTCGGATCACAACTTTATTATAGGACACC

113041   TTCCAACCAATGTTATCTAATCTTTAAATTCTAACGTGAATGAAAAGTATTCTTCTAGAA
113041   AAGGTTGGTTACAATAGATTAGAAATTTAAGATTGCACTTACTTTTCATAAGAAGATCTT

113101   GGGCTTTCTTGGCAAGACTATTAAAATAAGTATTGTTGATAGCAAGGGCAGAGAGAAACC
113101   CCCGAAAGAACCGTTCTGATAATTTTATTCATAACAACTATCGTTCCCGTCTCTCTTTGG

113161   AGTTTAGCAAGATGTCATAGTGGAGAAGTATTCTAGTAGTAGTCTCAGTCTACCAGGTAT
113161   TCAAATCGTTCTACAGTATCACCTCTTCATAAGATCATCATCAGAGTCAGATGGTCCATA

113221   CTCCCACCAACTTTTGTCTGGTTCATACCTGATGTGCTTCCATCCAGACATTCCTTAACT
113221   GAGGGTGGTTGAAAACAGACCAAGTATGGACTACACGAAGGTAGGTCTGTAAGGAATTGA

113281   TCCCAAGTCTGTGTTGCTTCCAAATGGCAATGATACTTCTTCCTTTCCTTTATTTATACC
113281   AGGGTTCAGACACAACGAAGGTTTACCGTTACTATGAAGAAGGAAAGGAAATAAATATGG

113341   AGTGTAACCATGCTTGCCGTAGAAATGAAATAATTTCACTGACATATAAATGTTTACTAA
113341   TCACATTGGTACGAACGGCATCTTTACTTTATTAAAGTGACTGTATATTTACAAATGATT

113401   TATAACATTATTGGTTTGACTCCCTTCTTTTTCTCTCTGTCCTACCCCCATCCTCCAAAA
113401   ATATTGTAATAACCAAACTGACGGAAGAAAAAGAGAGACAGGATGGGGGTAGGAGGTTTT

113461   TTCATATACATGCCTATTTTAAAATCAGAACATGCAAGCAAATGTAAAGTTGTTTTCAGT
113461   AAGTATATGTACGGATAAAATTTTAGTCTTGTACGTTCGTTTACATTTCAACAAAAGTCA

113521   AGACTTTCAAATTCGTGTGACACAGGCAAGCATATTAAACAATTTGGTGGACCGGGTGCA
113521   TCTGAAAGTTTAAGCACACTGTGTCCGTTCGTATAATTTGTTAAACCACCTGGCCCACGT
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FIGURE 4 (cont'd)

113581 GTGGTTCATGCCTATAATTCTAGCATTTTGGGAGGCCAAGGCAGGAGGATCACTTAAGCC
113581 CACCAAGTACGGATATTAAGATCGTAAAACCCTCCGGTTCCGTCCTCCTAGTGAATTCGG

113641 CAGGAATTCGAGACCAGCCTGGGCAACATAGTGAGACCCCGAATCTACAAAAAAATCAAA
113641 GTCCTTAAGCTCTGGTCGGACCCGTTGTATCACTCTGGGGCTTAGATGTTTTTTTAGTTT

113701 AACATTAGCTGAACATGGTGGTACATGCCTGTAGTCCCAGCTACTTGGAGGGGCTGAGGT
113701 TTGTAATCGACTTGTACCACCATGTACGGACATCAGGGTCGATGAACCTCCCCGACTCCA

113761 GGGAGGATGGCATAAGATCTGGAGGTCAAGGTCGCAGTGAGCTATGATCAAGCCACTGCA
113761 CCCTCCTACCGTATTCTAGACCTCCAGTTCCAGCGTCACTCGATACTAGTTCGGTGACGT

113821 CTACAGCCTGAATACAGGGTGAGACCATGTCTCTAAAAGTAAATTAAATAAATAAATAAA
113821 GATGTCGGACTTATGTCCCACTCTGGTACAGAGATTTTCATTTAATTTATTTATTTATTT

113881 TAAATAAATAAATAAATAAATAAATAAAATAAAATTTAAAAAGGTTTGGTTTTGGAAATG
113881 ATTTATTTATTTATTTATTTATTTATTTTATTTTAAATTTTTCCAAACCAAAACCTTTAC

113941 ACGTAATGTATTCAAGACAAATTATTGAATGAATTGGGTGTCTGGTAAAGGTTCTTGGAT
113941 TGCATTACATAAGTTCTGTTTAATAACTTACTTAACCCACAGACCATTTCCAAGAACCTA

114001 GGAACTTTTGACCCAGGTGTTAAAATGGTCTCCAAAGAACATGAAAAGGCTTTGAGCTTA
114001 CCTTGAAAACTGGGTCCACAATTTTACCAGAGGTTTCTTGTACTTTTCCGAAACTCGAAT

114061 CTGTGGTCAAAGAGTACTAGTAGTAATAGGACAAATGTTTAGAAACACACACGTTATCTA
114061 GACACCAGTTTCTCATGATCATCATTATCCTGTTTACAAATCTTTGTGTGTGCAATAGAT

114121 GGAGCATACCAGCATGGTTTCTCTGGAAAAGACTTTCAAAATAGATGAAATGTGCTATAA
114121 CCTCGTATGGTCGTACCAAAGAGACCTTTTCTGAAAGTTTTATCTACTTTACACGATATT

114181 ATAATTCTACAAAACCCTGAAGTAGACAAGACCCAACTGCTACATGCTGGCTGGCGCATT
114181 TATTAAGATGTTTTGGGACTTCATCTGTTCTGGGTTGACGATGTACGACCGACCGCGTAA

114241 GGGCATGACATTTACAAACCGTTGGTATAATTTTCAAACAGCTTGCCCTGTCCTAAATAT
114241 CCCGTACTGTAAATGTTTGGCAACCATATTAAAAGTTTGTCGAACGGGACAGGATTTATA

114301 GTTTGCAATTGGAAAGATATTTTTGAAGCTCAGTAATTTTTGTTTTATTAAAGAAAAATA
114301 CAAACGTTAACCTTTCTATAAAAACTTCGAGTCATTAAAAACAAAATAATTTCTTTTTAT

114361 TCAACCAAGTACAGAAGGTTCGACGACAAGTTGCAAGTGGAAATACTTTCCCACACTAAT
114361 AGTTGGTTCATGTCTTCCAAGCTGCTGTTCAACGTTCACCTTTATGAAAGGGTGTGATTA

114421 GATTTGCTAGCATGAAAAATAGGTTATTATGGAGGAAATTTTTTCTTGACTTCATAGCTG
114421 CTAAACGATCGTACTTTTTATCCAATAATACCTCCTTTAAAAAAGAACTGAAGTATCGAC

114481 TAATTTATTTTAAAAGCTATTTTAAAACATGAGACGTGAAATGCCAAGAGGCATGTAGGG
114481 ATTAAATAAAATTTTCGATAAAATTTTGTACTCTGCACTTTACGGTTCTCCGTACATCCC

114541 GGTCACCACTATTTGCCAGATAGGGGAAATTGTCCAAAGATAAGTAAGGGTGAGCAGAGC
114541 CCAGTGGTGATAAACGGTCTATCCCCTTTAACAGGTTTCTATTCATTCCCACTCGTCTCG

114601 AAAAACAATTCTGCTTATTTACAAAAGAGTTTTCTTTTCTTTTCTTTTTCAGGACACAGA
114601 TTTTTGTTAAGACGAATAAATGTTTTCTCAAAAGAAAAGAAAAGAAAAAGTCCTGTGTCT

114661 ACTCAGCTTGTTTTCAATTAATTTGCCTGATTTTCTGCAGTTCATTTACTTTTGAACAAC
114661 TGAGTCGAACAAAAGTTAATTAAACGGACTAAAAGACGTCAAGTAAATGAAAACTTGTTG

114721 ATAATTGCAATTGTAGACTGAGAGAAATTGAAACTTTCAAAGAGCCATATTTCTATTGCA
114721 TATTAACGTTAACATCTGACTCTCTTTAACTTTGAAAGTTTCTCGGTATAAAGATAACGT

114781 GATATATTTTCCTGCTCTTCCAAATCTACTTACAGCATGAGTTCTTCTTTTAAATATTCA
114781 CTATATAAAAGGACGAGAAGGTTTAGATGAATGTCGTACTCAAGAAGAAAATTTATAAGT

114841 AATATTTTGAATATTGCCAAGAGCTTTGATTTCCATTTTTATCTCTTGTGGGTTTATAAA
114841 TTATAAAACTTATAACGGTTCTCGAAACTAAAGGTAAAAATAGAGAACACCCAAATATTT

114901 TTAAGAAAAAATACTCATCTTATTTTTTTAAACCTCTCTATTTTTATTGCCCTTTATTCA
114901 AATTCTTTTTTATGAGTAGAATAAAAAAATTTGGAGAGATAAAAATAACGGGAAATAAGT

FIGURE 4 (cont'd)

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114961  AATAACTTGTTGACAAACTTTGAACTTCAACCACTGAGGTAAAAGAACAAGAATTAAACA
114961  TTATTGAACAACTGTTTGAAACTTGAACTTGGTGACTCCATTTTCTTGTTCTTAATTTGT

115021  GATAGTTTAAACACATAGCTTAAAAGGATCTTTTTCCCATTTCCTATCCTTGAGCAAAGA
115021  CTATCAAATTTGTGTATCGAATTTTCCTAGAAAAAGGGTAAAGGATAGGAACTCGTTTCT

115081  ATATATTCAAACACTTTGGCAGAAGTCAATGAGGTTATACCACTAATTCCATGATGAAAA
115081  TATATAAGTTTGTGAAACCGTCTTCAGTTACTCCAATATGGTGATTAAGGTACTACTTTT

115141  TCAACTGAATGTGATACTGAAAGAGAAGGAAGAGAATTGTCACTGTAAAGTCAACTGTTA
115141  AGTTGACTTACACTATGACTTTCTCTTCCTTCTCTTAACAGTGACATTTCAGTTGACAAT

115201  GTCATATTAGGAAAAAAAATACATACAATACAATTTCTCAAATAAAGTCCAAATATACAT
115201  CAGTATAATCCTTTTTTTTATGTATGTTATGTTAAAGAGTTTATTTCAGGTTTATATGTA

115261  TCAACGTTTAAAAATAATGAGTATTTCAGATATTTGAACTCAGTCTGTTCTTTATTCCAT
115261  AGTTGCAAATTTTTATTACTCATAAAGTCTATAAACTTGAGTCAGACAAGAAATAAGGTA

115321  AAAAGATATAGGTAAGCCGTGCACAGTGGCTCACAACTATAATCCCAGCACTTTGGCACT
115321  TTTTCTATATCCATTCGGCACGTGTCACCGAGTGTTGATATTAGGGTCGTGAAACCGTGA

115381  TTGGGAGGCTGAGGTGGGAGGATCACATGAGCCCAGCCTGGGCAACATAGGGAGACCCCT
115381  AACCCTCCGACTCCACCCTCCTAGTGTACTCGGGTCGGACCCGTTGTATCCCTCTGGGGA

115441  ATCTTTACAAAATAAAATATAAAATATAAAACCTAGTTGGGCATGGCAGCATACACCTGT
115441  TAGAAATGTTTTATTTTATATTTTATATTTTGGATCAACCCGTACCGTCGTATGTGGACA

115501  AGTCCCAGGTGCTCAGGAGACTGAGACAGGAGGATCACTTGGGCCTGGGAGGTCGAGGCT
115501  TCAGGGTCCACGAGTCCTCTGACTCTGTCCTCCTAGTGAACCCGGACCCTCCAGCTCCGA

115561  GCAATGAGCCAAGATTATGCCACTGCATTCCAGCCTGGGTGACAGGGCAAGACCCTGTCT
115561  CGTTACTCGGTTCTAATACGGTGACGTAAGGTCGGACCCACTGTCCCGTTCTGGGACAGA

115621  TAAAAAAAAAAAAAAAAGAAAGAGACAAACGTAGAAAGAGTACCAAATTTGGAGCCAATC
115621  ATTTTTTTTTTTTTTTTCTTTCTCTGTTTGCATCTTTCTCATGGTTTAAACCTCGGTTAG

115681  AGATCAGACCTGGGTTCAAATTGAGTTTCTGTCACTTACTTCCTTTGTGGCCCTGGAGAT
115681  TCTAGTCTGGACCCAAGTTTAACTCAAAGACAGTGAATGAAGGAAACACCGGGACCTCTA

115741  GCCCTTCAACCTCCTTGAACCTTAGTTTCCTCATCTGTAAAATGGGGATGATAGTACTCA
115741  CGGGAAGTTGGAGGAACTTGGAATCAAAGGAGTAGACATTTTACCCCTACTATCATGAGT

115801  CCCTTAAAATTACAGAACTTGGCATAATAGCGGGTGCTTGATAAATGGTAGCTATAATTA
115801  GGGAATTTTAATGTCTTGAACCGTATTATCGCCCACGAACTATTTACCATCGATATTAAT

115861  TTAATATTATATAATACATTGTTCTCCTTTATGGTAAAGTAGGTTTTAAGACACTGATTT
115861  AATTATAATATATTATGTAACAAGAGGAAATACCATTTCATCCAAAATTCTGTGACTAAA

115921  TTTTGTTTTGTTTTGTTTTTGGAGACAGAGTCTCACTCCGTCACCCAGGCTGGACTGCAG
115921  AAAACAAAACAAAACAAAAACCTCTGTCTCAGAGTGAGGCAGTGGGTCCGACCTGACGTC

115981  TGACGTGATCTTGGTTCACTGCAACCTCTGCCTCCTGAGTTCAAGCGATTCTCCTGCCTC
115981  ACTGCACTAGAACCAAGTGACGTTGGAGACGGAGGACTCAAGTTCGCTAAGAGGACGGAG

116041  AGCCTCCTGAGTAGCTGGGATTACAGGCACCCGCCACCATGCCTGGCTAATTTTTGTATT
116041  TCGGAGGACTCATCGACCCTAATGTCCGTGGGCGGTGGTACGGACCGATTAAAAACATAA

116101  TTTAGTAGAGACAGGGTTTTACCAGGTTGGCCAGGCTGGTCTCAAACTCCTGACCTCAAG
116101  AAATCATCTCTGTCCCAAAATGGTCCAACCGGTCCGACCAGAGTTTGAGGACTGGAGTTC

116161  TAATCTGCCTGCCTCAGCCTCCCCAAATGCAGAGATTACAGGCATGAGCCACCGTGCCCG
116161  ATTAGACGGACGGAGTCGGAGGGGTTTACGTCTCTAATGTCCGTACTCGGTGGCACGGGC

116221  GCCTAAGACACTGTTAACACGGAGCATGCATCAAGCAGCATTTGGGATGCATCAATTTTG
116221  CGGATTCTGTGACAATTGTGCCTCGTACGTAGTTCGTCGTAAACCCTACGTAGTTAAAAC
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FIGURE 4 (cont'd)

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116281   TGAGACTTTATACAAGTTAACAAATAAGAAGGCAAAAAAGAAGGCATATGTTAAAGTATA
116281   ACTCTGAAATATGTTCAATTGTTTATTCTTCCGTTTTTTCTTCCGTATACAATTTCATAT

116341   CCATGTGTCTTGTGGTGATAATCTTATATTTTATATTCTGATAATCTCATATATAAATCT
116341   GGTACACAGAACACCACTATTAGAATATAAAATATAAGACTATTAGAGTATATATTTAGA

116401   GTGACCTTGAAGTAGGTTACTTAACACCTCGATGTGTTCACCAGTAAGATGGTGTGCCAC
116401   CACTGGAACTTCATCCAATGAATTGTGGAGCTACACAAGTGGTCATTCTACCACACGGTG

116461   TTCCAGCTTTCCCTTAAAGGATGATTGTGACCTTGTCTAAGTGCAATCAGAATGTTAAGC
116461   AAGGTCGAAAGGGAATTTCCTACTAACACTGGAACAGATTCACGTTAGTCTTACAATTCG

116521   AGAACAGTAAGTATTGCAATTGTTTTGCATGCCTTTTCCTTTAAAATATACTTGTTATTT
116521   TCTTGTCATTCATAACGTTAACAAAACGTACGGAAAAGGAAATTTTATATGAACAATAAA

116581   TTTATATTCCATGCAGGGTGAATTTAAGGTGTCAGAGAGATACCTCACCATGGATGACTT
116581   AAATATAAGGTACGTCCCACTTAAATTCCACAGTCTCTCTATGGAGTGGTACCTACTGAA

116641   GACAACAGCCCTGGAGGGGAACAGAGTGAGAGAGATGTTTGGCTCTGGTACAGCCTGTGT
116641   CTGTTGTCGGGACCTCCCCTTGTCTCACTCTCTCTACAAACCGAGACCATGTCGGACACA

116701   TGTTTGCCCAGTTTCTGATATACTGTACAAAGGCGAGGTACGACAAGTATTTCCTCATTT
116701   ACAAACGGGTCAAAGACTATATGACATGTTTCCGCTCCATGCTGTTCATAAAGGAGTAAA

116761   CCTATCATTTCCAATCACATTAAATTACATTTAATTTAAGTGTATGAATAAAATTGTATC
116761   GGATAGTAAAGGTTAGTGTAATTTAATGTAAATTAAATTCACATACTTATTTTAACATAG

116821   TGGACCCAGACCCAAGATGCAAAAGTTTTGTCGTTGTTGTTGTTTTTCTTTATTTTAAAG
116821   ACCTGGGTCTGGGTTCTACGTTTTCAAAACAGCAACAACAACAAAAAGAAATAAAATTTC

116881   AGATGGAGTCTCGCTGTGTTGCCCAGGCTGGAGTGCAGTGGCTATTCACTGGTGTGATCA
116881   TCTACCTCAGAGCGACACAACGGGTCCGACCTCACGTCACCGATAAGTGACCACACTAGT

116941   TAGCTCACTGCAGCCTCAAACTCCTGGGCTCACGCAATCCTTCTGCTTCAGCCTCCTGAG
116941   ATCGAGTGACGTCGGAGTTTGAGGACCCGAGTGCGTTAGGAAGACGAAGTCGGAGGACTC

117001   TTGCTGGGATTACAGGAGTGCGCCACCGCACCATGCTAGGTCTTTTTTGTTGTTGTTTTT
117001   AACGACCCTAATGTCCTCACGCGGTGGCGTGGTACGATCCAGAAAAAACAACAACAAAAA

117061   GTTTTTTAACTTGGCACTACAAAAAAAATAACTGGGACAGTTTATCCAGATGAAACTGTA
117061   CAAAAAATTGAACCGTGATGTTTTTTTTATTGACCCTGTCAAATAGGTCTACTTTGACAT

117121   TTAGCATATATCTACTATGTTTCCAGTGATTTCATGTAAGCTTAAACATGGTGGGAAGTT
117121   AATCGTATATAGATGATACAAAGGTCACTAAAGTACATTCGAATTTGTACCACCCTTCAA

117181   AGTTTTGTCCTTGGACACGTGTAAGATCTGTCTTACCTACATGTCGGGATTGGAGCTATG
117181   TCAAAACAGGAACCTGTGCACATTCTAGACAGAATGGATGTACAGCCCTAACCTCGATAC

117241   CCGACAGTCTTCTACTCTTCTCTCTTCCTTCCTACCAGCTCACTAGGGAAGGCTCTATAG
117241   GGCTGTCAGAAGATGAGAAGAGAGAAGGAAGGATGGTCGAGTGATCCCTTCCGAGATATC

117301   GTAGTTACATTTCAGTTTCTGGTTAACCAAAAGTACTTCCAAACCACTGGATTAGGAATG
117301   CATCAATGTAAAGTCAAAGACCAATTGGTTTTCATGAAGGTTTGGTGACCTAATCCTTAC

117361   GCAAATAGTTATGGAAAATGCATTCGAGTGGTCAATCCCTTGATTTTTTTTTACTATTAA
117361   CGTTTATCAATACCTTTTACGTAAGCTCACCAGTTAGGGAACTAAAAAAAAATGATAATT

117421   TGCTGTTATCATTAATAGTAAGTAGACCACTTTACAAGAATTATTCATTGGCAAACCTGG
117421   ACGACAATAGTAATTATCATTCATCTGGTGAAATGTTCTTAATAAGTAACCGTTTGGACC

117481   TGCATTTACTAAAATCTTACAAAAGGAATTTGAGGATTTGGTTGGAAGAAATGTTCTCCT
117481   ACGTAAATGATTTTAGAATGTTTTCCTTAAACTCCTAAACCAACCTTCTTTACAAGAGGA

117541   CTTAGTAAATTAGTCTGATTTTATATGTGCCATACTTTTGTTTTCTTGTCAAATTGTTTT
117541   GAATCATTTAATCAGACTAAAATATACACGGTATGAAAACAAAAGAACAGTTTAACAAAA

117601   GCTTTTCACTTTATAACAAAGCTCCAATACTTATGATTAACATTGCCATCTAACTTTATA
117601   CGAAAAGTGAAATATTGTTTCGAGGTTATGAATACTAATTGTAACGGTAGATTGAAATAT
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FIGURE 4 (cont'd)

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117661  ACTTAAAGCCATCTAAGTATTAGTCTTATAATGTGAACTGGCTTAAGTTATTCATATTAT
117661  TGAATTTCCCTACATTCATAATCAGAATATTACACTTGACCGAATTCAATAAGTATAATA

117721  AGCAGATCCTTGAACAACACAGGGATTAGGGGTGTCAACCCCCATGCAGTTGAAAAATCC
117721  TCGTCTAGGAACTTGTTGTGTCCCTAATCCCCACAGTTGGGGGTACGTCAACTTTTTAGG

117781  ACATACAACTTTTTTTGTTTGTTTGTTTTTTTAAACGGGGTCTTTCTCTGTCACCTGTAC
117781  TGTATGTTGAAAAAAACAAACAAACAAAAAAATTTGCCCCAGAAAGAGACAGTGGACATG

117841  TGGAGTGCAGGGGCACAATCTCGGCTCACTGCAACCTCCGCCTCCCAAGCTCAAGCGATC
117841  ACCTCACGTCCCCGTGTTAGAGCCGAGTGACGTTGGAGGCGGAGGGTTCGAGTTCGCTAG

117901  CTCTCACCTCAGTCTCCCAAGTAGCTGGGACCACAGGTGTGCACCACCACACCCAGCTAA
117901  GAGAGTGGAGTCAGAGGGTTCATCGACCCTGGTGTCCACACGTGGTGGTGTGGGTCGATT

117961  TTTTAGTATTTTTTTGTAGAGACGGGGTTTCAAGATGTTTCACAGGCTGGTCTCAAACTCT
117961  AAAATCATAAAAAACATCTCTGCCCCAAAGTTCTACAAAGTGTCCGACCAGAGTTTGAGA

118021  TGAGTTCAAGTGATTCACCTGCCTTGACCTCCCAAAGTGCTGGTATTACAGGCGTGAGTC
118021  ACTCAAGTTCACTAAGTGGACGGAACTGGAGGGTTTCACGACCATAATGTCCGCACTCAG

118081  ACCATGCCCGGCCCACATATAACTTTTGACTTCCCAAAAACTTAACTACTAGTAGCCTGC
118081  TGGTACGGGCCGGGTGTATATTGAAAACTGAAGGGTTTTTGAATTGATGATCATCGGACG

118141  TGTTCACCGGAAGCCTTATCAACAACAAAAACAGTCGATTGGCACATATTTTGTATGTTA
118141  ACAAGTGGCCTTCGGAATAGTTGTTGTTTTTGTCAGCTAACCGTGTATAAAACATACAAT

118201  TGTATGTTATATATGTATTCTTACAATAAAGTAAGTTACGAAAATCATGGGGAAGGGAAA
118201  ACATACAATATATACATAAGAATGTTATTTCATTCAATGCTTTTAGTACCCCTTCCCTTT

118261  ATATATTTACTATTCATTACATGGAAGTGGATCATCATAAAGGTCTTCATCCTCATTGTC
118261  TATATAAATGATAAGTAATGTACCTTCACCTAGTAGTATTTCCAGAAGTAGGAGTAACAG

118321  CATCATGTTGAGTAGGCTGAGGAGGAGGAGGAGGAGGGATTGGTCTTGCTGTTTTAG
118321  GTAGTACAACTCATCCGACTCCTCCTCCTCCTCCTCCCTAACCAGAACGACAAAATC

118381  GAGTGGCAGAGGCAGAAGAAAGTCCACGTATAAGTGAACTTGTGTAGTTCAAACCCGTGT
118381  CTCACCGTCTCCGTCTTCTTTCAGGTGCATATTCACTTGAACACATCAAGTTTGGGCACA

118441  TGTTCAAGTGTCAACCGTAAATGCAAACTCCACTGGTTTTCAAATTTTACTTTAGAGTTA
118441  ACAAGTTCACAGTTGGCATTTACGTTTGAGGTGACCAAAAGTTTAAAATGAAATCTCAAT

118501  TTTTCCCTCAGCTGATTGGAGTTTTGCTCAACTCCTCTGACTTTAATAATGGCTGCTTCA
118501  AAAAGGGAGTCGACTAACCTCAAAACGAGTTGAGGAGACTGAAATTATTACCGACGAAGT

118561  TTTGTTGAGGTTTTAGAACTTGCTTTTAAGGGATTGCTCTTGACATAATTGCATCAACAG
118561  AAACAACTCCAAAATCTTGAACGAAAATTCCCTAACGAGAACTGTATTAACGTAGTTGTC

118621  ATAGACTGTTTCATGGGAGAAGAATTGTTCTGTTTCATGTCAATACTTACATTGATAAGA
118621  TATCTGACAAAGTACCCTCTTCTTAACAAGACAAAGTACAGTTATGAATGTAACTATTCT

118681  ATGCATCAAGGTAATGTGATCCATCCACTGAAGTTGTCATTAGGCCAGATTTTTTTTAAG
118681  TACGTAGTTCCATTACACTAGGTAGGTGACTTCAACAGTAATCCGGTCTAAAAAAAATTC

118741  TTGAATTATTATTTCACTTCTAGAAATAAGAAGTTTATAAAGTTTAGCATAATTTTAATG
118741  AACTTAATAATAAAGTGAAGATCTTTATTCTTCAAATATTTCAAATCGTATTAAAATTAC

118801  ATCCAGGCTTAGGAAGCATTTACAGCCAAAAAGTAAGTATATATAATTATCATATTATAC
118801  TAGGTCCGAATCCTTCGTAAATGTCGGTTTTTCATTCATATATATTAATAGTATAATATG

118861  TAAACGGTATAATATGAAAAGTGTTTGAGAGCACAGACTATCTCCTAAAATCAAACTATC
118861  ATTTCCCATATTATACTTTTCACAAACTCTCGTGTCTGATAGAGGATTTTAGTTTGATAG

118921  AAAACCTGCAAGCCAGCAAGGCATGAGTAGGCATGACTCAGATACAAATTAGAAGCATGA
118921  TTTTGGACGTTCGGTCGTTCCGTACTCATCCGTACTGAGTCTATGTTTAATCTTCGTACT
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FIGURE 4 (cont'd)

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118981  AATCTCTTTCAGCCATGCATTTAATCATGCTATCCAATATTGTGGAGGTAGTGGCCCCTG
118981  TTAGAGAAAGTCGGTACGTAAATTAGTACGATAGGTTATAACACCTCCATCACCGGGGAC

119041  GAAGTTTACCTTGGGCCAGAGATAGGTATAGAAGCCCCTTTTATGAAGTCATAGACTTGC
119041  CTTCAAATGGAACCCGGTCTCTATCCATATCTTCGGGGAAAATACTTCAGTATCTGAACG

119101  TTTAATTTATGCTCCCAGAATGACTTGCATTAAACTGTGGCAAAATATCTTTGAGTTCTC
119101  AAATTAAATACGAGGGTCTTACTGAACGTAATTTGACACCGTTTTATAGAAACTCAAGAG

119161  ATATTAGCCAGAGGGTTAATATGTAGAAGACAATCATTCATCCTTACAGATTCTCAGAAT
119161  TATAATCGGTCTCCCAATTATACATCTTCTGTTAGTAAGTAGGAATGTCTAAGAGTCTTA

119221  CTTGGAAGAGGTAGGGTTCTTTAAGTTTAGCCACTATTTTAGGTAACTGTAGCTCCTCCT
119221  GAACCTTCTCCATCCCAAGAAATTCAAATCGGTGATAAAATCCATTGACATCGAGGAGGA

119281  TGGTTCTTCAAATGATCCTGAAGGCTGGTATACAAACCAGTTATGCCCTAAAATTAATTG
119281  ACCAAGAAGTTTACTAGGACTTCCGACCATATGTTTGGTCAATACGGGATTTTAATTAAC

119341  GTAGGTAGGCAATGTATAACCTGTCATTGGCTAGTTTTTATTCAAATTTTGGATATGAAA
119341  CATCCATCCGTTACATATTGGACAGTAACCGATCAAAAATAAGTTTAAAACCTATACTTT

119401  GTCTTTGGCATAAGGTGCTAGCACTCAGAGTCAGTAGGTTTTAGTGCTATTCCTTAACTT
119401  CAGAAACCGTATTCCACGATCGTGAGTCTCAGTCATCCAAAATCACGATAAGGAATTGAA

119461  CAGTGGAATTGCCTTAGTATAGCAGAATTGCTTGAGTGTCTTATCTGTTATCACCATATA
119461  GTCACCTTAACGGAATCATATCGTCTTAACGAACTCACAGAATAGACAATAGTGGTATAT

119521  CATGAGTACCCTCAAATTATCTCATTTCCCTTTCTTTTGTAGACAATACACATTCCAACT
119521  GTACTCATGGGAGTTTAATAGAGTAAAGGGAAAGAAAACATCTGTTATGTGTAAGGTTGA

119581  ATGGAGAATGGTCCTAAGCTGGCAAGCCGCATCTTGAGCAAATTAACTGATATCCAGGTA
119581  TACCTCTTACCAGGATTCGACCGTTCGGCGTAGAACTCGTTTAATTGACTATAGGTCCAT

119641  AAGCTTTTCTTTTCTTTTCTTTTCTTTCCTTTTCTTTTCTTTTTTTTATGTCACCTTATT
119641  TTCGAAAAGAAAAGAAAAGAAAAGAAAGGAAAAGAAAAGAAAAAAAATACAGTGGAATAA

119701  TCTGTCAGAGCTTACAACTAAATTATATTTCAATGAAGAGGATTAAATAATACAATTTGA
119701  AGACAGTCTCGAATGTTGATTTAATATAAAGTTACTTCTCCTAATTTATTATGTTAAACT

119761  GATCAATAAGTTAAATTTAAGGAAGATATTCCCAACACAATGTGTGGGCATGAGCAAAGC
119761  CTAGTTATTCAATTTAAATTCCTTCTATAAGGGTTGTGTTACACACCCGTACTCGTTTCG

119821  AGAAATGGGAAAGAAGATGTATGTTTTAAAAAAAGAAAGAAAATATTGTTCAGGACTCCA
119821  TCTTTACCCTTTCTTCTACATACAAAATTTTTTTCTTTCTTTTATAACAAGTCCTGAGGT

119881  CATTACTTAACATTAAAAAATAGATGTAATTTTTGGTAACATTTAAAAATCTCATTAAGA
119881  GTAATGAATTGTAATTTTTTATCTACATTAAAAACCATTGTAAATTTTTAGAGTAATTCT

119941  AGGATAACATAACTTTTGTTAAAAAAAGGAAGAAAAAATTTGAAAGTAGAAGCAACTTCA
119941  TCCTATTGTATTGAAAACAATTTTTTTCCTTCTTTTTTAAACTTTCATCTTCGTTGAAGT

120001  GGAAGAAAATTACAGTGCATGTGATTCCAACACTGAGATATAATCACTGTTAATTTTTTA
120001  CCTTCTTTTAATGTCACGTACACTAAGGTTGTGACTCTATATTAGTGACAATTAAAAAAT

120061  TGTCTTTTTATTTTTGAGCTGGAGTTTCACTCTTGTTGCCCAGGCTGGAGTACCATGGCA
120061  ACAGAAAAATAAAAACTCGACCTCAAAGTGAGAACAACGGGTCCGACCTCATGGTACCGT

120121  CGATCTTGGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGCAATTTTCCTACCTCAGCCT
120121  GCTAGAACCGAGTGACGTTGGAGACGGAGGGCCCAAGTTCGTTAAAAGGATGGAGTCGGA

120181  CCCGAGTAGCTGGGATTATAGGTGTGCGCCACCATGCCCAGCTAATTTTTGTGTTTTTAG
120181  GGGCTCATCGACCCTAATATCCACACGCGGTGGTACGGGTCGATTAAAAACACAAAAATC

120241  TAGAGATGGGATTTCACCATGTTGGCCAGGCTGGTCTTGAACTCCTGACCTAAGGTAATC
120241  ATCTCTACCCTAAAGTGGTACAACCGGTCCGACCAGAACTTGAGGACTGGATTCCATTAG

120301  CACCTGCCTTGGCCTCCTAAATTGTTGGGATTACAGGCATGAACCACTGTGCCCTGCCAT
120301  GTGGACGGAACCGGAGGATTTAACAACCCTAATGTCCGTACTTGGTGACACGGGACGGTA
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FIGURE 4 (cont'd)

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120361  TTTTTGATGTCTTAACCTTCAATATTTTGTAAGCATTTATATACTTTATTTATTTATTTA
120361  AAAAACTACAGAATTGGAAGTTATAAAACATTCGTAAATATATGAAATAAATAAATAAAT

120421  TTTATTTATTTATTTATTTACTTATTTATTTTTGAGACTAAGTCTCGCTGTGTCACCCAG
120421  AAATAAATAAATAAATAAATGAATAAATAAAAACTCTGATTCAGAGCGACACAGTGGGTC

120481  GCTGGAGAACAGTGGCATGATCTCAGCTCACTACAACCTCCACCTCCTGGGTTCAAGCGA
120481  CGACCTCTTGTCACCGTACTAGAGTCGAGTGATGTTGGAGGTGGAGGACCCAAGTTCGCT

120541  TTCTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGTCTCATGCCACCGTTCCCGGC
120541  AAGAAGACGGAGTCGGAGGGCTCATCGACCCTAATGTCCAGAGTACGGTGGCAAGGGCCG

120601  TAATTTTTGTATTTTTAGTAGAGATGAGGTTTTGCCCTGTTGGCCAGGCTGGTCTTGAAC
120601  ATTAAAAACATAAAAATCATCTCTACTCCAAAACGGGACAACCGGTCCGACCAGAACTTG

120661  TCTTGACCTCAGGTGATCCACCCGCCTTGGCTTCCCAAAGTGCTGGGATTACAGCCGTGA
120661  AGAACTGGAGTCCACTAGGTGGGCGGAACCGAAGGGTTTCACGACCCTAATGTCGGCACT

120721  GCCACCATGCCCAGCCAGTATACTTTTAGATAGTTATTTTTTCCTAACAAAATGGATCA
120721  CGGTGGTACGGGTCGGTCATATGAAAATCTATCAATAAAAAAGGATTGTTTTACCCTAGT

120781  TATTGTACATAATTTTGTTACATGTTTTTTCACTGAATAAATGCTTTGCTTTTTTATATC
120781  ATAACATGTATTAAAACAATGTACAAAAAAGTGACTTATTTACGAAACGAAAAAATATAG

120841  AATAACTAGTTTTCTCCAACACCATTTATAAAGTTTAATTGAATTCCATTATATTGATGT
120841  TTATTCATCAAAAGAGGTTGTGGTAAATATTTCAAATTAACTTAAGGTAATATAACTACA

120901  ACCATAATTTTTTTAAAAAATTATATTATTGAACATTTATGTTGTTGGCAATTTTTTTTT
120901  TGGTATTAAAAAAATTTTTTAATATAATAACTTGTAAATACAACAACCGTTAAAAAAAAA

120961  CACTAGTATGGACAGTACATCCTCGATTACTTCCTAAGGATAAATCTGGGATCAAAGAGT
120961  GTGATCATACCTGTCATGTAGGAGCTAATGAAGGATTCCTATTTAGACCCTAGTTTCTCA

121021  ATACACGTCTATTTTTTCATACTGCTAACTTTGTTTTGCCTATTTTTTTTCTGAGCAATA
121021  TATGTGCAGATAAAAAAGTATGACGATTGAAACAAAACGGATAAAAAAAAGACTCGTTAT

121081  ATCTACAGTAATGCCTCATCAGGCAGTTAAGCAGGCATGCTAAATACCAGATAACACTGG
121081  TAGATGTCATTACGGAGTAGTCCGTCAATTCGTCCGTACGATTTATGGTCTATTGTGACC

121141  GCTACTCAGAAAAGAGATTATCCTGTAATTTGCAAGCATTTCACAAGTTAGAAGACTTTG
121141  CGATGAGTCTTTTCTCTAATAGGACATTAAACGTTCGTAAAGTGTTCAATCTTCTGAAAC

121201  TTGAAGCCAGTTACTATCCTTGTCAATTAGTAAAAATATCCAAGAGGGCCTGAGACTTAC
121201  AACTTCGGTCAATGATAGGAACAGTTAATCATTTTTATAGGTTCTCCCGGACTCTGAATG

121261  ATTGAAAAGTAAAATAAAGTTTGATCATTTGAGTGATGTCGGATGGCATTAAGTCATGAA
121261  TAACTTTTCATTTTATTTCAAACTAGTAAACTCACTACAGCCTACCGTAATTCAGTACTT

121321  ACTAAGTGAAACTTAAAGGTGGCTGAGAATGCAACAGGCCTCCAGAGAGCAATGGAGGTC
121321  TGATTCACTTTGAATTTCCACCGACTCTTACGTTGTCCGGAGGTCTCTCGTTACCTCCAG

121381  CTTGGGTAGTGATAAAAATGGCATTTCTGGCTGGGTGCAGTGGCTCACACCTATAATCCC
121381  GAACCCATCACTATTTTTACCGTAAAGACCGACCCACGTCACCGAGTGTGGATATTAGGG

121441  AACACTATGGGAGGCCAAGACAGGAGGATCGCTTGAGGCCAGGTGTTCAAGACTAGCCTA
121441  TTGTGATACCCTCCGGTTCTGTCCTCCTAGCGAACTCCGGTCCACAAGTTCTGATCGGAT

121501  GGCAACATAGTGAGAACCTTCCTCTAAAAAAAGGGAAATAAAATAAAAATAAAAGTTTAA
121501  CCGTTGTATCACTCTTGGAAGGAGATTTTTTTCCCTTTATTTTATTTTTATTTTCAAATT

121561  AAGAGAGTTTAAAAGGCAGTTTTAAAAGAGACTTACTCAGCAAGTTTTCTGCCAAATTTA
121561  TTCTCTCAAATTTTCCGTCAAAATTTTCTCTGAATGAGTCGTTCAAAAGACGGTTTAAAT

121621  CAGTATTAAAAAGAAAGAAAGTGTGTTTTTGTTTCTGTTTGTTTTTTTGAGACAGAGTCT
121621  GTCATAATTTTTCTTTCTTTCACACAAAAACAAAGACAAACAAAAAAACTCTGTCTCAGA
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FIGURE 4 (cont'd)

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121681  TACTCTGTTGCTCAGGCTGGGGTGCAGTGGTGCAATCTCAGCTCACTGCAACCCCTCCCT
121681  ATGAGACAACGAGTCCGACCCCACGTCACCACGTTAGAGTCGAGTGACGTTGGGGACGGA

121741  CCTGGGTTCAAGTGATTCTTGTGCCTCAGCCTCCCACACAGCAGGGATTATGGGCATGCA
121741  GGACCCAAGTTCACTAAGAACACGGAGTCGGAGGGTGTGTCGTCCCTAATACCCGTACGT

121801  CCATCATGCCTGGCTAATTTTTGTATTTTTAGTAGAGTCGAGGTTTCGCCATGTTGGCCA
121801  GGTAGTACGGACCGATTAAAAACATAAAAATCATCTCAGCTCCAAAGCGGTACAACCGGT

121861  GGCTGGTCTCAAACTCCTAGCCTCAAGTGATTTGCCCACCTTAGCCTCCCAAAGTGCTGA
121861  CCGACCAGAGTTTGAGGATCGGAGTTCACTAAACGGGTGGAATCGGAGGGTTTCACGACT

121921  GATTACAGGCATGAGCCACCGCACCCTGGCCTTGATTGTGGTTTTTTAATCAATGAGCTG
121921  CTAATGTCCGTACTCGGTGGCGTGGGACCGGAACTAACACCAAAAAATTAGTTACTCGAC

121981  CCATACTTCTGCTCTCCAGCAAAGGTTTTCTATGAGAATTTTCTGTAAGCTAAGTAAAGG
121981  GGTATGAAGACGAGAGGTCGTTTCCAAAAGATACTCTTAAAAGACATTCGATTCATTTCC

122041  AATATCTTAATATTGGAAGAAATAAAATTTAGTCAGAGTTGTTTTCTACCTTTGTACACA
122041  TTATAGAATTATAACCTTCTTTATTTTAAATCAGTCTCAACAAAAGATGGAAACATGTGT

122101  GCAACACTTACAAGTAATTTGAAGAGTAGCTAATAAAAATTTCTGCATGGATGGCTTAGG
122101  CGTTGTGAATGTTCATTAAACTTCTCATCGATTATTTTTAAAGACGTACCTACCGAATCC

122161  CATTTTAATTTTTTTAAGGTTGCCTGAGTAAATCTGAAAATAATAAATTATTACAGTTTT
122161  GTAAAATTAAAAAAATTCCAACGGACTCATTTAGACTTTTATTATTTAATAATGTCAAAA

122221  GCTCAAATAAAGAACACAAATAGAACAAAAAATACATAACTGGCTAGATTACATGAAAGC
122221  CGAGTTTATTTCTTGTGTTTATCTTGTTTTTTATGTATTGACCGATCTAATGTACTTTCG

122281  CTTTTTCCAAAACAGAGGTTTAGAGGCCAGGGCAAATAGGCAGGAAAAATAAATAAAGGG
122281  GAAAAAGGTTTTGTCTCCAAATCTCCGGTCCCGTTTATCCGTCCTTTTTATTTATTTCCC

122341  CATCCAAATTGGAAAAGAAGAAGTTAAATTAGCTTTCTTAGCAGATGACATTATCTTACA
122341  GTAGGTTTAACCTTTTCTTCTTCAATTTAATCGAAAGAATCGTCTACTGTAATAGAATGT

122401  CCTAGAAAAACCTAAAGACTCCCTCAAAAAACCTGTAGAACTGATAAATGAATTCAGTAA
122401  GGATCTTTTTGGATTTCTGAGGGAGTTTTTTGGACATCTTGACTATTTACTTAAGTCATT

122461  AGTTGCAGGATATAAAATCAACATATAAAAATCAGTAGAATTTATATATGCTAACAGTGA
122461  TCAACGTCCTATATTTTAGTTGTATATTTTTAGTCATCTTAAATATATACGATTGTCACT

122521  ACAATCTGAAAAAGAAATCAAGAAAGCAATCCCATTTATAATAGCCACAAAAAGTATAAA
122521  TGTTAGACTTTTTCTTTAGTTCTTTCGTTAGGGTAAATATTATCGGTGTTTTTCATATTT

122581  ATACCTAGGAATCAATCTAACCAAAGACATGAGAGATCTATACAAGGAAAAGTATAAAAC
122581  TATGGATCCTTAGTTAGATTGGTTTCTGTACTCTCTAGATATGTTCCTTTTCATATTTTG

122641  TATGATTTAAAAAATTGAAGAAAACACACAAAGGTGGAAAGATATTCCATATTCATGGAT
122641  ATACTAAATTTTTTAACTTCTTTTGTGTGTTTCCACCTTTCTATAAGGTATAAGTACCTA

122701  TGGAAGAATTAATTTTGTTAAAATGACTATACTACACAAAGCAATTTACAGATTCAATGC
122701  ACCTTCTTAATTAAAACAATTTTACTGATATGATGTGTTTCGTTAAATGTCTAAGTTACG

122761  AATCCCTATTAAAATACTGATGACTTTCTTCACAGAAATAGAAAAAACAATCCTAAAATG
122761  TTAGGGATAATTTTATGACTACTGAAAGAAGTGTCTTTATCTTTTTTGTTAGGATTTTAC

122821  TATATGGAGCTAAAAAGACCCCAAATAGCCAAAGCAATCTTGAGCAAAAAGAACAAAGTT
122821  ATATACCTCGATTTTTCTGGGGTTTATCGGTTTCGTTAGAACTCGTTTTTCTTGTTTCAA

122881  AGAATCACCACACTACCTTACTTCAAAATTTATTATAAAACTATAATAACCAAAACAGCA
122881  TCTTAGTGGTGTGATGGAATGAAGTTTTAAATAATATTTTGATATTATTGGTTTTGTCGT

122941  TAGTACTGATATAAAAACAGACATAGTAGACCAGTGGGACAGAATAGAGAACCCAGATAC
122941  ATCATGACTATATTTTTGTCTGTATCATCTGGTCACCCTGTCTTATCTCTTGGGTCTATG

123001  CTAACTCCACATGTTTACAACCAACTCATCTTTGACAAAGGTGCCAAGAACTGTAACGGC
123001  GATTCAGGTGTACAAATGTTGGTTGAGTAGAAACTGTTTCCACGGTTCTTGACATTGCCC
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FIGURE 4 (cont'd)

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123061  GAAGACAGTCTTTTCAATAAATGGTGCTGGGAAAATTGGATAATTATATGCAGAAGAATG
123061  CTTCTGTCAGAAAAGTTATTTACCACGACCCTTTTAACCTATTAATATACGTCTTCTTAC

123121  AAACTAGATTCGCTTCTCTTACCATACACAGAAATCAAATGAAAGTATATTAATGACTTG
123121  TTTGATCTAAGCGAAGAGAATGGTATGTGTCTTTAGTTTACTTTCATATAATTACTGAAC

123181  AATCTTAGACCTGAAACTATGAAATTACTTGAAGAAAACATTAAGGAAATGCTTCAGGAC
123181  TTAGAATCTGGACTTTGATACTTTAATGAACTTCTTTTGTAATTCCTTTACGAAGTCCTG

123241  ATTGGTCTAAGCAAAGATCTCATTCTGTCACTCAGGCTGGAGTGTAGTGGCATGAACCTG
123241  TAACCAGATTCGTTTCTAGAGTAAGACAGTGAGTCCGACCTCACATCACCGTACTTGGAC

123301  GCTCATTGTGGCATTGACCTCCTGGGCTCAAGCAATTCTCCCACCTTGGCTTTCCATGTA
123301  CGAGTAACACCGTAACTGGAGGACCCGAGTTCGTTAAGAGGGTGGAACCGAAAGGTACAT

123361  GCTAGAACCACAGGTGCATGCCACCACATTCCACTAATTTTTAAATTTTTTGTAGAGATG
123361  CGATCTTGGTGTCCACGTACGGTGGTGTAAGGTGATTAAAAATTTAAAAAACATCTCTAC

123421  GAGTCTCACCATCTTGCCCAGGCTGGTCTCGAACTCCTGAACTCAAGGGATCCTCCTGTC
123421  CTCAGAGTGGTAGAACGGGTCCGACCAGAGCTTGAGGACTTGAGTTCCCTAGGAGGACAG

123481  TCAGCCTCCCAAAGTGCTGAGATTACTAGCATAAGCCACTGTCCCTGGCCAGCGAAGATT
123481  AGTCGGAGGGTTTCACGACTCTAATGATCGTATTCGGTGACAGGGACCGGTCGCTTCTAA

123541  TCTTATGTAAGACCTGAAAAAGCATAGGCTATCAAAGCAAAAATAGGCAATTGGGATTAT
123541  AGAATACATTCTGGACTTTTTCGTATCCGATAGTTTCGTTTTTATCCGTTAACCCTAATA

123601  GTCAAGCTGGAAAGCTTCTCCACAGCAAAGAAAACAATCCACAAAGGGAATAGATTACCC
123601  CAGTTCGACCTTTCGAAGAGGTGTCGTTTCTTTTGTTAGGTGTTTCCCTTATCTAATGGG

123661  AAAGAATGGATGAAAATATTTGCAAACTATCAATCTGACAAGGGATTAATAACCAGAGTC
123661  TTTCTTACCTACTTTTATAAACGTTTGATAGTTAGACTGTTCCCTAATTATTGGTCTCAG

123721  TATAAGGAGCTCAAACAACTGTATAGGAAAAATCTAGTAATCTGGTTTTAAAATGGGCAT
123721  ATATTCCTCGAGTTTGTTGACATATCCTTTTTAGATCATTAGACCAAAATTTTACCCGTA

123781  GAGACCTGATTAGAAAACTCAACAGAAAAAAAAATTTGATTAAAAATGGATAAAAGATCT
123781  CTCTGGACTAATCTTTTGAGTTGTCTTTTTTTTTAAACTAATTTTTACCTATTTTCTAGA

123841  GAATGGACATTTCTCAAAAGAAGACAGACAAATGGCCAGGAGGTACATGAAAAAATGCGC
123841  CTTACCTGTAAAGAGTTTTCTTCTGTCTGTTTACCGGTCCTCCATGTACTTTTTTACGCG

123901  AACATCACTAATTATCAGAGAAATGCAAAACAAAACCACAATGTAAAATCCACTTGCCCT
123901  TTGTAGTGATTAATAGTCTCTTTACGTTTTGTTTTGGTGTTACATTTTAGGTGAACGGGA

123961  AGTTAAAATGGCTTGTATTAAAAAAAAAAAAAAAAACAGGCAATAACAGATGCTGGGAGG
123961  TCAATTTTACCGAACATAATTTTTTTTTTTTTTTTTGTCCGTTATTGTCTACGACCCTCC

124021  ATGTGGAGAAAGGGAACCATCATATATTGTTGGTTGAAATATAAATAGTACAGCCACTAT
124021  TACACCTCTTTCCCTTGGTAGTATATAACAACCAACTTTATATTTATCATGTCGGTGATA

124081  GGAGAACAGTATGGAGGGTCCTCCAAAAATAAAAGTAGAACTAGAACTTCCGTGTGATCC
124081  CCTCTTGTCATACCTCCCAGGAGGTTTTTATTTTCATCTTGATCTTGAAGGCACACTAGG

124141  AGCAATTCTACCACCGGGTATATATCCAAAAGAAAAAAATTAGTATATCAAAGAGATATC
124141  TCGTTAAGATGGTGGCCCATATATAGGTTTTCTTTTTTTAATCATATAGTTTCTCTATAG

124201  TGCACTCCCATGTTTATTGCAATAGTATTCACAATAGCCAAGATATGGAATTAACCTAAA
124201  ACGTGAGGGTACAAATAACGTTATCATAAGTGTTATCGGTTCTATACCTTAATTGGATTT

124261  TGTCTGTCAACAGATAAATGGATAAAGAGAATGTGGCATAAAGATATATATATATATATA
124261  ACAGACAGTTGTCTATTTACCTATTTCTCTTACACCGTATTTCTATATATATATATATAT

124321  TATACACACACACACACACACACACACAATGTGGTACTATTCAGCCATAAAAAAGAATGA
124321  ATATGTGTGTGTGTGTGTGTGTGTGTGTTACACCATGATAAGTCGGTATTTTTTCTTACT
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FIGURE 4 (cont'd)

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124381  AATCCTGTCATTTGCAGCAACATGTATGGAACTGGAGGCCATTTTGTTAAGTGAAATAAG
124381  TTAGGACAGTAAACGTCGTTGTACATACCTTGACCTCCGGTAAAACAATTCACTTTATTC

124441  CGAGGGACCGAAAGACAAACATCACATGTTCTCATGCAGGTGCTAAAAAAGTAGATCCTA
124441  GCTCCCTGGCTTTCTGTTTGTAGTGTACAAGAGTACGTCCACGATTTTTTCATCTAGGAT

124501  TGAAGACAGAGAGTAGATTAGAGGTTACCAGAGGCCGAGAAGGGGAGTGGAAGTAGAGG
124501  ACTTCTGTCTCTCATCTAATCTCCAATGGTCTCCGGCTCTTCCCCTCACCTTCATCTCC

124561  ATAAAGGAAAAAAACAAGAATATAAATGTATTTATTACCATTAAACTGAACATTTAAAAA
124561  TATTTCCTTTTTTTGTTCTTATATTTACATAAATAATGGTAATTTGACTTGTAAATTTTT

124621  TTGTAAAGATGGTAAATTATATATGTGTATTTTATCTTAATTAAAATTTTAAAAATCAGG
124621  AACATTTCTACCATTTAATATATACACATAAAATAGAATTAATTTTAAAATTTTTAGTCC

124681  AGTTTAGAAATTTTTAAGAGAAGTGTGCCCATAGTGATAAGAAAGAAAGACCCTTTTGGA
124681  TCAAATCTTTAAAAATTCTCTTCACACGGGTATCACTATTCTTTCTTTCTGGGAAAACCT

124741  AAATTTTCTTGAACAAATTATACAGTATTTTCTTAAACAAATTGTACATTCTGTAGCAGT
124741  TTTAAAAGAACTTGTTTAATATGTCATAAAAGAATTTGTTTAACATGTAAGACATCGTCA

124801  TAATACACCAAATAAGATTTCAGGGTTACCTCTTGGAGATTGTATGAAATAAAAACATTT
124801  ATTATGTGGTTTATTCTAAAGTCCCAATGGAGAACCTCTAACATACTTTATTTTTGTAAA

124861  AGGTGGGCATGATGGCTCATTCCTGTAATCCTAAAACTTTGGGAGGCTGATGCAGGAACA
124861  TCCACCCGTACTACCGAGTAAGGACATTAGGATTTTGAAACCCTCCGACTACGTCCTTGT

124921  ATACTTGAGGCTAGTACTTCAAGACGAGCCTAGGCAACATAGTAAGACCCAGTCTCCACA
124921  TATGAACTCCGATCATGAAGTTCTGCTCGGATCCGTTGTATCATTCTGGGTCAGAGGTGT

124981  AAACAACCAAAAAAAATAGCAAGTGTGGTGGCACACACCTGTAGTTCCAGCTACTCAGGA
124981  TTTGTTGGTTTTTTTTATCGTTCACACCACCGTGTGTGGACATCAAGGTCGATGAGTCCT

125041  GGCTGAGGCAGGAGGAACACTTGAGGCCAGGAATGTGAGACTGCAGTGGGCTATGATTGT
125041  CCGACTCCGTCCTCCTTGTGAACTCCGGTCCTTACACTCTGACGTCACCCGATACTAACA

125101  GCCACAGCACTCCACTCCAGCCTTCACTGTAGAAAGAGACCCTGTCTCGAAAGGAAGGAG
125101  CGGTGTCGTGAGGTGAGGTCGGAAGTGACATCTTTCTCTGGGACAGAGCTTTCCTTCCTC

125161  GGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAATGAAGGAAGGAAGGAAGGAAGGAAGGAA
125161  CCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTTACTTCCTTCCTTCCTTCCTTCCTTCCTT

125221  GGAAGGAAATGTAAACTCATTTGATTTGGCTGTAAAGGATTAATAGAAAAGGAAAACGTA
125221  CCTTCCTTTACATTTGAGTAAACTAAACCGACATTTCCTAATTATCTTTTCCTTTTGCAT

125281  GTCACTAGGCTGAGAAAAATTGAACTCTATTGAATTGGTATAAAGATCTAAGTGGAGGTG
125281  CAGTGATCCGACTCTTTTTAACTTGAGATAACTTAACCATATTTCTAGATTCACCTCCAC

125341  TTTGGCAGACATGATCATGAAGCTTTCACTGAGGAAGGAAACTCTAGGAGGCAAAAGCAG
125341  AAACCGTCTGTACTAGTACTTCGAAAGTGACTCCTTCCTTTGAGATCCTCCGTTTTCGTC

125401  AAATGCAACTCATCAAAATTGAAATGGTGACAAAATATGTGCATTCAAACCTGAAAGTGA
125401  TTTACGTTGAGTAGTTTTAACTTTACCACTGTTTTATACACGTAAGTTTGGACTTTCACT

125461  CTGAAAGAGAAGCCCAAACACACAATTTTGGGGTAAGATGGGAAACCATTACCAAAGTTC
125461  GACTTTCTCTTCGGGTTTGTGTGTTAAAACCCCATTCTACCCTTTGGTAATGGTTTCAAG

125521  TCAGAAAGAGCATTTTTAAAAGTAAGATTATAGAAGCCAAAAGGATATGTAGTAGTCTGT
125521  AGTCTTTCTCGTAAAAATTTTCATTCTAATATCTTCGGTTTTCCTATACATCATCAGACA

125581  TCTCACACTGCTGTAACGAACTACCTGAGACTGGGTAGTTTGTAAAGAAAAGAGGTTTTA
125581  AGAGTGTGACGACATTGCTTGATGGACTCTGACCCATCAAACATTTCTTTTCTCCAAAAT

125641  TTGACGCTCAGTTCTGCAGGCCATACAGGAGACATGGCTGGGGAGGCCTCAGGAAACTTA
125641  AACTGCGAGTCAAGACGTCCGGTATGTCCTCTGTACCGACCCCTCCGGAGTCCTTTGAAT

125701  CAGTCATGGCGGAAGGCAAAGGGGAAGCCAGTACATATTACATGGTGGGAACAGGAGGAG
125701  GTCAGTACCGCCTTCCGTTTCCCCTTCGGTCATGTATAATGTACCACCCTTGTCCTCCTC
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FIGURE 4 (cont'd)

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125761   GAGAGGGAGGGTGGGAGGTGCCACTCACTTTTTAAAACAAACAGATCTCCTTAGAACTCA
125761   CTCTCCCTCCCACCCTCCACGGTGAGTGAAAAATTTTGTTTGTCTAGAGGAATCTTGAGT

125821   CTCACTATCATGAGAACAGCAAGGGGGAGGTTTGCTCCCATGATGCAATTACCTGACACC
125821   GAGTGATAGTACTCTTGTCGTTCCCCCTCCAAACGAGGGTACTACGTTAATGGACTGTGG

125881   AGGCCCTTCCTCCAACATGGGGGATTACAATTCCACATGAGATTTGGGTGGGGACACAAA
125881   TCCGGGAAGGAGGTTGTACCCCCTAATGTTAAGGTGTACTCTAAACCCACCCCTGTGTTT

125941   TTCAAACCATATCAGAATGTTAGTGACTAAAGTAAATGTTCTTGTTTAACTCTTTAATGT
125941   AAGTTTGGTATAGTCTTACAATCACTGATTTCATTTACAAGAACAAATTGAGAAATTACA

126001   GTATATTGAGTGCAAGCCATATGCAGGGGCTATTCTAGGTACTGGTGGTTTACTCAAGAA
126001   CATATAACTCACGTTCGGTATACGTCCCCGATAAGATCCATGACCACCAAATGAGTTCTT

126061   AAAGGGGGCAAAAAAATGAAGAAGGTGGCCAGGCATGGTGGCTTACGCCTGTAATCCCAA
126061   TTTCCCCCGTTTTTTTACTTCTTCCACCGGTCCGTACCACCGAATGCGGACATTAGGGTT

126121   CACTTTGGGAGACTGAGACGTGAGAATTGCTTGAGCCCAGGAGTTTGAGATCAGCCTGGT
126121   GTGAAACCCTCTGACTCTGCACTCTTAACGAACTCGGGTCCTCAAACTCTAGTCGGACCA

126181   AACATGGCAAATCCCTGTCTCTACAAAAAAATGCAAACAAACAAACAAACAAACAAACAA
126181   TTGTACCGTTTAGGGACAGAGATGTTTTTTTACGTTTGTTTGTTTGTTTGTTTGTTTGTT

126241   ATTAATCGGGCATGGTGTCACATGTCTGTAGTCCCAGCTACAGGTTGAGGTGGGAAGATG
126241   TAATTAGCCCGTACCACAGTGTACAGACATCAGGGTCGATGTCCAACTCCACCCTTCTAC

126301   CCTTAAGCCTAGGGAGGTTGAGGCTGCAGTCAGCCATGATAGCACCACTGCACTCCAGCC
126301   GGAATTCGGATCCCTCCAACTCCGACGTCAGTCGGTACTATCGTGGTGACGTGAGGTCGG

126361   TGGGCAACAGAGTGAGACCCCATCTGAAAAAAAAAGAAGTCAAAACAAATGAAAAAAAAA
126361   ACCCGTTGTCTCACTCTGGGGTAGACTTTTTTTTTCTTCAGTTTTGTTTACTTTTTTTTT

126421   AAAAAGTCAAAACAAATATTCAGTGTAAATGTGAGACCATGTAAAAAAGTTTAAAAGTAA
126421   TTTTTCAGTTTTGTTTATAAGTCACATTTACACTCTGGTACATTTTTTCAAATTTTCATT

126481   AATATATAGTTTAAGCAGAGGATGGGAGACGGGGAAAAAACCTTTTCTCCCTAACTTTAT
126481   TTATATATCAAATTCGTCTCCTACCCTCTGCCCCTTTTTTGGAAAAGAGGGATTGAAATA

126541   ATACTCCCTCTATAAATTAGTGCTTATGGCCAATAAGAAATGAATAATTTCTTTTTTCAC
126541   TATGAGGGAGATATTTAATCACGAATACCGGTTATTCTTTACTTATTAAAGAAAAAAGTG

126601   CGTTGGTAGTAAAGTATAATGGTAGTTAACACAAAAAACTAAATGATATATTCAGAACCT
126601   GCAACCATCATTTCATATTACCATCAATTGTGTTTTTTGATTTACTATATAAGTCTTGGA

126661   CATACTAAACAAAGAAACAAAGGCATGCAATCACAGGACAGGTGGAAACAGTGGTTCTGA
126661   GTATGATTTGTTTCTTTGTTTCCGTACGTTAGTGTCCTGTCCACCTTTGTCACCAAGACT

126721   ACTAACCACAAACCAGAACTACCAAATGTGCTACAAATTGTTTAGTAACAAAGGACCATC
126721   TGATTGGTGTTTGGTCTTGATGGTTTACACGATGTTTAACAAATCATTGTTTCCTGGTAG

126781   CCTTCAGAATTGAAGAGCACGTCTCAGTTATCTCATGCCTATGTGCATGGAACTTAAAGT
126781   GGAAGTCTTAACTTCTCGTGCAGAGTCAATAGAGTACGGATACACGTACCTTGAATTTCA

126841   CTCAAAATTACTCTTACAAGATGGCAAATTGAGGCTGTCAGCTAAGCTCCTAGATTGTCT
126841   GAGTTTTAATGAGAATGTTCTACCGTTTAACTCCGACAGTCGATTCGAGGATCTAACAGA

126901   GTTTCTCCAAGAAAAATAAATTTCAGTAATTATTAAGGAAAAAGCATAGAATTGCATCAT
126901   CAAAGAGGTTCTTTTTATTTAAAGTCATTAATAATTCCTTTTTCGTATCTTAACGTAGTA

126961   GTTTTACATTTCATTACTTTTGGCATGACATGGGAGCATGGATGTTTTCTACAAAGTGCT
126961   CAAAATGTAAAGTAATGAAAACCGTACTGTACCCTCGTACCTACAAAAGATGTTTCACGA

127021   CTGATAAATTGAAGAAGAGGCCAACAACAGCCACCGAAAAAACCTTCAAGATTCTTGCCA
127021   GACTATTTAACTTCTTCTCCGGTTGTTGTCGGTGGCTTTTTTGGAAGTTCTAAGAACGGT
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FIGURE 4 (cont'd)

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127081  GTATGGCTCAGGGGAAAAATTCCCTCATAACCACAGATTTGACTTTTCAACTTCTGTACT
127081  CATACCGAGTCCCCTTTTTAAGGGAGTATTGGTGTCTAAACTGAAAAGTTGAAGACATGA

127141  TCTGCATATGAGTAATAATCTCTGAGGTTAAGTATTCATCCCATTTAGCTAATTGTCCAC
127141  AGACGTATACTCATTATTAGAGACTCCAATTCATAAGTAGGGTAAATCGATTAACAGGTG

127201  ATAACTCCCTGGGTCTTAGATTGCTCTATAAATACCTCCTAAGAGAAGAATTTTTCAAAT
127201  TATTGAGGGACCCAGAATCTAACGAGATATTTATGGAGGATTCTCTTCTTAAAAAGTTTA

127261  GACAGTTTCGTTTTTCCTTTTTCTTCTTTTAAAGCAACAAAGAAAAGCACGTCTGTGTTT
127261  CTGTCAAAGCAAAAAGGAAAAAGAAGAAAATTTCGTTGTTTCTTTTCGTGCAGACACAAA

127321  ATATTTAACCAAACTTAAACTTGGAGAGCATTGGCCGTGTTGTCGACGTGTTTCTTTTCT
127321  TATAAATTGGTTTGAATTTGAACCTCTCGTAACCGGCACAACAGCTGCACAAAGAAAAGA

127381  CTACTGTTAAATTCCTTACTGTTCCAGTTACTCACCATCATACTCACCTTTGCCTCTGCC
127381  GATGACAATTTAAGGAATGACAAGGTCAATGAGTGGTAGTATGAGTGGAAACGGAGACGG

127441  ACTTGGGGTCCTCTGTTCTGCAGTTGTGTTCTGCTCTCTGATGCCTCCAGGTTTTGCTGC
127441  TGAACCCCAGGAGACAAGACGTCAACACAAGACGAGAGACTACGGAGGTCCAAAACGACG

127501  ACCTTCTAGAAATTGCTCACCTGGATAAGGCCTTGGCTGTCCTTTATGACTCATCTCGTT
127501  TGGAAGATCTTTAACGAGTGGACCTATTCCGGAACCGACAGGAAATACTGAGTAGAGCAA

127561  CAGAAGCCTTTTGAATCTCTCTTGAAGAATATTCCCTTTGCTCAGTCCAAATACACATTC
127561  GTCTTCGGAAAACTTAGAGAGAACTTCTTATAAGGGAAACGAGTCAGGTTTATGTGTAAG

127621  ACTCACTTGAATGCTGCTTCTTCCTCCAGTTTCACAGTGCTGGGGATGATCCCGTAAGGC
127621  TGAGTGAACTTACGACGAAGAAGGAGGTCAAAGTGTCACGACCCCTACTAGGGCATTCCG

127681  CTTTAAATTACATTATAATTAGTCATGCACTTCTCTCTGCTCTGGGGCTGTTTGAATCGT
127681  GAAATTTAATGTAATATTAATCAGTACGTGAAGAGAGACGAGACCCCGACAAACTTAGCA

127741  TCACTCTCTTTATACCTCCAGTGTTCAGCACAGAGCCTAGGGTATAATGCGTATGCAGTA
127741  AGTGAGAGAAATATGGAGGTCACAAGTCGTGTCTCGGATCCCATATTACGCATACGTCAT

127801  ATGTTTCTTGAAGGAGTGAATGGGCAAGTGAAACACCAAACAAATACTAAAGAGCAAAAC
127801  TACAAAGAACTTCCTCACTTACCCGTTCACTTTGTGGTTTGTTTATGATTTCTCGTTTTG

127861  ATGTATTGCTCTTGTATATTAACACATTCCGAGAAGAGATGGGAGGAAGGTCTTGAATAA
127861  TACATAACGAGAACATATAATTGTGTAAGGCTCTTCTCTACCCTCCTTCCAGAACTTATT

127921  TATCAAATTATTTCTTAAGAGATCTTGATTTAGATTTTTTTCAAAATGAGATACATGTTG
127921  ATAGTTTAATAAAGAATTCTCTAGAACTAAATCTAAAAAAAGTTTTACTCTATGTACAAC

127981  ACACTGCTGTCAACAAATAATCACATAAAAGCTAGAGCCTGGCTTTTAAGTATCAGGGGG
127981  TGTGACGACAGTTGTTTATTAGTGTATTTTCGATCTCGGACCGAAAATTCATAGTCCCCC

128041  AGCATGTGTGAATAATCAGCATTGCTGCTGTTGAAGCTCCATAAAGTGGGAAGCAGCGAC
128041  TCGTACACACTTATTAGTCGTAACGACGACAACTTCGAGGTATTTCACCCTTCGTCGCTG

128101  TGCAAAGATCCAGAGATGGACATCTGAAGCATAGGAAAGGGGCAGCTTGAATGAGATAGG
128101  ACGTTTCTAGGTCTCTACCTGTAGACTTCGTATCCTTTCCCCGTCGAACTTACTCTATCC

128161  AGCAGGATCTGTATTGATTGCAGGTCACCAGATAGAATTAAAAAAATCTATGTTCTCACT
128161  TCGTCCTAGACATAACTAACGTCCAGTGGTCTATCTTAATTTTTTTAGATACAAGAGTGA

128221  AGTGGCTACAGTTTTCAAGGACAAATGACTATTAGTGGTTATTGTATTTTTCTTGTTTTC
128221  TCACCGATGTCAAAAGTTCCTGTTTACTGATAATCACCAATAACATAAAAAGAACAAAAG

128281  AATGGAGCAGCTCCATGACTTAGTTACATAAGAAGTTAAAGGCTCCACCCCCTTCCCTAC
128281  TTACCTCGTCGAGGTACTGAATCAATGTATTCTTCAATTTCCGAGGTGGGGGAAGGGATG

128341  CAATGTCTTAAGCTGTCCTCCGTGTGCATACAAACTTTGTTTCCAGACTGCCCTCGTGTG
128341  GTTACAGAATTCGACAGGAGGCACACGTATGTTTGAAACAAAGGTCTGACGGGAGCACAC

128401  ACTCAGTCCCTGGACCACCTTCCCAGCCCCTTCTGTTTCCACCACATCCTCCTCCACGTG
128401  TGAGTCAGGGACCTGGTCGAAGGGTCGGGGAAGACAAAGGTCGTGTAGGAGGAGGTGCAC
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FIGURE 4 (cont'd)

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128461  TTACAGCATTACAAAGCTTTGCACAGCCTTTCAATAGGGTTTAGAGCAAGAATCACACAT
128461  AATGTCCTAATGTTTCGAAACGTGTCGGAAAGTTATCCCAAATCTCGTTCTTACTGTCTA

128521  TGCTACCTGGTAGGCAGCACTGACTATAGTTTTATTGGCGTTGCGTAGAGTGACTGCATG
128521  ACGATGGACCATCCGTCGTGACTGATATCAAAATAACCGCAACGCATCTCACTGACGTAC

128581  ACATGCAGGTTGTGCTTTTGTTTTGCCAGGAATTTAAAGGCATTTAGCAAAGCCGTATGA
128581  TGTACGTCCAACACGAAAACAAAACGGTCCTTAAATTTCCGTAAATCGTTTCGGCATACT

128641  AATTATCTGCCTTATGTACCTCGAATGTGAGGTAATGAACTTGTCATTAGTCGTGTTTTA
128641  TTAATAGACGGAATACATGGAGCTTACACTCCATTACTTGAACAGTAATCAGCACAAAAT

128701  GTTTAGTGTTCTCGCTGGAATTTGCAAAAGATTAAAATTCTGCACATTTCATTAAGTCTT
128701  CAAATCACAAGAGCGACCTTAAACGTTTTCTAATTTTAAGACGTGTAAAGTAATTCAGAA

128761  CCACATGGGCTCAAAATACCATCCCGCAGGCTCGACCTGACTTGCCACGTTGCTTTGACA
128761  GGTGTACCCGAGTTTTATGGTAGGGCGTCCGAGCTGGACTGAACGGTGCAACGAAACTGT

128821  CCATCTCTGATTCCAGTGAACAAAACTAAGTAAGTGTGACTTACAGCCGCCCTACCAAAC
128821  GGTAGAGACTAAGGTCACTTGTTTTGATTCATTCACACTGAATGTCGGCGGGATGGTTTG

128881  ATTGAAGGTGTGAGCCTGCACTGTTGTTTTGTAATGACAATGACAAGAGTATAATGACAA
128881  TAACTTCCACACTCGGACGTGACAACAAAACATTACTGTTACTGTTCTCATATTACTGTT

128941  GAGTATAATGACATCCTAGTCCATGAAGACATGTTTTCTCTTTTCCCTCCCTCTATGTAT
128941  CTCATATTACTGTAGGATCAGGTACTTCTGTACAAAAGAGAAAAGGGAGGGAGATACATA

129001  ACTTACTTACTCTTAAGGAAATAATATAATTTCTATTTCTGCTTAAATCTGCCATCTCTA
129001  TGAATGAATGAGAATTCCTTTATTATATTAAAGATAAAGACGAATTTAGACGGTAGAGAT

129061  CTTAGAATTATTTTCCCTTGAAAAATTAAATTGCATTATCCATCAGCCAAATGGAAAATC
129061  GAATCTTAATAAAAGGGAACTTTTTAATTTAACGTAATAGGTAGTCGGTTTACCTTTTAG

129121  TGATTACTAAATGCCTACTTCTAGACATTATGAATTACCTGTAATATCACATTTCTTGGG
129121  ACTAATGATTTACGGATGAAGATCTGTAATACTTAATGGACATTATAGTGTAAAGAACCC

129181  CACTTCTCAGAATGCTATGATTTTACATAAAAGCATAAATTACAGAATGAGAAGAGTAAA
129181  GTGAAGAGTCTTACGATACTAAAATGTATTTTCGTATTTAATGTCTTACTCTTCTCATTT

129241  GCTTAGTGCATATTATGCAGGTTCGCAGAGTGATATGTGGCCTACGACTGTCATTGTAAT
129241  CGAATCACGTATAATACGTCCAAGCGTCTCACTATACACCGGATGCTGACAGTAACATTA

129301  CAAAATTGATTTTTGATCATTTATAAAACTAAAACAACTAATTGAAAGCAAATTTACTTT
129301  GTTTTAACTAAAAACTAGTAAATATTTTGATTTTGTTGATTAACTTTCGTTTAAATGAAA

129361  AACTGATGAAATTCAAGATGAAGTGACAGTAGTCATGAATCACAGTTCTGTAGATCTGCT
129361  TTGACTACTTTAAGTTCTACTTCACTGTCATCAGTACTTAGTGTCAAGACATCTAGACGA

129421  AAAATGCCAATGAACTGTTATTAATGGTGAAAGTGTTTAATATATTAATGGGAATCCAAG
129421  TTTTACGGTTACTTGACAATAATTACCACTTTCACAAATTATATAATTACCCTTAGGTTC

129481  TAAGGAAAATAAAACACATATTTTGCCCTTACCTTAAGTCATGTTGACATCATACATAAA
129481  ATTCCTTTTATTTTGTGTATAAAACGGGAATGGAATTCAGTACAACTGTAGTATGTATTT

129541  TCAGGTAGAATTTGAAGATGTTTCATCCAGCATTCATCATGAAGCAACAGAGTCAATAGC
129541  AGTCCATCTTAAACTTCTACAAAGTAGGTCGTAAGTAGTACTTCGTTGTCTCAGTTATCG

129601  GGGCAGTTACAGTCTGTAGGCAATGCTTTCTGGTGTGGATTATGCAAGAAACTTACAGTC
129601  CCCGTCAATGTCAGACATCCGTTACGAAAGACCACACCTAATACGTTCTTTGAATGTCAG

129661  ATTTGGCTTCCTTTATTCCCCTTTGCATGTAAACTACCAGGTGGTAGGTAGACCCATTCT
129661  TAAACCGAAGGAAATAAGGGGAAACGTACATTTGATGGTCCACCATCCATCTGGGTAAGA

129721  TGGCTGCCAGTATTTTTACCACTTGGATAGATTCTGCTCTCTGAGGTCTTTAAGACAAAC
129721  ACCGACGGTCATAAAAATGGTGAACCTATCTAAGACGAGAGACTCCAGAAATTCTGTTTG
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FIGURE 4 (cont'd)

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129781  ACACCACATGTACATTGTGATATAGGAGAAAGAACATCAGACAGAGGCAGAGAACTGGGC
129781  TGTGGTGTACATGTAACACTATATCCTCTTTCTTGTAGTCTGTCTCCGTCTCTTGACCCG

129841  TTGTCAAAATTAAGGGTGACCTAGAGCCTTAGTGTCCTTATATGTAAGATGAGAAGCTTG
129841  AACAGTTTTAATTCCCACTGGATCTCGGAATCACAGGAATATACATTCTACTCTTCGAAC

129901  GATTAAAATTCATTGCTCCTTACACTTGATTTTTATGCAGCAGAACTTTCTTCAAAAGAG
129901  CTAATTTTAAGTAACGAGGAATGTGAACTAAAAATACGTCGTCTTGAAAGAAGTTTTCTC

129961  ATCACTCCTGGAATCCCAATATACAAAATGGATAAAAGTAGGATTGTTCTGAAGTAAAGA
129961  TAGTGAGGACCTTAGGGTTATATGTTTTACCTATTTTCATCCTAACAAGACTTCATTTCT

130021  AGTAAAATCCAGAGCCCCACTTATTTGAGTCATCTCCTACCTTTTAGATGGTTATTAACA
130021  TCATTTTAGGTCTCGGGGTGAATAAACTCAGTAGAGGATGGAAAATCTACCAATAATTGT

130081  TTGTTTCTAGTTCAGAAATTCTGATGTTTTATATTAATTTAAACTAAAGTTAAATTAGGA
130081  AACAAAGATCAAGTCTTTAAGACTACAAAATATAATTAAATTTGATTTCAATTTAATCCT

130141  CTAGAAGAGCCATTTCGTGTGAAAATAGACATAGTCTGAGTGATTTAGGCAAACCCATAG
130141  GATCTTCTCGGTAAAGCACACTTTTATCTGTATCAGACTCACTAAATCCGTTTGGGTATC

130201  TGACAGATTTAGTGGCCTGATACACTGGCTTGGAAAGATCTGTTCCAAGTCAGTCTCAAT
130201  ACTGTCTAAATCACCGGACTATGTGACCGAACCTTTCTAGACAAGGTTCAGTCAGAGTTA

130261  ACACAAGGCTCGGTGAACACATGGCGAGCAGTCTTGGTGGTGGTCAAGAACATGGAATTT
130261  TGTGTTCCGAGCCACTTGTGTACCGCTCGTCAGAACCACCACCAGTTCTTGTACCTTAAA

130321  GCTGTGACAGAGAGCTTGGTTAGGGTCTGGGCTCTTCCATCTGTTAACTGCAAACTTGAG
130321  CGACACTCTCTCGAACCAATCCCAGACCCGAGAAGGTAGACAATTGACGTTTGAACTC

130381  CAAGTTATTCAATCTCCCTAATATTCAGTTTTCTCATTCATAAAATGGATTGATAATGGT
130381  GTTCAATAAGTTAGAGGGATTATAAGTCAAAAGAGTAAGTATTTTACCTAACTATTACCA

130441  ACCTTCTATGTACAGTTACTGTGGGTATTAAATGAGGTAATAAGCCTGTAAAACTCCTGG
130441  TGGAAGATACATGTCAATGACACCCATAATTTACTCCATTATTCGGACATTTTGAGGACC

130501  CATGATGACATTGGCCTACATTAATTGCTCACAGAGTGAGAACTTATTATAAACACAGGC
130501  GTACTACTGTAACCGGATGTAATTAACGAGTGTCTCACTCTTGAATAATATTTGTGTCCG

130561  ATTTTTGTTGAATGACTGACTGATTGAATGAATGAATATAGAACTAGCTTTCTATTTGTG
130561  TAAAAACAACTTACTGACTGACTAACTTACTTACTTATATCTTGATCGAAAGATAAACAC

130621  ATGTATGGAATATCTCTATTTCATTTAATTTCATTTTGAATATTAAAATTCAGGCTTGCT
130621  TACATACCTTATAGAGATAAAGTAAATTAAAGTAAAACTTATAATTTTAAGTCCGAACGA

130681  TTTAAACCAAAGTATTTGCTGATGCAAAGAATGAAATTCTGACTATGATACAGTTACATA
130681  AAATTTGGTTTCATAAACGACTACGTTTCTTACTTTAAGACTGATACTATGTCAATGTAT

130741  ACTTTTGAAGAAATAAGAAAAATGCTAACACAGCATGAACAACTTTGATTTAGAGAACAG
130741  TGAAAACTTCTTTATTCTTTTTACGATTGTGTCGTACTTGTTGAAACTAAATCTCTTGTC

130801  AGTCTCTGTTAAAATCCATGGGACTTGTCAACTTCATATTTTTGTTTATGAGCATAAAAC
130801  TCAGAGACAATTTTAGGTACCCTGAACAGTTGAAGTATAAAAACAAATACTCGTATTTTG

130861  ACTCTTTAGTGCATGTCGGAATCATTTGATGCTTGCTGAATCACAGGTTGCTGGAACCCA
130861  TGAGAAATCACGTACAGCCTTAGTAAACTACGAACGACTTAGTGTCCAACGACCTTGGGT

130921  TCCCCAGATTCTGATTCAGTCTGAGATGAGGTCTGGGAATTTGCATTTTTAACTTGTTGT
130921  AGGGGTCTAAGACTAAGTCAGACTCTACTCCAGACCCTTAAACGTAAAAATTGAACAACA

130981  CTGGTGATGCTGATGCTAGTGGTCTGAGAATACACTTTGAGGATCACTTTTTCACAGTAA
130981  GACCACTACGACTACGATCACCAGACTCTTATGTGAAACTCCTAGTGAAAAAGTGTCATT

131041  AAGTCACAGTCATTAAGCAAGTTAACTCAATGAGAAATGATAATGAAAAGGCATGTACCT
131041  TTCAGTGTCAGTAATTCGTTCAATTGAGTTACTCTTTACTATTACTTTTCCGTACATGGA

131101  AAATAGATAAAGGACCTATACCAGCTATGAATTTGAGTTCACCAATAATTCTAAAATTTG
131101  TTTATCTATTTCCTGGATATGGTCGATACTTAAACTCAAGTCGTTATTAACATTTTAAAC
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FIGURE 4 (cont'd)

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131161  TAATTCTTTTCAGCTATTTGGTTTTTAAAAAACTCCCTATGTATGCTTTTATCTTATGTT
131161  ATTAAGAAAAGTCCATAAACCAAAAATTTTTTGAGGGATACATACGAAAATAGAATACAA

131221  TTATATGGTGTCCCTCTTTTCCTCTCTTTCTCTCTAATCCAGTTTTTAATGTGAACATGT
131221  AATATACCACAGGGAGAAAAGGAGAGAAAGAGAGATTAGGTCAAAAATTACACTTGTACA

131281  TTAATGTGAAAATGTTGTTCAAAGCAGAAGCGAACCTTTTGTGTAACCTTGGCGGTATTA
131281  AATTACACTTTTACAACAAGTTTCGTCTTCGCTTGGAAAACACATTGGAACCGCCATAAT

131341  AGTTTGTTTGTAAGCTATTTCTGCCCTGTTAGCTTCTGTACTGAAACACGTTTTCTTGCT
131341  TCAAACAAACATTCGATAAAGACGGGACAATCGAAGACATGACTTTGTGCAAAAGAACGA

131401  TTTGTTGCAGTATGGAAGAGAAGAGAGCGACTGGACAATTGTGCTATCCTGAATGGAAAA
131401  AAACAACGTCATACCTTCTCTTCTCTCGCTGACCTGTTAACACGATAGGACTTACCTTTT

131461  TAGAGGATACAATGGAAAATAGAGGATACCAACTGTATGCTACTGGGACAGACTGTTGCA
131461  ATCTCCTATGTTACCTTTTATCTCCTATGGTTGACATACGATGACCCTGTCTGACAACGT

131521  TTTGAATTGTGATAGATTTCTTTGGCTACCTGTGCATAATGTAGTTTGTAGTATCAATGT
131521  AAACTTAACACTATCTAAAGAAACCGATGGACACGTATTACATCAAACATCATAGTTACA

131581  GTTACAAGAGTGATTGTTTCTTCATGCCAGAGAAAATGAATTGCAATCATCAAATGGTGT
131581  CAATGTTCTCACTAACAAAGAAGTACGGTCTCTTTTACTTAACGTTAGTAGTTTACCACA

131641  TTCATAACTTGGTAGTAGTAACTTACCTTACCTTACCTAGAAAAACATTAATGTAAGCCA
131641  AAGTATTGAACCATCATCATTGAATGGAATGGAATGGATCTTTTTGTAATTACATTCGGT

131701  TATAACATGGGATTTTCCTCAATGATTTTAGTGCCTCCTTTTGTACTTCACTCAGATACT
131701  ATATTGTACCCTAAAAGGAGTTACTAAAATCACGGAGGAAAACATGAAGTGAGTCTATGA

131761  AAATAGTAGTTTATTCTTTAATATAAGTTACATTCTGCTCCTCAAACAAATGCAATTTTT
131761  TTTATCATCAAATAAGAAATTATATTCAATGTAAGACGAGGAGTTTGTTTACGTTAAAAA

131821  TGTGTGTGTTTGAAAGCTAATTTGAGAAAATTTCATAGGTTACATTTCCTGCAGCCTATC
131821  ACACACACAAACTTTCGATTAAACTCTTTTAAAGTATCCAATGTAAAGGACGTCGGATAG

131881  TTTATCCACAGAAAGTGTTTTCTTTTTTTTAAATCAAGACTTTTAAAACTGGATTTCCTC
131881  AAATAGGTGTCTTTCACAAAAGAAAAAAAATTTAGTTCTGAAAATTTTGACCTAAAGGAG

131941  CCATCACTGTTTTTTGAAGGTCCTCCAAGTCCGTGTTAAGGTAAATATCTGTTTTCTTCC
131941  GGTAGTGACAAAAAACTTCCAGGAGGTTCAGGCACAATTCCATTTATAGACAAAAGAAGG

132001  TGATGTCACAGCCTGAGCATACTCTGTGCATTAGGAAGACCTGAGTGCATTTCCCACCAT
132001  ACTACAGTGTCGGACTCGTATGAGACACGTAATCCTTCTGGACTCACGTAAAGGGTGGTA

132061  TGTCCTTTCCACATTATGTTGTAGCTGGCTGGCTGTCAGGCGACTACAAGACTGAGGGTC
132061  ACAGGAAAGGTGTAATACAACATCGACCGACCGACAGTCCGCTGATGTTCTGACTCCCAG

132121  TTGTGCCTTATAGATCTTTGTATCCCCCATGGCTGACATATAGTAGGTACTCAGTAAATG
132121  AACACGGAATATCTAGAAACATAGGGGGTACCGACTGTATATCATCCATGAGTCATTTAC

132181  GTTTTATAATGAATCAGTGAACATTTTGCTTCTATAGAAGTGTACCTTCTTTGTTTCTAT
132181  CAAAATATTACTTAGTCACTTGTAAAACGAAGATATCTTCACATGGAAGAAACAAAGATA

132241  ATTATGAAACCTCTTTATTAGAATTTGTGATTGATTCTGACAGTGTATAGATTTACCTTA
132241  TAATACTTTGGAGAAATAATCTTAAACACTAACTAAGACTGTCACATATCTAAATGGAAT

132301  TATTGTCTTTATTTTCCATGAGCTACTAAGTCATTAGAGATACTCTGAAGCATAGTTAGT
132301  ATAACAGAAATAAAAGGTACTCGATGATTCAGTAATCTCTATGAGACTTCGTATCAATCA

132361  TTAGGAAATCACTTCATATTGATTGTATTAGAATTATCTTGGAATTGAAGATATATCCCT
132361  AATCCTTTAGTGAAGTATAACTAACATAATCTTAATAGAACCTTAACTTCTATATAGGGA

132421  AGAGCAGGGGACCCCAACCCCCAGGCCATGGGCCACACAGCAGGAAGAGGTGAGTGGTGG
132421  TCTCGTCCCCTGGGGTTGGGGGTCCGGTACCCGGTGTGTCGTCCTTCTCCACTCACCACC
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FIGURE 4 (cont'd)

132481 GCCATTGAGGAGCTTCATCTGTATTTATGGCTACTTCCCATCACTCGAATTACCACCTGA
132481 CGGTAACTCCTCGAAGTAGACATAAATACCGATGAAGGGTAGTGAGCTTAATGGTGGACT

132541 ACTCCACCTCTTGTCAGCTCAGTGGCAGCATTAGATTCTCATAGGAGCACAAATCCTATT
132541 TGAGGTGGAGAACAGTCGAGTCACCGTCGTAATCTAAGAGTATCCTCGTGTTTAGGATAA

132601 GTGAACTCTGCATGCAAGGGATCTAGGCTATGCGCTCCTTATGAGAATCTAATGCTTGAT
132601 CACTTGAGACGTACGTTCCCTAGATCCGATACGCGAGGAATACTCTTAGATTACGAACTA

132661 GACCTGAGGTGTAACAGTTTCATCCTGAAACCACCCTTCACCCTGCAGTCTGTGGAAAAA
132661 CTGGACTCCACATTGTCAAAGTAGGACTTTGGTGGGAAGTGGGACGTCAGACACCTTTTT

132721 TTGTCTTCCACAAAACTGGTCCCTGGTGCCAAAAATGTTGGGGACCACTGCTCTAGAGAG
132721 AACAGAAGGTGTTTTGACCAGGGACCACGGTTTTTACAACCCCTGGTGACGAGATCTCTC

132781 AGGTCATGATATCATACCAACCAAATGGAAATGACAAATGTTTTATGTCAAGTGTTAATT
132781 TCCAGTACTATAGTATGGTTGGTTTACCTTTACTGTTTACAAAATACAGTTCACAATTAA

132841 GCAGAAATAAATCTTTTTTTTTTTTTTTTGGTAGAAAACAAAGAGGCATACTCTGATTTT
132841 CGTCTTTATTTAGAAAAAAAAAAAAAAAACCATCTTTTGTTTCTCCGTATGAGACTAAAA

132901 TATACTCTGTTTTTGCAGGTGCTCTTTTCTTTGAATGGAGATTTGATGAGCAAGTGGTTA
132901 ATATGAGACAAAAACGTCCACGAGAAAAGAAACTTACCTCTAAACTACTCGTTCACCAAT

132961 GGATGCAGGGAGAGCTACTATGGGTGATATTTTCCTTGTTTAGGAGCTGTGAGTTAAAAT
132961 CCTACGTCCCTCTCGATGATACCCACTATAAAAGGAACAAATCCTCGACACTCAATTTTA

133021 TGTATCCTTTGTGGTTTATCTAAGGAAAGTCAAATCTTGACAGAAAACATTTTTCCTTGG
133021 ACATAGGAAACACCAAATAGATTCCTTTCAGTTTAGAACTGTCTTTTGTAAAAAGGAACC

133081 AAGGTCAACTCTCAGACATTGTATTTTGGTTTCCCTCAGTCCTCATAACTTCCTTCTTGC
133081 TTCCAGTTGAGAGTCTGTAACATAAAACCAAAGGGAGTCAGGAGTATTGAAGGAAGAACG

133141 TGAACATATTTTATTCTCTTTTCAGAGAAGGAAAATAAAAAGGATTCTAAAAGTTTGATG
133141 ACTTGTATAAAATAAGAGAAAAGTCTCTTCCTTTTATTTTTCCTAAGATTTTCAAACTAC

133201 CATTGGAAAAATTTCCTTGAGGCATTTAGCAACACATAGAAAATGGGCTTTGATTCTTTT
133201 GTAACCTTTTTAAAGGAACTCCGTAAATCGTTGTGTATCTTTTACCCGAAACTAAGAAAA

133261 CCAAAACTTTTAGCCATAGGGTCTTTTATAGACAGGGATAGTAAAATGAAAATTGAGAAA
133261 GGTTTTGAAAATCGGTATCCCAGAAAATATCTGTCCCTATCATTTTACTTTTAACTCTTT

133321 TATAAGATGAAAAGGAATGATAAAAATATCTTTTAGGGGGCTTTTAATTGGTGATCTGAA
133321 ATATTCTACTTTTCCTTACTATTTTTATAGAAAATCCCCCGAAAATTAACCACTAGACTT

133381 ATCTTGGGAGAAGCTGTTCTTTTCAGGCCTGAGGTGCTCTTGACTGTCGCCTGCGCACTG
133381 TAGAACCCTCTTCGACAAGAAAAGTCCGGACTCCACGAGAACTGACAGCGGACGCGTGAC

133441 TGTACCCCGAGCAACATTCTAAGGGTGTGCTTTCGCCTTGGCTAACTCCTTTGACCTCAT
133441 ACATGGGGCTCGTTGTAAGATTCCCACACGAAAGCGGAACCGATTGAGGAAACTGGAGTA

133501 TCTTCATATAGTAGTCTAGGAAAAAGTTGCAGGTAATTTAAACTGTCTAGTGGTACATAG
133501 AGAAGTATATCATCAGATCCTTTTTCAACGTCCATTAAATTTGACAGATCACCATGTATC

133561 TAACTAAATTTCTATTCCTATGAGAAATGAGAATTATTTATTTGCCATCAACACATTTTA
133561 ATTGATTTAAAGATAAGGATACTCTTTACTCTTAATAAATAAACGGTAGTTGTGTAAAAT

133621 TACTTTGCATCTCCAAATTTATTGTGGCGAGACTTGTCCATTGTGAAAGTTAGAGAACAT
133621 ATGAAACGTAGAGGTTTAAATAACACCGCTCTGAACAGGTAACACTTTCAATCTCTTGTA

133681 TATGTTTGTATCATTTCTTTCATAAAACCTCAAGAGCATTTTTAAGCCCTTTTCATCAGA
133681 ATACAAACATAGTAAAGAAAGTATTTTGGAGTTCTCGTAAAAATTCGGGAAAAGTAGTCT

133741 CCCAGTGAAAACTAAGGATAGATGTTTAAAAACTGGAGGTCTCCTGATAAGGAGAACACA
133741 GGGTCACTTTTGATTCCTATCTACAAATTTTTGACCTCCAGAGGACTATTCCTCTTGTGT

133801 ATCCACCATTGTCATTTAAGTAATAAGACAGGAAATTGACCTTGACGCTTTCTTGTTAAA
133801 TAGGTGGTAACAGTAAATTCATTATTCTGTCCTTTAACTGGAACTGCGAAAGAACAATTT

FIGURE 4 (cont'd)

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133861  TAGATTTAACAGGAACATCTGCACATCTTTTTTCCTTGTGCACTATTTGTTTAATTGCAG
133861  ATCTAAATTGTCCTTGTAGACGTGTAGAAAAAAGGAACACGTGATAAACAAATTAACGTC

133921  TGGATTAATACAGCAAGAGTGCCACATTATAACTAGGCAATTATCCATTCTTCAAGACTT
133921  ACCTAATTATGTCGTTCTCACGGTGTAATATTGATCCGTTAATAGGTAAGAAGTTCTGAA

133981  AGTTATTGTCACACTAATTGATCGTTTAAGGCATAAGATGGTCTAGCATTAGGAACATGT
133981  TCAATAACAGTGTGATTAACTAGCAAATTCCGTATTCTACCAGATCGTAATCCTTGTACA

134041  GAAGCTAATCTGCTCAAAAAGATCAACAAATTAATATTGTTGCTGATATTTGCATAATTG
134041  CTTCGATTAGACGAGTTTTTCTAGTTGTTTAATTATAACAACGACTATAAACGTATTAAC

134101  GCTGCAATTATTTAATGTTTAATTGGGTTGATCAAATGAGATTCAGCAATTCACAAGTGC
134101  CGACGTTAATAAATTACAAATTAACCCAACTAGTTTACTCTAAGTCGTTAAGTGTTCACG

134161  ATTAATATAAACAGAACTGGTGGCACTTAAAATGATAATGATTAACTTATATTGCATGTT
134161  TAATTATATTTGTCTTGACCACCGTGAATTTTACTATTACTAATTGAATATAACGTACAA

134221  CTCTTCCTTTCACTTTTTTCAGTTTCTACATTTCAGACCGAGCTTGTCAGCTTTTTTGAA
134221  GAGAAGGAAAGTGAAAAAAGTCAAAGATGTAAAGTCTGGCTCGAACAGTCGAAAAAACTT

134281  AACACATCAGTAGAAACCAAGATTTTAAAATGAAGTGTCAAGACAAAGGCAAAACCTGAG
134281  TTGTGTAGTCATCTTTGGTTCTAAAATTTTACTTCACAGTTCTGTTTCCGTTTTGGACTC

134341  CAGTTCCTAAAAAGATTTGCTGTTAGAAATTTTCTTTGTGGCAGTCATTTATTAAGGATT
134341  GTCAAGGATTTTTCTAAACGACAATCTTTAAAAGAAACACCGTCAGTAAATAATTCCTAA

134401  CAACTCGTGATACACCAAAAGAAGAGTTGACTTCAGAGATGTGTTCCATGCTCTCTAGCA
134401  GTTGAGCACTATGTGGTTTTCTTCTCAACTGAAGTCTCTACACAAGGTACGAGAGATCGT

134461  CAGGAATGAATAAATTTATAACACCTGCTTTAGCCTTTGTTTTCAAAAGCACAAAGGAAA
134461  GTCCTTACTTATTTAAATATTGTGGACGAAATCGGAAACAAAAGTTTTCGTGTTTCCTTT

134521  AGTGAAAGGGAAAGAGAAACAAGTGACTGAGAAGTCTTGTTAAGGAATCAGGTTTTTTCT
134521  TCACTTTCCCTTTCTCTTTGTTCACTGACTCTTCAGAACAATTCCTTAGTCCAAAAAAGA

134581  ACCTGGTAAACATTCTCTATTCTTTTCTCAAAAGATTGCTGTAAGAAAAAATGTAAGACA
134581  TGGACCATTTGTAAGAGATAAGAAAAGAGTTTTCTAACGACATTCTTTTTTACATTCTGT

134641  AAAAAAAAAAAAAAAAACAAACAGAGGCAGAGGCAGGCAGTAGCAAGAAAGCAGAGCGTA
134641  TTTTTTTTTTTTTTTTTGTTTGTCTCCGTCTCCGTCCGTCATCGTTCTTTCGTCTCGCAT

134701  ACATCAGCTAGATGGTAACATGCAATGTCAGCTCTCTTGAAGACATGGGAAACCTAAGTT
134701  TGTAGTCGATCTACCATTGTACGTTACAGTCGAGAGAACTTCTGTACCCTTTGGATTCAA

134761  ACACCTTGGGTTAAAATTCTTCACCATATTAGTTTTGTTGCTTCATAAAATTTACCTAAG
134761  TGTGGAACCCAATTTTAAGAAGTGGTATAATCAAAACAACGAAGTATTTTAAATGGATTC

134821  CAAGTGGTCTTGCTTGCCTCAAATCCAAGCAGTCTTGAACACTTGGAGGCAATTAATGAG
134821  GTTCACCAGAACGAACGGAGTTTAGGTTCGTCAGAACTTGTGAACCTCCGTTAATTACTC

134881  TATATCTTAGTCAAAAGAATTGTTGGAGCTTTTTATTAAAGCTACAGTTTCAGTTCTGCT
134881  ATATAGAATCAGTTTTCTTAACAACCTCGAAAAATAATTTCGATGTCAAAGTCAAGACGA

134941  TTTGGGGAATTGTGCTATGAAAGCAGCTGCCAAAATAAGCTCATTTATTTTCTTCAATCC
134941  AAACCCCTTAACACGATACTTTCGTCGACGGTTTTATTCGAGTAAATAAAAGAAGTTAGG

135001  CACTCAGTGCTCAGTCACTATATTCTGTTTCCTTTTTTTTTTTCAAGTTGCATATTTGGT
135001  GTGAGTCACGAGTCAGTGATATAAGACAAAGGAAAAAAAAAAAGTTCAACGTATAAACCA

135061  TTCCCCTTATGATTGGGAAAGATGAATTTTCAGCAGAAAACATTGTTTGTTCACTTTCAA
135061  AAGGGGAATACTAACCCTTTCTACTTAAAAGTCGTCTTTTGTAACAAACAAGTGAAAGTT

135121  AGAGTGATAGTTTCTAAAACATTTAGAGCAATAAATATTCATCAGAGGTACCAAGTAAGC
135121  TCTCACTATCAAAGATTTTGTAAATCTCGTTATTTATAAGTAGTCTCCATGGTTCATTCG
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FIGURE 4 (cont'd)

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135181   CGGCAGAAGAGTTAAGGGTTAGAGAAATCCCTTATTTCATGTCTTGACTCTAAAATTATC
135181   GCCGTCTTCTCAATTCCCAATCTCTTTAGGGAATAAAGTACAGAACTGAGATTTTAATAG

135241   AAAGTACTTTTCCTTGTAATGTGGATTTCTTCTTATGCGGATATGCAAAAACTTCAGTTA
135241   TTTCATGAAAAGGAACATTACACCTAAAGAAGAATACGCCTATACGTTTTTGAAGTCAAT

135301   TACGTAGTAATGCTAGCAGGTAATTTTAGTAGACATTTTATAACAACTGTCACTTTGTTT
135301   ATGCATCATTACGATCGTCCATTAAAATCATCTGTAAAATATTGTTGACAGTGAAACAAA

135361   CGCCACATGTAGAGTTTGTTCAGCTATTTTCCAGATATCTCCCCACAAAAGGAGGCAAAG
135361   GCGGTGTACATCTCAAACAAGTCGATAAAAGGTCTATAGAGGGGTGTTTTCCTCCGTTTC

135421   GGTACCAGCTTTTCAATGAGCATTACCTATTACTTGGCAAAGATGATGAAGACTCTATTA
135421   CCATGGTCGAAAAGTTACTCGTAATGGATAATGAACCGTTTCTACTACTTCTGAGATAAT

135481   ATAGTTCATTTGATAAATGTTGACATAACCAACAATAGAGATTAGGAAGTTAGTTTTAAG
135481   TATCAAGTAAACTATTTACAACTGTATTGGTTGTTATCTCTAATCCTTCAATCAAAATTC

135541   AAATCAATGGCATATAGACATTACCCTCATGGAGTTTGTATTCTACTACTTGAACTGATT
135541   TTTAGTTACCGTATATCTGTAATGGGAGTACCTCAAACATAAGATGATGAACTTGACTAA

135601   GTAGCTATAAAAGCATAGTTAGATAGCTGAATAGTTAGATCATAAGCAAAGAAGGCCAGA
135601   CATCGATATTTTCGTATCAATCTATCGACTTATCAATCTAGTATTCGTTTCTTCCGGTCT

135661   ACACATCTCTTATCAAGAAATCAATGAATAGTTTATCTCATTTTTAAAGCAACTTTATCC
135661   TGTGTAGAGAATAGTTCTTTAGTTACTTATCAAATAGAGTAAAAATTTCGTTGAAATAGG

135721   TTCTTTAATTCCTTCCTTTCTTCTAGTGCAAAACTACTTAATAAGGTTGGTGTTTAGGTT
135721   AAGAAATTAAGGAAGGAAAGAAGATCACGTTTTGATGAATTATTCCAACCACAAATCCAA

135781   AGTGTTCACACCATTCCTCATCTGGTGTGAATTACCTTCTCTTTCTTTACTATTTACTAC
135781   TCACAAGTGTGGTAAGGAGTAGACCACACTTAATGGAAGAGAAAGAAATGATAAATGATG

135841   CAACCTAGTACATGTGTTGACTGAATTCTTTTCAAACAATGTTGAGTTATCATGGTGCAC
135841   GTTGGATCATGTACACAACTGACTTAAGAAAAGTTTGTTACAACTCAATAGTACCACGTG

135901   CTAATAAATTAACACCACAGATTACAGCATCCTTGCTGATTTTCTCAGCAAAGCCAGATT
135901   GATTATTTAATTGTGGTGTCTAATGTCGTAGGAACGACTAAAAGAGTCGTTTCGGTCTAA

135961   AGATGGAAATAAACAAAGAAAATGATCCTAGAGTGAATTTTTCTAGAAAATATCTATTAT
135961   TCTACCTTTATTTGTTTCTTTTACTAGGATCTCACTTAAAAAGATCTTTTATAGATAATA

136021   GAACCATGCTGTTTAAAGTATTAGCTTGAAGGTGATGGATCCAGCTATTCAGAAAATAAC
136021   CTTGGTACGACAAATTTCATAATCGAACTTCCACTACCTAGGTCGATAAGTCTTTTATTG

136081   TTTCATATAACCATGATTTTGCACAGTATGAGGTCTTAAATGTGTGGAAAGAGATAAATT
136081   AAAGTATATTGGTACTAAAACGTGTCATACTCCAGAATTTACACACCTTTCTCTATTTAA

136141   TTTTATCATTACCACAAACCCCTTTTAAAGATTCAAAGGTGGAAGAAAGTGATTTATTTT
136141   AAAATAGTAATGGTGTTTGGGGAAAATTTCTAAGTTTCCACCTTCTTTCACTAAATAAAA

136201   TTCTCTTCAGCATACATATATAAAAGACTTGTCAGATGTTTAATTTGGGGAGGTTGATAA
136201   AAGAGAAGTCGTATGTATATATTTTCTGAACAGTCTACAAATTAAACCCCTCCAACTATT

136261   TGAAACATATCAACAGAGTATAGTAGTTATAGTAGTGTTTGTGGGTAAATAATTTCCTGG
136261   ACTTTGTATAGTTGTCTCATATCATCAATATCATCACAAACACCCATTTATTAAAGGACC

136321   GGTCAGACATATATAAACATATTTGCTTCAAAATGATAAAGGCATGAAATCAGTCTTAAA
136321   CCAGTCTGTATATATTTGTATAAACGAAGTTTTACTATTTCCGTACTTTAGTCAGAATTT

136381   AATTGAAATGGGGGTGATGGGGGAGAAAAAGAAGAACAAATTTGAAGTGCCCTTTCAAAT
136381   TTAACTTTACCCCCACTACCCCCTCTTTTTCTTCTTGTTTAAACTTCACGGGAAAGTTTA

136441   CTGCTGGATACAAGTATTGAAGTTTTAAGTCATCTTATTCTGTCTGAAAGTGTATTTTTC
136441   GACGACCTATGTTCATAACTTCAAAATTCAGTAGAATAAGACAGACTTTCACATAAAAAG

136501   ATTCTACAATAGACCCAATCAACAAGACGTATAACTTGAGTTGCATCATGTTCACTTTAT
136501   TAAGATGTTATCTGGGTTAGTTGTTCTGCATATTGAACTCAACGTACTACAAGTCAAATA
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FIGURE 4 (cont'd)

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136561  CTAATCTACTGTTCGGATCGTAACAATTCATGTAGCCTCTGGTGTAAGAATCAATTAAAA
136561  CATTAGATGACAACCCTACCATTCTTAACTACATCCGACACCACATTCTTACTTAATTTT

136621  TATAGTTTCACTGGCTTTTCTCTACATATCCACTATCACAATGGCTAGGTTTCCTGTTGC
136621  ATATCAAAGTGACCGAAAAGAGATGTATAGGTGATAGTGTTACCGATCCAAAGGACAACG

136681  TCACTATTGGATTCTGGAGAAAAATTTAATGAAAGATGATATCAGAGGAAGAATAAGTGG
136681  AGTGATAACCTAAGACCTCTTTTTAAATTACTTTCTACTATAGTCTCCTTCTTATTCACC

136741  AGGTAGAGAAGAAAGGAATGATAGAGGAGGGGAAAAAAACAAAACATATTTTTGTGTTAT
136741  TCCATCTCTTCTTTCCTTACTATCTCCTCCCCTTTTTTTGTTTTGTATAAAAACACAATA

136801  CCAAAGGAGCTTTTTCCTTATTCTGTCAAGCATTGAGATCTTCTTCAGCTTTCAATGTAG
136801  GGTTTCCTCGAAAAAGGAATAAGACAGTTCGTAACTCTAGAAGAAGTCGAAAGTTACATC

136861  TTGCTAAATACAAATAATGCTACTAGGTAGTGACTAAATATAGCAAACACTTCATCAGAT
136861  AACGATTTATGTTTATTACGATGATCCATCACTGATTTATATCGTTTGTGAAGTAGTCTA

136921  ATTAGAATTAGGTCACACTATTGAGGTTATAATCTGAAGGTTGTGTTACATAGAAACCAC
136921  TAATCTTAATCCAGTGTGATAACTCCAATATTAGACTTCCAACACAATGTATCTTTGGTG

136981  TTTAGATTATTATCAACTTGGACTAGGCTTTATTTTATAATAGCATAGTAAGTAATATCT
136981  AAATCTAATAATAGTTGAACCTGATCCGAAATAAAATATTATCGTATCATTCATTATAGA

137041  ATTGTGTCATTTCTTCAACCATTTTATTCTAAGATCCATGAAGCTTCTTGAGGCCAAATA
137041  TAACACAGTAAACAAGTTCGTAAAATAAGATTCTAGGTACTTCGAAGAACTCCGGTTTAT

137101  AAATAATAAGTTTAGACAAGAAGTAGATTGTGACTTTTTTCCCTTAGAGATACTATTTAC
137101  TTTATTATTCAAATCTGTTCTTCATCTAACACTGAAAAAAGGGAATCTCTATGATAAATG

137161  TATCTCCTATCCTGATAGGTGGAAGGTTTACTGAATTGGAAATTGGTTGACTATTAGTTT
137161  ATAGAGGATAGGACTATCCACCTTCCAAATGACTTAACCTTTAACCAACTGATAATCAAA

137221  TTAACTAAAATGTGCAATAACACATTGCAGTTTCCTCAAACTAGTTTCCTATGATCATTA
137221  AATTGATTTTACACGTTATTGTGTAACGTCAAAGGAGTTTGATCAAAGGATACTAGTAAT

137281  AACTCATTCTCAGGGTTAAGAAAGGAATGTAAATTTCTGCCTCAATTTGTACTTCATCAA
137281  TTGAGTAAGAGTCCCAATTCTTTCCTTACATTTAAAGACGGAGTTAAACATGAAGTAGTT

137341  TAAGTTTTTGAAGAGTGCAGATTTTTAGTCAGGTCTTAAAAATAAACTCACAAATCTGGA
137341  ATTCAAAAACTTCTCACGTCTAAAAATCAGTCCAGAATTTTTATTTGAGTGTTTAGACCT

137401  TGCATTTCTAAATTCTGCAAATGTTTCCTGGGGTGACTTAACAAGGAATAATCCCACAAT
137401  ACGTAAAGATTTAAGACGTTTACAAAGGACCCCACTGAATTGTTCCTTATTAGGGTGTTA

137461  ATACCTAGCTACCTAATACATGGAGCTGGGGCTCAACCCACTGTTTTTAAGGATTTGCGC
137461  TATGGATCGATGGATTATGTACCTCGACCCCGAGTTGGGTGACAAAAATTCCTAAACGCG

137521  TTACTTGTGGCTGAGGAAAAATAAGTAGTTCGAGGAAGTAGTTTTTAAATGTGAGCTTAT
137521  AATGAACACCGACTCCTTTTTATTCATCAAGCTCCTTCATCAAAAATTTACACTCGAATA

137581  AGATAGAAACAGAATATCAACTTAATTATGAAATTGTTAGAACCTGTTCTCTTGTATCTG
137581  TCTATCTTTGTCTTATAGTTGAATTAATACTTTAACAATCTTGGACAAGAGAACATAGAC

137641  AATCTGATTGCAATTACTATTGTACTGATAGACTCCAGCCATTGCAAGTCTCAGATATCT
137641  TTAGACTAACGTTAATGATAACATGACTATCTGAGGTCGGTAACGTTCAGAGTCTATAGA

137701  TAGCTGTGTAGTGATTCTTGAAATTCTTTTTAAGAAAAATTGAGTAGAAAGAAATAAACC
137701  ATCGACACATCACTAAGAACTTTAAGAAAAATTCTTTTTAACTCATCTTTCTTTATTTGG

137761  CTTTGTAAATGAGGCTTGGCTTTTGTGAAAGATCATCCGCAGGCTATGTTAAAAGCATTT
137761  GAAACATTTACTCCGAACCGAAAACACTTTCTAGTAGGCGTCCGATACAATTTTCCTAAA

137821  TAGCTCACTAAAAGTGTAATAATGGAAATGTGGAAAATATCGTAGGTAAAGGAAACTACC
137821  ATCGAGTGATTTTCACATTATTACCTTTACACCTTTTATAGCATCCATTTCCTTTGATGG
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FIGURE 4 (cont'd)

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137881  TCATGCTCTGAAGGTTTTGTAGAAGCACAATTAAACATCTAAAATGGCTTTGTTACACCA
137881  AGTACGACACTTCCAAAACATCTTCGTGTTAATTTGTAGATTTTACCGAAACAATGTGGT

137941  GAGCCATCTGGTGTGAAGAACTCTATATTTGTATGTTGAGAGGGCATGGAATAATTGTAT
137941  CTCGGTAGACCACACTTCTTGAGATATAAACATACAACTCTCCCGTACCTTATTAACATA

138001  TTTGCTGGCAATAGACACATTCTTTATTATTTGCAGATTCCTCATCAAATCTGTAATTAT
138001  AAACGACCGTTATCTGTGTAAGAAATAATAAACGTCTAAGGAGTAGTTTAGACATTAATA

138061  GCACAGTTTCTGTTATCAATAAAACAAAAGAATCCTGTTTGTGTGGTTTCATGAAATCAG
138061  CGTGTCAAAGACAATAGTTATTTTGTTTTCTTAGGACAAACACACCAAAGTACTTTAGTC

138121  CATTGTTGAATGCATGAAGTAATAATGCTAAATTAACATTTTTATGATGTCTCAAGGTTT
138121  GTAACAACTTACGTACTTCATTATTACGATTTAATTGTAAAAATACTACAGAGTTCCAAA

138181  CTGGTCAAGGGAAGTAAATGTAGGATAGTATTTTTACACCAAAATGACACAGAGAGAATT
138181  GACCAGTTCCCTTCATTTACATCCTATCATAAAAATGTGGTTTTACTGTGTCTCTCTTAA

138241  GAGCACACCAGAAAGACCAGAAACCACACCACTGGATAGAGATTCAATATGTTTCTTTTT
138241  CTCGTGTGGTCTTTCTGGTCTTTGGTGTGGTGACCTATCTCTAAGTTATACAAAGAAAAA

138301  CAAACATTTGGACAAGAAAAAAATGGGCATTTAAAAATTCTTCCTTCCCCTGGTTATGGA
138301  GTTTGTAAACCTGTTCTTTTTTTACCCGTAAATTTTTAAGAAGGAAGGGGACCAATACCT

138361  TTTATCTGTAGTAAAACTTAGCTTTGTCGTTTGAGATTTGCACAGAATGGGGGGAGTAGA
138361  AAATAGACATCATTTTGAATCGAAACAGCAAACTCTAAACGTGTCTTACCCCCCTCATCT

138421  TTACCTCTTCCCATTCATTGTCATAATGGATCTACATCACTGATAAACACCATACTTCTA
138421  AATGGAGAAGGGTAAGTAACAGTATTACCTAGATGTAGTGACTATTTGTGGTATGAAGAT

138481  TATGTGGTTAACTAGCTTTAGAATAAAAGACACTTTAAAAAGTAAAAGGCCTAGAGATCT
138481  ATACACCAATTGATCGAAATCTTATTTTCTGTGAAATTTTTCATTTTCCGGATCTCTAGA

138541  TCAATGAAGTGTCCCTTTTAGCCAAACCAGGCCTTGCAGAAATTGTCCTCAAAAGCACCA
138541  AGTTACTTCACAGGGAAAATCGGTTTGGTCCGGAACGTCTTTAACAGGAGTTTTCGTGGT

138601  AGGGAGAACAAAGCCAAGTGCAGAATTACCCAAGGGTCACACATTTTGTATTCATTTTCT
138601  TCCCTCTTGTTTCGGTTCACGTCTTAATGGGTTCCCAGTGTGTAAAACATAAGTAAAAGA

138661  TATAATTTGCCCAAATGATTTGAAGTACAGCAAAACCTGAAGTTTTGCAAAGAGTTACTG
138661  ATATTAAACGGGTTTACTAAACTTCATGTCGTTTTGGACTTCAAAACGTTTCTCAATGAC

138721  TAAACTGAACTTAAAAATGTCAGAGTGCTCGGTGACCCACTTCTCCAGACCCTGTCAACC
138721  ATTTGACTTGAATTTTTACAGTCTCACGAGCCACTGGGTGAAGAGGTCTGGGACAGTTGG

138781  TGTGAAAATATTGGCCTTTATTCAGATCTCTCAAGAAGTTACGCGCAGAGTTTGGAAGGT
138781  ACACTTTTATAACCGGAAATAAGTCTAGAGAGTTCTTCAATGCGCGTCTCAAACCTTCCA

138841  CTAGGCAAAGGTTATTAGTCAAGTGTTCTTACAGTGTCAACGCTCAATTCCCACAAGCGT
138841  GATCCGTTTCCAATAATCAGTTCACAAGAATGTCACAGTTGCGAGTTAAGGGTGTTCGCA

138901  GAGAAAGAGAGACCTGTCATTCCTGAGGGTGATGACATACATTTACTGGAGCTTATATAA
138901  CTCTTTCTCTCTGGACAGTAAGGACTCCCACTACTGTATGTAAATGACCTCGAATATATT

138961  TTTATCAGATAAGACAGCAGTTTCCTTCAGGGTAGAAAGTGTGTTTTCTACATTGATTTA
138961  AAATAGTCTATTCTGTCGTCAAAGCAAGTCCCATCTTTCACACAAAAGATGTAACTAAAT

139021  GTACAAAACAAAAAGAAAAGGGGATATTTCAAATTTTATAATTATTTTTCTGCTAAGCTG
139021  CATGTTTTGTTTTTCTTTTCCCCTATAAAGTTTAAAATATTAATAAAAAGACGATTCGAC

139081  ATTCAGTGTGATTTAAGCATATTTTTCAAATCATGAATCTGATTCCATATACATATGTGC
139081  TAAGTCACACTAAATTCGTATAAAAAGTTTAGTACTTAGACTAAGGTATATGTATACACG

139141  CTTATATTGTGATAATTTATTTTTAAGTGAAATATGCTATCATAGCCTGACTTTATGTAT
139141  GAATATAACACTATTAAATAAAAATTCACTTTATACGATAGTATCGGACTGAAATACATA

139201  AGTGGTGACAACTTCCACGATCGCATTTCTGTAACCAAACGGCCGACACCTGAGGTGTAC
139201  TCACCACTGTTGAACGTCCTAGCGTAAAGACATTGGTTTGCCGGCTGTCGACTCCACATC
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FIGURE 4 (cont'd)

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139261   ATGCTTCCTATGGTCTGTAGAATAATCACTGGGCTTGTTCTCTAGCTATGTCTGTATGCA
139261   TACGAAGGATACCAGACATCTTATTAGTGACCCGAACAAGAGATCGATACAGACATACGT

139321   ATCGCGACAGTGTTGATCAAAACCCATGATCATTCTCTCCAAAGGTCTTTGTCACTAAGC
139321   TAGCGCTGTCACAACTAGTTTTGGGTACTAGTAAGAGAGGTTTCCAGAAACAGTGATTCG

139381   CACTAGGGATTCTGAAAAGTTCGTGAGCTGAAACAAATAAATTGAGTTGGAAGATT
139381   GTGATCCCTAAGACTTTTCAAGCACTCGACTTTGTTTATTTAACTCAACCTTCTAA
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FIGURE 5

>hg19_refGene_NM_001220776 range=chr7:50342378-50472798 5'pad=0 3'pad=0 strand=+ repeatMasking=none

IKZF1 runs on plus strand.

YELLOW: SUB-REGION OF INTEREST TOWARDS WHICH AN EXAMPLE OF A BISULPHITE CONVERSION AND METHYLATION SPECIFIC ASSAY IS GIVEN

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   1  CCTGTCTCTGGTGTGCCCTGGCCCCCGACTTGGAGGCCTCCTGGGCCAGGCCAAGACCTT
   1  GGACAGAGACCACACGGGACCGGGGGCTGAACCTCCGGAGGACCCGGTCCGGTTCTGGAA

  61  CCCCGGCAGCGATGGTCTCCAGCCACACTCAACTGCCCTGAAGGGACATTTCCTGCTTAT
  61  GGGGCCGTCGCTACCAGAGGTCGGTGTGAGTTGACGGGACTTCCCTGTAAAGGACGAATA

 121  TCCCTTGCCCGGCTGTGTCCTCCACCCGGAAGGCCTGTGCCTTCTTCGCCTGCATGTCCT
 121  AGGGAACGGGCCGACACAGGAGGTGGGCCTTCCGGACACGGAAGAAGCGGACGTACAGGA

 181  ACCCTGAGGAGGCTCCCTTGGTCTTTCATCGCTCTCCCTATGGGTCTTCACGCCTTCCCG
 181  TGGGACTCCTCCGAGGGAACCAGAAAGTAGCGAGAGGGATACCCAGAAGTGCGGAAGGGC

 241  AACCACCGCGCCCAAGCAGGAGCACGTTCTCGGCCCTCTTCACAGGGCGCTCCTCCTCAC
 241  TTGGTGGCGCGGGTTCGTCCTCGTGCAAGAGCCGGGAGAAGTGTCCCGCGAGGAGGAGTG

 301  AGGGGTGCCCGGGATTTTTATTCTGTGCCTTCCTGGTGGCTCCTACAAGTCTGGAAGGGC
 301  TCCCCACGGGCCCTAAAAATAAGACACGGAAGGACCACCGAGGATGTTCAGACCTTCCCG

 361  AGGAGGCGCATCTCACTCCTCTGGGTCCCCTCCCCTAGCGCCTGCCGGGAGCCCAGGCTG
 361  TCCTCCGCGTAGAGTGAGGAGACCCAGGGGAGGGGATCGCGGACGGCCCTCGGGTCCGAC

 421  CATTTGTGGAATTCATGACTTTTTCTCTCCTGCTCAAGCTGAACACATTGCTGGCTCCTG
 421  GTAAACACCTTAAGTACTGAAAAAGAGAGGACGAGTTCGACTTGTGTAACGACCGAGGAC

 481  CTCGGGTGGAGCCCGGCTAATTAGAGTGAGGGGCTCCCCGTAGGGCGAAGGGGTGCGCTG
 481  GAGCCCACCTCGGGCCGATTAATCTCACTCCCCGAGGGGCATCCCGCTTCCCCACGCGAC

 541  TCAGATGTGGCATTCCCGTTTTACGGAGACACACGGTGTCTTACACGCCAGGGAGAGGTC
 541  AGTCTACACCGTAAGGGCAAAATGCCTCTGTGTGCCACAGAATGTGCGGTCCCTCTCCAG

 601  TGAGACGCAAAGAGCCGTCGAGCGGGCTGCGGGATTGCTTCGCTGTCACCTCCGCCTGCA
 601  ACTCTGCGTTTCTCGGCAGCTCGCCCGACGCCCTAACGAAGCGACAGTGGAGGCGGACGT

 661  GCCACCCTTCCGCACGCACTTGTGTGTGCACCCAGGCCAACATGGAAGGCGCCATCCTAA
 661  CGGTGGGAAGGCGTGCGTGAACACACACGTGGGTCCGGTTGTACCTTCCGCGGTAGGATT

 721  CTTCTGCCGTGAGCAGGTGGGAGGGAAGAGAGACGAGAGGTATTCCATTGGTTGTCTGGG
 721  GAAGACGGCACTCGTCCACCCTCCCTTCTCTCTGCTCTCCATAAGGTAACCAACAGACCC

 781  AAAATGAATTGCACCTTCCCCTCCCTTGCGGAGGATCAACTTTTCCCACCCCCTCGGGTG
 781  TTTTACTTAACGTGGAAGGGGAGGGAACGCCTCCTAGTTGAAAAGGGTGGGGGAGCCCAC

 841  GGCACTCGCATCCTGGGGCCGGAGCCTGAACCCGGGAGCCAAGGGGCCCCAGTTCCAGGG
 841  CCGTGAGCGTAGGACCCCGGCCTCGGACTTGGGCCCTCGGTTCCCCGGGGTCAAGGTCCC

 901  ACGTGAAGCTGAGCGTACAGCGGGCGCTCCCAGACACTGGGGAAAGTGCTTTACGATGTC
 901  TGCACTTCGACTCGCATGTCGCCCGCGAGGGTCTGTGACCCCTTTCACGAAATGCTACAG

 961  CCGAGTCCCTCCAGTCTCGCCAGCGGGGCGAGCGTGAGGGTGCCCCGACCGACCAGCGGC
 961  GGCTCAGGGAGGTCAGAGCGGTCGCCCCGCTCGCACTCCCACGGGGCTGGCTGGTCGCCG

1021  CCCGGGTGCAGGGTGGCGGGCCCGGCGGCGCGCGTCCCCCTCCCCCTCCTGGCGGCCCGC
1021  GGGCCCACGTCCCACCGCCCGGGCCGCCGCGCGCAGGGGGAGGGGGAGGACCGCCGGGCG

1081  ACGTGTCGCCCGCGCCGCGCCCCCACGGGTTACGCGCGGGTCCCGCAGCGCCGCGGCCGA
1081  TGCACAGCGGGCGCGGCGCGGGGGTGCCCAATGCGCGCCCAGGGCGTCGCGGCGCCGGCT

1141  GCCGGGCTGCCCGGCCCGCGGACACAGCGCCGGCCGCCGCATCCCGTGCGGGGCCGCGGC
1141  CGGCCCGACGGGCCGGGCGCCTGTGTCGCGGCCGGCGGCGTAGGGCACGCCCCGGCGCCG
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1201   GCGATGCTGCGCTGGAATGAGGAAGCGCGGCGGCGAGGGGAGGGCCCGGGCGCGGTGCGC
1201   CGCTACGACGCGACCTTACTCCTTCGCGCCGCCGCTCCCCTCCCGGGCCCGCGCCACGCG

1261   GCGGGGGTGGCGGCGGCGCGCCGAGCGGGCCCGGCGCGGGCGAGCGGGCTGCAGCCGGCG
1261   CGCCCCCACCGCCGCCGCGCGGCTCGCCCGGGCCGCGCCCGCTCGCCCGACGTCGGCCGC

1321   GCGGCGCCAGCAGGTACGGCCCGCACCCGCCGCCGCCCCGGCGGCCTTTGGGGGCTGAGC
1321   CGCCGCGGTCGTCCATGCCGGGCGTGGGCGGCGGCGGGGCCGCCGGAAACCCCCGACTCG

1381   CGGAGCCCGGCGCGATTGCAAAGTTTTCGTGCGCGGCCCCTCTGGCCCGGAGTTGCGCCT
1381   GCCTCGGGCCGCGCTAACGTTTCAAAAGCACGCGCCGGGGAGACCGGGCCTCAACGCGGA

1441   GAGACGCGCGCCGCGCGAGCCGGGGGACTCGGCGACGGGGCGGGGACGGGACGACGCACC
1441   CTCTGCGCGCGGCGCGCTCGGCCCCCTGAGCCGCTGCCCCGCCCCTGCCCTGCTGCGTGG

1501   CTCTCCGTGTCCCGCTCTGCGCCCTTCTGCGCGCCCCGCTCCCTGTACCGGAGCAGCGAT
1501   GAGAGGCACAGGGCGAGACGCGGGAAGACGCGCGGGGCGAGGGACATGGCCTCGTCGCTA

1561   CCGGGAGGCGGCCGAGAGGTGCGCGCGGGGCCGAGCCGGCTGCGGGGCAGGTCGAGCAGG
1561   GGCCCTCCGCCGGCTCTCCACGCGCGCCCCGGCTCGGCCGACGCCCCGTCCAGCTCGTCC

1621   GACCGCCAGCGTGCGTCACCCCAAAGTTTGCGGGGTGGCAGGGCGCGCGCTCTGGCCACC
1621   CTGGCGGTCGCACGCAGTGGGGTTTCAAACGCCCCACCGTCCCGCGCGCGAGACCGGTGG

1681   CGCCGCTCTGGGCGGCAGCTGGTGGCAACGCAAGGGCGCGGCGGGGGCGGCCGGCGCGGA
1681   GCGGCGAGACCCGCCGTCGACCACCGTTGCGTTCCCGCGCCGCCCCCGCCGGCCGCGCCT

1741   GGGGGCCAGGTACGGGGCCCGCGGGCGGCGCTGTGCGCGCGGGGCAGCCGGTCGGCCGGG
1741   CCCCCGGTCCATGCCCCGGGCGCCCGCCGCGACACGCGCGCCCCGTCGGCCAGCCGGCCC

1801   AGCGCGAAAGCCTGGTCTGAGCCGGCTGGGGGCGGGGAGTGTGGCGGAGAAATGGGGAAC
1801   TCGCGCTTTCGGACCAGACTCGGCCGACCCCCGCCCCTCACACCGCCTCTTTACCCCTTG

1861   AATGCGAGTGAGCAACTTCAGGAAGTCATTGTGAAAGAAAGCTGGGAAGAGCTCCGCGGC
1861   TTACGCTCACTCGTTGAAGTCCTTCAGTAACACTTTCTTTCGACCCTTCTCGAGGCGCCG

1921   CAAGTTAGCAGGACACTCTAACAAGTGACTGCGCGGCCCGCGCCCGGGGCGGTGACTGCG
1921   GTTCAATCGTCCTGTGAGATTGTTCACTGACGCGCCGGGCGCGGGCCCCGCCACTGACGC

1981   GCAAGCCCCCTGGGTCCCCGCGCGGCGCATCCCAGCCTGGGCGGGACGCTCGGCCGCGGC
1981   CGTTCGGGGGACCCAGGGGCGCGCCGCGTAGGGTCGGACCCGCCCTGCGAGCCGGCGCCG

2041   GAGGCGGGCAAGCCTGGCAGGGCAGAGGGAGCCCCGGCTCCGAGGTTGCTCTTCGCACCC
2041   CTCCGCCCGTTCGGACCGTCCCGTCTCCCTCGGGGCCGAGGCTCCAACGAGAAGCGTGGG

2101   GAGGATCAGTCTTGGCCCCAAAGCGCGACGCACAAATCCACGTGAGTGTTTTCAAATTGA
2101   CTCCTAGTCAGAACCGGGGTTTCGCGCTGCGTGTTTAGGTGCACTCACAAAAGTTTAACT

2161   ATTTCAATAGGAAAACTTGGGGTAACTGGTGAATTTAAAAAAAAAAAAACACAGTAAAGA
2161   TAAAGTTATCCTTTTGAACCCCATTGACCACTTAAATTTTTTTTTTTTTGTGTCATTTCT

2221   AAAGCGGTAAGGTTGGTAGACCCTGGTGTCGCTCAGGTCCGCCTCTCTTTTCTGAGGACA
2221   TTTCGCCATTCCAACCATCTGGGACCACAGCGAGTCCAGGCGGAGAGAAAAGACTCCTGT

2281   GTGAGAGAGTTCACTTCTGTCAAGCGTCTGTTGCTCTGCACTGTGCCAGCAGGTGCAGGA
2281   CACTCTCTCAAGTGAAGACAGTTCGCAGACAACGAGACGTGACACGGTCGTCCACGTCCT

2341   CCAGGCCCACATGGGACACTTCTGAGCAGCCCCGCTGTCACCAGGAGAGGAGTTCTAGCT
2341   GGTCCGGGTGTACCCTGTGAAGACTCGTCGGGGCGACAGTGGTCCTCTCCTCAAGATCGA

2401   CCCAACCATATTTAAATTTATGTAGACCTACATATACCCACGGAAGTCAGCCTTTATAAA
2401   GGGTTGGTATAAATTTAAATACATCTGGATGTATATGGGTGCCTTCAGTCGGAAATATTT

2461   GTCGTGTGTAAAGAGTTTTCCTTATATTTGAGCCGGGAGCTTTCTTTTTATACTATAAAT
2461   CAGCACACATTTCTCAAAAGGAATATAAACTCGGCCCTCGAAAGAAAAATATGATATTTA

2521   ATGATGAGATCGAGTCTGAACTTAATTTCTGCAAGAGAGGAATTATCCCGGCTTTGAAAA
2521   TACTACTCTAGCTCAGACTTGAATTAAAGACGTTCTCTCCTTAATAGGGCCGAAACTTTT

2581   GTTAGTCCTTTTGCTGACCGCAGGTTTGACGCTCAAGTCACCAAACCTTCTCAGGAAAAC
2581   CAATCAGGAAAACGACTGGCGTCCAAACTGCGAGTTCAGTGGTTTGGAAGAGTCCTTTTG

2641   CCTTAGTAATATTAAGGCATCAGGTTACTTGCCGTTATATTTGAAATGTATTTTAAATAT
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2641  GCAATCATTATAATTCCGTAGTCCAATGAACGCCAATATAAACTTTACATAAAATTTATA

2701  TTGTCAAGCATCGCTGCTGATGCCTAAGGAACCTCGTGAGGGCTTGTTTTTCCTTCTAAT
2701  AACAGTTCGTAGCGACGACTACGGATTCCTTGGAGCACTCCCGAACAAAAAGGAAGATTA

2761  TTGGAGGCATCTAATGACCGAAAACCGTAGCGATTCCATAGGGTCTGACCAGGCACAGCT
2761  AACCTCCGTAGATTACTGGCTTTTGGCATCGCTAAGGTATCCCAGACTGGTCCGTGTCGA

2821  TTCAAATGCAGCTTCCCTCTCTCTAGGGACTGCAGCCCACCCAGACTGAATTTCAATGCG
2821  AAGTTTACGTCGAAGGGAGAGAGATCCCTGACGTCGGGTGGGTCTGACTTAAAGTTACGC

2881  GTGCGCTTTGCTTAGGTTACCCACTCACAATTTCCCACTGCGCCGCAGGCAGTATATTTC
2881  CACGCGAAACGAATCCAATGGGTGAGTGTTAAAGGGTGACGCGGCGTCCGTCATATAAAG

2941  AGCTTTGAGATACCTTGTTTTAAAATTCCAGACAAAATGGTGTTGAGGAAATGTCTCCTT
2941  TCGAAACTCTATGGAACAAAATTTTAAGGTCTGTTTTACCACAACTCCTTTACAGAGGAA

3001  ACTAGTCCCATCAACTTCTGTTAAAAGAGGAAAATTTATGGAATTTGAAAATACTGCGTA
3001  TGATCAGGGTAGTTGAAGACAATTTTCTCCTTTTAAATACCTTAAACTTTTATGACGCAT

3061  TGATATTTAAACTTTCATAGACATTCAAATGCTTTTAAGGCCAGGTTCAATTTGGTTATG
3061  ACTATAAATTTGAAAGTATCTGTAAGTTTACGAAAATTCCGGTCCAAGTTAAACCAATAC

3121  AGTCGAGGGGTGGGGGGGACCCACATAGAAATGTCCTGGGTCCTCTTGAGTTTATTTCTT
3121  TCAGCTCCCCACCCCCCCTGGGTGTATCTTTACAGGACCCAGGAGAACTCAAATAAAGAA

3181  TGTTTGAAGATGTTTGTTCAATGAGTTTTATTGTACTCATCTTTTATATGGAATTTTAAA
3181  ACAAACTTCTACAAACAAGTTACTCAAAATAACATGAGTAGAAAATATACCTTAAAATTT

3241  AAGTAACAATTTCAGTATTATTTATATTAGAATGTGTCAGAATTATTTCCGTGACAAATC
3241  TTCATTGTTAAAGTCATAATAAATATAATCTTACACAGTCTTAATAAAGGCACTGTTTAG

3301  AGATCATTTGGGCTATGGCTTAAAATGTACACGAGGCAAATATTCATGACAAGAAGATTC
3301  TCTAGTAAACCCGATACCGAATTTTACATGTGCTCCGTTTATAAGTACTGTTCTTCTAAG

3361  ACCTTCTTACGCTGGCATCTTGTAAAATCCAGAACAACTTAAAGAAATAATGTGTACACA
3361  TGGAAGAATGCGACCGTAGAACATTTTAGGTCTTGTTGAATTTCTTTATTACACATGTGT

3421  TACAAATAATGATGTCACATTAAAAATACTACACTATTCTTGCTTGATGGAATGTATCTG
3421  ATGTTTATTACTACAGTGTAATTTTTATGATGTGATAAGAACGAACTACCTTACATAGAC

3481  ATTTCCAATTTCACCATGAACATATTTCATACATTTTTTACATGAAAAAAAACGTGACTC
3481  TAAAGGTTAAAGTGGTACTTGTATAAAGTATGTAAAAAATGTACTTTTTTTTGCACTGAG

3541  TTAACTCTCACAGTCAATCAGAGCTGGTGACCAGAACATTTTATTGAACTAAATGGTCAT
3541  AATTGAGAGTGTCAGTTAGTCTCGACCACTGGTCTTGTAAAATAACTTGATTTACCAGTA

3601  GTTTTCTTCCCCTTTTGTTTCACGGTGAGAGTTGAAGGAAGGAGTTTAGAAACTCTCCAG
3601  CAAAAGAAGGGGAAAACAAAGTGCCACTCTCAACTTCCTTCCTCAAATCTTTGAGAGGTC

3661  TACTTGTTTAATTCATCAGTGTTCTAATTAGAGTGGTACCTCTTGGAAAACTACACACCC
3661  ATGAACAAATTAAGTAGTCACAAGATTAATCTCACCATGGAGAACCTTTTGATGTGTGGG

3721  CCCTAATGCAGAAACATCATAGCAATAATCACCCACCCTCAGGGTCTCCAGGAGACCACA
3721  GGGATTACGTCTTTGTAGTATCGTTATTAGTGGGTGGGAGTCCCAGAGGTCCTCTGGTGT

3781  AGGGCTGCAGATAAAAGTCTGGATGTGTTAGGTTTGACCCTTTCGAAGAGTTTTACACAG
3781  TCCCGACGTCTATTTTCAGACCTACACAATCCAAACTGGGAAAGCTTCTCAAAATGTGTC

3841  GCTCCTAAAGAGAAGATCAGCTGTGGCCGTTTGTAGCCATTTCCTTTGTCGAAAAACTAA
3841  CGAGGATTTCTCTTCTAGTCGACACCGGCAAACATCGGTAAAGGAAACAGCTTTTTGATT

3901  GATCGCAGTGAATGTATTAGCCAAGAGGTCTAAAGCCCTGTTGTACTGCAGGCCACTGTC
3901  CTAGCGTCACTTACATAATCGGTTCTCCAGATTTCGGGACAACATGACGTCCGGTGACAG

3961  TTCCTTGTTTGACTAGAGACTTGGAGTTTGAGAACAGTGGTTCTTTGGTTTGGATACATT
3961  AAGGAACAAACTGATCTCTGAACCTCAAACTCTTGTCACCAAGAAACCAAACCTATGTAA

4021  TTTTGTTCTTGATTTGGATGTGTGTGTTTCATGCGTGGTTAATATAGCATATTTTCAATA
4021  AAAACAAGAACTAAACCTACACACACAAAGTACGCACCAATTATATCGTATAAAAGTTAT

4081  TAAATGTCAAAAATTTTGAAATAGGAAAGAACTCTCTATATATTAATGTACTTATACACA
4081  ATTTACAGTTTTTAAAACTTTATCCTTTCTTGAGAGATATATAATTACATGAATATGTGT
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4141 CACTTCAAGATTATGCATTTATTAACAGATACATGAAATAAATTCCATGTGCATATGCAC
4141 GTGAAGTTCTAATACGTAAATAATTGTCTATGTACTTTATTTAAGGTACACGTATACGTG

4201 ATATGCACACAGAGCGTGCACACACACAGCATGCACACAGCGTGGAGTGAGAGGCATGGG
4201 TATACGTGTGTCTCGCACGTGTGTGTGTCGTACGTGTGTCGCACCTCACTCTCCGTACCC

4261 GCAGTGTGGAAGAGTTTTAACATCAAACAGACCTGAAATGAGTATTAAAGGCCCCCTTTA
4261 CGTCACACCTTCTCAAAATTGTAGTTTGTCTGGACTTTACTCATAATTTCCGGGGGAAAT

4321 TTTTTAAACTTTTACTAAAACAAGATGGATTTCCCTATGTTATATAATGGTGAATTTTAG
4321 AAAAATTTGAAAATGATTTTGTTCTACCTAAAGGATACAATATATTACCACTTAAAATC

4381 GCATAAATAACGTTTTTTGAGTGTTGCATAATTGTACGTATTAATGTAATGTAACTGTGG
4381 CGTATTTATTGCAAAAAACTCACAACGTATTAACATGCATAATTACATTACATTGACACC

4441 TTAACGAAGAATTCATCAAGGATATCACTGTTTTGTGGCATTTTTTTTTTCCTCCTCTAA
4441 AATTGCTTCTTAAGTAGTTCCTATAGTGACAAAACACCGTAAAAAAAAAAGGAGGAGATT

4501 TCTTTGGACTTGTGAAATAATTTCACTATGAAATAAATGTTGGTTCTTGTCATATTCTAA
4501 AGAAACCTGAACACTTTATTAAAGTGATACTTTATTTACAACCAAGAACAGTATAAGATT

4561 GGGAGATTGATGTAAGTGGCTCCACTCCAGCTTACAGAAGGTAAACCACGACCTTTTTGC
4561 CCCTCTAACTACATTCACCGAGGTGAGGTCGAATGTCTTCCATTTGGTGCTGGAAAAACG

4621 GTTCTCTGAAAACGCTTGTCTTCCGATGCCTCTGTTTCTAAGACTGACAAGCACTCTGGG
4621 CAAGAGACTTTTGCGAACAGAAGGCTACGGAGACAAAGATTCTGACTGTTCGTGAGACCC

4681 GGCACTGTGACGCCTGCTTCTAGCGGCAGAGTTGCTGCAGCTCCTGTCCTGGCTGTGAAC
4681 CCGTGACACTGCGGACGAAGATCGCCGTCTCAACGACGTCGAGGACAGGACCGACACTTG

4741 ATTGTTCTCTCTCTGGTGTCTCTATGTTCATAACTACAGAGACTTCAGCTCTATTCCATT
4741 TAACAAGAGAGAGACCACAGAGATACAAGTATTGATGTCTCTGAAGTCGAGATAAGGTAA

4801 TCATATTTGTGCTGAATAATCATTCCATTTTATGGCAGAAAACACAAGATGTAAAAGCAA
4801 AGTATAAACACGACTTATTAGTAAGGTAAAATACCGTCTTTTGTGTTCTACATTTTCGTT

4861 CAAGTGACCCATCCTTTGAAGCTTACAAGAAGAGAAACATTAATCTATTTCACGTCTTGA
4861 GTTCACTGGGTAGGAAACTTCGAATGTTCTTCTCTTTGTAATTAGATAAAGTGCAGAACT

4921 AAACAGATCAGTTTTATTTTGCTCAAAAAGGGCACATGTACATTTTTGATCTAGGTCTTA
4921 TTTGTCTAGTCAAAATAAAACGAGTTTTTCCCGTGTACATGTAAAAACTAGATCCAGAAT

4981 GAAACGTAGAGTTTCAGAGGATCAGCATTATACACACTGTCACACACACACACACTTAAA
4981 CTTTGCATCTCAAAGTCTCCTAGTCGTAATATGTGTGACAGTGTGTGTGTGTGTGAATTT

5041 ATTCAGATGAGGAACAAGATAGGAATGAGGTTTTGTTAGGGACGCAGAGCACCTAAAACC
5041 TAAGTCTACTCCTTGTTCTATCCTTACTCCAAAACAATCCCTGCGTCTCGTGGATTTTGG

5101 AAAGGATATCGACAGTAACAAAGCTGTTTTTACTGTAGTGCTGACTGAACACTCATGCTG
5101 TTTCCTATAGCTGTCATTGTTTCGACAAAAATGACATCACGACTGACTTGTGAGTACGAC

5161 GTGTCTTCATGTGGACCATGGCTTTCTTGTATTTCTTTGCAGTTTAATAAATGACTTCAT
5161 CACAGAAGTACACCTGGTACCGAAAGAACATAAAGAAACGTCAAATTATTTACTGAAGTA

5221 ATCTCAGGTTACCTTTCCACATCTCCTGGAATATATGTTTATGTCCTTAAAGTTTCAGTG
5221 TAGAGTCCAATGGAAAGGTGTAGAGGACCTTATATACAAATACAGGAATTTCAAAGTCAC

5281 TCGTCACTTTAGTAGCTTTAGTTTGAGTTTTTAAATGTTTGGTAATATTCCAACAAATAT
5281 AGCAGTGAAATCATCGAAATCAAACTCAAAAATTTACAAACCATTATAAGGTTGTTTATA

5341 TTTTTAAGACATTATGAAACCTTATGAAGTGCCATATATTACAAGTGAGATAAAACAGCA
5341 AAAAATTCTGTAATACTTTGGAATACTTCACGGTATATAATGTTCACTCTATTTTGTCGT

5401 AGCAAAAGAAGGTTTGCAGAAGGTTTTTAAGTGGCGAAGTGCGGGCCTGCCCATTTTGGT
5401 TCGTTTTCTTCCAAACGTCTTCCAAAAATTCACCGCTTCACGCCCGGACGGGTAAAACCA

5461 GTCTCCTTGGTGGTTACTCCTGAGAAGGGCCTGGAGGAAGAGCAACTGAGGCCTAATCTA
5461 CAGAGGAACCACCAATGAGGACTCTTCCCGGACCTCCTTCTCGTTGACTCCGGATTAGAT

5521 CAGGCAACTGCCAAATTGTTTCAGTTGACGTTTTTCCCTCTCATGTTTGACTATAATAAA
5521 GTCCGTTGACGGTTTAACAAAGTCAACTGCAAAAAGGGAGAGTACAAACTGATATTATTT

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5581  TAGGTAGTTGCCAGTGGAGCCTTCAGCCAACCACCTGGTAATAAACTGTTAAAAATGGTG
5581  ATCCATCAACGGTCACCTCGGAAGTCGGTTGGTGGACCATTATTTGACAATTTTTACCAC

5641  CAAACCCTAGGTCACAGGTGTGGGGGCATTTGTCTTGCCTGTTAACAGGCCTGGCCTTA
5641  GTTTGGGATCCAGTGTCCACACCCCCGTAAACAGAACGGACAATTGTCCGGACCGGAAT

5701  ATTCTTTTCTCCCATGGCCATTTCTGCCTTTGGGGAACTCACAATTCCTGTTGACTAAAA
5701  TAAGAAAAGAGGGTACCGGTAAAGACGGAAACCCCTTGAGTGTTAAGGACAACTGATTTT

5761  GAGCACCCTTTTCCACCACAAGCCTGACAAATCAGACGTCCACATAATTTCTGAACTCGT
5761  CTCGTGGGAAAAGGTGGTGTTCGGACTGTTTAGTCTGCAGGTGTATTAAAGACTTGAGCA

5821  TTTGGTTAGGACAGGAAGCACAGGCTCCCTTCCTGTCTGTGTTTTCCTAAGAGAAAACGG
5821  AAACCAATCCTGTCCTTCGTGTCCGAGGGAAGGACAGACACAAAAGGATTCTCTTTTGCC

5881  TCTTCCCTCCTTTTTTGCATATTTGGCAAGTGGTTCCACCTTTCTCTGCACCCTGGTGGA
5881  AGAAGGGAGGAAAAAACGTATAAACCGTTCACCAAGGTGGAAAGAGACGTGGGACCACCT

5941  GTGTGAAGGCAGCAGAGGAACCTTTTGGAGGAGGAAGAGGACACAGAGGCCCTGTAGCCA
5941  CACACTTCCGTCGTCTCCTTGGAAAACCTCCTCCTTCTCCTGTGTCTCCGGGACATCGGT

6001  GGCACCAAGATCCCTCCCAGGTGGCTGGGTCTGAGGGGAACTCCGAGCAGCCCTAGGTCC
6001  CCGTGGTTCTAGGGAGGGTCCACCGACCCAGACTCCCCTTGAGGCTCGTCGGGATCCAGG

6061  TCAAAGTCTGGATTTGTGTGGAAAAGGCAGCTCTCACTTGGCCTTGGCGAGGCCTCGGTT
6061  AGTTTCAGACCTAAACACACCTTTTCCGTCGAGAGTGAACCGGAACCGCTCCGGAGCCAA

6121  GGTTGGTGAGTGCCACACGGTTTCTTTGTGTGCTTGCATGGATTGGAATAGCCATTGTGT
6121  CCAACCACTCACGGTGTGCCAAAGAAACACACGAACGTACCTAACCTTATCGGTAACACA

6181  TCTTCCGTCTTCCCTGCTGGTGTTTCCACAGTGGGTGGCCTGAGCCCAGAGCAGCTCCCC
6181  AGAAGGCAGAAGGGACGACCACAAAGGTGTCACCCACCGGACTCGGGTCTCGTCGAGGGG

6241  ATATCCCTGTGCAGGCCACCTGTCTCGGGTGATGGAGAGCATCATTATGCTCCGTCTGAA
6241  TATAGGGACACGTCCGGTGGACAGAGCCCACTACCTCTCGTAGTAATACGAGGCAGACTT

6301  CGCTCTGCTTTCGGATGGCCCCATGCTCCACCTCCTGATAGCTCGTGGCGCGGGGCCACG
6301  GCGAGACGAAAGCCTACCGGGGTACGAGGTGGAGGACTATCGAGCACCGCGCCCCGGTGC

6361  GCTTAACAAATGGCTGAAAATGGGTCCTAATTAGTGGAAAAGTGCTTTCTTCATATTTTC
6361  CGAATTGTTTACCGACTTTTACCCAGGATTAATCACCTTTTCACGAAAGAAGTATAAAAG

6421  TCACTCGAGTGTGCAGTGATTCATTTTTCTTCTGCAATCAGCTCACTGCTAAAGTAAATC
6421  AGTGAGCTCACACGTCACTAAGTAAAAAGAAGACGTTAGTCGAGTGACGATTTCATTTAG

6481  TGACTCTCTTCCCGCCATTGCACACCAAAAGTTAACTCTAATGGGTAGGAGGTTAGGTTT
6481  ACTGAGAGAAGGGCGGTAACGTGTGGTTTTCAATTGAGATTACCCATCCTCCAATCCAAA

6541  GTTGAGAGAGCAATGCAGTAAAAAGAGGGGATCCAATGTGGTCTTGTCTGTCTGGTCTTC
6541  CAACTCTCTCGTTACGTCATTTTTCTCCCCTAGGTTACACCAGAACAGACAGACCAGAAG

6601  CTTTCTTCGTTTTTTCCTCCCTTGTCTTCTCTGTCATTCCCTTCCCTCCATTTGCCTTGC
6601  GAAAGAAGCAAAAAAGGAGGGAACAGAAGAGACAGTAAGGGAAGGGAGGTAAACGGAACG

6661  CTTTCCTGTCCTTCCCTTCCCTTCCTTCCCCTCTTTCTTTCTATAATTGGTGGGGGGTTT
6661  GAAAGGACAGGAAGGGAAGGGAAGGAAGGGGAGAAAGAAAGATATTAACCACCCCCCAAA

6721  GCACAGACTGCCAAAACACTAAGAACTGTGTAAAGTGTTTTTGAATGGCCTTACACATAT
6721  CGTGTCTGACGGTTTTGTGATTCTTGACACATTTCACAAAAACTTACCGGAATGTGTATA

6781  TGAAGTAGATTTTTATGCTCCATTTTTGAGATCACACACTAAAATCTATACCTTTAAAGC
6781  ACTTCATCTAAAAATACGAGGTAAAAACTCTAGTGTGTGATTTTAGATATGGAAATTTCG

6841  ATTTTCTGTTAGTTTGAAACTATTTGAAAATGAACAATGTGGTTTAGATTAGAGTCCTGT
6841  TAAAAGACAATCAAACTTTGATAAACTTTTACTTGTTACACCAAATCTAATCTCAGGACA

6901  TCTGAAGCTAGGAGTTCCACTATGAATATTGATTTATCAGTTTTTGACAAATTTTTGTTG
6901  AGACTTCGATCCTCAAGGTGATACTTATAACTAAATAGTCAAAAACTGTTTAAAAACAAC

6961  TTATACCAGATTTTCACTGGCAAACCTAGAGCAAATAAAATTCCACATAAGATACTTCCC
6961  AATATGGTCTAAAAGTGACCGTTTGGATCTCGTTTATTTTAAGGTGTATTCTATGAAGGG

7021  TAGACCTAATGGGAAAAATGTTTAATTTAGAGTCTTTAGGAGAAATGAGAATGAGGAATT
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7021  ATCTGGATTACCCTTTTTACAAATTAAATCTCAGAAATCCTCTTTACTCTTACTCCTTAA

7081  GACCTTTTGTAAGCTTACTTCTCAGGCACTCTGAAGTGTGTTCCAGTGCTTTTAATGGAA
7081  CTGGAAAACATTCGAATGAAGACTCCGTGAGACTTCACACAAGGTCACGAAAATTACCTT

7141  ACTAGAGAGAGCCAGCAACCCCCTAGTGTGAGCCCCACTTTTAACCGGAAAAAGTGACCT
7141  TGATCTCTCTCGGTCGTTGGGGGATCACACTCGGGGTGAAAATTGGCCTTTTTCACTGGA

7201  TTTCCTCCTCCTTTGTGCTGAGTTTTGCGTAGGGCAGAAAATTAAGCTGATATTCAAAGA
7201  AAAGGAGGAGGAAACACGACTCAAAACGCATCCCGTCTTTTAATTCGACTATAAGTTTCT

7261  GATTCACTGCAAAAACATATTGATAAATCGTATATTCTATTTCATTAAATTAAAACCATA
7261  CTAAGTGACGTTTTTGTATAACTATTTAGCATATAAGATAAAGTAATTTAATTTTGGTAT

7321  CTGCTAATTATCTCAGGTTGTTAAACATAAGGCAATTAATTATCATTTTAAAAGTTGGTA
7321  GACGATTAATAGAGTCCAACAATTTGTATTCCGTTAATTAATAGTAAAATTTTCAACCAT

7381  GGAAGTTGTGAGTACTTTTGCAGTATGAGTGTTTTCCCGCTTTAGTATGAGGTTGTGTAT
7381  CCTTCAACACTCATGAAAACGTCATACTCACAAAAGGGCGAAATCATACTCCAACACATA

7441  GTTTGCTTGAATTTACAGAATTTTCACTTTAAGAGCAGACAATGTTTTGTTAAAGAAATG
7441  CAAACGAACTTAAATGTCTTAAAAGTGAAATTCTCGTCTGTTACAAAACAATTTCTTTAC

7501  AAATTTGCTAAAAAGGAGCATGTAAAGTGAAACATTAAAAATAAATAATTTCAACTTACT
7501  TTTAAACGATTTTTCCTCGTACATTTCACTTTGTAATTTTTATTTATTAAAGTTGAATGA

7561  TAAGAGCTGCAGAAAAATCTGATTGCTGTGTTTAAAATGAATTTTCCCACATTTCGCTCT
7561  ATTCTCGACGTCTTTTTAGACTAACGACACAAATTTTACTTAAAAGGGTGTAAAGCGAGA

7621  CTTATGGACAGGAGCATTTTCTGTCAGCTTATAAATAAAGACATGCCCATTTTTTGTACC
7621  GAATACCTGTCCTCGTAAAAGACAGTCCAATATTTATTTCTGTACGGGTAAAAAACATGG

7681  CCCACAAATGAGGAAGTTGTAAGCTCTCTGAGGTTTTACTGATGAGCCCCCTCCCCCTGG
7681  GGGTGTTTACTCCTTCAACATTCGAGAGACTCCAAAATGACTACTCGGGGGAGGGGGACC

7741  GTTTGCATGAAGAGATCATAGGCCACAAATAAAGGACTACAAAATGGGGTCTAAACTATC
7741  CAAACGTACTTCTCTAGTATCCGGTGTTTATTTCCTGATGTTTTACCCCAGATTTGATAG

7801  CTGGTGGGGCCTGATACCCACGTTTCGCATGGACCTTACGATGTGATGAATGGTTTTGGC
7801  GACCACCCCGGACTATGGGTGCAAAGCGTACCTGGAATGCTACACTACTTACCAAAACCG

7861  ATGAGTGTCTTAAGAATGCTTCCAGATTCGGGTTACAGGACAGCCAGCGCTGAGCTCCCT
7861  TACTCACAGAATTCTTACGAAGGTCTAAGCCCAATGTCCTGTCGGTCGCGACTCGAGGGA

7921  ATTGCAGAACAAAGTAGGAATCTAGAACTTTCTTGCTAACAGGATCCAGCTAAAACACCA
7921  TAACGTCTTGTTTCATCCTTAGATCTTGAAAGAACGATTGTCCTAGGTCGATTTTGTGGT

7981  AGTTAGATTCTTAAATGATGTTCTTTTCTGTCATTATTTGATTGTTGTCAGTAGCAGTAA
7981  TCAATCTAAGAATTTACTACAAGAAAAGACAGTAATAAACTAACAACAGTCATCGTCATT

8041  TTGTTACCAAGCCATTGATGCTTCTATTCTTCCCTTTGCCCTTCTGAGACACAGCTCATT
8041  AACAATGGTTCGGTAACTACGAAGATAAGAAGGGAAACGGGAAGACTCTGTGTCGAGTAA

8101  TTGACTTCAGTGGAACCCCTCGAAGGTGGGGTGATGAGCAAGGTGAATTTTCAAAGTAAA
8101  AACTGAAGTCACCTTGGGGAGCTTCCACCCCACTACTCGTTCCACTTAAAAGTTTCATTT

8161  GCTACTAAGAGACCAAACTACAATTTAAGGAACCTGATTTTTGAATCAAATTCCATATAC
8161  CGATGATTCTCTGGTTTGATGTTAAATTCCTTGGACTAAAAACTTAGTTTAAGGTATATG

8221  TGTGGGTATAGTTCAACATAGATTAATTTCTTATAGTTATTATGAAAAAAATCTCATCTT
8221  ACACCCATATCAAGTTGTATCTAATTAAAGAATATCAATAATACTTTTTTTAGAGTAGAA

8281  GATGATAGCTGATAATTTTCTGCGTGTCCTAAACAAAACAGAGGTCAGAATTCAGTCCCT
8281  CTACTATCGACTATTAAAACACCCACAGCATTTGTTTTGTCTCCAGTCTTAAGTCAGGGA

8341  TGGGGAAAATTTCCAATTAGTAGGAAACCAAGTGGCCTACCTTAGTTTGAAGACACCCAT
8341  ACCCCTTTTAAAGGTTAATCATCCTTTGGTTCACCGGATGGAATCAAACTTCTGTGGGTA

8401  CAGGATGTCTGCACCTTTTCATCCTCTCTGGAGGAAAGACTAAATACCCATTATTGTATA
8401  GTCCTACAGACGTGGAAAAGTAGGAGAGACCTCCTTTCTGATTTATGGGTAATAACATAT

8461  TAGGTCAGGCCAAAGCAGCCTTTTATATTGCAAGGAATAAGAGGTAAATAGATATATGTG
8461  ATCCAGTCCGGTTTCGTCGGAAAATATAACGTTCCTTATTCTCCATTTATCTATATACAC
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8521  CAACAATGAATCCCCTAATGTGTTTACTCTAGAACACATGTTCTTTCTGTATTTATATGT
8521  GTTGTTACTTAGGGGATTACACAAATGAGATCTTGTGTACAAGAAAGACATAAATATACA

8581  AGATTTTGTAGATCTTGTCTTACCACCTGCTAATGGTAGATACTGTATCTAAATAAGTTG
8581  TCTAAAACATCTAGAACAGAATGGTGGACGATTACCATCTATGACATAGATTTATTCAAC

8641  AGGAAAATTTATAGTACCTAGGAATGTGTCCTCAGTGGGCCAATCAATCAATCATGACTT
8641  TCCTTTTAAATATCATGGATCCTTACACAGGAGTCACCCGGTTAGTTAGTTAGTACTGAA

8701  CAGGTTATTTTTAATAAATATACACGTATGGGTTCATAAACAATGGGATGTTCTTGTGAA
8701  GTCCAATAAAAATTATTTATATGTGCATACCCAAGTATTTGTTACCCTACAAGAACACTT

8761  GATCTAAATAATTTTACTTCTTTGGGACTAAATAAAATATAGCTTTTGCCAAATAAACTC
8761  CTAGATTTATTAAAATGAAGAAACCCTGATTTATTTTATATCGAAAACGGTTTATTTGAG

8821  ACACAAGCACTTATTTTAATAGAAGTCAAATGGCTTTGCAGAAACTTCAGTTTTACAGGT
8821  TGTGTTCGTGAATAAAATTATCTTCAGTTTACCGAAACGTCTTTGAAGTCAAAATGTCCA

8881  GCATTGTTTGAAATGTTACGGGTATACAAGTGGATTTCTCTATTATGTACAGTGTTAAGT
8881  CGTAACAAACTTTACAATGCCCATATGTTCACCTAAAGAGATAATACATGTCACAATTCA

8941  TTGAGTTTCAAAATGTCCACCTGAAATGATTTACTTGTACGTTAAGATAATTTAACTGCT
8941  AACTCAAAGTTTTACAGGTGGACTTTACTAAATGAACATGCAATTCTATTAAATTGACGA

9001  AAGAAGGCAAGATAAAGCATTCTTTGTGACACCATATGGCCTTGCTGAGGGAAAAACTTA
9001  TTCTTCCGTTCTATTTCGTAAGAAACACTGTGGTATACCGGAACGACTCCCTTTTTGAAT

9061  CTGTTATAAGTTTGTGTTTATCTCTCTTTTTAAAAAAAATGAAGAAAAAAAACGTTTAAA
9061  GACAATATTCAAACACAAATAGAGAGAAAAATTTTTTTTACTTCTTTTTTTTGCAAATTT

9121  ATAATGGGAACACAGCAGTTCCTGGGGTCCTCTGTCTCTTTATCTTATTATAGTAAATTA
9121  TATTACCCTTGTGTCGTCAAGGACCCCAGGAGACAGAGAAATAGAATAATATCATTTAAT

9181  CCAAAAAAATAATGACCTGGGGCATGTCTGTGTGGACCCTTCTTTTAGAGGCAGTTTCTG
9181  GGTTTTTTTATTACTGGACCCCGTACAGACACACCTGGGAAGAAAATCTCCGTCAAAGAC

9241  TGTTTTGTAAAGCTGTAGGTTCTATTTTCATTGCACTTCATATTGCTGCACAGCTCCTGA
9241  ACAAAACATTTCGACATCCAAGATAAAAGTAACGTGAAGTATAACGACGTGTCGAGGACT

9301  CCATGCATGAAGGTCCTCTGAAATCGGTAAGAGGGCAGAAGAAAATGATTCTAAACTTAG
9301  GGTACGTACTTCCAGGAGACTTTAGCCATTCTCCCGTCTTCTTTTACTAAGATTTGAATC

9361  ATTTTTTTAACTTAAGTGATGAAGTGTGAAACGCCATTTATATTTGAGGAAGCTACCTAG
9361  TAAAAAAATTGAATTCACTACTTCACACTTTGCGGTAAATATAAACTCCTTCGATGGATC

9421  GAAGTGGCTCATGTCGATGGCCCAAATCAGAAGAGGGCCTGTAAAAGCTTCTATCAATTT
9421  CTTCACCGAGTACAGCTACCGGGTTTAGTCTTCTCCCGGACATTTTCGAAGATAGTTAAA

9481  TGACTGTGTATGCTTCTACCATGGCGGCTCAATAAACAGCAGTATTAGTTTAAGAGTGGA
9481  ACTGACACATACGAAGATGGTACCGCCGAGTTATTTGTCGTCATAATCAAATTCTCACCT

9541  TGGTACAGTAGTATAGACGGGAAGCCTCTCCTCTCCGTGTGAACCGTGCACCCCTATGAG
9541  ACCATGTCATCATATCTGCCCTTCGGAGAGGAGAGGCACACTTGGCACGTGGGGATACTC

9601  AGGGTAGAGACAATACAATATGCCTGTAACGTCAGGACAGACAGTCATGGCCAGCTTGAA
9601  TCCCATCTCTGTTATGTTATACGGACATTGCAGTCCTGTCTGTCAGTACCGGTCGAACTT

9661  CTCCAGCCCTGGGCTTCTTGCAGCAACAAACGTGAACACAGAGGACTGTCTCCAACTCCA
9661  GAGGTCGGGACCCGAAGAACGTCGTTGTTTGCACTTGTGTCTCCTGACAGAGGTTGAGGT

9721  CTTTCTCTATTTTTAAAACAACTTTTTGAATACAGTATCTGCCATCTTTTCTTATACCTC
9721  GAAAGAGATAAAAATTTTGTTGAAAAACTTATGTCATAGACGGTAGAAAAGAATATGGAG

9781  ACTTTGAAACAGGTGGCTCCACTGTGGCATTTAAAATGTTCTGTTTCTTTTCCCTCTGTA
9781  TGAAACTTTGTCCACCGAGGTGACACCGTAAATTTTACAAGACAAAGAAAAGGGAGACAT

9841  TCAAATACCTCTTTACCAAGAAAACATTCAAACAGCATAGTTTTTAACTGTATTTTGAAA
9841  AGTTTATGGAGAAATGGTTCTTTTGTAAGTTTGTCGTATCAAAAATTGACATAAAACTTT

9901  GGTTTCCTTAGTTCCCTTTGACCCTTCCTCTTTTGCATATCAGTTCCTGGCCATAAAAAT
9901  CCAAAGGAATCAAGGGAAACTGGGAAGGAGAAAACGTATAGTCAAGGACCGGTATTTTTA
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10021   GGAACAAACCGCAGGAGGAGTTTTCTGTGGCTCAGTTAAATGTCGGGGGAGGGTGGTGTG
10021   CCTTGTTTGGCGTCCTCCTCAAAAGACACCGAGTCAATTTACAGCCCCCTCCCACCACAC

10081   AAAGCCAAATTGGATTCCTGCTTTCCTGTTTAAATCTTGTTTTTCATTGTTATTTGCACC
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10141   AGCAATACTCTGTGGAATAATCATGAAAATGTGTAGATTGGCAGCTAATTTTTGAAAAAT
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10201   GAAAAGAATCAGAAATGAAATAAGAGTGCTCGGAAGTTTTTATGTTCTCTCAACCTGTTT
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10261   TGTCAAATTGTTACGAAAACCTATAAGGTCTCTTTGACTAGATACAAAGACTTTGCACAT
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10321   TGCCTTAGCTTTCTCTTGAAGCATTTCCTTTTTTAAAATACAGTGTAATTCACAGTGATA
10321   ACGGAATCGAAAGAGAACTTCGTAAAGGAAAAAATTTTATGTCACATTAAGTGTCACTAT

10381   TGATAGATTTGCAAAAGTAAAATCTACCAGTCTGAAGATGAAAGGACTTGTCTCTTAGCA
10381   ACTATCTAAACGTTTTCATTTTAGATGGTCAGACTTCTACTTTCCTGAACAGAGAATCGT

10441   GGAATAATGGGTTTTATTAAAGAGGTCTGTGACCTAAGGCATTTTAAATAAATTACAGGC
10441   CCTTATTACCCAAAATAATTTCTCCAGACACTGGATTCCGTAAAATTTATTTAATGTCCG

10501   TTGGTCCCTGTCTCCCCCATGTATCTACTCCCTTCAATATAAGCATCATTGAGTATTTAA
10501   AACCAGGGACAGAGGGGGTACATAGATGAGGGAAGTTATATTCGTAGTAACTCATAAATT

10561   GGAAATAACCCCAAATGTAACTCTAGTGTAGCTTCACTTGTCAGGGAGGAAAAAGTAAAT
10561   CCTTTATTGGGGTTTACATTGAGATCACATCGAAGTGAACAGTCCCTCCTTTTTCATTTA

10621   AGCATACATTTGGCCAAATAACCAGAACTTTACTGTAGAAGTTTTATGATGAAATTTGCC
10621   TCGTATGTAAACCGGTTTATTGGTCTTGAAATGACATCTTCAAAATACTACTTTAAACGG

10681   TTTAGTGCAGAGTATTACAAAGATCATGTTTAGTTTCTAGCAGTATATAAGTAGCATCCA
10681   AAATCACGTCTCATAATGTTTCTAGTACAAATCAAAGATCGTCATATATTCATCGTAGGT

10741   TCCTTATCTGTCATGCATTTGGAGTGTGCGACCCCTGCACTGGGCTGCAACATTCTGATG
10741   AGGAATAGACAGTACGTAAACCTCACACGCTGGGGACGTGACCCGACGTTGTAAGACTAC

10801   GGCAAGAGTGCTAGGGAGAAAGAGGCATCACCATCAGACTGCACGGGTTCAAGTGTCAGC
10801   CCGTTCTCACGATCCCTCTTTCTCCGTAGTGGTAGTCTGACGTGCCCAAGTTCACAGTCG

10861   TCTGTGGTTGATTAGCTGTGTGACCTGGGGAAAGCTATTTCTCTTAGCCTTGGTTCTCTC
10861   AGACACCAACTAATCGACACACTGGACCCCTTTCGATAAAGAGAATCGGAACCAAGAGAG

10921   ATCTATAAAATGGAGATAATGATGCAGATGCCTTGGGTTTAATTGGGAGAGTTAAAGACA
10921   TAGATATTTTACCTCTATTACTACGTCTACGGAACCCAAATTAACCCTCTCAATTTCTGT

10981   CATTTACATATTTAGCAAGTAGGTGTTGAATTCTAGCTCTACATTGGACACTATGCCAGG
10981   GTAAATGTATAAATCGTTCATCCACAACTTAAGATCGAGATGTAACCTGTGATACGGTCC

11041   TGCTCAAATAAACAAGTGGACAAGACAGACAACACCCATGGTCTTATGAGGCTTAACCAT
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11101   TTGCCTCTTCAATGCCAGAAACTTAGTAGGTTGATTAGATAAAGCCAGTGAGTACCAGTA
11101   AACGGAGAAGTTACGGTCTTTGAATCATCCAACTAATCTATTTCGGTCACTCATGGTCAT

11161   TCCTTTTCTTTGCAGCCTTTTCCTGGCACACTAAAAATACTCAGTACATATGAAATATCA
11161   AGGAAAAGAAACGTCGGAAAAGGACCGTGTGATTTTTATGAGTCATGTATACTTTATAGT

11221   CTGGACAAAGAATCCCCCTTAGAGTACCAGTGGAGAAGGAAGGCATTTGCTTAAAAGCAA
11221   GACCTGTTTCTTAGGGGGAATCTCATGGTCACCTCTTCCTTCCGTAAACGAATTTTCGTT

11281   ACCAACAGAAAGACATTGTAAGGCAGTTGTTTAAGTCTCAGAGACCTATAATTTTTTTCT
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11341   TTTTTCTTTTTTTTTCATCTCGCTCTGTCGCCCAGGCTGGAGTGCAGTGGCACAATCTCAG
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11401   CTCACTGCAAGCTCCACCTTCCGGGTTCATGCCATTCTTCTGCCTCAGCCTCCCAAGTAG
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11401 GAGTGACGTTCGAGGTGGAAGGCCCAAGTACGGTAAGAAGACGGAGTCGGAGGGTTCATC

11461 CAGAGACTACAGGCGCCCCGCCACCACACCTGGCTAATTTTTTGTATTTTTACTGGAGACG
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11521 GGGTTTCGCCGTGTTAGCCAGGATGGTCTTGATCTCCTGACCTCATGATCCGCCTGCCTC
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11641 CTTAAAGCTTGTAGAATTACTGTGTGCTACCAACAGACAGGCTAATTTTGAGTGACCCTC
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12061 GAGGAGTGGACCTTCGTCGTTGACGGGTCCCGACAACCTACAAAGAGGGGTCCCCTGTCG

12121 CAGGTCCCAGTCCCGCCTCGGTGTGGAAGGAGGAAAGGCAGGGTCCAGGAAGCTGTTTCA
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12181 GGACAGGCCCAAGGTCCCCCAGGGATGCCTTTCAGGGTCAGCGGAGGCTGTAAATCAGCA
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12961  TGTGAAAACATGCCATTAGCTTGCTTTGTGATTAACTCCTTTTACTGAATGTGAGCTCCT
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13081  CCATGTGGGAGAGGAGGGGCTCAGTAAGTGCTTTGTAAAATACACAGCCGAAGTGATGCA
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13141  CGTGCTAACAAAGGAGTGTGACAGCACTTAAGTGCCCTTCTAGACACTTCAGGCTCCCCT
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13201  TTGTAAGCTGTCTTGGAAGAGGCCACATTTCCTTTCCCTCAAACAGTTTCTCATTGTTTG
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13261  ATTATTCTTTTAGCCTTTCTCTGGAAGCAAAGCCACTTTTACGAGAAAGTCACTGCTTTT
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13321  TCATCTCAAGAGATGCAAGTTTGGAGTTTGGGGAAGTTTTCAGGTGCCCGTCAAGTCATC
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13381  CTTTATGATGTCAGACGAGTCAGGCCACAGAATTCACAGGGCTCAGTGCAGACCGAAAAC
13381  GAAATACTACAGTCTGCTCAGTCCGGTGTCTTAAGTGTCCCGAGTCACGTCTGGCTTTTG

13441  TTGAGGCCTCTTGTTCAGAAATTATTAAAAATTTTGGTGAACATCACCCCAAGCAAAGAG
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13561  CAGAAACAATGTGGTTGAAATTGTGTATGCACTTGGAAGTGAGATGGATTGCAAAACACA
13561  GTCTTTGTTACACCAACTTTAACACATACGTGAACCTTCACTCTACCTAACGTTTTGTGT

13621  GGTCTCCATGCTGGGGCAGGAGTGGTGATAGGGCATGGAGTGGAAATGTCCAGCAGGCCC
13621  CCAGAGGTACGACCCCGTCCTCACCACTATCCCGTACCTCACCTTTACAGGTCGTCCGGG

13681  ACGTGCGAAAATGCAGAGCTCTCTGGCTCTTGCAGACTTGGCTGCTGACAATAGACGCGC
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13741  TCCAGGAAGGTGCTCGCTGTGGTGTGATCTGCTGCCCACCCCTAGCTCCCTCCAGGAGAC
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13801  TGGTGCGGGGACTGTTTGCAAATGACTGCAAAAGTAAGAAGGTTCCCACAGAGCAGAGCT
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13861  TGATTTGGGGACCAGCCGAGGGCAGTTTGTCAGGATTCCGGCTTGAAACTGTTCTCACAT
13861  ACTAAACCCCTGGTCGGCTCCCGTCAAACAGTCCTAAGGCCGAACTTTGACAAGAGTGTA

13921  CTCACCGCCTGAAAGGACGAGTGTGTCCAGAGGACTTAGCATTGATCACCTCTGTCTCCA
13921  GAGTGGCGGACTTTCCTGCTCACACAGGTCTCCTGAATCGTAACTAGTGGAGACAGAGGT

13981  TGCAGCAAACTCAGAGGCTCAGCCCGCATTCCACTGGAAGGGCGTTTGCCAGTGGTGTTG
13981  ACGTCGTTTGAGTCTCCGAGTCGGGCGTAAGGTGACCTTCCCGCAAACGGTCACCACAAC

14041  GTTGGAAGAGCCTTGACTTTGCCTTAGGAAACATCTTTTTTTAAGAATTGAAAATAACTT
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14101  GAGTATGCAACAGTAGGGCATTTGTTATATAAATTAGTTGACTAGTGTGTAGCCAGTAAA
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14161  ATGATGATGGTGGTGTGTATTTGTTAAATAAAAAGATATGTGTGGTATTAAATTAAAAAA
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17341  TTTTCCGATCGAATAAAAAGAAAATCTCACTCCGAAGCATAAATAATGTTATATTAACCG

17401  ACATTCTTTGTGTAATTCTCACATTTATATCTTAAATATAATTCTCATGAATGAGAATTA
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17461  TATAATTCTCTTTTTGTATATCATTGAATATTTTCACTTAATTTTTAATTTTTTTAATCG
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17761  TGTAATTTTGTCTCCTTTAACAAATCTCTCCCTATCTTCCACTCCCCCGACCTTTCCAGC
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22081  TCCTCACTTGGTTCCAGGGCCCCATGCATCTAAGGGTGTCTCAGAGCATCCTGCAGTGCT
22081  AGGAGTGAACCAAGGTCCCGGGGTACGTAGATTCCCACAGAGTCTCGTAGGACGTCACGA

22141  CCAGCATGATCGCAGGGAAAAGCTATAGGAGGAAAAGAGTCAATAAAGTTTAGTTTCTCA
22141  GGTCGTACTAGCGTCCCTTTTCGATATCCTCCTTTTCTCAGTTATTTCAAATCAAAGAGT

22201  ACCTCCCACCTCCACCCCATAATAATGACAGCTGGTTAATCATGAGACGCGTGCACACCC
22201  TGGAGGGTGGAGGTGGGGTATTATTACTGTCGACCAATTAGTACTCTGCGCACGTGTGGG

22261  CACACGCCCTGTACATGTTTACTCATTGGGATAGCATGTCAGGCCAGAAGGCTCCATGGT
22261  GTGTGCGGGACATGTACAAATGAGTAACCCTATCGTACAGTCCGGTCTTCCGAGGTACCA

22321  CATTTCTATGAAGGTACTTTAGCAGGTCTTCAAGAAGGCAAGTGGCCTGGGTCCCTGCCT
22321  GTAAAGATACTTCCATGAAATCGTCCAGAAGTTCTTCCGTTCACCGGACCCAGGGACGGA

22381  CCCCAAATTGCAAGCTCCCTGCTTTATGTAGGAGACCTATGTGTATATTACAGTTCTGTG
22381  GGGGTTTAACGTTCGAGGGACGAAATACATCCTCTGGATACACATATAATGTCAAGACAC

22441  TAAGATTATTTTGTTATTCTTACCCCCACACCCACCCCCCAACCCCCCGCTGCCACCAAA
22441  ATTCTAATAAAACAATAAGAATGGGGGTGTGGGTGGGGGGTTGGGGGGCGACGGTGGTTT

22501  AAAAAAAAAAAAAAATTCCTCTGACAACCTTCATAAAGTCCTGGGAGTTTGAACACCATT
22501  TTTTTTTTTTTTTTTAAGGAGACTGTTGGAAGTATTTCAGGACCCTCAAACTTGTGGTAA

22561  GCTCTAGGAAGTCATCTTATACAAAAATAAGAGTTGTGAGGTGGTTCATATACCTCCTGC
22561  CGAGATCCTTCAGTAGAATATGTTTTTATTCTCAACACTCCACCAAGTATATGGAGGACG

22621  GTTCTCCTATTTGGAGTTTTTCCCCATTTATGAAAGAGGTGAAAACGCTAAGATATTTAG
22621  CAAGAGGATAAACCTCAAAAAGGGGTAAATACTTTCTCCACTTTTGCGATTCTATAAATC

22681  CAATTATTACTTTAAACATTTTCTATTTATAGGCCGGGCGCAGTGGCTCATGCCTGTAAT
22681  GTTAATAATGAAATTTGTAAAAGATAAATATCCGGCCCGCGTCACCGAGTACGGACATTA

22741  CCCAGCGCTTGGGAGGCCAAGGCAGGCAGATCACGAGGTCAGGAGATCGAGACCATCTTG
22741  GGGTCGCGAACCCTCCGGTTCCGTCCGTCTAGTGCTCCAGTCCTCTAGCTCTGGTAGAAC

22801  GCTAACACGGTGAAACCCTGTCTCTACTAAAAAAATACAAAAATTTAGTTGGGCATGGTG
22801  CGATTGTGCCACTTTGGGACAGAGATGATTTTTTTATGTTTTTAAATCAACCCGTACCAC

22861  GGGGATACCTGTGGTCCCAGCTACTCGGGAGGCTGAGACAGGAGAATGGCTTGAACCTGG
22861  CCCCTATGGACACCAGGGTCGATGAGCCCTCCGACTCTGTCCTCTTACCGAACTTGGACC

22921  GAGGCCGAGCTTGCAGTGAGCCAAGATCGCGCCACTGCACTCCAGCCTGGGTGACAGAGC
22921  CTCCGGCTCGAACGTCACTCGGTTCTAGCGCGGTGACGTGAGGTCGGACCCACTGTCTCG

22981  AAGACTCTGTCTCGAAAAAAAAAAAAAATTCTATTTACAGCAGTGAAAATAGTAGTGACT
22981  TTCTGAGACAGAGCTTTTTTTTTTTTTTAAGATAAATGTCGTCACTTTTATCATCACTGA

23041  TAATGCACATTGCCAAGGCTTTAGCATAACATGAACACTTTCACTCAATGTCTCTCTGGC
23041  ATTACGTGTAACGGTTCCGAAATCGTATTGTACTTGTGAAAGTGAGTTACAGAGAGACCG
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23101  CTTTTGTTTTTCCTTGGGAAATTCTTATAATCCTGCTCCGTCTTTAACTATTCATTTTGT
23101  GAAAACAAAAAGGAACCCTTTAAGAATATTAGGACGAGGCAGAAATTGATAAGTAAAACA

23161  ATTGGCTATCCAAATATACCCAATAATGCTCTTTCTGAAAATATGCCAATTGTGGTAATT
23161  TAACCGATAGGTTTATATGGGTTATTACGAGAAAGACTTTTATACGGTTAACACCATTAA

23221  ACAGCTAAGCTGGAATATTAAATTGTGATGTCTGTTTTCCAGAGAATGAAGTAGTATTCC
23221  TGTCGATTCGACCTTATAATTTAACACTACAGACAAAAGGTCTCTTACTTCATCATAAGG

23281  CCAGAGCATAGGCTTGGTGCCTGTGCAGGTTCTATTTTAAATATTCCAGGAAGGGTTGTT
23281  GGTCTCGTATCCGAACCACGGACACGTCCAAGATAAAATTTATAAGGTCCTTCCCAACAA

23341  TTATATACTGAGGATGATTTTACTGGTCTTGCCAGTCGTCTGAAATGCTGGTATTACTCT
23341  AATATATGACTCCTACTAAAATGACCAGAACGGTCAGCAGACTTTACGACCATAATGAGA

23401  TGTGGAAGGTTTATTCAAACAAACAAGGACATTTCACACAATACCTAGTCATGTTTTTCA
23401  ACACCTTCCAAATAAGTTTGTTTGTTCCTGTAAAGTGTGTTATGGATCAGTACAAAAAGT

23461  GACATTTTAATGTTTGGTTCATCATTTGCACACACTCTCAAAAATCTAGGTTTGTCTATG
23461  CTGTAAAATTACAAACCAAGTAGTAAACGTGTGTGAGAGTTTTTAGATCCAAACAGATAC

23521  TGTTCATATCATTTTGCCTGTTGCCAGCTCAGTCAGCAGGCACACTCTCCCAGGCTGTTG
23521  ACAAGTATAGTAAAACGGACAACGGTCGAGTCAGTCGTCCGTGTGAGAGGGTCCGACAAC

23581  CTGTTTTGTTAGACTTCTTCAGGACCTTCATCTAAAATGGTCTTCCACACGTAGCTATAC
23581  GACAAAACAATCTGAAGAAGTCCTGGAAGTAGATTTTACCAGAAGGTGTGCATCGATATG

23641  TGCATAAGTTCACATCATCTGTTTCTTGCATGTGGGTTGTGTCTCAACTCAAGTTTAAGT
23641  ACGTATTCAAGTGTAGTAGACAAAGAACGTACACCCAACACAGAGTTGAGTTCAAATTCA

23701  TAGATTTGGAAGGGCGGAAACTATAGGAGTTGCAGCTTCAGTGGAGAAAAGAGCATTTCC
23701  ATCTAAACCTTCCCGCCTTTGATATCCTCAACGTCGAAGTCACCTCTTTTCTCGTAAAGG

23761  TACTAGTTATGGCTTCCCAAGGAAGGTTAGATTCCTCAGAGTAGGAGTGATTCCCCAATG
23761  ATGATCAATACCGAAGGGTTCCTTCCAATCTAAGGAGTCTCATCCTCACTAAGGGGTTAC

23821  CTAGAACCTTTGGTCAAATATAATTCTAATCCAGTCAAAATAAATACAGGTATTCTGTAA
23821  GATCTTGGAAACCAGTTTATATTAAGATTAGGTCAGTTTTATTTATGTCCATAAGACATT

23881  AACCCGATTTCATTTTGTAAATCCTACTTTGTATAGTATAAGCAATTTTTGTATTTGTGT
23881  TTGGGCTAAAGTAAAACATTTAGGATGAAACATATCATATTCGTTAAAAACATAAACACA

23941  GGATTATATTTTATTTTCCTATTTCAAAGAGAAGAATTTGTATTAGCAGACTCCCTTTGC
23941  CCTAATATAAAATAAAAGGATAAAGTTTCTCTTCTTAAACATAATCGTCTGAGGGAAACG

24001  ATGCGGAGAGGGGATCATTTTCCCAGTAGGCATGGGGTTCCCTTCCATTCCTTGTCCAGT
24001  TACGCCTCTCCCCTAGTAAAAGGGTCATCCGTACCCCAAGGGAAGGTAAGGAACAGGTCA

24061  CTTCTTTTCCCCACTAAGTTAAGTCAAACTAAGCAGCTGGTAAGATATTCCCTGGTTCTT
24061  GAAGAAAAGGGGTGATTCAATTCAGTTTGATTCGTCGACCATTCTATAAGGGACCAAGAA

24121  GCAAAGAAAGTGAGCAGATGGCAGAATGTATAGCTCTAAGCAGAATACCTGGTGTGGTAT
24121  CGTTTCTTTCACTCGTCTACCGTCTTACATATCGAGATTCGTCTTATGGACCACACCATA

24181  CCTCAAACACAAATTGACAGGAGGGTGTGGTGTGGCAAGCTCATTGTGGGGGTAAATTGG
24181  GGAGTTTGTGTTTAACTGTCCTCCCACACCACACCGTTCGAGTAACACCCCCATTTAACC

24241  AATAAGCTTACAGGGGGAAGAGTTGACAAAAGATAGGAAGAACCTTAAAAATATAGATGC
24241  TTATTCGAATGTCCCCCTTCTCAACTGTTTTCTATCCTTCTTGGAATTTTTATATCTACG

24301  CTTTTATGCAGTGATAAAATGTCTAGATATTTATACTGTGGTGATTATTAGGAATATGTG
24301  GAAAATACGTCACTATTTTACAGATCTATAAATATGACACCACTAATAATCCTTATACAC

24361  CAAAGATTGGCTATTAGGATGTTCATTACAGTGTTGTTTAATAATTATAAAAGGACAGAA
24361  GTTTCTAACCGATAATCCTACAAGTAATGTCACAACAAATTATTAATATTTTCCTGTCTT

24421  AGCAATGTGGACTCAAAAATAGGAAAAGAATTTAAATAAATCCTAGTGTACCCGTTATAC
24421  TCGTTACACCTGAGTTTTTATCCTTTTCTTAAATTTATTTAGGATCACATGGGCAATATG

24481  ATGAAATTATGGAAATATGACCCTGAGCATGGAAATATGTACATGAGAATGTCTAAAAGC
24481  TACTTTAATACCTTTATACTGGGACTCGTACCTTTATACATGTACTCTTACAGATTTTCG

24541  TAGTTCATTTTGAAAAACAAAATAATGTCACCTCATATTATTTATAGTATATAAAGATGA
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24541 ATCAAGTAAAACTTTTTGTTTTATTACAGTGGAGTATAATAAATATCATATATTTCTACT

24601 TTTTAAGAGTGGCAGTGTCTGGGATTATAGGTGATTGTATTTCTTCCCTTTTGCACATCT
24601 AAAATTCTCACCGTCACAGACCCTAATATCCACTAACATAAAGAAGGCAAAACGTGTAGA

24661 ATGTTCTCTCATTTGTATTGTGTGGGGAGAAGTGACTTTTTTTATAAAAAGAAAAAGGTA
24661 TACAAGAGAGTAAACATAACACACCCCTCTTCACTGAAAAAAATATTTTTCTTTTTCCAT

24721 TATGCATCCCAGCAGAGAAGCACTGGCTCCACCCAGTACCTGCCTCCTCATGCCACCCTC
24721 ATACGTAGGGTCGTCTCTTCGTGACCGAGGTGGGTCATGGACGGAGGAGTACGGTGGGAG

24781 TCAAGCCAAAAGCCGGGGGAAGCCCAGGCACCTTGACCATGACCGCCCGAGACTCACACT
24781 AGTTCGGTTTTCGGCCCCCTTCGGGTCCGTGGAACTGGTACTGGCGGGCTCTGAGTGTGA

24841 TCTTCTTTCTCATCAGGGAAGGAAAGCCCCCCTGTAAGCGATACTCCAGATGAGGGCGAT
24841 AGAAGAAAGAGTAGTCCCTTCCTTTCGGGGGGACATTCGCTATGAGGTCTACTCCCGCTA

24901 GAGCCCATGCCGATCCCCGAGGACCTCTCCACCACCTCGGGAGGACAGCAAAGCTCCAAG
24901 CTCGGGTACGGCTAGGGGCTCCTGGAGAGGTGGTGGAGCCCTCCTGTCGTTTCGAGGTTC

24961 AGTGACAGAGTCGTCGGTAAGTGGGTCACCAGCGGCCTCTGTGCCTGTGAAACCTTTATC
24961 TCACTGTCTCAGCACCCATTCACCCAGTGGTCGCCGGAGACACGGACACTTTGGAAATAG

25021 TCTTTGTATTTTTCCAAGACAGTGATGAAGGGATGCAAGTCATTTTATCCATTGTGTTCC
25021 AGAAACATAAAAAGGTTCTGTCACTACTTCCCTACGTTCAGTAAAATAGGTAACACAAGG

25081 CTCAACTGGCATATTAAAGAAATATGGCACAAAGATCAGCAGGATGGGGGTCCTCTGGTG
25081 GAGTTGACCGTATAATTTCTTTATACCGTGTTTCTAGTCGTCCTACCCCCAGGAGACCAC

25141 TGTGGGAGGATGGACACTCACAGGCCAGCATGGCCGTGAGAGCCACACACCCCGCAAAAT
25141 ACACCCTCCTACCTGTGAGTGTCCGGTCGTACCGGCACTCTCGGTGTGTGGGGCGTTTTA

25201 GTCCAAGTTGAGGAGCAATCCTGCCCAGGGACGCGTCTCTGTCACTGTCCTCTGTCCTCA
25201 CAGGTTCAACTCCTCGTTAGGACGGGTCCCTGCGCAGAGACAGTGACAGGAGACAGGAGT

25261 CTGCACTTGCAGGAATATCAAATGTTATGGATTGTAGATCGTGAAAATTACACACTTACG
25261 GACGTGAACGTCCTTATAGTTTACAATACCTAACATCTAGCACTTTTAATGTGTGAATGC

25321 TGTTTTGGCAACAGTGCTTTTCAGTGTTTGGGGTTAGAACAAGCCACATCTGGCCATTTT
25321 ACAAAACCGTTGTCACGAAAAGTCACAAACCCCAATCTTGTTCGGTGTAGACCGGTAAAA

25381 ATGTTATCCCTCTAATCTCTAGTTCTTAAATTTCAGATTTAACTGAAAATAGAAAGTTTC
25381 TACAATAGGGAGATTAGAGATCAAGAATTTAAAGTCTAAATTGACTTTTATCTTTCAAAG

25441 ATAAATGGTAATTTTTAAATGTTAGAAAAAAATCAAAGCACACATTTACATACCTTTTCC
25441 TATTTACCATTAAAAATTTACAATCTTTTTTTAGTTTCGTGTGTAAATGTATGGAAAAGG

25501 ATAAAAAAGTGTGTGTGAAACCATCTGCAACTCCACTGGTTAACTTACACATGCGACAGT
25501 TATTTTTTCACACACACTTTGGTAGACGTTGAGGTGACCAATTGAATCTGTACGCTGTCA

25561 TTGTGTTTGGAAAACTTCACCCACCCTCTTTATTTCAAGAAACCAAACACGGAGAGAAGT
25561 AACACAAACCTTTTGAAGTGGGTGGGAGAAATAAAGTTCTTTGGTTTCTGCCTCTCTTCA

25621 TCAGTGAATTAACCAAGGTGAAATGACAGAGTCAGAATTGAACTGAATTTCTGACTGAAA
25621 AGTCACTTAATTGGTTCCACTTTACTGTCTCAGTCTTAACTTGACTTAAAGACTGACTTT

25681 AACTAGTTCTCGCTCCATTATACCATGTTCTAATGAGCTAATGAGTCAACAGTTCCCTGG
25681 TTGATCAAGAGCGAGGTAATATGGTACAAGATTACTCGATTACTCAGTTGTCAAGGGACC

25741 AATACCTCTTTTCTTCTTTAAAAACAGAAACAGCTGTGATACTGAGACCTACCTATTGCC
25741 TTATGGACAAAAGAAGAAATTTTTCTCTTTCTCGACACTATGACTCTCGATGGATAACCG

25801 ATAAAAGAATATGAAGGACATACAGGTAAAATGAGGTAGACTGGATCAATGTGGGTCAGC
25801 TATTTTCTTATACTTCCTGTATGTCCATTTTACTCCATCTGACCTAGTTACACCCAGTCG

25861 TACATAAGCCCCCATAGCCAAGGAGGGAACATGTATGTAAAATTCTCAGGCTTATGAGAA
25861 ATGTATTCGGGGGTATCGGTTCCTCCCTTGTACATACATTTTAAGAGTCCGAATACTCTT

25921 TCACAACTGTATGTCTATAGGACATCCTAATGCAATAATGGGAAAATGTGATAACTGAAT
25921 AGTGTTGACATACAGATATCCTGTAGGATTACGTTATTACCCTTTTACACTATTGACTTA

25981 TTTATCTACATGTATAGAAAACATATTTTGGGCCGGGCATGGTGGCTCAAGCTTGTAATC
25981 AAATAGATGTACATATCTTTTGTATAAAACCCGGCCCGTACCACCGAGTTCGAACATTAG

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26041  CCAGCACTTTGGGAGGCCGAGGCTGGCGGATCACAAGGTCAGGAAATCGAGACCATCCTG
26041  GGTCGTGAAACCCTCCGGCTCCGACCGCCTAGTGTTCCAGTCCTTTAGCTCTGGTAGGAC

26101  GCTAACACGGTGAAACCCTGTCTCTACTAAAAATACAAAAAATTAGCCGGGCGTAGTGGT
26101  CGATTGTGCCACTTTGGGACAGAGATGATTTTTATGTTTTTTAATCGGCCCGCATCACCA

26161  GGGCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATGGCGTGAACCCGGCA
26161  CCCGCGGACATCAGGGTCGATGAGCCCTCCGACTCCGTCCTCTTACCGCACTTGGGCCGT

26221  GGCGGAGCTTGCAGTGAGCCGAGATTGCGCCACTGCACTCCAGCCTGGATGACAGAGCCA
26221  CCGCCTCGAACGTCACTCGGCTCTAACGCGGTGACGTGAGGTCGGACCTACTGTCTCGGT

26281  GACTCCATCTCAAAAAAAAAAAAAAAAAAGAAAAAGTAAAGAAAACATATTTTGTATGTT
26281  CTGAGGTAGAGTTTTTTTTTTTTTTTTTTCTTTTTCATTTCTTTTGTATAAAACATACAA

26341  TTTTATGTGTCTTAGAAACCAAGTGGACTAGGTATAATGGTTCTTTTTTTTTTTAACTCA
26341  AAAATACACAGAATCTTTGGTTCACCTGATCCATATTACCAAGAAAAAAAAAAATTGAGT

26401  GCAGCACAGTTAATGGCACAAACAGATAAAGATGGTGGCTAAAGCCATTTGGTGTAGATG
26401  CGTCGTGTCAATTACCGTGTTTGTCTATTTCTACCACCGATTTCGGTAAACCACATCTAC

26461  AATCCAGAAAACAAGTACATTTATGAATTATTTTACCCTATTGGAAAATGGCTACTATAT
26461  TTAGGTCTTTTGTTCATGTAAATACTTAATAAAATGGGATAACCTTTTACCGATGATATA

26521  GTGGAAAGTAGAGGGGAAGAGAAATGAACTTGTGAATTATCTACTCTATTCTACCAAAGA
26521  CACCTTTCATCTCCCCTTCTCTTTACTTGAACACTTAATAGATGAGATAAGATGGTTTCT

26581  AAGATACATATATCATTTCAGGGTTTTCCAAAGTTGGGATGCAAAGGATCATGTTTCATT
26581  TTCTATGTATATAGTAAAGTCCCAAAAGGTTTCAACCCTACGTTTCCTAGTACAAAGTAA

26641  TTAATTTATGTATTTATTTTTGAGATTGTCTTCTATGTATTGCAAGTGATACTGGTTTTA
26641  AATTAAATACATAAATAAAAACTCTAACAGAAGATACATAACGTTCACTATGACCAAAAT

26701  CCATGCACTGTACCACTACGAGGGTTCCTTTCAAAACACATTCATATAAATTAAAAAATC
26701  GGTACGTGACATGGTGATGCTCCCAAGGAAAGTTTTGTGTAAGTATATTTAATTTTTTAG

26761  AGTTTAAATAAAAACATCAAGTCAATAGTAGTACATAGATATGATAAAAGTTTGCAAAAG
26761  TCAAATTTATTTTTGTAGTTCAGTTATCATCATGTATCTATACTATTTTCAAACGTTTTC

26821  TGGCACAGGAATAGTCATTGGGTGGTGATGTTCCCTGATTTTTTTAGTCCCTGAAGCACC
26821  ACCGTGTCCTTATCAGTAACCCACCACTACAAGGGACTAAAAAAATCAGGGACTTCGTGG

26881  CAGCGCCAAGGGTACTGTTCTTCCTGCTTAACACAGGAGCAAACAGATGCTCACACCCTG
26881  GTCGCGGTTCCCATGACAAGAAGGACGAATTGTGTCCTCGTTTGTCTACGAGTGTGGGAC

26941  CCCAAGAACACAGAGGCTCAGGGACTGAACCAGAAGAAATGATCCATTAACCATGTAAAT
26941  GGGTTCTTGTGTCTCCGAGTCCCTGACTTGGTCTTCTTTACTAGGTAATTGGTACATTTA

27001  GAACAGAGAGCCTGGATGTCAGAGTGAGGAGGCCAGCTCGGGTCGCTGTGGAGAAAGAGA
27001  CTTGTCTCTCGGACCTACAGTCTCACTCCTCCGGTCGAGCCCAGCGACACCTCTTTCTCT

27061  TGGGCTCTCCCTGGAATCCCTGCAGCTGCCCTTAGAGGCTGTGAGCCATCGTGGCTAGGG
27061  ACCCGAGAGGGACCTTAGGGACGTCGACGGGAATCTCCGACACTCGGTAGCACCGATCCC

27121  CATCTTTAGAGAACTGAAAGTCAGGCCGATTCCTGGAGAGTGAAGAATAGCACACGTGCC
27121  GTAGAAATCTCTTGACTTTCAGTCCGGCTAAGGACCTCTCACTTCTTATCGTGTGCACGG

27181  TTCAAAACAGTGTCAGTATCCTGTCCCTTACGGACGTCATATTGTTGGTGGGTTTTCCTG
27181  AAGTTTTGTCACAGTCATAGGACAGGGAATGCCTGCAGTATAACAACCACCCAAAAGGAC

27241  GGTGGGAGATCACCCAGTATCTGGTTGGCATTACTGATGGGTTCCCAGAGCTGTCTTTTG
27241  CCACCCTCTAGTGGGTCATAGACCAACCGTAATGACTACCCAAGGGTCTCGACAGAAAAC

27301  GTTCAAAGTCCTGCCCTCGGTCCCAGCTGCCCCCAGCACAGGTGTCACCTTGGAGTCAGG
27301  CAAGTTTCAGGACGGGAGCCAGGGTCGACGGGGGTCGTGTCCACAGTGGAACCTCAGTCC

27361  GGCGGGTTTGTCATAGCCCATGGGTCCTGGCCCTGCCCTTTATCATGTTTGACATGATTT
27361  CCGCCCAAACAGTATCGGGTACCCAGGACCGGGACGGGAAATAGTACAAACTGTACTAAA

27421  TCAGTCTACTTTTCCTTCAGGATGTAATTTAGAAAATATGATTTCAGAATTGTGAAATTT
27421  AGTCAGATGAAAAGGAAGTCCTACATTAAATCTTTTATACTAAAGTCTTAACACTTTAAA
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27481  AAAAACCCTAGAAAACCTCTTTGCTTTGCTTGTAAATAGCAGTTGATGCAGCCCTGTGGA
27481  TTTTTGGGATCTTTTGGAGAAACGAAACGAACATTTATCGTCAACTACGTCGGGACACCT

27541  CAGGCGGGAACAGCCATGTGACGTGGGCACTGAGATGATTTGGGAGATTGAATGCTCCTC
27541  GTCCGCCCTTGTCGGTACACTGCACCCGTGACTCTACTAAACCCTCTAACTTACGAGGAG

27601  AGTGGGGCTAGAGGCCACAGGAGTGATAGGTTACTGTAAAGAAAGCAAAAAAGATGCAAA
27601  TCACCCCGATCTCCGGTGTCCTCACTATCCAATGACATTTCTTTCGTTTTTTCTACGTTT

27661  AGCCTACATGACAAACCAGGCACGACACAAAGGAGAGGCTTGAGAAGAGGAAGTGAAGGA
27661  TCGGATGTACTGTTTGGTCCGTGCTGTGTTTCCTCTCCGAACTCTTCTCCTTCACTTCCT

27721  GCCAGAGGATTCCACAAGACCGAAGTGCCCAAGGAGACATGGAGGGAAGAGAGGGCTCTT
27721  CGGTCTCCTAAGGTGTTCTGGCTTCACGGGTTCCTCTGTACCTCCCTTCTCTCCCGAGAA

27781  CACAGAGCTGAGTTTAGAGACCACCCTCCATGGTTCTGGAAGGAAACCAGCCAGCTTTCA
27781  GTGTCTCGACTCAAATCTCTGGTGGGAGGTACCAAGACCTTCCTTTGGTCGGTCGAAAGT

27841  TATGTGGTGACAGGCTGTTCATTAATTTGTAGTGTACAGCATTAAATAAATGAAGTATGT
27841  ATACACCACTGTCCGACAAGTAATTAAACATCACATGTCGTAATTTATTTACTTCATACA

27901  ACAGAACATTAGGAAACAATATAAAAAGGTAGGGGAATTCGTGGATAAAGGGAATAACCT
27901  TGTCTTGTAATCCTTTGTTATATTTTTCCATCCCCTTAAGCACCTATTTCCCTTATTGGA

27961  GGGTACCATATTTCATCACATTATTCCATGGGAATAAGTCATCAGTGCAAAGGACTGTAA
27961  CCCATGGTATAAAGTAGTGTAATAAGGTACCCTTATTCAGTAGTCACGTTTCCTGACATT

28021  GGAGTGCACAGCAGGAAATGAAAAGACAGAAGCAGTGGGGCCGAGAGGAGGAAATGGAGT
28021  CCTCACGTGTCGTCCTTTACTTTTCTGTCTTCGTCACCCCGGCTCTCCTCCTTTACCTCA

28081  TGCTGAAATGCAGGGTGAGCAGCAGGGGCGGAGAGTGCCCTGTGGGTAAGGCACACCTCA
28081  ACGACTTTACGTCCCACTCGTCGTCCCCGCCTCTCACGGGACACCCATTCCGTGTGGAGT

28141  GAAGGGACAGGTCCAGGCCCTCTCCTCCCTGGCCTGGAGCTTCTGGCAAGGCTTTTCTTC
28141  CTTCCCTGTCCAGGTCCGGGAGAGGAGGGACCGGACCTCGAAGACCGTTCCGAAAAGAAG

28201  TCTGAGCCTCACTTTCCTCTTTTGAAGGTGGCAATAGTAACTGAACCTGCATCANNNNNN
28201  AGACTCGGAGTGAAAGGAGAAAACTTCCACCGTTATCATTGACTTGGACGTAGTNNNNNN

28261  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
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28381  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
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28621  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN

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28801  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
28801  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN

28861  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
28861  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN

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28921  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN

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29041  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN

29101  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
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29401  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
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29461  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN

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71401  TGGAAATTTAGAAGAGATTCTAGTGCAGACAACTTCATCCCACCCCCGCTGCCCACAGAG
71401  ACCTTTAAATCTTCTCTAAGATCACGTCTGTTGAAGTAGGGTGGGGGCGACGGGTGTCTC

71461  CTAGCCATGTGCACGGTGTGTTTGAACAATGTTATGTTGCTGCTGTGCACAGAGATCCCC
71461  GATCGGTACACGTGCCACACAAACTTGTTACAATACAACGACGACACGTGTCTCTAGGGG

71521  AGTCTCATAAAACATACTGGATGGAAGGCTGTCGAGAGATCATCAGGCCCCAGTGCATAA
71521  TCAGAGTATTTTGTATGACCTACCTTCCGACAGCTCTCTAGTAGTCCGGGGTCACGTATT

71581  GTTCTTCCTAAGCATCCTTAACAGGTGATCACCTCGCCTATTGAGAACCCTCAGGAGGCA
71581  CAAGAAGGATTCGTAGGAATTGTCCACTAGTGGAGCGGATAACTCTTGGGAGTCCTCCGT

71641  GCCCACTTACGGAAGCACTGATTGTTACAAAAGCCCTGAACTAAATCTGCTTGTCTCTAA
71641  CGGGTGAATGCCTTCGTGACTAACAATGTTTTCGGGACTTGATTTAGACGAACAGAGATT

71701  AGCCAGCCCTGCAGATGTCTGCAGTGTAACTACTTTCTCTTCTCTCAAGCAGTTCAGCCC
71701  TCGGTCGGGACGTCTACAGACGTCACATTGATGAAAGAGAAGAGAGTTCGTCAAGTCGGG

71761  TTCAAATCATTGACAACAGCTCTACAAAGCCCTCTAAATAGCCCGTTCTCCTGGCTAAAG
71761  AAGTTTAGTAACTGTTGTCGAGATGTTTCGGGAGATTTATCGGGCAAGAGGACCGATTTC

71821  TGTGTTGGTTTCCTCAGCATATGATGAAATAAACACCATGATGCCTTTGCCTTGCTTTTT
71821  ACACAACCAAAGGAGTCGTATACTACTTTATTTGTGGTACTACGGAAACGGAACGAAAAA

71881  CTTGCTGGTCTCACTCTTCCCTGGCATTCTTCAATGTGCCCAAGTCCTTCCTAGAACATT
71881  GAACGACCAGAGTGAGAAGGGACCGTAAGAAGTTACACGGGTTCAGGAAGGATCTTGTAA

71941  GCACCCAAAGGGCCTTCCTGGTCTTTCCAGGGAATGCAGAATGAAAAAGAAATCCCATCC
71941  CGTGGGTTTCCCGGAAGGACCAGAAAGGTCCCTTACGTCTTACTTTTTCTTTAGGGTAGG

72001  CCTGCCTCGAAAGGAGCTCTTCTGTGTGTAAGTGTACCTTCCCCCTCAGGGCATAATGGG
72001  GGACGGAGCTTTCCTCGAGAAGACACACATTCACATGGAAGGGGGAGTCCCGTATTACCC

72061  AAACAGTTTGCCAAAGCTAACTGTGTAATTTCACATGACTCACTGCCGTTAGTCTGAGAA
72061  TTTGTCAAACGGTTTCGATTGACACATTAAAGTGTACTGAGTGACGGCAATCAGACTCTT

72121  AGCATGGCATATTAAACTCATTTTCCATGCTTCCCAACTTTATTTACTATTCCATTTCTG
72121  TCGTACCGTATAATTTGAGTAAAAGGTACGAAGGGTTGAAATAAATGATAAGGTAAAGAC

72181  AGGGGCAGAGAGCTGAGCAGGAATAACACCTTCCTTGCTCCTCCTAATGGGGCACATGTG
72181  TCCCCGTCTCTCGACTCGTCCTTATTGTGGAAGGAACGAGGAGGATTACCCCGTGTACAC

72241  CACATATAAAATTGTGTTCGATCTTTGCAGCCACGACCCATGTTAACTGTCAACTGAGAA
72241  GTGTATATTTTAACACAAGCTAGAAACGTCGGTGCTGGGTACAATTGACAGTTGACTCTT

72301  CTCATGAGTCAGTTTCTCAGGAACAGCCCTGAAGACATTATCTCCTGCATCTTGTATTTG
72301  GAGTACTCAGTCAAAGAGTCCTTGTCGGGACTTCTGTAATAGAGGACGTAGAACATAAAC

72361  TGCCTTTGATATTTGGAGGGAAGGGTAGGATCTGGCAATTATCGTTATCTCATTTGGTTC
72361  ACGGAAACTATAAACCTCCCTTCCCATCCTAGACCGTTAATAGCAATAGAGTAAACCAAG

72421  AGTGTATTTCATTTCAGCCTGTTAAGATCTTTTGGAAATACTGTATGTGCTAGTTACAGG
72421  TCACATAAAGTAAAGTCGGACAATTCTAGAAAACCTTTATGACATACACGATCAATGTCC

72481  GACAGTGATAAATAAGACAGCATTCCTGTCCTTGAGATGCTATTTCCACAGCTCCATGAG
72481  CTGTCACTATTTATTCTGTCGTAAGGACAGGAACTCTACGATAAAGGTGTCGAGGTACTC

72541  ATGCCTAGTTAAAAACAGAGCCTTTTTTGGAAACAGCCTACTAATCTGTTAAAATAATAA
72541  TACGGATCAATTTTTGTCTCGGAAAAAACCTTTGTCGGATGATTAGACAATTTTATTATT

72601  TGGAAAAAGATAAAGTTAGCATACCTGAGCTGCAAGGGCTGCCTCCTGGTCTGATCTCTG
72601  ACCTTTTTCTATTTCAATCGTATGGACTCGACGTTCCCGACGGAGGACCAGACTAGAGAC

72661  ATAAGGATCAGATCCTAGAGCCTCTGAGATCCCTGTCCTCCCTGTCTGCACAAGCACTCG
72661  TATTCCTAGTCTAGGATCTCGGAGACTCTAGGGACAGGAGGGACAGACGTGTTCGTGAGC

72721  CAGAAGGAGAAACAGTTTACGGTGGTTCATCATGACTTTGAACCAAGCTTAAAGTCAAAG
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72721 GTCTTCCTCTTTGTCAAATGCCACCAAGTAGTACTGAAACTTGGTTCGAATTTCAGTTTC

72781 TCATACTCTTTAAACCATTGGAAACCAAGTTTTTGCGAGTTGCCTAAAGTGGGCAAAAAT
72781 AGTATGAGAAATTTGGTAACCTTTGGTTCAAAAACGCTCAACGGATTTCACCCGTTTTTA

72841 CCCACAATGCACCTGAGCACAAGCAGGAAAACATGCCATTGTCTCCCCAGGAGCCCTCCT
72841 GGGTGTTACGTGGACTCGTGTTCGTCCTTTTGTACGGTAACAGAGGGGTCCTCGGGAGGA

72901 TGACTTCTACTTTACTTTATCCATTGACACTAGTCTTATAAGTAGCTTTGTCTGTCCAAT
72901 ACTGAAGATGAAATGAAATAGGTAACTGTGATCAGAATATTCATCGAAACAGACAGGTTA

72961 TTTTAATTGAATTTCGTTTTTATTTTCGTGAGTGGAAATATCACTTTGAAAGAAATCAGT
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73021 CCTCTCCTGAAATCCAGAATTCCTGGAGCTCAGTTTACATGTTTGACGCGTGTCACATGA
73021 GGAGAGGACTTTAGGTCTTAAGGACCTCGAGTCAAATGTACAAACTGCGCACAGTGTACT

73081 TTCCACAAGTCACTCAAGGGCAGGAGGATTACCATCGATACGGAAAGATTTCTTAGAAAG
73081 AAGGTGTTCAGTGAGTTCCCGTCCTCCTAATGGTAGCTATGCCTTTCTAAAGAATCTTTC

73141 CTTAAGTGAAAGGGAAACCAGGGAGAAAGTGTGCTTCGTGAGAATAGGTATGCGGACGGC
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73201 TCTTTGTGACGCTCTGTGCAACCCTCGTGTTTGCATTGAACCAAGCTGTGCTGCAGATGG
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73261 ACACCCATCCCATTTCCCCGACTCATACCAGGGAGGCCCACTTTGCAAGGTACACAGAGG
73261 TGTGGGTAGGGTAAAGGGGCTGAGTATGGTCCCTCCGGGTGAAACGTTCCATGTGTCTCC

73321 GGACCACAGAGCAGGGGGCCATGCAGGGGACCAAGGGACATTTTAGTGTAACCAAAGTGT
73321 CCTGGTGTCTCGTCCCCCGGTACGTCCCCTGGTTCCCTGTAAAATCACATTGGTTTCACA

73381 GAAGTATGCCCTTTATTTCAAAAGAATAAAGAAAATCACAGGTTTTCCCGCTGATATGCC
73381 CTTCATACGGGAAATAAAGTTTTCTTATTTCTTTTAGTGTCCAAAAGGGCGACTATACGG

73441 AGGGACATTTCCAAGAGAATTCCTTTTTTGAGAGAAATCTCCTTTGATATCCCATCAGTC
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73501 AGCCATACTGCATAATTGTTAGATAGTGAAAGAAATTCATTTTTTAAGTTTGTCAGAAAA
73501 TCGGTATGACGTATTAACAATCTATCACTTTCTTTAAGTAAAAAATTCAAACAGTCTTTT

73561 ATAAATTCTTTGAAGTCTTAAATTGTTGCCTCCGGACATGACATATCTGGCTCTTCCAGA
73561 TATTTAAGAAACTTCAGAATTTAACAACGGAGGCCTGTACTGTATAGACCGAGAAGGTCT

73621 ATCCATGTTAGTCCTAGCTGAGGAAGAAGGAGAAGGAGAGGGGCGTTTGTTGATTATTGA
73621 TAGGTACAATCAGGATCGACTCCTTCTTCCTCTTCCTCTCCCCGCAAACAACTAATAACT

73681 TTTTGTAAGATGCCCCACACGTTGGCTATTAGCAGAATTCTCACTTCTAAAAGGAAAATG
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73741 TCACACTCGATACAAGTTACTCTTTGTCAATAAAAACCCTGTAAGAAACTCCATTTTGTG

73801 CTCCTTAAGATGCTGCTTCCTTATTGCTATGGGACCAAGATTAGAGCAAGAACATAGTGG
73801 GAGGAATTCTACGACGAAGGAATAACGATACCCTGGTTCTAATCTCGTTCTTGTATCACC

73861 TTTTCAGACCCTGGACATCATCCACAGCCGCAGCAGAGGCCCTGCCCACTTGAACAATGA
73861 AAAAGTCTGGGACCTGTAGTAGGTGTCGGCGTCGTCTCCGGGACGGGTGAACTTGTTACT

73921 GACAGGCCACCATTTTGTTTCGAGAATGAGCAAAGTGAACCACCATGCCAGATATTGTTA
73921 CTGTCCGGTGGTAAAACAAAGCTCTTACTCGTTTCACTTGGTGGTACGGTCTATAACAAT

73981 AGTCAGCAACTCTTCTGAAGATGGACATAGTAAAAAATAAACAAACAAGGCAGCACTTGA
73981 TCAGTCGTTGAGAAGACTTCTACCTGTATCATTTTTTATTTGTTTGTTCCGTCGTGAACT

74041 GATGGTCATGGCAGAGCAATCTCAACAAGCGATTTGTTATTTTGCACAGTGATGTACCCA
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74101 CTCATTGAATAAAATGCACCAGAACCATGCACTACAGATGCTAAGGAGAGTTGTCCTTCA
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74221 GCAGGCATGGCCCTTTCTATGCTTCACAGATGAGGAAGGTCCCTGGCACAGGTCCAGTCT
74221 CGTCCGTACCGGGAAAGATACGAAGTGTCTACTCCTTCCAGGGACCGTGTCCAGGTCAGA

74281 CCAGCATGGCCTAGAGGTGGCAGGTGCTACTTAGCATCGCCAGCCTCCTGCTTGGTCATG
74281 GGTCGTACCGGATCTCCACCGTCCACGATGAATCGTAGCGGTCGGAGGACGAACCAGTAC

74341 GGGTCAGCCAGTTTATAACACGAACGGAGGTTAATGAACTGATCTTCCCATCGCACAACT
74341 CCCAGTCGGTCAAATATTGTGCTTGCCTCCAATTACTTGACTAGAAGGGTAGCGTGTTGA

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74461 CTGTCTAGTGTAGGCCTGTGTGTTCATGGCCTTTCTTGCCACCAAAAGATCAACTATTAG
74461 GACAGATCACATCCGGACACACAAGTACCGGAAACAACGGTGGTTTTCTAGTTGATAATC

74521 CTGAATAACATACTGAGACATGTTGGTGTTGTGTTCTAAATAGCACTAGTAAACTGTTAG
74521 GACTTATTGTATGACTCTGTACAACCACAACACAAGATTTATCGTGATCATTTGACAATC

74581 GGAAATCTGACTATATAGCTACTATCCAGTCTAGTTTTTCTTGCGAAGTGTTTGTTGAGT
74581 CCTTTAGACTGATATATCGATGATAGGTCAGATCAAAAAGAACGCTTCACAAACAACTCA

74641 GTGTAATGAGGAGTAAGGAAGGTGAATAAGAAATGGCCTGAGTCTTTATAAAATAAGCAA
74641 CACATTACTCCTCATTCCTTCCACTTATTCTTTACCGGACTCAGAAATATTTTATTCGTT

74701 GGAGAGAAAACAGTTTTGATGAGAAGCGCATGGAATTTTTAGAAGATAGGACGTGTATTA
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74761 TGTACCTATAAGAATGGGTAGGATTTTAGAAGAGATGGATGGGGAAAAGGAACAGGGAGT
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74821 GGGAACAAAACGTGGACCAAGGAAGAGCAGGTTTAGCCATGGAAGCCTCACCGCCGGCTT
74821 CCCTTGTTTTGCACCTGGTTCCTTCTCGTCCAAATCGGTACCTTCGGAGTGGCGGCCGAA

74881 TGGTTTATCGTGGGCCAAGGGGACAGACCCTGTGGGGAGGGCTGGCAGCAGGGAGGTCTT
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74941 CCAGAAGTCTATCCTGCAGGCAGTAACAGCCACCCAGTCTATAAGCTGAGTGGGCATGGG
74941 GGTCTTCAGATAGGACGTCCGTCATTGTCGGTGGGTCAGATATTCGACTCACCCGTACCC

75001 GGTGATGGGGAATGGGTGGGGAGTTATTGGGGTAACTTACCCCAAAATGATAGCTAGCTG
75001 CCACTACCCCTTACCCACCCCTCAATAACCCCATTGAATGGGGTTTTACTATCGATCGAC

75061 GAACCATTTATTCTATTGCATTTTATCAATAAATCTTATAGGAAGTACCATCCTAGTGAA
75061 CTTGGTAAATAAGATAACGTAAAATAGTTATTTAGAATATCCTTCATGGTAGGATCACTT

75121 AACCCTGTCACATTGAGGGCATTCATGCTTATGTTTTAAAACATGTTATTGGGTCTATGA
75121 TTGGGACAGTGTAACTCCCGTAAGTACGAATACAAAATTTTGTACAATAACCCAGATACT

75181 AAAATAAGGCTGAAACCTATGAGCACCCTCCATGCAAAGTTTCAGTCAAGACTTTGGAAA
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75241 CAAGACAGTGTCTTACTCACTTTATAAATTCATTCAGAAAGCCGTAGGTTTGAAAATTCC
75241 GTTCTGTCACAGAATGAGTGAAATATTTAAGTAAGTCTTTCGGCATCCAAACTTTTAAGG

75301 AAACTTAGATGTAAGAAGCTCTGAGAAACACATGAAATCACCCCCACATCAGTAGAGATG
75301 TTTGAATCTACATTCTTCGAGACTCTTTGTGTACTTTAGTGGGGGTGTAGTCATCTCTAC

75361 TCTCAGCAGACATGGGAAGAGGGGCAGCAGGGTGTAGGGAGGTGGGGCAGCCCCGGGGTG
75361 AGAGTCGTCTGTACCCTTCTCCCCGTCGTCCCACATCCCTCCACCCCGTCGGGGCCCCAC

75421 GGCCTTGCAGGCTGGGCTTGAATCCCATGGCCACCACCGTCCGCTGGGAGGCCTGGAGCC
75421 CCGGAACGTCCGACCCGAACTTAGGGTACCGGTGGTGGCAGGCGACCCTCCGGACCTCGG

75481 GGCTGCCCACTCTCTGACCAGCACATGTTGATGCTGTATCCTTGAAGGGACCGTGGTCTG
75481 CCGACGGGTGAGAGACTGGTCGTGTACAACTACGACATAGGAACTTCCCTGGCACCAGAC

75541 ACATCCTGTGATGCAGACCTGAATCCAGCACCCACAGGGTCTGCACATTCCCTCTTTGAG
75541 TGTAGGACACTACGTCTGGACTTAGGTCGTGGGTGTCCCAGACGTGTAAGGGAGAAACTC

75601 GTGGAGCCCAGCTCCAGAGGCTGGTCCCTGACTCTGTTTCTCAAGAAGCCTGTACAGATG
75601 CACCTCGGGTCGAGGTCTCCGACCAGGGACTGAGACAAAGAGTTCTTCGGACATGTCTAC

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75661  TTCCCCTCACCACTGTTTCCAGTCACCTTTGGCTTTCACGGTGCAGATGCTAAGTTTGAT
75661  AAGGGGAGTGGTGACAAAGGTCAGTGGAAACCGAAAGTGCCACGTCTACGATTCAAACTA

75721  TTTCAGAGCCCATCTGGGAATTTAGTGAACTGAACAGGTAGCATTTCTGAACCCACCCAT
75721  AAAGTCTCGGGTAGACCCTTAAATCACTTGACTTGTCCATCGTAAAGACTTGGGTGGGTA

75781  AACCCATGCCCTCCCCACTGATTTTGAAAGAGAGTTTGCTGCAGGTGACTTTGCAGCTGG
75781  TTGGGTACGGGAGGGGTGACTAAAACTTTCTCTCAAACGACGTCCACTGAAACGTCGACC

75841  GTAGAGAATCTTGGGGCAGGATTCCGAGGCAGGCAGATGAGTGAGGATAAATTGGGTTCT
75841  CATCTCTTAGAACCCCGTCCTAAGGCTCCGTCCGTCTACTCACTCCTATTTAACCCAAGA

75901  GACGGCACGTTACACCAGTGGACTCTAACGACGACCTCACCTCGTGCACAGATAATTCTG
75901  CTGCCGTGCAATGTGGTCACCTGAGATTGCTGCTGGAGTGGAGCACGTGTCTATTAAGAC

75961  CCTTGTGCTTAACCGTTACAAATGTGTCACTGAAGTGTGAACATATTATGCTGTTACATT
75961  GGAACACGAATTGGCAATCTTTACACAGTGACTTCACACTTGTATAATACGACAATCTAA

76021  TCCCATCATTTCTGTTCTTTCATTCCCTCTCATTTGCATTGGTTACTCATAAATGTAGAT
76021  AGGGTAGTAAAGACAAGAAAGTAAGGGAGAGTAAACGTAACCAATGAGTATTTACATCTA

76081  CTTTGGTATGATTTGTACAACTGCCGGGTGTCAATCTGTGAAAGAAATAGCAGAGCAAGC
76081  GAAACCATACTAAACATGTTGACGGCCCACAGTTAGACACTTTCTTTATCGTCTCGTTCG

76141  TGGGCTCTGGTAGCGCTTTATCCCTGCGTGCTGGCTTGCCCGGGTTGACTCAGAGGCAGT
76141  ACCCGAGACCATCGCGAAATAGGGACGCACGACCGAACGGGCCCAACTGAGTCTCCGTCA

76201  CTCACATTCAGCTGCGCTGGGGCCAAGGACCCAGGGAGCCAAGTGTGTTTCTGTTTTCTG
76201  GAGTGTAAGTCGACGCGACCCCGGTTCCTGGGTCCCTCGGTTCACACAAAGACAAAAGAC

76261  TATTTAGCAATTTAAGACCTGCGTTTAAATACTAGCTATGCATTCTAGCAAAAGAGGTTT
76261  ATAAATCGTTAAATTCTGGACGCAAATTTATGATCGATACGTAAGATCGTTTTCTCCAAA

76321  ATATTTTAACACAGTAACTCTTAATTGTTTAATTCAGTTCGTGTGTTACCTCTCGGAATA
76321  TATAAAATTGTGTCATTGAGAATTAACAAATTAAGTCAAGCACACAATGGAGAGCCTTAT

76381  AAATAGTGGAAGCCAATTAACTATAGACTTCATTAGTTTGGATTTAAGATCACCAAAACA
76381  TTTATCACCTTCGGTTAATTGATATCTGAAGTAATCAAACCTAAATTCTAGTGGTTTTGT

76441  TTTACCACATCTCAATTGTTCATTACATGCTCTCTCTTTTTTAATGCAGTTTTTATAATA
76441  AAATGGTGTAGAGTTAACAAGTAATGTACGAGAGAGAAAAAATTACGTCAAAAATATTAT

76501  TGGGGAGTGGGGGTGTGGATTTAACCATTATATTTTTATGATATTGGGAGTAGATTTAAC
76501  ACCCCTCACCCCCACACCTAAATTGGTAATATAAAAATACTATAACCCTCATCTAAATTG

76561  CATTATGTAAATTGGATTTTTAATTTTAAAAAGTCACTTATCTTGATGTAAAATCATGT
76561  GTAATACATTTAACCTAAAAATTAAAATTTTTCAGTGAATAGAACTACATTTTAGTACA

76621  CTTAGTAACCTTGATAAACTAAGTTTTGCATGATTACACCTTAAGGTTAAAACATATTTC
76621  GAATCATTGGAACTATTTGATTCAAAACGTACTAATGTGGAATTCCAATTTTGTATAAAG

76681  ATTTCATCATTTCCCAGAAGGGGCACTGAATTCACCCATTTCCTGTTTTTCATCTCAGAA
76681  TAAAGTAGTAAAGGGTCTTCCCCGTGACTTAAGTGGGTAAAGGACAAAAAGTAGAGTCTT

76741  TGTTCTGTGTTTCCTCCATATCTACTTTCCCGGCAGCAGGACCCTGGAAGCAGTCACACC
76741  ACAAGACACAAAGGAGGTATAGATGAAAGGGCCGTCGTCCTGGGACCTTCGTCAGTGTGG

76801  AACCTCATTTACCCCACCTGAGATTTGTGCGCTTTGAACATAGTTGCAATCAAATCAACA
76801  TTGGAGTAAATGGGGTGGACTCTAAACACGCGAAACTTGTATCAACGTTAGTTTAGTTGT

76861  ATATCTTTGCTCAGAAATGGATATGTGAAGTAAAATGTGCTGCCCTGTTCATGTATGAAA
76861  TATAGAAACGAGTCTTTACCTATACACTTCATTTTACACGACGGGACAAGTACATACTTT

76921  TCATTCAGCTAGCTGGCCAGTGAGCCCTTCATTGCAACAAAGATTTTTCTAGAGCCCCTG
76921  AGTAAGTCGATCGACCGGTCACTCGGGAAGTAACGTTGTTTCTAAAAAGATCTCGGGGAC

76981  CACTATCTGGGGCTATGTCAGGCCTCACACTCCTGCTCACACCTTTGGAGGCTACCTTGG
76981  GTGATAGACCCCGATACAGTCCGGAGTGTGAGGACGAGTGTGCAAACCTCCGATGGAACC

77041  CCAGTATTACCTTAATCCAGCATTTAGGGGAAGGAGCATTTCAAGACTAAATTTTCTAAA
77041  GGTCATAATGGAATTAGGTCGTAAATCCCCTTCCTCGTAAAGTTCTGATTTAAAAGATTT

77101  CTGCTCAAGCCTACCTCATTTTATTTCTTGTGTATTTTAACACTTTTGGATGAGGACTCT
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77101   GACGAGTTCGGATGGAGTAAAATAAAGAACACATAAAATTGTGAAAACCTACTCCTGAGA

77161   TCCTAGAACCTACTAACAATTCCCCCCCGCCCCCATGCCAAGATTCTTTAAAGACTTTCT
77161   AGGATCTTGGATGATTGTTAAGGGGGGGCGGGGGTACGGTTCTAAGAAATTTCTGAAAGA

77221   TGAAAACGCTTCAGTCTTTTCTTCTTAGCTCAAAAGTACTATCCTAAATACTAGCTCTGG
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77281   CATTACAGGGAGTTAATTTGTGGGCACACACAGTAAATTATAAACCCCTTAAGCAGAGAA
77281   GTAATGTCCCTCAATTAAACACCCGTGTGTGTCATTTAATATTTGGGGAATTCGTCTCTT

77341   GATTGTATTATCAGTTTATTAGTTTTCTTATTCATTCCTTCAGCACACATTTCTGTTGCC
77341   CTAACATAATAGTCAAATAATCAAAAGAATAAGTAAGGAAGTCGTGTGTAAAGACAACGG

77401   TCCAATGCAGCAGAGAAATTGACTTCTACAGTTTCCACAACAGTCCAGATTTCAACTGTG
77401   AGGTTACGTCGTCTCTTTAACTGAAGATGTCAAAGGTGTTGTCAGGTCTAAAGTTGACAC

77461   TAGTGCTCTTTCAGCCAGAAAGTACACTTGTGTTTCCCTGGCCATAGGTCCTGAACCTCA
77461   ATCACGAGAAAGTCGGTCTTTCATGTGAACACAAAGGGACCGGTATCCAGGACTTGGAGT

77521   CTTCTGAAAAGTCATTGTGCATAGAGAGCTAATAGCTGTACCCTAAATGATCCTGGCTTT
77521   GAAGACTTTTCAGTAACACGTATCTCTCGATTATCGACATGGGATTTACTAGGACCGAAA

77581   GAATTCTCTTATCTGCTTCCATACTATTATCTGTCTCTTCCTCTGCATTCTAATTTGCTA
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77641   CTTCTAATCTGCTGGGAATTACAATAAGAAAGAACCATTTAATCATTTTTACAACTGTGC
77641   GAAGATTAGACGACCCTTAATGTTATTCTTTCTTGGTAAATTAGTAAAAATGTTGACACG

77701   CTAAAGAGAGTGTGTGTAAGTGCCGAGAGAGTGTATGAGGGACTTGCCCATGAGTAAATG
77701   GATTTCTCTCACACACATTCACGGCTCTCTCACATACTCCCTGAACGGGTACTCATTTAC

77761   CATGAATTTTAGGTCAAGGGTTTTTTGCTTCTCTTTTGGTTGATTACCTCAGAGATCAGT
77761   GTACTTAAAATCCAGTTCCCAAAAAACGAAGAGAAAACCAACTAATGGAGTCTCTAGTCA

77821   TTTACTTTCTTTCTCATTCTTGACCTATCATCACTAGCTGATATGGATGATGTGTACAAC
77821   AAATGAAAGAAAGAGTAAGAACTGGATAGTAGTGATCGACTATACCTACTACACATGTTG

77881   TTCTGAGTAAGAATAATGTCAATGGGACGGGATGGGATTGGCTGGTGATTCTGTTGATCT
77881   AAGACTCATTCTTATTACAGTTACCCTGCCCTACCCTAACCGACCACTAAGACAACTAGA

77941   TAAAGTTTATATATTTTAAGTTTAGTGTTTCAGAATGAGACCAAAGCGGTGACATTTTCA
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78001   ACCTCTTCGGTCTCTCTTCAGTTTTTTCATTTTAACTTTTTGTTGTGCTTCTATCACTTA
78001   TGGAGAAGCCAGAGAGAAGTCAAAAAAGTAAAATTGAAAAACAACACGAAGATAGTGAAT

78061   AAGGAAGCCTCCAAGTTGAAATCAAATACTAATGACATTTTTATCTAATGTATAAATGTG
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78121   TTTTTATTATTTATTAGGAAATTTATTTTACTTGGCCCTCAGCCATGACATATCATGGCA
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78181   TAATCACTATCCTAAATTTGTATATCTTATCCTTGCATAAGGTAAGACTTTCTATGAATT
78181   ATTAGTGATAGGATTTAAACATATAGAATAGGAACGTATTCCATTCTGAAAGATACTTAA

78241   ACACATATTTGTATTTTCCTCTCTTACATATTTTAAGAATTTTTTTATACTTTGTTTTCT
78241   TGTGTATAAACATAAAAGGAGAGAATGTATAAAATTCTTAAAAAAATATGAAACAAAAGA

78301   GCAAATGAAATATTGCTCATAAGCCAGGTGATGGCTGTCCACGCCTCTTTTCCCCTGCTT
78301   CGTTTACTTTATAACGAGTATTCGGTCCACTACCGACAGGTGCGGAGAAAAGGGGACGAA

78361   ACCCTTGCTTAGATCTTATGGTAGAATCTTTTCATAGAAGACACAGAAAGACATGAAAGA
78361   TGGGAACGAATCTAGAATACCATCTTAGAAAAGTATCTTCTGTGTCTTTCTGTACTTTCT

78421   AAGAGCTGGAGAAGCCTGAGGGGCTGCCCAGTGAGTGGTCTGCTAGGATGCTGTGCCACA
78421   TTCTCGACCTCTTCGGACTCCCCGACGGGTCACTCACCAGACGATCCTACGACACGGTGT

78481   GCCCAGGCACAGGAGGCAGGGAGAGCAATGGGGCCCTTCCCTTCCACCAACATTCAGCAG
78481   CGGGTCCGTGTCCTCCGTCCCTCTCGTTACCCCGGGAAGGGAAGGTGGTTGTAAGTCGTC

78541   AATTTGCAGCTCCATGTTTCCAAAGCTTCCAGGGCACTTGCATTTAGAGAGAGAGAGCAA
78541   TTAAACGTCGAGGTACAAAGGTTTCGAAGGTCCCGTGAACGTAAATCTCTCTCTCTCGTT
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78601  GCAAGCTGCCTTTCCTCTTCCTCAGTTCTGCCAGCCACACTCTTGCCATGATGAGCAGTT
78601  CGTTCGACGGAAAGGAGAAGGAGTCAAGACGGTCGGTGTGAGAACGGTACTACTCGTCAA

78661  TCAGCCAAAAGCTCCTTCCCCTGCCCTAACACCTCCTGCAAGGCCTGAGGTCTGGAAGCC
78661  AGTCGGTTTTCGAGGAAGGGGACGGGATTGTGGAGGACGTTCCGGACTCCAGACCTTCGG

78721  ACCTGCGCCTGCTGGCCCCTCCTTTCTTGTTTCTGCAATGGATGTTGTGGCCCTGTGAGG
78721  TGGACGCGGACGACCGGGGAGGAAAGAACAAAGACGTTACCTACAACACCGGGACACTCC

78781  GAGAAGAGAAAAAGAAGTTGCCCTCCTCCCTCTATCCTCACCTCCTGCCATGCTGTCACC
78781  CTCTTCTCTTTTTCTTCAACGGGAGGAGGGAGATAGGAGTGGAGGACGGTACGACAGTGG

78841  CTTATAAGAGAGAAGGGCTAACCATCCAGGCTAATCCTCCAGTGATGCAGGAGAGGACAT
78841  GAATATTCTCTCTTCCCGATTGGTAGGTCCGATTAGGAGGTCACTACGTCCTCTCCTGTA

78901  CCTGGCCGGAAGAGTCAGAGCTTCCAGGTGAGCTCAGGTGGGTCAGCCCCCGAGGCTGTG
78901  GGACCGGCCTTCTCAGTCTCGAAGGTCCACTCGAGTCCACCCAGTCGGGGGCTCCGACAC

78961  AAGAGCCCAGGGGCCAGTAGATGCCACTTTTGCTCCAGGAAGAATCTTCAACTGTGTCCT
78961  TTCTCGGGTCCCCGGTCATCTACGGTGAAAACGAGGTCCTTCTTAGAAGTTGACACAGGA

79021  TTTTATTCAAGGGGCTCTCTTTTCAGCCAATCTCTAGATGTACTAGTCACAAACACTCGC
79021  AAAATAAGTTCCCCGAGAGAAAAGTCGGTTAGAGATCTACATGATCAGTGTTTGTGAGCG

79081  ATTTATTAAAATGTATCCATGATCCCACAATCCTTTTACATATTTCTCTCCAGGAGTATC
79081  TAAATAATTTTACATAGGTACTAGGGTGTTAGGAAAATGTATAAAGAGAGGTCCTCATAG

79141  ACATTTCTGAGGGCCCTGTGCCTGTTTTCTGCAGGAAGTTGCTGTTGTCCCGGGTCCCCC
79141  TGTAAAGACTCCCGGGACACGGACAAAAGACGTCCTTCAACGACAACAGGGCCCAGGGGG

79201  TGCCCCCAGCACCTCTGTTACAAGAAGCAGACCCTTCATGCCACACTGGGACCCAGGGAG
79201  ACGGGGGTCGTGGAGACAATGTTCTTCGTCTGGGAAGTACGGTGTGACCCTGGGTCCCTC

79261  GCCCCAAGCCAGGATGCTGGGATCTTAGTAAAGGTTGGAATGATGTCAGAACATAGAGGA
79261  CGGGGTTCGGTCCTACGACCCTAGAATCATTTCCAACCTTACTACAGTCTTGTATCTCCT

79321  GGCAGAATTCCCCCCATAGCATCATCCTGGAGGGCGCTGATTTGTGTGCTCTGCCAGGTT
79321  CCGTCTTAAGGGGGGTATCGTAGTAGGACCTCCCGCGACTAAACACACGAGACGGTCCAA

79381  CATCTGTGACTCAGGATTTAAAAGCCCCAGGTGTGGTGTCCCTTCTGTGCCTGCAAGGTG
79381  GTAGACACTGAGTCCTAAATTTTCGGGGTCCACACCACAGGGAAGACACGGACGTTCCAC

79441  CGTCTTTAGCAGTTCTCCCTGGTGTGGAAGGATCAGTGGTTCTTGCAGCCTAGGCACCCT
79441  GCAGAAATCGTCAAGAGGGACCACACCTTCCTAGTCACCAAGAACGTCGGATCCGTGGGA

79501  CCACAGCAAGCCCAACACAGGTGCTGTGAGCAGCTGGTTCATGAACGGTGATCCTGGGGA
79501  GGTGTCGTTCGGGTTGTGTCCACGACACTCGTCGACCAAGTACTTGCCACTAGGACCCCT

79561  GAAGAGGAGGATGAAAATGGAAAACCAGTGCAAAGGTGTGTCATCCAGTTGGTTACTGCT
79561  CTTCTCCTCCTACTTTTACCTTTTGGTCACGTTTCCACACAGTAGGTCAACCAATGACGA

79621  GTGGGTGCCCGGGCTTCCATCCCACCAGAGCCCCCACTAGCCAGGGCAGCCTGGCGGAGG
79621  CACCCACGGGCCCGAAGGTAGGGTGGTCTCGGGGGTGATCGGTCCCGTCGGACCGCCTCC

79681  TGAGCATCATTCTGCTTTCTGGCTGCACCTGTGTGGACAGAGCCCGTTCCAAAGCCTCCC
79681  ACTCGTAGTAAGACGAAAGACCGACGTGGACACACCTGTCTCGGGCAAGGTTTCGGAGGG

79741  AGGCACAGGGCAGACATCAAGCAAGGGGCAGAGCTGGGGCGAGGGCTCTGGGTGCCCCCG
79741  TCCGTGTCCCGTCTGTAGTTCGTTCCCCGTCTCGACCCCGCTCCCGAGACCCACGGGGGC

79801  TTATTGAACACAGGCCTGAAGGGAGCCTAAGAGGTGGCTGGCAGGAGATACTACAAGGCA
79801  AATAACTTGTGTCCGGACTTCCCTCGGATTCTCCACCGACCGTCCTCTATCATGTTCCGT

79861  GAAAGACAGGGCAGCAGTCTTTGTACTGTACGTTTTTGTTTTTAAGAGAGAACAAAAAG
79861  CTTTCTGTCCCGTCGTCAGAAACATGACATGCAAAAACAAAAATTCTCTCTTGTTTTTC

79921  TCAAGGTTGAGAGATGAGAAATACTCTTGCCAAAAAGAGAACACCAAAATCCTGGAGTCA
79921  AGTTCCAACTCTCTACTCTTTATGAGAACGGTTTTTCTCTTGTGGTTTTAGGACCTCAGT

79981  CGGGTCTTCCATTACCCTCTCTAGCATTTCTGCTTGTCTTTTCCCTAGTATTGGTGAAGA
79981  GCCCAGAAGGTAATGGGAGAGATCGTAAAGACGAACAGAAAAGGGATCATAACCACTTCT
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80041  TAAAAATTTCATTGGTTGGGTATGGCAACCAATGTCCGGGACACCAGTGGTCCGACAGAG

80101  CCCATGATGGGGATGGAGAGTGGTTAGTGCAGAAACTTAGACCTCCCCTCCAGCTTGTTG
80101  GGGTACTACCCCTACCTCTCACCAATCACGTCTTTGAATCTGGAGGGGAGGTCGAACAAC

80161  AATGCCCTGAAGTTTATCTAGAAGGGAAGATACTCAAGCGTAGGATTTCAGTGATGCATT
80161  TTACGGGACTTCAAATAGATCTTCCCTTCTATGAGTTCGCATCCTAAAGTCACTACGTAA

80221  TGGACAGCATCAGTACTATGCTTCAGCGTCAAAAACGTCACTTTGGGTAGGAACAATACA
80221  ACCTGTCGTAGTCATGATACGAAGTCGCAGTTTTTGCAGTGAAACCCATCCTTGTTATGT

80281  TAATGCGTGGCAATGCCTTTTGTGACACCTGTTCAGGAGATTCCCATAGGAAGCTTCTGA
80281  ATTACGCACCGTTACGGAAAACACTGTGGACAAGTCCTCTAAGGGTATCCTTCGAAGACT

80341  GGCAGAGTCCTCAGGTGAGGAGGGGGACAGGCCTGGGTCTTGGGGGAAGGTGGAGATGAC
80341  CCGTCTCAGGAGTCCACTCCTCCCCCTGTCCGGACCCAGAACCCCCTTCCACCTCTACTG

80401  CAGCCTCATGCCTCTCTCCCCAGTGGCCTCAGTCTCCATCAGGCAAATCTTGAGAAGCCT
80401  GTCGGAGTACGGAGAGAGGGGTCACCGGAGTCAGAGGTAGTCCGTTTAGAACTCTTCGGA

80461  CCTCCATTCTGCAGGCAAATGACTGAGATGTGTGAGCTCTGCTTCCCAACAGGCGGAAAT
80461  GGAGGTAAGACGTCCGTTTACTGACTCTACACACTCGAGACGAAGGGTTGTCCGCCTTTA

80521  TCACATGGGGAAGGGCACCTGTGAATGGCCTTCTAGAACTATCAGGAAGTTCTGGATTTA
80521  AGTGTACCCCTTCCCGTGGACACTTACCGGAAGATCTTGATAGTCCTTCAAGACCTAAAT

80581  GTACCCTGTGAGAGCAGATGGTCCTGGGTGCACTCGGATGATCCTGCCTAGCCAGCTGGA
80581  CATGGGACACTCTCGTCTACCAGGACCCACGTGAGCCTACTAGGACGGATCGGTCGACCT

80641  TTGCAGAGTGGTCATCATTATCAGTGAGCTATTGAGGGGTTGAGAGCAGTCAGTGTCATG
80641  AACGTCTCACCAGTAGTAATAGTCACTCGATAACTCCCCAACTCTCGTCAGTCACAGTAC

80701  TATAAGGATGGGTTGGGGTACCGGCCAACGCCCGCCTTGAGGCCTGGCCGCCGGATGGGA
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80761  GGCGAGAGCACAAGAGAGTCCTGGCTAGGTGTGCCCCGCTCTGCAGGGCCACACCATCCA
80761  CCGCTCTCGTGTTCTCTCAGGACCGATCCACACGGGGCGAGACGTCCCGGTGTGGTAGGT

80821  CTGGAAACCCTGTGCCCACTGGGCTGCGTGCTAAGAGGCTGTGGCCAATGCTCTTGTCCA
80821  GACCTTTGGGACACGGGTGACCCGACGCACGATTCTCCGACACCGGTTACGAGAACAGGT

80881  AATTTTACTGAATCTGCAGTCTCTCTTAATTCACTCCAAAGTTTAATGTGTTAGCTTGCG
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80941  AATAAATAAATAAATAAATAAATAAATAAATAAATGGAAAGAAACAGTCCTCAGAAAGTC
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81001  CCAGTCAAATTTTAATTCCAACAGATATTCAGCAGTTTCCTCTAAGAACAATGAGAGTTC
81001  GGTCAGTTTAAAATTAAGGTTGTCTATAAGTCGTCAAAGGAGATTCTTGTTACTCTCAAG

81061  TGGGGCTAGCCAGTGTTTCTCTTGGAAAATAAGGAAGAGGGAAAGCGGTGCATTCATTTA
81061  ACCCCGATCGGTCACAAAGAGAACCTTTTATTCCTTCTCCCTTTCGCCACGTAAGTAAAT

81121  AAAACCTGCCCTAGGGAGGCAGCGTTCCCTGTGAACTCCGAGGCCACAGTGAGCAGAGCA
81121  TTTTGGACGGGATCCCTCCGTCGCAAGGGACACTTGAGGCTCCGGTGTCACTCGTCTCGT

81181  GGCTGGAGGCCTCCCGGCTGTCCTGCCCCTCCTGCCACATGCCTGTGAAAATGCTAGATA
81181  CCGACCTCCGGAGGGCCGACAGGACGGGGAGGACGGTGTACGGACACTTTTACGATCTAT

81241  AGGACTTTTTCTCAGCAACTTCCACGCTCCTTCAGTGGGGATGTCTTTGACTCAGAGCTC
81241  TCCTGAAAAAGAGTCGTTGAAGGTGCGAGGAAGTCACCCCTACAGAAACTGAGTCTCGAG

81301  TGCCACTGGTTATCTCCACGAACAGAAAATGCCACAGATGGGTTAATTCACTGTGTTGTT
81301  ACGGTGACCAATAGAGGTGCTTGTCTTTTACGGTGTCTACCCAATTAAGTGACACAACAA

81361  CTCATTTTCCCTCAGTTTCAGGCTTTTCTCTCCTTGCCTGTTTTCCTCGCTTAAAAAATG
81361  GAGTAAAAGGGAGTCAAAGTCCGAAAAGAGAGGAACGGACAAAAGGAGCGAATTTTTTAC

81421  ATGTGGGGGTCCCTAAACGCATCTACCCCGATAGATTTATGTTTTCTTTTCCATTAGTCC
81421  TACACCCCCAGGGATTTGCGTAGATGGGGCTATCTAAATACAAAAGAAAAGGTAATCAGG

81481  ACTTTGCGTCTCAGCCCTAAAATTAAGTTTTTGATTATAATGTAAGGAAGTTTTACCATA
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81541 AAAATTGAGACCGAAAAATTTATGTTTTCTTTTTATTGTCTTACCGGAAGATCTTGATAG

81601 AGGAACTTCTGGATCTAGTACCCTGTGGGGACAGATGGTCTGGAGCCAGCGCACTTGGAT
81601 TCCTTGAAGACCTAGATCATGGGACACCCCTGTCTACCAGACCTCGGTCGCGTGAACCTA

81661 GATCTCTCTCAGCCATCTGGACCATAGAGTGAACTTGTTACTGTCCCTCCAAGGCTGACA
81661 CTAGAGAGAGTCGGTAGACCTGGTATCTCACTTGAACAATGACAGGGAGGTTCCGACTGT

81721 ACTATGAGCTCATACTCTTCTAGCAGTTTAATTTAGACCCAAGAAAGGCTGTGTGTGTGT
81721 TGATACTCGAGTATGAGAAGATCGTCAAATTAAATCTGGGTTCTTTCCGACACACACACA

81781 GAATTTGTCACAGTGTCTGAGTCTGTCTTTGTGCCTCTGTTTCTGTGTCTGTCTGTGTGT
81781 CTTAAACACTCTCACACACTCACACAGAAACACGGACACAAAGACACACACAGACACACA

81841 ACATGTGTGTCTGTGGGGTGTGTCTGTGTGTGCACGGCTGTGTGTCTGTGCGTGTGCATG
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81901 GCTTTGTCTGTGTGTGTGCGCACGCACTCTGCTAACCTACTCAATGCAATTCCTTACTCT
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81961 TACTTCCCTTTCTGTCACTTCTCCATAATTCTTTGTATTTCGGTTGGGCTGGTATCTCGC
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82081 GGCTTTTACAATATAGCCAGGAGGATGTGGAAACCCAGTTACAAGATGACACACAAGCAC
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82141 AGTGTCACAATCGCTGTGCTTGGGCCCTACCTCCTGCAGACCAGGGTGGGACGGTGTCTC
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82201 TGGATATGGAGGGAAGGGCGGAAGATCACGGGGTGGCAGAAGGCCCGACTGTCCGGTCTT
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82261 CTGGAAGCTGGGGTCTCGTGGTCGCTGGGCTGGTGGTGCTCTAAAACCTAGAGTAACCGA
82261 GACCTTCGACCCCAGAGCACCAGCGACCCGACCACCACGAGATTTTGGATCTCATTGGCT

82321 GAGCAGGATGACTGCACCCCTGACTGCCGACTCACCGGGCTTCGGAGGGCCATGGGTGTG
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82381 TGATTCCACTTGTGATCCTCCTACTTCCCCAGCCCACCCTGGTGGTCTCCCACTTCTCTC
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82441 TCTCTGCCTGTGGAGTGTTATAACCGACTCCTTCTTCTAGGCATCTCCATCCCAACCCCA
82441 AGAGACGGACACCTCACAATATTGGCTGAGGAAGAAGATCCGTAGAGGTAGGGTTGGGGT

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82501 CTGGTCAAGGGAATTTGGTGGAGGGTGGTGTCCTGGGGGTGTTCGTCCCTGGAGAGTGTC

82561 TTCCTGTTGCCTGGGGACTTCATCTCAGCTTCCAAGGCCTCTGGAACCAGGCCCTGCATC
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82621 CTGGGCATGACTGTCCCCATGATTCTCTGAGCCAGCCACCACCCCACCACCCCCCCACCG
82621 GACCCGTACTGACAGGGGTACTAAGAGACTCGGTCGGTGGTGGGGTGGTGGGGGGGTGGC

82681 CCAAGTCCACTGCTGACCCTGCTGTAGCCCCCCACCTCCACTTGTTGAGATTCCCTCTTC
82681 GGTTCAGGTGACGACTGGGACGACATCGGGGGGTGGAGGTGAACAACTCTAAGGGAGAAG

82741 CTGCTTCTCATTTTGAATGTCACCCTTCTGTGACTTCTCACAACCCCCCTGCCACCCCTC
82741 GACGAAGAGTAAAACTTACAGTGGGAAGACACTGAAGAGTGTTGGGGGGACGGTGGGGAG

82801 CCTCCAGTTGCCATGGCTTAGTCTTCCTAAGAACATGTGCTGCTTCCCAGTACCCAGGGC
82801 GGAGGTCAACGGTACCGAATCAGAAGGATTCTTGTACACGACGAAGGGTCATGGGTCCCG

82861 TGCTGTGCACCGTGGCACGTGAGTTTCGGTGCATCTTCCTCCTGCTGTTTATAAATTGCA
82861 ACGACACGTGGCACCGTGCACTCAAAGCCACGTAGAAGGAGGACGACAAATATTTAACGT

82921 ACATCCCTGGACAGATCTTGGATTTTCCCTCTATAATTTCTCTGGAGACTCCCTCGGGGT
82921 TGTAGGGACCTGTCTAGAACCTAAAAGGGAGATATTAAAGAGACCTCTGAGGGAGCCCCA

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82981  TTGCACACACATCTGTGGAATGCCCAAGTTGGAGATGGTCCTCCCTGATGTGTAGTGTGG
82981  AACGTGTGTGTAGACACCTTACGGGTTCAACCTCTACCAGGAGGGACTACACATCACACC

83041  GCTATTCAGAGGGCCTCATTTCATAAACTCATTAACAGCTAGGACGCGAAGACTTGGAGA
83041  CGATAAGTCTCCCGGAGTAAAGTATTTGAGTAATTGTCGATCCTGCGCTTCTGAACCTCT

83101  AGTTAGCTCAGGACACACGGAGTGGGAGGGAGGCAACGAGTTAAGAAATGGGCTTTGGAG
83101  TCAATCGAGTCCTGTGTGCCTCACCCTCCCTCCGTTGCTCAATTCTTTACCCGAAACCTC

83161  TGCCTCGAATTTGGCCTCCACTTTTCTTTTCTACTGTCTTACCTGGTCTTAGGCAGGTCG
83161  ACGGAGCTTAAACCGGAGGTGAAAAGAAAAGATGACAGAATGGACCAGAATCCGTCCAGC

83221  GGTGACCATCTGGAGTCGGAGTTTCTCTCATTTGTAAAGCGGGGGTGATATTTTTCTCAC
83221  CCACTGGTAGACCTCAGCCTCAAAGAGAGTAAACATTTCGCCCCCACTATAAAAAGAGTG

83281  AGGGCTGCTTCAAGGGTTAACAAAGTTAATGTCTAGGAAGGACATAGCATAGCACCTTCA
83281  TCCCGACGAAGTTCCCAATTGTTTCAATTACAGATCCTTCCTGTATCGTATCGTGGAAGT

83341  CCTGGTTGCAAGCCCCTGGAGTCACATGGCAACAGCTGTGGAACCAGGTAAATGACTTGA
83341  GGACCAACGTTCGGGGACCTCAGTGTACCGTTGTCGACACCTTGGTCCATTTACTGAACT

83401  CTTACATGTTACACGCTCTTAGTTGTTCGATTTGTAAATGGGAAGAGTGTGTGACCCAAA
83401  GAATGTACAATGTGCGAGAATCAACAAGCTAAACATTTACCCTTCTCACACACTGGGTTT

83461  TTAGTCGTTTCCAGATATTTCCTGGTAAATGGTTGTTGAATCATAAAACTAGAAAGATGG
83461  AATCAGCAAAGGTCTATAAAGGACCATTTACCAACAACTTAGTATTTTGATCTTTCTACC

83521  GAAAGAAAGGGAGGAACCCCCCTTACTTCGAAGAAGTGTTGTTGATGTGAAGGACAGGAC
83521  CTTTCTTTCCCTCCTTGGGGGGAATGAAGCTTCTTCACAACAACTACACTTCCTGTCCTG

83581  TTTTTGAGACACTCTCATCCTAAGAAACAGCTGATATCTACTAGGAAAAAACATGACATT
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83641  TGAAGTTTCTTCCTAAGAGATGTGAGGTTTTGACAGAAGTGCCAGGAAGCCAGAGGTGTG
83641  ACTTCAAAGAAGGATTCTCTACACTCCAAAACTGTCTTCACGGTCCTTCGGTCTCCACAC

83701  TGAGTAGTGGGCCAATCTCGCGTGAAGGCTGTGGGACGGGGCAGGAGAGGGGCAGCCAGC
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83761  ATTTCCTGAGCGCCAGCTAATGGCGGGGACCTGGCACCTTTGCTCTGTGACTCTCCAGCT
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83821  GTATGGTGACATGAGGCTGGCGTTTTCTTTGGTTTCATACGTGAGGAAGCTGAGGCTTGG
83821  CATACCACTGTACTCCGACCGCAAAAGAAACCAAAGTATGCACTCCTTCGACTCCGAACC

83881  TGATGTCCTGTGCATGGCTCGGACTCCAGAGCTACTCAGAGGCAGAGGCCGTCTGTAAAC
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83941  ACCTTCAGGTGGTTGGAGGCAGGGTGCTGCAGCCAATGCTGATCACTCACAAGCCAAGGC
83941  TGGAAGTCCACCAACCTCCGTCCCACGACGTCGGTTACGACTAGTGAGTGTTCGGTTCCG

84001  TTTATTGTAAGGGCTAAATAAAATAACATATGCCTAGCATTTATACAGCACGGGGCTTTT
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84061  TAGGAAATAGTGAGACGACCATGGAGAGGTGGAGGAAGAGAGAAGGGAAAGAAGAAAAAG
84061  ATCCTTTATCACTCTGCTGGTACCTCTCCACCTCCTTCTCTCTTCCCTTTCTTCTTTTTC

84121  AAAAAAAAAGCCTTAAAGAGTTTCTTAAGAGAACTATATATTACAAAGTCCTTGGAGTTT
84121  TTTTTTTTTCGGAATTTCTCAAAGAATTCTCTTGATATATAATGTTTCAGGAACCTCAAA

84181  TTTTTCCCTGGTTAGACATAAGTTTACATGAAACGTTAAACGGCTTAAAGTAGCCACATC
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84241  TCCTTCCTTATGTCTTCTCACAGCCACTTGTGAGTTTCTTATCAAGATACAGAATTATGG
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84301  CCAAGTGCGGTAGCTCACACGTGTAATCCCAGCACTTTGAGAGACTGAGGTGGAAGGATC
84301  GGTTCACGCCATCGAGTGTGCACATTAGGGTCGTGAAACTCTCTGACTCCACCTTCCTAG

84361  ATGTGTGCTCAGGAGTTTCAGACCAACCTAGGCAATATGGTAAAACCCTGTCTCTACAAA
84361  TACACACGAGTCCTCAAAGTCTGGTTGGATCCGTTATACCATTTTGGGACAGAGATGTTT
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84421  AAAATACAAAAATTAGCTGGGCATGGTGGCATATTCCAATAGTTCCAGGCACTCGGGAGG
84421  TTTTATGTTTTTAATCGACCCGTACCACCGTATAAGGTTATCAAGGTCCGTGAGCCCTCC

84481  CTGAGACAGGAGGATTGCTTGAGCCCAAGAGGTCAAGACTGCAGTGAGCTGTGATCGAGC
84481  GACTCTGTCCTCCTAACGAACTCGGGTTCTCCAGTTCTGACGTCACTCGACACTAGCTCG

84541  CACTGCACTACAGCCTGGGCCACAGAGCAAGATCCTGTCTCAAAAAATAAAATAAAATAA
84541  GTGACGTGATGTCGGACCCGGTGTCTCGTTCTAGGACAGAGTTTTTTATTTTATTTTATT

84601  AATAAATTCTGCAACAAGTCACAATTCCTTGCTCAGAAATCTCTACAGGTGTGCTTCTTT
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84661  GTTAAGAAATGGAGGAAACATGAATTTCATCCTGACTTCTGAGTCTTGTAGAGACCAGAT
84661  CAATTCTTTACCTCCTTTGTACTTAAAGTAGGACTGAAGACTCAGAACATCTCTGGTCTA

84721  CTGACTCCTGCAGCCTTCTGCCCACAGAGCTGGCAGGCGGGGAATGTGCGCAGAGTGAG
84721  GACTGAGGACGTCGGAAGACGGGTGTCTCGACCGTCCGCCCCTTACACGCGTCTCACTC

84781  GAGGAGCTGATCTGACATTCCGAACAGTGGAGACTGCTGCCTATTTGGCCGCACCACTGT
84781  CTCCTCGACTAGACTGTAAGGCTTGTCACCTCTGACGACGGATAAACCGGCGTGGTGACA

84841  CCTTCTGCATGGAAAAGTCACAGTAAATAATGGACTCTCTACCTGTGAGTCGATTTTACT
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84901  GAGCTGCCTTTTTAAATATATGTGTAGAAAGGGCGATCTCTGTGTGTCATTTGCACATGT
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85081  GACAGCCAGTTCAGCTACAGTTATGCCAGATTGCCTGCACTCTGATCTTTACCATCACCA
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85141  GACTCTCAGCTTGAGCTCATGCCTGAGAAATCCACTTTCTGGGAGGAAGGCAGAAGAAAC
85141  CTGAGAGTCGAACTCGAGTACGGACTCTTTAGGTGAAAGACCCTCCTTCCGTCTTCTTTG

85201  TGCCAAGGCAGCACTGAAGACTTGACCTCCACCTGTAGTGGGTCAGGTCACCAGACGCT
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85261  GGCTGACTCCCCAGGATTTCTCAGCAGAGTATTACACAAATACCCCTTCCTTAAAGATTA
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85321  GCAACCACTTAAAGACACAAAGTGTCCAGCACTGTACCCATGCCCCGACAGCGGCGGCATT
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85441  TGGAATTCTGACAGGGACCCGTTGGCCTTCTGGAAGGCAGGGACAGCAGAGGATCCACCC
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85561  TGGAATCTTTGAGGCTGACACCCTGCCAGCCCTGGGGATGAGAGGGAATGGCCGTGTCTG
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85621  TCTGCAGAGCCTGAGGAGGAGCTGAGCACAGCCTCCAGAGTTCTCTTCAGTTGATCGCTT
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85681  AGGTGGACAAAGGCCACAGAAATGGATTTAAACTCCTCAGCCCTTTCTTTGCATGTTTGT
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85741  TCTCATTTGAAGTCAGAAGTGATATGTCCTACACCTCAAGAACGTGTGAAATGCACATAC
85741  AGAGTAAACTTCAGTCTTCACTATACAGGATGTGGAGTTCTTGCACACTTTACGTGTATG

85801  AATAACCCCATTTCAGGAAGCCAAGTCCAGCTTAACAGTCAAAACATTTCCTTCAGTCTT
85801  TTATTGGGGTAAAGTCCTTCGGTTCAGGTCGAATTGTCAGTTTTGTAAAGGAAGTCAGAA

85861  TAGTCCTTCACTTTGCCGAACTCCCTTTACACCGGCAGCAACAGTTTAACCTGTTGCTT
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85921  GACATTCTCACACGATGACCCTTTTGGTGTAGATTTTGTGCACACGTCAATGTAGTCGAT

85981  GAGCACATGCTAAACAGTTGATCAAAGGCTCTTGCCTTGTGGCCCACGCTGCAGACACTC
85981  CTCGTGTACGATTTGTCAACTAGTTTCCGAGAACGGAACACCGGGTGCGACGTCTGTGAG

86041  TGACGACTGCCGAGCTCCGCAGCCCCATGTCGTCCCTTCCGCACTGCCTGCTGTGCCTCT
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86101  CCTCTCCATGTGGCAGGCAACACAGCCAGTCATCACCATGTGGCTCTGCCCGGCCGCTGCC
86101  GGAGAGGTACACCGTCCCTTGTGTCGGTCAGTAGTGGTACACCGAGACGGGCCGCGACGG

86161  CCAGCATGTCCTGACAGGGCCTAGATATGGAAAGGTGGCTCTCCATGCACACACCCCAAG
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86221  CCCCTCCTGCCCGCCGTGTGACCCACACTCTTATGGGCAGCCCAGTTATTTTGTAGCATT
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86281  TCCCTTCCTTATCATTTTGGCCCAGTGATCCAGCACAAATCTCCCTTATTAGAATAAAAT
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86341  TTGGAATGACAAAATTAAATTTCATTTTTCACTTATATTGAGGACCTCACACTCTTCACC
86341  AACCTTACTGTTTTAATTTAAAGTAAAAAGTGAATATAACTCCTGGAGTGTGAGAAGTGG

86401  CCTGCCACGATCCCTGACAAGAGCCTTCCTATCTAATCATTGTTCCTCCAGCCCTCTTAG
86401  GGACGGTGCTAGGGACTGTTCTCGGAAGGATAGATTAGTAACAAGGAGGTCGGGAGAATC

86461  TTTTCTTCAGCCTTTCTTGATTGCCTGAATGTCCCTTTCCCTTCTCCTTTTAAAGCATGA
86461  AAAAGAAGTCGGAAAGAACTAACGGACTTACAGGGAAAGGGAAGAGGAAAATTTCGTACT

86521  ACCAAGCTTTCTTACCCCGTTCTCATTATCATTTTTGCATTTTCTTCTTTGCATATGATT
86521  TGGTTCGAAAGAATGGGGCAAGAGTAATAGTAAAAACGTAAAAGAAGAAACGTATACTAA

86581  CTCCTTAAATTATAAAACTTGGGGGTAATTTCTAGAGGTGCCATCATAGTGCTTCTGTCT
86581  GAGGAATTTAATATTTTGAACCCCCATTAAAGATCTCCACGGTAGTATCACGAAGACAGA

86641  ACTCAGTGTCTTTAGAATCAGCAAATATCATTTTTACAAAAAAGTAGTATTTCTTCCAAA
86641  TGAGTCACAGAAATCTTAGTCGTTTATAGTAAAAATGTTTTTTCATCATAAAGAAGGTTT

86701  AAAGAGTAAGCAAGAAGGTTACAACACTGGGAAAATATCCCTAAGCCTGTTCTTCAACCT
86701  TTTCTCATTCGTTCTTCCAATGTTGTGACCCTTTTATAGGGATTCGGACAAGAAGTTGGA

86761  GTTGAATGTTTTCCCCTAAATTGTTATATGGAGATCCTGGACCCGGAAGTTGGCTGACAT
86761  CAACTTACAAAAGGGGATTTAACAATATACCTCTAGGACCTGGGCCTTCAACCGACTGTA

86821  GAAACAGGCCTAGCAGGGCAGCTGAGGAAATGCTCCAACCTCAGGATCCAGGAAGATTGC
86821  CTTTGTCCGGATCGTCCCGTCGACTCCTTTACGAGGTTGGAGTCCTAGGTCCTTCTAACG

86881  ACATGGCACCAAAACAATCATTTAAAAGCTAATCCTGGCCAGGCACAGTGGCTCACGCCT
86881  TGTACCGTGGTTTTGTTAGTAAATTTTCGATTAGGACCGGTCCGTGTCACCGAGTGCGGA

86941  GTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCTGATCACAAGGTCAAGAGATCGAGACC
86941  CATTAGGGTCGTGAAACCCTCCGGCTCCACCCGACTAGTGTTCCAGTTCTCTAGCTCTGG

87001  ATCCTGACCAACATGGTGAAACCCCATCTCTACCAAAAGTACAAATATTAGCTGGGCATG
87001  TAGGACTGGTTGTACCACTTTGGGGTAGAGATGGTTTTCATGTTTATAATCGACCCGTAC

87061  GTGGTGCGCGCCTGTAGTCCCAGCTACCCGGGAGGCTGAGGCAGGAGAATCACTTGAACC
87061  CACCACGCGCGGACATCAGGGTCGATGGGCCCTCCGACTCCGTCCTCTTAGTGAACTTGG

87121  CGGGAGGAGGAGGTTGCAGTGAGCCAAGATCATGCCACTGCACTCCAGCCTGGTGACAGA
87121  GCCCTCCTCCTCCAACGTCACTCGGTTCTAGTACGGTGACGTGAGGTCGGACCACTGTCT

87181  GCAAGACTCCATCTCAAAAAAGAAAAAAAAAGCTAATCCCATAAAAGAACCATCATTTTG
87181  CGTTCTGAGGTAGAGTTTTTTCTTTTTTTTTCGATTAGGGTATTTTCTTGGTAGTAAAAC

87241  AACCTGCTGTTTCCTTTCTTGTACTCTTTAGAAGTACCCATTTCTCCCTTTCTAAGCCAT
87241  TTGGACGACAAAGGAAAGAACATGAGAAATCTTCATGGGTAAAGAGGGAAAGATTCGGTA

87301  AGGTGTATTAATTGGAGCTTTTTCTATCTTAATTAGTTCACTGTGAACAATTAAAATTGT
87301  TCCACATAATTAACCTCGAAAAAGATAGAATTAATCAAGTGACACTTGTTAATTTTAACA
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87361  GTTAATAAAACAAAAACAAAAATAGGACTGGTGCCTAGTTGTACTACATGAAGAGAGAAA
87361  CAATTATTTTGTTTTTGTTTTTATCCTGACCACGGATCAACATGATGTACTTCTCTCTTT

87421  GGGCCAGACATTGGTTTTTCCTAATCTTCTGTCAAGTTCTCCAAATCATCTGCTCTGGAA
87421  CCCGGTCTGTAACCAAAAAGGATTAGAAGACAGTTCAAGAGGTTTAGTAGACGAGACCTT

87481  GGTAGCTCCAACAGCTGGGATTTGAAGTAAAGCATAGTGACTTTGGCCATCACTGACATG
87481  CCATCGAGGTTGTCGACCCTAAACTTCATTTCGTATCACTGAAACCGGTAGTGACTGTAC

87541  TCCCATTTGAAGCAACCAAAACTGTCCCTCGACCTGACACTCATCCCTGAAACACCATGA
87541  AGGGTAAACTTCGTTGGTTTTGACAGGGAGCTGGACTGTGAGTAGGGACTTTGTGGTACT

87601  GGGTAAGTGAGGCGCTTCGGAAGGTCCACTCAACCCCATTGCCAGATAGAGTAAGTGTCT
87601  CCCATTCACTCCGCGAAGCCTTCCAGGTGAGTTGGGGTAACGGTCTATCTCATTCACAGA

87661  GCCAGGGGCATTTGGAGCTGAAGGGAAGACTGTACAGACTCACGGTTTGCAGGCACTGAA
87661  CGGTCCCCGTAAACCTCGACTTCCCTTCTGACATGTCTGAGTGCCAAACGTCCGTGACTT

87721  GGCGTTTTCCTGCCTTCTTTTTCACCTTCAGTGGACTTGCAAAGCACTAGCCCTATTGTT
87721  CCGCAAAAGGACGGAAGAAAAAGTGGAAGTCACCTGAACGTTTCGTGATCGGGATAACAA

87781  TTTCCCATCTGGGAAACATGGTGAATGTTGGTTGGTTGTAGCTAATCCTATGGGTCTTGA
87781  AAAGGGTAGACCCTTTGTACCACTTACAACCAACCAACATCGATTAGGATACCCAGAACT

87841  GGTCTTTGTTGACAAGAAGGTAGATGTTATCTTTATCTGCGTGTGGCTTTCTACTAAAAC
87841  CCAGAAACAACTGTTCTTCCATCTACAATAGAAATAGACGCACACCGAAAGATGATTTTG

87901  ATGAGCTACAGGGCTCTCTTTTTTGTTTTAAAGCATTTTTCCATAAGGTTCACCCTTACT
87901  TACTCGATGTCCCGAGAGAAAAAACAAAATTTCGTAAAAAGGTATTCCAAGTGGGAATGA

87961  ATTGCTTATCTGAATAATATTACCTGCTGAGAAGTTTATTCATTGCTCACCAGTTGTAGG
87961  TAACGAATAGACTTATTATAATGGACGACTCTTCAAATAAGTAACGAGTGGTCAACATCC

88021  GAGATTTTGACACAGGACTGGAGGATTTTTTTCTCATCGTAACAGTGCAGACCCATGGAA
88021  CTCTAAAACTGTGTCCTGACCTCCTAAAAAAAGAGTAGCATTGTCACGTCTGGGTACCTT

88081  AGCTTGGAAGCAGTTGTGACCGGATAAGAGCAGGTTGAGGATGATAATCTTAGGGCAATG
88081  TCGAACCTTCGTCAACACTGGCCTATTCTCGTCCAACTCCTACTATTAGAATCCCGTTAC

88141  AGCAGGTTGATTGAGAGGGGTGCCTGAAAGCAAGGTCCCCATGATGCAAGCAAACAAACT
88141  TCGTCCAACTAACTCTCCCCACGGACTTTCGTTCCAGGGGTACTACGTTCGTTTGTTTGA

88201  CACATGCCAGACGGTGGACAGGAAACACAGGCAGGATGTGGTGCAGGCTGGGCTGCCTTG
88201  GTGTACGGTCTGCCACCTGTCCTTTGTGTCCGTCCTACACCACGTCCGACCCGACGGAAC

88261  GCTGGGCAAAGGCAGGGGCTTCATGGCCATGCTGGGATGTGACGTGGTTGGAAAACAATA
88261  CGACCCGTTTCCGTCCCCGAAGTACCGGTACGACCCTACACTGCACCAACCTTTTGTTAT

88321  AGAATGGAGACCTCTCCAAAGACCTCAGACATAATTTGGCCATGAGAGGCAAGGGTAGAG
88321  TCTTACCTCTGGAGAGGTTTCTGGAGTCTGTATTAAACCGGTACTCTCCGTTCCCATCTC

88381  GCGAGCCCCCTGTGGGTTGGAATGTATGGAATCCAGATGAAGCACCATCAACATGCATGG
88381  CGCTCGGGGGACACCCAACCTTACATACCTTAGGTCTACTTCGTGGTAGTTGTACGTACC

88441  GCTACATAGGAGAGCTGGGTCTGGGGGAAAAGATGGGATTTGGGTTTGGGTGTGCATGTT
88441  CGATGTATCCTCTCGACCCAGACCCCCTTTTCTACCCTAAACCCAAACCCACACGTACAA

88501  CCAGGCATGGAGGGAAGAATGGGCAGAATGACGAGGATCAAGCCCTGGTGGAGCCCCCAG
88501  GGTCCGTACCTCCCTTCTTACCCGTCTTACTGCTCCTAGTTCGGGACCACCTCGGGGGTC

88561  ACCAGGGCCCTGGGCATATTTCCACTTGCCTTCTTCTGCAAACTTTTGTGTGCCTGTTGG
88561  TGGTCCCGGGACCCGTATAAAGGTGAACGGAAGAAGACGTTTGAAAACACACGGACAACC

88621  GTGGAAGGTACTATGCTGGGGCCATCCAGGATCCGGAGCAGTGTAAGACATCATGGCCTG
88621  CACCTTCCATGATACGACCCCGGTAGGTCCTAGGCCTCGTCACATTCTGTAGTACCGGAC

88681  CATGGTGTGACCCTTGACATCTGAAAAGAACGAGCTGGTGGAGTGGGAAGGAGACAAGTG
88681  GTACCACACTGGGAACTGTAGACTTTTCTTGCTCGACCACCTCACCCTTCCTCTGTTCAC

88741  GCAGCAGAGTTGACATCATCAGGACTGACTGCAGGACAGGCGGTGAAACGAGCCACTGAG
88741  CGTCGTCTCAACTGTAGTAGTCCTGACTGACGTCCTGTCCGCCACTTTGCTCGGTGACTC
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88801  GAGTTACCCAGTGCCCTGGGGAGCTTAGATGTGAGACTTACACCACCCAGCACTCCCCAG
88801  CTCAATGGGTCACGGGACCCCTCGAATCTACACTCTGAATGTGGTGGGTCGTGAGGGGTC

88861  CTCTGTGTCCCTGGGTCCCACTGAACTTGATTGTATTTTAGTTGCCTCTTTTCTAAGACC
88861  GAGACACAGGGACCCAGGGTGACTTGAACTAACATAAAATCAACGGAGAAAAGATTCTGG

88921  GGAGCAACAATACCTTCCTTGAGTGTGCATGTGCAGTCCATAGATGGCAGCCAGTGTTCT
88921  CCTCGTTGTTATGGAAGGAACTCACACGTACACGTCAGGTATCTACCGTCGGTCACAAGA

88981  CTTCCCATGAGAAGACTCTGACCCTCCTCACTAGACGGTGGTCTAAAAACAAATGGATCC
88981  GAAGGGTACTCTTCTGAGACTGGGAGGAGTGATCTGCCACCAGATTTTTGTTTACCTAGG

89041  ATCCACAGAAGGTCTGAAAGGTTTTCATAGAATCTTGACTTGGTAGCACTTCAGGATCTA
89041  TAGGTGTCTTCCAGACTTTCCAAAAGTATCTTAGAACTGAACCATCGTGAAGTCCTAGAT

89101  ACTCGTGCTTTCCAGAAGTGTGGCCTGTGGTGTTCTGTCTGGAGTATTTGGTCCTCCCAT
89101  TGAGCACGAAAGGTCTTCACACCGGACACCACAAGACAGACCTCATAAACCAGGAGGGTA

89161  CCACCTCCACCTTGCTGTCCTGTCCTGTGACTCTCACTAGCTCAGTCACCGGGTCAGGAA
89161  GGTGGAGGTGGAACGACAGGACAGGACACTGAGAGTGATCGAGTCAGTGGCCCAGTCCTT

89221  GCCCTGCCATGAAATGCTAGATTTGGAGGCATTGCCAAGGTACCACAAACCATACTCAAA
89221  CGGGACGGTACTTTACGATCTAAACCTCCGTAACGGTTCCATGGTGTTTGGTATGAGTTT

89281  CAAGGTCATAATAGACTAGTGATCTCACTGTGGCTAACAGGTTCATGTGATTTAAAGAAT
89281  GTTCCAGTATTATCTGATCACTAGAGTGACACCGATTGTCCAAGTACACTAAATTTCTTA

89341  GACAGCATTTTTTCTAAATTTTATAAATTTTATAAATTTCTCCTAAATACAAATCTGAAT
89341  CTGTCGTAAAAAAGATTTAAAATATTTAAAATATTTAAAGAGGATTTATGTTTAGACTTA

89401  GTGTTTACCTTTAGACAGATTTTCCCAGAAAATTGTCAGTGTTCTCGAATTTCAAAGTAG
89401  CACAAATGGAAATCTGTCTAAAAGGGTCTTTTAACAGTCACAAGAGCTTAAAGTTTCATC

89461  ATCAGATCTCCTCCCTCTAGTTTTGAAAATCTCAACTAGGTTTAGCCTCTCCCCAGAGTG
89461  TAGTCTAGAGGAGGGAGATCAAAACTTTTAGAGTTGATCCAAATCGGAGAGGGGTCTCAC

89521  ACAACGGCACAAGAAGTTTATAATTTTATGCACAGCTAAATGCAAACTGAAAAGTGTGGT
89521  TGTTGCCGTGTTCTTCAAATATTAAAATACGTGTCGATTTACGTTTGACTTTTCACACCA

89581  TTGTGGGTATTTCATTTTTCCCATAATGTTCATCAATTTGGCAATTCAAATAGGATTCAG
89581  AACACCCATAAAGTAAAAAGGGTATTACAAGTAGTTAAACCGTTAAGTTTATCCTAAGTC

89641  AATCCAAGGTGTTCGCAGCATTTTATATGAAAATGTGCCTGAGAGTTTGGGGAATAGAAA
89641  TTAGGTTCCACAAGCGTCGTAAAATATACTTTTACACGGACTCTCAAACCCCTTATCTTT

89701  TTCTTACCAAATAAGTTAAATTTGCTCTTGATAAGAATATATTTTGTAAAATGTAGAAAA
89701  AAGAATGGTTTATTCAATTTAAACGAGAACTATTCTTATATAAAACATTTTACATCTTTT

89761  CTGAGAAAAAAAGTTTGACACCTGTTTTATCTGCATCCTTTTATTAAACAGTGGCCTGAA
89761  GACTCTTTTTTTCAAACTGTGGACAAAATAGACGTAGGAAAATAATTTGTCACCGGACTT

89821  TTTACTAAAGGACAGAGAACAGGGTTGAGAGGTAATCACTGAATAATAGCTTCGCTAATC
89821  AAATGATTTCCTGTCTCTTGTCCCAACTCTCCATTAGTGACTTATTATCGAAGCGATTAG

89881  CCACAGTGACTGCTTCTTATGACAAGCAAGAGGGTCAACTTAGAGGCAGGACTGTCTTCA
89881  GGTGTCACTGACGAAGAATACTGTTCGTTCTCCCAGTTGAATCTCCGTCCTGACAGAAGT

89941  GGGGCAAAAGCAAGTCAGCACCTACAAACCTCTCCAAGAGAGTGAGAAAAAGCAGGTTGT
89941  CCCCGTTTTCGTTCAGTCGTGGATGTTTGGAGAGGTTCTCTCACTCTTTTTCGTCCAACA

90001  ATGGCTCATTTTGCAGCTTGCCAGAAGCAATGTGGGAATATTGTCAGACTGCACAGACCT
90001  TACCGAGTAAAACGTCGAACGGTCTTCGTTACACCCTTATAACAGTCTGACGTGTCTGGA

90061  GGGGCCAGCTGGCTCCTAGAGTGCGAGGAGCTCTCAGTGACTGCTGTGCATACTCACCTG
90061  CCCCGGTCGACCGAGGATCTCACGCTCCTCGAGAGTCACTGACGACACGTATGAGTGGAC

90121  CTCTGTGACTTTGTTCAGTCCCTACCCTGGATGTGTGGTGAAGGGTGCCAGGCTTAGCTG
90121  GAGACACTGAAACAAGTCAGGGATGGGACCTACACACCACTTCCCACGGTCCGAATCGAC

90181  CTGGACCAGTGAGGTCCCTGAGGGGGCAGGGCTAAGAGCTGTAGCAGTCCCACTTGACCA
90181  GACCTGGTCACTCCAGGGACTCCCCCGTCCCGATTCTCGACATCGTCAGGGTGAACTGGT

90241  GTCATTGATTCACTGGTTGGCAATTTGTTCATTGACGGGACACCATTACTCCCCATGCCT
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90241  CAGTAACTAAGTGACCAACCCTTAAACAAGTAACTCCCCTGTGGTAATGAGGGGTACGGA

90301  CACGTGCAGGTGAGTGTGTGTATATTTGCATTAACACACAAACACACTTATGTGTGTCCC
90301  GTGCACGTCCACTCACACACATATAAACGTAATTGTGTGTTTGTGTGAATACACACAGGG

90361  TGTATGTGCAGCTGCAGTACCTTACACATCTTCCAGTGCCTCTCAAGCATCATAAAAACA
90361  ACATACACGTCGACGTCATGGAATGTGTAGAAGGTCACGGAGAGTTCGTAGTATTTTTGT

90421  GCTTCCACAAAACCTCTACTACCCACCTGGCATCCACAGAGCTCCCAGTGATTGGCTCCC
90421  CGAAGGTGTTTTGGAGATGATGGGTGGACCGTAGGTGTCTCGAGGGTCACTAACCGAGGG

90481  AAAAGATACTGAACTTTGGCATGGAACAGAGTGAGTTTCCACATTTGCTGTTGTACATAA
90481  TTTTCTATGACTTGAAACCGTACCTTGTCTCACTCAAAGGTGTAAACGACAACATGTATT

90541  TTACCTGTCCAGCTAGAATAGTACACACTTCTTTTACTGAGCCCAGAAGTTTATGTGCCT
90541  AATGGACAGGTCGATCTTATCATGTGTGAAGAAAATGACTCGGGTCTTCAAATACACGGA

90601  GAACACGGATGGTACAGGAACAAGGGTGAGCGCTTATCAATTCAGCATTACTCTGGAGAC
90601  CTTGTGCCTACCATGTCCTTGTTCCCACTCGCGAATAGTTAAGTCGTAATGAGACCTCTG

90661  ATGAAACAAACTAATAGGTACAGCTATATTTTGTTTTTTAAACAATTTTGTGAACCACAT
90661  TACTTTGTTTGATTATCCATGTCGATATAAAACAAAAAATTTGTTAAAACACTTGGTGTA

90721  ATTTGGGACAAAAATCAACAAGTAAATTTGAATTACACTAGGCAAAGGACTGATTCTTTT
90721  TAAACCCTGTTTTTAGTTGTTCATTTAAACTTAATGTCATCCGTTTCCTGACTAAGAAAA

90781  GAAACGTGATTGACATTCAACGTCTAACTTTCCAAAAGAAGACATACATGTGGCCCACAA
90781  CTTTGCACTAACTGTAAGTTGCAGATTGAAAGGTTTTCTTCTGTATGTACACCGGGTGTT

90841  TCATATGAAATAAAGTTCATCATCATTGATCATTAGAGAAATGCAAATCAAAACCACAAT
90841  AGTATACTTTATTTCAAGTAGTAGTAACTAGTAATCTCTTTACGTTTAGTTTTGGTGTTA

90901  GAGATACCATCTCACACCAGTCAGAATGGTTATTAATAAAAAGTCAAAGAATGACAGTTG
90901  CTCTATGGTAGAGTGTGGTCAGTCTTACCAATAATTATTTTTCAGTTTCTTACTGTCAAC

90961  CTGGTGAGGTTGTAGAGAAAAAGGAACGCTTATACACTGTTGAGGGGATTGTAAATTAGT
90961  GACCACTCCAACATCTCTTTTTCCTTGCGAATATGTGACAACTCCCCTAACATTTAATCA

91021  TCAACCATGTGGAAGACAGTGTGGCAATTCCTCAAAGACCTATATACCATTTGACCCAGC
91021  AGTTGGTACACCTTCTGTCACACCGTTAAGGAGTTTCTGGATATATGGTAAACTGGGTCG

91081  AATCCCATTACTGCATATATACCCAAAGGAATATGAGTCATTCTACCGTAAGACACATGC
91081  TTAGGGTAATGACGTATATATGGGTTTCCTTATACTCAGTAAGATGGCATTCTGTGTACG

91141  ACGCATTTGTTTGTTGCAGCACTATTCACGATAGCAAAAACATGGAATCAACCTACATGC
91141  TGCGTAAACAAACAACGTCGTGATAAGTGCTATCGTTTTTGTACCTTAGTTGGATGTACG

91201  CCATCAATGATAGACTGGATAAAGAAAATGTGGTACATATACCCCATGGAATACTATGCA
91201  GGTAGTTACTATCTGACCTATTTCTTTTACACCATGTATATGGGGTACCTTATGATACGT

91261  GCCATAAGAAAAAGAATGAGATCATGCCCTTTGCAGGAACATGGATGGAGCTGGAGGCCA
91261  CGGTATTCTTTTTCTTACTCTAGTACGGGAAACGTCCTTGTACCTACCTCGACCTCCGGT

91321  TTATCCTTAGCAAACTAACCCAGGAACAGAAAACCAAGTGCAGATGTTCTCACTTTTAAG
91321  AATAGGAATCGTTTGATTGGGTCCTTGTCTTTTGGTTCACGTCTACAAGAGTGAAAATTC

91381  TGTGAGCTGAATGAGGAGAATACATGGGCACATAGAGGGGCCTATCAGAGGGTGGAGGGT
91381  ACACTCGACTTACTCCTCTTATGTACCCGTGTATCTCCCCGGATAGTCTCCCACCTCCCA

91441  GGGAGAAGGAAGAGTATCAGAAAAAATAACAGGTAGTAGATTTAATACCGGATGACAAAA
91441  CCCTCTTCCTTCTCATAGTCTTTTTTATTGTCCATCATCTAAATTATGGCCTACTGTTTT

91501  CAATCTGTATAACAAACCCCCATGACATGAGTTTACCTATATAACAAACCCGCACATGTA
91501  GTTAGACATATTGTTTGGGGGTACTGTACTCAAATGGATATATTGTTTGGGCGTGTACAT

91561  CTCCTGAACTTAAAAGTTAAATTAAAAAAAAATTAATGTCTAATAATATATTACAGTATT
91561  GAGGACTTGAATTTTCAATTTAATTTTTTTTTAATTACAGATTATTATATAATGTCATAA

91621  CTTCATATTCAATGGCAATGTGTGAAGTGGCAAGTGTCTTGACAGAATTCGGTGTTTCAA
91621  GAAGTATAAGTTACCGTTACACACTTCACCGTTCACAGAACTGTCTTAAGCCACAAAGTT

91681  GGCTTACACTTTGATGCCCAAGACTGCACAAGGCTACATTTTCTACTGGTGAGACAAATT
91681  CCGAATGTGAAACTACGGGTTCTGACGTGTTCCGATGTAAAAGATGACCACTCTGTTTAA
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91741  CCAGACGCATTGCATTCAGATCTAATCTCTTAGCTCCTTAATCTTCAGGGTACTGGTAAA
91741  GGTCTGCGTAACGTAAGTCTAGATTAGAGAATCGAGGAATTAGAAGTCCCATGACCATTT

91801  CATGAAGACCTCCCCAGTGCTGTAGTCATCATGATATGTACAGCAGGTGGCTGAGCTCTG
91801  GTACTTCTGGAGGGGTCACGACATCAGTAGTACTATACATGTCGTCCACCGACTCGAGAC

91861  GATGTAGACTGCAGGGATATATTAGGAAGTTAATTCTCAAGGCAAGTCATCTTCAAGCAC
91861  CTACATCTGACGTCCCTATATAATCCTTCAATTAAGAGTTCCGTTCAGTAGAAGTTCGTG

91921  CATATCAGCATGATCAGCAATATAAGTAGTATCTCAGTGCTTTGTTGTTTAGTCAGAGTT
91921  GTATAGTCGTACTAGTCGTTATATTCATCATAGAGTCACGAAACAACAAATCAGTCTCAA

91981  TTGTACTCTATCACCCATTGTAATGTTCCTATTTGCAAAAGGTAATACATACCCTTTAAA
91981  AACATGAGATAGTGGGTAACATTACAAGGATAAACGTTTTCCATTATGTATGGGAAATTT

92041  ACATCTTTGCTTTTTCTCCCATTATCGAGATGCTAGCAGCTTCATAAAGCAGAATAACTA
92041  TGTAGAAACGAAAAAGAGGGTAATAGCTCTACGATCGTCGAAGTATTTCGTCTTATTGAT

92101  AGGGCAAACAGATTATATAAAGGGTTGGAGCTCAATGAAGACAACAAGAACAGCAAAGGT
92101  TCCCGTTTGTCTAATATATTTCCCAACCTCGAGTTACTTCTGTTGTTCTTGTCGTTTCCA

92161  TATTGTAAAACTGGCTGCTTGCAGGCCAACAAGCACATCCATATGGAGGCAATCAGTTTA
92161  ATAACATTTTGACCGACGAACGTCCGGTTGTTCGTGTAGGTATACCTCCGTTAGTCAAAT

92221  TGCTACCTCTGTCTGTTTGATGGGATTCATAATATTGACTTTATCCATTAGATTTGGACT
92221  ACGATGGAGACAGACAAACTACCCTAAGTATTATAACTGAAATAGGTAATCTAAACCTGA

92281  ACCAGGGAATAAAATAAGCAGATGGAGAGTAAGGATTTGCTAGGAAATAATTCAGCCAGT
92281  TGGTCCCTTATTTTATTCGTCTACCTCTCATTCCTAAACGATCCTTTATTAAGTCGGTCA

92341  CACTTTGAAAGCTGTTCAAGAAACAGCTTTCAAAGTGTCTCTCAAACTATGTTTGCCCAT
92341  GTGAAACTTTCGACAAGTTCTTTGTCGAAAGTTTCACAGAGAGTTTGATACAAACGGGTA

92401  TATCCCAATAATTTATTTCCCAATAATTTCATGGGAAAAGAAGGAAGTTCTGTGGTCAGA
92401  ATAGGGTTATTAAATAAAGGGTTATTAAAGTACCCTTTTCTTCCTTCAAGACACCAGTCT

92461  TAAATCTGGAAAACACTGGTTTAAGCAAAGTTCAGTAGGTCTGCTTCCCTGCAGGTCACC
92461  ATTTAGACCTTTTGTGACCAAATTCGTTTCAAGTCATCCAGACGAAGGGACGTCCAGTGG

92521  TCAGAGTCTTTACTCTGCTAACCTAGGAACTCATCCAACAAGTTTAATTTAACAGCTACA
92521  AGTCTCAGAAATGAGACGATTGGATCCTTGAGTAGGTTGTTCAAATTAAATTGTCGATGT

92581  CTGTGTACGTCACTTTAACAGTCACTGAGCTGTGACTCTTGGGGGAAAGATTGTGCGTGT
92581  GACACATGCAGTGAAATTGTCAGTGACTCGACACTGAGAACCCCCTTTCTAACACGCACA

92641  GTGTGTGTGTGTGTACACATGTGTGCACATGTGCAGAATCTACCAAATCTTAAGAGAAAG
92641  CACACACACACACATGTGTACACACGTGTACACGTCTTAGATGGTTTAGAATTCTCTTTC

92701  GAACATGCTGGGAAACTGTCCTGTGAAAGAGAATAGAAACCTGAAGATTTGAGGCAGTGA
92701  CTTGTACGACCCTTTGACAGGACACTTTCTCTTATCTTTGGACTTCTAAACTCCGTCACT

92761  TAGCATTTATGAAAGCAGCAGATAAGGACTAATCACCAAAAGGGGTAGCTCTTTTGTTGG
92761  ATCGTAAATACTTTCGTCGTCTATTCCTGATTAGTGGTTTTCCCCATCGAGAAAACAACC

92821  TTGGGGAAAACAGGAATTTTTCCCCCACCCAATGTGCTGCATTTTCTAATTTTCTATGAA
92821  AACCCCTTTTGTCCTTAAAAAGGGGGTGGGTTACACGACGTAAAAGATTAAAAGATACTT

92881  CACTTCCTAAGAAAAAGCTGAATGAAGAACATTTGCGATGCAATCAGCTCATTAAGAAAC
92881  GTGAAGGATTCTTTTTCGACTTACTTCTTGTAAACGCTACGTTAGTCGAGTAATTCTTTG

92941  ACGCACTTTTGTGGAGATACGTGCTGTCCCAGGAGATGCTCTGCGAGGAGCCGAGTGTTT
92941  TGCGTGAAAACACCTCTATGCACGACAGGGTCCTCTACGAGACGCTCCTCGGCTCACAAA

93001  GGACTGGAGCTGCTGAATGGTTTCTCACAGTTCTAGAATGTTTGGGGCTGCACCCTCTAA
93001  CCTGACCTCGACGACTTACCAAAGAGTGTCAAGATCTTACAAACCCCGACGTGGGAGATT

93061  GATGTTGAACCCATCAGTAATTGCTCCAAACCACTTTATGGGATATAATGCTGTGAGTTG
93061  CTACAACTTGGGTAGTCATTAACGAGGTTTGGTGAAATACCCTATATTACGACACTCAAC

93121  ACACCTGAGGGGATTGTGGTCCTGTTCATGAGTAATTACTTTTCTGTTGCCTATAGAAGG
93121  TGTGGACTCCCCTAACACCAGGACAAGTACTCATTAATGAAAAGACAACGGATATCTTCC
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93181  GCCAGCAATACCAGATCAGTACCTGAACAGTCCTTTTCAGTAATAAAACGTTCTTTTTTA
93181  CGGTCGTTATCGTCTACTCATCGACTTGTCACCAAAACTCATTATTTTGCAAGAAAAAAT

93241  AAAAAAAGTAATGCTTTCTGTTAAACTCTGACTATACTCTCTCCTGGTATCACAACCCAG
93241  TTTTTTTCATTACGAAAGACAATTTGAGACTGATATGAGAGAGGACCATAGTGTTGGGTC

93301  CTTTCTTTTTGCCTTCTTTATTGCAGTTACATATGGGCCTGATGACTTTAGGGATTTCCA
93301  GAAAGAAAAACGGAAGAAATAACGTCAATGTATACCCGGACTACTGAAATCCCTAAAGGT

93361  TGCAATAATTCCCAAATCTTTCTCTCGTAAGTATATGCCTTGCTTCTGGAAAACAAAAGC
93361  ACGTTATTAAGGGTTTAGAAAGAGAGCATTCATATACGGAACGAAGACCTTTTGTTTTCG

93421  ATGCCTTCATCTCCTATCATGTAAATATCGTACGTGCATGTTCCTTCATCAACCCCCGAC
93421  TACGGAAGTAGAGGATAGTACATTTATAGCATGCACGTACAAGGAAGTAGTTGGGGGCTG

93481  ATACATTAAATATTCACTGTTCTATTCGTTAGACACCTACCATATCATTTTTGGGTATTT
93481  TATGTAATTTATAAGTGACAAGATAAGCAATCTGTGGATGGTATAGTAAAAACCCATAAA

93541  ATACCATAAAGTGCAAAACGAAGGTCTAGGCAGTTGTGCGGTGTCCTGGGAGCATGGCAG
93541  TATGGTATTTCACGTTTTGCTTCCAGATCCGTCAACACGCCACAGGACCCTCGTACCGTC

93601  TGGAGTAACAGTAAGGGTTGGAGTCACAGTAGCACTGATGGGATTGTTACTTCGCAGATG
93601  ACCTCATTGTCATTCCCAACCTCAGTGTCATCGTGACTACCCTAACAATGAAGCGTCTAC

93661  CTGCTGGACAGCTTTGAGATTACTCCTGTAATCCTTTTTATTGAGTGTCAGGATAAAATG
93661  GACGACCTGTCGAAACTCTAATGAGGACATTAGGAAAAATAACTCACAGTCCTATTTTAC

93721  GCCATATTTTCTGTCACCAACAAAGAACTGAACATGGTTTCAAGATAATTTTTACAATTT
93721  CGGTATAAAAGACAGTGGTTGTTTCTTGACTTGTACCAAAGTTCTATTAAAAATGTTAAA

93781  TGTGGGACAGGAGAAGGAGATATGCTCTTCATCTGTGGTTCTGGAGTATTAATTTCAGAA
93781  ACACCCTGTCCTCTTCCTCTATACGAGAAGTAGACACCAAGACCTCATAATTAAAGTCTT

93841  CTGAGAAGAGAAAATTGCAGGCCTCCAGGCCGTTATTCTGTGGTGCATCGCTGCTGGAGC
93841  GACTCTTCTCTTTTAACGTCCGGAGGTCCGGCAATAAGACACCACGTAGCGACGACCTCG

93901  CAACGTACTGTTCCTGCTTGGTGCCCGCAGGACCTTCTCTGATCTGAGCTGTTAAACCAA
93901  GTTGCATGACAAGGACGAACCACGGGCGTCCTGGAAGAGACTAGACTCGACAATTTGGTT

93961  AAACAGATGTGAATTTCATTTTTCTTTTTTAGATATTGAGCTGATAAATGATAAATATAT
93961  TTTGTCTACACTTAAAGTAAAAAGAAAAAATCTATAACTCGACTATTTACTATTTATATA

94021  TTGGGTAACATCCTCAAATGAGTACTTTAAAGAACAGAGAGTGCTTTTGAAAATGTATAG
94021  AACCCATTGTAGGAGTTTACTCATGAAATTTCTTGTCTCTCACGAAAACTTTTACATATC

94081  AGAGCTGAATATTTAAAGCCATACAAGTTGATAATCCCCTTAGGACCTGTATTAGTAAAT
94081  TCTCGACTTATAAATTTCGGTATGTTCAACTATTAGGGGAATCCTGGACATAATCATTTA

94141  CCTCTAATACTATAAAGCAACATCAGAAAACAGGTCGCATTTGTTAACACTGTGACAATT
94141  GGAGATTATGATATTTCGTTGTAGTCTTTTGTCCAGCGTAAACAATTGTGACACTGTTAA

94201  ATAATTATAGGCTCTAATTTGAACAGTGCCAGTAACAGTTAAAGACAGGTGTCTCACATC
94201  TATTAATATCCGAGATTAAACTTGTCACGGTCATTGTCAATTTCTGTCCACAGAGTGTAG

94261  CTGGTTATCAAAAACTATCTGGTGTCTAAGGAATTTAACAGTATCAAAGTACATCTTTTT
94261  GACCAATAGTTTTTGATAGACCACAGATTCCTTAAATTGTCATAGTTTCATGTAGAAAAA

94321  GCTCACAAACTAGATTGGCTACTTTTCCAGCCTATAGAAGTTACAGAAATCTTTCTTTTA
94321  CGAGTGTTTGATCTAACCGATGAAAAGGTCGGATATCTTCAATGTCTTTAGAAAGAAAAT

94381  CTGATATTCCTTTGATTCCACTTTAAAGCAATAGCTTGATACCTACTTTTTGAGATGTAT
94381  GACTATAAGGAAACTAAGGTGAAATTTCGTTATCGAACTATGGATGAAAAACTCTACATA

94441  ATGTATGTACTTGTAAATGCTTATATATGTGTATTTGTTTACACGTGAGCTTATATGAAC
94441  TACATACATGAACATTTACGAATATATACACATAAACAAATGTGCACTCGAATATACTTG

94501  ATATAAAACATTATGGTATTGGACAGAGAAATGATATTGATTTGAAGAATCATATTGTTG
94501  TATATTTTGTAATACCATAACCTGTCTCTTTACTATAACTAAACTTCTTAGTATAACAAC

94561  AAGTATTTTGAGAAGTCAAATGCACTTGAGAGTAAGCTAATGCATCCTAAAACATGTTTC
94561  TTCATAAAACTCTTCAGTTTACGTGAACTCTCATTCGATTACGTAGGATTTTGTACAAAG

94621  TGTGAAGTCTGAGGAAGGTGTCAGCCAGAGCATATGTTGAAGCAGACCCTTCAGTGAAGC
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94621 ACACTTCAGACTCCTTCCACAGTCGGTCTCGTATACAACTTCGTCTGGGAAGTCACTTCG

94681 CTTCAGTCTGTAAGAATCGCTGCATGTGAAGATGTGTTAATGTTATGATAGTTACAGTTT
94681 GAAGTCAGACATTCTTAGCGACGTACACTTCTACACAATTACAATACTATCAATGTCAAA

94741 TTATAAAAGAGATGATATACACTTGGATATGCTTTCTGTCTATATTTATGCAAATGTGTC
94741 AATATTTTCTCTACTATATGTGAACCTATACGAAAGACAGATATAAATACGTTTACACAG

94801 CATAAGGTATTGGTGTCTCTCTTTCTCTCCCACTCTCCCCAGTGTTGGAATTGTGACTAT
94801 GTATTCCATAACCACAGAGAGAAAGAGAGGGTGAGAGGGGTCACAACCTTAACACTGATA

94861 CTTCTCACACAAGCGGCTACTTGGTCTTGATGCCTTCCCCCGCAAAACAGCAACCAAACT
94861 GAAGAGTGTGTTCGCCGATGAACCAGAACTACGGAAGGGGGCGTTTTGTCGTTGGTTTGA

94921 GTTCTGGGCCAATATCACCACCTTGTGGTCATGATGAAGAATTGCCCCCTTTGCCCTCAA
94921 CAAGACCCGGTTATAGTGGTGGAACACCAGTACTACTTCTTAACGGGGGAAACGGGAGTT

94981 CACCTCTTTTCTTCTTGAAAATTAAAAACAACCCCTTTCACCCCCTCTACTGTCCTTATT
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95041 CCAGTTTGTGTCCGTAGTTGCTGGAGGAAAGAAAATGCCTATTGCTCTTTTTTTTATTCT
95041 GGTCAAACACAGGCATCAACGACCTCCTTTCTTTTACGGATAACGAGAAAAAAAATAAGA

95101 CTTTATCTGTTTACTCTTCTGCCTTTCTTTTCTCTCCCTGACTTCATTCCATTTAAAGGC
95101 GAAATAGACAAATGAGAAGACGGAAAGAAAAGAGAGGGACTGAAGTAAGGTAAATTTCCG

95161 CTTAAATTGCAAATAACGAAAAAAGTATTTTCTAATAATATACCCTAGTGGACGAAAAC
95161 GAATTTAACGTTTATTGCTTTTTTCATAAAAGATTATTATATGGGATCACCTGCTTTTG

95221 AACCTTCTACATTTTAAATGATATTAAGTTATAATAAATGGTTCCATGAACTTTAAAACG
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95281 CTTAAAAGTTTTATAAATCTCTTTTAGAGGCAACACAAAAATATCTATATATATATCTTC
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95461 AAGTAAAATATTGAGCATTTCAAGCTTACATGGCCTAAACTCACACTAGAGTGACTACTT
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95761 GGATTCTCCAGATTCTTCAATCCAAACTTGTCTATCTACCAAAGTCCACCTTCCATACAG
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95821 GGGTGTGGGGTCTCTCTTAGTACTGTTGGGTGCCAATAACATAGAAGCCCTCCAAGATAG
95821 CCCACACCCCAGAGAGAATCATGACAACCCACGGTTATTGTATCTTCGGGAGGTTCTATC

95881 GTCAATGAGATTTTAATTTTTCCCAACTTTAAATAGCATCTGGGAAGGAAAGCAGCTTTT
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95941 GACTAGGAGTTTGAAAACATCCACTCTTCATATTTATTGTCACATTTATTGAGTAATAAA
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96001 ATTGGGCTCTTGTCCATTATCTCTCAGTCAATGAAAGAGCCCACGGTGGGCATGAGCCAG
96001 TAACCCGAGAACAGGTAATAGAGAGTCAGTTACTTTCTCGGGTGCCACCCGTACTCGGTC

96061 AGTGTTCCGGAGAAAGAGAGGACCAGTCTCCATTTCATGTTCTATATTTAATCAGTTCAA
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96121 TTCAGCACCTTACTGAGTTTGACATTTTTCTAAGTAATGGGGTGGGGGGTTACAAAATAT
96121 AAGTCGTGGAATGACTCAAACTGTAAAAAGATTCATTACCCCACCCCCCAATGTTTTATA

96181 TTATAACTATCTTTCCTATCTTCAGGGAGATGTACCATTTCACTGAAGCAATACCACAGC
96181 AATATTGATAGAAAGGATAGAAGTCCCTCTACATGGTAAAGTGACTTCGTTATGGTGTCG

96241 TAAGCAGTTCCAGCTCCGAGTAACAGAGGAAGGAGTGAGCGATTTAGGAACTCACAGAAG
96241 ATTCGTCAAGGTCGAGGCTCATTGTCTCCTTCCTCACTCGCTAAATCCTTGAGTGTCTTC

96301 GGCACGGCCAGGCAACTCGCGCCCTGGCAAATGTTCCATAGAGACAGCATCCATGGGGTT
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96361 GAACCAAGCACAATGCCTGCAAATCGGGCAGGCGGGTTCATGGAATTGATTCTAGGGCAG
96361 CTTGGTTCGTGTTACGGACCTTTAGCCCGTCCGCCCAAGTACCTTAACTAAGATCCCGTC

96421 GTATGATCAGCACCATTTAAGGAGTGGCAGTTGTTAAGAAACTGAAGGGATTTCTCATAT
96421 CATACTAGTCGTGGTAAATTCCTCACCGTCAACAATTCTTTGACTTCCCTAAAGAGTATA

96481 GGCATTTTCAACAGAATTCAGCAGGAGCCTTGCATATCCCTTGGGATGGGTTCCGGGGTA
96481 CCGTAAAAGTTGTCTTAAGTCGTCCTCGGAACGTATAGGGAACCCTACCCAAGGCCCCAT

96541 TTATGGAGCTGCCAGGAGGTGCTCAGCTTCAGTAAGTGCCAGTCATTCCTTCCCAACCTC
96541 AATACCTCGACGGTCCTCCACGAGTCGAAGTCATTCACGGTCAGTAAGGAAGGGTTGGAG

96601 CTCCTTCATTAGTGGAAGTATCAGCTGGTGTCATTGCCTTCTTCAGGAGGATGGATTTCA
96601 GAGGAAGTAATCACCTTCATAGTCGACCACAGTAACGGAAGAAGTCCTCCTACCTAAAGT

96661 AAATGAAGCGCCAACAAAACTCACATTCTCGCAGAGCCTCCCTCACAACTGCATGTGTTC
96661 TTTACTTCCCGGTTGTTTTGAGTGTAAGAGCGTCTCGGAGGCAGTGTTGACGTACACAAG

96721 ACTGCCATCAACAGGCCAACACCCACTTGTTCTTTTCTTCTAGGTAAAGGAAAAGGTCTG
96721 TGACGGTAGTTGTCCGGTTGTGGGTGAACAAGAAAAGAAGATCCATTTCCTTTTCCAGAC

96781 TGGGACAAAGGCCCTGAACTCCTCACTCCTTGAATGGGAGGCATATTGGTGGAGGCTGTC
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96841 ACACAACTACAGGTGGCAGCAACCTGCCATCAGGGTTCCCATCAGCCTCCAGGGCTTGCT
96841 TGTGTTGATGTCCACCGTCCTTGGACGGTAGTCCCAAGGGTAGTCGGAGGTCCCGAACGA

96901 TCTCTGCCCTGTGTGTGGACACCTTCCATCACTGGAAACCCCTCTCTCAGAAGAACCACT
96901 AGAGACGGGACACACACCTGTGGAAGGTAGTGACCTTTGGGGAGAGAGTCTTCTTGGTGA

96961 TCTTGCCCTCATCTCCCACTTGCCTCTCCTCGGCACCTTCTCCACCCTCAGGGGCCAAGC
96961 AGAACGGGAGTAGAGGGTGAACGGAGAGGAGCCGTGGAAGAGGTGGGAGTCCCCGGTTCG

97021 TGAGGAAGTGTGCATCCTGTGCCACCAACCTTGCTCGCAGGAATTAGTTTCAGTCCCCAG
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97081 TGACTGACTCTTCCAAACCTGCACCAGCCTATGCTGCCCTTTTGAAAGGAGGCGTGCGTA
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97441 AAACAGTAAGCAAGTTGCTTGTATTCTCCTCCTAGCTGGATAAGAGACCCCCGTTTTCAT
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97501 GGACAGCCTCCTTGGGTGGACAGAAGTCTCCTGATCTTGTCTATGTAACCAGCACCCACT
97501 CCTGTCGGAGGAACCCACCTGTCTTCAGAGGACTAGAACAGATACATTGGTCGTGGGTGA

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97561  TTGCATTTTTCCGCAAAGAAAAGAGGAGCTTAACCCCATTTACGGGAAATCCACGCACTG
97561  AACGTAAAAAGGCGTTTCTTTTCTCCTCGAATTGGGGTAAATGCCCTTTAGGTGCGTGAC

97621  CTTGAATCTTACGCGCCCCGTGGTGACGGTGTTGCCCACTCTGTTCCCTTCCCACCAAAT
97621  GAACTTAGAATGCGCGGGGCACCACTGCCACAACGGGTGAGACAAGGGAAGGGTGGTTTA

97681  CCTGCCAGCACCTGGCAGTCATCCAGTCCTTGTCTTAGACTTCACCAACCTTTCCCGTCA
97681  GGACGGTCGTGGACCGTCAGTAGGTCAGGAACAGAATCTGAAGTGGTTGGAAAGGGCAGT

97741  TAACATGGCTTAGAAGTTGTCCGAATAGTGCTAGAAGCTTTCAGCCCTGGAATGCTCAGC
97741  ATTGTACCGAATCTTCAACAGGCTTATCACGATCTTCGAAAGTCGGGACCTTACGAGTCG

97801  ATCTGCCATCTAACTTCCATTTAAAACGTTTTGAGCATTTGCTGATACAGGTTCCTCTGT
97801  TAGACGGTAGATTGAAGGTAAATTTTGCAAAACTCGTAAACGACTATGTCCAAGGAGACA

97861  CCTTTCCCCATTATTTTCAGTTCCTTGGCCTTGCCCATAGTGATCTGTGGATATTGTCTG
97861  GGAAAGGGGTAATAAAAGTCAAGGAACCGGAACGGGTATCACTAGACACCTATAACAGAC

97921  CATACTCTTTTTTAGAAACCTAGAGCATCGCAGTGTCCTTAATTTTCCTCTTCAAACTCT
97921  GTATGAGAAAAAATCTTTGGATCTCGTAGCGTCACAGGAATTAAAAGGAGAAGTTTGAGA

97981  ATATATTCCTGAGCTGATCATCCCTACTGCTGTTCCTACAGAACTGTGTGACTAATCTTC
97981  TATATAAGGACTCGACTAGTAGGGATGACGACAAGGATGTCTTGACACACTGATTAGAAG

98041  TATATATGTCCCTACATCTAGCCATCTAGGTGGAGATCTAGGTACCTATCTCCCTAAAAT
98041  ATATATACAGGGATGTAGATCGGTAGATCCACCTCTAGATCCATGGATAGAGGGATTTTA

98101  TGTACTTGGTATCCACATTGACCTCAGGACAGTATGTGATAGGCTCTTGTGCCTTTTCGA
98101  ACATGAACCATAGGTGTAACTGGAGTCCTGTCATACACTATCCGAGAACACGGAAAAGCT

98161  CTAGGAGTTTGAAAACATCCACTCTTCATATTTATTGTCACATTTGTTGAATAATAAAAT
98161  GATCCTCAAACTTTTGTAGGTGAGAAGTATAAATAACAGTGTAAACAACTTATTATTTTA

98221  TGGGCTCTTGTCCATTATGTCTCAGTCAGTGAAAGAGCCCAGGGTGGGCCTGAGCCAGAG
98221  ACCCGAGAACAGGTAATACAGAGTCAGTCACTTTCTCGGGTCCCACCCGGACTCGGTCTC

98281  TGTTTGTGTCCCTAGTTCTCTTTTGGTTCTGTTACAGCTCTCAGTGACAGTGTCATTGAG
98281  ACAAACACAGGGATCAAGAGAAAACCAAGACAATGTCGAGAGTCACTGTCACAGTAACTC

98341  GCTAACAAGGACAGAGTACTGCTTTCAGCCACCATTTGTCCAATGAGTGGCTGATCTCCA
98341  CGATTGTTCCTGTCTCATGACGAAAGTCGGTGGTAAACAGGTTACTCACCGACTAGAGGT

98401  GGCCTCTGGCTTTGAGAACATCTGTGATATCTAAGGCAGCATCCATTGTGGGCTTTCCCC
98401  CCGGAGACCGAAACTCTTGTAGACACTATAGATTCCGTCGTAGGTAACACCCGAAAGGGG

98461  CATGCTTCTGTTTCCTTCCTGTCACATAGCTTTGCCTCCTCCTGCAAGCAGCCTGCTGTA
98461  GTACGAAGACAAAGGAAGGACAGTGTATCGAAACGGAGGAGGACGTTCGTCGGACGACAT

98521  GCAGAACCGGTGTTCCTGAAGCCAGAAACCCAAAGGTCGTGTCCAATGCTTCCCTGCTGT
98521  CGTCTTGGCCACAAGGACTTCGGTCTTTGGGTTTCCAGCACAGGTTACGAAGGGACGACA

98581  TCTGCTCCCCACCTGCAAGCGCCCACACACTGATCAACAGCACACGCCATAGAGCATGCC
98581  AGACGAGGGGTGGACGTTCGCGGGTGTGTGACTAGTTGTCGTGTGCGGTATCTCGTACGG

98641  AAAGAATCCCAGAAATACTCATTCTTAATGATCCAGAAGAACAAGTGATAGCTTCTGGCA
98641  TTTCTTAGGGTCTTTATGAGTAAGAATTACTAGGTCTTCTTGTTCACTATCGAAGACCGT

98701  AGTTCTAATAGGCCATATGTGCCCATGGGAAAGCAAGAGTCAATTCTCTCTAGCTGGTTG
98701  TCAAGATTATCCGGTATACACGGGTACCCTTTCGTTCTCAGTTAAGAGAGATCGACCAAC

98761  CCTCTGAATTTATGAAGTCAAGCCGCGTAGGGGAACATGCCAAGAGGATTATCCCAATGC
98761  GGAGACTTAAATACTTCAGTTCGGCGCATCCCCTTGTACGGTTCTCCTAATAGGGTTACG

98821  CTGTTCTGCGTGGTGTCCTTTTTCTAGCCTCGGAAGCACTAGGCCTACACCTTCGCTATA
98821  GACAAGACGCACCACAGGAAAAAGATCGGAGCCTTCGTGATCCGGATGTGGAAGCGATAT

98881  GCCCTCGTCTTAGCGCCTGTATTTGAAAAACTTGCCACACCAATCTTAATTTGCTCCATT
98881  CGGGAGCAGAATCGCGGACATAAACTTTTTGAACGGTGTGGTTAGAATTAAACGAGGTAA

98941  GTGTTCTAATCTCATTTTAAAAACCACAAGGTAAATGATTAAAAATAATCTTAGATTAAG
98941  CACAAGATTAGAGTAAAATTTTTGGTGTTCCATTTACTAATTTTTATTAGAATCTAATTC

99001  GAGTACACAGATCTTTGCAGCCTCATTGTGTTTCCAGAGCGGGCTAGTGTAGACACTGGT
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 99061  CTTGTTCCTCCCGGATCTCTTAATCGAAAGAGGGTCTTTCTACGTGTCGGAGATGGACTC

 99121  AGTACCAATTCCAGAGAACTCAATGGTCATTAAGCACCATTGCCTCGACAGCCAGCCAGC
 99121  TCATGGTTAAGGTCTCTTGAGTTACCAGTAATTCGTGGTAACGGAGCTGTCGGTCGGTCG

 99181  CTCACTTGCCTGCCTATCTCCTTTATTTTCCAAGTATCTTGTCCCTGGCAGTGGGGAGAG
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 99241  GTTAGCAGGAGGCTGCTCAGATGCTCTCGGTCTCTGATCTTCAGGATCTGAAGGGGAGAG
 99241  CAATCGTCCTCCGACGAGTCTACGAGAGCCAGAGACTAGAAGTCCTAGACTTCCCCTCTC

 99301  CATTTGAAGAATCCCCATTGCTGGATTTCTCAGGACAATCCTGCATAATGCCAGGATCTG
 99301  GTAAACTTCTTAGGGGTAACGACCTAAAGAGTCCTGTTAGGACGTATTACGGTCCTAGAC

 99361  ATGGAGGAGACAGGCAGCTCTGTTAATCCTCTGGTGCATCCTCACTTCTGTGGTCTCCAA
 99361  TACCTCCTCTGTCCGTCGAGACAATTAGGAGACCACGTAGGAGTGAAGACACCAGAGGTT

 99421  GTCCACCATGTCCCAGTTAATTCATTTCATTATTCATCTGTAAGTCATTTCCCTAAAGAG
 99421  CAGGTGGTACAGGGTCAATTAAGTAAAGTAATAAGTAGACATTCAGTAAAGGGATTTCTC

 99481  CTAATAAGAAAACACTGGCAGTACAATCAGCCCTCCATATCCATGGGTTCAGCCTCTGGA
 99481  GATTATTCTTTTGTGACCGTCATGTTAGTCGGGAGGTATAGGTACCCAAGTCGGAGACCT

 99541  AATTCAACCCACTGTGGCTTGAAAATACAGTATTCAAGAGACATGGAACCTGTGGATATA
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 99601  GAAGGCAGATTTTTCGTATCCATAGGTTCTATAGGGCCATTTTAGGGACTTGCACATCTA
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 99661  CAGACCTTCAGGAGTCTCAGAACTGATGCACTGCAGATACCAAGAGATGACTGTAAGTGG
 99661  GTCTGGAAGTCCTCAGAGTCTTGACTACGTGACGTCTATGGTTCTCTACTGACATTCACC

 99721  TTAGGAATTTGGATGCTGGGGCCAGGCTGCCTGCAGTTACCTTCCAGCTCTGCCACTTGC
 99721  AATCCTTAAACCTACGACCCCGGTCCGACGGACGTCAATGGAAGGTCGAGACGGTGAACG

 99781  CAGCTATGTGACCTTAGCAAGTTGTTCAACCTCTCTGTGCCTTGGCTTCTTCAACTGTAA
 99781  GTCGATACACTGGAATCGTTCAACAAGTTGGAGAGACACGGAACCGAAGAAGTTGACATT

 99841  AATAGGATAATGATAGCACTTCCCTTATGGAGTCCTTGTGAAGGTTAAATGGCAGAGTAC
 99841  TTATCCTATTACTATCGTGAAGGGAATACCTCAGGAACACTTCCAATTTACCGTCTCATG

 99901  AATTAATGTGCTGTGTGCCCAGCGTGTGGTATTGGGGTTAGGTGAAAGACTGTACTGGGA
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 99961  TCACTGGGGGTGAGCCTCCATGTGCCATGCCCCAACCACTATCCTCAGCTAACTTCTTGT
 99961  AGTGACCCCCACTCGGAGGTACACGGTACGGGGTTGGTGATAGGAGTCGATTGAAGAACA

100021  CTGTCAGTGTTAGGCTGGTGCTATAATAATTTCCATTTTCATGGATGAGGAAATCAAGGC
100021  GACAGTCACAATCCGACCACGATATTATTAAAGGTAAAAGTACCTACTCCTTTAGTTCCG

100081  ACAGAGAAGTTACATGACTTGCCTAAGATCTCAGTGCTTTTAAATAGTGCAGCTAAGATT
100081  TGTCTCTTCAATGTACTGAACGGATTCTAGAGTCACGAAAATTTATCACGTCGATTCTAA

100141  CCAGACCAGGTATTTTTATTTCAGTGTCTGGACTGTAGATCTCTAAATCGAGAGGAACTC
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100201  CCTGAATAAAATAAGCTTGGAGTGCTGTTAACTAAGTTGGTTATTTAAGACAGTTGTTCT
100201  GGACTTATTTTATTCGAACCTCACGACAATTGATTCAACCAATAAATTCTGTCAACAAGA

100261  CAGTCCTCAGTGTACATTAGAATCTTCTGGAGGGTATGTTAAAACAGACTGCTGGGCCCA
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100321  CCGAGAGTTCCTGAGCCTGCAACTCTGGGTTGAGCCTGAGAGTCTGTGCTTCTAGTAAGT
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100381  TCTCAGGTGATGCTTATGCTGCTTCTCCCAAATTTTGAGAACCATTGATTGAAAATGTTG
100381  AGAGTCCACTACGAATACGACGAAGAGGGTTTAAAACTCTTGGTAACTAACTTTTACAAC

100441  ATCAAAAATTATGTGGTCTAGGCTGAGCACAGTGGCTCACAACTGTAATCTCAACACTTT
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100501  GGGAGGCCAAGTCAGGTGGATCACTGAGCTCAGGAGTTCGAGAGCAGCCTGGTCAACATG
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100561  ACAAGACCCATCTCTACAAAAAACACCAAAAAAAAATGGCTGGATGTGGTGGTGCACACC
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100621  TGTAGTCACAACTACTGGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCGGGAGACAGAG
100621  ACATCAGTGTTGATGACCCCTCCGACTCCACCCTCCTAGTGAACTCGGGCCCTCTGTCTC

100681  CAAGACCCTGTCTCAAAAAAGAAACATTTAGTCTTGATTGTCATCTATCTCATTGATCAT
100681  GTTCTGGGACAGAGTTTTTTCTTTGTAAATCAGAACTAACAGTAGATAGAGTAACTAGTA

100741  TTTACTTGGCAAAATTTACCTACTTACTCTTATTAGTCTGTAAAAATGGTTATTAAAATG
100741  AAATGAACCGTTTTAAATGGATGAATGAGAATAATCAGACATTTTTACCAATAATTTTAC

100801  GTGGCTTTCAGTGTAACTACAAATTCTCTTAGTCATTATAGTGTTGGATTCACCAATGTA
100801  CACCGAAAGTCACATTGATGTTTAAGAGAATCAGTAATATCACAACCTAAGTGGTTACAT

100861  TCATCAGTCAGTGTTTCTGAAGTGTGTAAATGAAATAACTCCTACTTTCTTTAGGAAGAA
100861  AGTAGTCAGTCACAAAGACTTCACACATTTACTTTATTGAGGATGAAAGAAATCCTTCTT

100921  AAATATTCAAATGACATAATTACCTTGTGATGTGTGACTTAAAGGTAACAGTAATGCAGA
100921  TTTATAAGTTTACTGTATTAATGGAACACTACACACTGAATTTCCATTGTCATTACGTCT

100981  GTCAATAGTGGTCATTGTATTCAAGACACTAAAAGTTCACCTCCCACCCCCCCCCCCCAC
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101101  CTACATTCATAAACTATCCCAATTAACCCTTCAGCAAGTGGAAGAAGTGTAAGAAAGGAT
101101  GATGTAAGTATTTGATAGGGTTAATTGGGAAGTCGTTCACCTTCTTCACATTCTTTCCTA

101161  ACCTCTTCTTTAGAACACAGGGTTTGTTTTTATGTTATTTAAGATAAACAGGAATTCAAA
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101221  TGGTCATGTACCAAAGCAACACAAAGAACTTCCGGAAATCTGAAAGGGAACTGTGGTCAG
101221  ACCAGTACATGGTTTCGTTGTGTTTCTTGAAGGCCTTTAGACTTTCCCTTGACACCAGTC

101281  AACTCTGAGCATTTTTATGTTTACTGAGTTTTGTCCCAAAGTTTATTAATGTTTACATGC
101281  TTGAGACTCGTAAAAATACAAATGACTCAAAACAGGGTTTCAAATAATTACAAATGTACG

101341  CACAAGGAAAGGTAGCATCACAATAAGAGACGTTTTTCAGGCTTGATAACCACTTATTAG
101341  GTGTTCCTTTCCATCGTAGTGTTATTCTCTGCAAAAAGTCCGAACTATTGGTGAATAATC

101401  GTATTTTGCCAAACAAGTTCACACATCCTAGAGAGCTGGATTGTGTGACCCAGAACCCAC
101401  CATAAAACGGTTTGTTCAAGTGTGTAGGATCTCTCGACCTAACACACTGGGTCTTGGGTG

101461  CCTCTAGGGCAAGGTGCCCATCTGATGGGTAGGGTGTAGGAGTAGGCCTCAGACCACTCC
101461  GGAGATCCCGTTCCACGGGTAGACTACCCATCCCACATCCTCATCCGGAGTCTGGTGAGG

101521  TGACGTGAACCTGCTTAAAGTGAGGGCCCAATTCTAAAGTGGGAACTATGTAAATACCTT
101521  ACTGCACTTGGACGAATTTCACTCCCGGGTTAAGATTTCACCCTTGATACATTTATGGAA

101581  TCTAGTGCATTTTCAGATAATCGCCACTGGGCCTATGGATGGAGAGGGCTGGCAGATCTC
101581  AGATCACGTAAAAGTCTATTAGCGGTGACCCGGATACCTACCTCTCCCGACCGTCTAGAG

101641  CCTGTAACCCCAGGTGCATCCCGAGGCCTGCCACCGAAGCCCACTCAAGGCTGAATGCAC
101641  GGACATTGGGGTCCACGTAGGGCTCCGGACGGTGGCTTCGGGTGAGTTCCGACTTACGTG

101701  GGCGAGCTCAGGCTGCTCTCCCCTTGGTATTTGCTAAGAACTTCTGTTTAGTAGCTCTCC
101701  CCGCTCGAGTCCGACGAGAGGGGAACCATAAACGATTCTTGAAGACAAATCATCGAGAGG

101761  ACACCTATTTGATTGTCTTTTTGCTGCTGTGTTGTTTTGTTGAGTTTTTTTTTTGCAATG
101761  TGTGGATAAACTAACAGAAAAACGACGACACAACAAAACAACTCAAAAAAAAAACGTTAC

101821  ACACTGAGTGGCCTCCTGTATTGTTTCTTTCAGCCAGTAATGTTAAAGTAGAGACTCAGA
101821  TGTGACTCACCGGAGGACATAACAAAGAAAGTCGGTCATTACAATTTCATCTCTGAGTCT

101881  GTGATGAAGAGAATGGGCGTGCCTGTGAAATGAATGGGGAAGAATGTGCGGAGGATTTAC
101881  CACTACTTCTCTTACCCGCACGGACACTTTACTTACCCCTTCTTACACGCCTCCTAAATG
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101941  GAATGCTTGATGCCTCGGGAGAGAAAATGAATGGCTCCCACAGGGACCAAGGCAGCTCGG
101941  CTTACGAACTACGGAGCCCTCTCTTTTACTTACCGAGGGTGTCCCTGGTTCCGTCGAGCC

102001  CTTTGTCGGGAGTTGGAGGCATTCGACTTCCTAACGGAAAACTAAAGTGTGATATCTGTG
102001  GAAACAGCCCTCAACCTCCGTAAGCTGAAGGATTGCCTTTTGATTTCACACTATAGACAC

102061  GGATCATTTGCATCGGGCCCAATGTGCTCATGGTTCACAAAAGAAGCCACACTGGTAAGG
102061  CCTAGTAAACGTAGCCCGGGTTACACGAGTACCAAGTGTTTTCTTCGGTGTGACCATTCC

102121  CCTGGCTCAGTTTTTCCTTTAGTGGCCTGGAGAAGGTGCATGGGGTTTGAAGGAGGAAAG
102121  GGACCGAGTCAAAAAGGAAATCACCGGACCTCTTCCACGTACCCCAAACTTCCTCCTTTC

102181  CATCCTGTCTTCCTTGTGTTCTGAGCATGTTTCTAATTGACTGGTAGCTCAGTTGTTGCA
102181  GTAGGACAGAAGGAACACAAGACTCGTACAAAGATTAACTGACCATCGAGTCAACAACGT

102241  AGCGATTGGTTCCAAGTGGTACCGAGTCATAGAGTCCTTGTTCTGGTACAGCCTTGTAAA
102241  TCGCTAACCAAGGTTCACCATGGCTCAGTATCTCAGGAACAAGACCATGTCGGAACATTT

102301  GGACTTCTCAACACGTACCAATTCCACCCTATAAATAAAACAAGGGAAAAGTGAACAGCA
102301  CCTGAAGACTTGTGCATGGTTAAGGTGGGATATTTATTTTGTTCCCTTTTCACTTGTCGT

102361  TCACATGAGAGGCTTGGCGAGGGCTGCTATTATAGTAACACATACTAAGTAGTCTCAGCT
102361  AGTGTACTCTCCGAACCGCTCCCGACGATAATATCATTGTGTATGATTCATCAGAGTCGA

102421  GAGCCCTCAGGGTACGTGTGCTGAGTGGTCACCCTCCACAAAACAAAAAATCCTGATACA
102421  CTCGGGAGTCCCATGCACACGACTCACCAGTGGGAGGTGTTTTGTTTTTTAGGACTATGT

102481  CCAAAACTTACTCCTCAAAGTTTCCACTGAGAAACCATGAGTAAAATGTGTGTTTAAATT
102481  GGTTTTGAATGAGGAGTTTCAAAGGTGACTCTTTGGTACTCATTTTACACACAAATTTAA

102541  GTATCCAAACTAACAGGGTTTGATGTTTAGAAACAATAATCAATGATGGAATAGCAGCAA
102541  CATAGGTTTGATTGTCCCAAACTACAAATCTTTGTTATTAGTTACTACCTTATCGTCGTT

102601  AATCGAGTTTTCAGAAAGACCTCAGATGAGCTTTCAAATGGCTTGCCCTCTAACAGGAAA
102601  TTAGCTCAAAAGTCTTTCTGGAGTCTACTCGAAAGTTTACCGAACGGGAGATTGTCCTTT

102661  GACTTTGAATCAGATGCTTCTATTGCCACTGGTTATCAGCTCAAATTCCTAAAGAACTTC
102661  CTGAAACTTAGTCTACGAAGATAACGGTGACCAATAGTCGAGTTTAAGGATTTCTTGAAG

102721  ATCCCAAATACCCTGTCTTGCTGAAAGGTTTACTGGAAGTATAAGAGAATGTCATGTTCT
102721  TAGGGTTTATGGGACAGAACGACTTTCCAAATGACCTTCATATTCTCTTACAGTACAAGA

102781  GTGTCCAGAAAGGAAGGAACACGGGCACCCTAGTGTCAGCGAGTTGTGCTCAGGCTCACA
102781  CACAGGTCTTTCCTTCCTTGTGCCCGTGGGATCACAGTCGCTCAACACGAGTCCGAGTGT

102841  GGATGCCCCCTCACCAGAGGCGTGGGAACACGGCGAGCCCCAGCTGGCCGCGCTCTGCCA
102841  CCTACGGGGGAGTGGTCTCCGCACCCTTGTGCCGCTCGGGGTCGACCGGCGCGAGACGGT

102901  CTGTTTCTAATAGCCGGTCACGTTGATGGAAGTGTCACAGAGTTGTCCAACAGAACTGTC
102901  GACAAAGATTATCGGCCAGTGCAACTACCTTCACAGTGTCTCAACAGGTTGTCTTGACAG

102961  CAGTCAGAAAACCACCACTCATGGTGCTGGAGTGTCTTAGAAGTAAAATATGAATAACAC
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103021  ACACTTATTTAACTATAGGCAGGAGGTTTCTTATGAATTGAAGAGAAACTTTTCTTTGCG
103021  TGTGAATAAATTGATATCCGTCCTCCAAAGAATACTTAACTTCTCTTTGAAAAGAAACGC

103081  TGGGAAGCTGTTCTAAAGTTGGGTAAAACACAATAGATCCACCACCTCTAGCAGCCACTG
103081  ACCCTTCGACAAGATTTCAACCCATTTTGTGTTATCTAGGTGGTGGAGATCGTCGGTGAC

103141  ATAGCTGAAACGTGAAACATAGAGACCCTAAGCTATCACTGCCTCTGAGCTGGCATTGTT
103141  TATCGACTTTGCACTTTGTATCTCTGGGATTCGATAGTGACGGAGACTCGACCGTAACAA

103201  AGGTCATCATAAAGCTAGCGTCTCCCACTGCAAAACCCAAGAGGAAAAAAATAGTTCAAA
103201  TCCAGTAGTATTTCGATCGCAGAGGGTGACGTTTTGGGTTCTCCTTTTTTTATCAACTTT

103261  ATCCTATTTTAAAGGCCTAGCAGATTCTATAAGATACCTTGGGAAAATGATGACGATGAC
103261  TAGGATAAAATTTCCGGATCGTCTAAGATATTCTATGGAACCCTTTTACTACTGCTACTG

103321  TTGAAATCAGACCCTCGTATGCTGCTTCCGTGGGGGCGAACAAAAATATGTTCATCAAAA
103321  AACTTTAGTCTGGGAGCATACGACGAAGGCACCCCCGCTTGTTTTTATACAAGTAGTTTT

103381  ATTAAGCAGAAATGCAGAAAATTTTGTGAGCCAAAAAAGCTGTGTTATCAGGAAATGCAG
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103441 ATATTTGTGGGGTTGTAATTTTTTATATTTGAATCGGGCGGTTTTCAAAATGATCTATTC
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103561 CATAAAAATTCAACTTCTAAAATTAAGCAAACTTTGCTTTTTCTAATGGCCCCTTTATCC
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103681 AGAGTAGTCCCAGCCTCGCCTTTGTAATGAGGTGGAAATTAACATGAAGGTAGGCTACCC
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103741 TGTGATAGACACTTAACAGGATACTCGGGGACCCATGGTAATACATCCCTGATAAGGAAT
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104161 AACTCATGAATTGTTTTCATCATGCATTTCCACTTGCCTAAATATAAAGGGTCCCAGGTA
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104221 GATACAGAAATACCTGGTTTGGCCAAACTTGGTTTGAATAACTAGACATGCTAGAAAAGG
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104281 TTTTCATTTTCCTGGCATCTGAGTGGAATATGTTAGAAAAGGCATGCTTTCTGAATTCTC
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104401 CTCTAGAGCACTTGTATGTTGAGACGAAGTCTGGACCCCCCTCCGTCCTCTCGTTCGTAA

104461 CCTAACAAGCTCCCAGCTTGTGGAGCACAGAGCCGCCTCAGGCAGCAGGGCAGTGCAGCT
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104521 GAGCAGTGACAGTGAACAGGGCCATTCAGAGGGCTCTCCACCTGGGGCTTAGGTACGACG
104521 CTCGTCACTGTCACTTGTCCCGGTAAGTCTCCCGAGAGGTGGACCCCGAATCCATGCTGC

104581 GGAATCCCCACTGGACAGGCTAGGACTTGCACTGTGGCCATTGTTCCTCCTCCTGCCCAT
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104641 GCCTGAGTCAGCTTCTCAGTCCCTTCCAGGATACACTGAGAGCATTCAGGGGCCGTCTCG
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104701 CCTCTGCCCATATCCCCACGTTGGTGAAGTACCACTGGCGCCATTTTCTAATCAGCTCAT
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104761 CGGCACCAGCACGTCACTTCCCCTGTTGTGCAGCTCAGTTTTATATTTCTGACTCGGGTG
104761 GCCGTGGTCGTGCAGTGAAGGGGACAACACGTCGAGTCAAAATATAAAGACTGAGCCCAC

104821 TAATAGTAACATCTTCCCCACCAATGTCTCAGGGTTATTGTGAGAACCAGAGAGGAGAGA
104821 ATTATCATTGTAGAAGGGGTGGTTACAGAGTCCCAATAACACTCTTGGTCTCTCCTCTCT

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104881  GGTAGGAAGGAAGCAGGAAATGCAGGGTGCAAATACACCACATTATTATTCTAAATAATG
104881  CCATCCTTCCTTCGTCCTTTACGTCCCACGTTTATGTGGTGTAATAATAAGATTTATTAC

104941  GGATTTTTAATAACAAAGACCAAGAAGATTGTCTGTGCCTATCTAGTTCCCATCTGTAAG
104941  CCTAAAAATTATTGTTTCTGGTTCTTCTAACAGACACGGATAGATCAAGGGTAGACATTC

105001  ATAAAAAGGTGCAGTCCCTGAGCCTCCTAAAAACAGCACCCTAATGGCACTGCTCCTCCC
105001  TATTTTTCCACGTCAGGGACTCGGAGGATTTTTGTCGTGGGATTACCGTGACGAGGAGGG

105061  AGGTATGATTGCAGTAGACCTACGTCAGTTCTTGCAGTTCAAACACATTTTTTCACTTTC
105061  TCCATACTAACGTCATCTGGATGCAGTCAAGAACGTCAAGTTTGTGTAAAAAAGTGAAAG

105121  TTCTGAAATGCCCTCAAATTCTATGACATAGTATCCATGAAGACTTCCCTTTTTACCCAG
105121  AAGACTTTACGGGAGTTTAAGATACTGTATCATAGGTACTTCTGAAGGGAAAAATGGGTC

105181  TGAAGTTACTAGAGGGGGTTCAAACCTTCTTACAGAGGGTTCCTAAAATGGGAGATCTGT
105181  ACTTCAATGATCTCCCCCAAGTTTGGAAGAATGTCTCCCAAGGATTTTACCCTCTAGACA

105241  GGAGTCATTGGGATTAAAAATTAAATTTCAAATTCATGACATCAATGTCCTCATCCCAGT
105241  CCTCAGTAACCCTAATTTTTAATTTAAAGTTTAAGTACTGTAGTTACAGGAGTAGGGTCA

105301  TAAATAAAAGTAAATACAACCTTGAAGAAATTTGACCTACTCAGCTGCAATAGCTGTTGA
105301  ATTTATTTTCATTTATGTTGGAACTTCTTTAAACTGGATGAGTCGACGTTATCGACAACT

105361  CCTGCAGAAGCCAAATGATGGACCCCGGCCACGCAAGAACACACATGGCGTGGGCTGCGT
105361  GGACGTCTTCGGTTTACTACCTGGGGCCGGTGCGTTCTTGTGTGTACCGCACCCGACGCA

105421  TCTTGTGCCCCAGCTCCATGGACGTGTCTTCTTAGCTGTGGACCCCTCCAAAGGAAACTG
105421  AGAACACGGGGTCGAGGTACCTGCACAGAAGAATCGACACCTGGGGAGGTTTCCTTTGAC

105481  CTTGAGTGGAGTGCTCTGTATTGTCACTCCTGGGAATGCTCTCTTAACACCCCCATGCCT
105481  GAACTCACCTCACGAGACATAACAGTGAGGACCCTTACGAGAGAATTGTGGGGGTACGGA

105541  TGTGCTATGTGTTCATACCAGCATAGGCACTCAGAAGCAAAAAAGGTTTCCAGTGAAATT
105541  ACACGATACACAAGTATGGTCGTATCCGTGAGTCTTCGTTTTTTCCAAAGGTCACTTTAA

105601  TGTTTGCAGGCAGGTATTAAGACATCAGACACTGCAGGATCCAAGTGAACCCCTCCCCGC
105601  ACAAACGTCCGTCCATAATTCTGTAGTCTGTGACGTCCTAGGTTCACTTGGGGAGGGGCG

105661  CTGCCTGCCTGCCCTGCTCTGCTCTGCAGAAGGGCATGTGTCTGTACCAATCTGCCCTTT
105661  GACGGACGGACGGGACGAGACGAGACGTCTTCCCGTACACAGACATGGTTAGACGGGAAA

105721  CTGTCTGCGATGGGCAGAGACCCTGGCTCTGCCTCCTGTTTTCCCTGTAGCCCTCCAGAC
105721  GACAGACGCTACCCGTCTCTGGGACCGAGACGGAGGACAAAAGGGACATCGGGAGGTCTG

105781  CTGGGGAGAGACATGGGACTCCAGCACCTGCCCAGCACGGAAGGGGGTCTTTCCCAGGTG
105781  GACCCCTCTCTGTACCCTGAGGTCGTGGACGGGTCGTGCCTTCCCCCAGAAAGGGTCCAC

105841  TAAGTGTAGGGCTGCATTCACTAATTTAGGGTCATACCACAAACACTGTTGTGTCACCAG
105841  ATTCACATCCCGACGTAAGTGATTAAATCCCAGTATGGTGTTTGTGACAACACAGTGGTC

105901  GATGTTGTCACATGCTTATTGTGAGCATTTTTGTGACATGAGCTTTCTCCTGAGAGGCCA
105901  CTACAACAGTGTACGAATAACACTCGTAAAAACACTGTACTCGAAAGAGGACTCTCCGGT

105961  CCCTGTCCAAATGAGAGCTGTAGTTGGAGGCACATCCGTCTCATGCTGCCTGGGTCTCCC
105961  GGGACAGGTTTACTCTCGACATCAACCTCCGTGTAGGCAGAGTACGACGGACCCAGAGGG

106021  TGCACCAGCTCACTCTACTTTTCCTTTTTATCCACTTGGAGTTAAATGCACACATTTATG
106021  ACGTGGTCGAGTGAGATGAAAAGGAAAAATAGGTGAACCTCAATTTACGTGTGTAAATAC

106081  CACAAGTGCACAGAAGGCCCAGAACTGTTCCTAATAGATAATTAAATGATCTCTCTCCAG
106081  GTGTTCACGTGTCTTCCGGGTCTTGACAAGGATTATCTATTAATTTACTAGAGAGAGGTC

106141  TGGAAACTCTCCTGGGCTACCTGGCTGCTAGCTGTTTTAGCCTCTTCATCCAGTATTGAT
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106201  TTACATGCATCGGTTTGTAACTCAGACAGTATAGTTAGTTAGTTTGTTTCACCATCACCT
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106261  TCCAACCTGCTTACGTTTAAACTCCTTCTCTCTGCTTAGCTAATACAGATTTCTGTAAGG
106261  AGGTTGGACGAATGCAAATTTGAGGAAGAGAGACGAATCGATTATGTCTAAAGACATTCC

106321  ATTTGGAGAAATACCAGATACCTCCTGGTTAGTATCAGGACCTCTCCATTGGCCTATAAT
106321  TAAACCTCTTTATGGTCTATGGAGGACCAATCATAGTCCTGGAGAGGTAACCGGATATTA
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106441  AAAAAAAGTGATGATAATCATGAAATTCAAGTGTCAATATAGACTTTTAAATCTGGTGTG
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106501  GATGTTAATAGTGCCAGATATGCTTCTGTGTAATCATTTTTGAGAAGTGCTGTCTTCTTT
106501  CTACAATTATCACGGTCTATACGAAGACACATTAGTAAAAACTCTTCACGACAGAAGAAA

106561  ACCATAATCACATTAATCAATCGGGAAATGGTTAAATAGACATTTTAATACATTGTTTTT
106561  TGGTATTAGTGTAATTAGTTAGCCCTTTACCAATTTATCTGTAAAATTATGTAACAAAAA

106621  TCCTGAGAAAAAAAGTGACTCCAGGAAATATGTTGTTACAATATCTCAACACCAGGAATT
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106681  GTGGTCACATAGCATTCTTCTTCTAAATAAAGCATTTGTTTTACAAAAGAGTTTCATGTT
106681  CACCAGTGTATCGTAAGAAGAAGATTTATTTCGTAAACAAAATGTTTTCTCAAAGTACAA

106741  TACTTAAACGTGACAAATGTATCACTCTTCGAAGTGACAGTTAAATGAAATGTTCCCTGA
106741  ATGAATTTGCACTGTTTACATAGTGAGAAGCTTCACTCTCAATTTACTTTACAAGGGACT

106801  TTTAGATTCCAAGACCTGTGACTACTCAGTAGGACAATAGCATATTTCTTTTACTCAGAT
106801  AAATCTAAGGTTCTGGACACTGATGAGTCATCCTGTTATCGTATAAAGAAAATGAGTCTA

106861  ACCTGTTTATCCCTTTGTCAGCTCCAGAATGGAGACACAGGTGCTGCCACACAGAGGAGA
106861  TGGACAAATAGGGAAACAGTCGAGGTCTTACCTCTGTGTCCACGACGGTGTGTCTCCTCT

106921  GGGTCAGGTGTTTTCTTAGTCACAAATGCAGCAGTCTCACCCCTGAAAGAATTCCTTCAT
106921  CCCAGTCCACAAAAGAATCAGTGTTTACGTCGTCAGAGTGGGGACTTTCTTAAGGAAGTA

106981  AACAACTAAATTGCACCTCTTAGAATACCTGTACTTAAAATATAATTTGTCTTCTATGGA
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107041  TATAGACAAATAATAGCTTAAATGTTTTAGGATTTGTAAAGAAAGAAAAAGCTAGAAATC
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107101  TCAATGCAACTCTGACTTGTATGTCCTGCCATAGGAAGGTTTGGGACTTTTCTTTGGAAG
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107161  ATGGGAGGCTTCCTTCACAGTTTCTTAACTTCTCATTTTATTCAATCTTTCTCCATCTCT
107161  TACCCTCCGAAGGAAGTGTCAAAGAATTGAAGAGTAAAATAAGTTAGAAAGAGGTAGAGA

107221  CTCTCTCTTTCTCTCATCCTCACGCTCTCTGTCTGTCTCTCTCCTGATTTGTCTGCTTAG
107221  GAGAGAGAAAGAGAGTAGGAGTGCGAGAGACAGACAGAGAGAGGACTAAACAGACGAATC

107281  GGACAGACAGGTAATGGAGAAGAAATTGAAAGGGAAAATACAGGGAAAATGTAAATGAAA
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107341  AGAAGTTATTATAACTGTTATAATGAAGTGCCTTTCATTTAAATATAAGAATGTAACGCT
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107401  GAAATGAACTTGTGATCCTGAAATGCATTTTTAATGAGTTTCCTTTTTATTTTGCTGCTT
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107461  GTCACCGTATAAAATTTCTGGGAAACTTTTTTCGGTGTAATTTTTTGGGGTGGTTTACGG

107521  ACAACACGCAAAATTGGATATTGGTTTATTCCAAAACTGCTGATCAGGAAGAGTGGCTCT
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107581  TCATCACAAAATGTTGCAGTCACTTTATTTAAATGAGTTTGAATTTGCATTGTGATGTGC
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107641  CATTCTGATTTAGGGAAAAAAAATTAGATTTTCAGATCAAATTGACCCAGCCAGTGAAGC
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107701  GTTAAGGAGCTGGCAGGTTTAGTCTGAAAGCCTCATGTTCTATCAAACCTGCAGCCGGTG
107701  CAATTCCTCGACCGTCCAAATCAGACTTTCGGAGTACAAGATAGTTTGGACGTCGGCCAC

107761  GAAGTCACCAGGCCCCCGTGGGAAACAACTTTCTCGTAGCATCGTCCTCATGTCCCCACG
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107821  CTGAGTTTAGTTCTCACCAGCTCTCCTCTCTCCGTCCCAGGAGAACGGCCCTTCCAGTGC
107821  GACTCAAATCAAGAGTGGTCGAGAGGAGAGAGGCAGGGTCCTCTTGCCGGGAAGGTCACG

107881  AATCAGTGCGGGGCCTCATTCACCCAGAAGGGCAACCTGCTCCGGCACATCAAGCTGCAT
107881  TTAGTCACGCCCCGGAGTAAGTGGGTCTTCCCGTTGGACGAGGCCGTGTAGTTCGACGTA

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108001  CTCACTGGCCACCTGAGGACGCACTCCGGTAGGTCCCCTGGATGCAGTCCGGGGCTGTCT
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108061  GGGTGTCCCGGGATTCCTCCACTCTGCCCGCCTGGGTCCCGGATTGTGTCCTTGCTGGCT
108061  CCCACAGGGCCCTAAGGAGGTGAGACGGGCGGACCCAGGGCCTAACACAGGAACGACCGA

108121  AACCCTGAGTCCCTCCCAGCTCGCAGTCCTGCATCGGGTGTGAGCTGTTGCTTCTTTGAC
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108181  ATTGCCCCATCCCCCCTCCCCATATTCTCCTTTTCCCACTGCACCAGGGAGATTGGGCGC
108181  TAACGGGGTAGGGGGGAGGGGTATAAGAGGAAAAGGGTGACGTGGTCCCTCTAACCCGCG

108241  AGGACCCCCATGCACATACACACACAGAAGTCTCACCTTAGGTAGCATGTTTCAGAACAG
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108301  GCCTCCTCATCCCGTTTGTCAGGCTGGTATGGTTTCCCTAAAGGATTTTGCGGGAAATGT
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108361  TTTCACCAAGTGTACTGCTAAGACCCAAAACGTTTTCAAGTACAATTCTTTCTGTTGTTA
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108481  AGAAGGGTGATTTAGGGCGCACCCACCCAGACTGAGCCCCGTGTGGCTCTCACACCAAAA
108481  TCTTCCCACTAAATCCCGCGTGGGTGGGTCTGACTCGGGGCACACCGAGAGTGTGGTTTT

108541  ACCAGCCAAGCCCACAGTTACAGAGGCCAGTCTGGGGCTGTTACCAGATTTTAGACAGCA
108541  TGGTCGGTTCCGGTGTCAATGTCTCCGGTCAGACCCCGACAATGGTCTAAAATCTGTCGT

108601  GCCTTTCTCTTTGAATTAGACAGTTAAAGTACAACCCACATAATCTGGAGTCTTGACAAG
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108661  ATCATCATAGGCATAAACGCTCTATCATTCTCAAAACAGTCTCAGCCTGCAAAGTTCAAA
108661  TAGTAGTATCCGTATTTGCGAGATAGTAAGAGTTTTGTCAGAGTCGGACGTTTCAAGTTT

108721  TCCACTAAAGTTTGGTTAGATCCTCTGCCTCCTGAGAAATGGTCCTGGGTGTTTCATTAT
108721  AGGTGATTTCAAACCAATCTAGGAGACGGAGGACTCTTTACCAGGACCCACAAAGTAATA

108781  CCAGCAGTCCCATAATTCTACAGGGCAGAGGAAGAGAGGGCTCTTGGCCGGCCTGTCATG
108781  GGTCGTCAGGGTATTAAGATGTCCCGTCTCCTTCTCTCCCGAGAACCGGCCGGACAGTAC

108841  GATCATGTTTGCCTACAGTGTGGTCTATACAACATGACATGGCACAGGTCTCCTTCATAC
108841  CTAGTACAAACGGATGTCACACCAGATATGTTGTACTGTACCGTGTCCAGAGGAAGTATG

108901  CGTCCAGTTGGGGATATTTGCTGTAGCATACTGCATGAGACTTCGGAGGCGAAAGGTTGA
108901  GCAGGTCAACCCCTATAAACGACATCGTATGACGTACTCTGAAGCCTCCGCTTTCCAACT

108961  TGGCTTTTGTCCTTCCCCTCAAGGAGCTTCCTGCCCCAGCCAGCCACCAGCCAGGGCCCT
108961  ACCGAAAACAGGAAGGGGAGTTCCTCGAAGGACGGGGTCGGTCGGTGGTCGGTCCCGGGA

109021  TCTCCAAGCAGCAGCCTCTCTAAGCCGGTGCCCTGGGGGATGGCAATGCCTCAGACCAGC
109021  AGAGGTTCGTCGTCGGAGAGATTCGGCCACGGGACCCCCTACCGTTACGGAGTCTGGTCG

109081  TACTCCTCACCCACCCTGGCTACCAGGATAAGCAGCAGCCTCCCTCAGCGACGCAGACGT
109081  ATGAGGAGTGGGTGGGACCGATGGTCCTATTCGTCGTCGGAGGGAGTCGCTGCGTCTGCA

109141  GTGTTCTTTGTGAAATATCTGCAGCGGCCCAGGCCATCTCTTCCCAAATGTGATGCGTGT
109141  CACAAGAAACACTTTATAGACGTCGCCGGGTCCGGTAGAGAAGGGTTTACACTACGCACA

109201  ATTTGATGGTTGAGGGTTTTAGAGGCTGCTCATTGTGTCCATCTCTTTATCACACATTTA
109201  TAAACTACCAACTCCCAAAATCTCCGACGAGTAACACAGGTAGAGAAATAGTGTGTAAAT
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109261 CTGAGCACCCCTGGGTGCCCATTCTGCACAGAAGACCTCAGGTGCACACAAGGAAAGCAC
109261 GACTCGTGGGGACCCACGGGTAAGACGTGTCTTCTGGAGTCCACGTGTGTTCCTTTCGTG

109321 CAATGTGTTACAGGAGGCATGACAGAGTGTCTGAGGGGACAGTGGGAGCATAAGGAAGGG
109321 GTTACACAATGTCCTCCGTACTGTCTCACAGACTCCCCTGTCACCCTCGTATTCCTTCCC

109381 GACACTGGGTCCTGGGGTCGAAAGTCAGGAGAGACTTCCCATAGAAGGGAGGGGCTTCTG
109381 CTGTCACCCAGGACCCCACCTTTCAGTCCTCTCTGAAGGGTATCTTCCCTCCCCGAAGAC

109441 AAGTACATGCTGGAAGGCGAGTGTCTGAGGTTTGCTTTAGAGACATTCTAAACTAGTGTG
109441 TTCATGTACGACCTTCCGCTCACAGACTCCAAACGAAATCTCTGTAAGATTTGATCACAC

109501 TGAGTCGGCAGTAATCCCAGAGAGGGGTGCGGCACCCATGTTGGCAAGAACTCGGTCTCA
109501 ACTCAGCCGTCATTAGGGTCTCTCCCCACGCCGTGGGTACAACCGTTCTTGAGCCAGAGT

109561 CTCCTGGCAGGTGGTCCCTGCAGTAGTTCACCCAGTTGGCTGGAGACAAAAAGGAGAGGA
109561 GAGGACCGTCCACCAGGGACGTCATCAAGTGGGTCAACCGACCTCTGTTTTTCCTCTCCT

109621 GTCACAGGGGCTGGTGCATCACCTCCTCTCCATCCTGACCTCCTTCCTGGCGGTGCACAT
109621 CAGTGTCCCCGACCACGTAGTGGAGGAGAGGTAGGACTGGAGGAAGGACCGCCACGTGTA

109681 GGAGAAGGATCCCCACATGCTCGCCATCAGAAAATTGTCATGATTTGGGTGATTTGACTT
109681 CCTCTTCCTAGGGGTGTACGAGCGGTAGTCTTTTAACAGTACTAAACCCACTAAACTGAA

109741 CCTAAAAACTTCCAAGAAAGGAGCTATACCAAGCTGAGGAGTTGCTTGCCCGAGAGGGCG
109741 GGATTTTTGAAGGTTCTTTCCTCGATATGGTTCGACTCCTCAACGAACGGGCTCTCCCGC

109801 GGCAGATCAGCAGGGGGGCCATGGAGTGGGACACTTGCCTTGTTACAGAGGGACAGGGAG
109801 CCGTCTAGTCGTCCCCCCGGTACCTCACCCTGTGAACGGAACAATGTCTCCCTGTCCCTC

109861 AACAGGTGGTTCCCCTGAGATAGGAAGACAGTAGCATGACGGTGAGCATCTTTAAATGTT
109861 TTGTCCACCAAGGGGACTCTATCCTTCTGTCATCGTACTGCCACTCGTAGAAATTTACAA

109921 CACATGGGTCATGAGCATGTATGGTGGTCCCACCTGGAGACAAAGGTGGTACCTGGGCCT
109921 GTGTACCCACTACTCGTACATACCACCAGGGTGGACCTCTGTTTCCACCATGGACCCGGA

109981 GATAAGCAAGGCCCATGGAGGCCTCAGCTAAGAGAACTGTGCAGTCTGTCTGCCATGCTA
109981 CTATTCGTTCCGGGTACCTCCGGAGTCGATTCTCTTGACACGTCAGACAGACGGTACGAT

110041 ACCAGTGGTCTAGGAAGAAGCTTCACATCTGTTGTTTCTAAGGAGCCATGTAGACATAGA
110041 TGGTCACCAGATCCTTCTTCGAAGTGTAGACAACAAAGATTCCTCGGTACATCTGTATCT

110101 CACAGTTGGCAGCAATATTGCCTTGGGTTAGTGGGAAGCACCACTTCCCATGTCAGTGGA
110101 GTGTCAACCGTCGTTATAACGGAACCCAATCACCCTTCGTGGTGAAGGGTACAGTCACCT

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110161 TTTGTGTCTGTGAGCAAGAATCCAACTGTGGTTGGTATCCAGTAGTAGTGAGGATCTAAT

110221 CTCTGATTGCAATGGAATCTCTCATGCCCATCAGTCCTTAAAAGCAGAGCTGCTCTCTTT
110221 GAGACTAACGTTACCTTAGAGAGTACGGGTAGTCAGGAATTTTCGTCTCGACGAGAGAAA

110281 CCTTTCTTGTTGTGGAGTTAGGAACATGTAGTGGAGTATTTTATGTTATTCTGGCTCCAG
110281 GGAAAGAACAACACCTCAATCCTTGTACATCACCTCATAAAATACAATAAGACCGAGGTC

110341 GCCTATGTATTTCATTTGAGGCATGATGGTTTCCTATTCTAAGTACCACTAAGTATTGAG
110341 CGGATACATAAAGTAAACTCCGTACTACCAAAGGATAAGATTCATGGTGATTCATAACTC

110401 TAGTTATAAAATGGTGGTAGACTTTGGACTGTGTATTTCTATTCTGGATCCACGGATGAG
110401 ATCAATATTTTACCACCATCTGAAACCTGACACATAAAGATAAGACCTAGGTGCCTACTC

110461 CAAGTGGAGAAAACCCATCATGGATGCAGGGCTGCTGGGGATCTGTCTGTCCGAAAATGC
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110521 TATAGAGACACACACTGCTCTTGGGGAAAAAAACAGTGATGATTTCTTCAAAATGATTTC
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110581 ACTGAAGTGAAATAAGGACTTTGGCCTTGCTCTGGCAAATTCAAATGTGGCCACACTCTA
110581 TGACTTCACTTTATTCCTGAAACCGGAACGAGACCGTTTAAGTTTACACCGGTGTGAGAT

110641 CTCCATTGTGGAATGGTGACTCCCCTGTCCCATGAAAAACCAGGATCAACATCACAGCTT
110641 GAGGTAACACCTTACCACTGAGGGGACAGGGTACTTTTTGGTCCTAGTTGTAGTGTCGAA

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110701  TCTCTAGCAACTGGTGGTGGCCTGAGGTCTTATGAACTAGCATGTTAGCAGGGATAGAGT
110701  AGAGATCGTTGACCACCACCGGACTCCAGAATACTTGATCGTACAATCGTCCCTATCTCA

110761  TAGGGAATTTGTCCGATGCTGACAGCAAGAGGGTGCTGGGGGACCTGGAGGGGTGGAGAA
110761  ATCCCTTAAACAGGCTACGACTGTCGTTCTCCCACGACCCCCTGGACCTCCCCACCTCTT

110821  GTGATCTCCCTTCCTGCCTCATGGCTTCCTTTGGAAGTTGCAAGCTTAGAATTTCTTTCC
110821  CACTAGAGGGAAGGACGGAGTACCGAAGGAAACCTTCAACGTTCGAATCTTAAAGAAAGG

110881  CAAAGAATATTGGACTATGCTTCAAGAGACACTTGAGTTCAGTTGCTTACAGTGAACATA
110881  GTTTCTTATAACCTGATACGAAGTTCTCTGTGAACTCAAGTCAACGAATGTCACTTGTAT

110941  CTTCTTATGTTCCAGAGTTAAACTCAATCATATTTTCAGAAAAATAGATATTCAGACATC
110941  GAAGAATACAAGGTCTCAATTTGAGTTAGTATAAAAGTCTTTTTATCTATAAGTCTGTAG

111001  ATGTCATATTTACAGGAAGCTATTTGATCATGGAATTTACTGAAGTGACAGCTTTTTCAG
111001  TACAGTATAAATGTCCTTCGATAAACTAGTACCTTAAATGACTTCACTGTCGAAAAAGTC

111061  GAAAGGGTATCGAGTGGTTATCTATATCCTATTAATTTCTAAAAGCAATGCTCAATAAAA
111061  CTTTCCCATAGCTCACCAATAGATATAGGATAATTAAAGATTTTCGTTACGAGTTATTTT

111121  TGTGCAATTTTAGGCAATATTCTGTGTTTCAACATTATTTCCTTATGTTGGGGGTACATC
111121  ACACGTTAAAATCCGTTATAAGACACAAAGTTGTAATAAAGGAATACAACCCCCATGTAG

111181  ACTTTATATAGATAAAGAAAGATCCTTTTCATTCTCTATTAAATGGTCGAGAAGTCAAAT
111181  TGAAATATATCTATTTCTTTCTAGGAAAAGTAAGAGATAATTTACCAGCTCTTCAGTTTA

111241  TTTGGCTTTCATGTTGGTCTTCTTACTGTAGCTTCTGTTCACCTAAGAAAGAGATTTAAC
111241  AAACCGAAAGTACAACCAGAAGAATGACATCGAAGACAAGTGGATTCTTTCTCTAAATTG

111301  CAACATAAGCTTTGGCTAAACCATTGTACCAAACATTTCTATTTGGATGCTCTTAACTTT
111301  GTTGTATTCGAAACCGATTTGGTAACATGGTTTGTAAAGATAAACCTACGAGAATTGAAA

111361  TATACAATACTTTGAAATGTGTTCAATAAAACAACATGAGAAAGAAGTAGAAGATTCTGC
111361  ATATGTTATGAAACTTTACACAAGTTATTTTGTTGTACTCTTTCTTCATCTTCTAAGACG

111421  TATTAGGTTGGAAATTGATATTCCTTACATAAGTGATTAAAGATACTTTATTCAGTTTAT
111421  ATAATCCAACCTTTAACTATAAGGAATGTATTCACTAATTTCTATGAAATAAGTCAAATA

111481  CCCTTAAAATGGTATCTACTGAAGTCCTTAAACTTAGGCATGATATTAATTCCTGGCTAG
111481  GGGAATTTTACCATAGATGACTTCAGGAATTTGAATCCGTACTATAATTAAGGACCGATC

111541  TCTTTCTTTTTCCTAAAATATCACTCAATAAAATCCAAGAAGGACTAAAACTCATTATAT
111541  AGAAAGAAAAAGGATTTTATAGTGAGTTATTTTAGGTTCTTCCTGATTTTGAGTAATATA

111601  AGAACTGCACTGCCCAATACAGCAGCCACTAGCCACATGCAGTATTTTTAATTATAATAA
111601  TCTTGACGTGACGGGTTATGTCGTCGGTGATCGGTGTACGTCATAAAAATTAATATTATT

111661  CTTAAAATTAAACAAAATTAAAACTTCAGCCCTCAGTGGCACTAGCCACACTTTTTGTGT
111661  GAATTTTAATTTGTTTTAATTTTGAAGTCGGGAGTCACCGTGATCGGTGTGAAAAACACA

111721  CCAACAGCTACATATGGCTGGTGGCTGCCATATTGGACAGCACTAATAGAGAGCATTTCT
111721  GGTTGTCGATGTATACCGACCACCGACGGTATAACCTGTCGTGATTATCTCTCGTAAAGA

111781  ATCATCATAGGAAGTTCTGTTGAACAAGGCTGATCTGGAAGCTACACCATCCTAAAGCTC
111781  TAGTAGTATCCTTCAAGACAACTTGTTCCGACTAGACCTTCGATGTGGTAGGATTTCGAG

111841  TTTGGCAAGAAAGCAGAGCTTTTCCATAAGCTCAGTTTATGAACAATATATTTTGTATTT
111841  AAACCGTTCTTTCGTCTCGAAAAGGTATTCGAGTCAAATACTTGTTATATAAAACATAAA

111901  TCTATGTATATGTATATGAGAATACGTATACATAGAAATATATGAAAATACATATACATA
111901  AGATACATATACATATACTCTTATGCATATGTATCTTTATATACTTTTATGTATATGTAT

111961  TAAATATACATATACATAAAATAGAAATACATATACATAGAAAATACAAAATATTTTGTA
111961  ATTTATATGTATATGTATTTTATCTTTATGTATATGTATCTTTTATGTTTTATAAAACAT

112021  TTACATATACATATGCATGGAAATACAAAATATTTTGTATTATATAATGCAAATGTAAGA
112021  AATGTATATGTATACGTACCTTTATGTTTTATAAAACATAATATATTACGTTTACATTCT

112081  TATATTTATATTATGTAAGAAAATACATTTGTGCAATAAAACGCTTATTTCATTCAAGCA
112081  ATATAAATATAATACATTCTTTTATGTAAACACGTTATTTTGCCAATAAAGTAACTTCGT

112141  TATTTGTCCAGCATGGTTTCTTAGAGACTGAAGTTACCCAGTTTAGCACCTGGAACTGAA
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112141  ATAAACAGGTCGTACCAAAGAATCTCTGACTTCAATGGGTCAAATCGTGGACCTTGACTT

112201  TTCACTCTGGCTGTGTTAGATGTAGCACCAGCGTCATGACAGATCCAGCCCACAGCATAG
112201  AAGTGAGACCGACACAATCTACATCGTGGTCGCAGTACTGTCTAGGTCGGGTGTCGTATC

112261  ACTGAGGCCTACTCTGGAGGCAAATCTGCAGACAATGTGGCCAACACATGGGCCTTCCTC
112261  TGACTCCGGATGAGACCTCCGTTTAGACGTCTGTTACACCGGTTGTGTACCCGGAAGGAG

112321  ACATCTCTGTCCAGTCGCTGGCATCCACGTTATAACACAGCAGTGGCTCGTTTTCTCCAG
112321  TGTAGAGACAGGTCAGCGACCGTAGGTGCAATATTGTGTCGTCACCGAGCAAAAGAGGTC

112381  TTAAAGGCTAGGCTTCCGTGATTGAAGCAGGAGAGAATTTGGTAGTCAGTAAAGTAGACA
112381  AATTTCCGATCCGAAGGCACTAACTTCGTCCTCTCTTAAACCATCAGTCATTTCATCTGT

112441  AACTAAGACAAAACAAGAGTCGCATGAGTTCTTGGTACAATTAAAGAAACCCTTGGCCAC
112441  TTGATTCTGTTTTGTTCTCAGCGTACTCAAGAACCATGTTAATTTCTTTGGGAACCGGTG

112501  CAACGTTTTTAAATTCAGGAATTTCACCAAGTCCGTAACAGTTTTAGCTCTCAAGGGTAG
112501  GTTGCAAAAATTTAAGTCCTTAAAGTGGTTCAGGCATTGTCAAAATCGAGAGTTCCCATC

112561  AATTTTTTTTTTAACTTTTTTGGTAATAATTGTATTGCATGCATTCCCCTTACACAGAAG
112561  TTAAAAAAAAAATTGAAAAAACCATTATTAACATAACGTACGTAAGGGGAATGTGTCTTC

112621  GCTGGCATTTAATTGGGGTCTTGAACTCAATTGTGTTTTCTGCAGTTGGTAAACCTCACA
112621  CGACCGTAAATTAACCCCAGAACTTGAGTTAACACAAAAGACGTCAACCATTTGGAGTGT

112681  AATGTGGATATTGTGGCCGAAGCTATAAACAGCGAAGCTCTTTAGAGGAACATAAAGAGC
112681  TTACACCTATAACACCGGCTTCGATATTTGTCGCTTCGAGAAATCTCCTTGTATTTCTCG

112741  GCTGCCACAACTACTTGGAAAGCATGGGCCTTCCGGGCACACTGTACCCAGGTAAGCGCT
112741  CGACGGTGTTGATGAACCTTTCGTACCCGGAAGGCCCGTGTGACATGGGTCCATTCGCGA

112801  GCTGCTCGGAGGCCAGCCTGGTGGGCTCTCCCCCCAGCACGGTGGGGAAGGAGGGCGCTC
112801  CGACGAGCCTCCGGTCGGACCACCCGAGAGGGGGGTCGTGCCACCCCTTCCTCCCGCGAG

112861  TGCATGCAGCCTTAGGAGCAGAGCCTTGGGCCTGCTTCCTGCCGGGGCTAGGAGGGAGGG
112861  ACGTACGTCGGAATCCTCGTCTCGGAACCCGGACGAAGGACGGCCCCGATCCTCCCTCCC

112921  AAGTTTTTGGCCAATAGCATCAGTTTCACCAGAAGCACGTTGTGCTTCCCAGCTTTCTAG
112921  TTCAAAAACCGGTTATCGTAGTCAAAGTGGTCTTCGTGCAACACGAAGGGTCGAAAGATC

112981  GTCCTCATCTGACCAGAGAGAGCTTGATTTTAAAACCCTTCCCACTTCCAATCGGGAGAA
112981  CAGGAGTAGACTGGTCTCTCTCGAACTAAAATTTTGGGAAGGGTGAAGGTTAGCCCTCTT

113041  ACTCCTAGGATAGCAGTGACCTTGAAAGTTTTGGGGTTGTTTTTTGGATGTTGGTGATTT
113041  TGAGGATCCTATCGTCACTGGAACTTTCAAAACCCCAACAAAAAACCTACAACCACTAAA

113101  TAAAACAACAACAAAAAAAACACCTCAAGTAGTGATATTTCTTTGTAAACAAAATAAAAT
113101  ATTTTGTTGTTGTTTTTTTTGTGGAGTTCATCACTATAAAGAAACATTTGTTTTATTTTA

113161  GTAAAATATTGTTTTGAAACAATTTTTTAACAAAGTTGATCAAATAAGAACTTTCAGGCT
113161  CATTTTATAACAAAACTTTGTTAAAAAATTGTTTCAACTAGTTTATTCTTGAAAGTCCGA

113221  GTGATTTTAAGCATCAGTTCAGACTGAGGGCAGGGTATCCACTCCTGCATGGAGTGTGAG
113221  CACTAAAATTCGTAGTCAAGTCTGACTCCCGTCCCATAGGTGAGGACGTACCTCACACTC

113281  GTTGAAGTTTGTTGGAAGCCCCTGGTAGTTGATAATATTGAGGTTGTTGAAGGATGAGAG
113281  CAACTTCAAACAACCTTCGGGGACCATCAACTATTATAACTCCAACAACTTCCTACTCTC

113341  GAAAGGTCGCTTCTTTCTTAGGAGCTGTGATGCTCCACTGTATTGCATAACGAGATAGCA
113341  CTTTCCAGCGAAGAAAGAATCCTCGACACTACGAGGTGACATAACGTATTGCTCTATCGT

113401  CTTGATTCAGACCCCAGAGCCTGTAGAATAAATGATGTGGAGAGAGTATTGAAAAAGCCT
113401  GAACTAAGTCTGGGGTCTCGGACATCTTATTTACTACACCTCTCTCATAACTTTTTCGGA

113461  GGATTTATCTGGGGGAATGGCAATGTTATAAAAGGTTCTTCCCTAATTTTTTAAGAGATA
113461  CCTAAATAGACCCCCTTACCGTTACAATATTTTCCAAGAAGGGATTAAAAAATTCTCTAT

113521  AGCAATTTATAAAGAGATCAAATAAAACTAATCTCTTTCAAAACAGTATTCATTTAGCAC
113521  TCGTTAAATATTTCTCTAGTTTATTTTGATTAGAGAAAGTTTTGTCATAAGTAAATCGTG

113581  TACCCCTGGAAAAATCATCACTAGACTGTGAGTCGAAATTTAACGAATGGAGGAAAATTT
113581  ATGGGGACCTTTTTAGTAGTGATCTGACACTCAGCTTTAAATTGCTTACCTCCTTTTAAA
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113641  ATTAAGCCTCATTCACCTTTCGGACTTTAACAAATGGTTCAAAAGGGAAAATTCACCAGA
113641  TAATTCGGAGTAAGTGGAAAGCCTGAAATTGTTTACCAAGTTTTCCCTTTTAAGTGGTCT

113701  GTACCCTCAGATTATTAATGGCAGATGAGAGCAGGAAAAAAGAATGTTGAGAATGGCTAA
113701  CATGGGAGTCTAATAATTACCGTCTACTCTCGTCCTTTTTTCTTACAACTCTTACCGATT

113761  AAATTCATTCCAATTAGTCTTGGCATGGAGAGGCAACATCTCACCTGGCCAGAGCCCTGC
113761  TTTAAGTAAGGTTAATCAGAACCGTACCTCTCCGTTGTAGAGTGGACCGGTCTCGGGACG

113821  AGCCAGAGTGCTGTCTCCTCTGCCAGTCAGCCAGGGATCTGGGGCTTACAGGCGATTCCT
113821  TCGGTCTCACGACAGAGGAGACGGTCAGTCGGTCCCTAGACCCCGAATGTCCGCTAAGGA

113881  CCAGGCCTCAATCTTCTCACCTGTGAAATGGGAAGATACCATTAAATTGTCATTTGGCTT
113881  GGTCCGGAGTTAGAAGAGTGGACACTTTACCCTTCTATGGTAATTTAACAGTAAACCGAA

113941  CTTTCAAAATCTCAGGTCTAGAATGGAAAGGCATTGAAGGTGAGTGGAAGAGAAGAAACT
113941  GAAAGTTTTAGAGTCCAGATCTTACCTTTCCGTAACTTCCACTCACCTTCTCTTCTTTGA

114001  GGATGTTAAAATAATAATAATGTAACAGTTATTAATTCACATGGCCAGACCCCAGGGCAG
114001  CCTACAATTTTATTATTATTACATTGTCAATAATTAAGTGTACCGGTCTGGGGTCCCGTC

114061  AAGACTAATGGACGAGAGGATGATTATGTTCCTTTGAAATAAAATGTCAACATTCAAATA
114061  TTCTGATTACCTGCTCTCCTACTAATACAAGGAAACTTTATTTTACAGTTGTAAGTTTAT

114121  TTGTTTTTTTCTGTAAAAAATAAGTGAATGGGTCTTGGAAGGAAGTGCTCCTAATGATGT
114121  AACAAAAAAAGACATTTTTTATTCACTTACCCAGAACCTTCCTTCACGAGGATTACTACA

114181  AGTTTACATATTAATGCTTAATAAACCATTTTATTTACTCAACAAATATTCACTGAGGAC
114181  TCAAATGTATAATTACGAATTATTTGGTAAAATAAATGAGTTGTTTATAAGTGACTCCTG

114241  TTATAATCAATAATACCAAGCCCTATTGAATACAGTAATCTAATATACACATAGAATTGA
114241  AATATTAGTTATTATGGTTCGGGATAACTTATGTCATTAGATTATATGTGTATCTTAACT

114301  AAAGACAAAATGAACAAAAGAAACAGACAGTATATCATTTCTGTTTCCTCCACTGTTTTC
114301  TTTCTGTTTTACTTGTTTTCTTTGTCTGTCATATAGTAAAGACAAAGGAGGTGACAAAAG

114361  ATTACTAAAGAAACAAGCTGCAGTACACAGCCGGCTGAGAGCTGCTTCCGGGGGAGCAGG
114361  TAATGATTTCTTTGTTCGACGTCATGTGTCGGCCGACTCTCGACGAAGGCCCCCTCGTCC

114421  AGAAGCAGCACTCATTTCACTGAGACCTGGGTTTGAGTTCTCTGTTTTTGAATGTGACCC
114421  TCTTCGTCGTGAGTAAAGTGACTCTGGACCCAAACTCAAGAGACAAAAACTTACACTGGG

114481  AGAGCTCATCGCTTAAATGCGACTGATAATTCGTGCCTGGCCACCCTCATAGCAGCGCTC
114481  TCTCGAGTAGCGAATTTACGCTGACTATTAAGCACGGACCGGTGGGAGTATCGTCGCGAG

114541  TGAAAGAAACATAAAGGAGTGGATACACGTGTGAGCAGGAGCCTAGACATGTGTCAGGTA
114541  ACTTTCTTTGTATTTCCTCACCTATGTGCACACTCGTCCTCGGATCTGTACACAGTCCAT

114601  CTTACCTAAACATGGATGTTTAGGTCACTGACATACTGACACCATCAAGCTAATTCTTCT
114601  GAATGGATTTGTACCTACAAATCCAGTGACTGTATGACTGTGGTAGTTCGATTAAGAAGA

114661  CTATTGGTCTCTATGTCAGTAAGGCTACGTGCCAGTAATGTGTATTAAATATTACCCTGT
114661  GATAACCAGAGATACAGTCATTCCGATGCACGGTCATTACACATAATTTATAATGGGACA

114721  GGTGAGTATCAATTTCACCCTAAAATGTTCATTTATTCCCTTTGGTGGTTAAGTTACTTG
114721  CCACTCATAGTTAAAGTGGGATTTTACAAGTAAATAAGGGAAACCACCAATTCAATGAAC

114781  GACTACCACAGTGATGCCTCTATGTCCCCACACTCAGGAGGTATGAAAGCGTCTCTAGGA
114781  CTGATGGTGTCACTACGGAGATACAGGGGTGTGAGTCCTCCATACTTTCGCAGAGATCCT

114841  AGGAGCAGTGGTCTGGTCTCAGTGTGGCAGCAGACAAAGCCAGGCTCGCACTTAATTACA
114841  TCCTCGTCACCAGACCAGAGTCACACCGTCGTCTGTTTCGGTCCGAGCGTGAATTAATGT

114901  TTGAATTATTTCTGTCTGGTATGGCCTCAAAAGGTGCAAAATGATCATAAATATCTTTCG
114901  AACTTAATAAAGACAGACCATACCGGAGTTTTCCACGTTTTACTAGTATTTATAGAAAGC

114961  ACAGTCACCTTTGGTTTTTGCCCTTGCCAGCACCTGGCCCTTGTAGGTGCTGCTGGTTTA
114961  TGTCAGTGGAAACCAAAAACGGGAACGGTCGTGGACCGGGAACATCCACGACGACCAAAT

115021  AGGAACTTGGAGTATTAAGGGGATCCATAAAAGGACTTTGACAGAAGTCTTCCTGAACTG
115021  TCCTTGAACCTCATAATTCCCCTAGGTATTTTCCTGAAACTGTCTTCAGAAGGACTTGAC
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115081  TGCTTAGGGCCAGGAAGGCAGGCAGGGGCTTGGTCATTTCAGCTGTGCTGTACCCGGATG
115081  ACGAATCCCGGTCCTTCCGTCCGTCCCCGAACCAGTAAAGTCGACACGACATGGGCCTAC

115141  AGTGGAAACTGTGCCTTCTGATGCATCTCTCCTCCTCTGTTCCCCTCTAAGAACCCCTTG
115141  TCACCTTTGACACGGAAGACTACGTAGAGAGGAGGAGACAAGGGGAGATTCTTGGGGAAC

115201  TCTGTGCTCAGATGGATGAGCAAGTAGTCTCTTCTCCCACCCCAAAAACCTCCTTAGATG
115201  AGACACGAGTCTACCTACTCGTTCATCAGAGAAGAGGGTGGGGTTTTTGGAGGAATCTAC

115261  GGGTGGATTCAGTAAAATCAAAGCCTCAGTTAGGCAATATAGGAAAAGATGAATTTTTGT
115261  CCCACCTAAGTCATTTTAGTTTCGGAGTCAATCCGTTATATCCTTTTCTACTTAAAAACA

115321  GAATATAATTTTCTTTAGTAAAAGGCTTTTGGTCACCTCTTATAATTTCTCAATGTCTTT
115321  CTTATATTAAAAGAAATCATTTTCCGAAAACCAGTGGAGAATATTAAAGAGTTACAGAAA

115381  ATGGAAAAAATAAGTTTCTCTTGAGCCTTTGGTGCACAAACAGAGTCACCAGCCCTTGGA
115381  TACCTTTTTTATTCAAAGAGAACTCGGAAACCACGTGTTTGTCTCAGTGGTCGGGAACCT

115441  GGTGCATGCATCTAATGACAGAGCAGCCTGTGACTCGCGAGCATCAGGCTCACTTGTTCC
115441  CCACGTACGTAGATTACTGTCTCGTCGGACACTGAGCGCTCGTAGTCCGAGTGAACAAGG

115501  TTGCTGTGATTGACTCTGGGGGGTGGAGGCTTTTGGGAGGCCCTGCGCCATGGTGCAGAG
115501  AACGACACTAACTGAGACCCCCCACCTCCGAAAACCCTCCGGCACGCGGTACCACGTCTC

115561  GAAGACCCCTGACCTCTGGGAGCCCTGGGCAGGCTGTGGGTGTGGCTTGGCAGAGAAGGA
115561  CTTCTGGGGACTGGAGACCCTCGGGACCCGTCCGACACCCACACCGAACCGTCTCTTCCT

115621  TGGACATGTCAGGAAGCATATTAGCTTAATAGATGAAGTGTGTGACCAGTGTAATTGGGT
115621  ACCTGTACAGTCCTTCGTATAATCGAATTATCTACTTCACACACTGGTCACATTAACCCA

115681  TTTATGGATTTATATTTATCTTGCATATAAATCAGGGTGTGGCCTATATATGTTTGCCCA
115681  AAATACCTAAATATAAATAGAACGTATATTTAGTCCCACACCGGATATATACAAACGGGT

115741  TTTAATAAAAAACACATATTCCAAATGTTAAAATATAAAATATACCAGCAACAATAGCCA
115741  AAATTATTTTTTGTGTATAAGGTTTACAATTTTATATTTTATATGGTCGTTGTTATCGGT

115801  ATTTGAAATATATGTTTTCAAAGTAACATTCATAATAGCAATGAAGACATAAATACTTAG
115801  TAAACTTTATATACAAAAGTTTCATTGTAAGTATTATCGTTACTTCTGTATTTATGAATC

115861  AAATGAAGAAAACCAGCAAGCCATAGTGAGGCAAGAAAGAAAACATGGGAGATTGGAGAG
115861  TTTACTTCTTTTGGTCGTTCGGTATCACTCCCTTCTTTCTTTTGTACCCTCTAACCTCTC

115921  GTAGAGAGGTCTGGATGCCGTCCATGGGCCTCTGCCCAAATTAGTGTATCATTTCAACAT
115921  CATCTCTCCACACCTACGGCAGGTACCCGGACACGGGTTTAATCACATAGTAAAGTTGTA

115981  AAAACTGGCTTGTAAATTTTACTGGAATCTGGTAACCATGTATCATAAAGTATCTGGATA
115981  TTTTGACCCAACATTTAAAATGACCTTAGACCATTGGTACATAGTATTTCATACACCTAT

116041  TATACATGAGATAATTGGCAACTTTTTAGAACAAGAATAATGTCAACTGATGTATGAAAA
116041  ATATGTACTCTATTAACCGTTGAAAAATCTTCTTCTTATTACAGTTCACTACATACTTTT

116101  TGTAGCTGAAATGGATGGAACTCTTTGAAGAATAGACAAACAAATCAATAATAGAGATGG
116101  ACATCGACTTTACCTACCTTGAGAAACTTCTTATCTGTTTGTTTAGTTATTATCTCTACC

116161  ATACCCTACTGAAGACCCCATGATAAATCAGCATGAAATATCCGAGGCAGGAGCAAGCAT
116161  TATGGGATGACTTCTGGGGTACTATTTAGTCGTACTTTATAGGCTCCGTCCTCCTTCGTA

116221  AAGGCAGGAACGGTATTGGAAGAATTGATCAGGCATTTAAGATAATCAGTTTACATTATC
116221  TTCCGTCCTTGCCATAACCTTCTTAACTAGTCCGTAAATTCTATTAGTCAAATGTAATAG

116281  ATCTCCTTATACACTAGGATAAATTGCCGGGAAATGAAAGAGTTATATTTTTATAACTCC
116281  TAGAGGAATATGTGATCCTATTTAACGGCCCTTTACTTTCTCAATATAAAAATATTGAGG

116341  AACCACAATAACTGATGTAAATATAGATCCAGCTATGCAGGATACAAAGTTGTATCTTCA
116341  TTGGTGTTATTGACTACATTTATATCTAGGTCGATACGTCCTATGTTTCAACATAGAAGT

116401  ATTATGGAAAGAGATGACATAGAACAATTGAGAATGACTAGAAATGGCCCACACATCAGC
116401  TAATACCTTTCTCTACTGTATCTTGTTAACTCTTACTGATCTTTACCGGGTGTGTAGTCG

116461  ATTTACCTCCATAATTTCTAAATTTTCTACAGCAGTCAGGGGTGCTTTGATTTTCAGGAG
116461  TAAATGGAGGTATTAAAGATTTAAAAGATGTCGTCAGTCCCCACGAAACTAAAAGTCCTC

116521  TTTGTTGTATGCTCAGGGATAAGGGGCTCTGGGTTTTTCCTCCACATTGCCCAGATCTGC
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116521  AAACAACATACGAGTCCCTATTCCCCGAGACCCAAAAAGGAGGTGTAACGGGTCTAGACG

116581  TGTAGGCTCTTGGGGGCCACATTTTTGTATCTCCGTTCACTGTGCTGGTCCATGAAGTCA
116581  ACATCCGAGAACCCCCGGTGTAAAAACATAGAGGCAAGTGACACGACCAGGTACTTCAGT

116641  GATGTTAGATCACACACTTCTTTGCGTCTCAGAGGGCTGCTGTTAGGGACTGACTGAGGT
116641  CTACAATCTAGTGTGTGAAGAAACGCAGAGTCTCCCGACGACAATCCCTGACTGACTCCA

116701  AGCAGATTTGGGAGTATTATGAAAAGTTAAAAGGACTTGTCAAAGGGACATCAATACTTA
116701  TCGTCTAAACCCTCATAATACTTTTCAATTTTCCTGAACAGTTTCCCTGTAGTTATGAAT

116761  ATCCCAGTCCAGCCTCTGGTGATGGTGGTGGTGCCTGTGCATTTGGACTTAAAGAGGATG
116761  TAGGGTCAGGTCGGAGACCACTACCACCACCACGGACACGTAAACCTGAATTTCTCCTAC

116821  ATGTGTGGTGAGCAGCTGTTGGAGGAAGAAGCATTTGCAGGTGGCTGGTCATTGGCATTG
116821  TACACACCACTCGTCGACAACCTCCTTCTTCGTAAACGTCCACCGACCAGTAACCGTAAC

116881  CTCCGGCTGCCTCTGCCTGTCTGGAAGTGTTGCTGGGAAGATTAGAATTAATCTCTAGGA
116881  GAGGCCGACGGAGACGGACAGACCTTCACAACGACCCTTCTAATCTTAATTAGAGATCCT

116941  AGGGCCTGGCTCTTGTAGGCACTTAACAAATGTCAGATTTAACATTGGACGCGACTGAAC
116941  TCCCGGACCGAGAACATCCGTGAATTGTTTACAGTCTAAATTGTAACCTGCGCTGACTTG

117001  CCTTTAAACATAAGCCTTTCTAAACTGGCCTCTCTGTCTTTGACTTTAGTCATTAAAGAA
117001  GGAAATTTGTATTCGGAAAGATTTGACCGGAGAGACAGAAACTGAAATCAGTAATTTCTT

117061  GAAACTAATCACAGTGAAATGGCAGAAGACCTGTGCAAGATAGGATCAGAGAGATCTCTC
117061  CTTTGATTAGTGTCACTTTACCGTCTTCTGGACACGTTCTATCCTAGTCTCTCTAGAGAG

117121  GTGCTGGACAGACTAGCAAGTAACGTCGCCAAACGTAAGAGCTCTATGCCTCAGAAATTT
117121  CACGACCTGTCTGATCGTTCATTGCAGCGGTTTGCATTCTCGAGATACGGAGTCTTTAAA

117181  CTTGGTAAGAGTTAAATGTTTGCTGTCTCTTAAAAAAAAACTATGTGGGTGTTTTAGATG
117181  GAACCATTCTCAATTTACAAACGACAGAGAATTTTTTTTTGATACACCCACAAAATCTAC

117241  CAAGTAGAAATGAGTTCAGGGTGGAAGAAAGGGAAAAAAATCTTATTTTTTCAAAAGGAA
117241  GTTCATCTTTACTCAACTCCCACCTTCTTTCCCTTTTTTTAGAATAAAAAAGTTTTCCTT

117301  AAATTGGTAAGCTTAACATTCCTTAAATATCTTAGAATTTTTTCCAATAAGTATCTTAAA
117301  TTTAACCATTCGAATTGTAAGGAATTTATAGAATCTTAAAAAAGGTTATTCATAGAATTT

117361  AATAACAAACCTCCCATCAGTTTTTCCTAGATTTGATTTTGCAGCATCTGGGGCCTGCCC
117361  TTATTGTTTGGAGGGTAGTCAAAAAGGATCTAAACTAAAACGTCGTAGACCCCGGACGGG

117421  TGTGATCTGCCTGTGGACATCGCTCTTAGGGGCGGCTGCACCAGCGTGCACAGGGTGGAG
117421  ACACTAGACGGACACCTGTAGCGAGAATCCCCGCCGACGTGGTCGCACGTGTCCCACCTC

117481  AGTTTGGGCCTGGCTCGTCCGGGGGACACCACACTGCAGGACACTCCAGGCCTGGCCGGC
117481  TCAAACCCGGACCGAGCAGGCCCCCTGTGGTGTGACGTCCTGTGAGGTCCGGACCGGCCG

117541  TTCTCAGAGCTTCAGATCCTCATTTTTCATATGAAGCTCCTAATGCTCCCCTTATGGGGC
117541  AAGAGTCTCGAAGTCTAGGAGTAAAAAGTATACTTCGAGGATTACGAGGGGAATACCCCC

117601  ACTCTGAAGGGTTAATGGGAGGAATCATACAGTGACTGACCCCTGAGAAGTGTCCAGTGA
117601  TGAGACTTCCCAATTACCCTCCTTAGTATGTCACTGACTGGGGACTCTTCACAGGTCACT

117661  AGACAGGGCTTAGCTAGGATTGCTGTTTTGCCTAATGCTCTGCGGGATTAAAAAAAAAGA
117661  TCTGTCCCGAATCGATCCTAACGACAAAACGGATTACGAGACGCCCTAATTTTTTTTTCT

117721  AGAAGAAGAACAAGACCATTCGTCTCTCTAGGAGCATTGCCCAGAGTAGGTATTAGACAC
117721  TCTTCTTCTTGTTCTGGTAAGCAGAGAGATCCTCGTAACGGGTCTCATCCATAATCTGTG

117781  ACCAACACCACCATCCAGCCAGACGCTGCAGGGACAGTGAGCCAGGGTCCGAGTGGAAAG
117781  TGGTTGTGGTGGTAGGTCGGTCTGCGACGTCCCTGTCACTCGGTCCCAGGCTCACCTTTC

117841  GCGCTAGGCTTGGCAACCAGCTCAGAGTCAATACAGAGCCACCGCCACTCACCAACTCTC
117841  CGCGATCCGAACCCTTGGTCGAGTCTCAGTTATGTCTCGGTGGCGGTGAGTGGTTGAGAC

117901  TCAGCTTAGTAAAATGGCTCTGCCCCTAGAGCCCTGGTTCCATCCTTTAGTATCTCACAG
117901  AGTCGAATCATTTTACCGAGACGGGGATCTCGGGACCAAGGTAGGAAATCATAGAGTGTC

117961  GGTGATTGTGAATATCCCATGACTCCAAGATTGAGAAAACGTTTAGAATCCCTCGGTGTG
117961  CCACTAACACTTATAGGGTACTGAGGTTCTAACTCTTTTGCAAATCTTAGGGAGCCACAC
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118021  AAGGTTAACTCTGTCCGGAAAGAGGACCAGTAAAAGCTTCATGAGGCTGAGATGCACTTT
118021  TTCCAATTGAGACAGGCCTTTCTCCTGGTCATTTTCGAAGTACTCCGACTCTACGTGAAA

118081  GGAAGAGGAATAGAGTTTCAGCACATTCTAGGTGTTGGAGGAATGGGGGAATCTAGGCAG
118081  CCTTCTCCTTATCTCAAAGTCGTGTAAGATCCACAACCTCCTTACCCCCTTAGATCCGTC

118141  ATGTTTAAAATCAATGAGAAACCAGAATGCTGACCATGAGGGTTGGAGTGGGGGCCTAAG
118141  TACAAATTTTAGTTACTCTTTGGTCTTACGACTGGTACTCCCAACCTCACCCCCGGATTC

118201  GACATGACGGAGGAGCAGGGTGTGTTCCCAGCTTAACTCAGGTACCCATGGGGAAGCAGG
118201  CTGTACTGCCTCCTCGTCCCACACAAGGGTCGAATTGAGTCCATGGGTACCCCTTCGTCC

118261  AAAAGTGAAGGTGTCCTAGGCAGCTCTGCCACAGGATGAATGGCTTCAGATGCCAGGTGA
118261  TTTTCACTTCCACAGGATCCGTCGAGACGGTGTCCTACTTACCGAAGTCTACGGTCCACT

118321  GCGAGGGACCCTTCATTCAGTCAGCAGGAAAGAAGCACTGGCATATTTTTTATGAGAACA
118321  CGCTCCCTGGGAAGTAAGTCAGTCGTCCTTTCTTCGTGACCGTATAAAAAATACTCTTGT

118381  AAGGCTAGGATAGTAAAGACAGCAAGTACCAAAAAATGACTGGAAAAGGGAGACTGTGGA
118381  TTCCGATCCTATCATTTCTGTCGTTCATGGTTTTTTACTGACCTTTTCCCTCTGACACCT

118441  GGCAGTGGCAGCAGGCATGGAAAGAAGGGCTTGTGAAGGGGAAGGGGTGGTGTCAGAGGA
118441  CCGTCACCGTCGTCCGTACCTTTCTTCCCGAACACTTCCCCTTCCCCACCACAGTCTCCT

118501  ACATAGGGCTGGGGGCAGGGATTAGGTGAGGGAAACCATGAGTCACACTGATTCTAGAGT
118501  TGTATCCCGACCCCCGTCCCTAATCCACTCCCTTTGGTACTCAGTGTGACTAAGATCTCA

118561  AGTGTGCCCTTGATGAAAAGGATAACACCAGGTTCTAGGAAAAGATGGGGTTCTGTTTTT
118561  TCACACGGGAACTACTTTTCCTATTGTGGTCCAAGATCCTTTTCTACCCCAAGACAAAAA

118621  GACGTGTTGATTTTCAAGGACTTCTGGTGTTTGTGACACATGGGGAAATTGTGGTGGGAG
118621  CTGCACAACTAAAAGTTCCTGAAGACCACAAACACTGTGTACCCCTTTAACACCACCCTC

118681  AGAGGTGGGGCCAGAACAGGGGCTGGTGAGGCCAAGGGTCCCAGAGGGCACCTGTTGACC
118681  TCTCCACCCCGGTCTTGTCCCCGACCACTCCGGTTCCCAGGGTCTCCCGTGGACAACTGG

118741  TGCAGGATGACATGAAGGGGGAAGGACAGAGGCAAGGCCAAGTCCTGGGCACCAGCCTCC
118741  ACGTCCTACTGTACTTCCCCCTTCCTGTCTCCGTTCCGGTTCAGGACCCGTGGTCGGAGG

118801  CTCTTGCAGCTTCAAATAGGGCTCCATTTTGACCTTTTGATTAATTAGAGGTTTGTCATA
118801  GAGAACGTCGAAGTTTATCCCGAGGTAAAACTGGAAAACTAATTAATCTCCAAACAGTAT

118861  GGTTGGGGGTTGAGAGGAGCAAGGGAGAGAAGGATTCAGTGTACAAAAAGAATGAAAGCC
118861  CCAACCCCCAACTCTCCTCGTTCCCTCTCTTCCTAAGTCACATGTTTTTCTTACTTTCGG

118921  ACTGGCTGAGCCAGTGGGGAGTTGTCCACACACACATGAGCCTTTGGACCATGAGAACGA
118921  TGACCGACTCGGTCACCCCTCAACAGGTGTGTGTGTACTCGGAAACCTGGTACTCTTGCT

118981  GGGAGGCCTTGCCTTCCTGAACGGAGTAGGAGTGAGGTCCTGTGCTGAGCGTAAGCAGTG
118981  CCCTCCGGAACGGAAGGACTTGCCTCATCCTCACTCCAGGACACGACTCGCATTCGTCAC

119041  CGATTCCCACAGCACTGCCCACAGACCCCACGGGCTGCCTCCTGAGCAGCCAGCATCTGC
119041  CCTAAGGGTGTCGTGACGGGTGTCTGGGGTGCCCGACGGAGGACTCGTCGGTCGTAGACG

119101  CTGGGGTGGACACAGTGACAGAGAGATGGGTGGTGACTGGGGTATGGGCAGAGATAAGGC
119101  GACCCCACCTGTGTCACTGTCTCTCTACCCACCACTGACCCCATACCCGTCTCTATTCCG

119161  AGCAAGTGTGTGCAAGGGGAGTGAAGGGTTACTGACCTTAAGAAGCAGGGATGGCGTCCT
119161  TCGTTCACACACGTTCCCCTCACTTCCCAATGACTGGAATTCTTCGTCCCTACCGCAGGA

119221  CTGTCAGGTGAGGAGCCTGGAGAATGCTTTGGTGAATGAACGTTTGCAGCCCCTTTTAGC
119221  GACAGTCCACTCCTCGGACCTCTTACGAAACCACTTACTTGCAAACGTCGGGGAAAATCG

119281  TTTTGGAGACTTGAAACCAAAGGAGAGATTCATCTGTGAAACTCTACTGGAGCCACTCCC
119281  AAAACCTCTGAACTTTGGTTTCCTCTCTAAGTAGACACTTTGAGATGACCTCGGTGAGGG

119341  CAACCCCCACCCTTGTGAGACCACAATGTGGGCGTTGGCTTGAGATGCTTCTGTGTTAGT
119341  GTTGGGGGTGGGAACACTCTGGTGTTACACCCGCAACCGAACTCTACGAAGACACAATCA

119401  AGAAGAAATAAACAACACAGTGCTCTGATGAGGCAAAGCGAAGATGAAAAAGGAGTTCCC
119401  TCTTCTTTATTTGTTGTGTCACGAGACTACTCCGTTTCGCTTCTACTTTTTCCTCAAGGG
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119461  AGGGGACATAGTAGGAACAGTGGACGAGGGTAGCAGAAGAGGAGTTTGGAGCAAAAGACT
119461  TCCCCTGTATCATCCTTGTCACCTGCTCCCATCGTCTTCTCCTCAAACCTCGTTTTCTGA

119521  CACAAGCAGCTGCATAATCTGTTGGTGCTTGGCAGTTCATTTGTAAAAATGATGCCTCTT
119521  GTGTTCGTCGACGTATTAGACAACCACGAACCGTCAAGTAAACATTTTTACTACGGAGAA

119581  CCTGCCCTAAAATACCTACCTTACCCCCGCTTCAACTTGATGAGATTTCCATCAGTCACT
119581  GGACGGGATTTTATGGATGGAATGGGGGCGAAGTTGAACTACTCTAAAGGTAGTCAGTGA

119641  CCCAATGTGTCACAGCTTCTGCAGCCCTAAAATTAAAAGGTGAGTGAGTCTCTGAGGCCC
119641  GGGTTACACAGTGTCGAAGACGTCGGGATTTTAATTTTCCACTCACTCAGAGACTCCGGG

119701  CTCTCCACTTCTCGGATGCTGAGTTTAGCCTTCATGTGAATGTGGAAAGACTAGGAATAC
119701  GAGAGGTGAAGAGCCTACGACTCAAATCGGAAGTACACTTACACCTTTCTGATCCTTATG

119761  AGCTGTTATCACACAAGCTGGCCCAATAGTGGTTCAGTTGAGAGAGCCCCATCGTTCAGA
119761  TCGACAATAGTGTGTTCGACCGGGTTATCACCAAGTCAACTCTCTCGGGGTAGCAAGTCT

119821  GTCAGCTCCAGCTAGGAGTGACTGGTGGCCTTGAGCATGGTGCTGGGCTTAGTGTTGCCA
119821  CAGTCGAGGTCGATCCTCACTGACCACCGGAACTCGTACCACGACCCGAATCACAACGGT

119881  TCTGTGGAATGGGTGTGGGTCTGTTGCCCTGCCTCCTCCCAGAGCTATTCTGAGGCTCAG
119881  AGACACCTTACCCACACCCAGACAACGGGACGGAGGAGGGTCTCGATAAGACTCCGAGTC

119941  AAGGGGTGATGGATGTGATGGTGCTCCCAACACTAGAAAGCATCTTAAGAATGTAAGATT
119941  TTCCCCACTACCTACACTACCACGAGGGTTGTGATCTTTCGTAGAATTCTTACATTCTAA

120001  TTCATGATGACTGTTGCTCAGAGTGGCTATTATAGTTTTGCTTTATTGTTCTATAACCTA
120001  AAGTACTACTGACAACGAGTCTCACCGATAATATCAAAACGAAATAACAAGATATTGGAT

120061  TGATTAAAATTTTTACCTTAAACTTTGACGTGAGTGTGAATAAGTATTTGTTTTGCCAGC
120061  ACTAATTTTAAAAATGGAATTTGAAACTGCACTCACACTTATTCATAAACAAAACGGTCG

120121  AACATTCCTCACCACTGGGGCCATTAAAGATCTCCCCCTCTGAGACCATCAAATACAGGT
120121  TTGTAAGGAGTGGTGACCCCGGTAATTTCTAGAGGGGGAGACTCTGGTAGTTTATGTCCA

120181  CAACAGGACTGATTAATCTAATTAGAAAAGGGCTTGTATTAAATAGCAATGATAATTGTT
120181  GTTGTCCTGACTAATTAGATTAATCTTTTCCCGAACATAATTTATCGTTACTATTAACAA

120241  GTTTTTAGTCTGTCTGGTGTTTGACTTGGGAACGTTTTTAAAATAGAGAAAAGCACAAAG
120241  CAAAAATCAGACAGACCACAAACTGAACCCTTGCAAAAATTTTATCTCTTTTCGTGTTTC

120301  AGGAAAACAACAATTACCAATATTCCTGCTACCCATTATAATTATCTAGGTATATTTTCT
120301  TCCTTTTGTTGTTAATGGTTATAAGGACGATGGGTAATATTAATAGATCCATATAAAAGA

120361  TCTTTTGTAAGAAAAAGAAACCCTGTTATATTGTTAAAATAACACAAAGTTAATATAAAG
120361  AGAAAACATTCTTTTTCTTTGGGACAATATAACAATTTTATTGTGTTTCAATTATATTTC

120421  AATTTTAATGCAAAGATTAATGTTTTCAAATCACCACAAAACCCAACATCCAGAAATTAC
120421  TTAAAATTACGTTTCTAATTACAAAAGTTTAGTGGTGTTTTGGGTTGTAGGTCTTTAATG

120481  CAATATTAAAAGTAGAAAAGTATCATTCTAAATATTTTCTGTTGCATATGTATGTGAGTG
120481  GTTATAATTTTCATCTTTTCATAGTAAGATTTATAAAAGACAACGTATACATACACTCAC

120541  GATAGGCTGATGAATTAGGTGGATTGATGGATAGGTAAATATGAAATAAATACTTTCATA
120541  CTATCCGACTACTTAATCCACCTAACTACCTATCCATTTATACTTTATTTATGAAAGTAT

120601  AATATTCCAACTTATCATACATGCCTTAAATTCAAGAGGTGAAAAAAGACCCAAACAAAA
120601  TTATAAGGTTGAATAGTATGTACGGAATTTAAGTTCTCCACTTTTTTCTGGGTTTGTTTT

120661  CTAGAGAAGCGGCTTATTTTAAATATCCTCTGACATAAAGGAATATTATATTTAAAGGAT
120661  GATCTCTTCGCCGAATAAAATTTATAGGAGACTGTATTTCCTTATAATATAAATTTCCTA

120721  CCTCTAAGATTAAAAATATGTACTATGAAAAACATTAAGAAATTTGAATTTTTTTTAATC
120721  GGAGATTCTAATTTTTATACATGATACTTTTTGTAATTCTTTAAACTTAAAAAAAATTAG

120781  CATTTGTTTCAATTTAAGCAGCATCTACTGGCTCACTGCTTTGAAAAATAAGGACAGTAT
120781  GTAAACAAAGTTAAATTCGTCGTAGATGACCGAGTGACGAAACTTTTTATTCCTGTCATA

120841  TCCAGTTCACATTCAGTGTTCCAGTGTTCACATTATCTTATTATTTTTACATTGTCCAGC
120841  AGGTCAAGTGTAAGTCACAAGGTCACAAGTGTAATAGAATAATAAAAATGTAACAGGTCG

120901  TTTGTAATATTCACATTCTATTCTGTAATCATAATTCATAGTAGTTTAGTTATTTATTAC
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120901  AAACATTATAAGTGTAAGATAAGACATTAGTATTAAGTATCATCAAATCAATAAATAATG

120961  TAACTCTATTTAAATAGATTCAAGGATCAGACCCTGCCCTTTTCTTCTTATTTATGTTTA
120961  ATTGAGATAAATTTATCTAAGTTCCTAGTCTGGGACGGGAAAAGAAGAATAAATACAAAT

121021  TTTTGATTAATCTCTTAATTGATTGGACTTTACATTCAAGCAACTTTTTTAAAAAAAAGT
121021  AAAACTAATTAGAGAATTAACTAACCTGAAATGTAAGTTCGTTGAAAAAATTTTTTTTCA

121081  TTCTATAGATGTTCTATTTCTATCATTGTATTGTTTTTGAGGATGTTGGCCTGTTGCCTT
121081  AAGATATCTACAAGATAAAGATAGTAACATAACAAAAACTCCTACAACCGGACAACGGAA

121141  TGTATTTGATGAGCATTTTGACAGAGTCTATGGTCTTGGGCCACTCTTTCTTTTTCTCCC
121141  ACATAAACTACTCGTAAAACTGTCTCAGATACCAGAACCCGGTGAGAAAGAAAAAGAGGG

121201  TTGAGAACTTTTTAGATTTTGCTGATGGCATTGCTTGTTGAATGTTGCTGTGGAAACATC
121201  AACTCTTGAAAAATCTAAAACGACTACCGTAACGAACAACTTACAACGACACCTTTGTAG

121261  AAGTCTAGTGTAACTGTTTCTTCTTCAAGGTGATTTGCATTTTATTCCTGAATGCCTGAG
121261  TTCAGATCACATTGACAAAGAAGAAGTTCCACTAAACGTAAAATAAGGACTTACGGACTC

121321  GGTTCTTTATTTAACCTTGAAGTTAAATACCCTAATTAGGATGTATCTTGGTCTATTCAT
121321  CCAAGAAATAAATTGGAACTTCAATTTATGGGATTAATCCTACATAGAACCAGATAAGTA

121381  TCGGAATAAAAAATTCCTGCCATTTTGTCTAGAGAGTCCCTTTTTTTTCTCTTTATTTCT
121381  AGCCTTATTTTTTAAGGACGGTAAAACAGATCTCTCAGGGAAAAAAAAGAGAAATAAAGA

121441  GGGAAATTCTCTTTTATATAAATATGTTTTGTTCCATCTATTGTGATCTCTGTTGAGGGA
121441  CCCTTTAAGAGAAAATATATTTATACAAAACAAGGTAGATAACACTAGAGACAACTCCCT

121501  TACCAGTTGTCCATATGTTAGATAATTTGTCTTCCATATCTGTTAACAGTTCTTAAAGTT
121501  ATGGTCAACAGGTATACAATCTATTAAACAGAAGGTATAGACAATTGTCAAGAATTTCAA

121561  TTTTGTTTATTTCTTTGTCTATTTTTACATTTACTCACTGTTCTCTTGTGGTTTTCCTCT
121561  AAAACAAATAAAGAAACAGATAAAAATGTAAATGAGTGACAAGAGAACACCAAAAGGAGA

121621  GTCAGTAATTTAATTTTTAGTAGTTCCTGTTCTATTACTTGCTATTTTTAATCCATGCAT
121621  CAGTCATTAAATTAAAAATCATCAAGGACAAGATAATGAACGATAAAAATTAGGTACGTA

121681  TAATTTTATAATAATATTATTTTGCTCCTTATTTTGTCTCCTGAGACCCGAAATCTCTTT
121681  ATTAAAATATTATTATAATAAAACGAGGAATAAAACAGAGGACTCTGGGCTTTAGAGAAA

121741  TTTCCTCTTACTCTGTTGCTTTTGCATTTTATTTTGAATACTTTTAAAATTGATTCCATG
121741  AAAGGAGAATGAGACAACGAAAACGTAAAATAAAACTTATGAAAATTTTAACTAAGGTAC

121801  TTATGAAGCAATTATGAGGCATTTCCTCTCTTGTTGGAATTAACGATTTTTTCCCCTAGG
121801  AATACTTCGTTAATACTCCGTAAAGGAGAGAACAACCTTAATTGCTAAAAAAGGGGATCC

121861  AGGGACTCTATGGTCTGTGTTTTACTTCCTTTCTTCCCCTGTATTTCTAGAAAATATTTT
121861  TCCCTGAGATACCAGACACAAAATGAAGGAAAGAAGGGGACATAAAGATCTTTTATAAAA

121921  CCTAGTAACCCTGACATTTCTTTTCATCTTGCTTATTCTAGTTGGTCTGATATAGCTTGA
121921  GGATCATTGGGACTGTAAAGAAAAGTAGAACGAATAAGATCAACCAGACTATATCGAACT

121981  TTGACATTTCAGCCTTCTTCCCACTATATTTTTTTTTCCTGTGAGAGCTATTGGGTTTTC
121981  AACTGTAAAGTCGGAAGAAGGGTGATATAAAAAAAAAGGACACTCTCGATAACCCAAAAG

122041  TAAATCCTGAAAGAATGCCAAAGATGGGGTTGGAGGAGTTTGGTGAGGCAAAGTGCAGCC
122041  ATTTAGGACTTTCTTACGGTTTCTACCCCAACCTCCTCAAACCACTCCGTTTCACGTCGG

122101  TTTGTTAAAATACTTTTCCTTTGCTCTCTCTCCCTCATCTGAAATTTAGTTAAATACCCT
122101  AAACAATTTTATGAAAAGGAAACGAGAGAGAGGGAGTAGACTTTAAATCAATTTATGGGA

122161  AAGCCATCAGCACTGTACCTAGTTGGGGAATGCTTTCATCCCCACAGGAGATTCTCTGGG
122161  TTCGGTAGTCGTGACATGGATCAACCCCTTACGAAAGTAGGGGTGTCCTCTAAGAGACCC

122221  GCTTTGGGCCATCTTCCCCTTCAGTGTAGACCACAGAGGACTTTGCTTCTGTCCCAGGCA
122221  CGAAACCCGGTAGAAGGGGAAGTCACATCTGGTGTCTCCTGAAACGAAGACAGGGTCCCT

122281  GCCCGCAGGGGCTCACTTCTCCATGTTCATCTGATTCTTGTCAGCCAAGGTTTCAAATGC
122281  CGGGCGTCCCCGAGTGAAGAGGTACAAGTAGACTAAGAACAGTCGGTTCCAAAGTTTACG

122341  TTTTCTGATCAGAACAGGGAAAAGATACCTATCTGAATCATGTCTTTATAGATATGAGGC
122341  AAAAGACTAGTCTTGTCCCTTTTCTATGGATAGACTTAGTACAGAAATATCTATACTCCG
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122401 TATGAGGGAAAATTCTGAGGTTATTCTTGACTCACACCTAAAGATTTGGAAATGAGATTA
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122521 TGTATGTGTGTTCTCACACACGCCATAATGAAATGCATATTATATATAATTATGTGTATA
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122581 TATAATATTCTATGACTATACATGACATGTTCCTTTAGCTGATTGCTGTTAAGAGAAATT
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122641 TATAGGTTTTATTTTTCTTGTTTTGTTGGGTATTAAGGAAGAGAAATTCTATGGTAATT
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122701 TTCATGTGGCACAGTAATCTGGCATATATGTTGATTTTTTTCCTACACCCATTTGTTGTG
122701 AAGTACACCGTGTCATTAGACCGTATATACAACTAAAAAAAGGATGTGGGTAAACAACAC

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122941 GAGGGATAGACTTGGATACAAACTAGAATGGATTCATTCTTCTCTGGAGTTAGTGTAACA
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123001 AGACATTTAGCTGCTCAACACAAAAACAGAAACAAAAAAATTGTGTGGTTTCAGCAGTGC
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123121 TCAGCTTCATAGGGTTTTCATCCTGTTCTGTTTCTGGGAGGGCGTAACTGGCCATGCACA
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123241 GGAAACCAGGCTATTATATGATACATATCCATTACAAAATAAGACATGAAACTCAAAGGT
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123301 ACTTTATGGTATAATGGGGCATATATTCCTGGACAATTCTTAATGGTCACAGATTTTATA
123301 TGAAATACCATATTACCCCGTATATAAGGACCTGTTAAGAATTACCAGTGTCTAAAATAT

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123481 CCCTCACCAGCCATCATCAGCCATAACCTGCACATTGGGGAAGTTTTGACTTATCCCTCA
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123541 CTTTTGCCCCTCTTCAAGCTGTTCTTTCCACAGTGAATGAGAAGGCCACTTCTTCCTTCA
123541 GAAAACGGGGAGAAGTTCGACAAGAAAGGTGTCACTTACTCTTCCGGTGAAGAAGGAAGT

123601 AACCTTTCAGTGGTTTCCATTTTCCTTTAGACAAAGTCTCTGCCTAGCTGGCCTCTGCCT
123601 TTGGAAAGTCACCAAAGGTAAAAGGAAATCTGTTTCAGAGACGGATCGACCGGAGACGGA

123661 GCCCCTCCTGCCTACCTCTCGAGCACTGCCCCCACCTAGGGCTCTGGTTCCCCAACCTTC
123661 CGGGGAGGACGGATGGAGAGCTCGTGACGGGGGTGGATCCCGAGACCAAGGGGTTGGAAG

123721 ACTCGGTCCTGCCACACCTCCCAGCCCCTTCTCCCTTCAGAACTTTCCTTCTTGTTGTCC
123721 TGAGCCAGGACGGTGTGGAGGGTCGGGGAAGAGGGAAGTCTTGAAAGGAAGAACAACAGG

123781 CCAACACTGGGACACAAAACCCTCCTTATCAACCCTCCTTATCTGGCTGACTCTTACAAG
123781 GGTTGTGACCCTGTGTTTTGGGAGGAATAGTTGGGAGGAATAGACCGACTGAGAATGTTC

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123841  ATCAGAAACCTGTGTAATGCTCTCATGGCACGCTCCCCTTGTCTTCGTGGATTTCTCAGA
123841  TAGTCTTTGGACACATTACGAGAGTACCGTGCGAGGGGAACAGAAGCACCTAAAGAGTCT

123901  TGGGAAGGAATTATCCATGCAATCACACATAAACTTCTACCTACCCTCCCCTAGTAGCTG
123901  ACCCTTCCTTAATAGGTACGTTAGTGTGTATTTGAAGATGGATGGGAGGGGATCATCGAC

123961  TCTGCTGCTAAGGATGGGGACCATTCTCACTTACTCACTGTTCTGTCCCTCTGCCCAGTC
123961  AGACGACGATTCCTACCCCTGGTAAGAGTGAATGAGTGACAAGACAGGGAGACGGGTCAG

124021  CAGATGTGTTGAAGGATGGAAATATACAGAGTAGTGGTAAAATATAAACCGTTCAGACAT
124021  GTCTACACAACTTCCTACCTTTATATGTCTCATCACCATTTTATATTTGGCAAGTCTGTA

124081  TCCAAGGATGGGCTCATGTGCTTTGACTCATTAATGTACCACTGCTGAAAACAGAACACA
124081  AGGTTCCTACCCGAGTACACGAAACTGAGTAATTACATGGTGACGACTTTTGTCTTGTGT

124141  GCCGCAGTCTTGCCAGTAAGAGTGCAGTTACTGTAATTAATGAATTTGCTAATTAAGCCA
124141  CGGCGTCAGAACGGTCATTCTCACGTCAATGACATTAATTACTTAAACGATTAATTCGGT

124201  TGATTTCATACTGAACTTATGACCAACATATTGAGAAGGTGTGTCTTCAAGAAAATTTAT
124201  ACTAAAGTATGACTTGAATACTGGTTGTATAACTCTTCCACACAGAAGTTCTTTTAAATA

124261  TTTTTGTATTAAGATATTTACTCCAAAGCTAATTGAAGAAGCCAAATCTAGGCTCTGGTT
124261  AAAAACATAATTCTATAAATGAGGTTTCGATTAACTTCTTCGGTTTAGATCCGAGACCAA

124321  TCACCATTGCCAGGGAAATGAGCTCATGGACTCCTATGAACTGATGATCTTAGATCAGAA
124321  AGTGGTAACGGTCCCTTTACTCGAGTACCTGAGGATACTTGACTACTAGAATCTAGTCTT

124381  GTTTCTCAAGGCCAGGGCCCAATCACTGCTGAGGCGTCAACAGTAGTTCCTTGTACATCA
124381  CAAAGAGTTCCGGTCCCGGGTTAGTGACGACTCCGCAGTTGTCATCAAGGAACATGTAGT

124441  ATAATTCTCATTACTTTTAAAAAATAACAGATGAATAGCAACTATTTTCCCTGTAGCTCC
124441  TATTAAGAGTAATGAAAATTTTTTATTGTCTACTTATCGTTGATAAAAGGGACATCGAGG

124501  CTTGCTGTGCCTCCTACCCTCCACCACATGTTTCTGGGGAGCCCTGCTTCGGGCCTGCCA
124501  GAACGACACGGAGGATGGGAGGTGGTGTACAAAGACCCCTCGGGACGAAGCCCGGACGGT

124561  ACTACAGAGAATTACTTTTGAGTATCCCTTCCACTCTCATCTCAAGACAGAGTTCATCTA
124561  TGATGTCTCTTAATGAAAACTCATAGGGAAGGTGAGAGTAGAGTTCTGTCTCAAGTAGAT

124621  CCTTTGGGTTATTTGTCAAAAATGTGTCATTTTATTACAAAAAATATACAATCATCATGT
124621  GGAAACCCAATAAACAGTTTTTACACAGTAAAATAATGTTTTTTATATGTTAGTAGTACA

124681  ATTTTGATTAAATTTTACACTAGATTATTAAAATTATTAAATACAATTATTAAAATTAAT
124681  TAAAACTAATTTAAAATGTGATCTAATAATTTTAATAATTTATGTTAATAATTTTAATTA

124741  AATTTAACATATCACATATTTTAAATATATTGTATATAATGAATAATAATATAATTATTG
124741  TTAAATTGTATAGTGTATAAAATTTATATAACATATATTACTTATTATTATATTAATAAC

124801  TCTATTTTAATTCAATAAATGTATAGTAAGTTAGCCAGTTGTAAATTACTGAGAACACTC
124801  AGATAAAATTAAGTTATTTACATATCATTCAATCGGTCAACATTTAATGACTCTTGTGAG

124861  TACTGAAAAAGCATCATTTCAAATACACTATTTAAAATATTAAATGAAATACAATAACAT
124861  ATGACTTTTTCGTAGTAAAGTTTATGTGATAAATTTTATAATTTACTTTATGTTATTGTA

124921  AATTAAACTAATCTTTGGTTCCCCTATTTATGTATTCATTTATCCAACAAAATCTCCTTA
124921  TTAATTTGATTAGAAACCAAGGGGATAAATACATAAGTAAATAGGTTGTTTTAGAGGAAT

124981  AGTGCTTATAATGGGTAGGTCCTGGCTCGGTGTCCCCTAGACAGACGCATGGGCCTTCCC
124981  TCACGAATATTACCCATCCAGGACCGAGCCACAGGGGATCTGTCTGCGTACCCGGAAGGG

125041  CCAGCCCGTCAGTATGGTGCAGGTGTCATGTGTCCGCAGGTGTGTGTGTATGTGTGCAGG
125041  GGTCGGGCAGTCATACCACGTCCACAGTACACAGGCGTCCACACACACATACACACGTCC

125101  TGTGGGGTCCGCAGGCGTGCTGGGCCCCCAGGCCGTGTTCCCCTTCCCCTCCCCGGTTGT
125101  ACACCCCAGGCGTCCGCACGACCCGGGGGTCCGGCACAAGGGGAAGGGGAGGGGCCAACA

125161  AGATTTCAGCTGTTGCTGCCAGACCTGACCGGTTCCGGAGGTGGCCGCGCCCCACTCACT
125161  TCTAAAGTCGACAACGACGGTCTGGACTGGCCAAGGCCTCCACCGGCGCGGGGTGAGTGA

125221  GTCGCCTGCTTTCCACAGGGGACAAGCGCCTGTCCGACACGCCCTACGACAGCAGCGCCA
125221  CAGCGGACGAAAGGTGTCCCCTGTTCGCGGACAGGCTGTGCGGGATGCTGTCGTCGCGGT

125281  GCTACGAGAAGGAGAACGAAATGATGAAGTCCCACGTGATGGACCAAGCCATCAACAACG
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125281   CGATGCTCTTCCTCTTGCTTTACTACTTCAGGGTGCACTACCTGGTTCGGTAGTTGTTGC

125341   CCATCAACTACCTGGGGCCCGAGTCCCTGCCCCCGCTGGTGCAGACGCCCCCGGGCGGTT
125341   GGTAGTTGATGGACCCCGGGCTCAGGGACGGGGGCGACCACGTCTGCGGGGGCCCGCCAA

125401   CCGAGGTGGTCCCGGTCATCAGCCCGATGTACCAGCTGCACAAGCCGCTCGCGGAGGGCA
125401   GGCTCCACCAGGGCCAGTAGTCGGGCTACATGGTCGACGTGTTCGGCGAGCGCCTCCCGT

125461   CCCCGCGCTCCAACCACTCGGCCCAGGACAGCGCCGTGGAGAACCTGCTGCTGCTCTCCA
125461   GGGGCGCGAGGTTGGTGAGCCGGGTCCTGTCGCGGCACCTCTTGGACGACGACGAGAGGT

125521   AGGCCAAGTTGGTGCCCTCGGAGCGCGAGGCGTCCCCGAGCAACAGCTGCCAAGACTCCA
125521   TCCGGTTCAACCACGGGAGCCTCGCGCTCCGCAGGGGCTCGTTGTCGACGGTTCTGAGGT

125581   CGGACACCGAGAGCAACAACGAGGAGCAGCGCAGCGGTCTCATCTACCTGACCAACCACA
125581   GCCTGTGGCTCTCGTTGTTGCTCCTCGTCGCGTCGCCAGAGTAGATGGACTGGTTGGTGT

125641   TCGCCCCGCACGCGCGCAACGGGCTGTCGCTCAAGGAGGAGCACCGCGCCTACGACCTGC
125641   AGCGGGGCGTGCGCGCGTTGCCCGACAGCGAGTTCCTCCTCGTGGCGCGGATGCTGGACG

125701   TGCGCGCCGCCTCCGAGAACTCGCAGGACGCGCTCCGCGTGGTCAGCACCAGCGGGGAGC
125701   ACGCGCGGCGGAGGCTCTTGAGCGTCCTGCGCGAGGCGCACCAGTCGTGGTCGCCCCTCG

125761   AGATGAAGGTGTACAAGTGCGAACACTGCCGGGTGCTCTTCCTGGATCACGTCATGTACA
125761   TCTACTTCCACATGTTCACGCTTGTGACGGCCCACGAGAAGGACCTAGTGCAGTACATGT

125821   CCATCCACATGGGCTGCCACGGCTTCCGTGATCCTTTTGAGTGCAACATGTGCGGCTACC
125821   GGTAGGTGTACCCGACGGTGCCGAAGGCACTAGGAAAACTCACGTTGTACACGCCGATGG

125881   ACAGCCAGGACCGGTACGAGTTCTCGTCGCACATAACGCGAGGGGAGCACCGCTTCCACA
125881   TGTCGGTCCTGGCCATGCTCAAGAGCAGCGTGTATTGCGCTCCCCTCGTGGCGAAGGTGT

125941   TGAGCTAAAGCCCTCCCGCGCCCCCACCCCAGACCCCGAGCCACCCCAGGAAAAGCACAA
125941   ACTCGATTTCGGGAGGGCGCGGGGGTGGGGTCTGGGGCTCGGTGGGGTCCTTTTCGTGTT

126001   GGACTGCCGCCTTCTCGCTCCCGCCAGCAGCATAGACTGGACTGGACCAGACAATGTTGT
126001   CCTGACGGCGGAAGAGCGAGGGCGGTCGTCGTATCTGACCTGACCTGGTCTGTTACAACA

126061   GTTTGGATTTGTAACTGTTTTTTGTTTTTTGTTTGAGTTGGTTGATTGGGGTTTGATTTG
126061   CAAACCTAAACATTGACAAAAAACAAAAAACAAACTCAACCAACTAACCCCAAACTAAAC

126121   CTTTTGAAAAGATTTTTATTTTTAGAGGCAGGGCTGCATTGGGAGCATCCAGAACTGCTA
126121   GAAAACTTTTCTAAAAATAAAAATCTCCGTCCCGACGTAACCCTCGTAGGTCTTGACGAT

126181   CCTTCCTAGATGTTTCCCCAGACCGCTGGCTGAGATTCCCTCACCTGTCGCTTCCTAGAA
126181   GGAAGGATCTACAAAGGGGTCTGGCGACCGACTCTAAGGGAGTGGACAGCGAAGGATCTT

126241   TCCCCTTCTCCAAACGATTAGTCTAAATTTTCAGAGAGAAATAGATAAAACACGCCACAG
126241   AGGGGAAGAGGTTTGCTAATCAGATTTAAAAGTCTCTCTTTATCTATTTTGTGCGGTGTC

126301   CCTGGGAAGGAGCGTGCTCTACCCTGTGCTAAGCACGGGGTTCGCGCACCAGGTGTCTTT
126301   GGACCCTTCCTCGCACGAGATGGGACACGATTCGTGCCCCAAGCGCGTGGTCCACAGAAA

126361   TTCCAGTCCCCAGAAGCAGAGAGCACAGCCCCTGCTGTGTGGGTCTGCAGGTGAGCAGAC
126361   AAGGTCAGGGGTCTTCGTCTCTCGTGTCGGGGACGACACACCCAGACGTCCACTCGTCTG

126421   AGGACAGGTGTGCCGCCACCCAAGTGCCAAGACACAGCAGGGCCAACAACCTGTGCCCAG
126421   TCCTGTCCACACGGCGGTGGGTTCACGGTTCTGTGTCGTCCCGGTTGTTGGACACGGGTC

126481   GCCAGCTTCGAGCTACATGCATCTAGGGCGGAGAGGCTGCACTTGTGAGAGAAAATACTA
126481   CGGTCGAAGCTCGATGTACGTAGATCCCGCCTCTCCGACGTGAACACTCTCTTTTATGAT

126541   TTTCAAGTCATATTCTGCGTAGGAAAATGAATTGGTTGGGGAAAGTCGTGTCTGTCAGAC
126541   AAAGTTCAGTATAAGACGCATCCTTTTACTTAACCAACCCCTTTCAGCACAGACAGTCTG

126601   TGCCCTGGGTGGAGGGAGACGCCGGGCTAGAGCCTTTGGGATCGTCCTGGATTCACTGGC
126601   ACGGGACCCACCTCCCTCTGCGGCCCGATCTCGGAAACCCTAGCAGGACCTAAGTGACCG

126661   TTTGCGGAGGCTGCTCAGATGGCCTGAGCCTCCCGAGGCTTGCTGCCCCCTAGGAGGAGA
126661   AAACGCCTCCGACGAGTCTACCGGACTCGGAGGGCTCCGAACGACGGGGGATCCTCCTCT

126721   CTGTCTTCCCGTGGGCATATCTGGGGAGCCCTGTTCCCCGCTTTTTCACTCCCATACCTT
126721   GACAGAAGGGCACCCGTATAGACCCCTCGGGACAAGGGGCGAAAAAGTGAGGGTATGGAA
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126781  TAATGGCCCCCAAAATCTGTCACTACAATTTAAACACCAGTCCCGAAATTTGGATCTTCT
126781  ATTACCGGGGGTTTTAGACAGTGATGTTAAATTTGTGGTCAGGGCTTTAAACCTAGAAGA

126841  TTCTTTTTGAATCTCTCAAACGGCAACATTCCTCAGAAACCAAAGCTTTATTTCAAATCT
126841  AAGAAAAACTTAGAGAGTTTGCCGTTGTAAGGAGTCTTTGGTTTCGAAATAAAGTTTAGA

126901  CTTCCTTCCCTGGCTGGTTCCATCTAGTACCAGAGGCCTCTTTTCCTGAAGAAATCCAAT
126901  GAAGGAAGGGACCGACCAAGGTAGATCATGGTCTCCGGAGAAAAGGACTTCTTTAGGTTA

126961  CCTAGCCCTCATTTTAATTATGTACATCTGTTTGTAGCCACAAGCCTGAATTTCTCAGTG
126961  GGATCGGGAGTAAAATTAATACATGTAGACAAACATCGGTGTTCGGACTTAAAGAGTCAC

127021  TTGGTAAGTTTCTTTACCTACCCTCACTATATATTATTCTCGTTTTAAAACCCATAAAGG
127021  AACCATTCAAAGAAATGGATGGGAGTGATATATAATAAGAGCAAAATTTTGGGTATTTCC

127081  AGTGATTTAGAACAGTCATTAATTTTCAACTCAATGAAATATGTGAAGCCCAGCATCTCT
127081  TCACTAAATCTTGTCAGTAATTAAAAGTTGAGTTACTTTATACACTTCGGGTCGTAGAGA

127141  GTTGCTAACACACAGAGCTCACCTGTTTGAAACCAAGCTTTCAAACATGTTGAAGCTCTT
127141  CAACGATTGTGTGTCTCGAGTGGACAAACTTTGGTTCGAAAGTTTGTACAACTTCGAGAA

127201  TACTGTAAAGGCAAGCCAGCATGTGTGTCCACACATACATAGGATGGCTGGCTCTGCACC
127201  ATGACATTTCCGTTCGGTCGTACACACAGGTGTGTATGTATCCTACCGACCGAGACGTGG

127261  TGTAGGATATTGGAATGCACAGGGCAATTGAGGGACTGAGCCAGACCTTCGGAGAGTAAT
127261  ACATCCTATAACCTTACGTGTCCCGTTAACTCCCTGACTCGGTCTGGAAGCCTCTCATTA

127321  GCCACCAGATCCCCTAGGAAAGAGGAGGCAAATGGCACTGCAGGTGAGAACCCCGCCCAT
127321  CGGTGGTCTAGGGGATCCTTTCTCCTCCGTTTACCGTGACGTCCACTCTTGGGGCGGGTA

127381  CCGTGCTATGACATGGAGGCACTGAAGCCCGAGGAAGGTGTGTGGAGATTCTAATCCCAA
127381  GGCACGATACTGTACCTCCGTGACTTCGGGCTCCTTCCACACACCTCTAAGATTAGGGTT

127441  CAAGCAAGGGTCTCCTTCAAGATTAATGCTATCAATCATTAAGGTCATTACTCTCAACCA
127441  GTTCGTTCCCAGAGGAAGTTCTAATTACGATAGTTAGTAATTCCAGTAATGAGAGTTGGT

127501  CCTAGGCAATGAAGAATATACCATTTCAAATATTTACAGTACTTGTCTTCACCAACACTG
127501  GGATCCGTTACTTCTTATATGGTAAAGTTTATAAATGTCATGAACAGAAGTGGTTGTGAC

127561  TCCCAAGGTGAAATGAAGCAACAGAGAGGAAATTGTACATAAGTACCTCAGCATTTAATC
127561  AGGGTTCCACTTTACTTCGTTGTCTCTCCTTTAACATGTATTCATGGAGTCGTAAATTAG

127621  CAAACAGGGGTTCTTAGTCTCAGCACTATGACATTTTGGGCTGACTACTTATTTGTTAGG
127621  GTTTGTCCCCAAGAATCAGAGTCGTGATACTGTAAAACCCGACTGATGAATAAACAATCC

127681  CGGGAGCTCTCCTGTGCATTGTAGGATAATTAGCAGTATCCCTGGTGGCTACCCAATAGA
127681  GCCCTCGAGAGGACACGTAACATCCTATTAATCGTCATAGGGACCACCGATGGGTTATCT

127741  CGCCAGTAGCACCCCGAATTGACAACCCAAACTCTCCAGACATCACCAACTGTCCCCTGC
127741  GCGGTCATCGTGGGGCTTAACTGTTGGGTTTGAGAGGTCTGTAGTGGTTGACAGGGGACG

127801  GAGGAGAAATCACTCCTGGGGGAGAACCACTGACCCAAATGAATTCTAAACCAATCAAAT
127801  CTCCTCTTTAGTGAGGACCCCCTCTTGGTGACTGGGTTTACTTAAGATTTGGTTAGTTTA

127861  GTCTGGGAAGCCCTCCAAGAAAAAAAATAGAAAAGCACTTGAAGAATATTCCCAATATTC
127861  CAGACCCTTCGGGAGGTTCTTTTTTTTATCTTTTCGTGAACTTCTTATAAGGGTTATAAG

127921  CCGGTCAGCAGTATCAAGGCTGACTTGTGTTCATGTGGAGTCATTATAAATTCTATAAAT
127921  GGCCAGTCGTCATAGTTCCGACTGAACACAAGTACACCTCAGTAATATTTAAGATATTTA

127981  CAATTATTCCCCTTCGGTCTTAAAAATATATTTCCTCATAAACATTTGAGTTTTGTTGAA
127981  GTTAATAAGGGGAAGCCAGAATTTTTATATAAAGGAGTATTTGTAAACTCAAAACAACTT

128041  AAGATGGAGTTTACAAAGATACCATTCTTGAGTCATGGATTTCTCTGCTCACAGAAGGGT
128041  TTCTACCTCAAATGTTTCTATGGTAAGAACTCAGTACCTAAAGAGACGAGTGTCTTCCCA

128101  GTGGCATTTGGAAACGGGAATAAACAAAATTGCTGCACCAATGCACTGAGTGAAGGAAGA
128101  CACCGTAAACCTTTGCCCTTATTTGTTTTAACGACGTGGTTACGTGACTCACTTCCTTCT

128161  GAGACAGAGGATCAAGGGCTTTAGACAGCACTCCTTCAATATGCAATCACAGAGAAAGAT
128161  CTCTGTCTCCTAGTTCCCGAAATCTGTCGTGAGGAAGTTATACGTTAGTGTCTCTTTCTA
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128221  GCGCCTTATCCAAGTTAATATCTCTAAGGTGAGAGCCTTCTTAGAGTCAGTTTGTTGCAA
128221  CGCGGAATAGGTTCAATTATAGAGATTCCACTCTCGGAAGAATCTCAGTCAAACAACGTT

128281  ATTTCACCTACTCTGTTCTTTTCCATCCATCCCCCTGAGTCAGTTGGTTGAAGGGAGTTA
128281  TAAAGTGGATGAGACAAGAAAAGGTAGGTAGGGGGACTCAGTCAACCAACTTCCCTCAAT

128341  TTTTTTCAAGTGGAATTCAAACAAAGCTCAAACCAGAACTGTAAATAGTGATTGCAGGAA
128341  AAAAAAGTTCACCTTAAGTTTGTTTCGAGTTTGGTCTTGACATTTATCACTAACGTCCTT

128401  TTCTTTTCTAAACTGCTTTGCCCTTTCCTCTCACTGCCTTTTATAGCCAATATAAATGTC
128401  AAGAAAAGATTTGACGAAACGGGAAAGGAGAGTGACGGAAAATATCGGTTATATTTACAG

128461  TCTTTGCACACCTTTTGTTGTGGTTTTATATTGTAACACCATTTTTCTTTGAAACTATTG
128461  AGAAACGTGTGGAAAACAACACCAAAATATAACATTGTGGTAAAAAGAAACTTTGATAAC

128521  TATTTAAAGTAAGGTTTCATATTATGTCAGCAAGTAATTAACTTATGTTTAAAAGGTGGC
128521  ATAAATTTCATTCCAAAGTATAATACAGTCGTTCATTAATTGAATACAAATTTTCCACCG

128581  CATATCATGTACCAAAAGTTGCTGAAGTTTCTCTTCTAGCTGGTAAAGTAGGAGTTTGCA
128581  GTATAGTACATGGTTTTCAACGACTTCAAAGAGAAGATCGACCATTTCATCCTCAAACGT

128641  TGACTTCACACTTTTTTTGCGTAGTTTCTTCTGTTGTATGATGGCGTGAGTGTGTGTCTT
128641  ACTGAAGTGTGAAAAAAACGCATCAAAGAAGACAACATACTACCGCACTCACACACAGAA

128701  GGGTACCGCTGTGTACTACTGTGTGCCTAGATTCCATGCACTCTCGTTGTGTTTGAAGTA
128701  CCCATGGCGACACATGATGACACACGGATCTAAGGTACGTGAGAGCAACACAAACTTCAT

128761  AATATTGGAGACCGGAGGGTAACAGGTTGGCCTGTTGATTACAGCTAGTAATCGCTGTGT
128761  TTATAACCTCTGGCCTCCCATTGTCCAACCGGACAACTAATGTCGATCATTAGCGACACA

128821  CTTGTTCCGCCCCCTCCCTGACACCCCAGCTTCCCAGGATGTGGAAAGCCTGGATCTCAG
128821  GAACAAGGCGGGGGAGGGACTGTGGGGTCGAAGGGTCCTACACCTTTCGGACCTAGAGTC

128881  CTCCTTGCCCCATATCCCTTCTGTAATTTGTACCTAAAGAGTGTGATTATCCTAATTCAA
128881  GAGGAACGGGGTATAGGGAAGACATTAAACATGGATTTCTCACACTAATAGGATTAAGTT

128941  GAGTCACTAAAACTCATCACATTATCATTGCATATCAGCAAAGGGTAAAGTCCTAGCACC
128941  CTCAGTGATTTTGAGTAGTGTAATAGTAACGTATAGTCGTTTCCCATTTCAGGATCGTGG

129001  AATTGCTTCACATACCAGCATGTTCCATTTCCAATTTAGAATTAGCCACATAATAAAATC
129001  TTAACGAAGTGTATGGTCGTACAAGGTAAAGGTTAAATCTTAATCGGTGTATTATTTTAG

129061  TTAGAATCTTCCTTGAGAAAGAGCTGCCTGAGATGTAGTTTTGTTATATGGTTCCCCACC
129061  AATCTTAGAAGGAACTCTTTCTCGACGGACTCTACATCAAAACAATATACCAAGGGGTGG

129121  GACCATTTTTGTGCTTTTTTCTTGTTTTGTTTTGTTTTGACTGCACTGTGAGTTTTGTAG
129121  CTGGTAAAAACACGAAAAAAGAACAAAACAAAACAAAACTGACGTGACACTCAAAACATC

129181  TGTCCTCTTCTTGCCAAAACAAACGCGAGATGAACTGGACTTATGTAGACAAATCGTGAT
129181  ACAGGAGAAGAACGGTTTTGTTTGCGCTCTACTTGACCTGAATACATCTGTTTAGCACTA

129241  GCCAGTGTATCCTTCCTTTCTTCAGTTCCAGCAATAATGAATGGTCAACTTTTTTAAAAT
129241  CGGTCACATAGGAAGGAAAGAAGTCAAGGTCGTTATTACTTACCAGTTGAAAAAATTTTA

129301  CTAGATCTCTCTCATTCATTTCAATGTATTTTTACTTTAAGATGAACCAAAATTATTAGA
129301  GATCTAGAGAGAGTAAGTAAAGTTACATAAAAATGAAATTCTACTTGGTTTTAATAATCT

129361  CTTATTTAAGATGTACAGGCATCAGAAAAAAGAAGCACATAATGCTTTTGGTCCGATGGC
129361  GAATAAATTCTACATGTCCGTAGTCTTTTTTCTTCGTGTATTACGAAAACCAGGCTACCG

129421  ACTCACTGTGAACATGTGTAACCACATATTAATATGCAATATTGTTTCCAATACTTTCTA
129421  TGAGTGACACTTGTACACATTGGTGTATAATTATACGTTATAACAAAGGTTATGAAAGAT

129481  ATACAGTTTTTTATAATGTTGTGTGTGGTGATTGTTCAGGTCGAATCTGTTGTATCCAGT
129481  TATGTCAAAAAATATTACAACACACACCACTAACAAGTCCAGCTTAGACAACATAGGTCA

129541  ACAGCTTTAGGTCTTCAGCTGCCCTTCTGGCGAGTACATGCACAGGATTGTAAATGAGAA
129541  TGTCGAAATCCAGAAGTCGACGGGAAGACCGCTCATGTACGTGTCCTAACATTTACTCTT

129601  ATGCAGTCATATTTCCAGTCTGCCTCTATGATGATGTTAAATTATTGCTGTTTAGCTGTG
129601  TACGTCAGTATAAAGGTCAGACGGAGATACTACTACAATTTAATAACGACAAATCGACAC

129661  AACAAGGGATGTACCACTGGAGGAATAGAGTATCCTTTTGTACACATTTTGAAATGCTTC
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129661  TTGTTCCCTACATGGTGACCTCCTTATCTCATAGGAAAACATGTGTAAAACTTTACGAAG

129721  TTCTGTAGTGATAGAACAAATAAATGCAACGAATACTCTGTCTGCCCTATCCCGTGAAGT
129721  AAGACATCACTATCTTGTTTATTTACGTTGCTTATGAGACAGACGGGATAGGGCACTTCA

129781  CCACACTGGCGTAAGAGAAGGCCCAGCAGAGCAGGAATCTGCCTAGACTTTCTCCCAATG
129781  GGTGTGACCGCATTCTCTTCCGGGTCGTCTCGTCCTTAGACGGATCTGAAAGAGGGTTAC

129841  AGATCCCAATATGAGAGGGAGAAGAGATGGGCCTCAGGACAGCTGCAATACCACTTGGGA
129841  TCTAGGGTTATACTCTCCCTCTTCTCTACCCGGAGTCCTGTCGACGTTATGGTGAACCCT

129901  ACACATGTGGTGTCTTGATGTGGCCAGCGCAGCAGTTCAGCACAACGTACCTCCCATCTA
129901  TGTGTACACCACAGAACTACACCGGTCGCGTCGTCAAGTCGTGTTGCATGGAGGGTAGAT

129961  CAACAGTGCTGGACGTGGGAATTCTAAGTCCCAGTCTTGAGGGTGGGTGGAGATGGAGGG
129961  GTTGTCACGACCTGCACCCTTAAGATTCAGGGTCAGAACTCCCACCCACCTCTACCTCCC

130021  CAACAAGAGATACATTTCCAGTTCTCCACTGCAGCATGCTTCAGTCATTCTGTGAGTGGC
130021  GTTGTTCTCTATGTAAAGGTCAAGAGGTGACGTCGTACGAAGTCAGTAAGACACTCACCG

130081  CGGGCCCAGGGCCCTCACAATTTCACTACCTTGTCTTTTACATAGTCATAAGAATTATCC
130081  GCCCGGGTCCCGGGAGTGTTAAAGTGATGGAACAGAAAATGTATCAGTATTCTTAATAGG

130141  TCAACATAGCCTTTTGACGCTGTAAATCTTGAGTATTCATTTACCCTTTTCTGATCTCCT
130141  AGTTGTATCGGAAAACTGCGACATTTAGAACTCATAAGTAAATGGGAAAAGACTAGAGGA

130201  GGAAACAGCTGCCTGCCTGCATTGCACTTCTCTTCCCGAGGAGTGGGGTAAATTTAAAAG
130201  CCTTTGTCGACGGACGGACGTAACGTGAAGAGAAGGGCTCCTCACCCCATTTAAATTTTC

130261  TCAAGTTATAGTTTGGATGTTAGTATAGAATTTTGAAATTGGGAATTAAAAATCAGGACT
130261  AGTTCAATATCAAACCTACAATCATATCTTAAAACTTTAACCCTTAATTTTTAGTCCTGA

130321  GGGGACTGGGAGACCAAAAATTTCTGATCCCATTTCTGATGGATGTGTCACACCTTTTCT
130321  CCCCTGACCCTCTGGTTTTTAAAGACTAGGGTAAAGACTACCTACACAGTGTGGAAAAGA

130381  GTCAAAATAAAATGTCTTGGAGGTTATGACTCCTTGGTGAA
130381  CAGTTTTATTTTACAGAACCTCCAATACTGAGGAACCACTT
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