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(71) Applicant: **ALLEN INSTITUTE** [US/US]; 615 Westlake Avenue North, Seattle, Washington 98109 (US).

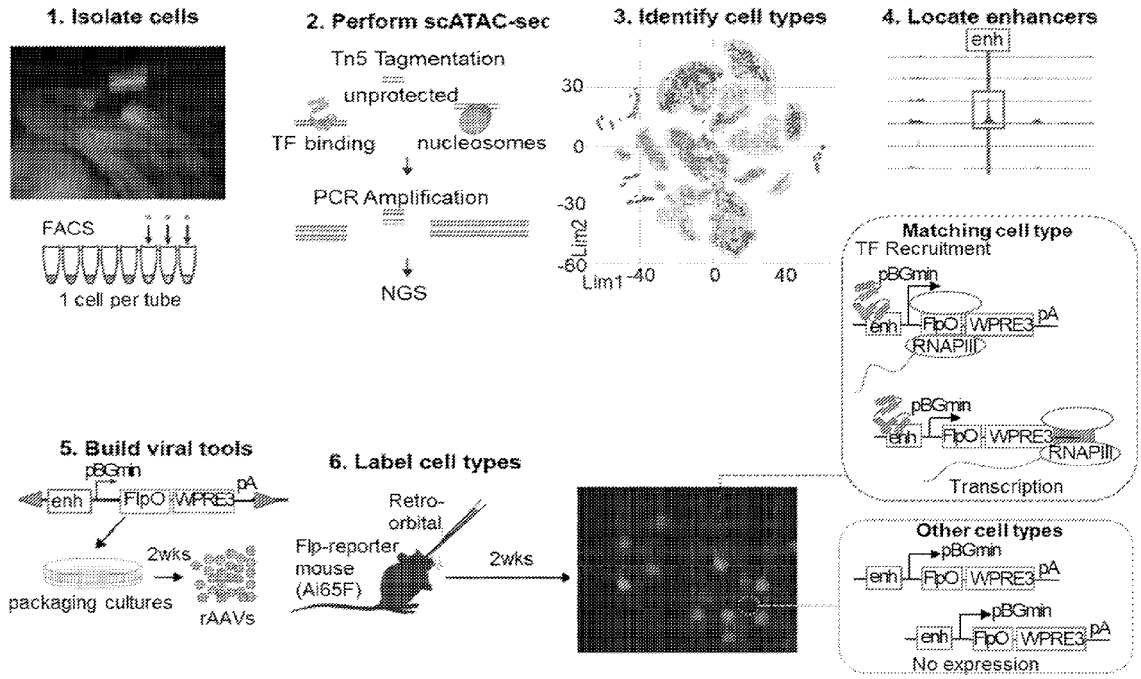
(72) Inventors: **DAIGLE, Tanya**; 615 Westlake Avenue North, Seattle, Washington 98109 (US). **LEIN, Edward Sebastian**; 615 Westlake Avenue North, Seattle, Washington 98109 (US). **LEVI, Boaz P.**; 615 Westlake Avenue North, Seattle, Washington 98109 (US). **MICH, John K.**; 615 Westlake Avenue North, Seattle, Washington 98109 (US). **TASIC, Bosiljka**; 615 Westlake Avenue North, Seattle, Washington 98109 (US). **TING, Jonathan**; 615 Westlake Avenue North, Seattle, Washington 98109 (US). **ZENG, Hongkui**; 615 Westlake Avenue North, Seattle, Washington 98109 (US).

(74) Agent: **WINGER, C. Rachal** et al.; Lee & Hayes PC, 601 W. Riverside Avenue Suite 1400, Spokane, Washington 99201 (US).

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(54) Title: ARTIFICIAL EXPRESSION CONSTRUCTS FOR MODULATING GENE EXPRESSION IN STRIATAL NEURONS

FIG. 1



(57) **Abstract:** Artificial expression constructs for modulating gene expression in striatal neurons are described. The artificial expression constructs can be used to express heterologous genes in striatal neurons including in striatal medium spiny neuron-pan, striatal medium spiny neuron-indirect pathway, striatal medium spiny neuron-direct pathway, striatal interneuron-cholinergic, and Drd3+ medium spiny neurons in olfactory tubercle. The artificial expression constructs can be used for many purposes, including to research and treat movement disorders such as Parkinson's disease and Huntington's disease.

[Continued on next page]

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— *as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii))*

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ARTIFICIAL EXPRESSION CONSTRUCTS FOR MODULATING GENE EXPRESSION IN STRIATAL NEURONS

CROSS-REFERENCE TO RELATED APPLICATION

[0001] This application claims priority to U.S. Provisional Patent Application No. 63/066,008 filed on August 14, 2020, which is incorporated herein by reference in its entirety as if fully set forth herein.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

[0002] This invention was made with government support under MH114126 awarded by the National Institutes of Health. The government has certain rights in the invention.

REFERENCE TO SEQUENCE LISTING

[0003] The Sequence Listing associated with this application is provided in text format in lieu of a paper copy and is hereby incorporated by reference into the specification. The name of the text file containing the Sequence Listing is 2JG2543.txt. The text file is 367 KB, was created on August 13, 2021 and is being submitted electronically via EFS-Web.

FIELD OF THE DISCLOSURE

[0004] The current disclosure provides artificial expression constructs for modulating gene expression in striatal neurons. The artificial expression constructs can be used for many purposes, including in the research and treatment of movement disorders.

BACKGROUND OF THE DISCLOSURE

[0005] To fully understand the biology of the brain, different cell types need to be distinguished and defined and, to further study them, artificial expression constructs that can label and perturb them need to be identified. In mouse, recombinase driver lines have been used to great effect to label cell populations that share marker gene expression. However, the creation, maintenance, and use of such lines that label cell types with high specificity can be costly, frequently requiring triple transgenic crosses, which yield a low frequency of experimental animals. Furthermore, those tools require germline transgenic animals and thus are not applicable to humans.

[0006] A movement disorder is a neurological disturbance that involves one or more muscles or muscle groups. Movement disorders affect a significant portion of the population, causing disability as well as distress. Movement disorders include Parkinson's disease, Huntington's chorea, progressive supranuclear palsy, Wilson's disease, Tourette's syndrome, epilepsy, tardive

dyskinesia, and various chronic tremors, tics and dystonias.

[0007] Parkinson's disease is a movement disorder of increasing occurrence in aging populations. It affects one percent of the population over the age of 60 in the United States, such that the cumulative lifetime risk of an individual developing the disease is 1 in 40. Symptoms include pronounced tremor of the extremities, bradykinesia, rigidity and postural change. A perceived pathophysiological cause of Parkinson's disease is progressive destruction of dopamine producing cells in the basal ganglia which include the pars compacta of the substantia nigra. Parkinson's disease is a progressive disorder which can begin with mild limb stiffness and infrequent tremors and progress over a period of ten or more years to frequent tremors and memory impairment, to uncontrollable tremors and dementia.

[0008] Huntington's disease (HD) is a dominantly inherited neurodegenerative genetic disorder that affects muscle coordination and leads to cognitive decline and psychiatric problems. HD is due to mutations in the gene encoding for huntingtin, and it is the most common genetic cause of abnormal involuntary writhing movements called chorea. The most prominent early effects in HD are in a part of the basal ganglia called the neostriatum, which is composed of the caudate nucleus and putamen. Symptoms of the disease can vary between individuals, but usually progress predictably. The earliest symptoms are often subtle problems with mood or cognition, followed by a general lack of coordination and an unsteady gait. In advanced stages of the disease, uncoordinated, jerky body movements become more apparent, along with a decline in mental abilities, as well as behavioral and psychiatric problems. Physical abilities are gradually impeded until coordinated movement becomes very difficult, and mental abilities generally decline into dementia. Although the genetic basis of the pathology is well known there is not yet a cure for HD.

SUMMARY OF THE DISCLOSURE

[0009] The current disclosure provides artificial expression constructs that drive gene expression in striatal neurons. The artificial expression constructs can be used for many purposes, including in the research and treatment of movement disorders.

[0010] Particular embodiments of the artificial expression constructs utilize the following enhancers to drive gene expression within targeted central nervous system cell populations as follows:

striatal medium spiny neuron-pan: eHGT_608h, eHGT_609h, eHGT_633h, eHGT_634h, eHGT_635h, eHGT_636h, eHGT_351h, eHGT_367h, eHGT_450h, eHGT_447h, eHGT_744m, eHGT_782m, eHGT_785m, and eHGT_441h;

striatal medium spiny neuron-indirect pathway: eHGT_612h, eHGT_613h, eHGT_614h, eHGT_617h, eHGT_618h, eHGT_619h, eHGT_620h, eHGT_442h, eHGT_444h, eHGT_445h, eHGT_452h, and eHGT_784m;

striatal medium spiny neuron-direct pathway: eHGT_610h, eHGT_611h, eHGT_615h, eHGT_616h, eHGT_627h, eHGT_628h, eHGT_629h, eHGT_446h, eHGT_779m, eHGT_780m, eHGT_781m, and eHGT_783m;

striatal interneuron-cholinergic: eHGT_622h, eHGT_623h, eHGT_624h, eHGT_625h, eHGT_630h, eHGT_631h, eHGT_735m, eHGT_736m, eHGT_737m, eHGT_738m, eHGT_739m, eHGT_740m, eHGT_741m, eHGT_742m, eHGT_743m, eHGT_746m, eHGT_747m, eHGT_748m, eHGT_749m, eHGT_750m, and eHGT_751m;

Drd3+ medium spiny neurons in olfactory tubercle: eHGT_621h.

[0011] In particular embodiments, the artificial enhancer elements include a concatenated core of an enhancer. Examples include a core or concatenated core of eHGT_367h, eHGT_441h, eHGT_445h, eHGT_444h, eHGT_452h, eHGT_779m, eHGT_743m, eHGT_621h, eHGT_780m, eHGT_447h, eHGT_351h, and/or eHGT_450h. These artificial enhancer elements can provide higher levels and more rapid onset of transgene expression compared to a single full length original (native) enhancer.

[0012] In particular embodiments, the enhancer core includes the sequence as set forth in any one of SEQ ID NOs: 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, and 226. In particular embodiments, these cores are concatenated and have 2, 3, 4, 5, 6, 7, 8, 9, or 10 copies of the core sequence. SEQ ID NOs: 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, and 227 provide three-copy concatemers of the described enhancer cores.

[0013] Particular embodiments of the artificial expression constructs utilize core2_eHGT_367h, 3xcore2_eHGT_367h, 3xcore_eHGT_441h, 3xCore-eHGT_447h, and/or 3xcore2_eHGT_351h to drive gene expression within striatal medium spiny neuron-pan.

[0014] Particular embodiments of the artificial expression constructs utilize 3xcore2_eHGT_445h, 3xCore2_eHGT_444h, 3xcore2_eHGT_452h, 3xcore2_eHGT_450h, and/or 3xcore3_eHGT_450h to drive gene expression within striatal medium spiny neuron-indirect pathway.

[0015] Particular embodiments of the artificial expression constructs utilize 3xcore2_eHGT_779m and/or 3xCore2_eHGT_780m to drive gene expression within striatal medium spiny neuron-direct pathway.

[0016] Particular embodiments of the artificial expression constructs utilize 3xcore2_eHGT_743m to drive gene expression within striatal interneuron-cholinergic.

[0017] Particular embodiments of the artificial expression constructs utilize 3xcore-eHGT_621h to drive gene expression within Drd3+ medium spiny neurons in olfactory tubercle.

[0018] Particular embodiments provide artificial expression constructs including the features of vectors described herein including vectors: CN2438, CN2439, CN2451, CN2463, CN2464, CN2465, CN2466, CN2013, CN2025, CN2229, CN2442, CN2443, CN2444, CN2447, CN2448, CN2449, CN2450, CN2467, CN2421, CN2231, CN2236, CN2237, CN2440, CN2441, CN2445, CN2446, CN2457, CN2458, CN2459, CN2232, CN2233, CN2452, CN2453, CN2454, CN2455, CN2460, CN2461, CN2628, CN2641, CN2642, CN2643, CN2629, CN2630, CN2745, CN2746, CN2631, CN2747, CN2632, CN2644, CN2748, CN2633, CN2634, CN2635, CN2609, CN2610, CN2749, CN2626, CN2611, CN2750, CN2614, CN2485, CN2486, CN2739, CN2740, CN2765, CN2766, CN2514, CN2555, CN2907, CN2909, CN2921, CN2982, CN3044, CN3038, CN3344, CN3281, CN3346, CN3566, CN2912, CN2913, CN2966, CN2203, and CN2700.

BRIEF DESCRIPTION OF THE FIGURES

[0019] Some of the drawings submitted herein are better understood in color. Applicant considers the color versions of the drawings as part of the original submission and reserves the right to present color images of the drawings in later proceedings.

[0020] FIG. 1: Putative enhancers were selected from the Icahn School of Medicine Brain Open Chromatin Atlas (BOCA) associated with Fullard et al, 2018 Genome Research (doi:10.1101/gr.232488.117) or the snATAC-seq dataset available through the open access web portal called CATlas (Cis-element Atlas): catlas.org/mousebrain/#!/. These regions were cloned upstream of a minimal promoter in an AAV genomic backbone, which was used to generate recombinant adeno-associated viral vectors (rAAVs) or plasmid AAVs (pAAVs). These viral tools were delivered retro-orbitally to label specific striatal populations. In cells with a matching cell type, enhancers recruit their cognate transcription factors to drive cell type-specific expression. In other cells, viral genomes are present, but transcripts are not expressed.

[0021] FIGs. 2A,2B. (2A) Fluorescent reporter expression in mouse brain tissue following retro-orbital injection of CN2514 serotype PHPeB. Scale bar: 1 mm. (2B) Higher magnification view of SYFP2 expression in the boxed dorsal striatum region from FIG. 2A. Scale bar: 500 microns. Abbreviations: Ctx-cortex, Hipp-hippocampus, Str-striatum, SNr-substantia nigra pars reticulata, GPe-globus pallidus external. CP-caudoputamen, CB-cerebellum.

[0022] FIGs. 3A-3G. A C57Bl/6J (wild-type) mouse was injected with 1.0E+12 viral genomes of CN2514 serotype PHP.eB virus via the retro-orbital sinus. Representative two-photon tomography (TissueCyte) images of the native SYFP2 fluorescence in coronal brain sections are

shown four weeks post-injection. FIGs. 3A, 3C, 3E show the full coronal section at different planes in the brain (moving anterior to posterior) and (3B, 3D, 3F) show higher magnification view of the boxed areas in the corresponding FIGs. 3A, 3C, and 3E, respectively. Abbreviations: PALd = dorsal pallidum (3G) TissueCyte imaging datasets were processed using an established informatics pipeline (Oh et al., Nature 2014, 508: 207-214) and registered to the CCFv3.0 (Wang et al., Cell 2020, 181(4):936-953.e20). Segmented pixel counts or voxels for each brain region were used for analysis and density dot plots of these data in all cortical (left = left hemisphere and right = right hemisphere) and subcortical structures are shown. Dark black, large circles = brain regions with most SYFP2 signal and small, light circles = brain regions with little to no SYFP2 signal. See FIG. 21 for full list of abbreviated brain structures.

[0023] FIGs. 4A, 4B. (4A) Fluorescent reporter expression in mouse brain tissue following retro-orbital injection of CN2555 serotype PHPeB. Scale bar: 1 mm. (4B) Higher magnification view of SYFP2 expression in the boxed dorsal striatum region from FIG. 4A. Scale bar: 500 microns.

[0024] FIGs. 5A-5G. A C57Bl/6J (wild-type) mouse was injected with 1.0E+12 viral genomes of CN2555 serotype PHP.eB virus via the retro-orbital sinus. Representative two-photon tomography (TissueCyte) images of the native SYFP2 fluorescence in coronal brain sections are shown four weeks post-injection. FIGs. 5A, 5C, 5E show the full coronal section at different planes in the brain (moving anterior to posterior) and (5B, 5D, 5F) show higher magnification view of the boxed areas in the corresponding FIGs. 5A, 5C, 5E, respectively. (5G) TissueCyte imaging datasets were processed using an established informatics pipeline (Oh et al., Nature 2014, 508: 207-214) and registered to the CCFv3.0 (Wang et al., Cell 2020, 181(4):936-953.e20). Segmented pixel counts or voxels for each brain region were used for analysis and density dot plots of these data in all cortical (left = left hemisphere and right = right hemisphere) and subcortical structures are shown. Dark black, large circles = brain regions with most SYFP2 signal and small, light circles = brain regions with little to no SYFP2 signal. See FIG. 21 for full list of abbreviated brain structures.

[0025] FIGs. 6A, 6B. (6A) Fluorescent reporter expression in mouse brain tissue following retro-orbital injection of CN2025 serotype PHPeB. Scale bar: 1 mm. (6B) Higher magnification view of SYFP2 expression in the boxed dorsal striatum region from FIG. 6A. Scale bar: 100 microns.

[0026] FIGs. 7A-7G. A C57Bl/6J (wild-type) mouse was injected with 1.0E+12 viral genomes of CN2025 serotype PHP.eB virus via the retro-orbital sinus. Representative two-photon tomography (TissueCyte) images of the native SYFP2 fluorescence in coronal brain sections are shown four weeks post-injection. FIGs. 7A, 7C, 7E show the full coronal section at different planes in the brain (moving anterior to posterior) and (7B, 7D, 7F) show higher magnification view of the

boxed areas in the corresponding FIGs. 7A, 7C, and 7E, respectively. (7G) TissueCyte imaging datasets were processed using an established informatics pipeline (Oh et al., Nature 2014, 508: 207-214) and registered to the CCFv3.0 (Wang et al., Cell 2020, 181(4):936-953.e20). Segmented pixel counts or voxels for each brain region were used for analysis and density dot plots of these data in all cortical (left = left hemisphere and right = right hemisphere) and subcortical structures are shown. Dark black, large circles = brain regions with most SYFP2 signal and small, light circles = brain regions with little to no SYFP2 signal. See FIG. 21 for full list of abbreviated brain structures.

[0027] FIGs. 8A-8C. (8A) Fluorescent reporter expression in mouse brain tissue following retro-orbital injection of CN2233 serotype PHPeB. Scale bar: 1 mm. (8B) Higher magnification view of SYFP2 expression in the dorsal striatum region from FIG. 8A. Scale bar: 100 microns. (8C) Fluorescent reporter expression in rat brain tissue following injection of CN2233 serotype PHPeB into the lateral ventricle at P2 and tissue harvest at P19. Scale bar: 1 mm. Abbreviation: OT-olfactory tubercle.

[0028] FIGs. 9A-9G. A C57Bl/6J (wild-type) mouse was injected with 1.0E+12 viral genomes of CN2233 serotype PHP.eB virus via the retro-orbital sinus. Representative two-photon tomography (TissueCyte) images of the native SYFP2 fluorescence in coronal brain sections are shown four weeks post-injection. FIGs. 9A, 9C, 9E show the full coronal section at different planes in the brain (moving anterior to posterior) and (9B, 9D, 9F) show higher magnification view of the boxed areas in the corresponding FIGs. 9A, 9C, 9E, respectively. (9G) TissueCyte imaging datasets were processed using an established informatics pipeline (Oh et al., Nature 2014, 508: 207-214) and registered to the CCFv3.0 (Wang et al., Cell 2020, 181(4):936-953.e20). Segmented pixel counts or voxels for each brain region were used for analysis and density dot plots of these data in all cortical (left = left hemisphere and right = right hemisphere) and subcortical structures are shown. Dark black, large circles = brain regions with most SYFP2 signal and small, light circles = brain regions with little to no SYFP2 signal. See FIG. 21 for full list of abbreviated brain structures.

[0029] FIGs. 10A, 10B. (10A) Fluorescent reporter expression in mouse brain tissue following retro-orbital injection of CN2236 serotype PHPeB. Scale bar: 1 mm. (10B) Higher magnification view of SYFP2 expression in the boxed dorsal striatum region from FIG. 10A. Scale bar: 100 microns.

[0030] FIGs. 11A-11G. A C57Bl/6J (wild-type) mouse was injected with 1.0E+12 viral genomes of CN2236 serotype PHP.eB virus via the retro-orbital sinus. Representative two-photon tomography (TissueCyte) images of the native SYFP2 fluorescence in coronal brain sections are

shown four weeks post-injection. FIGs. 11A, 11C, 11E show the full coronal section at different planes in the brain (moving anterior to posterior) and (11B, 11D, 11F) show higher magnification view of the boxed areas in the corresponding FIGs. 11A, 11C, 11E, respectively. (11G) TissueCyte imaging datasets were processed using an established informatics pipeline (Oh et al., Nature 2014, 508: 207-214) and registered to the CCFv3.0 (Wang et al., Cell 2020, 181(4):936-953.e20). Segmented pixel counts or voxels for each brain region were used for analysis and density dot plots of these data in all cortical (left = left hemisphere and right = right hemisphere) and subcortical structures are shown. Dark black, large circles = brain regions with most SYFP2 signal and small, light circles = brain regions with little to no SYFP2 signal. See FIG. 21 for full list of abbreviated brain structures.

[0031] FIGs. 12A, 12B. (12A) Fluorescent reporter expression in mouse brain tissue following retro-orbital injection of CN2237 serotype PHPeB. Scale bar: 1 mm. (12B) Higher magnification view of SYFP2 expression in the boxed dorsal striatum region from FIG. 12A. Scale bar: 500 microns.

[0032] FIGs. 13A-13G. A C57Bl/6J (wild-type) mouse was injected with 1.0E+12 viral genomes of CN2237 serotype PHP.eB virus via the retro-orbital sinus. Representative two-photon tomography (TissueCyte) images of the native SYFP2 fluorescence in coronal brain sections are shown four weeks post-injection. FIGs. 13A, 13C, 13E show the full coronal section at different planes in the brain (moving anterior to posterior) and (13B, 13D, 13F) show higher magnification view of the boxed areas in the corresponding FIGs. 13A, 13C, 13E, respectively. (13G) TissueCyte imaging datasets were processed using an established informatics pipeline (Oh et al., Nature 2014, 508: 207-214) and registered to the CCFv3.0 (Wang et al., Cell 2020, 181(4):936-953.e20). Segmented pixel counts or voxels for each brain region were used for analysis and density dot plots of these data in all cortical (left = left hemisphere and right = right hemisphere) and subcortical structures are shown. Dark black, large circles = brain regions with most SYFP2 signal and small, light circles = brain regions with little to no SYFP2 signal. See FIG. 21for full list of abbreviated brain structures.

[0033] FIG. 14A-14C: In vivo stereotaxic injection of CN2700 (packaged as serotype PHP.eB) into macaque caudate and putamen region. (14A) anti-DARPP-32 signal reveals Basal ganglia brain structures. (14B) Fluorescent reporter mTFP1 expression was detected in caudate and putamen. Scale bar: 1 mm. (14C) Higher magnification view of mTFP1 expression in the boxed putamen region from FIG. 14B. Scale bar: 500 microns. Abbreviations: GPi-globus pallidus internal segment.

[0034] FIGs. 15A-15C. (15A) Fluorescent reporter expression in mouse brain tissue following

retro-orbital injection of CN2609 serotype PHPeB. Scale bar: 1 mm. (15B) Higher magnification view of SYFP2 expression in the dorsal striatum region (box) from FIG. 19A showing neuronal profiles. Scale bar: 250 microns. (15C) Higher magnification view of SYFP2 signal in the white boxed region in FIG. 15A and containing GPe and SNr structures. Prominent axon signal is detected in SNr but not GPe. Scale bar: 1 mm.

[0035] FIGs. 16A-16G. A C57Bl/6J (wild-type) mouse was injected with 1.0E+12 viral genomes of CN2609 serotype PHP.eB virus via the retro-orbital sinus. Representative two-photon tomography (TissueCyte) images of the native SYFP2 fluorescence in coronal brain sections are shown four weeks post-injection. FIGs. 16A, 16C, 16E show the full coronal section at different planes in the brain (moving anterior to posterior) and (16B, 16D, 16F) show higher magnification view of the boxed areas in the corresponding FIGs. 16A, 16C, 16E, respectively. (16G) TissueCyte imaging datasets were processed using an established informatics pipeline (Oh et al., Nature 2014, 508: 207-214) and registered to the CCFv3.0 (Wang et al., Cell 2020, 181(4):936-953.e20). Segmented pixel counts or voxels for each brain region were used for analysis and density dot plots of these data in all cortical (left = left hemisphere and right = right hemisphere) and subcortical structures are shown. Dark black, large circles = brain regions with most SYFP2 signal and small, light circles = brain regions with little to no SYFP2 signal. See FIG. 21for full list of abbreviated brain structures.

[0036] FIGs. 17A-17H. (17A) Fluorescent reporter expression in mouse brain tissue following retro-orbital injection of CN2631 serotype PHPeB. Scale bar: 1 mm. (17B) Higher magnification view of SYFP2 expression in the boxed dorsal striatum region from FIG. 17A. Scale bar: 100 microns. (17C) anti-GFP signal in mouse caudoputamen following retro-orbital injection of CN2631 serotype PHPeB. (17D) Anti-ChAT signal in the same region from FIG. 17A. (17E) Overlay of signal from FIGs. 17C and 17D showing colocalization of anti-GFP and anti-ChAT signal. Scale bar: 100 microns. (17F-17H) Enhancer: eHGT_743m; Animal: 557822; Vector: CN2631; Region: dorsal striatum. Multiplexed fluorescent in situ hybridization (mFISH) analysis of CN2631 labeling specificity in mouse dorsal striatum region showing 90% (9/10) of labeled neurons are ChAT positive striatal cholinergic interneurons. (17F) SYFP2 probe signal, (17G) overlay of SYFP2 and ChAT probe signals, and (17H) ChAT probe signal. Circles represent SYFP2+/ChAT+ cells and diamonds represent SYFP2+/ChAT- cells.

[0037] FIGs. 18A-18G. A C57Bl/6J (wild-type) mouse was injected with 1.0E+12 viral genomes of CN2631 serotype PHP.eB virus via the retro-orbital sinus. Representative two-photon tomography (TissueCyte) images of the native SYFP2 fluorescence in coronal brain sections are shown four weeks post-injection. FIGs. 18A, 18C, 18E show the full coronal section at different

planes in the brain (moving anterior to posterior) and (18B, 18D, 18F) show higher magnification view of the boxed areas in the corresponding FIGs. 18A, 18C, 18E, respectively. (18G) TissueCyte imaging datasets were processed using an established informatics pipeline (Oh et al., Nature 2014, 508: 207-214) and registered to the CCFv3.0 (Wang et al., Cell 2020, 181(4):936-953.e20). Segmented pixel counts or voxels for each brain region were used for analysis and density dot plots of these data in all cortical (left = left hemisphere and right = right hemisphere) and subcortical structures are shown. Dark black, large circles = brain regions with most SYFP2 signal and small, light circles = brain regions with little to no SYFP2 signal. See FIG. 21 for full list of abbreviated brain structures.

[0038] FIGs. 19A-19E. (19A) Fluorescent reporter expression in mouse brain tissue following retro-orbital injection of CN2451 serotype PHPeB. Scale bar: 1 mm. (19B) Higher magnification view of SYFP2 expression in the boxed region from FIG. 19A. Scale bar: 1 mm. (19C) Fluorescent reporter expression in rat brain tissue following injection of CN2451 serotype PHPeB into the lateral ventricle at P2 and tissue harvest at P19. Scale bar: 1 mm. (19C-19E) Multiplexed fluorescent in situ hybridization (mFISH) analysis of CN2451 labeling specificity in mouse olfactory tubercle region showing 68/71 or 96% of labeled neurons are Drd3 positive neurons. (19C) SYFP2 probe signal, (19D) overlay of SYFP2 and Drd3 probe signals, and (19E) Drd3 probe signal. Circles represent SYFP2+/Drd3+ cells and diamonds represent SYFP2+/Drd3- cells.

[0039] FIGs. 20A, 20B. (20A) Vector designs for enhancer-driven AADC expression in striatal medium spiny neurons. (20B) Anti-HA antibody staining of the mouse striatum after retro-orbital injection of AAV virus packaged with PHP.eB. Image is a montage of a sagittal section of a mouse brain.

[0040] FIG. 21. Table of abbreviations of brain structures.

[0041] FIGs. 22A-22C. (22A) Enhancer names, lengths, and sequences including eHGT_608h (SEQ ID NO: 1); eHGT_609h (SEQ ID NO: 2); eHGT_621h (SEQ ID NO: 3); Core-eHGT_621h (SEQ ID NO: 202); 3xCore-eHGT_621h (SEQ ID NO: 203); eHGT_633h (SEQ ID NO: 4); eHGT_634h (SEQ ID NO: 5); eHGT_635h (SEQ ID NO: 6); eHGT_636h (SEQ ID NO: 7); eHGT_351h (SEQ ID NO: 8); core2_eHGT_351h (SEQ ID NO: 204); 3xcore2_eHGT_351h (SEQ ID NO: 205); eHGT_367h (SEQ ID NO: 9); core2_eHGT_367h (SEQ ID NO: 206); 3xcore2_eHGT_367h (SEQ ID NO: 207); eHGT_441h (SEQ ID NO: 10); core_eHGT_441h (SEQ ID NO: 208); 3xcore_eHGT_441h (SEQ ID NO: 209); eHGT_612h (SEQ ID NO: 11); eHGT_613h (SEQ ID NO: 12); eHGT_614h (SEQ ID NO: 13); eHGT_617h (SEQ ID NO: 14); eHGT_618h (SEQ ID NO: 15); eHGT_619h (SEQ ID NO: 16); eHGT_620h (SEQ ID NO: 17); eHGT_442h

(SEQ ID NO: 18); eHGT_444h (SEQ ID NO: 19); core2_eHGT_444h (SEQ ID NO: 210); 3xcore2_eHGT_444h (SEQ ID NO: 211); eHGT_445h (SEQ ID NO: 20); core2_eHGT_445h (SEQ ID NO: 212); 3xcore2_eHGT_445h (SEQ ID NO: 213); eHGT_450h (SEQ ID NO: 21); core2_eHGT_450h (SEQ ID NO: 214); 3xcore2_eHGT_450h (SEQ ID NO: 215); core3_eHGT_450h (SEQ ID NO: 216); 3xcore3_eHGT_450h (SEQ ID NO: 217); eHGT_452h (SEQ ID NO: 22); core2_eHGT_452h (SEQ ID NO: 218); 3xcore2_eHGT_452h (SEQ ID NO: 219); eHGT_610h (SEQ ID NO: 23); eHGT_611h (SEQ ID NO: 24); eHGT_615h (SEQ ID NO: 25); eHGT_616h (SEQ ID NO: 26); eHGT_627h (SEQ ID NO: 27); eHGT_628h (SEQ ID NO: 28); eHGT_629h (SEQ ID NO: 29); eHGT_446h (SEQ ID NO: 30); eHGT_447h (SEQ ID NO: 31); Core-eHGT_447h (SEQ ID NO: 220); 3xCore-eHGT_447h (SEQ ID NO: 221); eHGT_622h (SEQ ID NO: 32); eHGT_623h (SEQ ID NO: 33); eHGT_624h (SEQ ID NO: 34); eHGT_625h (SEQ ID NO: 35); eHGT_630h (SEQ ID NO: 36); eHGT_631h (SEQ ID NO: 37); eHGT_735m (SEQ ID NO: 39); eHGT_736m (SEQ ID NO: 40); eHGT_737m (SEQ ID NO: 41); eHGT_738m (SEQ ID NO: 42); eHGT_739m (SEQ ID NO: 43); eHGT_740m (SEQ ID NO: 44); eHGT_741m (SEQ ID NO: 45); eHGT_742m (SEQ ID NO: 46); eHGT_743m (SEQ ID NO: 47); core2_eHGT_743m (SEQ ID NO: 222); 3xcore2_eHGT_743m (SEQ ID NO: 223 eHGT_744m (SEQ ID NO: 48); eHGT_746m (SEQ ID NO: 49); eHGT_747m (SEQ ID NO: 50); eHGT_748m (SEQ ID NO: 51); eHGT_749m (SEQ ID NO: 52); eHGT_750m (SEQ ID NO: 53); eHGT_751m (SEQ ID NO: 54); eHGT_779m (SEQ ID NO: 55); core2_eHGT_779m (SEQ ID NO: 224); 3xcore2_eHGT_779m (SEQ ID NO: 225); eHGT_780m (SEQ ID NO: 56); Core2_eHGT_780m (SEQ ID NO: 226); 3xCore2_eHGT_780m (SEQ ID NO: 227); eHGT_781m (SEQ ID NO: 57); eHGT_782m (SEQ ID NO: 58); eHGT_783m (SEQ ID NO: 59); eHGT_784m (SEQ ID NO: 60); and eHGT_785m (SEQ ID NO: 61). (22B) Vector names, lengths (between ITRs), and sequences including CN2438 (SEQ ID NO: 62); CN2439 (SEQ ID NO: 63); CN2451 (SEQ ID NO: 64); CN2463 (SEQ ID NO: 65); CN2464 (SEQ ID NO: 66); CN2465 (SEQ ID NO: 67); CN2466 (SEQ ID NO: 68); CN2013 (SEQ ID NO: 69); CN2025 (SEQ ID NO: 70); CN2229 (SEQ ID NO: 71); CN2442 (SEQ ID NO: 72); CN2443 (SEQ ID NO: 73); CN2444 (SEQ ID NO: 74); CN2447 (SEQ ID NO: 75); CN2448 (SEQ ID NO: 76); CN2449 (SEQ ID NO: 77); CN2450 (SEQ ID NO: 78); CN2467 (SEQ ID NO: 79); CN2421 (SEQ ID NO: 80); CN2231 (SEQ ID NO: 81); CN2236 (SEQ ID NO: 82); CN2237 (SEQ ID NO: 83); CN2440 (SEQ ID NO: 84); CN2441 (SEQ ID NO: 85); CN2445 (SEQ ID NO: 86); CN2446 (SEQ ID NO: 87); CN2457 (SEQ ID NO: 88); CN2458 (SEQ ID NO: 89); CN2459 (SEQ ID NO: 90); CN2232 (SEQ ID NO: 91); CN2233 (SEQ ID NO: 92); CN2452 (SEQ ID NO: 93); CN2453 (SEQ ID NO: 94); CN2454 (SEQ ID NO: 95); CN2455 (SEQ ID NO: 96); CN2460 (SEQ ID NO: 97); CN2461 (SEQ ID NO: 98); CN2628 (SEQ ID NO: 100); CN2641 (SEQ ID NO: 101);

CN2642 (SEQ ID NO: 102); CN2643 (SEQ ID NO: 103); CN2629 (SEQ ID NO: 104); CN2630 (SEQ ID NO: 105); CN2745 (SEQ ID NO: 106); CN2746 (SEQ ID NO: 107); CN2631 (SEQ ID NO: 108); CN2747 (SEQ ID NO: 109); CN2632 (SEQ ID NO: 110); CN2644 (SEQ ID NO: 111); CN2748 (SEQ ID NO: 112); CN2633 (SEQ ID NO: 113); CN2634 (SEQ ID NO: 114); CN2635 (SEQ ID NO: 115); CN2609 (SEQ ID NO: 116); CN2610 (SEQ ID NO: 117); CN2749 (SEQ ID NO: 118); CN2626 (SEQ ID NO: 119); CN2611 (SEQ ID NO: 120); CN2750 (SEQ ID NO: 121); CN2614 (SEQ ID NO: 122); CN2485 (SEQ ID NO: 228); CN2486 (SEQ ID NO: 229); CN2739 (SEQ ID NO: 230); CN2740 (SEQ ID NO: 231); CN2765 (SEQ ID NO: 232); CN2766 (SEQ ID NO: 233); CN2514 (SEQ ID NO: 234); CN2555 (SEQ ID NO: 235); CN2907 (SEQ ID NO: 236); CN2909 (SEQ ID NO: 237); CN2921 (SEQ ID NO: 238); CN2982 (SEQ ID NO: 239); CN3044 (SEQ ID NO: 240); CN3038 (SEQ ID NO: 241); CN3344 (SEQ ID NO: 242); CN3281 (SEQ ID NO: 243); CN3346 (SEQ ID NO: 244); CN3566 (SEQ ID NO: 245); CN2912 (SEQ ID NO: 246); CN2913 (SEQ ID NO: 247); CN2966 (SEQ ID NO: 248); CN2203 (SEQ ID NO: 249); and CN2700 (SEQ ID NO: 250). (22C) Exemplary sequences of subcomponents for use with artificial expression constructs disclosed herein including Beta-Globin Minimal Promoter (pBGmin/minBGlobin/minBGprom) (SEQ ID NO: 123); minCMV Promoter (SEQ ID NO: 124); Mutated minCMV Promoter (SacI RE site removed) (SEQ ID NO: 125); minRho Promoter (SEQ ID NO: 126); minRho* Promoter (SEQ ID NO:127); Hsp68 minimal Promoter (proHsp68) (SEQ ID NO: 128); SYFP2 (SEQ ID NO: 129); EGFP (SEQ ID NO: 130); Optimized Flp recombinase (FlpO) (SEQ ID NO: 131); Improved Cre recombinase (iCre) (SEQ ID NO: 132); SP10 insulator (SP10ins) (SEQ ID NO: 133); 3xSP10ins (SEQ ID NO: 134); 3xHA tag nucleotide sequence (SEQ ID NO: 251); WPRE3 (SEQ ID NO: 135); WPRE (SEQ ID NO: 136); BGHpA (SEQ ID NO: 137); HGHpA (SEQ ID NO: 138); P2A (SEQ ID NO: 139); T2A (SEQ ID NO: 140); E2A (SEQ ID NO: 141); F2A (SEQ ID NO: 142); Exemplary Plasmid Backbone 1 – Left ITR (SEQ ID NO: 143); Exemplary Plasmid Backbone 1 – Right ITR (SEQ ID NO: 144); Exemplary Plasmid Backbone 2 – Left ITR (SEQ ID NO: 145); Exemplary Plasmid Backbone 2 – Right ITR (SEQ ID NO: 146); PHP.eB capsid (SEQ ID NO: 147); AAV9 VP1 capsid protein (SEQ ID NO: 148); tet-Transactivator version 2 (tTA2) (SEQ ID NO: 149); Aromatic L-amino acid decarboxylase (AADC) mRNA (SEQ ID NO: 150); rAAV-hAADC-vector gene insert (SEQ ID NO: 151); Tyrosine hydroxylase (TH) mRNA (SEQ ID NO: 152); GTP cyclohydrolase I (CH1) mRNA (SEQ ID NO: 153); Glucocerebrosidase (SEQ ID NO: 154); GBA1 gene product Isoform 2 (SEQ ID NO: 155); GBA1 gene product Isoform 3 (SEQ ID NO: 156); Human Huntingtin gene of exon 1 (SEQ ID NO: 157); Target sequence of human huntingtin gene of exon 1 (SEQ ID NO: 158); GTPase HRas (SEQ ID NO: 159); GCaMP6m (SEQ ID NO: 160); GCaMP6s (SEQ ID NO: 161); and GCaMP6f (SEQ ID

NO: 162).

DETAILED DESCRIPTION

[0042] To fully understand the biology of the brain, different cell types need to be distinguished and defined and, to further study them, artificial expression constructs that can label and perturb them need to be identified (Tasic, Curr. Opin. Neurobiol. 50, 242–249 (2018); Zeng & Sanes, Nat. Rev. Neurosci. 18, 530–546 (2017)). In mouse, recombinase driver lines have been used to great effect to label cell populations that share marker gene expression (Daigle et al., Cell 174, 465–480.e22 (2018); Taniguchi, et al., Neuron 71, 995–1013 (2011); Gong et al., J. Neurosci. 27, 9817–9823 (2007)). However, the creation, maintenance, and use of such lines that label cell types with high specificity can be costly, frequently requiring triple transgenic crosses, which yield a low frequency of experimental animals. Furthermore, those tools require germline transgenic animals and thus are not applicable to humans.

[0043] A movement disorder is a neurological disturbance that involves one or more muscles or muscle groups. Movement disorders affect a significant portion of the population, causing disability as well as distress. Movement disorders include Parkinson's disease, Huntington's chorea, progressive supranuclear palsy, multiple system atrophy (MSA), Aromatic L-amino acid decarboxylase (AADC) deficiency, Wilson's disease, Tourette's syndrome, epilepsy, tardive dyskinesia, and various chronic tremors, tics and dystonias.

[0044] Parkinson's disease is a movement disorder of increasing occurrence in aging populations. It affects one percent of the population over the age of 60 in the United States, such that the cumulative lifetime risk of an individual developing the disease is 1 in 40. Symptoms include pronounced tremor of the extremities, bradykinesia, rigidity and postural change. A perceived pathophysiological cause of Parkinson's disease is progressive destruction of dopamine producing cells in the basal ganglia which include the pars compacta of the substantia nigra. Parkinson's disease is a progressive disorder which can begin with mild limb stiffness and infrequent tremors and progress over a period of ten or more years to frequent tremors and memory impairment, to uncontrollable tremors and dementia. Although not a cure for Parkinson’s disease, dopamine replacement, including treatment with the dopamine precursor levodopa (L-DOPA), is an effective therapeutic strategy.

[0045] In vivo, dopamine is synthesized from tyrosine by two enzymes, tyrosine hydroxylase (TH) and aromatic L-amino acid decarboxylase (AADC). In particular embodiments, TH can be a truncated form of the TH gene which avoids end-product feed-back inhibition by dopamine. Functional activity of TH depends on the availability of its cofactor tetrahydrobiopterin (BH4). GTP

cyclohydrolase I (CH1) is the enzyme that catalyses the rate limiting step on the pathway of BH4-synthesis, to ensure that sufficient levels of the dopamine precursor, L-Dopa, are produced in vivo.

[0046] AADC is the enzyme responsible for the final step in the synthesis of dopamine. AADC deficiency is a rare genetic disorder believed to arise from mutation of the DDC gene (dopa decarboxylase). AADC deficiency results in severe developmental failures, global muscular hypotonia and dystonia, severe, long-lasting seizures known as oculo-gyric crises, frequent hospitalizations (including prolonged stays in intensive care), and the need for life-long care. Symptoms and severity vary depending on the type of underlying genetic mutation which abrogates AADC enzyme function. In particular embodiments, AADC includes human AADC (hAADC).

[0047] Mutations in *GBA1*, the gene encoding the lysosomal enzyme glucocerebrosidase (GCase), are linked to increased risk of Parkinson disease and Gaucher disease. Mutations in GBA1 may result in degradation of the enzyme and thus affect its function. Furthermore, the severity of PD symptoms correlate with the degree of enzyme activity reduction. GCase is a membrane-associated lysosomal hydrolase with 497 amino acids that cleaves, by hydrolysis, the beta-glucosidic linkage of glucocerebroside.

[0048] Tardive dyskinesia (TD) is a chronic disorder of the nervous system, characterized by involuntary, irregular rhythmic movements of the mouth, tongue, and facial muscles. The upper extremities also may be involved. These movements may be accompanied, to a variable extent, by other involuntary movements and movement disorders. These include rocking, writhing, or twisting movements of the trunk (tardive dystonia), forcible eye closure (tardive blepharospasm), an irresistible impulse to move continually (tardive akathisia), jerking movements of the neck (tardive spasmodic torticollis), and disrupted respiratory movements (respiratory dyskinesia).

[0049] Focal dystonias are a class of related movement disorders involving the intermittent sustained contraction of a group of muscles. The spasms of focal dystonia can last many seconds at a time, causing major disruption of the function of the affected area. Some of the focal dystonias are precipitated by repetitive movements; writer's cramp is the best-known example. Focal dystonia can involve the face (e.g., blepharospasm, mandibular dystonia), the neck (torticollis), the limbs (e.g., writer's cramp), or the trunk. Dystonia can occur spontaneously or can be precipitated by exposure to neuroleptic drugs and other dopamine receptor blockers (tardive dystonia).

[0050] A tic is an abrupt repetitive movement, gesture, or utterance that often mimics a normal type of behavior. Motor tics include movements such as eye blinking, head jerks or shoulder

shrugs, but can vary to more complex purposive appearing behaviors such as facial expressions of emotion or meaningful gestures of the arms and head. Gilles de la Tourette syndrome (TS) is the most severe tic disorder. Patients with TS have multiple tics, including at least one vocal (phonic) tic. TS becomes apparent in early childhood with the presentation of simple motor tics, for example, eye blinking or head jerks. Initially, tics may come and go, but in time tics become persistent and severe, and begin to have adverse effects on the child and the child's family. Phonic tics manifest, on average, 1 to 2 years after the onset of motor tics.

[0051] Huntington's disease (HD) is a dominantly inherited neurodegenerative genetic disorder that affects muscle coordination and leads to cognitive decline and psychiatric problems. HD is due to mutations in the gene encoding for huntingtin, and it is the most common genetic cause of abnormal involuntary writhing movements called chorea. The most prominent early effects in HD are in a part of the basal ganglia called the neostriatum, which is composed of the caudate nucleus and putamen. Symptoms of the disease can vary between individuals, but usually progress predictably. The earliest symptoms are often subtle problems with mood or cognition, followed by a general lack of coordination and an unsteady gait. In advanced stages of the disease, uncoordinated, jerky body movements become more apparent, along with a decline in mental abilities, as well as behavioral and psychiatric problems. Physical abilities are gradually impeded until coordinated movement becomes very difficult, and mental abilities generally decline into dementia.

[0052] The problematic genetic mutation within the HTT gene involves a DNA segment of the huntingtin gene known as the CAG trinucleotide repeat. Normally, the CAG segment in the huntingtin gene of humans is repeated multiple times, i.e. 10-35 times. People with 36 to 39 CAG repeats may develop signs and symptoms of Huntington disease, while people with 40 or more repeats almost always develop the disorder. The increase in the size of the CAG repeat leads to the production of an elongated (mutated) huntingtin protein. This protein is processed in the cell into smaller fragments that are cytotoxic and that accumulate and aggregate in neurons. This results in the disruption of normal function and eventual death of neurons. Hypotheses on the molecular mechanisms underlying the neurotoxicity of polyglutamine-expanded HTT protein and its resultant aggregates have been wide ranging, but include, caspase activation, dysregulation of transcriptional pathways, increased production of reactive oxygen species, mitochondrial dysfunction, disrupted axonal transport and/or inhibition of protein degradation systems within the cell.

[0053] The current disclosure provides artificial expression constructs that drive gene expression in striatal neurons. The artificial expression constructs can be used for many purposes, including in the research and treatment of movement disorders.

[0054] Particular embodiments of the artificial expression constructs utilize the following enhancers to drive gene expression within targeted central nervous system cell populations as follows:

striatal medium spiny neuron-pan: eHGT_608h, eHGT_609h, eHGT_633h, eHGT_634h, eHGT_635h, eHGT_636h, eHGT_351h, eHGT_367h, eHGT_450h, eHGT_447h, eHGT_744m, eHGT_782m, eHGT_785m, and eHGT_441h;

striatal medium spiny neuron-indirect pathway: eHGT_612h, eHGT_613h, eHGT_614h, eHGT_617h, eHGT_618h, eHGT_619h, eHGT_620h, eHGT_442h, eHGT_444h, eHGT_445h, eHGT_452h, and eHGT_784m;

striatal medium spiny neuron-direct pathway: eHGT_610h, eHGT_611h, eHGT_615h, eHGT_616h, eHGT_627h, eHGT_628h, eHGT_629h, eHGT_446h, eHGT_779m, eHGT_780m, eHGT_781m, and eHGT_783m;

striatal interneuron-cholinergic: eHGT_622h, eHGT_623h, eHGT_624h, eHGT_625h, eHGT_630h, eHGT_631h, eHGT_735m, eHGT_736m, eHGT_737m, eHGT_738m, eHGT_739m, eHGT_740m, eHGT_741m, eHGT_742m, eHGT_743m, eHGT_746m, eHGT_747m, eHGT_748m, eHGT_749m, eHGT_750m, and eHGT_751m;

Drd3+ medium spiny neurons in olfactory tubercle: eHGT_621h.

[0055] In particular embodiments, the artificial enhancer elements include a concatenated core of an enhancer. Examples include a core or concatenated core of eHGT_367h, eHGT_441h, eHGT_445h, eHGT_444h, eHGT_452h, eHGT_779m, eHGT_743m, eHGT_621h, eHGT_780m, eHGT_447h, eHGT_351h, and/or eHGT_450h. These artificial enhancer elements can provide higher levels and more rapid onset of transgene expression compared to a single full length original (native) enhancer.

[0056] In particular embodiments, the enhancer core includes the sequence as set forth in any one of SEQ ID NOs: 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, and 226. In particular embodiments, these cores are concatenated and have 2, 3, 4, 5, 6, 7, 8, 9, or 10 copies of the core sequence. SEQ ID NOs: 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, and 227 provide three-copy concatemers of the described enhancer cores.

[0057] Particular embodiments of the artificial expression constructs utilize core2_eHGT_367h, 3xcore2_eHGT_367h, 3xcore_eHGT_441h, 3xCore-eHGT_447h, and/or 3xcore2_eHGT_351h to drive gene expression within striatal medium spiny neuron-pan.

[0058] Particular embodiments of the artificial expression constructs utilize 3xcore2_eHGT_445h, 3xcore2_eHGT_444h, 3xcore2_eHGT_452h, 3xcore2_eHGT_450h, and/or 3xcore3_eHGT_450h to drive gene expression within striatal medium spiny neuron-indirect pathway.

[0059] Particular embodiments of the artificial expression constructs utilize 3xcore2_eHGT_779m and/or 3xCore2_eHGT_780m to drive gene expression within striatal medium spiny neuron-direct pathway.

[0060] Particular embodiments of the artificial expression constructs utilize 3xcore2_eHGT_743m to drive gene expression within striatal interneuron-cholinergic.

[0061] Particular embodiments of the artificial expression constructs utilize 3xcore-eHGT_621h to drive gene expression within Drd3+ medium spiny neurons in olfactory tubercle.

[0062] Particular embodiments provide artificial expression constructs including the features of vectors described herein including vectors:CN2438, CN2439, CN2451, CN2463, CN2464, CN2465, CN2466, CN2013, CN2025, CN2229, CN2442, CN2443, CN2444, CN2447, CN2448, CN2449, CN2450, CN2467, CN2421, CN2231, CN2236, CN2237, CN2440, CN2441, CN2445, CN2446, CN2457, CN2458, CN2459, CN2232, CN2233, CN2452, CN2453, CN2454, CN2455, CN2460, CN2461, CN2628, CN2641, CN2642, CN2643, CN2629, CN2630, CN2745, CN2746, CN2631, CN2747, CN2632, CN2644, CN2748, CN2633, CN2634, CN2635, CN2609, CN2610, CN2749, CN2626, CN2611, CN2750, CN2614, CN2485, CN2486, CN2739, CN2740, CN2765, CN2766, CN2514, CN2555, CN2907, CN2909, CN2921, CN2982, CN3044, CN3038, CN3344, CN3281, CN3346, CN3566, CN2912, CN2913, CN2966, CN2203, and CN2700.

[0063] Aspects of the disclosure are now described with the following additional options and detail: (i) Artificial Expression Constructs & Vectors for Targeted Expression of Genes in Targeted Cell Types; (ii) Compositions for Administration (iii) Cell Lines Including Artificial Expression Constructs; (iv) Transgenic Animals; (v) Methods of Use; (vi) Kits and Commercial Packages; (vii) Exemplary Embodiments; and (viii) Closing Paragraphs. These headings are provided for organizational purposes only and do not limit the scope or interpretation of the disclosure.

[0064] (i) Artificial Expression Constructs & Vectors for Targeted Expression of Genes in Targeted Cell Types. Artificial expression constructs disclosed herein include (i) an enhancer sequence that leads to targeted expression of a coding sequence within a targeted central nervous system cell type, (ii) a coding sequence that is expressed, and (iii) a promoter. The artificial expression construct can also include other regulatory elements if necessary or beneficial. These headings do not limit the interpretation of the disclosure and are provided for organizational purposes only.

[0065] In particular embodiments, an "enhancer" or an "enhancer element" is a cis-acting sequence that increases the level of transcription associated with a promoter and can function in either orientation relative to the promoter and the coding sequence that is to be transcribed and can be located upstream or downstream relative to the promoter or the coding sequence to be transcribed. There are art-recognized methods and techniques for measuring function(s) of enhancer element sequences. Particular examples of enhancer sequences utilized within artificial expression constructs disclosed herein include eHGT_608h, eHGT_609h, eHGT_621h, eHGT_633h, eHGT_634h, eHGT_635h, eHGT_636h, eHGT_351h, eHGT_367h, eHGT_441h, eHGT_612h, eHGT_613h, eHGT_614h, eHGT_617h, eHGT_618h, eHGT_619h, eHGT_620h, eHGT_442h, eHGT_444h, eHGT_445h, eHGT_450h, eHGT_452h, eHGT_610h, eHGT_611h, eHGT_615h, eHGT_616h, eHGT_627h, eHGT_628h, eHGT_629h, eHGT_446h, eHGT_447h, eHGT_622h, eHGT_623h, eHGT_624h, eHGT_625h, eHGT_630h, eHGT_631h, eHGT_735m, eHGT_736m, eHGT_737m, eHGT_738m, eHGT_739m, eHGT_740m, eHGT_741m, eHGT_742m, eHGT_743m, eHGT_744m, eHGT_746m, eHGT_747m, eHGT_748m, eHGT_749m, eHGT_750m, eHGT_751m, eHGT_779m, eHGT_780m, eHGT_781m, eHGT_782m, eHGT_783m, eHGT_784m, and eHGT_785m, and enhancer core core2_eHGT_367h,_and concatenated cores, such as 3xcore2_eHGT_367h, 3xcore_eHGT_441h, 3xCore-eHGT_621h, 3xCore-eHGT_447h, 3xcore2_eHGT_351h, 3xcore2_eHGT_445h, 3xcore2_eHGT_444h, 3xcore2_eHGT_452h, 3xcore2_eHGT_450h, 3xcore3_eHGT_450h, 3xcore2_eHGT_779m, 3xCore2_eHGT_780m, and 3xcore2_eHGT_743m.

[0066] In particular embodiments, a targeted central nervous system cell type enhancer is an enhancer that is uniquely or predominantly utilized by the targeted central nervous system cell type. A targeted central nervous system cell type enhancer enhances expression of a gene in the targeted central nervous system cell type.

[0067] When a heterologous coding sequence operatively linked to an enhancer disclosed herein leads to expression in a targeted cell type, it leads to expression of the administered heterologous coding sequence in the intended cell type.

[0068] When a heterologous coding sequence is selectively expressed in selected cells, it leads to expression of the administered heterologous coding sequence in the intended cell type and is not substantially expressed in other cell types, as explained in additional detail below. In particular embodiments, not substantially expressed in other cell types is less than 50% expression in a reference cell type as compared to a targeted cell type; less than 40% expression in a reference cell type as compared to a targeted cell type; less than 30% expression in a reference cell type

as compared to a targeted cell type; less than 20% expression in a reference cell type as compared to a targeted cell type; or less than 10% expression in a reference cell type as compared to a targeted cell type. In particular embodiments, a reference cell type refers to non-targeted cells. The non-targeted cells can be within the same anatomical structure as the targeted cells and/or can project to a common anatomical area. In particular embodiments, a reference cell type is within an anatomical structure that is adjacent to an anatomical structure that includes the targeted cell type. In particular embodiments, a reference cell type is a non-targeted cell with a different gene expression profile than the targeted cells.

[0069] In particular embodiments, the product of the coding sequence may be expressed at low levels in non-targeted cell types, for example at less than 1% or 1%, 2%, 3%, 5%, 10%, 15% or 20% of the levels at which the product is expressed in targeted cell types. In particular embodiments, the targeted central nervous system cell type is the only cell type that expresses the right combination of transcription factors that bind an enhancer disclosed herein to drive gene expression. Thus, in particular embodiments, expression occurs exclusively within the selected cell type.

[0070] In particular embodiments, targeted cell types (e.g. neuronal, and/or non-neuronal) can be identified based on transcriptional profiles, such as those described in Tasic et al., Nature, 563, 72-78 (2018) and Hodge et al., Nature 573, 61-68 (2019). For reference, the following description of cell types and distinguishing features is also provided:

[0071] Targeted Striatal Cell Classes:

[0072] The striatum (Str) is important in translating cortical activity into voluntary motor actions. Regarding the striatum, corresponding structures in human/primate are called the putamen, caudate, and ventral striatum containing the nucleus accumbens. In rodent, the striatum includes the dorsal striatum plus the nucleus accumbens. Thus, in human/primate, the putamen and caudate collectively are the equivalent of the rodent dorsal striatum.

[0073] Striatal cell Classes and Subclasses:

- Medium spiny neurons, pan: include 95% of striatal neurons and known to express GABA synthesis genes Gad1/GAD1 and Gad2/GAD2, as well as Ppp1r1b/PPP1R1B. Medium spiny neurons expressing Drd3 are herein referred to as Drd3+ medium spiny neurons.
- Medium spiny neurons, direct pathway-projecting: include nearly 50% of striatal neurons and are enriched for expression of Drd1/DRD1, Pdyn/PDYN, and Slc35d3/SLC35D3. The major axon projection from direct pathway medium spiny neurons is to the substantia nigra pars reticulata (SNr) or to the inner division of the globus pallidus (GPi).

- Medium spiny neurons, indirect pathway-projecting: include nearly 50% of striatal neurons and are enriched for expression of Drd2/DRD2, Adora2a/ADORA2A, Gpr6/GPR6, and Penk/PENK. The major axon projection from indirect pathway medium spiny neurons is to the external segment of the globus pallidus (GPe).
- Striatal interneuron-cholinergic: A rare interneuron population including 1% of striatal neurons. These local interneurons have large somata and aspiny dendrites and are known to express Chat/CHAT and release the neurotransmitter acetylcholine.

[0074] Neocortical GABAergic neuron Subclasses:

- All: Express GABA synthesis genes Gad1/GAD1 and Gad2/GAD2.
- Lamp5, Sncg, Serpinf1, and Vip GABAergic neurons: Developmentally derived from neuronal progenitors from the caudal ganglionic eminence (CGE) or preoptic area (POA).
- Sst and Pvalb GABAergic neurons: Developmentally derived from neuronal progenitors in the medial ganglionic eminence (MGE).
- Lamp5 GABAergic neurons: Found in many neocortical layers, especially upper (L1-L2/3), and have mainly neurogliaform and single bouquet morphology.
- *Lamp5_Lhx6* GABAergic neurons: A subset of *Lamp5* GABAergic neurons that co-express *Lamp5* and *Lhx6*.
- Sncg GABAergic neurons: Found in many neocortical layers, and have molecular overlaps with Lamp5 and Vip cells, but inconsistent expression of Lamp5 or Vip, with more consistent expression of Sncg.
- Serpinf1 GABAergic neurons: Found in many neocortical layers, and have molecular overlaps with Sncg and Vip cells, but inconsistent expression of Sncg or Vip, with more consistent expression of Serpinf1.
- Vip GABAergic neurons: Found in many neocortical layers, but especially frequent in upper layers (L1-L4), and highly express the neurotransmitter vasoactive intestinal peptide (Vip).
- Sst GABAergic neurons: Found in many neocortical layers, but especially frequent in lower layers (L5-L6). They highly express the neurotransmitter somatostatin (Sst), and frequently block dendritic inputs to postsynaptic neurons. Included in this subclass are sleep-active Sst Chodl neurons (which also express Nos1 and Tacr1) that are highly distinct from other Sst neurons but express some shared marker genes including Sst. In human, SST gene expression is often detected in layer 1 LAMP5+ GABAergic neuron subtypes.

- Pvalb GABAergic neurons: Found in many neocortical layers, but especially frequent in lower layers (L5-L6). They highly express the calcium-binding protein parvalbumin (Pvalb), express neuropeptide Tac1, and frequently dampen the output of postsynaptic neurons. Most fast-spiking GABAergic neurons express Pvalb strongly. Included in this subclass are chandelier cells, which have distinct, chandelier-like morphology and express the markers Cpne5 and Vipr2 in mouse, and NOG and UNC5B in human.
- Meis2: A distinct subclass defined by a single type, only neocortical GABAergic neuron type that expresses Meis2 gene, and does not express some other genes that are expressed by all other neocortical GABAergic neuron types (for example, Thy1 and Scn2b). This type is found in L6b and subcortical white matter.

[0075] Neocortical Glutamatergic neuron Subclasses:

- All: Express glutamate transmitters Slc17a6 and/or Slc17a7. They all express Snap25 and lack expression of Gad1/Gad2.
- L2/3 IT glutamatergic neurons: Primarily reside in Layer 2/3 and have mainly intratelencephalic (cortico-cortical) projections.
- L4 IT glutamatergic neurons: Primarily reside in Layer 4 and mainly have either local or intratelencephalic (cortico-cortical) projections.
- L5 IT glutamatergic neurons: Primarily reside in Layer 5 and have mainly intratelencephalic (cortico-cortical) projections. Also called L5a.
- L5 PT glutamatergic neurons: Primarily reside in Layer 5 and have mainly cortico-subcortical (pyramidal tract or corticofugal) projections. Also called L5b or L5 CF (corticofugal) or L5 ET (extratelencephalic). This subclass includes cells that are located in the primary motor cortex and neighboring areas and are corticospinal projection neurons, which are associated with motor neuron/movement disorders, such as ALS. This subclass includes thick-tufted pyramidal neurons, including distinctive cell types found only in specialized regions, e.g. Betz cells, Meynert cells, and von Economo cells.
- L5 NP glutamatergic neurons: Primarily reside in Layer 5 and have mainly nearby projections.
- L6 CT glutamatergic neurons: Primarily reside in Layer 6 and have mainly cortico-thalamic projections.
- L6 IT glutamatergic neurons: Primarily reside in Layer 6 and have mainly intratelencephalic (cortico-cortical) projections.
- L6 IT Car3 glutamatergic neurons: Most densely present in claustrum and endopyriform

nucleus, and sparsely throughout L6 in many cortical areas including the primary visual cortex. These cells have mainly intratelencephalic (cortico-cortical) projections. Additional marker genes for claustrum enriched neurons include *Gnb4* and *Ntng2*.

- L6b glutamatergic neurons: Primarily reside in the neocortical subplate (L6b), with local (near the cell body) projections and some cortico-cortical projections from VISp to anterior cingulate, and cortico-subcortical projections to the thalamus.
- CR neurons: A distinct subclass defined by a single type in L1, Cajal-Retzius cells express distinct molecular markers Lhx5 and Trp73.

[0076] The cerebellum is located at the posterior of the brain. The cerebellum processes inputs from the cerebral motor cortex, different brainstem nuclei, and sensory receptors. Two types of neurons play major roles in the cerebellar ciruit, including Purkinje cells and granule cells. The cerebellum also receives dopaminergic, serotonergic, noradrenergic, and cholinergic inputs.

- Cerebellar Purkinje cells: large GABAergic neurons that are the only projection neurons and the sole output from the cerebellum. Their cell bodies form a single layer, so called 'Purkinje cell layer', and they express parvalbumin.
- Deep cerebellar nucleus neurons: neurons located in the deep cerebellar nuclei structures. These include glutamatergic and GABAergic cells that express the gene Pvalb.

[0077] Non-neuronal Subclasses:

- Astrocytes: Neuroectoderm-derived glial cells which express the marker Aqp4 and often GFAP, but do not express neuronal marker SNAP25. They can have a distinct star-shaped morphology and are involved in metabolic support of other cells in the brain. Multiple astrocyte morphologies are observed in mouse and human
- Oligodendrocytes: Neuroectoderm-derived glial cells, which express the marker Sox10. This category includes oligodendrocyte precursor cells (OPCs). Oligodendrocytes are the subclass that is primarily responsible for myelination of neurons.
- VLMCs: Vascular leptomeningeal cells (VLMCs) are part of the meninges that surround the outer layer of the cortex and express the marker genes Lum and Col1a1.
- Pericytes: Blood vessel-associated cells that express the marker genes Kcnj8 and Abcc9. Pericytes wrap around endothelial cells and are important for regulation of capillary blood flow and are involved in blood-brain barrier permeability.
- SMCs: Specialized smooth-muscle cells which are blood vessel-associated cells that express the marker gene Acta2. SMCs cover arterioles in the brain and are involved in blood-brain barrier permeability.

- Endothelial cells: Cells that line blood vessels of the brain. Endothelial cells express the markers Tek and PDGF-B.
- Microglia: hematopoietic-derived immune cells, which are brain-resident macrophages, and perivascular macrophages (PVMs) that may be transitionally associated with brain tissue or included as a biproduct of brain dissection methods. Microglia are known to express Cx3cr1, Tmem119, and PTPRC (CD45).

[0078] Olfactory Tubercle (OT): The olfactory tubercle is a multi-sensory processing center that is located on the ventral surface of the frontal lobe. The olfactory tubercle has outputs directed towards the thalamus, ventral pallidum, nucleus accumbens, and in some primates the orbitofrontal cortex.

[0079] Cortex (Ctx) The cortex is the outer layer of the brain (also reffered to as the grey matter). The four lobes of the cortex include the frontal lobe, parietal lobe, temporal lobe, and occipital lobe.

[0080] Hippocampus (Hipp): The hippocampus is a C-shaped brain structure embedded deep into the temporal lobe. The hippocampus is the posterior part of limbic lobe while the frontal part is amygdala. The hippocampus is known to play a role in learning, memory and spatial navigation.

[0081] Caudoputamen (CP): The caudoputamen is also referred to as the dorsal striatum is one of the structures that form the basal ganglia.

[0082] Dorsal Pallidum (PALd): The dorsal pallidum is also referred to as the globus pallidus. The globus pallidus is a subcortical structure of the brain including an external (referred to as globus pallidus external segment (GPe)) and an internal (referred to as globus pallidus internal segment (GPi)) segment.

[0083] In particular embodiments, a coding sequence is a heterologous coding sequence that encodes an effector element. An effector element is a sequence that is expressed to achieve, and that in fact achieves, an intended effect. Examples of effector elements include reporter genes/proteins and functional genes/proteins.

[0084] Exemplary reporter genes/proteins include those expressed by Addgene ID#s 83894 (pAAV-hDlx-Flex-dTomato-Fishell_7), 83895 (pAAV-hDlx-Flex-GFP-Fishell_6), 83896 (pAAV-hDlx-GiDREADD-dTomato-Fishell-5), 83898 (pAAV-mDlx-ChR2-mCherry-Fishell-3), 83899 (pAAV-mDlx-GCaMP6f-Fishell-2), 83900 (pAAV-mDlx-GFP-Fishell-1), and 89897 (pcDNA3-FLAG-mTET2 (N500)). Exemplary reporter genes particularly can include those which encode an expressible fluorescent protein, or expressible biotin; blue fluorescent proteins (*e.g.* eBFP, eBFP2, Azurite, mKalama1, GFPuv, Sapphire, T-sapphire); cyan fluorescent proteins (*e.g.* eCFP, Cerulean, CyPet, AmCyanl, Midoriishi-Cyan, mTurquoise); green fluorescent proteins (*e.g.* GFP,

GFP-2, tagGFP, turboGFP, EGFP, Emerald, Azami Green, Monomeric Azami Green (mAzamigreen), CopGFP, AceGFP, avGFP, ZsGreenl, Oregon Green™(Thermo Fisher Scientific)); Luciferase; orange fluorescent proteins (mOrange, mKO, Kusabira-Orange, Monomeric Kusabira-Orange, mTangerine, tdTomato, dTomato); red fluorescent proteins (mKate, mKate2, mPlum, DsRed monomer, mCherry, mRuby, mRFP1, DsRed-Express, DsRed2, DsRed-Monomer, HcRed-Tandem, HcRedl, AsRed2, eqFP611, mRaspberry, mStrawberry, Jred, Texas Red™ (Thermo Fisher Scientific)); far red fluorescent proteins (e.g., mPlum and mNeptune); yellow fluorescent proteins (*e.g.*, YFP, eYFP, Citrine, SYFP2, Venus, YPet, PhiYFP, ZsYellowl); and tandem conjugates.

[0085] GFP is composed of 238 amino acids (26.9 kDa), originally isolated from the jellyfish Aequorea victoria/Aequorea aequorea/Aequorea forskalea that fluoresces green when exposed to blue light. The GFP from A. victoria has a major excitation peak at a wavelength of 395 nm and a minor one at 475 nm. Its emission peak is at 509 nm which is in the lower green portion of the visible spectrum. The GFP from the sea pansy (Renilla reniformis) has a single major excitation peak at 498 nm. Due to the potential for widespread usage and the evolving needs of researchers, many different mutants of GFP have been engineered. The first major improvement was a single point mutation (S65T) reported in 1995 in Nature by Roger Tsien. This mutation dramatically improved the spectral characteristics of GFP, resulting in increased fluorescence, photostability and a shift of the major excitation peak to 488 nm with the peak emission kept at 509 nm. The addition of the 37°C folding efficiency (F64L) point mutant to this scaffold yielded enhanced GFP (EGFP). EGFP has an extinction coefficient (denoted ε), also known as its optical cross section of 9.13X10-21 m^2/molecule, also quoted as 55,000 L/(mol•cm). Superfolder GFP, a series of mutations that allow GFP to rapidly fold and mature even when fused to poorly folding peptides, was reported in 2006.

[0086] The "yellow fluorescent protein" (YFP) is a genetic mutant of green fluorescent protein, derived from Aequorea victoria. Its excitation peak is 514 nm and its emission peak is 527 nm.

[0087] Exemplary functional molecules include functioning ion transporters, cellular trafficking proteins, enzymes, transcription factors, neurotransmitters, calcium reporters, channelrhodopsins, guide RNA, microRNA, nucleases, or designer receptors exclusively activated by designer drugs (DREADDs).

[0088] Ion transporters are transmembrane proteins that mediate transport of ions across cell membranes. These transporters are pervasive throughout most cell types and important for regulating cellular excitability and homeostasis. Ion transporters participate in numerous cellular processes such as action potentials, synaptic transmission, hormone secretion, and muscle

contraction. Many important biological processes in living cells involve the translocation of cations, such as calcium (Ca2+), potassium (K+), and sodium (Na+) ions, through such ion channels. In particular embodiments, ion transporters include voltage gated sodium channels (e.g., SCN1A), potassium channels (e.g., KCNQ2), and calcium channels (e.g. CACNA1C)).

[0089] In particular embodiments, the amino acid sequence of human sodium channel protein type 1 subunit alpha includes UniProtKB: P35498; the amino acid sequence of human potassium voltage-gated channel subfamily KQT member 2 includes UniProtKB: O43526; and/or the amino acid sequence of human voltage-dependent L-type calcium channel subunit alpha-1C includes UniProtKB: Q13936.

[0090] Exemplary enzymes, transcription factors, receptors, membrane proteins, cellular trafficking proteins, signaling molecules, and neurotransmitters include enzymes such as aromatic L-amino acid decarboxylase (AADC including human AADC (hAADC)), tyrosine hydroxylase (TH), GTP cyclohydrolase I (CH1), glucocerebrosidase (GCase), lactase, lipase, helicase, alpha-glucosidase, amylase; transcription factors such as SP1, AP-1, Heat shock factor protein 1, C/EBP (CCAA-T/enhancer binding protein), and Oct-1; receptors such as transforming growth factor receptor beta 1, platelet-derived growth factor receptor, epidermal growth factor receptor, vascular endothelial growth factor receptor, and interleukin 8 receptor alpha; membrane proteins, cellular trafficking proteins such as clathrin, dynamin, caveolin, Rab-4A, and Rab-11A; signaling molecules such as nerve growth factor (NGF), platelet-derived growth factor (PDGF), transforming growth factor β (TGFβ), epidermal growth factor (EGF), GTPase and HRas; and neurotransmitters such as cocaine and amphetamine regulated transcript, substance P, oxytocin, and somatostatin.

[0091] In particular embodiments, the nucleotide sequence encoding human aromatic L-amino acid decarboxylase (AADC) includes Accession No. M76180.1 shown as SEQ ID NO: 150 in FIG. 22C; the nucleotide sequence encoding human tyrosine hydroxylase (TH) includes Accession No. X05290.1 shown as SEQ ID NO: 152 in FIG. 22C; the nucleotide sequence encoding human GTP cyclohydrolase I (CH1) includes Accession No. U19523.1 shown as SEQ ID NO: 153 in FIG. 22C; and/or the amino acid sequence of human glucocerebrosidase includes Accession No. NP_000148.2 shown as SEQ ID NO: 154 in FIG. 22C. In particular embodiments, the amino acid sequence of the GBA1 gene as Isoform 1, Isoform 2, or Isoform 3 includes Accession Nos. NP_001005742.1, NP_001165282.1, or NP_001165283.1, respectively. In particular embodiments, the amino acid sequence of human lactase includes GenBank Accession No. EAX11622.1; the amino acid sequence of human lipase includes GenBank Accession No. AAA60129.1; the amino acid sequence of human helicase includes GenBank Accession No.

AMD82207.1; the amino acid sequence of human amylase includes GenBank Accession No. AAA51724.1; and/or the amino acid sequence of human alpha-glucosidase includes GenBank Accession No. ABI53718.1.

[0092] In particular embodiments, the amino acid sequence of human transcription factor SP1 includes UniProtKB/Swiss-Prot: P08047.3; the amino acid sequence of human transcription factor AP-1 includes NP_002219.1; the amino acid sequence of human heat shock factor protein 1 includes UniProtKB/Swiss-Prot: Q00613.1; the amino acid sequence of human CCAAT/enhancer-binding protein (C/EBP) beta isoform a includes NP_005185.2; and/or the amino acid sequence of human octamer-binding protein 1 (Oct-1) includes UniProtKB/Swiss-Prot: P14859.2.

[0093] In particular embodiments, the amino acid sequence of human transforming growth factor receptor beta 1 includes GenBank Accession No. CAF02096.2; the amino acid sequence of human platelet-derived growth factor receptor includes GenBank Accession No. AAA60049.1; the amino acid sequence of human epidermal growth factor receptor includes GenBank Accession No. CAA25240.1; the amino acid sequence of human vascular endothelial growth factor receptor includes GenBank Accession No. AAC16449.2; and/or the amino acid sequence of human interleukin 8 receptor alpha includes GenBank Accession No. AAB59436.1.

[0094] In particular embodiments, the amino acid sequence of human caveolin includes GenBank Accession No. CAA79476.1; the amino acid sequence of human dynamin includes GenBank Accession No. AAA88025.1; the amino acid sequence of human clathrin heavy chain 1 isoform 1 includes NP_004850.1; the amino acid sequence of human clathrin heavy chain 2 isoform 1 includes NP_009029.3; the amino acid sequence of human clathrin light chain A isoform a includes NP_001824.1; and/or the amino acid sequence of human clathrin light chain B isoform a includes NP_001825.1.

[0095] In particular embodiments, the amino acid sequence of human Ras-related protein Rab-4A isoform 1 includes NP_004569.2; the amino acid sequence of Ras-related protein Rab-11A includes UniProtKB/Swiss-Prot: P62491.3; the amino acid sequence of human platelet-derived growth factor includes GenBank Accession No. AAA60552.1; the amino acid sequence of human transforming growth factor-beta3 includes GenBank Accession No. AAA61161.1; the amino acid sequence of human nerve growth factor includes GenBank Accession No. CAA37703.1; the amino acid sequence of human epidermal growth factor (EGF) includes GenBank Accession No. CAA34902.2; and/or the amino acid sequence of human GTPase HRas can be found in FIG. 22C (SEQ ID NO: 159).

[0096] In particular embodiments, the amino acid sequence of human cocaine and amphetamine regulated transcript (Chain A) includes Protein Data Bank ID 1HY9_A; the amino acid sequence of Substance P includes positions 58-68 of Protachykinin-1; the amino acid sequence of human protachykinin-1 includes UniProtKB: P20366; the amino acid sequence of oxytocin includes positions 20-28 of oxytocin-neurophysin 1; the amino acid sequence of human oxytocin-neurophysin 1 includes UniProtKB: P01178; and/or the amino acid sequence of human somatostatin includes GenBank Accession No. AAH32625.1.

[0097] In particular embodiments, functional molecules include reporters of cell function and states such as calcium reporters. Intracellular calcium concentration is an important predictor of numerous cellular activities, which include neuronal activation, muscle cell contraction and second messenger signaling. A sensitive and convenient technique to monitor the intracellular calcium levels is through the genetically encoded calcium indicator (GECI). Among the GECIs, green fluorescent protein (GFP) based calcium sensors named GCaMPs are efficient and widely used tools. The GCaMPs are formed by fusion of M13 and calmodulin protein to N- and C-termini of circularly permutated GFP. Some GCaMPs yield distinct fluorescence emission spectra (Zhao et al., Science, 2011, 333(6051): 1888-1891). Exemplary GECIs with green fluorescence include GCaMP3, GCaMP5G, GCaMP6s, GCaMP6m, GCaMP6f, jGCaMP7s, jGCaMP7c, jGCaMP7b, and jGCaMP7f. Furthermore, GECIs with red fluorescence include jRGECO1a and jRGECO1b. AAV products containing GECIs are commercially available. For example, Vigene Biosciences provides AAV products including AAV8-CAG-GCaMP3 (Cat. No:BS4-CX3AAV8), AAV8-Syn-FLEX-GCaMP6s-WPRE (Cat. No:BS1-NXSAAV8), AAV8-Syn-FLEX-GCaMP6s-WPRE (Cat. No:BS1-NXSAAV8), AAV9-CAG-FLEX-GCaMP6m-WPRE (Cat. No:BS2-CXMAAV9), AAV9-Syn-FLEX-jGCaMP7s-WPRE (Cat. No:BS12-NXSAAV9), AAV9-CAG-FLEX-jGCaMP7f-WPRE (Cat. No:BS12-CXFAAV9), AAV9-Syn-FLEX-jGCaMP7b-WPRE (Cat. No:BS12-NXBAAV9), AAV9-Syn-FLEX-jGCaMP7c-WPRE (Cat. No:BS12-NXCAAV9), AAV9-Syn-FLEX-NES-jRGECO1a-WPRE (Cat. No:BS8-NXAAAV9), and AAV8-Syn-FLEX-NES-jRCaMP1b-WPRE (Cat. No:BS7-NXBAAV8).

[0098] In particular embodiments, the amino acid sequence of GCaMP6m includes SEQ ID NO: 160 in FIG. 22C; the amino acid sequence of GCaMP6s includes SEQ ID NO: 161 in FIG. 22C; and/or the amino acid sequence of GCaMP6f includes SEQ ID NO: 162 in FIG. 22C.

[0099] In particular embodiments calcium reporters include the genetically encoded calcium indicators GECI, NTnC; Myosin light chain kinase, GFP, Calmodulin chimera; Calcium indicator TN-XXL; BRET-based auto-luminescent calcium indicator; and/or Calcium indicator protein OeNL(Ca2+)-18u).

[0100] In particular embodiments, the amino acid sequence of myosin light chain kinase, Green fluorescent protein, Calmodulin chimera (Chain A) includes Protein Data Bank ID 3EKJ_A. In particular embodiments, the amino acid sequence of genetically-encoded green calcium indicator NTnC (chain A) includes PDB: 5MWC_The amino acid sequence of calcium indicator TN-XXL can include GenBank Accession No. ACF93133.1 and the amino acid sequence of BRET-based auto-luminescent calcium indicator can include GenBank Accession No. ADF42668.1. In particular embodiments, the amino acid sequence of calcium indicator protein OeNL(Ca2+)-18u includes GenBank Accession No. BBB18812.1.

[0101] In particular embodiments, functional molecules include modulators of neuronal activity like channelrhodopsins (e.g., channelrhodopsin-1, channelrhodopsin-2, and variants thereof). Channelrhodopsins are a subfamily of retinylidene proteins (rhodopsins) that function as light-gated ion channels. In addition to channelrhodopsin 1 (ChR1) and channelrhodopsin 2 (ChR2), several variants of channelrhodopsins have been developed. For example, Lin et al. (*Biophys J,* 2009, 96(5): 1803-14) describe making chimeras of the transmembrane domains of ChR1 and ChR2, combined with site-directed mutagenesis. Zhang et al. (*Nat Neurosci,* 2008, 11(6): 631-3) describe VChR1, which is a red-shifted channelrhodopsin variant. VChR1 has lower light sensitivity and poor membrane trafficking and expression. Other known channelrhodopsin variants include the ChR2 variant described in Nagel, et al., *Proc Natl Acad Sci USA,* 2003, 100(24): 13940-5), ChR2/H134R (Nagel, G., et al., *Curr Biol,* 2005, 15(24): 2279-84), and ChD/ChEF/ChIEF (Lin, J. Y., et al., *Biophys J,* 2009, 96(5): 1803-14), which are activated by blue light (470 nm) but show no sensitivity to orange/red light. Additional variants are described in Lin, *Experimental Physiology,* 2010, 96.1: 19-25 and Knopfel et al., *The Journal of Neuroscience,* 2010, 30(45): 14998-15004).

[0102] In particular embodiments, the amino acid sequence of channelopsin 1 [*Mesostigma viride*] includes UniProtKB: F8UVI5; the amino acid sequence of channelopsin 1 [Chlamydomonas yellowstonensis] includes GenBank Accession No. AER58217.1; the amino acid sequence of channelrhodopsin-2 [Volvox carteri f. nagariensis] includes UniProtKB: B4Y105; and/or the amino acid sequence of channel rhodopsin 2 includes GenBank Accession No. ABO64386.1.

[0103] In particular embodiments, functional molecules include DNA and RNA editing tools such CRISPR/CAS (e.g., guide RNA and a nuclease, such as Cas, Cas9 or cpf1). Functional molecules can also include engineered Cpf1s such as those described in US 2018/0030425, US 2016/0208243, WO/2017/184768 and Zetsche *et al.* (2015) *Cell* 163: 759-771; single gRNA (see e.g., Jinek *et al.* (2012) Science 337:816-821; Jinek *et al.* (2013) eLife 2:e00471; Segal (2013)

eLife 2:e00563) or editase, guide RNA molecules or homologous recombination donor cassettes. In particular embodiments, functional molecules include RNA (e.g. microRNA) that suppresses or inhibits the expression of a pathogenic huntingtin (HTT) gene.

[0104] In particular embodiments, the nucleotide sequence encoding the human huntingtin gene of exon 1 includes the sequence set forth SEQ ID NO: 157 in FIG. 22C. An example of the HTT protein sequence includes NCBI Accession No. NP_002102.4 and the encoding sequence includes NCBI Accession No. NM_002111.7. A sequence set forth in SEQ ID NO: 158 corresponds to a target sequence of the human huntingtin gene of exon 1. RNA sequences targeting the target sequence of the human huntingtin gene of exon 1 can be found in US Patent No. 10,174,321; US Application No. 16/302,140; and PCT Application No. WO2018US52103. Additional RNAi molecules designed to target the nucleotide sequence that encodes the poly-glutamine repeat proteins are described in U.S. Patent Nos. 9,169,483 and 9,181,544; International Patent Publication No. WO2015179525; and described elsewhere herein. The amino acid sequence of CRISPR-associated protein (Cas) is shown in GenBank Accession No. AKG27598.1; the amino acid sequence of Cas9 is shown in GenBank Accession No. AST09977.1; and the amino acid sequence of CRISPR-associated endonuclease Cpf1 is shown in UniProtKB/Swiss-Prot: U2UMQ6.1. In particular embodiments, the amino acid sequence of human ribonuclease 4 or ribonuclease L includes UniProtKB/Swiss-Prot: Q05823.2 and the amino acid sequence of human deoxyribonuclease II beta is shown in GenBank Accession No. AAF76893.1.

[0105] Exon 1 RNA sequence of the huntingtin (HTT) gene is set forth in SEQ ID NO: 157. The CAG repeat sequence is from nucleotides 367-429. Functional molecules can be used to disrupt or inhibit the expression of Exon 1 of HTT. In particular embodiments, double stranded RNAs are used to disrupt or inhibit the expression of Exon 1 of HTT. Exemplary double stranded RNAs include microRNA. In particular embodiments, doubles stranded RNAs target sequences of Exon H1 at the target sequences (Name, Nucleotide location) including H1, 185-205; H2, 186-206; H3, 189-209; H4, 191-211; H5, 194-214; H6, 196-216; H7, 250-270; H8, 261-281, H9, 310-330; H10, 311-331, H11, 339-359, H12, 345-365, H13, 454-474; H14, 459-479; H15, 477-497; H16, 486-506; H17, 492-512; H18, 498-518; H19, 549-569; H20, 557-577; H21, 558-578. In particular embodiments, 5′-CUUCGAGUCCCUCAAGUCCUU-3′ (SEQ ID NO: 158) is H12 which corresponds to a target sequence of the huntingtin gene of exon 1 (SEQ ID NO: 157) at nucleotides 345 to 365.

[0106] In particular embodiments, the double stranded RNA includes a first RNA sequence and a second RNA sequence attached via a linker or loop portion. Examples of loop portions can be

found in U.S. Pat. No. 9, 169,483. In particular embodiments, an RNA sequence has a sequence length of (i) at least 15 nucleotides; (ii) at least 19 nucleotides; or (iii) at least 19, at least 20, at least 21, at least 22, or at least 23 nucleotides. In particular embodiments, an RNA sequence has a sequence length of 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides. Exemplary RNA sequences to include as a first RNA sequence can be selected from SEQ ID NOs: 163-167.

[0107] Table 1. First RNA Sequences

SEQ ID NO:	RNA Sequence	Length
163	5′-AAGGACUUGAGGGACUCGA-3′	19
164	5′-AAGGACUUGAGGGACUCGAA-3′	20
165	5′-AAGGACUUGAGGGACUCGAAG-3′	21
166	5′-AAGGACUUGAGGGACUCGAAGG-3′	22
167	5′-AAGGACUUGAGGGACUCGAAGGC-3′	23

[0108] Exemplary RNA sequences to include as a second RNA sequence can be selected from SEQ ID NOs: 168-174.

[0109] Table 2. Second RNA Sequences

SEQ ID NO:	RNA Sequence	Length
168	5′-UCGAGUCCCUCAAGUCCUU-3′	19
169	5′-UUCGAGUCCCUCAAGUCCUU-3′	20
170	5′-CUUCGAGUCCCUCAAGUCCUU-3′	21
171	5′-CCUUCGAGUCCCUCAAGUCCUU-3′	22
172	5′-GCCUUCGAGUCCCUCAAGUCCUU-3′	23
173	5′-CUUCGAGUCUCAAGUCCUU-3′	19
174	5′-ACGAGUCCCUCAAGUCCUC-3′	19

[0110] In some cases, the double stranded RNA includes a pre-miRNA or pri-miRNA scaffold. A pri-miRNA scaffold includes a pre-miRNA scaffold. The pre-miRNA scaffold includes the double stranded RNA, i.e. the first RNA sequence and the second RNA sequence. In particular embodiments, the sequence of pre-miRNAs are listed in Table 3 below.

[0111] Table 3. Pre-miRNA scaffolds with SEQ ID NO: 165.

SEQ ID NO:	Name	Sequence
175	pre-miR451a	5′- CUUGGGAAUGGCAAGGAAGGACUUGAGGGACUCGAAGA CGAGUCCCUCAAGUCCUCUCUUGCUAUACCCAGA-3′
176	Pre-miR155	5′- UGCUGAAGGACUUGAGGGACUCGAAGGUUUUGGCCAC UGACUGACCUUCGAGUCUCAAGUCCUUCAGGA-3′

[0112] In particular embodiments, double stranded RNA sequences include full sequences or part of the sequences of SEQ ID NOs: 177-195. Additional RNA sequences targeting the target sequence of human hungtingtin gene of exon 1 can be found in US Patent No. 10,174,321; US

Application No. 16/302,140; U.S. Patent Nos. 9,169,483 and 9,181,544; International Patent Publication No. WO2015179525; or International Patent Application No. WO2018US52103.

[0113] Table 4.

SEQ ID NO:	Sequence
177	AUGAAGGCCUUCGAGUCCCUC
178	GGCGACCCUGGAAAAGCUGAU
179	UGGCGACCCUGGAAAAGCUGA
180	AUGGCGACCCUGGAAAAGCUG
181	CGACCAUGCGAGCCAGCA
182	AGUCGCUGAUGACCGGGA
183	ACGUCGUAAACAAGAGGA
184	GUCGACCAUGCGAGCCAGCAC
185	AUAGUCGCUGAUGACCGGGAU
186	UUACGUCGUAAACAAGAGGAA
187	AAAACUCGAGUGAGCGCUGAAGGCCUUCGAGUCCCUCAUGAGGGAC UCGAAGGCCUUCAUCGCCUACUAGUAAAA
188	AAAACUCGAGUGAGCGCUGAAGGCCUUCGAGUCUUUUAUGAGGGAC UCGAAGGCCUUCAUCGCCUACUAGUAAAA
189	AAAACUCGAGUGAGCGCAUGAAGGCCUUCGAGUCCCUCGAGGGACU CGAAGGCCUUCAUCCGCCUACUAGUAAAA
190	AAAACUCGAGUGAGCGCAUGAAGGCCUUCGAGUCUUUUGAGGGACU CGAAGGCCUUCAUCCGCCUACUAGUAAAA
191	CUCGAGUGAGCGCUCCCGGUCAUCAGCGACUAUUCCGUAAAGCCAC AGAUGGGGAUAGUCGCUGAUGACCGGGAUCGCCUACUAG
192	CUCGAGUGAGCGAUGCUGGCUCGCAUGGUCGAUACUGUAAAGCCAC AGAUGGGUGUCGACCAUGCGAGCCAGCACCGCCUACUAGA
193	CUCGAGUGAGCGCUCCUCUUGUUUACGACGUGAUCUGUAAAGCCAC AGAUGGGAUUACGUCGUAAACAAGAGGAACGCCUACUAGU
194	GCGUUUAGUGAACCGUCAGAUGGUACCGUUUAAACUCGAGUGAGCG AUGCUGGCUCGCAUGGUCGAUACUGUAAAGCCACAGAUGGGUGUCG ACCAUGCGAGCCAGCACCGCCUACUAGAGCGGCCGCCACAGCGGGG AGAUCCAGACAUGAUAAGAUACAUU
195	GCGUUUAGUGAACCGUCAGAUGGUACCGUUUAAACUCGAGUGAGCG CUCCCGGUCAUCAGCGACUAUUCCGUAAAGCCACAGAUGGGGAUAG UCGCUGAUGACCGGGAUCGCCUACUAGAGCGGCCGCCACAGCGGGG AGAUCCAGACAUGAUAAGAUACAUU

[0114] Additional effector elements include Cre, iCre, dgCre, FlpO, and tTA2. iCre refers to a codon-improved Cre. dgCre refers to an enhanced GFP/Cre recombinase fusion gene with an N terminal fusion of the first 159 amino acids of the Escherichia coli K-12 strain chromosomal dihydrofolate reductase gene (DHFR or folA) harboring a G67S mutation and modified to also include the R12Y/Y100I destabilizing domain mutation. FlpO refers to a codon-optimized form of FLPe that greatly increases protein expression and FRT recombination efficiency in mouse cells. Like the Cre/LoxP system, the FLP/FRT system has been widely used for gene expression (and

generating conditional knockout mice, mediated by the FLP/FRT system). tTA2 refers to tetracycline transactivator.

[0115] Exemplary expressible elements are expression products that do not include effector elements, for example, a non-functioning or defective protein. In particular embodiments, expressible elements can provide methods to study the effects of their functioning counterparts. In particular embodiments, expressible elements are non-functioning or defective based on an engineered mutation that renders them non-functioning. In these aspects, non-expressible elements are as similar in structure as possible to their functioning counterparts.

[0116] Exemplary self-cleaving peptides include the 2A peptides which lead to the production of two proteins from one mRNA. The 2A sequences are short (e.g., 20 amino acids), allowing more use in size-limited constructs. Particular examples include P2A, T2A, E2A, and F2A. In particular embodiments, the artificial expression constructs include an internal ribosome entry site (IRES) sequence. IRES allow ribosomes to initiate translation at a second internal site on a mRNA molecule, leading to production of two proteins from one mRNA.

[0117] Coding sequences encoding molecules (e.g., RNA, proteins) described herein can be obtained from publicly available databases and publications. Coding sequences can further include various sequence polymorphisms, mutations, and/or sequence variants wherein such alterations do not affect the function of the encoded molecule. The term “encode” or “encoding” refers to a property of sequences of nucleic acids, such as a vector, a plasmid, a gene, cDNA, mRNA, to serve as templates for synthesis of other molecules such as proteins.

[0118] The term “gene” may include not only coding sequences but also regulatory regions such as promoters, enhancers, insulators, and/or post-regulatory elements, such as termination regions. The term further can include all introns and other DNA sequences spliced from the mRNA transcript, along with variants resulting from alternative splice sites. The sequences can also include degenerate codons of a reference sequence or sequences that may be introduced to provide codon preference in a specific organism or cell type.

[0119] Promoters can include general promoters, tissue-specific promoters, cell-specific promoters, and/or promoters specific for the cytoplasm. Promoters may include strong promoters, weak promoters, constitutive expression promoters, and/or inducible promoters. Inducible promoters direct expression in response to certain conditions, signals or cellular events. For example, the promoter may be an inducible promoter that requires a particular ligand, small molecule, transcription factor or hormone protein in order to effect transcription from the promoter. Particular examples of promoters include minBglobin, CMV, minCMV, minCMV* (minCMV* is minCMV with a SacI restriction site removed) minRho, minRho* (minRho* is minRho with a SacI

restriction site removed), SV40 immediately early promoter, the Hsp68 minimal promoter (proHSP68), and the Rous Sarcoma Virus (RSV) long-terminal repeat (LTR) promoter. Minimal promoters have no activity to drive gene expression on their own but can be activated to drive gene expression when linked to a proximal enhancer element.

[0120] In particular embodiments, expression constructs are provided within vectors. The term vector refers to a nucleic acid molecule capable of transferring or transporting another nucleic acid molecule, such as an expression construct. The transferred nucleic acid is generally linked to, *e.g.*, inserted into, the vector nucleic acid molecule. A vector may include sequences that direct autonomous replication in a cell or may include sequences that permit integration into host cell DNA. Useful vectors include, for example, plasmids (*e.g.*, DNA plasmids or RNA plasmids), transposons, cosmids, bacterial artificial chromosomes, and viral vectors.

[0121] Viral vector is widely used to refer to a nucleic acid molecule that includes virus-derived components that facilitate transfer and expression of non-native nucleic acid molecules within a cell. The term adeno-associated viral vector refers to a viral vector or plasmid containing structural and functional genetic elements, or portions thereof, that are primarily derived from AAV. The term "retroviral vector" refers to a viral vector or plasmid containing structural and functional genetic elements, or portions thereof, that are primarily derived from a retrovirus. The term "lentiviral vector" refers to a viral vector or plasmid containing structural and functional genetic elements, or portions thereof, that are primarily derived from a lentivirus, and so on. The term "hybrid vector" refers to a vector including structural and/or functional genetic elements from more than one virus type.

[0122] Adenovirus vectors refer to those constructs containing adenovirus sequences sufficient to (a) support packaging of an artificial expression construct and (b) to express a coding sequence that has been cloned therein in a sense or antisense orientation. A recombinant Adenovirus vector includes a genetically engineered form of an adenovirus. Knowledge of the genetic organization of adenovirus, a 36 kb, linear, double-stranded DNA virus, allows substitution of large pieces of adenoviral DNA with foreign sequences up to 7 kb. In contrast to retrovirus, the adenoviral infection of host cells does not result in chromosomal integration because adenoviral DNA can replicate in an episomal manner without potential genotoxicity. Also, adenoviruses are structurally stable, and no genome rearrangement has been detected after extensive amplification.

[0123] Adenovirus is particularly suitable for use as a gene transfer vector because of its mid-sized genome, ease of manipulation, high titer, wide target-cell range, and high infectivity. Both ends of the viral genome contain 100-200 base pair inverted repeats (ITRs), which are cis elements necessary for viral DNA replication and packaging. The early (E) and late (L) regions of

the genome contain different transcription units that are divided by the onset of viral DNA replication. The E1 region (E1A and E1B) encodes proteins responsible for the regulation of transcription of the viral genome and a few cellular genes. The expression of the E2 region (E2A and E2B) results in the synthesis of the proteins for viral DNA replication. These proteins are involved in DNA replication, late gene expression, and host cell shut-off. The products of the late genes, including the majority of the viral capsid proteins, are expressed only after significant processing of a single primary transcript issued by the major late promoter (MLP). The MLP is particularly efficient during the late phase of infection, and all the mRNAs issued from this promoter possess a 5'-tripartite leader (TPL) sequence which makes them preferred mRNAs for translation.

[0124] Other than the requirement that an adenovirus vector be replication defective, or at least conditionally defective, the nature of the adenovirus vector is not believed to be crucial to the successful practice of particular embodiments disclosed herein. The adenovirus may be of any of the 42 different known serotypes or subgroups A-F. In particular embodiments, adenovirus type 5 of subgroup C is the preferred starting material in order to obtain a conditional replication-defective adenovirus vector for use in particular embodiments, since Adenovirus type 5 is a human adenovirus about which a great deal of biochemical and genetic information is known, and it has historically been used for most constructions employing adenovirus as a vector.

[0125] As indicated, the typical vector is replication defective and will not have an adenovirus E1 region. Thus, it will be most convenient to introduce the polynucleotide encoding the gene of interest at the position from which the E1-coding sequences have been removed. However, the position of insertion of the construct within the adenovirus sequences is not critical. The polynucleotide encoding the gene of interest may also be inserted in lieu of a deleted E3 region in E3 replacement vectors or in the E4 region where a helper cell line or helper virus complements the E4 defect.

[0126] Adeno-Associated Virus (AAV) is a parvovirus, discovered as a contamination of adenoviral stocks. It is a ubiquitous virus (antibodies are present in 85% of the US human population) that has not been linked to any disease. It is also classified as a dependovirus, because its replication is dependent on the presence of a helper virus, such as adenovirus. Various serotypes have been isolated, of which AAV-2 is the best characterized. AAV has a single-stranded linear DNA that is encapsidated into capsid proteins VP1, VP2 and VP3 to form an icosahedral virion of 20 to 24 nm in diameter.

[0127] The AAV DNA is 4.7 kilobases long. It contains two open reading frames and is flanked by two ITRs. There are two major genes in the AAV genome: rep and cap. The rep gene codes

for proteins responsible for viral replications, whereas cap codes for capsid protein VP1-3. Each ITR forms a T-shaped hairpin structure. These terminal repeats are the only essential cis components of the AAV for chromosomal integration. Therefore, the AAV can be used as a vector with all viral coding sequences removed and replaced by the cassette of genes for delivery. Three AAV viral promoters have been identified and named p5, p19, and p40, according to their map position. Transcription from p5 and p19 results in production of rep proteins, and transcription from p40 produces the capsid proteins.

[0128] AAVs stand out for use within the current disclosure because of their superb safety profile and because their capsids and genomes can be tailored to allow expression in targeted cell populations. scAAV refers to a self-complementary AAV. pAAV refers to a plasmid adeno-associated virus. rAAV refers to a recombinant adeno-associated virus.

[0129] Other viral vectors may also be employed. For example, vectors derived from viruses such as vaccinia virus, polioviruses and herpes viruses may be employed. They offer several attractive features for various mammalian cells.

[0130] Retroviruses are a common tool for gene delivery. "Retrovirus" refers to an RNA virus that reverse transcribes its genomic RNA into a linear double-stranded DNA copy and subsequently covalently integrates its genomic DNA into a host genome. Once the virus is integrated into the host genome, it is referred to as a "provirus." The provirus serves as a template for RNA polymerase II and directs the expression of RNA molecules which encode the structural proteins and enzymes needed to produce new viral particles.

[0131] Illustrative retroviruses suitable for use in particular embodiments, include: Moloney murine leukemia virus (M-MuLV), Moloney murine sarcoma virus (MoMSV), Harvey murine sarcoma virus (HaMuSV), murine mammary tumor virus (MuMTV), gibbon ape leukemia virus (GaLV), feline leukemia virus (FLV), spumavirus, Friend murine leukemia virus, Murine Stem Cell Virus (MSCV), Rous Sarcoma Virus (RSV), and lentivirus.

[0132] "Lentivirus" refers to a group (or genus) of complex retroviruses. Illustrative lentiviruses include: HIV (human immunodeficiency virus; including HIV type 1, and HIV type 2); visna-maedi virus (VMV); the caprine arthritis-encephalitis virus (CAEV); equine infectious anemia virus (EIAV); feline immunodeficiency virus (FIV); bovine immune deficiency virus (BIV); and simian immunodeficiency virus (SIV). In particular embodiments, HIV based vector backbones (i.e., HIV cis-acting sequence elements) can be used.

[0133] A safety enhancement for the use of some vectors can be provided by replacing the U3 region of the 5' LTR with a heterologous promoter to drive transcription of the viral genome during production of viral particles. Examples of heterologous promoters which can be used for this

purpose include, for example, viral simian virus 40 (SV40) (*e.g.*, early or late), cytomegalovirus (CMV) (*e.g.*, immediate early), Moloney murine leukemia virus (MoMLV), Rous sarcoma virus (RSV), and herpes simplex virus (HSV) (thymidine kinase) promoters. Typical promoters are able to drive high levels of transcription in a Tat-independent manner. This replacement reduces the possibility of recombination to generate replication-competent virus because there is no complete U3 sequence in the virus production system. In particular embodiments, the heterologous promoter has additional advantages in controlling the manner in which the viral genome is transcribed. For example, the heterologous promoter can be inducible, such that transcription of all or part of the viral genome will occur only when the induction factors are present. Induction factors include one or more chemical compounds or the physiological conditions such as temperature or pH, in which the host cells are cultured.

[0134] In particular embodiments, viral vectors include a TAR element. The term "TAR" refers to the "trans-activation response" genetic element located in the R region of lentiviral LTRs. This element interacts with the lentiviral trans-activator (tat) genetic element to enhance viral replication. However, this element is not required in embodiments wherein the U3 region of the 5' LTR is replaced by a heterologous promoter.

[0135] The "R region" refers to the region within retroviral LTRs beginning at the start of the capping group (i.e., the start of transcription) and ending immediately prior to the start of the poly(A) tract. The R region is also defined as being flanked by the U3 and U5 regions. The R region plays a role during reverse transcription in permitting the transfer of nascent DNA from one end of the genome to the other.

[0136] In particular embodiments, expression of heterologous sequences in viral vectors is increased by incorporating posttranscriptional regulatory elements, efficient polyadenylation sites, and optionally, transcription termination signals into the vectors. A variety of posttranscriptional regulatory elements can increase expression of a heterologous nucleic acid. Examples include the woodchuck hepatitis virus posttranscriptional regulatory element (WPRE; Zufferey *et al.*, 1999, J. Virol., 73:2886); the posttranscriptional regulatory element present in hepatitis B virus (HPRE) (Smith *et al.*, Nucleic Acids Res. 26(21):4818-4827, 1998); and the like (Liu *et al.*, 1995, Genes Dev., 9:1766). In particular embodiments, vectors include a posttranscriptional regulatory element such as a WPRE or HPRE. In particular embodiments, vectors lack or do not include a posttranscriptional regulatory element such as a WPRE or HPRE.

[0137] Elements directing the efficient termination and polyadenylation of a heterologous nucleic acid transcript can increase heterologous gene expression. Transcription termination signals are generally found downstream of the polyadenylation signal. In particular embodiments, vectors

include a polyadenylation signal 3' of a polynucleotide encoding a molecule (e.g., protein) to be expressed. The term "poly(A) site" or "poly(A) sequence" denotes a DNA sequence which directs both the termination and polyadenylation of the nascent RNA transcript by RNA polymerase II. Polyadenylation sequences can promote mRNA stability by addition of a poly(A) tail to the 3' end of the coding sequence and thus, contribute to increased translational efficiency. Particular embodiments may utilize BGHpA or SV40pA. In particular embodiments, a preferred embodiment of an expression construct includes a terminator element. These elements can serve to enhance transcript levels and to minimize read through from the construct into other plasmid sequences.

[0138] In particular embodiments, a viral vector further includes one or more insulator elements. Insulators elements may contribute to protecting viral vector-expressed sequences, e.g., effector elements or expressible elements, from integration site effects, which may be mediated by cis-acting elements present in genomic DNA and lead to deregulated expression of transferred sequences (*i.e.*, position effect; see, *e.g.*, Burgess-Beusse *et al.*, *PNAS., USA*, 99:16433, 2002; and Zhan *et al.*, *Hum. Genet.*, 109:471, 2001). In particular embodiments, viral transfer vectors include one or more insulator elements at the 3' LTR and upon integration of the provirus into the host genome, the provirus includes the one or more insulators at both the 5' LTR and 3' LTR, by virtue of duplicating the 3' LTR. Suitable insulators for use in particular embodiments include the chicken β-globin insulator (see Chung *et al.*, *Cell* 74:505, 1993; Chung *et al.*, *PNAS USA* 94:575, 1997; and Bell *et al.*, *Cell* 98:387, 1999), SP10 insulator (Abhyankar et al., *JBC* 282:36143, 2007), or other small CTCF recognition sequences that function as enhancer blocking insulators (Liu et al., *Nature Biotechnology*, 33:198, 2015).

[0139] Beyond the foregoing description, a wide range of suitable expression vector types will be known to a person of ordinary skill in the art. These can include commercially available expression vectors designed for general recombinant procedures, for example plasmids that contain one or more reporter genes and regulatory elements required for expression of the reporter gene in cells. Numerous vectors are commercially available, e.g., from Invitrogen, Stratagene, Clontech, etc., and are described in numerous associated guides. In particular embodiments, suitable expression vectors include any plasmid, cosmid or phage construct that is capable of supporting expression of encoded genes in mammalian cell, such as pUC or Bluescript plasmid series.

[0140] Particular embodiments of vectors disclosed herein include:

[0141] Table 5. Constructs and Construct Components

Construct Name	**Construct Components**
CN2438	rAAV-eHGT_608h-minBglobin-SYFP2-WPRE3-BGHpA

CN2439	rAAV-eHGT_609h-minBglobin-SYFP2-WPRE3-BGHpA
CN2451	rAAV-eHGT_621h-minBglobin-SYFP2-WPRE3-BGHpA
CN2463	rAAV-eHGT_633h-minBglobin-SYFP2-WPRE3-BGHpA
CN2464	rAAV-eHGT_634h-minBglobin-SYFP2-WPRE3-BGHpA
CN2465	rAAV-eHGT_635h-minBglobin-SYFP2-WPRE3-BGHpA
CN2466	rAAV-eHGT_636h-minBglobin-SYFP2-WPRE3-BGHpA
CN2013	rAAV-3xSP10ins-eHGT_351h-minRho*-SYFP2-WPRE3-BGHpA
CN2025	rAAV-3xSP10ins-eHGT_367h-minRho*-SYFP2-WPRE3-BGHpA
CN2229	rAAV-eHGT_441h-minBglobin-SYFP2-WPRE3-BGHpA
CN2442	rAAV-eHGT_612h-minBglobin-SYFP2-WPRE3-BGHpA
CN2443	rAAV-eHGT_613h-minBglobin-SYFP2-WPRE3-BGHpA
CN2444	rAAV-eHGT_614h-minBglobin-SYFP2-WPRE3-BGHpA
CN2447	rAAV-eHGT_617h-minBglobin-SYFP2-WPRE3-BGHpA
CN2448	rAAV-eHGT_618h-minBglobin-SYFP2-WPRE3-BGHpA
CN2449	rAAV-eHGT_619h-minBglobin-SYFP2-WPRE3-BGHpA
CN2450	rAAV-eHGT_620h-minBglobin-SYFP2-WPRE3-BGHpA
CN2467	rAAV-eHGT_442h-minBglobin-SYFP2-WPRE3-BGHpA
CN2421	rAAV-eHGT_444h-minBglobin-SYFP2-WPRE3-BGHpA
CN2231	rAAV-eHGT_445h-minBglobin-SYFP2-WPRE3-BGHpA
CN2236	rAAV-eHGT_450h-minBglobin-SYFP2-WPRE3-BGHpA
CN2237	rAAV-eHGT_452h-minBglobin-SYFP2-WPRE3-BGHpA
CN2440	rAAV-eHGT_610h-minBglobin-SYFP2-WPRE3-BGHpA
CN2441	rAAV-eHGT_611h-minBglobin-SYFP2-WPRE3-BGHpA
CN2445	rAAV-eHGT_615h-minBglobin-SYFP2-WPRE3-BGHpA
CN2446	rAAV-eHGT_616h-minBglobin-SYFP2-WPRE3-BGHpA
CN2457	rAAV-eHGT_627h-minBglobin-SYFP2-WPRE3-BGHpA
CN2458	rAAV-eHGT_628h-minBglobin-SYFP2-WPRE3-BGHpA
CN2459	rAAV-eHGT_629h-minBglobin-SYFP2-WPRE3-BGHpA
CN2232	rAAV-eHGT_446h-minBglobin-SYFP2-WPRE3-BGHpA
CN2233	rAAV-eHGT_447h-minBglobin-SYFP2-WPRE3-BGHpA
CN2452	rAAV-eHGT_622h-minBglobin-SYFP2-WPRE3-BGHpA
CN2453	rAAV-eHGT_623h-minBglobin-SYFP2-WPRE3-BGHpA
CN2454	rAAV-eHGT_624h-minBglobin-SYFP2-WPRE3-BGHpA
CN2455	rAAV-eHGT_625h-minBglobin-SYFP2-WPRE3-BGHpA
CN2460	rAAV-eHGT_630h-minBglobin-SYFP2-WPRE3-BGHpA
CN2461	rAAV-eHGT_631h-minBglobin-SYFP2-WPRE3-BGHpA
CN2628	rAAV-eHGT_735m-minBglobin-SYFP2-WPRE3-BGHpA
CN2641	rAAV-eHGT_736m-minBglobin-SYFP2-WPRE3-BGHpA
CN2642	rAAV-eHGT_737m-minBglobin-SYFP2-WPRE3-BGHpA

CN2643	rAAV-eHGT_738m-minBglobin-SYFP2-WPRE3-BGHpA
CN2629	rAAV-eHGT_739m-minBglobin-SYFP2-WPRE3-BGHpA
CN2630	rAAV-eHGT_740m-minBglobin-SYFP2-WPRE3-BGHpA
CN2745	rAAV-eHGT_741m-minBglobin-SYFP2-WPRE3-BGHpA
CN2746	rAAV-eHGT_742m-minBglobin-SYFP2-WPRE3-BGHpA
CN2631	rAAV-eHGT_743m-minBglobin-SYFP2-WPRE3-BGHpA
CN2747	rAAV-eHGT_744m-minBglobin-SYFP2-WPRE3-BGHpA
CN2632	rAAV-eHGT_746m-minBglobin-SYFP2-WPRE3-BGHpA
CN2644	rAAV-eHGT_747m-minBglobin-SYFP2-WPRE3-BGHpA
CN2748	rAAV-eHGT_748m-minBglobin-SYFP2-WPRE3-BGHpA
CN2633	rAAV-eHGT_749m-minBglobin-SYFP2-WPRE3-BGHpA
CN2634	rAAV-eHGT_750m-minBglobin-SYFP2-WPRE3-BGHpA
CN2635	rAAV-eHGT_751m-minBglobin-SYFP2-WPRE3-BGHpA
CN2609	rAAV-eHGT_779m-minBglobin-SYFP2-WPRE3-BGHpA
CN2610	rAAV-eHGT_780m-minBglobin-SYFP2-WPRE3-BGHpA
CN2749	rAAV-eHGT_781m-minBglobin-SYFP2-WPRE3-BGHpA
CN2626	rAAV-eHGT_782m-minBglobin-SYFP2-WPRE3-BGHpA
CN2611	rAAV-eHGT_783m-minBglobin-SYFP2-WPRE3-BGHpA
CN2750	rAAV-eHGT_784m-minBglobin-SYFP2-WPRE3-BGHpA
CN2614	rAAV-eHGT_785m-minBglobin-SYFP2-WPRE3-BGHpA
CN2485	rAAV-eHGT_452h-minBglobin-hAADC-Intron-WPRE3-BGHpA
CN2486	rAAV-eHGT_452h-minBglobin-hAADC-Intron-3xHA-WPRE3-BGHpA
CN2739	rAAV-3xSP10ins-eHGT_367h-minRho-hAADC-Intron-WPRE3-BGHpA
CN2740	rAAV-3xSP10ins-eHGT_367h-minRho-hAADC-Intron-3xHA-WPRE3-BGHpA
CN2765	pAAV-3xSP10ins-eHGT_367h-minBglobin-hAADC-Intron-WPRE3-BGHpA
CN2766	pAAV-3xSP10ins-eHGT_367h-minBglobin-hAADC-Intron-3xHA-WPRE3-BGHpA
CN2514	rAAV-3xSP10ins-core2_eHGT_367h-minRho*-SYFP2-WPRE3-BGHpA
CN2555	rAAV-3xSP10ins-3xcore2_eHGT_367h-minRho*-SYFP2-WPRE3-BGHpA
CN2907	rAAV-3xcore_eHGT_441h-minBglobin-SYFP2-WPRE3-BGHpA
CN2909	rAAV-3xcore2_eHGT_445h-minBglobin-SYFP2-WPRE3-BGHpA
CN2921	rAAV-3xcore2_eHGT_444h-minBglobin-SYFP2-WPRE3-BGHpA
CN2982	rAAV-3xcore2_eHGT_452h-minBglobin-SYFP2-WPRE3-BGHpA
CN3044	rAAV-3xcore2_eHGT_779m-minBglobin-SYFP2-WPRE3-BGHpA
CN3038	rAAV-3xcore2_eHGT_743m-minBglobin-SYFP2-WPRE3-BGHpA
CN3344	rAAV-3xCore-eHGT_621h-minBglobin-SYFP2-WPRE3-BGHpA
CN3281	rAAV-3xCore2_eHGT_780m-minBglobin-SYFP2-WPRE3-BGHpA
CN3346	rAAV-3xCore-eHGT_447h-minBglobin-SYFP2-WPRE3-BGHpA
CN3566	rAAV-3xSP10ins_3xcore2_eHGT_351h-minBglobin-SYFP2-WPRE3-BGHpA
CN2912	rAAV- 3xcore2_eHGT_450h-minBglobin-SYFP2-WPRE3-BGHpA

CN2913	rAAV-3xcore3_eHGT_450h-minBglobin-SYFP2-WPRE3-BGHpA
CN2966	rAAV-eHGT_743m-minBglobin-iCre-WPRE3-BGHpA
CN2203	rAAV-3xSP10ins-eHGT_367h-minRho*-iCre-WPRE3-BGHpA
CN2700	rAAV-eHGT_452h-minBglobin-mTFP1-WPRE3-BGHpA

[0142] Subcomponent sequences within the larger vector sequences can be readily identified by one of ordinary skill in the art and based on the contents of the current disclosure (see FIGs. 22C). Nucleotides between identifiable and enumerated subcomponents reflect restriction enzyme recognition sites used in assembly (cloning) of the constructs, and in some cases, additional nucleotides do not convey any identifiable function. These segments of complete vector sequences can be adjusted based on use of different cloning strategies and/or vectors. In general, short 6-nucleotide palindromic sequences reflect vector construction artifacts that are not important to vector function.

[0143] In particular embodiments vectors (e.g., AAV) with capsids that cross the blood-brain barrier (BBB) are selected. In particular embodiments, vectors are modified to include capsids that cross the BBB. Examples of AAV with viral capsids that cross the blood brain barrier include AAV9 (Gombash et al., Front Mol Neurosci. 2014; 7:81), AAVrh.10 (Yang, et al., Mol Ther. 2014; 22(7): 1299-1309), AAV1R6, AAV1R7 (Albright et al., Mol Ther. 2018; 26(2): 510), rAAVrh.8 (Yang, et al., supra), AAV-BR1 (Marchio et al., EMBO Mol Med. 2016; 8(6): 592), AAV-PHP.S (Chan et al., Nat Neurosci. 2017; 20(8): 1172), AAV-PHP.B (Deverman et al., Nat Biotechnol. 2016; 34(2): 204), AAV-PPS (Chen et al., Nat Med. 2009; 15: 1215), and PHP.eB. In particular embodiments, the PHP.eB capsid differs from AAV9 such that, using AAV9 as a reference, amino acids starting at residue 586: S-AQ-A (SEQ ID NO: 196) are changed to S-DGTLAVPFK-A (SEQ ID NO: 197). In particular embodiments, PHP.eb refers to the associated sequence provided in FIG. 22C.

[0144] AAV9 is a naturally occurring AAV serotype that, unlike many other naturally occurring serotypes, can cross the BBB following intravenous injection. It transduces large sections of the central nervous system (CNS), thus permitting minimally invasive treatments (Naso et al., BioDrugs. 2017; 31(4): 317), for example, as described in relation to clinical trials for the treatment of spinal muscular atrophy (SMA) syndrome by AveXis (AVXS-101, NCT03505099) and the treatment of CLN3 gene-Related Neuronal Ceroid-Lipofuscinosis (NCT03770572).

[0145] AAVrh.10, was originally isolated from rhesus macaques and shows low seropositivity in humans when compared with other common serotypes used for gene delivery applications (Selot et al., Front Pharmacol. 2017; 8: 441) and has been evaluated in clinical trials LYS-SAF302, LYSOGENE, and NCT03612869.

[0146] AAV1R6 and AAV1R7, two variants isolated from a library of chimeric AAV vectors (AAV1 capsid domains swapped into AAVrh.10 (also referred to as Rh10)), retain the ability to cross the BBB and transduce the CNS while showing significantly reduced hepatic and vascular endothelial transduction.

[0147] rAAVrh.8, also isolated from rhesus macaques, shows a global transduction of glial and neuronal cell types in regions of clinical importance following peripheral administration and also displays reduced peripheral tissue tropism compared to other vectors.

[0148] AAV-BR1 is an AAV2 variant displaying the NRGTEWD (SEQ ID NO: 198) epitope that was isolated during in vivo screening of a random AAV display peptide library. It shows high specificity accompanied by high transgene expression in the brain with minimal off-target affinity (including for the liver) (Körbelin et al., EMBO Mol Med. 2016; 8(6): 609).

[0149] AAV-PHP.S (Addgene, Watertown, MA) is a variant of AAV9 generated with the CREATE method that encodes the 7-mer sequence QAVRTSL (SEQ ID NO: 199), transduces neurons in the enteric nervous system, and strongly transduces peripheral sensory afferents entering the spinal cord and brain stem.

[0150] AAV-PHP.B (Addgene, Watertown, MA) is a variant of AAV9 generated with the CREATE method that encodes the 7-mer sequence TLAVPFK (SEQ ID NO: 200). It transfers genes throughout the CNS with higher efficiency than AAV9 and transduces the majority of astrocytes and neurons across multiple CNS regions.

[0151] AAV-PPS, an AAV2 variant crated by insertion of the DSPAHPS (SEQ ID NO: 201) epitope into the capsid of AAV2, shows a dramatically improved brain tropism relative to AAV2.

[0152] Additional capsids include PHP.V1, AAV1, AAV5, AAV8, AAV11, Hu11, AAV2-retro, AAV9-retro, CAP.B10, and CAP.B22. For additional information regarding capsids that cross the blood brain barrier, see Chan et al., Nat. Neurosci. 2017 Aug: 20(8): 1172-1179.

[0153] (ii) Compositions for Administration. Artificial expression constructs and vectors of the present disclosure (referred to herein as physiologically active components) can be formulated with a carrier that is suitable for administration to a cell, tissue slice, animal (e.g., mouse, non-human primate), or human. Physiologically active components within compositions described herein can be prepared in neutral forms, as freebases, or as pharmacologically acceptable salts.

[0154] Pharmaceutically-acceptable salts include the acid addition salts (formed with the free amino groups of the protein) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such

as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, histidine, procaine and the like.

[0155] Carriers of physiologically active components can include solvents, dispersion media, vehicles, coatings, diluents, isotonic and absorption delaying agents, buffers, solutions, suspensions, colloids, and the like. The use of such carriers for physiologically active components is well known in the art. Except insofar as any conventional media or agent is incompatible with the physiologically active components, it can be used with compositions as described herein.

[0156] The phrase "pharmaceutically-acceptable carriers" refer to carriers that do not produce an allergic or similar untoward reaction when administered to a human, and in particular embodiments, when administered intravenously (e.g. at the retro-orbital plexus).

[0157] In particular embodiments, compositions can be formulated for intravenous, intraparenchymal, intraocular, intravitreal, parenteral, subcutaneous, intracerebro-ventricular, intramuscular, intrathecal, intraspinal, intraperitoneal, oral or nasal inhalation, or by direct injection in or application to one or more cells, tissues, or organs.

[0158] Compositions may include liposomes, lipids, lipid complexes, microspheres, microparticles, nanospheres, and/or nanoparticles.

[0159] The formation and use of liposomes is generally known to those of skill in the art. Liposomes have been developed with improved serum stability and circulation half-times (see, for instance, U.S. Pat. No. 5,741,516). Further, various methods of liposome and liposome like preparations as potential drug carriers have been described (see, for instance U.S. Pat. Nos. 5,567,434; 5,552,157; 5,565,213; 5,738,868; and 5,795,587).

[0160] The disclosure also provides for pharmaceutically acceptable nanocapsule formulations of the physiologically active components. Nanocapsules can generally entrap compounds in a stable and reproducible way (Quintanar-Guerrero *et al.*, *Drug Dev Ind Pharm* 24(12):1113-1128, 1998; Quintanar-Guerrero *et al.*, *Pharm Res.* 15(7):1056-1062, 1998; Quintanar-Guerrero *et al.*, J. *Microencapsul*. 15(1):107-119, 1998; Douglas *et al.*, *Crit Rev Ther Drug Carrier Syst* 3(3):233-261, 1987). To avoid side effects due to intracellular polymeric overloading, such ultrafine particles can be designed using polymers able to be degraded *in vivo*. Biodegradable polyalkyl-cyanoacrylate nanoparticles that meet these requirements are contemplated for use in the present disclosure. Such particles can be easily made, as described in Couvreur *et al.*, *J Pharm Sci* 69(2):199-202, 1980; Couvreur *et al.*, *Crit Rev Ther Drug Carrier Syst*. 5(1)1-20, 1988; zur Muhlen *et al.*, *Eur J Pharm Biopharm*, 45(2):149-155, 1998; Zambaux *et al.*, *J Control Release* 50(1-3):31-40, 1998; and U.S. Pat. No. 5,145,684.

[0161] Injectable compositions can include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions (U.S. Pat. No. 5,466,468). For delivery via injection, the form is sterile and fluid to the extent that it can be delivered by syringe. In particular embodiments, it is stable under the conditions of manufacture and storage, and optionally contains one or more preservative compounds against the contaminating action of microorganisms, such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (*e.g.*, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and/or vegetable oils. Proper fluidity may be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion, and/or by the use of surfactants. The prevention of the action of microorganisms can be brought about by various antibacterial and/or antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In various embodiments, the preparation will include an isotonic agent(s), for example, sugar(s) or sodium chloride. Prolonged absorption of the injectable compositions can be accomplished by including in the compositions of agents that delay absorption, for example, aluminum monostearate and gelatin. Injectable compositions can be suitably buffered, if necessary, and the liquid diluent first rendered isotonic with sufficient saline or glucose.

[0162] Dispersions may also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. As indicated, under ordinary conditions of storage and use, these preparations can contain a preservative to prevent the growth of microorganisms.

[0163] Sterile compositions can be prepared by incorporating the physiologically active component in an appropriate amount of a solvent with other optional ingredients (e.g., as enumerated above), followed by filtered sterilization. Generally, dispersions are prepared by incorporating the various sterilized physiologically active components into a sterile vehicle that contains the basic dispersion medium and the required other ingredients (e.g., from those enumerated above). In the case of sterile powders for the preparation of sterile injectable solutions, preferred methods of preparation can be vacuum-drying and freeze-drying techniques which yield a powder of the physiologically active components plus any additional desired ingredient from a previously sterile-filtered solution thereof.

[0164] Oral compositions may be in liquid form, for example, as solutions, syrups or suspensions, or may be presented as a drug product for reconstitution with water or other suitable vehicle before use. Such liquid preparations may be prepared by conventional means with pharmaceutically acceptable additives such as suspending agents (e.g., sorbitol syrup, cellulose

derivatives or hydrogenated edible fats); emulsifying agents (e.g., lecithin or acacia); non-aqueous vehicles (e.g., almond oil, oily esters, or fractionated vegetable oils); and preservatives (e.g., methyl or propyl-p-hydroxybenzoates or sorbic acid). The compositions may take the form of, for example, tablets or capsules prepared by conventional means with pharmaceutically acceptable excipients such as binding agents (e.g., pregelatinized maize starch, polyvinyl pyrrolidone or hydroxypropyl methylcellulose); fillers (e.g., lactose, microcrystalline cellulose or calcium hydrogen phosphate); lubricants (e.g., magnesium stearate, talc or silica); disintegrants (e.g., potato starch or sodium starch glycolate); or wetting agents (e.g., sodium lauryl sulphate). Tablets may be coated by methods well-known in the art.

[0165] Inhalable compositions can be delivered in the form of an aerosol spray presentation from pressurized packs or a nebulizer, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g., gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch.

[0166] Compositions can also include microchip devices (U.S. Pat. No. 5,797,898), ophthalmic formulations (Bourlais *et al*., *Prog Retin Eye Res*, 17(1):33-58, 1998), transdermal matrices (U.S. Pat. No. 5,770,219 and U.S. Pat. No. 5,783,208) and feedback-controlled delivery (U.S. Pat. No. 5,697,899).

[0167] Supplementary active ingredients can also be incorporated into the compositions.

[0168] Typically, compositions can include at least 0.1% of the physiologically active components or more, although the percentage of the physiologically active components may, of course, be varied and may conveniently be between 1 or 2% and 70% or 80% or more or 0.5-99% of the weight or volume of the total composition. Naturally, the amount of physiologically active components in each physiologically-useful composition may be prepared in such a way that a suitable dosage will be obtained in any given unit dose of the compound. Factors such as solubility, bioavailability, biological half-life, route of administration, product shelf life, as well as other pharmacological considerations will be contemplated by one skilled in the art of preparing such pharmaceutical formulations, and as such, a variety of compositions and dosages may be desirable.

[0169] In particular embodiments, for administration to humans, compositions should meet sterility, pyrogenicity, and the general safety and purity standards as required by United States Food and Drug Administration (FDA) or other applicable regulatory agencies in other countries.

[0170] (iii) Cell Lines Including Artificial Expression Constructs. The present disclosure includes cells including an artificial expression construct described herein. A cell that has been transformed with an artificial expression construct can be used for many purposes, including in neuroanatomical studies, assessments of functioning and/or non-functioning proteins, and drug screens that assess the regulatory properties of enhancers.

[0171] A variety of host cell lines can be used, but in particular embodiments, the cell is a mammalian cell. In particular embodiments, the artificial expression construct includes eHGT_608h, eHGT_609h, eHGT_621h, eHGT_633h, eHGT_634h, eHGT_635h, eHGT_636h, eHGT_351h, eHGT_367h, eHGT_441h, eHGT_612h, eHGT_613h, eHGT_614h, eHGT_617h, eHGT_618h, eHGT_619h, eHGT_620h, eHGT_442h, eHGT_444h, eHGT_445h, eHGT_450h, eHGT_452h, eHGT_610h, eHGT_611h, eHGT_615h, eHGT_616h, eHGT_627h, eHGT_628h, eHGT_629h, eHGT_446h, eHGT_447h, eHGT_622h, eHGT_623h, eHGT_624h, eHGT_625h, eHGT_630h, eHGT_631h, eHGT_735m, eHGT_736m, eHGT_737m, eHGT_738m, eHGT_739m, eHGT_740m, eHGT_741m, eHGT_742m, eHGT_743m, eHGT_744m, eHGT_746m, eHGT_747m, eHGT_748m, eHGT_749m, eHGT_750m, eHGT_751m, eHGT_779m, eHGT_780m, eHGT_781m, eHGT_782m, eHGT_783m, eHGT_784m, eHGT_785m, core2_eHGT_367h, 3xcore2_eHGT_367h, 3xcore_eHGT_441h, 3xCore-eHGT_621h, 3xCore-eHGT_447h, 3xcore2_eHGT_351h, 3xcore2_eHGT_445h, 3xcore2_eHGT_444h, 3xcore2_eHGT_452h, 3xcore2_eHGT_450h, 3xcore3_eHGT_450h, 3xcore2_eHGT_779m, 3xCore2_eHGT_780m, or 3xcore2_eHGT_743m and/or CN2438, CN2439, CN2451, CN2463, CN2464, CN2465, CN2466, CN2013, CN2025, CN2229, CN2442, CN2443, CN2444, CN2447, CN2448, CN2449, CN2450, CN2467, CN2421, CN2231, CN2236, CN2237, CN2440, CN2441, CN2445, CN2446, CN2457, CN2458, CN2459, CN2232, CN2233, CN2452, CN2453, CN2454, CN2455, CN2460, CN2461, CN2628, CN2641, CN2642, CN2643, CN2629, CN2630, CN2745, CN2746, CN2631, CN2747, CN2632, CN2644, CN2748, CN2633, CN2634, CN2635, CN2609, CN2610, CN2749, CN2626, CN2611, CN2750, CN2614, CN2485, CN2486, CN2739, CN2740, CN2765, CN2766, CN2514, CN2555, CN2907, CN2909, CN2921, CN2982, CN3044, CN3038, CN3344, CN3281, CN3346, CN3566, CN2912, CN2913, CN2966, CN2203, or CN2700, and the cell line is a human, primate, or murine cell. Cell lines which can be utilized for transgenesis in the present disclosure also include primary cell lines derived from living tissue such as rat or mouse brains and organotypic cell cultures, including brain slices from animals such as rats or mice. The PC12 cell line (available from the American Type Culture Collection, ATCC, Manassas, VA) has been shown to express a number of neuronal marker proteins in response to Neuronal Growth Factor (NGF). The PC12 cell line is considered to be a

neuronal cell line and is applicable for use with this disclosure. JAR cells (available from ATCC) are a platelet derived cell-line that express some neuronal genes, such as the serotonin transporter gene, and may be used with embodiments described herein.

[0172] WO 91/13150 describes a variety of cell lines, including neuronal cell lines, and methods of producing them. Similarly, WO 97/39117 describes a neuronal cell line and methods of producing such cell lines. The neuronal cell lines disclosed in these patent applications are applicable for use in the present disclosure.

[0173] In particular embodiments, "neuronal" describes something that is of, related to, or includes, neuronal cells. Neuronal cells are defined by the presence of an axon and dendrites. The term "neuronal-specific" refers to something that is found, or an activity that occurs, in neuronal cells or cells derived from neuronal cells, but is not found in or occur in, or is not found substantially in or occur substantially in, non-neuronal cells or cells not derived from neuronal cells, for example glial cells such as astrocytes or oligodendrocytes.

[0174] In particular embodiments, non-neuronal cell lines may be used, including mouse embryonic stem cells. Cultured mouse embryonic stem cells can be used to analyze expression of genetic constructs using transient transfection with plasmid constructs. Mouse embryonic stem cells are pluripotent and undifferentiated. These cells can be maintained in this undifferentiated state by Leukemia Inhibitory Factor (LIF). Withdrawal of LIF induces differentiation of the embryonic stem cells. In culture, the stem cells form a variety of differentiated cell types. Differentiation is caused by the expression of tissue specific transcription factors, allowing the function of an enhancer sequence to be evaluated. (See for example Fiskerstrand *et al.*, *FEBS Lett* 458: 171-174, 1999).

[0175] Methods to differentiate stem cells into neuronal cells include replacing a stem cell culture media with a media including basic fibroblast growth factor (bFGF) heparin, an N2 supplement (*e.g.,* transferrin, insulin, progesterone, putrescine, and selenite), laminin and polyornithine. A process to produce myelinating oligodendrocytes from stem cells is described in Hu, *et al.,* 2009, *Nat. Protoc.* 4:1614-22. Bibel, *et al.,* 2007, *Nat. Protoc*. 2:1034-43 describes a protocol to produce glutamatergic neurons from stem cells while Chatzi, *et al.,* 2009, *Exp. Neurol.* 217:407-16 describes a procedure to produce GABAergic neurons. This procedure includes exposing stem cells to all-trans-RA for three days. After subsequent culture in serum-free neuronal induction medium including Neurobasal medium supplemented with B27, bFGF and EGF, 95% GABA neurons develop

[0176] U.S. Publication No. 2012/0329714 describes use of prolactin to increase neural stem cell numbers while U.S. Publication No. 2012/0308530 describes a culture surface with amino groups

that promotes neuronal differentiation into neurons, astrocytes and oligodendrocytes. Thus, the fate of neural stem cells can be controlled by a variety of extracellular factors. Commonly used factors include brain derived growth factor (BDNF; Shetty and Turner, 1998, *J. Neurobiol.* 35:395-425); fibroblast growth factor (bFGF; U.S. Pat. No.5,766,948; FGF-1, FGF-2); Neurotrophin-3 (NT-3) and Neurotrophin-4 (NT-4); Caldwell, *et al.,* 2001, *Nat. Biotechnol.* 1;19:475-9); ciliary neurotrophic factor (CNTF); BMP-2 (U.S. Pat. Nos. 5,948,428 and 6,001,654); isobutyl 3-methylxanthine; leukemia inhibitory growth factor (LIF; U.S. Patent No. 6,103,530); somatostatin; amphiregulin; neurotrophins (*e.g.,* cyclic adenosine monophosphate; epidermal growth factor (EGF); dexamethasone (glucocorticoid hormone); forskolin; GDNF family receptor ligands; potassium; retinoic acid (U.S. Patent No. 6,395,546); tetanus toxin; and transforming growth factor-α and TGF-β (U.S. Pat. Nos. 5,851,832 and 5,753,506).

[0177] In particular embodiments, yeast one-hybrid systems may also be used to identify compounds that inhibit specific protein/DNA interactions, such as transcription factors for eHGT_608h, eHGT_609h, eHGT_621h, eHGT_633h, eHGT_634h, eHGT_635h, eHGT_636h, eHGT_351h, eHGT_367h, eHGT_441h, eHGT_612h, eHGT_613h, eHGT_614h, eHGT_617h, eHGT_618h, eHGT_619h, eHGT_620h, eHGT_442h, eHGT_444h, eHGT_445h, eHGT_450h, eHGT_452h, eHGT_610h, eHGT_611h, eHGT_615h, eHGT_616h, eHGT_627h, eHGT_628h, eHGT_629h, eHGT_446h, eHGT_447h, eHGT_622h, eHGT_623h, eHGT_624h, eHGT_625h, eHGT_630h, eHGT_631h, eHGT_735m, eHGT_736m, eHGT_737m, eHGT_738m, eHGT_739m, eHGT_740m, eHGT_741m, eHGT_742m, eHGT_743m, eHGT_744m, eHGT_746m, eHGT_747m, eHGT_748m, eHGT_749m, eHGT_750m, eHGT_751m, eHGT_779m, eHGT_780m, eHGT_781m, eHGT_782m, eHGT_783m, eHGT_784m, eHGT_785m, core2_eHGT_367h, 3xcore2_eHGT_367h, 3xcore_eHGT_441h, 3xCore-eHGT_621h, 3xCore-eHGT_447h, 3xcore2_eHGT_351h, 3xcore2_eHGT_445h, 3xcore2_eHGT_444h, 3xcore2_eHGT_452h, 3xcore2_eHGT_450h, 3xcore3_eHGT_450h, 3xcore2_eHGT_779m, 3xCore2_eHGT_780m, or 3xcore2_eHGT_743m.

[0178] Transgenic animals are described below. Cell lines may also be derived from such transgenic animals. For example, primary tissue culture from transgenic mice (e.g., also as described below) can provide cell lines with the artificial expression construct already integrated into the genome. (for an example see MacKenzie & Quinn, *Proc Natl Acad Sci USA* 96: 15251-15255, 1999).

[0179] (iv) Transgenic Animals. Another aspect of the disclosure includes transgenic animals, the genome of which contains an artificial expression construct including eHGT_608h, eHGT_609h, eHGT_621h, eHGT_633h, eHGT_634h, eHGT_635h, eHGT_636h, eHGT_351h, eHGT_367h,

eHGT_441h, eHGT_612h, eHGT_613h, eHGT_614h, eHGT_617h, eHGT_618h, eHGT_619h, eHGT_620h, eHGT_442h, eHGT_444h, eHGT_445h, eHGT_450h, eHGT_452h, eHGT_610h, eHGT_611h, eHGT_615h, eHGT_616h, eHGT_627h, eHGT_628h, eHGT_629h, eHGT_446h, eHGT_447h, eHGT_622h, eHGT_623h, eHGT_624h, eHGT_625h, eHGT_630h, eHGT_631h, eHGT_735m, eHGT_736m, eHGT_737m, eHGT_738m, eHGT_739m, eHGT_740m, eHGT_741m, eHGT_742m, eHGT_743m, eHGT_744m, eHGT_746m, eHGT_747m, eHGT_748m, eHGT_749m, eHGT_750m, eHGT_751m, eHGT_779m, eHGT_780m, eHGT_781m, eHGT_782m, eHGT_783m, eHGT_784m, eHGT_785m, core2_eHGT_367h, 3xcore2_eHGT_367h, 3xcore_eHGT_441h, 3xCore-eHGT_621h, 3xCore-eHGT_447h, 3xcore2_eHGT_351h, 3xcore2_eHGT_445h, 3xcore2_eHGT_444h, 3xcore2_eHGT_452h, 3xcore2_eHGT_450h, 3xcore3_eHGT_450h, 3xcore2_eHGT_779m, 3xCore2_eHGT_780m, and 3xcore2_eHGT_743m operatively linked to a heterologous coding sequence. In particular embodiments, the genome of a transgenic animal includes CN2438, CN2439, CN2451, CN2463, CN2464, CN2465, CN2466, CN2013, CN2025, CN2229, CN2442, CN2443, CN2444, CN2447, CN2448, CN2449, CN2450, CN2467, CN2421, CN2231, CN2236, CN2237, CN2440, CN2441, CN2445, CN2446, CN2457, CN2458, CN2459, CN2232, CN2233, CN2452, CN2453, CN2454, CN2455, CN2460, CN2461, CN2628, CN2641, CN2642, CN2643, CN2629, CN2630, CN2745, CN2746, CN2631, CN2747, CN2632, CN2644, CN2748, CN2633, CN2634, CN2635, CN2609, CN2610, CN2749, CN2626, CN2611, CN2750, CN2614, CN2485, CN2486, CN2739, CN2740, CN2765, CN2766, CN2514, CN2555, CN2907, CN2909, CN2921, CN2982, CN3044, CN3038, CN3344, CN3281, CN3346, CN3566, CN2912, CN2913, CN2966, CN2203, and CN2700. In particular embodiments, when a non-integrating vector is utilized, a transgenic animal includes an artificial expression construct including eHGT_608h, eHGT_609h, eHGT_621h, eHGT_633h, eHGT_634h, eHGT_635h, eHGT_636h, eHGT_351h, eHGT_367h, eHGT_441h, eHGT_612h, eHGT_613h, eHGT_614h, eHGT_617h, eHGT_618h, eHGT_619h, eHGT_620h, eHGT_442h, eHGT_444h, eHGT_445h, eHGT_450h, eHGT_452h, eHGT_610h, eHGT_611h, eHGT_615h, eHGT_616h, eHGT_627h, eHGT_628h, eHGT_629h, eHGT_446h, eHGT_447h, eHGT_622h, eHGT_623h, eHGT_624h, eHGT_625h, eHGT_630h, eHGT_631h, eHGT_735m, eHGT_736m, eHGT_737m, eHGT_738m, eHGT_739m, eHGT_740m, eHGT_741m, eHGT_742m, eHGT_743m, eHGT_744m, eHGT_746m, eHGT_747m, eHGT_748m, eHGT_749m, eHGT_750m, eHGT_751m, eHGT_779m, eHGT_780m, eHGT_781m, eHGT_782m, eHGT_783m, eHGT_784m, eHGT_785m, core2_eHGT_367h, 3xcore2_eHGT_367h, 3xcore_eHGT_441h, 3xCore-eHGT_621h, 3xCore-eHGT_447h, 3xcore2_eHGT_351h, 3xcore2_eHGT_445h, 3xcore2_eHGT_444h, 3xcore2_eHGT_452h, 3xcore2_eHGT_450h,

3xcore3_eHGT_450h, 3xcore2_eHGT_779m, 3xCore2_eHGT_780m, or 3xcore2_eHGT_743m and/or CN2438, CN2439, CN2451, CN2463, CN2464, CN2465, CN2466, CN2013, CN2025, CN2229, CN2442, CN2443, CN2444, CN2447, CN2448, CN2449, CN2450, CN2467, CN2421, CN2231, CN2236, CN2237, CN2440, CN2441, CN2445, CN2446, CN2457, CN2458, CN2459, CN2232, CN2233, CN2452, CN2453, CN2454, CN2455, CN2460, CN2461, CN2628, CN2641, CN2642, CN2643, CN2629, CN2630, CN2745, CN2746, CN2631, CN2747, CN2632, CN2644, CN2748, CN2633, CN2634, CN2635, CN2609, CN2610, CN2749, CN2626, CN2611, CN2750, CN2614, CN2485, CN2486, CN2739, CN2740, CN2765, CN2766, CN2514, CN2555, CN2907, CN2909, CN2921, CN2982, CN3044, CN3038, CN3344, CN3281, CN3346, CN3566, CN2912, CN2913, CN2966, CN2203, or CN2700 within one or more of its cells.

[0180] Detailed methods for producing transgenic animals are described in U.S. Pat. No. 4,736,866. Transgenic animals may be of any nonhuman species, but preferably include nonhuman primates (NHPs), sheep, horses, cattle, pigs, goats, dogs, cats, rabbits, chickens, and rodents such as guinea pigs, hamsters, gerbils, rats, mice, and ferrets.

[0181] In particular embodiments, construction of a transgenic animal results in an organism that has an engineered construct present in all cells in the same genomic integration site. Thus, cell lines derived from such transgenic animals will be consistent in as much as the engineered construct will be in the same genomic integration site in all cells and hence will suffer the same position effect variegation. In contrast, introducing genes into cell lines or primary cell cultures can give rise to heterologous expression of the construct. A disadvantage of this approach is that the expression of the introduced DNA may be affected by the specific genetic background of the host animal.

[0182] Transgenic animals can be used to model movements disorders. For example, an animal model of Parkinson's disease includes daily delivery of conduritol-b-epoxide (CBE), an inhibitor of GCase to mice. A genetic model of Parkinson's disease is one in which mice carry a homozygous GBA1 mutation and are partially deficient in saposins (4L/PS-NA). An example of a non-human primate model of Parkinson's disease is one in which adult Macaca fascicularis are administered the neurotoxin 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine (MPTP) until they reach a severe and stable bilateral Parkinsonian syndrome, including akinesia, flexed posture, balance impairment and tremor.

[0183] In particular embodiments, transgenic animals can be used in animal models of Huntington's disease. In particular embodiments, the animal model is a LV-171-82Q Huntington's disease (HD) rat model. This model is based on the striatal overexpression of the first 171 amino acids of the HTT mutant fragment with 82 CAG repeats linked to a fragment of exon 67 containing

the SNP C/T. In particular embodiments, the animal model is a Hu128/21 HD mouse or a YAC128 HD mouse.

[0184] As indicated above in relation to cell lines, the artificial expression constructs of this disclosure can be used to genetically modify mouse embryonic stem cells using techniques known in the art. Typically, the artificial expression construct is introduced into cultured murine embryonic stem cells. Transformed ES cells are then injected into a blastocyst from a host mother and the host embryo re-implanted into the mother. This results in a chimeric mouse whose tissues are composed of cells derived from both the embryonic stem cells present in the cultured cell line and the embryonic stem cells present in the host embryo. Usually the mice from which the cultured ES cells used for transgenesis are derived are chosen to have a different coat color from the host mouse into whose embryos the transformed cells are to be injected. Chimeric mice will then have a variegated coat color. As long as the germ-line tissue is derived, at least in part, from the genetically modified cells, then the chimeric mice crossed with an appropriate strain can produce offspring that will carry the transgene.

[0185] In addition to the methods of delivery described above, the following techniques are also contemplated as alternative methods of delivering artificial expression constructs to target cells or targeted tissues and organs of an animal, and in particular, to cells, organs, or tissues of a vertebrate mammal: sonophoresis (*e.g.,* ultrasound, as described in U.S. Pat. No. 5,656,016); intraosseous injection (U.S. Pat. No. 5,779,708); microchip devices (U.S. Pat. No. 5,797,898); ophthalmic formulations (Bourlais *et al.*, *Prog Retin Eye Res*, 17(1):33-58, 1998); transdermal matrices (U.S. Pat. No. 5,770,219 and U.S. Pat. No. 5,783,208); feedback-controlled delivery (U.S. Pat. No. 5,697,899), and any other delivery method available and/or described elsewhere in the disclosure.

[0186] (v) Methods of Use. Methods disclosed herein include treating subjects (e.g., humans, veterinary animals (dogs, cats, reptiles, birds) livestock (e.g., horses, cattle, goats, pigs, chickens) and research animals (e.g., monkeys, rats, mice, fish) with compositions for administration disclosed herein. Within the current disclosure, a subject can also include an isolated cell, a network of cells, or a tissue slice.

[0187] Treating subjects includes delivering therapeutically effective amounts. Therapeutically effective amounts include those that provide effective amounts, prophylactic treatments and/or therapeutic treatments.

[0188] In particular embodiments, the disclosure includes the use of the artificial expression constructs described herein to modulate expression of a heterologous gene which is either partially or wholly encoded in a location downstream to that enhancer in an engineered sequence.

Thus, there are provided herein methods of use of the disclosed artificial expression constructs in the research, study, and potential development of medicaments for preventing, treating or ameliorating the symptoms of a disease, dysfunction, or disorder.

[0189] Particular embodiments include methods of administering to a subject an artificial expression construct including the enhancer eHGT_608h, eHGT_609h, eHGT_621h, eHGT_633h, eHGT_634h, eHGT_635h, eHGT_636h, eHGT_351h, eHGT_367h, eHGT_441h, eHGT_612h, eHGT_613h, eHGT_614h, eHGT_617h, eHGT_618h, eHGT_619h, eHGT_620h, eHGT_442h, eHGT_444h, eHGT_445h, eHGT_450h, eHGT_452h, eHGT_610h, eHGT_611h, eHGT_615h, eHGT_616h, eHGT_627h, eHGT_628h, eHGT_629h, eHGT_446h, eHGT_447h, eHGT_622h, eHGT_623h, eHGT_624h, eHGT_625h, eHGT_630h, eHGT_631h, eHGT_735m, eHGT_736m, eHGT_737m, eHGT_738m, eHGT_739m, eHGT_740m, eHGT_741m, eHGT_742m, eHGT_743m, eHGT_744m, eHGT_746m, eHGT_747m, eHGT_748m, eHGT_749m, eHGT_750m, eHGT_751m, eHGT_779m, eHGT_780m, eHGT_781m, eHGT_782m, eHGT_783m, eHGT_784m, eHGT_785m, core2_eHGT_367h, 3xcore2_eHGT_367h, 3xcore_eHGT_441h, 3xCore-eHGT_621h, 3xCore-eHGT_447h, 3xcore2_eHGT_351h, 3xcore2_eHGT_445h, 3xcore2_eHGT_444h, 3xcore2_eHGT_452h, 3xcore2_eHGT_450h, 3xcore3_eHGT_450h, 3xcore2_eHGT_779m, 3xCore2_eHGT_780m, and 3xcore2_eHGT_743m operatively linked to a heterologous coding sequence to drive expression of a gene in a targeted cell type.

[0190] In particular embodiments, the targeted cell type includes cells in the striatum including striatal interneuron-cholinergic, striatal medium spiny neuron-direct pathway, striatal medium spiny neuron-indirect pathway, striatal medium spiny neuron-pan, or Drd3+ medium spiny neurons.

[0191] In addition to targeting the striatum, some enhancers target additional brain regions and cell types.

[0192] In particular embodiments, 3xcore2_eHGT_367h additionally targets parafascicular nucleus in the thalamus; L2/3 IT neurons and L6 neurons in the cortex; and superior colliculus, CA1, and hilus neurons in the hippocampus.

[0193] In particular embodiments, core2_eHGT_367h additionally targets superior colliculus, CA1, and hilus neurons in the hippocampus; with scattered sparse expression in the cortex.

[0194] In particular embodiments, eHGT_743m additionally targets lateral septal nucleus putative cholinergic interneurons.

[0195] In particular embodiments, eHGT_779m additionally targets cells in the caudodorsal part of lateral septum and superior colliculus.

[0196] In particular embodiments, eHGT_780m additionally targets central amygdala nucleus, accessory olfactory nucleus (AON), upper band of L2/3 pyramidal neurons in Piriform area, piriform-amygdalar area, entorhinal, perirhinal, frontal areas especially motor cortex areas, and cells around the glomeruli in the olfactory bulb (OB).

[0197] In particular embodiments, eHGT_785m additionally targets central amygdala (CEA); cells around the glomeruli in OB; and L3 in caudal entorhinal cortex.

[0198] In particular embodiments, eHGT_452h additionally targets TTd (Taenia tecta, dorsal) putative excitatory neurons.

[0199] In particular embodiments, eHGT_444h additionally targets cortex, amygdala, and glomeruli in olfactory bulb.

[0200] In particular embodiments, eHGT_621h additionally targets cells around the glomeruli in OB; paraventricular hypothalamic nucleus; and lateral, medial and main intercalated (ITC) nucleus of the amygdala.

[0201] In particular embodiments, eHGT_619h additionally targets CA2 in the hippocampus.

[0202] In particular embodiments, eHGT_617h additionally targets CA3 and hilus neurons in the hippocampus; cells around the glomeruli in OB; molecular layer of piriform area; paraventricular nucleus of the thalamus; dorsal tip of interpeduncular nucleus; and dorsal tegmental nucleus.

[0203] In particular embodiments, eHGT_612h additionally targets posterior basolateral amygdala (BLA) neurons, CA2, CA3, and caudal CA1/Subiculum pyramidal neurons; superior colliculus cells; paraventricular nucleus of the thalamus; AON cells; and scattered cells in OB.

[0204] In particular embodiments, eHGT_610h additionally targets cells in cortical amygdalar area (COAp), piriform area L2, CEA, BLA, L5 neurons in retrosplenial (RSP) cortex, AON, and OB.

[0205] In particular embodiments, eHGT_742m additionally targets L2/3 neocortex.

[0206] Particular embodiments include methods of administering to a subject an artificial expression construct including CN2438, CN2439, CN2451, CN2463, CN2464, CN2465, CN2466, CN2013, CN2025, CN2229, CN2442, CN2443, CN2444, CN2447, CN2448, CN2449, CN2450, CN2467, CN2421, CN2231, CN2236, CN2237, CN2440, CN2441, CN2445, CN2446, CN2457, CN2458, CN2459, CN2232, CN2233, CN2452, CN2453, CN2454, CN2455, CN2460, CN2461, CN2628, CN2641, CN2642, CN2643, CN2629, CN2630, CN2745, CN2746, CN2631, CN2747, CN2632, CN2644, CN2748, CN2633, CN2634, CN2635, CN2609, CN2610, CN2749, CN2626, CN2611, CN2750, CN2614, CN2485, CN2486, CN2739, CN2740, CN2765, CN2766, CN2514, CN2555, CN2907, CN2909, CN2921, CN2982, CN3044, CN3038, CN3344, CN3281, CN3346, CN3566, CN2912, CN2913, CN2966, CN2203, and CN2700 to drive expression of a gene in a

targeted cell type.

[0207] Particular embodiments include methods of administering to a subject an artificial expression construct including CN2438, CN2439, CN2451, CN2463, CN2464, CN2465, CN2466, CN2013, CN2025, CN2229, CN2442, CN2443, CN2444, CN2447, CN2448, CN2449, CN2450, CN2467, CN2421, CN2231, CN2236, CN2237, CN2440, CN2441, CN2445, CN2446, CN2457, CN2458, CN2459, CN2232, CN2233, CN2452, CN2453, CN2454, CN2455, CN2460, CN2461, CN2628, CN2641, CN2642, CN2643, CN2629, CN2630, CN2745, CN2746, CN2631, CN2747, CN2632, CN2644, CN2748, CN2633, CN2634, CN2635, CN2609, CN2610, CN2749, CN2626, CN2611, CN2750, CN2614, CN2514, CN2555, CN2907, CN2909, CN2921, CN2982, CN3044, CN3038, CN3344, CN3281, CN3346, CN3566, CN2912, CN2913, CN2966, CN2203, and/or CN2700 wherein the gene encoding sequence is replaced with or supplemented with a sequence encoding a therapeutic gene product to drive expression of a gene in a targeted cell type.

[0208] A therapeutic gene product refers to a biochemical material resulting from the expression of a gene that produces an intended physiological effect meant to alleviate a condition. In particular embodiments, a therapeutic gene product includes AADC (e.g. hAADC), GCase, survival motor neuron 1 (SMN1), nerve growth factor (NFG), glutamic acid decarboxylase (GAD), glial derived neurotrophic factor (GDNF; e.g. neurturin (NTN)), tyrosine hydroxylase (TH), guanosine triphosphate cyclohydrolase (GCH), brain-derived neurotrophic factor (BDNF), or RNA suppressing or inhibiting the expression of a pathogenic hungtingtin (HTT) gene.

[0209] An "effective amount" is the amount of a composition necessary to result in a desired physiological change in the subject. Effective amounts are often administered for research purposes. Effective amounts disclosed herein can cause a statistically-significant effect in an animal model or in vitro assay relevant to the assessment of a movement disorder's development, progression, and/or resolution.

[0210] A "prophylactic treatment" includes a treatment administered to a subject who does not display signs or symptoms of a movement disorder or displays only early signs or symptoms of a movement disorder such that treatment is administered for the purpose of diminishing or decreasing the risk of developing the movement disorder further. Thus, a prophylactic treatment functions as a preventative treatment against a movement disorder. In particular embodiments, prophylactic treatments reduce, delay, or prevent the worsening of a movement disorder.

[0211] A "therapeutic treatment" includes a treatment administered to a subject who displays symptoms or signs of a movement disorder and is administered to the subject for the purpose of diminishing or eliminating those signs or symptoms of the movement disorder. The therapeutic treatment can reduce, control, or eliminate the presence or activity of the movement disorder

and/or reduce control or eliminate side effects of the movement disorder.

[0212] Function as an effective amount, prophylactic treatment or therapeutic treatment are not mutually exclusive, and in particular embodiments, administered dosages may accomplish more than one treatment type.

[0213] Exemplary movements disorders that can be treated include Parkinson's disease, Huntington's disease, ataxia, corticobasal ganglionic degeneration (CBGD), dyskinesia, dystonia, tremors, hereditary spastic paraplegia, multiple system atrophy, myoclonus, progressive supranuclear palsy, restless legs syndrome, Rett syndrome, spasticity, Sydenham's chorea, other choreas, athetosis, ballism, stereotypy, tardive dyskinesia/dystonia, tics, Tourette's syndrome, olivopontocerebellar atrophy (OPCA), diffuse Lewy body disease, hemibalismus, hemi-facial spasm, Wilson's disease, stiff man syndrome, akinetic mutism, psychomotor retardation, painful legs, moving toes syndrome, a gait disorder, a drug-induced movement disorder, or other movement disorders described herein.

[0214] In particular embodiments, methods to determine the efficacy of the treatments using constructs disclosed herein will be measured before treatment, during the first year after treatment, and at other times. In particular embodiments, efficacy of the treatments using constructs disclosed herein will be determined to be effective if the evaluated measurements can be maintained at a normal, non-movement disorder level, reduced to a non-movement disorder level, or reduced such that it is still elevated compared to a non-movement disorder individual, but is still less than the level which would be expected in an individual without treatment.

[0215] Therapeutically effective amounts disclosed herein can improve motor control and/or reduce tremors.

[0216] Therapeutically effective amounts can be assessed using developmental tests for cognitive and motor function, MRI and CT assessments, FDOPA Positron Emission Tomography (PET) putamen-specific radioactivity uptake values, CSF neurotransmitter metabolite values, and neurological evaluation.

[0217] In particular embodiments, additional methods for determining the efficacy of Parkinson's disease treatments include measuring metabolic activity of the subthalamic nucleus (STN), measuring the firing rate of internal globus pallidus (GPi) neurons and the proportion of spikes per burst and the number of burst events in the neuronal firing pattern.

[0218] For Huntington's disease, therapeutically effective amounts can additionally be assessed using standard evaluations for this disease including the Unified Huntington's Disease Ratings Scale (UHDRS) or the Prognostic Index for Huntington's Disease. The Prognostic Index for Huntington's Disease predicts the probability of a motor diagnosis by calculating the total motor

score (TMS) from the Unified Huntington's Disease Rating Scale (UHDRS), the Symbol Digit Modality Test (SDMT), base-line age, and cytosine-adenine-guanine (CAG) expansion. Potential biomarkers in brain imaging for premanifest and early progression of Huntington's disease include striatal volume, subcortical white-matter volume, cortical thickness, whole brain and ventricular volumes, functional imaging (e.g., functional MRI), PET (e.g., with fluorodeoxy glucose), and magnetic resonance spectroscopy (e.g., lactate). Potential biomarkers for quantitative clinical tools for premanifest and early progression of Huntington's disease include quantitative motor assessments, motor physiological assessments (e.g., transcranial magnetic stimulation), and quantitative eye movement measurements.

[0219] Numerous movement disorders affect infants and children and a number of motor and developmental tests can be utilized to assess therapeutically effective amounts within this context. Examples include the the Peabody Developmental Motor Scale (PDMS-II), Alberta Infant Motor Scale (AIMS), Bayley Scales of Infant and Toddler Development®-Third Edition (Bayley-III), or the Comprehensive Developmental Inventory for Infants and Toddlers (CDIIT).

[0220] PDMS-II is a skill-based measure of gross and fine motor development for infants and children from birth through 5 years of age. This tool separates motor development into gross and fine motor skills. Through a combination of the composite scores for the gross and fine motor skills, the examiner has a reliable estimate of the child's motor skills. It consists of 4 gross motor and 2 fine motor subtests, as follows: Reflexes (gross motor); Stationary (gross motor); Locomotion (gross motor); Object Manipulation (gross motor); Grasping (fine motor); and Visual-Motor Integration (fine motor).

[0221] Scoring the PDMS-II relies on raw scores, percentiles, standard scores, and age equivalents for the subtests, and quotients for the composites. Raw scores are total points accumulated by a child on a subtest. Developmental ages are often used to convey information to parents of young children. Age equivalents for PDMS-II are called "motor ages" which convey to parents that their child is "passing" on items that a child of a certain chronological age would typically pass. Age equivalents for PDMS-II subtests are generated from Table C.1 in the PDMS-II manual or by PDMS-II software scoring and report systems.

[0222] AIMS is a 58-item observational measure of infant motor performance for use from birth through the age of independent walking (18 months). It assesses the sequential development of motor milestones in terms of progressive development and integration of antigravity muscle control. The test assesses infant movement in 4 positions: prone, supine, sitting, and standing. The AIMS total score is calculated by summing the scores for the 58 items with a range of scores between 0 and 58. Higher scores indicate more mature motor development. The infant's score

can then be converted to a percentile and compared with age-equivalent peers from the normative sample.

[0223] Bayley-III offers a standardized assessment of cognitive and motor development for children between 1 and 42 months of age. The assessment measures cognitive, communication, physical, social/emotional, and adaptive areas of development to identify children with developmental delays. The test consists of 5 scales of development: Cognitive Scale, Language Scale, Motor Scale, Social Emotional Scale, and Adaptive Behavior Scale. It is possible to present results for developmental age corresponding to each subscale vs chronological age.

[0224] The diagnostic test of the CDIIT is one of the child developmental tests covering 5 developmental subtests used for children aged 3 to 72 months.

[0225] The amount of expression constructs and time of administration of such compositions will be within the purview of the skilled artisan having benefit of the present teachings. It is likely, however, that the administration of effective amounts of the disclosed compositions may be achieved by a single administration, such as for example, a single injection of sufficient numbers of infectious particles to provide an effect in the subject. Alternatively, in some circumstances, it may be desirable to provide multiple, or successive administrations of the artificial expression construct compositions or other genetic constructs, either over a relatively short, or a relatively prolonged period of time, as may be determined by the individual overseeing the administration of such compositions. For example, the number of infectious particles administered to a mammal may be 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, 10^{16}, or even higher, viral genomes/ml given either as a single dose or divided into two or more administrations as may be required to achieve an intended effect. In fact, in certain embodiments, it may be desirable to administer two or more different expression constructs in combination to achieve a desired effect. In particular embodiments, a patient receiving intravenous, intraparenchymal, intraspinal, retro-orbital, or intrathecal administration can be infused with from 10^5 to 10^{22} copies of the artificial expression construct. In particular embodiments, dosages for any one subject depends upon many factors, including the subject's size, surface area, age, the particular compound to be administered, sex, time and route of administration, general health, and other drugs being administered concurrently.

[0226] In certain circumstances it will be desirable to deliver the artificial expression construct in suitably formulated compositions disclosed herein either by pipette, retro-orbital injection, subcutaneously, intraocularly, intracisternally, intravitreally, parenterally, subcutaneously, intravenously, intraparenchymally, intracerebro-ventricularly, intramuscularly, intrathecally, intraspinally, intraperitoneally, by oral or nasal inhalation, or by direct application or injection to

one or more cells, tissues, or organs. The methods of administration may also include those modalities as described in U.S. Pat. No. 5,543,158; U.S. Pat. No. 5,641,515 and U.S. Pat. No. 5,399,363.

[0227] (vi) Kits and Commercial Packages. Kits and commercial packages contain an artificial expression construct described herein. The artificial expression construct can be isolated. In particular embodiments, the components of an expression product can be isolated from each other. In particular embodiments, the expression product can be within a vector, within a viral vector, within a cell, within a tissue slice or sample, and/or within a transgenic animal. Such kits may further include one or more reagents, restriction enzymes, peptides, therapeutics, pharmaceutical compounds, or means for delivery of the compositions such as syringes, injectables, and the like.

[0228] Embodiments of a kit or commercial package will also contain instructions regarding use of the included components, for example, in basic research, electrophysiological research, neuroanatomical research, and/or the research and/or treatment of a disorder, disease or condition.

[0229] The Exemplary Embodiments and Experimental Examples below are included to demonstrate particular embodiments of the disclosure. Those of ordinary skill in the art should recognize in light of the present disclosure that many changes can be made to the specific embodiments disclosed herein and still obtain a like or similar result without departing from the spirit and scope of the disclosure.

[0230] (vii) Exemplary Embodiments.

1. A core of the eHGT_351h, eHGT_367h, eHGT_441h, eHGT_444h, eHGT_445h, eHGT_447h, eHGT_450h, eHGT_452h, eHGT_621h, eHGT_743m, eHGT_779m, or eHGT_780m enhancer.

2. The core of embodiment 1, wherein the core has the sequence as set forth in SEQ ID NO: 202; SEQ ID NO: 204; SEQ ID NO: 206; SEQ ID NO: 208; SEQ ID NO: 210; SEQ ID NO: 212; SEQ ID NO: 214; SEQ ID NO: 216; SEQ ID NO: 218; SEQ ID NO: 220; SEQ ID NO: 222; SEQ ID NO: 224; or SEQ ID NO: 226.

3. The core of embodiments 1 or 2, wherein the core is concatenated into a concatemer including 2, 3, 4, 5, 6, 7, 8, 9, or 10 copies of the enhancer core.

4. The core of embodiment 3, wherein the concatenated core includes 2, 3, 4, 5, 6, 7, 8, 9, or 10 copies of SEQ ID NO: 202; SEQ ID NO: 204; SEQ ID NO: 206; SEQ ID NO: 208; SEQ ID NO: 210; SEQ ID NO: 212; SEQ ID NO: 214; SEQ ID NO: 216; SEQ ID NO: 218; SEQ ID NO: 220; SEQ ID NO: 222; SEQ ID NO: 224; and/or SEQ ID NO: 226.

5. The core of any of embodiments 3 or 4, wherein the concatenated core includes 3 copies of SEQ ID NO: 206.
6. The core of any of embodiments 3 or 4, wherein the concatenated core includes 3 copies of SEQ ID NO: 202.
7. The core of any of embodiments 3 or 4, wherein the concatenated core includes 3 copies of SEQ ID NO: 204.
8. The core of any of embodiments 3 or 4, wherein the concatenated core includes 3 copies of SEQ ID NO: 208.
9. The core of any of embodiments 3 or 4, wherein the concatenated core includes 3 copies of SEQ ID NO: 210.
10. The core of any of embodiments 3 or 4, wherein the concatenated core includes 3 copies of SEQ ID NO: 212.
11. The core of any of embodiments 3 or 4, wherein the concatenated core includes 3 copies of SEQ ID NO: 214.
12. The core of any of embodiments 3 or 4, wherein the concatenated core includes 3 copies of SEQ ID NO: 216.
13. The core of any of embodiments 3 or 4, wherein the concatenated core includes 3 copies of SEQ ID NO: 218.
14. The core of any of embodiments 3 or 4, wherein the concatenated core includes 3 copies of SEQ ID NO: 220.
15. The core of any of embodiments 3 or 4, wherein the concatenated core includes 3 copies of SEQ ID NO: 222.
16. The core of any of embodiments 3 or 4, wherein the concatenated core includes 3 copies of SEQ ID NO: 224.
17. The core of any of embodiments 3 or 4, wherein the concatenated core includes 3 copies of SEQ ID NO: 226.
18. The core of embodiment 5, wherein the concatenated core includes SEQ ID NO: 207.
19. The core of embodiment 6, wherein the concatenated core includes SEQ ID NO: 203.
20. The core of embodiment 7, wherein the concatenated core includes SEQ ID NO: 205.
21. The core of embodiment 8, wherein the concatenated core includes SEQ ID NO: 209.
22. The core of embodiment 9, wherein the concatenated core includes SEQ ID NO: 211.
23. The core of embodiment 10, wherein the concatenated core includes SEQ ID NO: 213.
24. The core of embodiment 11, wherein the concatenated core includes SEQ ID NO: 215.
25. The core of embodiment 12, wherein the concatenated core includes SEQ ID NO: 217.

26. The core of embodiment 13, wherein the concatenated core includes SEQ ID NO: 219.

27. The core of embodiment 14, wherein the concatenated core includes SEQ ID NO: 221.

28. The core of embodiment 15, wherein the concatenated core includes SEQ ID NO: 223.

29. The core of embodiment 16, wherein the concatenated core includes SEQ ID NO: 225.

30. The core of embodiment 17, wherein the concatenated core includes SEQ ID NO: 227.

31. An artificial expression construct including (i) an enhancer selected from eHGT_608h, eHGT_609h, eHGT_621h, eHGT_633h, eHGT_634h, eHGT_635h, eHGT_636h, eHGT_351h, eHGT_367h, eHGT_441h, eHGT_612h, eHGT_613h, eHGT_614h, eHGT_617h, eHGT_618h, eHGT_619h, eHGT_620h, eHGT_442h, eHGT_444h, eHGT_445h, eHGT_450h, eHGT_452h, eHGT_610h, eHGT_611h, eHGT_615h, eHGT_616h, eHGT_627h, eHGT_628h, eHGT_629h, eHGT_446h, eHGT_447h, eHGT_622h, eHGT_623h, eHGT_624h, eHGT_625h, eHGT_630h, eHGT_631h, eHGT_735m, eHGT_736m, eHGT_737m, eHGT_738m, eHGT_739m, eHGT_740m, eHGT_741m, eHGT_742m, eHGT_743m, eHGT_744m, eHGT_746m, eHGT_747m, eHGT_748m, eHGT_749m, eHGT_750m, eHGT_751m, eHGT_779m, eHGT_780m, eHGT_781m, eHGT_782m, eHGT_783m, eHGT_784m, eHGT_785m, core2_eHGT_367h, core2_eHGT_367h, core_eHGT_441h, Core-eHGT_621h, Core-eHGT_447h, core2_eHGT_351h, core2_eHGT_445h, core2_eHGT_444h, core2_eHGT_452h, core2_eHGT_450h, core3_eHGT_450h, core2_eHGT_779m, Core2_eHGT_780m, and core2_eHGT_743m; (ii) a promoter; and (iii) a heterologous encoding sequence.

32. The artificial expression construct of claim 4, wherein the enhancer is concatenated including 3xcore2_eHGT_743m, 3xcore2_eHGT_367h, 3xcore_eHGT_441h, 3xCore-eHGT_621h, 3xCore-eHGT_447h, 3xcore2_eHGT_351h, 3xcore2_eHGT_445h, 3xcore2_eHGT_444h, 3xcore2_eHGT_452h, 3xcore2_eHGT_450h, 3xcore3_eHGT_450h, 3xcore2_eHGT_779m, and 3xCore2_eHGT_780m.

33. The artificial expression construct of embodiments 31 or 32, wherein the heterologous encoding sequence encodes an effector element or an expressible element.

34. The artificial expression construct of embodiment 33, wherein the effector element includes a reporter protein or a functional molecule.

35. The artificial expression construct of embodiment 34, wherein the reporter protein includes a fluorescent protein.

36. The artificial expression construct of embodiment 34 or 35, wherein the functional molecule includes a functional ion transporter, enzyme, transcription factor, receptor, membrane protein, cellular trafficking protein, signaling molecule, neurotransmitter, calcium reporter, channelrhodopsin, CRISPR/CAS molecule, editase, guide RNA molecule, RNA, microRNA,

homologous recombination donor cassette, or a designer receptor exclusively activated by designer drug (DREADD).

37. The artificial expression construct of embodiment 36, wherein the functional molecule includes aromatic L-amino acid decarboxylase (AADC), tyrosine hydroxylase (TH), GTP cyclohydrolase I (CH1), tetrahydrobiopterin (BH4) and/ or glucocerebrosidase (GCase).

38. The artificial expression construct of embodiment 36, wherein the RNA suppresses or inhibits the expression of a pathogenic huntingtin (HTT) gene.

39. The artificial expression construct of embodiment 38, wherein the RNA sequence includes SEQ ID NOs: 163-195.

40. The artificial expression construct of embodiment 33, wherein the expressible element includes a non-functional molecule.

41. The artificial expression construct of embodiment 40, wherein the non-functional molecule includes a non-functional ion transporter, enzyme, transcription factor, receptor, membrane protein, cellular trafficking protein, signaling molecule, neurotransmitter, calcium reporter, channelrhodopsin, CRISPR/CAS molecule, editase, guide RNA molecule, RNA, microRNA, homologous recombination donor cassette, or a DREADD.

42. The artificial expression construct of any of embodiments 31-41, wherein the artificial expression construct is associated with a capsid that crosses the blood brain barrier.

43. The artificial expression construct of embodiment 42, wherein the capsid includes PHP.eB, AAV-BR1, AAV-PHP.S, AAV-PHP.B, AAV-PPS, PHP.V1, AAV1, AAV2, AAV5, AAV8, AAV9, AAV11, Rh10, Hu11, AAV2-retro, AAV9-retro, CAP.B10, or CAP.B22.

44. The artificial expression construct of any of embodiments 31-43, wherein the artificial expression construct includes or encodes a skipping element.

45. The artificial expression construct of embodiment 44, wherein the skipping element includes a 2A peptide and/or an internal ribosome entry site (IRES).

46. The artificial expression construct of embodiment 45, wherein the 2A peptide is selected from T2A, P2A, E2A, or F2A.

47. The artificial expression construct of any of embodiments 31-46, wherein the artificial expression construct includes or encodes a set of features selected from eHGT_608h, eHGT_609h, eHGT_621h, eHGT_633h, eHGT_634h, eHGT_635h, eHGT_636h, eHGT_351h, eHGT_367h, eHGT_441h, eHGT_612h, eHGT_613h, eHGT_614h, eHGT_617h, eHGT_618h, eHGT_619h, eHGT_620h, eHGT_442h, eHGT_444h, eHGT_445h, eHGT_450h, eHGT_452h, eHGT_610h, eHGT_611h, eHGT_615h, eHGT_616h, eHGT_627h, eHGT_628h, eHGT_629h, eHGT_446h, eHGT_447h, eHGT_622h, eHGT_623h, eHGT_624h, eHGT_625h, eHGT_630h,

eHGT_631h, eHGT_735m, eHGT_736m, eHGT_737m, eHGT_738m, eHGT_739m, eHGT_740m, eHGT_741m, eHGT_742m, eHGT_743m, eHGT_744m, eHGT_746m, eHGT_747m, eHGT_748m, eHGT_749m, eHGT_750m, eHGT_751m, eHGT_779m, eHGT_780m, eHGT_781m, eHGT_782m, eHGT_783m, eHGT_784m, eHGT_785m, core2_eHGT_367h, 3xcore2_eHGT_367h, 3xcore_eHGT_441h, 3xCore-eHGT_621h, 3xCore-eHGT_447h, 3xcore2_eHGT_351h, 3xcore2_eHGT_445h, 3xcore2_eHGT_444h, 3xcore2_eHGT_452h, 3xcore2_eHGT_450h, 3xcore3_eHGT_450h, 3xcore2_eHGT_779m, 3xCore2_eHGT_780m, 3xcore2_eHGT_743m, AAV, scAAV, rAAV, pAAV, minBglobin, CMV, minCMV, minRho, minRho*, AADC, TH, CH1, BH4 GCase, Intron, 3xHA, an RNA that suppresses or inhibits the expression of a pathogenic HTT gene, a gene whose expression treats a movement disorder, fluorescent protein (e.g. EGFP, SYFP2, GFP, mTFP1), Cre, iCre, dgCre, FlpO, tTA2, SP10ins, WPRE3, hGHpA, and/or BGHpA.

48. The artificial expression construct of any of embodiments 31-47, wherein the artificial expression construct includes or encodes a set of features selected from:

3xcore2_eHGT_743m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xSP10ins-core2_eHGT_367h-minRho*-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_608h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_609h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_621h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_633h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_634h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_635h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_636h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xSP10ins-eHGT_351h-minRho*-[gene encoding functional molecule]-WPRE3-BGHpA;

3xSP10ins-eHGT_367h-minRho*-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_441h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_612h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_613h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_614h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_617h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_618h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_619h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_620h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_442h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_444h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_445h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_450h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_452h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_610h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_611h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_615h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_616h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_627h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_628h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_629h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_446h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_447h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_622h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_623h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_624h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_625h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_630h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_631h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_735m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_736m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_737m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_738m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_739m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_740m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_741m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_742m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_743m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_744m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_746m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_747m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_748m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_749m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_750m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_751m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_779m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_780m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_781m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_782m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_783m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_784m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_785m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_452h-minBglobin-[gene encoding functional molecule]A-WPRE3-BGHpA;

3xSP10ins-eHGT_367h-minRho-[gene encoding functional molecule]-WPRE3-BGHpA;

3xSP10ins-eHGT_367h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xSP10ins-3xcore2_eHGT_367h-minRho*-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore_eHGT_441h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore2_eHGT_445h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore2_eHGT_444h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore2_eHGT_452h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore2_eHGT_779m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xCore-eHGT_621h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xCore2_eHGT_780m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xCore-eHGT_447h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xSP10ins_3xcore2_eHGT_351h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore2_eHGT_450h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore3_eHGT_450h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore2_eHGT_743m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xSP10ins-core2_eHGT_367h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_608h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_609h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_621h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_633h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_634h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_635h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_636h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xSP10ins-eHGT_351h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xSP10ins-eHGT_367h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_441h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_612h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_613h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_614h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_617h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_618h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_619h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_620h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_442h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_444h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_445h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_450h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_452h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_610h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_611h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_615h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_616h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_627h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_628h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_629h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_446h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_447h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_622h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_623h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_624h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_625h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_630h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_631h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_735m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_736m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_737m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_738m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_739m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_740m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_741m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_742m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_743m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_744m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_746m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_747m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_748m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_749m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_750m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_751m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_779m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_780m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_781m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_782m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_783m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_784m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_785m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_452h-[minimal promoter]-[gene encoding functional molecule]A-WPRE3-BGHpA;

3xSP10ins-3xcore2_eHGT_367h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore_eHGT_441h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore2_eHGT_445h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore2_eHGT_444h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore2_eHGT_452h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore2_eHGT_779m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xCore-eHGT_621h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xCore2_eHGT_780m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xCore-eHGT_447h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xSP10ins_3xcore2_eHGT_351h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore2_eHGT_450h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA; or

3xcore3_eHGT_450h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA

Wherein the functional molecule in each of the foregoing embodiments can be a therapeutic gene product.

49. The artificial expression construct of embodiment 48, wherein the functional molecule is a therapeutic gene product that treats a movement disorder.

50. A vector including an artificial expression construct of any of embodiments 31-49.

51. The vector of embodiment 50, wherein the vector includes a viral vector.

52. The vector of embodiment 51, wherein the viral vector includes a recombinant adeno-associated viral (AAV) vector or a plasmid (AAV).

53. An adeno-associated viral (AAV) vector including at least one heterologous encoding sequence, wherein the heterologous encoding sequence is under control of a promoter and an enhancer selected from eHGT_608h, eHGT_609h, eHGT_621h, eHGT_633h, eHGT_634h, eHGT_635h, eHGT_636h, eHGT_351h, eHGT_367h, eHGT_441h, eHGT_612h, eHGT_613h, eHGT_614h, eHGT_617h, eHGT_618h, eHGT_619h, eHGT_620h, eHGT_442h, eHGT_444h, eHGT_445h, eHGT_450h, eHGT_452h, eHGT_610h, eHGT_611h, eHGT_615h, eHGT_616h, eHGT_627h, eHGT_628h, eHGT_629h, eHGT_446h, eHGT_447h, eHGT_622h, eHGT_623h, eHGT_624h, eHGT_625h, eHGT_630h, eHGT_631h, eHGT_735m, eHGT_736m, eHGT_737m, eHGT_738m, eHGT_739m, eHGT_740m, eHGT_741m, eHGT_742m, eHGT_743m, eHGT_744m, eHGT_746m, eHGT_747m, eHGT_748m, eHGT_749m, eHGT_750m, eHGT_751m, eHGT_779m, eHGT_780m, eHGT_781m, eHGT_782m, eHGT_783m, eHGT_784m, eHGT_785m, core2_eHGT_367h, 3xcore2_eHGT_367h, 3xcore_eHGT_441h, 3xCore-eHGT_621h, 3xCore-eHGT_447h, 3xcore2_eHGT_351h, 3xcore2_eHGT_445h, 3xcore2_eHGT_444h, 3xcore2_eHGT_452h, 3xcore2_eHGT_450h, 3xcore3_eHGT_450h, 3xcore2_eHGT_779m, 3xCore2_eHGT_780m, and 3xcore2_eHGT_743m.

54. A transgenic cell including an artificial expression construct or vector of any of the preceding embodiments.

55. The transgenic cell of embodiment 54, wherein the transgenic cell is a striatal neuron.

56. The transgenic cell of embodiments 54 or 55, wherein the transgenic cell is a striatal interneuron-cholinergic cell, a striatal medium spiny neuron-direct pathway cell, a striatal medium spiny neuron-indirect pathway cell, a striatal medium spiny neuron-pan cell, or a Drd3+ medium spiny cell.

57. The transgenic cell of embodiments 54, wherein the transgenic cell includes cells in the thalamus, cortex, hippocampus, olfactory bulb, Taenia tecta dorsal, hypothalamus, or amygdala.

58. The transgenic cell of embodiments 57, wherein the cells in the thalamus include cells within the paraventricular nucleus or the parafascicular nucleus.

59. The transgenic cell of embodiments 57, wherein the cells in the cortex include L2/3 IT neurons or L6 neurons.

60. The transgenic cell of embodiments 57, wherein the cells in the hippocampus include superior colliculus, CA1, CA2, CA3, hilus, or lateral pathway axons.

61. The transgenic cell of embodiments 57, wherein the cells in the olfactory bulb include periglomerular cells or glomeruli cells.

62. The transgenic cell of embodiments 57, wherein the cells in the Taenia tecta dorsal include putative excitatory neurons.

63. The transgenic cell of embodiments 57, wherein the cells in the hypothalamus include cells within the paraventricular hypothalamic nucleus.

64. The transgenic cell of embodiments 57, wherein the cells in the amygdala include cells within the lateral, medial and main intercalated (ITC) nucleus, central amygdala (CEA) nucleus, or cortical amygdalar area (COAp).

65. The transgenic cell of embodiment 54, wherein the transgenic cell is (or is found within) a putative cholinergic interneuron in the lateral septal nucleus, caudodorsal part of the lateral septum, accessory olfactory nucleus (AON), upper band of L2/3 pyramidal neurons in Pir, piriform-amygdalar area, entorhinal, perirhinal, frontal areas especially motor cortex areas, L3 in caudal entorhinal cortex, molecular layer of piriform area, dorsal tip of the interpeduncular nucleus, dorsal tegmental nucleus, axons in the supragenual nucleus, posterior of the basolateral amygdala (BLA), CA2, CA3, caudal CA1/Subiculum pyramidal neurons, substantia innominata axon, piriform area L2, CEA dense, BLA sparse, L5, or retrosplenial (RSP) cells.

66. A non-human transgenic animal including an artificial expression construct, vector, or transgenic cell of any of the preceding embodiments.

67. The non-human transgenic animal of embodiment 66, wherein the non-human transgenic animal is a mouse or a non-human primate.

68. An administrable composition including an artificial expression construct, vector, or transgenic cell of any of the preceding embodiments.

69. A kit including an artificial expression construct, vector, transgenic cell, transgenic animal, and/or administrable compositions of any of the preceding embodiments.

70. A method for expressing a heterologous gene within striatal neurons in vivo or in vitro, the method including administering the administrable composition of embodiment 58 in a sufficient dosage and for a sufficient time to a sample or subject including the striatal neurons thereby expressing the gene within the striatal neurons.

71. The method of embodiment 70, wherein the heterologous gene encodes an effector element or an expressible element.

72. The method of embodiment 71, wherein the effector element includes a reporter protein or a

functional molecule.

73. The method of embodiment 72, wherein the reporter protein includes a fluorescent protein.

74. The method of embodiment 72 or 73, wherein the functional molecule includes a functional ion transporter, enzyme, transcription factor, receptor, membrane protein, cellular trafficking protein, signaling molecule, neurotransmitter, calcium reporter, channelrhodopsin, CRISPR/CAS molecule, editase, guide RNA molecule, RNA, microRNA, homologous recombination donor cassette, DREADD, and/or a therapeutic gene product.

75. The method of embodiment 74, wherein the functional molecule includes aromatic L-amino acid decarboxylase (AADC), improved Cre (iCre), monomeric teal fluorescent protein 1 (mTFP1), tyrosine hydroxylase (TH), GTP cyclohydrolase I (CH1), tetrahydrobiopterin (BH4) and/ or glucocerebrosidase (GCase).

76. The method of embodiment 74, wherein the RNA suppresses or inhibits the expression of a pathogenic huntingtin (HTT) gene.

77. The method of embodiment 76, wherein the RNA sequence includes SEQ ID NOs: 163-195.

78. The method of embodiment 71, wherein the expressible element includes a non-functional molecule.

79. The method of embodiment 78, wherein the non-functional molecule includes a non-functional ion transporter, enzyme, transcription factor, receptor, membrane protein, cellular trafficking protein, signaling molecule, neurotransmitter, calcium reporter, channelrhodopsin, CRISPR/CAS molecule, editase, guide RNA molecule, RNA, microRNA, homologous recombination donor cassette, or DREADD.

80. The method of any of embodiments 70- 79, wherein the administering includes pipetting.

81. The method of embodiment 80, wherein the pipetting is to a brain slice.

82. The method of embodiment 81, wherein the brain slice includes a striatal interneuron-cholinergic cell, a striatal medium spiny neuron-direct pathway cell, a striatal medium spiny neuron-indirect pathway cell, a striatal medium spiny neuron-pan cell, or a Drd3+ medium spiny cells.

83. The method of embodiment 81 or 82, wherein the brain slice is murine, human, or non-human primate.

84. The method of any of embodiments 70-79, wherein the administering includes administering to a living subject.

85. The method of embodiment 84, wherein the living subject is a human, non-human primate, or a mouse.

86. The method of embodiment 84 or 85, wherein the administering provides a therapeutically

effective amount.

87. The method of embodiment 86, wherein the therapeutically effective amount treats a movement disorder.

88. The method of embodiment 86, wherein the therapeutically effective amount provides an effective amount, a prophylactic treatment and/or a therapeutic treatment against a movement disorder.

89. The method of embodiment 87 or 88, wherein the movement disorder includes Parkinson's disease, Huntington's disease, ataxia, corticobasal ganglionic degeneration (CBGD), dyskinesia, dystonia, tremors, hereditary spastic paraplegia, multiple system atrophy, myoclonus, progressive supranuclear palsy, restless legs syndrome, Rett syndrome, spasticity, Sydenham's chorea, other choreas, athetosis, ballism, stereotypy, tardive dyskinesia/dystonia, tics, Tourette's syndrome, olivopontocerebellar atrophy (OPCA), diffuse Lewy body disease, hemibalismus, hemi-facial spasm, Wilson's disease, stiff man syndrome, akinetic mutism, psychomotor retardation, painful legs, moving toes syndrome, a gait disorder, or a drug-induced movement disorder.

90. The method of any of embodiments 84 -89, wherein the administering to a living subject is through injection.

91. The method of embodiment 90, wherein the injection includes intravenous injection, intraparenchymal injection into brain tissue, intracerebroventricular (ICV) injection, intra-cisterna magna (ICM) injection, or intrathecal injection.

92. An artificial expression construct including CN2438, CN2439, CN2451, CN2463, CN2464, CN2465, CN2466, CN2013, CN2025, CN2229, CN2442, CN2443, CN2444, CN2447, CN2448, CN2449, CN2450, CN2467, CN2421, CN2231, CN2236, CN2237, CN2440, CN2441, CN2445, CN2446, CN2457, CN2458, CN2459, CN2232, CN2233, CN2452, CN2453, CN2454, CN2455, CN2460, CN2461, CN2628, CN2641, CN2642, CN2643, CN2629, CN2630, CN2745, CN2746, CN2631, CN2747, CN2632, CN2644, CN2748, CN2633, CN2634, CN2635, CN2609, CN2610, CN2749, CN2626, CN2611, CN2750, CN2614, CN2485, CN2486, CN2739, CN2740, CN2765, CN2766, CN2514, CN2555, CN2907, CN2909, CN2921, CN2982, CN3044, CN3038, CN3344, CN3281, CN3346, CN3566, CN2912, CN2913, CN2966, CN2203, or CN2700.

[0231] (viii) Closing Paragraphs. Variants of the sequences disclosed and referenced herein are also included. Guidance in determining which amino acid residues can be substituted, inserted, or deleted without abolishing biological activity can be found using computer programs well known in the art, such as DNASTAR™ (Madison, Wisconsin) software. Preferably, amino acid changes in the protein variants disclosed herein are conservative amino acid changes, i.e., substitutions

of similarly charged or uncharged amino acids. A conservative amino acid change involves substitution of one of a family of amino acids which are related in their side chains.

[0232] In a peptide or protein, suitable conservative substitutions of amino acids are known to those of skill in this art and generally can be made without altering a biological activity of a resulting molecule. Those of skill in this art recognize that, in general, single amino acid substitutions in non-essential regions of a polypeptide do not substantially alter biological activity (see, e.g., Watson et al. *Molecular Biology of the Gene,* 4th Edition, 1987, The Benjamin/Cummings Pub. Co., p. 224). Naturally occurring amino acids are generally divided into conservative substitution families as follows: Group 1: Alanine (Ala), Glycine (Gly), Serine (Ser), and Threonine (Thr); Group 2: (acidic): Aspartic acid (Asp), and Glutamic acid (Glu); Group 3: (acidic; also classified as polar, negatively charged residues and their amides): Asparagine (Asn), Glutamine (Gln), Asp, and Glu; Group 4: Gln and Asn; Group 5: (basic; also classified as polar, positively charged residues): Arginine (Arg), Lysine (Lys), and Histidine (His); Group 6 (large aliphatic, nonpolar residues): Isoleucine (Ile), Leucine (Leu), Methionine (Met), Valine (Val) and Cysteine (Cys); Group 7 (uncharged polar): Tyrosine (Tyr), Gly, Asn, Gln, Cys, Ser, and Thr; Group 8 (large aromatic residues): Phenylalanine (Phe), Tryptophan (Trp), and Tyr; Group 9 (non-polar): Proline (Pro), Ala, Val, Leu, Ile, Phe, Met, and Trp; Group 11 (aliphatic): Gly, Ala, Val, Leu, and Ile; Group 10 (small aliphatic, nonpolar or slightly polar residues): Ala, Ser, Thr, Pro, and Gly; and Group 12 (sulfur-containing): Met and Cys. Additional information can be found in Creighton (1984) Proteins, W.H. Freeman and Company.

[0233] In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring interactive biologic function on a protein is generally understood in the art (Kyte and Doolittle, 1982, J. Mol. Biol. 157(1), 105-32). Each amino acid has been assigned a hydropathic index on the basis of its hydrophobicity and charge characteristics (Kyte and Doolittle, 1982). These values are: Ile (+4.5); Val (+4.2); Leu (+3.8); Phe (+2.8); Cys (+2.5); Met (+1.9); Ala (+1.8); Gly (−0.4); Thr (−0.7); Ser (−0.8); Trp (−0.9); Tyr (−1.3); Pro (−1.6); His (−3.2); Glutamate (−3.5); Gln (−3.5); aspartate (−3.5); Asn (−3.5); Lys (−3.9); and Arg (−4.5).

[0234] It is known in the art that certain amino acids may be substituted by other amino acids having a similar hydropathic index or score and still result in a protein with similar biological activity, i.e., still obtain a biological functionally equivalent protein. In making such changes, the substitution of amino acids whose hydropathic indices are within ±2 is preferred, those within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred. It is also

understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity.

[0235] As detailed in U.S. Pat. No. 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: Arg (+3.0); Lys (+3.0); aspartate (+3.0±1); glutamate (+3.0±1); Ser (+0.3); Asn (+0.2); Gln (+0.2); Gly (0); Thr (−0.4); Pro (−0.5±1); Ala (−0.5); His (−0.5); Cys (−1.0); Met (−1.3); Val (−1.5); Leu (−1.8); Ile (−1.8); Tyr (−2.3); Phe (−2.5); Trp (−3.4). It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent, and in particular, an immunologically equivalent protein. In such changes, the substitution of amino acids whose hydrophilicity values are within ±2 is preferred, those within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred.

[0236] As outlined above, amino acid substitutions may be based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like.

[0237] As indicated elsewhere, variants of gene sequences can include codon optimized variants, sequence polymorphisms, splice variants, and/or mutations that do not affect the function of an encoded product to a statistically-significant degree.

[0238] Variants of the protein, nucleic acid, and gene sequences disclosed herein also include sequences with at least 70% sequence identity, 80% sequence identity, 85% sequence, 90% sequence identity, 95% sequence identity, 96% sequence identity, 97% sequence identity, 98% sequence identity, or 99% sequence identity to the protein, nucleic acid, or gene sequences disclosed herein.

[0239] "% sequence identity" refers to a relationship between two or more sequences, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between protein, nucleic acid, or gene sequences as determined by the match between strings of such sequences. "Identity" (often referred to as "similarity") can be readily calculated by known methods, including those described in: Computational Molecular Biology (Lesk, A. M., ed.) Oxford University Press, NY (1988); Biocomputing: Informatics and Genome Projects (Smith, D. W., ed.) Academic Press, NY (1994); Computer Analysis of Sequence Data, Part I (Griffin, A. M., and Griffin, H. G., eds.) Humana Press, NJ (1994); Sequence Analysis in Molecular Biology (Von Heijne, G., ed.) Academic Press (1987); and Sequence Analysis Primer (Gribskov, M. and Devereux, J., eds.) Oxford University Press, NY (1992). Preferred methods to determine identity are designed to give the best match between the sequences tested. Methods to determine identity and similarity are codified in publicly available computer programs.

Sequence alignments and percent identity calculations may be performed using the Megalign program of the LASERGENE bioinformatics computing suite (DNASTAR, Inc., Madison, Wisconsin). Multiple alignment of the sequences can also be performed using the Clustal method of alignment (Higgins and Sharp CABIOS, 5, 151-153 (1989) with default parameters (GAP PENALTY=10, GAP LENGTH PENALTY=10). Relevant programs also include the GCG suite of programs (Wisconsin Package Version 9.0, Genetics Computer Group (GCG), Madison, Wisconsin); BLASTP, BLASTN, BLASTX (Altschul, et al., J. Mol. Biol. 215:403-410 (1990); DNASTAR (DNASTAR, Inc., Madison, Wisconsin); and the FASTA program incorporating the Smith-Waterman algorithm (Pearson, Comput. Methods Genome Res., [Proc. Int. Symp.] (1994), Meeting Date 1992, 111-20. Editor(s): Suhai, Sandor. Publisher: Plenum, New York, N.Y.. Within the context of this disclosure it will be understood that where sequence analysis software is used for analysis, the results of the analysis are based on the "default values" of the program referenced. As used herein "default values" will mean any set of values or parameters, which originally load with the software when first initialized.

[0240] Variants also include nucleic acid molecules that hybridizes under stringent hybridization conditions to a sequence disclosed herein and provide the same function as the reference sequence. Exemplary stringent hybridization conditions include an overnight incubation at 42 °C in a solution including 50% formamide, 5XSSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5XDenhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1XSSC at 50 °C. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, moderately high stringency conditions include an overnight incubation at 37°C in a solution including 6XSSPE (20XSSPE=3M NaCl; 0.2M NaH_2PO_4; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 µg/ml salmon sperm blocking DNA; followed by washes at 50°C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5XSSC). Variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

[0241] The term concatenate is broadly used to describe linking together into a chain or series. It

is used to describe the linking together of nucleotide or amino acid sequences into a single nucleotide or amino acid sequence, respectively. The term "concatamerize" should be interpreted to recite: "concatenate." In particular embodiments, enhancer are concatenated into 2, 3, 4, 5, 6, 7, 9, or 10 copies within a single artificial expression construct.

[0242] As will be understood by one of ordinary skill in the art, each embodiment disclosed herein can comprise, consist essentially of or consist of its particular stated element, step, ingredient or component. Thus, the terms "include" or "including" should be interpreted to recite: "comprise, consist of, or consist essentially of." The transition term "comprise" or "comprises" means has, but is not limited to, and allows for the inclusion of unspecified elements, steps, ingredients, or components, even in major amounts. The transitional phrase "consisting of" excludes any element, step, ingredient or component not specified. The transition phrase "consisting essentially of" limits the scope of the embodiment to the specified elements, steps, ingredients or components and to those that do not materially affect the embodiment. A material effect would cause a statistically significant reduction in targeted expression in the targeted cell population as determined by scRNA-Seq and the targeted cell population and enhancer pairings:

striatal medium spiny neuron-pan: eHGT_608h, eHGT_609h, eHGT_633h, eHGT_634h, eHGT_635h, eHGT_636h, eHGT_351h, eHGT_367h, eHGT_450h, eHGT_447h, eHGT_744m, eHGT_782m, eHGT_785m, eHGT_441h, core2_eHGT_367h, 3xcore2_eHGT_367h, 3xcore_eHGT_441h, 3xCore2_eHGT_444h, 3xCore-eHGT_447h, and 3xcore2_eHGT_351h;

striatal medium spiny neuron-indirect pathway: eHGT_612h, eHGT_613h, eHGT_614h, eHGT_617h, eHGT_618h, eHGT_619h, eHGT_620h, eHGT_442h, eHGT_444h, eHGT_445h, eHGT_452h, eHGT_784m, 3xcore2_eHGT_445h, 3xcore2_eHGT_444h, 3xcore2_eHGT_452h, 3xcore2_eHGT_450h, and 3xcore3_eHGT_450h;

striatal medium spiny neuron-direct pathway: eHGT_610h, eHGT_611h, eHGT_615h, eHGT_616h, eHGT_627h, eHGT_628h, eHGT_629h, eHGT_446h, eHGT_779m, eHGT_780m, eHGT_781m, eHGT_783m, 3xcore2_eHGT_779m and 3xCore2_eHGT_780m;

striatal interneuron-cholinergic: eHGT_622h, eHGT_623h, eHGT_624h, eHGT_625h, eHGT_630h, eHGT_631h, eHGT_735m, eHGT_736m, eHGT_737m, eHGT_738m, eHGT_739m, eHGT_740m, eHGT_741m, eHGT_743m, eHGT_742m, HGT_746m, eHGT_747m, eHGT_748m, eHGT_749m, eHGT_750m, eHGT_751m, and 3xcore2_eHGT_743m;

Drd3+ medium spiny neurons in olfactory tubercle: eHGT_621h and 3xcore-eHGT_621h.

[0243] In particular embodiments, artificial means not naturally occurring.

[0244] Unless otherwise indicated, all numbers expressing quantities of ingredients, properties such as molecular weight, reaction conditions, and so forth used in the specification and claims are to be understood as being modified in all instances by the term "about." Accordingly, unless indicated to the contrary, the numerical parameters set forth in the specification and attached claims are approximations that may vary depending upon the desired properties sought to be obtained by the present invention. At the very least, and not as an attempt to limit the application of the doctrine of equivalents to the scope of the claims, each numerical parameter should at least be construed in light of the number of reported significant digits and by applying ordinary rounding techniques. When further clarity is required, the term "about" has the meaning reasonably ascribed to it by a person skilled in the art when used in conjunction with a stated numerical value or range, i.e. denoting somewhat more or somewhat less than the stated value or range, to within a range of ±20% of the stated value; ±19% of the stated value; ±18% of the stated value; ±17% of the stated value; ±16% of the stated value; ±15% of the stated value; ±14% of the stated value; ±13% of the stated value; ±12% of the stated value; ±11% of the stated value; ±10% of the stated value; ±9% of the stated value; ±8% of the stated value; ±7% of the stated value; ±6% of the stated value; ±5% of the stated value; ±4% of the stated value; ±3% of the stated value; ±2% of the stated value; or ±1% of the stated value.

[0245] Notwithstanding that the numerical ranges and parameters setting forth the broad scope of the invention are approximations, the numerical values set forth in the specific examples are reported as precisely as possible. Any numerical value, however, inherently contains certain errors necessarily resulting from the standard deviation found in their respective testing measurements.

[0246] The terms "a," "an," "the" and similar referents used in the context of describing the invention (especially in the context of the following claims) are to be construed to cover both the singular and the plural, unless otherwise indicated herein or clearly contradicted by context. Recitation of ranges of values herein is merely intended to serve as a shorthand method of referring individually to each separate value falling within the range. Unless otherwise indicated herein, each individual value is incorporated into the specification as if it were individually recited herein. All methods described herein can be performed in any suitable order unless otherwise indicated herein or otherwise clearly contradicted by context. The use of any and all examples, or exemplary language (e.g., "such as") provided herein is intended merely to better illuminate the invention and does not pose a limitation on the scope of the invention otherwise claimed. No language in the specification should be construed as indicating any non-claimed element essential to the practice of the invention.

[0247] Groupings of alternative elements or embodiments of the invention disclosed herein are not to be construed as limitations. Each group member may be referred to and claimed individually or in any combination with other members of the group or other elements found herein. It is anticipated that one or more members of a group may be included in, or deleted from, a group for reasons of convenience and/or patentability. When any such inclusion or deletion occurs, the specification is deemed to contain the group as modified thus fulfilling the written description of all Markush groups used in the appended claims.

[0248] Certain embodiments of this invention are described herein, including the best mode known to the inventors for carrying out the invention. Of course, variations on these described embodiments will become apparent to those of ordinary skill in the art upon reading the foregoing description. The inventor expects skilled artisans to employ such variations as appropriate, and the inventors intend for the invention to be practiced otherwise than specifically described herein. Accordingly, this invention includes all modifications and equivalents of the subject matter recited in the claims appended hereto as permitted by applicable law. Moreover, any combination of the above-described elements in all possible variations thereof is encompassed by the invention unless otherwise indicated herein or otherwise clearly contradicted by context.

[0249] Furthermore, numerous references have been made to patents, printed publications, journal articles and other written text throughout this specification (referenced materials herein). Each of the referenced materials are individually incorporated herein by reference in their entirety for their referenced teaching.

[0250] In closing, it is to be understood that the embodiments of the invention disclosed herein are illustrative of the principles of the present invention. Other modifications that may be employed are within the scope of the invention. Thus, by way of example, but not of limitation, alternative configurations of the present invention may be utilized in accordance with the teachings herein. Accordingly, the present invention is not limited to that precisely as shown and described.

[0251] The particulars shown herein are by way of example and for purposes of illustrative discussion of the preferred embodiments of the present invention only and are presented in the cause of providing what is believed to be the most useful and readily understood description of the principles and conceptual aspects of various embodiments of the invention. In this regard, no attempt is made to show structural details of the invention in more detail than is necessary for the fundamental understanding of the invention, the description taken with the drawings and/or examples making apparent to those skilled in the art how the several forms of the invention may be embodied in practice.

[0252] Definitions and explanations used in the present disclosure are meant and intended to be controlling in any future construction unless clearly and unambiguously modified in the following examples or when application of the meaning renders any construction meaningless or essentially meaningless. In cases where the construction of the term would render it meaningless or essentially meaningless, the definition should be taken from Webster's Dictionary, 3rd Edition or a dictionary known to those of ordinary skill in the art, such as the Oxford Dictionary of Biochemistry and Molecular Biology (Ed. Anthony Smith, Oxford University Press, Oxford, 2004).

CLAIMS

What is claimed is:

1. An artificial expression construct comprising (i) an enhancer selected from 3xcore2_eHGT_743m or core2_eHGT_367h; (ii) a promoter; and (iii) a heterologous encoding sequence.

2. The artificial expression construct of claim 1, wherein the enhancer comprises 3xcore2_eHGT_743m, the promoter is minBglobin, and the heterologous encoding sequence encodes human aromatic L-amino acid decarboxylase.

3. The artificial expression construct of claim 1, wherein the enhancer comprises core2_eHGT_367h, the promoter is minRho*, and the heterologous encoding sequence encodes human aromatic L-amino acid decarboxylase.

4. A core of the eHGT_351h, eHGT_367h, eHGT_441h, eHGT_444h, eHGT_445h, eHGT_447h, eHGT_450h, eHGT_452h, eHGT_621h, eHGT_743m, eHGT_779m, or eHGT_780m enhancer.

5. The core of claim 4, wherein the core has the sequence as set forth in SEQ ID NO: 202; SEQ ID NO: 204; SEQ ID NO: 206; SEQ ID NO: 208; SEQ ID NO: 210; SEQ ID NO: 212; SEQ ID NO: 214; SEQ ID NO: 216; SEQ ID NO: 218; SEQ ID NO: 220; SEQ ID NO: 222; SEQ ID NO: 224; or SEQ ID NO: 226.

6. The core of claim 4, wherein the core is concatenated into a concatemer comprising 2, 3, 4, 5, 6, 7, 8, 9, or 10 copies of the enhancer core.

7. The core of claim 6, wherein concatenated core comprises 2, 3, 4, 5, 6, 7, 8, 9, or 10 copies of SEQ ID NO: 202; SEQ ID NO: 204; SEQ ID NO: 206; SEQ ID NO: 208; SEQ ID NO: 210; SEQ ID NO: 212; SEQ ID NO: 214; SEQ ID NO: 216; SEQ ID NO: 218; SEQ ID NO: 220; SEQ ID NO: 222; SEQ ID NO: 224; and/or SEQ ID NO: 226.

8. The core of claim 6, wherein the concatenated core comprises 3 copies of SEQ ID NO: 206.

9. The core of claim 6, wherein the concatenated core comprises 3 copies of SEQ ID NO: 202.

10. The core of claim 6, wherein the concatenated core comprises 3 copies of SEQ ID NO: 204.

11. The core of claim 6, wherein the concatenated core comprises 3 copies of SEQ ID NO: 208.

12. The core of claim 6, wherein the concatenated core comprises 3 copies of SEQ ID NO: 210.

13. The core of claim 6, wherein the concatenated core comprises 3 copies of SEQ ID NO: 212.

14. The core of claim 6, wherein the concatenated core comprises 3 copies of SEQ ID NO: 214.

15. The core of claim 6, wherein the concatenated core comprises 3 copies of SEQ ID NO: 216.

16. The core of claim 6, wherein the concatenated core comprises 3 copies of SEQ ID NO: 218.

17. The core of claim 6, wherein the concatenated core comprises 3 copies of SEQ ID NO: 220.

18. The core of claim 6, wherein the concatenated core comprises 3 copies of SEQ ID NO: 222.

19. The core of claim 6, wherein the concatenated core comprises 3 copies of SEQ ID NO: 224.

20. The core of claim 6, wherein the concatenated core comprises 3 copies of SEQ ID NO: 226.

21. The core of claim 8, wherein the concatenated core comprises SEQ ID NO: 207.

22. The core of claim 9, wherein the concatenated core comprises SEQ ID NO: 203.

23. The core of claim 10, wherein the concatenated core comprises SEQ ID NO: 205.

24. The core of claim 11, wherein the concatenated core comprises SEQ ID NO: 209.

25. The core of claim 12, wherein the concatenated core comprises SEQ ID NO: 211.

26. The core of claim 13, wherein the concatenated core comprises SEQ ID NO: 213.

27. The core of claim 14, wherein the concatenated core comprises SEQ ID NO: 215.

28. The core of claim 15, wherein the concatenated core comprises SEQ ID NO: 217.

29. The core of claim 16, wherein the concatenated core comprises SEQ ID NO: 219.

30. The core of claim 17, wherein the concatenated core comprises SEQ ID NO: 221.

31. The core of claim 18, wherein the concatenated core comprises SEQ ID NO: 223.

32. The core of claim 19, wherein the concatenated core comprises SEQ ID NO: 225.

33. The core of claim 20, wherein the concatenated core comprises SEQ ID NO: 227.

34. An artificial expression construct comprising (i) an enhancer selected from core2_eHGT_743m, core2_eHGT_367h, eHGT_608h, eHGT_609h, eHGT_621h, eHGT_633h, eHGT_634h, eHGT_635h, eHGT_636h, eHGT_351h, eHGT_367h, eHGT_441h, eHGT_612h, eHGT_613h, eHGT_614h, eHGT_617h, eHGT_618h, eHGT_619h, eHGT_620h, eHGT_442h, eHGT_444h, eHGT_445h, eHGT_450h, eHGT_452h, eHGT_610h, eHGT_611h, eHGT_615h,

eHGT_616h, eHGT_627h, eHGT_628h, eHGT_629h, eHGT_446h, eHGT_447h, eHGT_622h, eHGT_623h, eHGT_624h, eHGT_625h, eHGT_630h, eHGT_631h, eHGT_735m, eHGT_736m, eHGT_737m, eHGT_738m, eHGT_739m, eHGT_740m, eHGT_741m, eHGT_742m, eHGT_743m, eHGT_744m, eHGT_746m, eHGT_747m, eHGT_748m, eHGT_749m, eHGT_750m, eHGT_751m, eHGT_779m, eHGT_780m, eHGT_781m, eHGT_782m, eHGT_783m, eHGT_784m, eHGT_785m, core_eHGT_441h, Core-eHGT_621h, Core-eHGT_447h, core2_eHGT_351h, core2_eHGT_445h, core2_eHGT_444h, core2_eHGT_452h, core2_eHGT_450h, core3_eHGT_450h, core2_eHGT_779m, and Core2_eHGT_780m; (ii) a promoter; and (iii) a heterologous encoding sequence.

35. The artificial expression construct of claim 4, wherein the enhancer is concatenated comprising 3xcore2_eHGT_743m, 3xcore2_eHGT_367h, 3xcore_eHGT_441h, 3xCore-eHGT_621h, 3xCore-eHGT_447h, 3xcore2_eHGT_351h, 3xcore2_eHGT_445h, 3xcore2_eHGT_444h, 3xcore2_eHGT_452h, 3xcore2_eHGT_450h, 3xcore3_eHGT_450h, 3xcore2_eHGT_779m, and 3xCore2_eHGT_780m

36. The artificial expression construct of claim 34, wherein the heterologous encoding sequence encodes an effector element or an expressible element.

37. The artificial expression construct of claim 36, wherein the effector element comprises a reporter protein or a functional molecule.

38. The artificial expression construct of claim 37, wherein the reporter protein comprises a fluorescent protein.

39. The artificial expression construct of claim 37, wherein the functional molecule comprises a functional ion transporter, enzyme, transcription factor, receptor, membrane protein, cellular trafficking protein, signaling molecule, neurotransmitter, calcium reporter, channelrhodopsin, CRISPR/CAS molecule, editase, guide RNA molecule, RNA, microRNA, homologous recombination donor cassette, or a designer receptor exclusively activated by designer drug (DREADD).

40. The artificial expression construct of claim 39, wherein the functional molecule comprises aromatic L-amino acid decarboxylase (AADC), improved Cre (iCre), monomeric teal fluorescent protein 1 (mTFP1), tyrosine hydroxylase (TH), GTP cyclohydrolase I (CH1), tetrahydrobiopterin (BH4) and/ or glucocerebrosidase (GCase).

41. The artificial expression construct of claim 39, wherein the mRNA suppresses or inhibits the expression of a pathogenic huntingtin (HTT) gene.

42. The artificial expression construct of claim 41, wherein the RNA sequence comprises SEQ ID NOs: 163-195.

43. The artificial expression construct of claim 36, wherein the expressible element comprises a non-functional molecule.

44. The artificial expression construct of claim 43, wherein the non-functional molecule comprises a non-functional ion transporter, enzyme, transcription factor, receptor, membrane protein, cellular trafficking protein, signaling molecule, neurotransmitter, calcium reporter, channelrhodopsin, CRISPR/CAS molecule, editase, guide RNA molecule, RNA, homologous recombination donor cassette, or a DREADD.

45. The artificial expression construct of claim 34, wherein the artificial expression construct is associated with a capsid that crosses the blood brain barrier.

46. The artificial expression construct of claim 45, wherein the capsid comprises PHP.eB, AAV-BR1, AAV-PHP.S, AAV-PHP.B, AAV-PPS, PHP.V1, AAV1, AAV2, AAV5, AAV8, AAV9, AAV11, Rh10, Hu11, AAV2-retro, AAV9-retro, CAP.B10, or CAP.B22.

47. The artificial expression construct of claim 34, wherein the artificial expression construct comprises or encodes a skipping element.

48. The artificial expression construct of claim 47, wherein the skipping element comprises a 2A peptide and/or an internal ribosome entry site (IRES).

49. The artificial expression construct of claim 48, wherein the 2A peptide is selected from T2A, P2A, E2A, or F2A.

50. The artificial expression construct of claim 34, wherein the artificial expression construct comprises or encodes a set of features selected from 3xcore2_eHGT_743m, core2_eHGT_367h, eHGT_608h, eHGT_609h, eHGT_621h, eHGT_633h, eHGT_634h, eHGT_635h, eHGT_636h, eHGT_351h, eHGT_367h, eHGT_441h, eHGT_612h, eHGT_613h, eHGT_614h, eHGT_617h, eHGT_618h, eHGT_619h, eHGT_620h, eHGT_442h, eHGT_444h, eHGT_445h, eHGT_450h, eHGT_452h, eHGT_610h, eHGT_611h, eHGT_615h, eHGT_616h, eHGT_627h, eHGT_628h, eHGT_629h, eHGT_446h, eHGT_447h, eHGT_622h, eHGT_623h, eHGT_624h, eHGT_625h, eHGT_630h, eHGT_631h, eHGT_735m, eHGT_736m, eHGT_737m, eHGT_738m, eHGT_739m, eHGT_740m, eHGT_741m, eHGT_742m, eHGT_743m, eHGT_744m, eHGT_746m, eHGT_747m, eHGT_748m, eHGT_749m, eHGT_750m, eHGT_751m, eHGT_779m, eHGT_780m, eHGT_781m, eHGT_782m, eHGT_783m, eHGT_784m, eHGT_785m, 3xcore2_eHGT_367h, 3xcore_eHGT_441h, 3xCore-eHGT_621h, 3xCore-eHGT_447h, 3xcore2_eHGT_351h, 3xcore2_eHGT_445h, 3xcore2_eHGT_444h, 3xcore2_eHGT_452h, 3xcore2_eHGT_450h, 3xcore3_eHGT_450h, 3xcore2_eHGT_779m, 3xCore2_eHGT_780m, AAV, scAAV, rAAV, pAAV, minBglobin, CMV, minCMV, minRho, minRho*, AADC, TH, CH1, BH4 GCase, Intron, 3xHA, an RNA that suppresses or inhibits the

expression of a pathogenic HTT gene, a gene whose expression treats a movement disorder, fluorescent protein, Cre, iCre, dgCre, FlpO, tTA2, SP10ins, WPRE3, hGHpA, and/or BGHpA.

51. The artificial expression construct of claim 34, wherein the artificial expression construct comprises or encodes a set of features selected from:

3xcore2_eHGT_743m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xSP10ins-core2_eHGT_367h-minRho*-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_608h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_609h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_621h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_633h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_634h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_635h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_636h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xSP10ins-eHGT_351h-minRho*-[gene encoding functional molecule]-WPRE3-BGHpA;

3xSP10ins-eHGT_367h-minRho*-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_441h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_612h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_613h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_614h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_617h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_618h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_619h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_620h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_442h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_444h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_445h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_450h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_452h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_610h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_611h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_615h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_616h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_627h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_628h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_629h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_446h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_447h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_622h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_623h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_624h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_625h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_630h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_631h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_735m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_736m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_737m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_738m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_739m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_740m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_741m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_742m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_743m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_744m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_746m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_747m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_748m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_749m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_750m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_751m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_779m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_780m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_781m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_782m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_783m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_784m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_785m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_452h-minBglobin-[gene encoding functional molecule]A-WPRE3-BGHpA;

3xSP10ins-eHGT_367h-minRho-[gene encoding functional molecule]-WPRE3-BGHpA;

3xSP10ins-eHGT_367h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xSP10ins-3xcore2_eHGT_367h-minRho*-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore_eHGT_441h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore2_eHGT_445h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore2_eHGT_444h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore2_eHGT_452h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore2_eHGT_779m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xCore-eHGT_621h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xCore2_eHGT_780m-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xCore-eHGT_447h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xSP10ins_3xcore2_eHGT_351h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore2_eHGT_450h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore3_eHGT_450h-minBglobin-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore2_eHGT_743m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xSP10ins-core2_eHGT_367h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_608h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_609h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_621h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_633h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_634h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_635h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_636h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xSP10ins-eHGT_351h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xSP10ins-eHGT_367h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_441h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_612h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_613h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_614h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_617h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_618h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_619h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_620h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_442h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_444h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_445h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_450h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_452h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_610h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_611h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_615h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_616h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_627h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_628h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_629h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_446h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_447h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_622h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

eHGT_623h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_624h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_625h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_630h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_631h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_735m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_736m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_737m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_738m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_739m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_740m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_741m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_742m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_743m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_744m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_746m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_747m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_748m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_749m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_750m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_751m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_779m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_780m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_781m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_782m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_783m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_784m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_785m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;
eHGT_452h-[minimal promoter]-[gene encoding functional molecule]A-WPRE3-BGHpA;

3xSP10ins-3xcore2_eHGT_367h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore_eHGT_441h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore2_eHGT_445h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore2_eHGT_444h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore2_eHGT_452h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore2_eHGT_779m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xCore-eHGT_621h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xCore2_eHGT_780m-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xCore-eHGT_447h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xSP10ins_3xcore2_eHGT_351h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA;

3xcore2_eHGT_450h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA; or

3xcore3_eHGT_450h-[minimal promoter]-[gene encoding functional molecule]-WPRE3-BGHpA.

wherein the functional molecule optionally comprises a therapeutic gene product.

52. The artificial expression construct of claim 51, wherein the functional molecule is a therapeutic gene product that treats a movement disorder.

53. A vector comprising an artificial expression construct of any of claim 34.

54. The vector of claim 53, wherein the vector comprises a viral vector.

55. The vector of claim 54, wherein the viral vector comprises a recombinant adeno-associated viral (AAV) vector.

56. An adeno-associated viral (AAV) vector comprising at least one heterologous encoding sequence, wherein the heterologous encoding sequence is under control of a promoter and an enhancer selected from 3xcore2_eHGT_743m, core2_eHGT_367h, eHGT_608h, eHGT_609h, eHGT_621h, eHGT_633h, eHGT_634h, eHGT_635h, eHGT_636h, eHGT_351h, eHGT_367h,

eHGT_441h, eHGT_612h, eHGT_613h, eHGT_614h, eHGT_617h, eHGT_618h, eHGT_619h, eHGT_620h, eHGT_442h, eHGT_444h, eHGT_445h, eHGT_450h, eHGT_452h, eHGT_610h, eHGT_611h, eHGT_615h, eHGT_616h, eHGT_627h, eHGT_628h, eHGT_629h, eHGT_446h, eHGT_447h, eHGT_622h, eHGT_623h, eHGT_624h, eHGT_625h, eHGT_630h, eHGT_631h, eHGT_735m, eHGT_736m, eHGT_737m, eHGT_738m, eHGT_739m, eHGT_740m, eHGT_741m, eHGT_742m, eHGT_743m, eHGT_744m, eHGT_746m, eHGT_747m, eHGT_748m, eHGT_749m, eHGT_750m, eHGT_751m, eHGT_779m, eHGT_780m, eHGT_781m, eHGT_782m, eHGT_783m, eHGT_784m, eHGT_785m, 3xcore2_eHGT_367h, 3xcore_eHGT_441h, 3xCore-eHGT_621h, 3xCore-eHGT_447h, 3xcore2_eHGT_351h, 3xcore2_eHGT_445h, 3xcore2_eHGT_444h, 3xcore2_eHGT_452h, 3xcore2_eHGT_450h, 3xcore3_eHGT_450h, 3xcore2_eHGT_779m, and 3xCore2_eHGT_780m.

57. A transgenic cell comprising an artificial expression construct of claim 34.

58. The transgenic cell of claim 57, wherein the transgenic cell is a striatal neuron.

59. The transgenic cell of claim 58, wherein the striatal neuron is a striatal interneuron-cholinergic cell, a striatal medium spiny neuron-direct pathway cell, a striatal medium spiny neuron-indirect pathway cell, a striatal medium spiny neuron-pan cell, or a Drd3+ medium spiny cells.

60. A non-human transgenic animal comprising an artificial expression construct of claim 34.

61. The non-human transgenic animal of claim 60, wherein the non-human transgenic animal is a mouse or a non-human primate.

62. An administrable composition comprising an artificial expression construct of claim 34.

63. A kit comprising an artificial expression construct of claim 34.

64. A method for expressing a heterologous gene within striatal neurons in vivo or in vitro, the method comprising administering the administrable composition of claim 62 in a sufficient dosage and for a sufficient time to a sample or subject comprising the striatal neurons thereby expressing the gene within the striatal neurons.

65. The method of claim 64, wherein the heterologous gene encodes an effector element or an expressible element.

66. The method of claim 65, wherein the effector element comprises a reporter protein or a functional molecule.

67. The method of claim 66, wherein the reporter protein comprises a fluorescent protein.

68. The method of claim 66, wherein the functional molecule comprises a functional ion transporter, enzyme, transcription factor, receptor, membrane protein, cellular trafficking protein, signaling molecule, neurotransmitter, calcium reporter, channelrhodopsin, CRISPR/CAS

molecule, editase, guide RNA molecule, RNA, homologous recombination donor cassette, or a DREADD.

69. The method of claim 68, wherein the functional molecule comprises aromatic L-amino acid decarboxylase (AADC), improved Cre (iCre), monomeric teal fluorescent protein 1 (mTFP1), tyrosine hydroxylase (TH), GTP cyclohydrolase I (CH1), tetrahydrobiopterin (BH4) and/ or glucocerebrosidase (GCase).

70. The method of claim 68, wherein the RNA suppresses or inhibits the expression of a pathogenic huntingtin (HTT) gene.

71. The method of claim 70, wherein the RNA sequence comprises SEQ ID NOs: 163-195.

72. The method of claim 65, wherein the expressible element comprises a non-functional molecule.

73. The method of claim 72, wherein the non-functional molecule comprises a non-functional ion transporter, enzyme, transcription factor, receptor, membrane protein, cellular trafficking protein, signaling molecule, neurotransmitter, calcium reporter, channelrhodopsin, CRISPR/CAS molecule, editase, guide RNA molecule, RNA, homologous recombination donor cassette, or DREADD.

74. The method of claim 64, wherein the administering comprises pipetting.

75. The method of claim 74, wherein the pipetting is to a brain slice.

76. The method of claim 75, wherein the brain slice comprises a striatal interneuron-cholinergic cell, a striatal medium spiny neuron-direct pathway cell, a striatal medium spiny neuron-indirect pathway cell, a striatal medium spiny neuron-pan cell, or a Drd3+ medium spiny cells.

77. The method of claim 75, wherein the brain slice is murine, human, or non-human primate.

78. The method of claim 64, wherein the administering comprises administering to a living subject.

79. The method of claim 78, wherein the living subject is a human, non-human primate, or a mouse.

80. The method of claim 78, wherein the administering provides a therapeutically effective amount.

81. The method of claim 80, wherein the therapeutically effective amount treats a movement disorder.

82. The method of claim 80, wherein the therapeutically effective amount provides an effective amount, a prophylactic treatment and/or a therapeutic treatment against a movement disorder.

83. The method of claim 81 or 82, wherein the movement disorder comprises Parkinson's

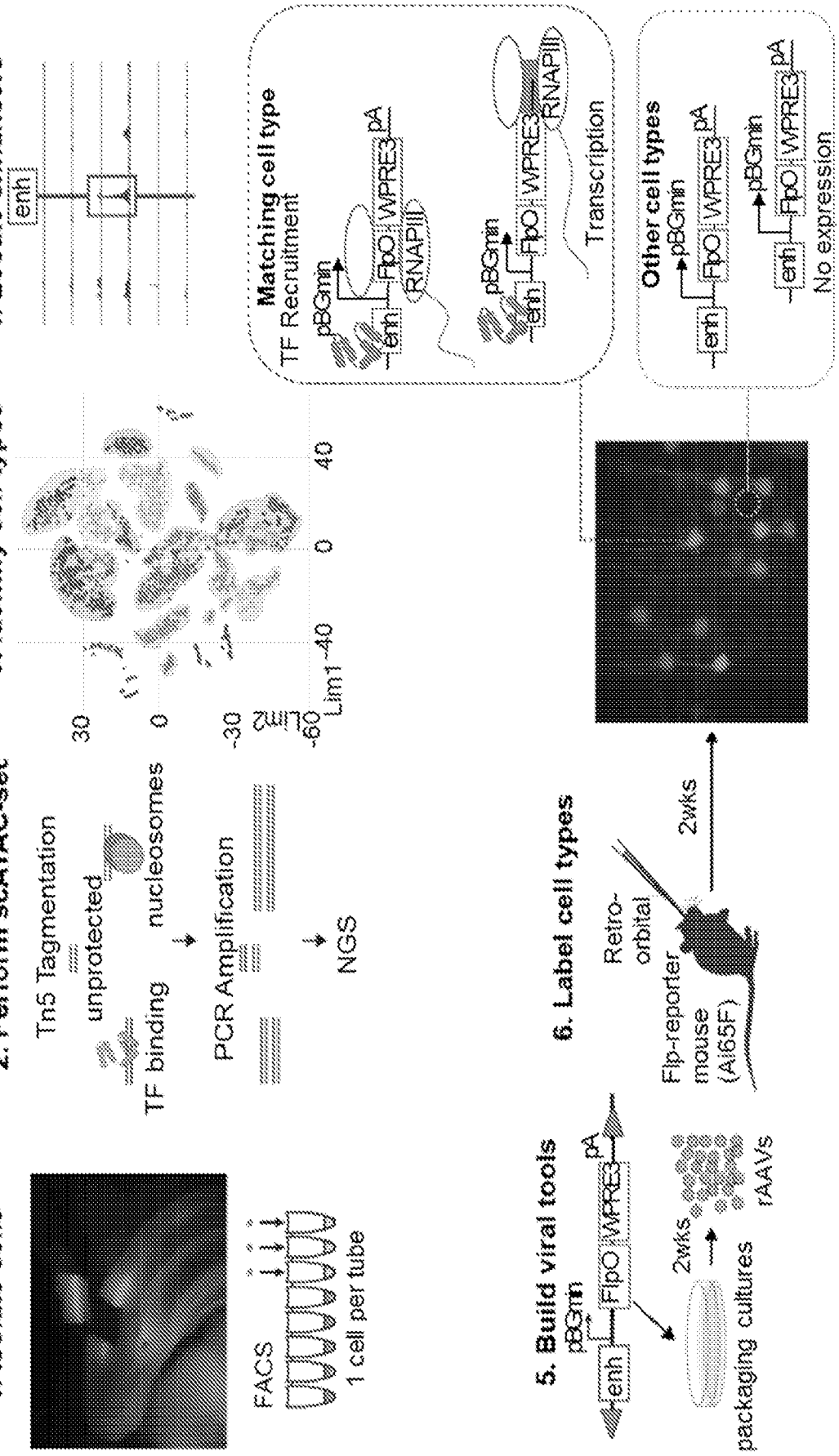
disease, Huntington's disease, ataxia, corticobasal ganglionic degeneration (CBGD), dyskinesia, dystonia, tremors, hereditary spastic paraplegia, multiple system atrophy, myoclonus, progressive supranuclear palsy, restless legs syndrome, Rett syndrome, spasticity, Sydenham's chorea, other choreas, athetosis, ballism, stereotypy, tardive dyskinesia/dystonia, tics, Tourette's syndrome, olivopontocerebellar atrophy (OPCA), diffuse Lewy body disease, hemibalismus, hemi-facial spasm, Wilson's disease, stiff man syndrome, akinetic mutism, psychomotor retardation, painful legs, moving toes syndrome, a gait disorder, or a drug-induced movement disorder.

84. The method of claim 78, wherein the administering to a living subject is through injection.

85. The method of claim 84, wherein the injection comprises intravenous injection, intraparenchymal injection into brain tissue, intracerebroventricular (ICV) injection, intra-cisterna magna (ICM) injection, or intrathecal injection.

86. An artificial expression construct comprising CN3038, CN2514, CN2438, CN2439, CN2451, CN2463, CN2464, CN2465, CN2466, CN2013, CN2025, CN2229, CN2442, CN2443, CN2444, CN2447, CN2448, CN2449, CN2450, CN2467, CN2421, CN2231, CN2236, CN2237, CN2440, CN2441, CN2445, CN2446, CN2457, CN2458, CN2459, CN2232, CN2233, CN2452, CN2453, CN2454, CN2455, CN2460, CN2461, CN2628, CN2641, CN2642, CN2643, CN2629, CN2630, CN2745, CN2746, CN2631, CN2747, CN2632, CN2644, CN2748, CN2633, CN2634, CN2635, CN2609, CN2610, CN2749, CN2626, CN2611, CN2750, CN2614, CN2485, CN2486, CN2739, CN2740, CN2765, CN2766, CN2555, CN2907, CN2909, CN2921, CN2982, CN3044, CN3344, CN3281, CN3346, CN3566, CN2912, CN2913, CN2966, CN2203, and CN2700.

FIG. 1


1. Isolate cells
FACS
1 cell per tube
2. Perform scATAC-seq
Tn5 Tagmentation
unprotected
nucleosomes
TF binding
PCR Amplification
NGS
3. Identify cell types
30
0
-30
-60
Lim1
-40
0
40
4. Locate enhancers
enh
Matching cell type
TF Recruitment
pBGmin
enh
FlpO
WPRE3
pA
RNAPII
Transcription
Other cell types
No expression
5. Build viral tools
2wks
rAAVs
packaging cultures
6. Label cell types
Retro-orbital
Flp-reporter mouse (Ai65F)
2wks

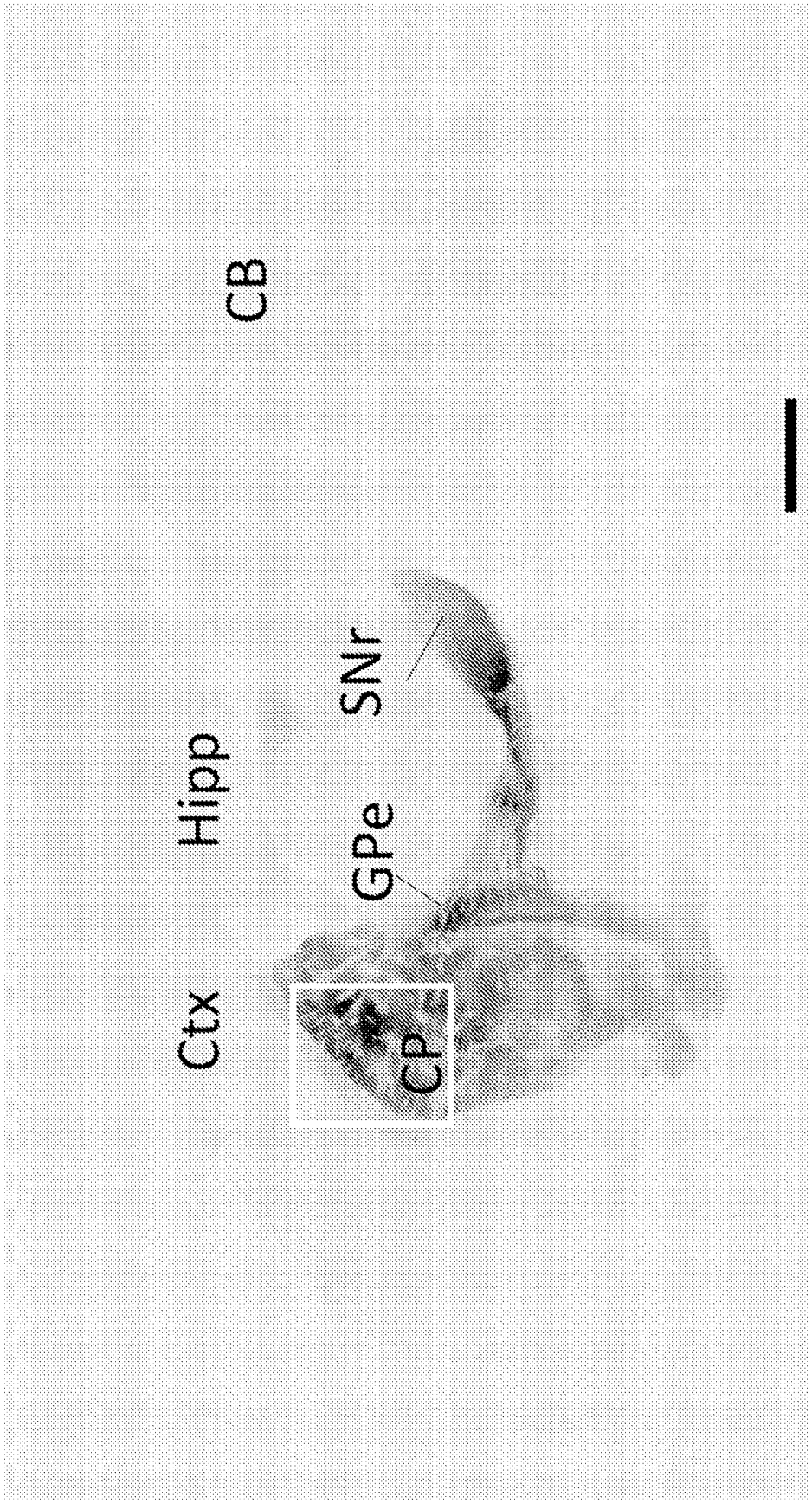


FIG. 2A

FIG. 2B

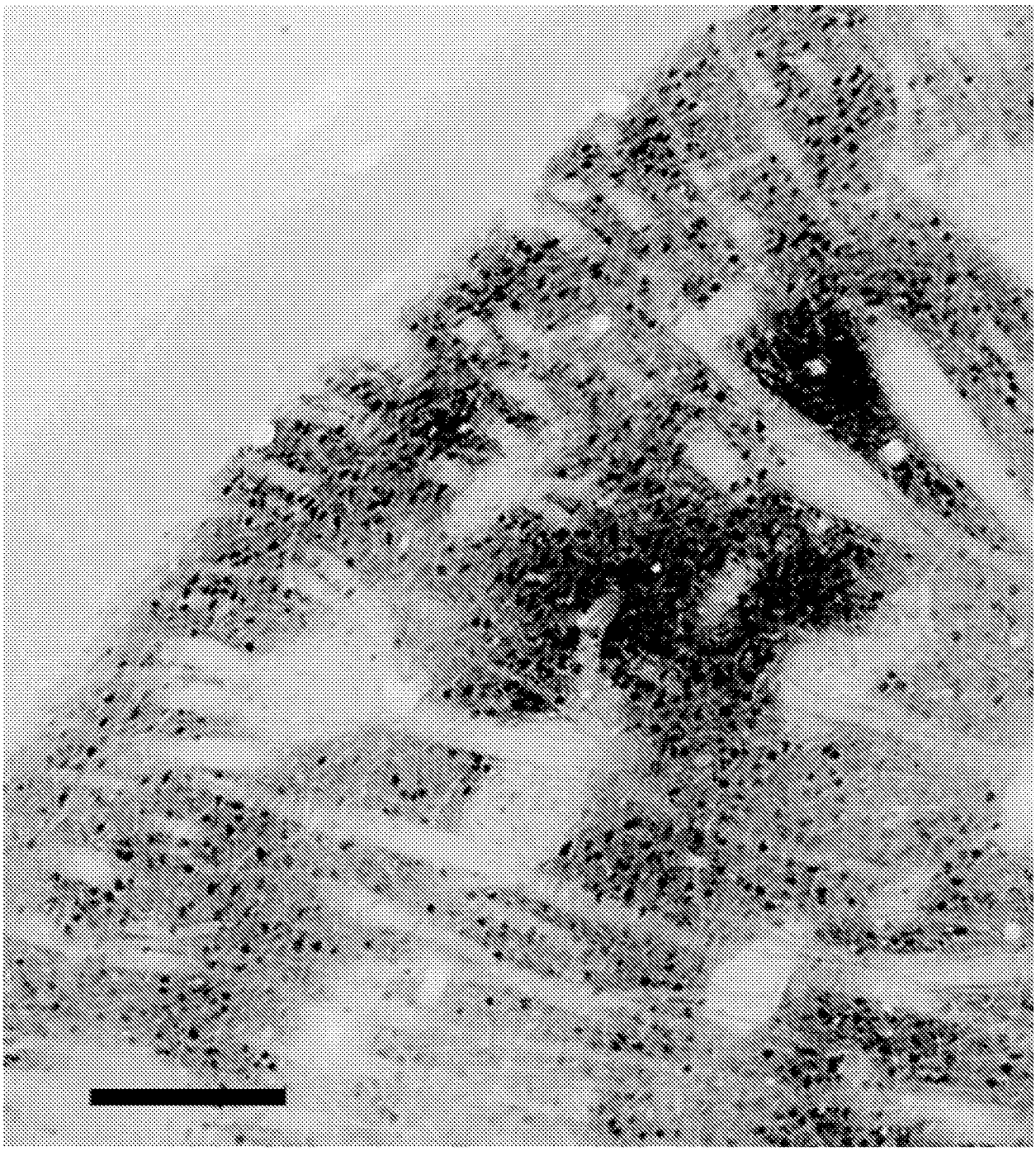


FIG. 3A

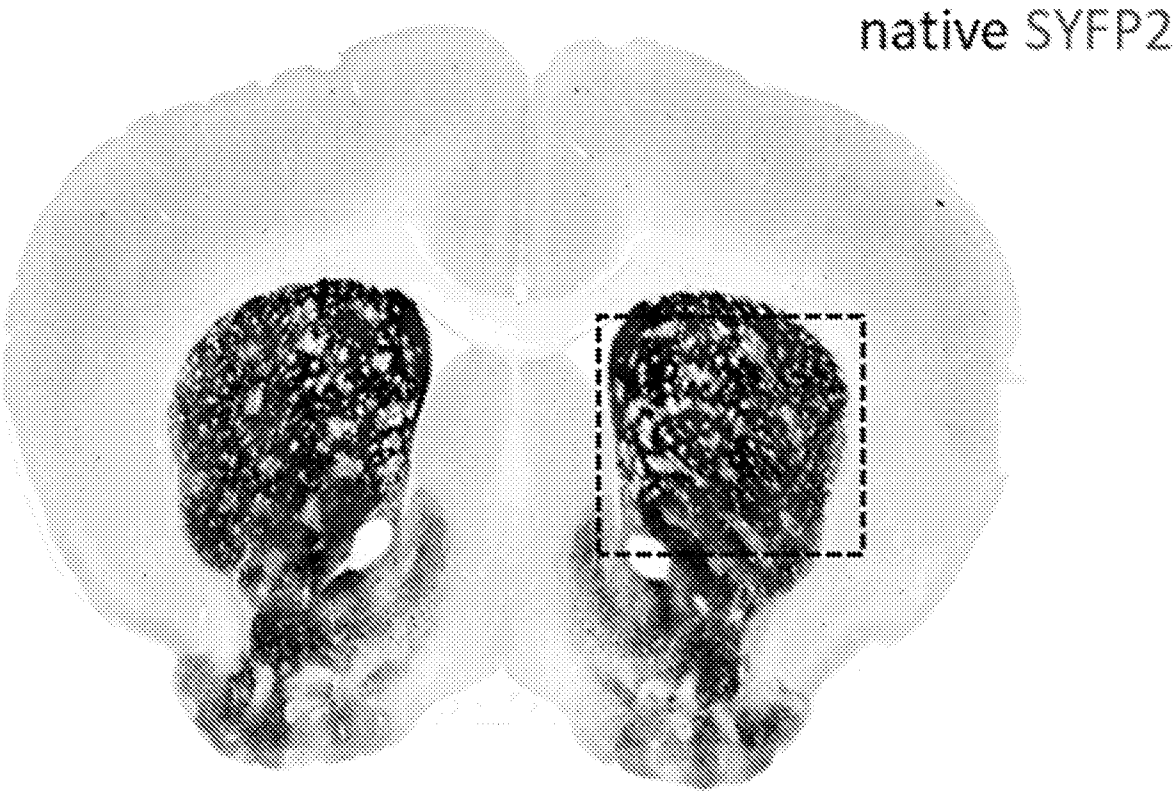


FIG. 3B

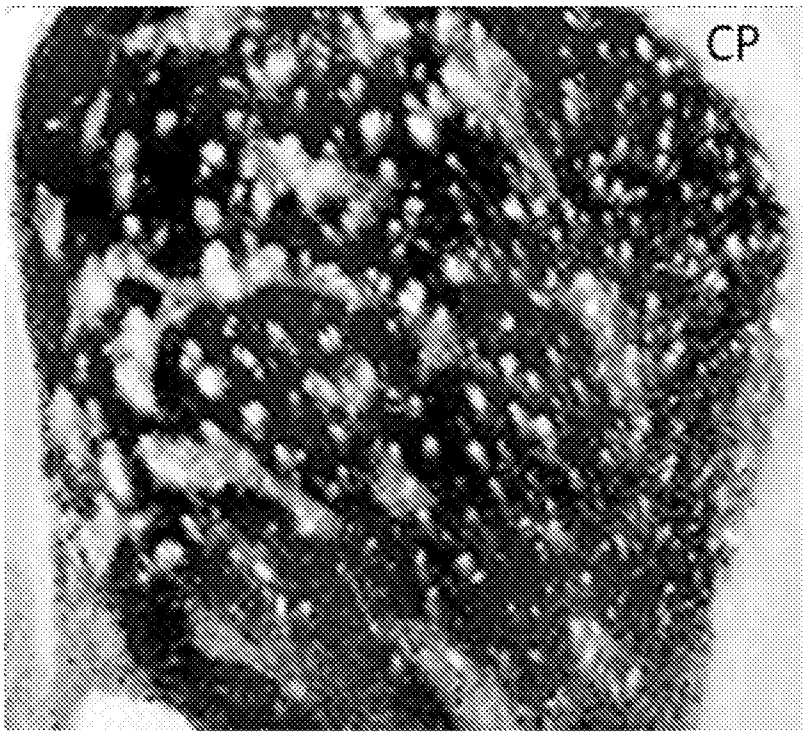


FIG. 3C

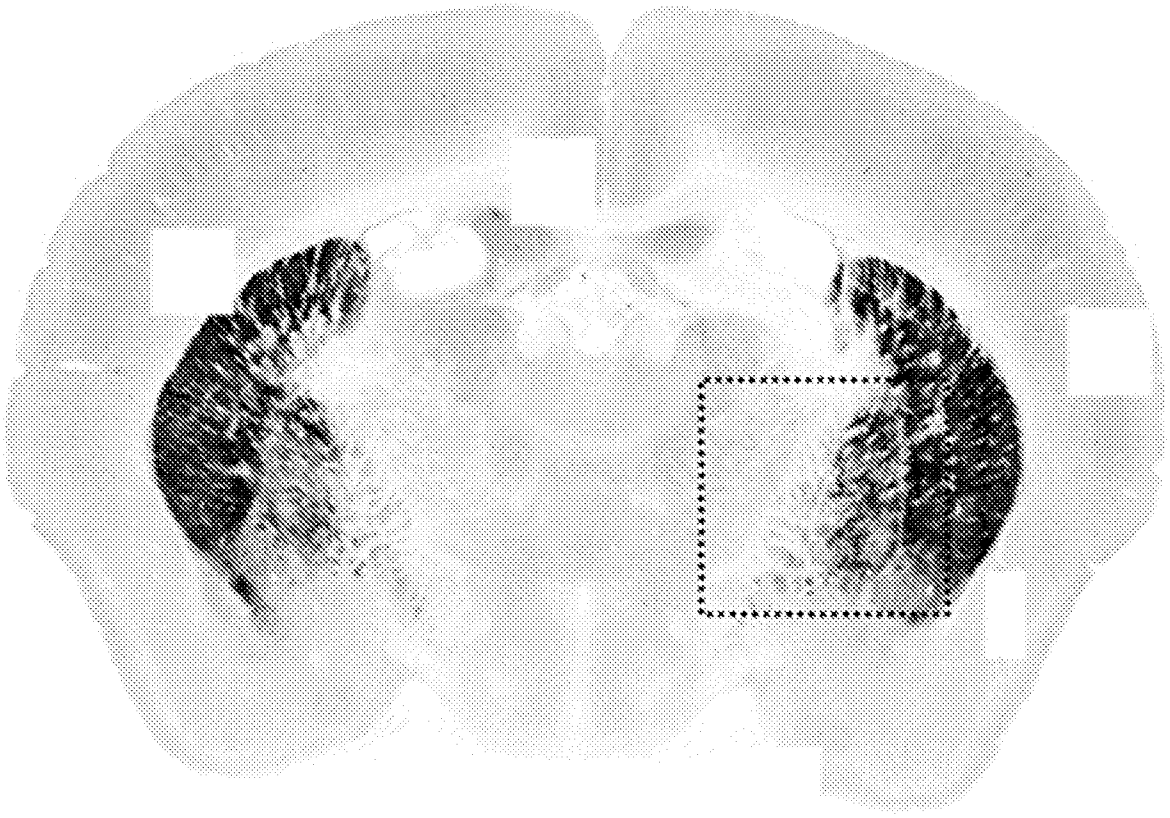


FIG. 3D

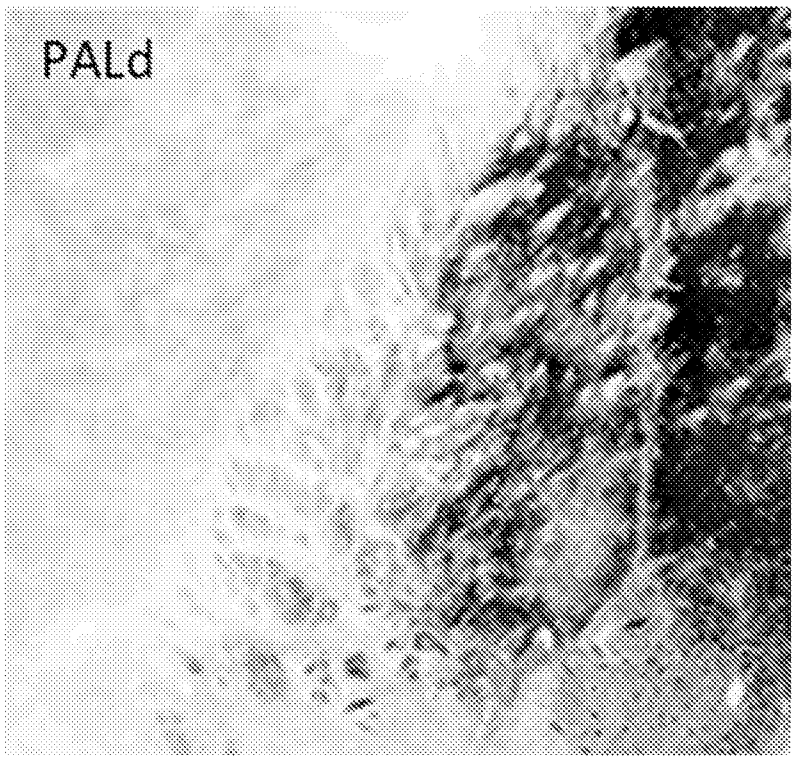


FIG. 3E

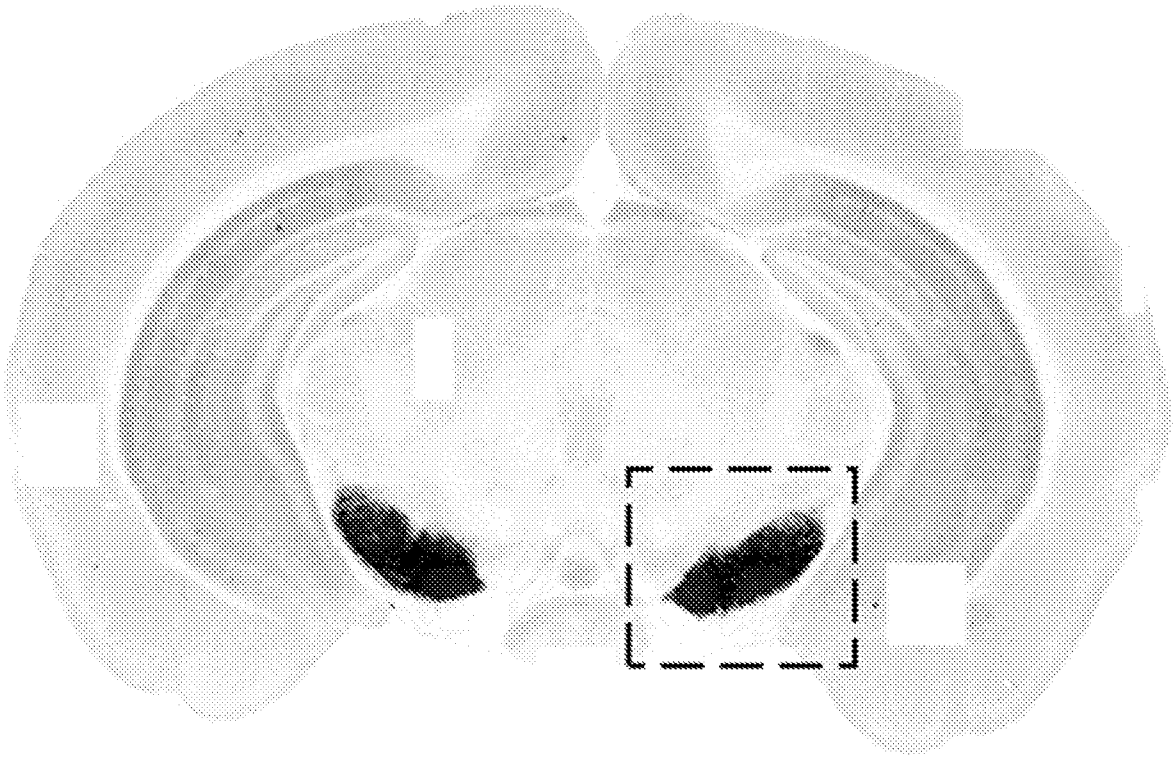


FIG. 3F

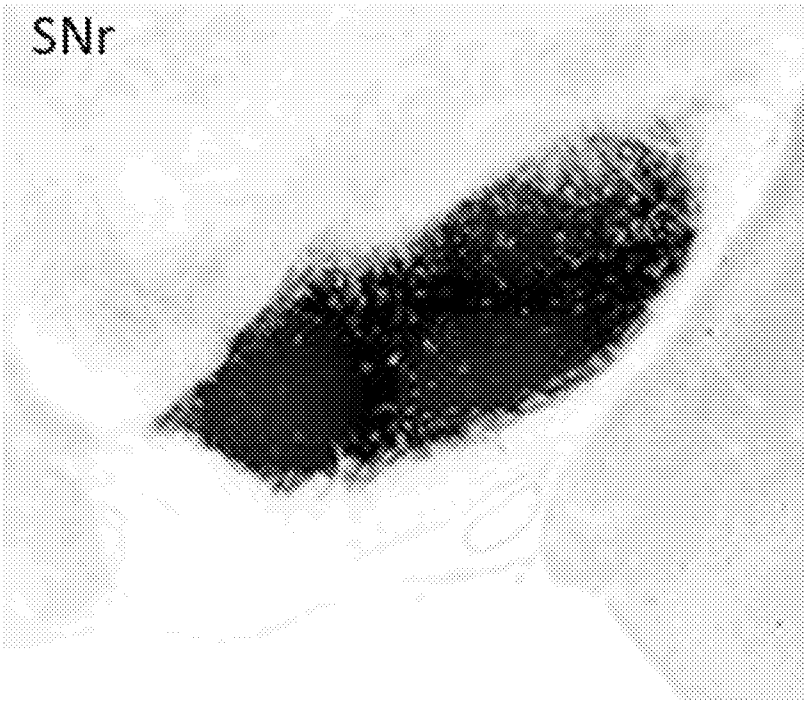


FIG. 3G

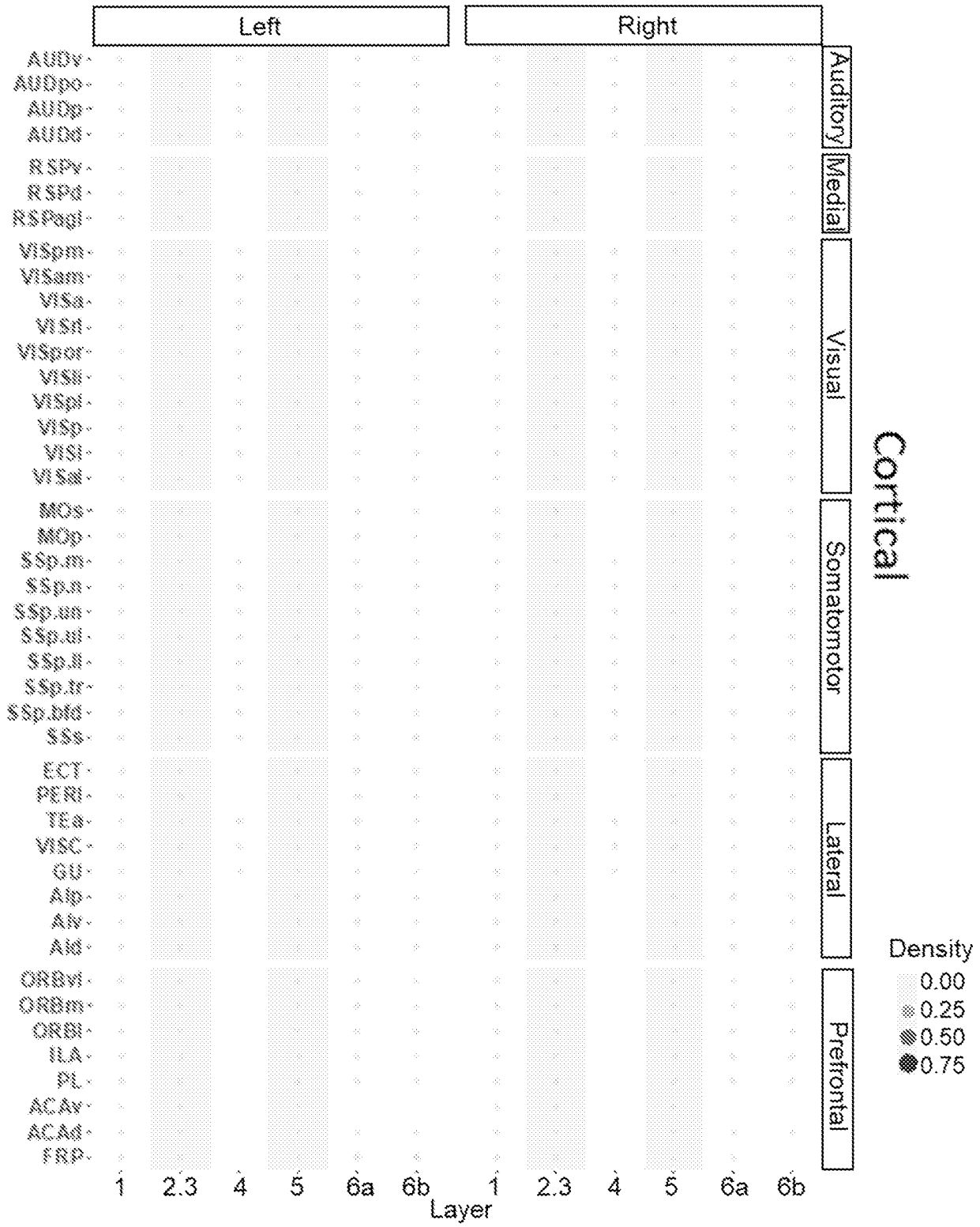

Left
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Lateral
Prefrontal
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VISam
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VISrl
VISpor
VISli
VISpl
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VISl
VISal
MOs
MOp
SSp.m
SSp.n
SSp.un
SSp.ul
SSp.ll
SSp.tr
SSp.bfd
SSs
ECT
PERI
TEa
VISC
GU
AIp
AIv
AId
ORBvl
ORBm
ORBl
ILA
PL
ACAv
ACAd
FRP
1
2.3
4
5
6a
6b
Layer
Density
0.00
0.25
0.50
0.75

FIG. 3G cont'd

FIG. 3G cont'd


Subcortical
Density
0.0
0.2
0.4
0.6
Right
Left
Right
Left
Right
Left
Right
Left
Right
Left
Right
Left
Right
Left

FIG. 4A

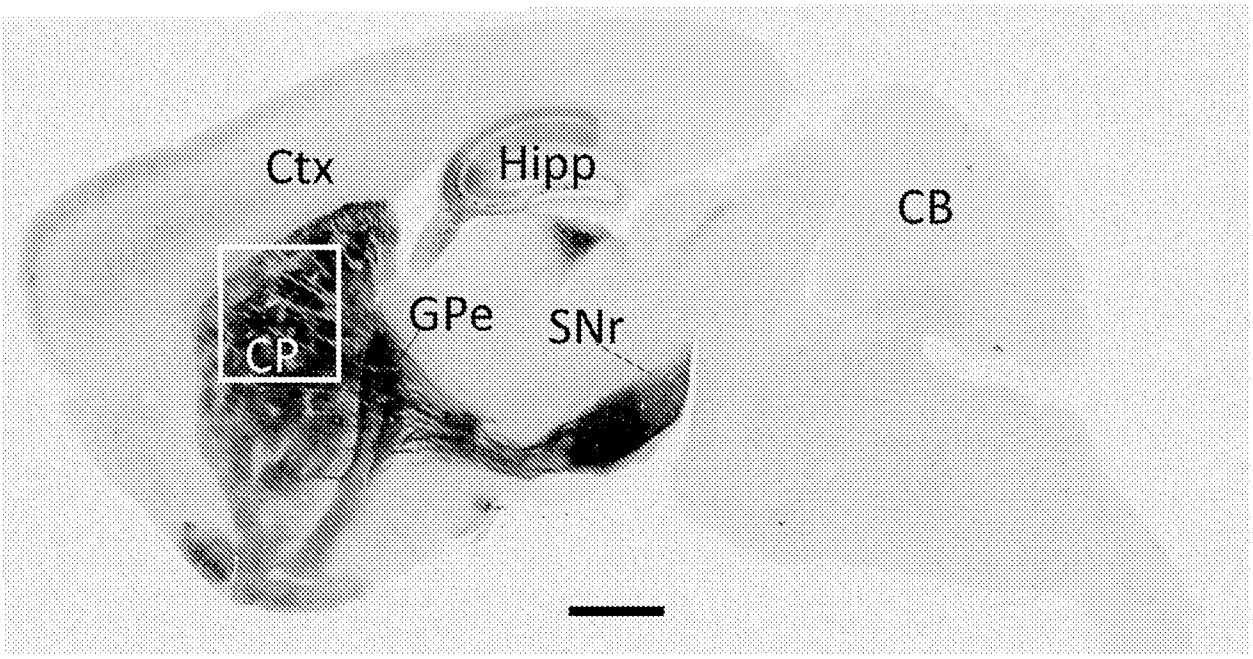


FIG. 4B

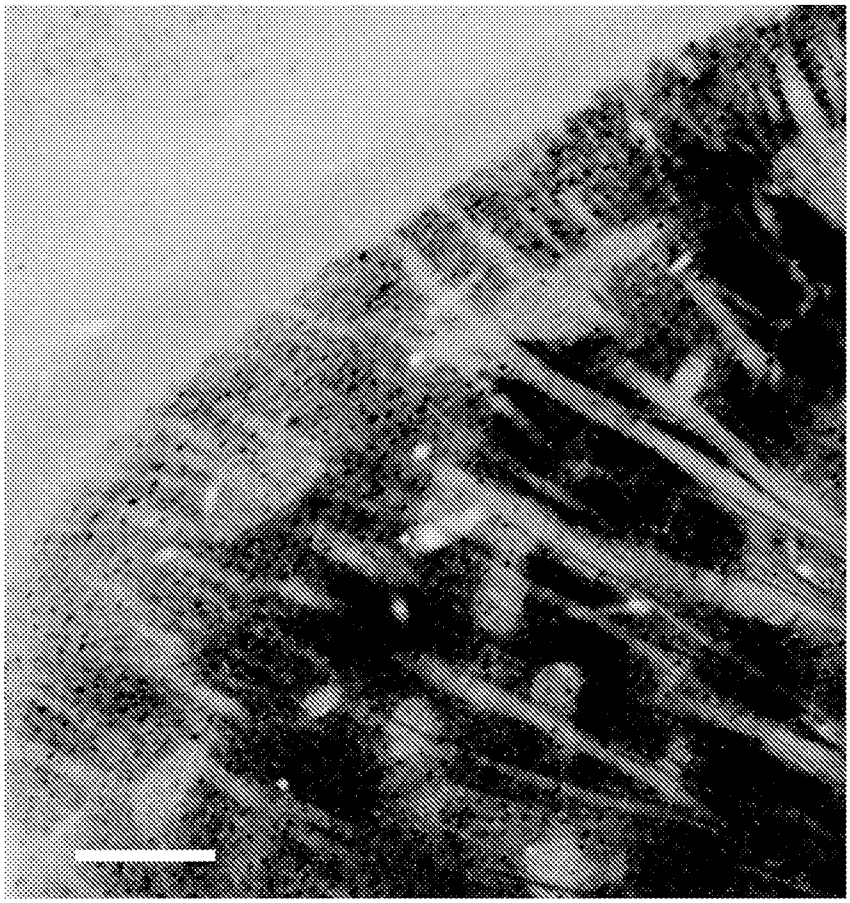


FIG. 5A

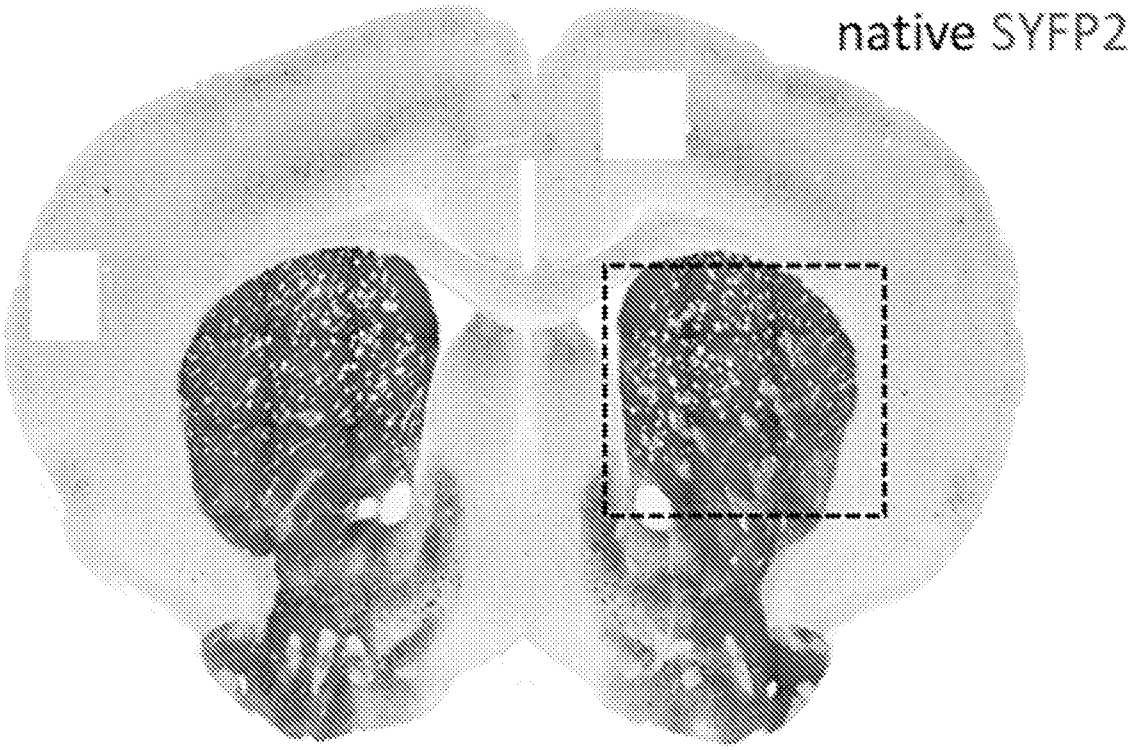


FIG. 5B

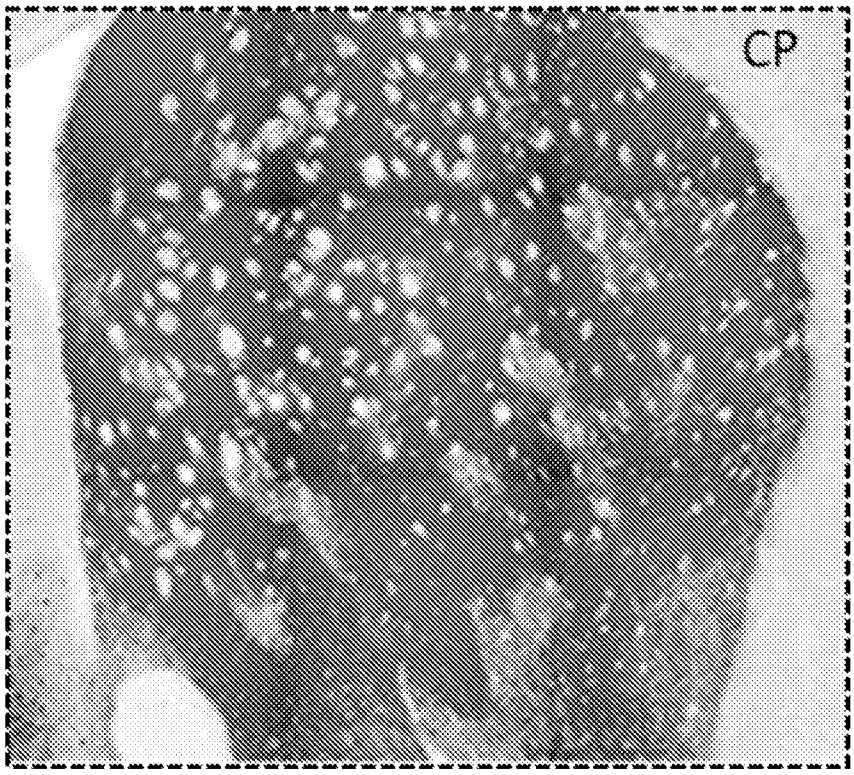


FIG. 5C

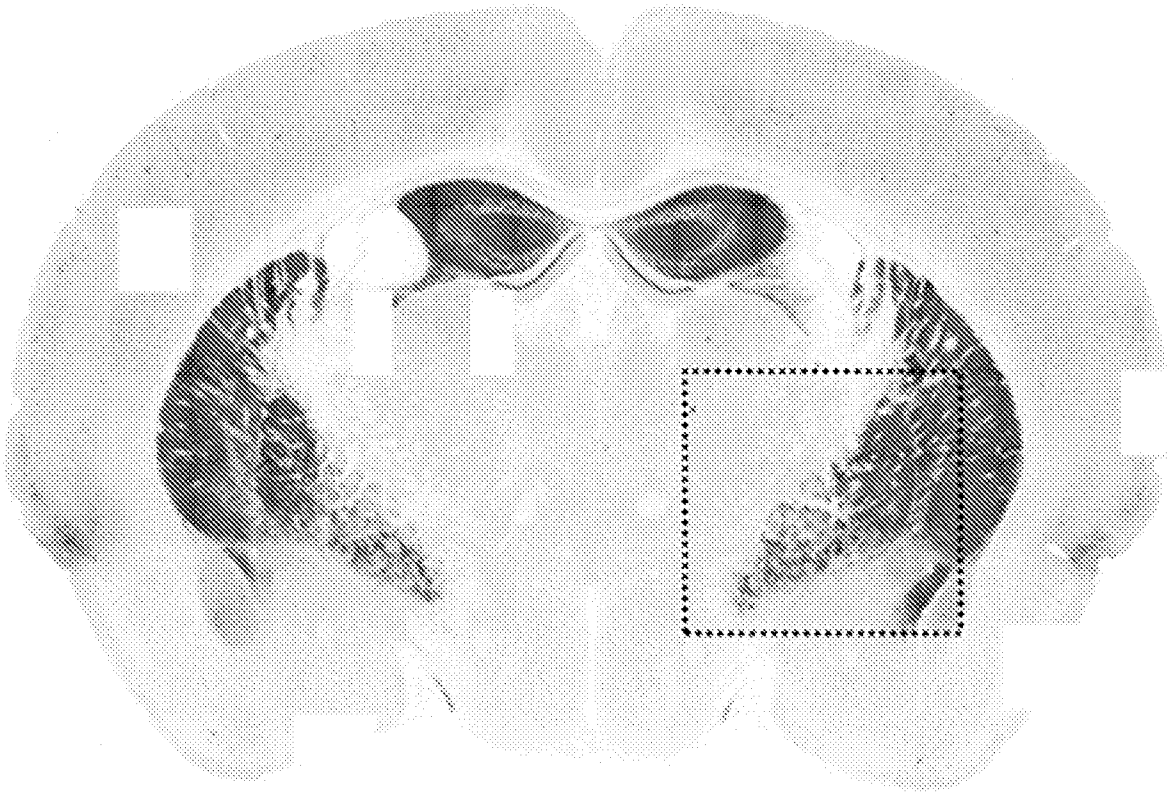


FIG. 5D

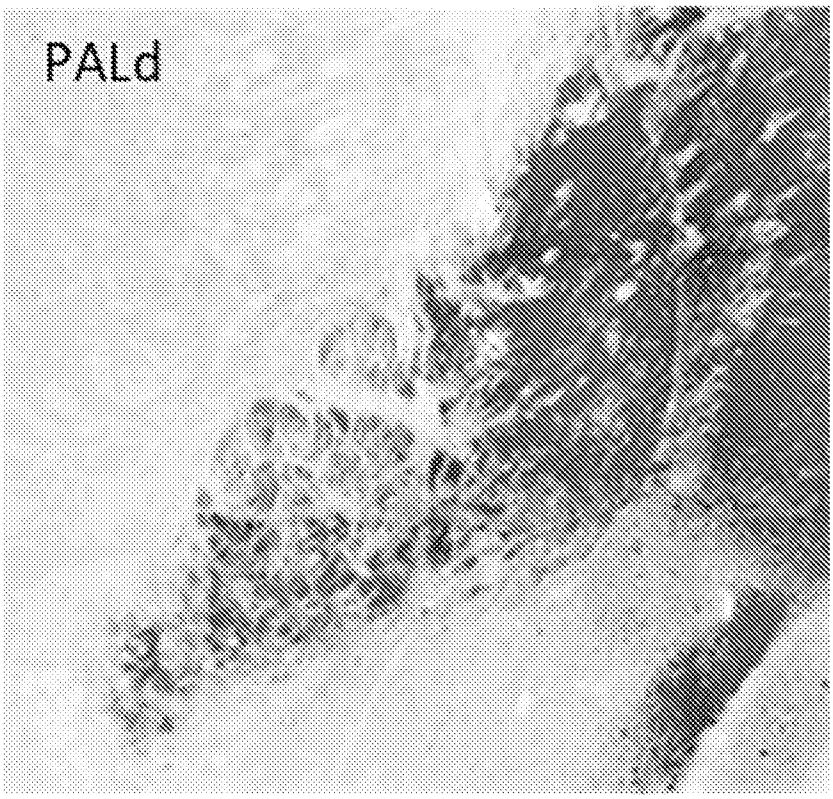


FIG. 5E

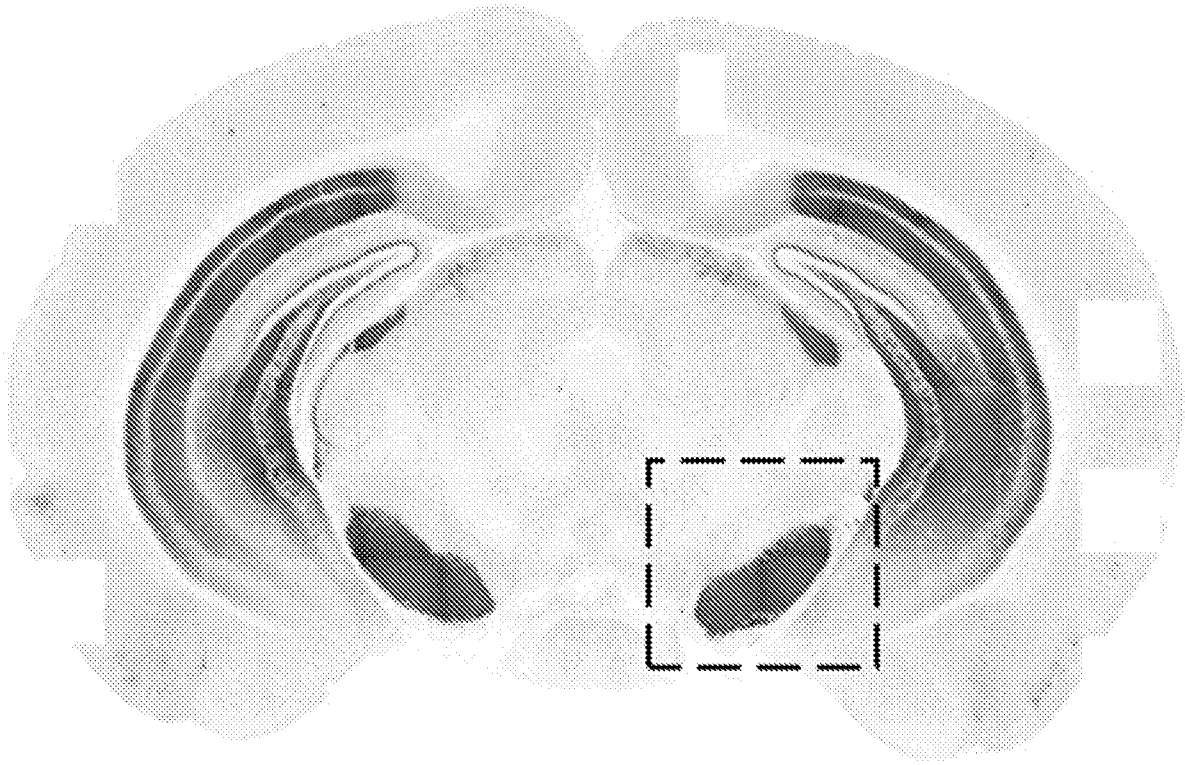


FIG. 5F

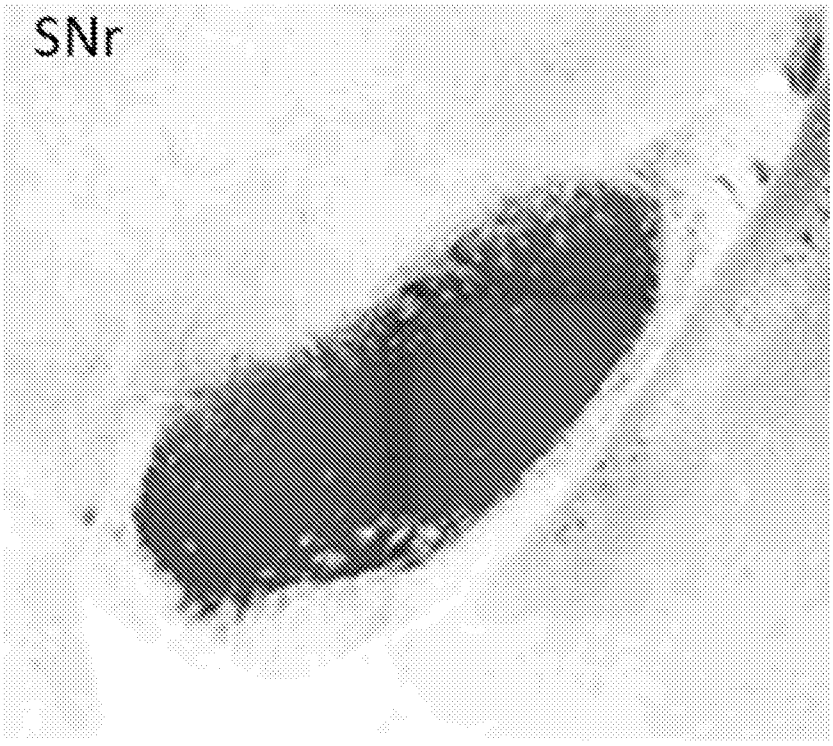


FIG. 5G

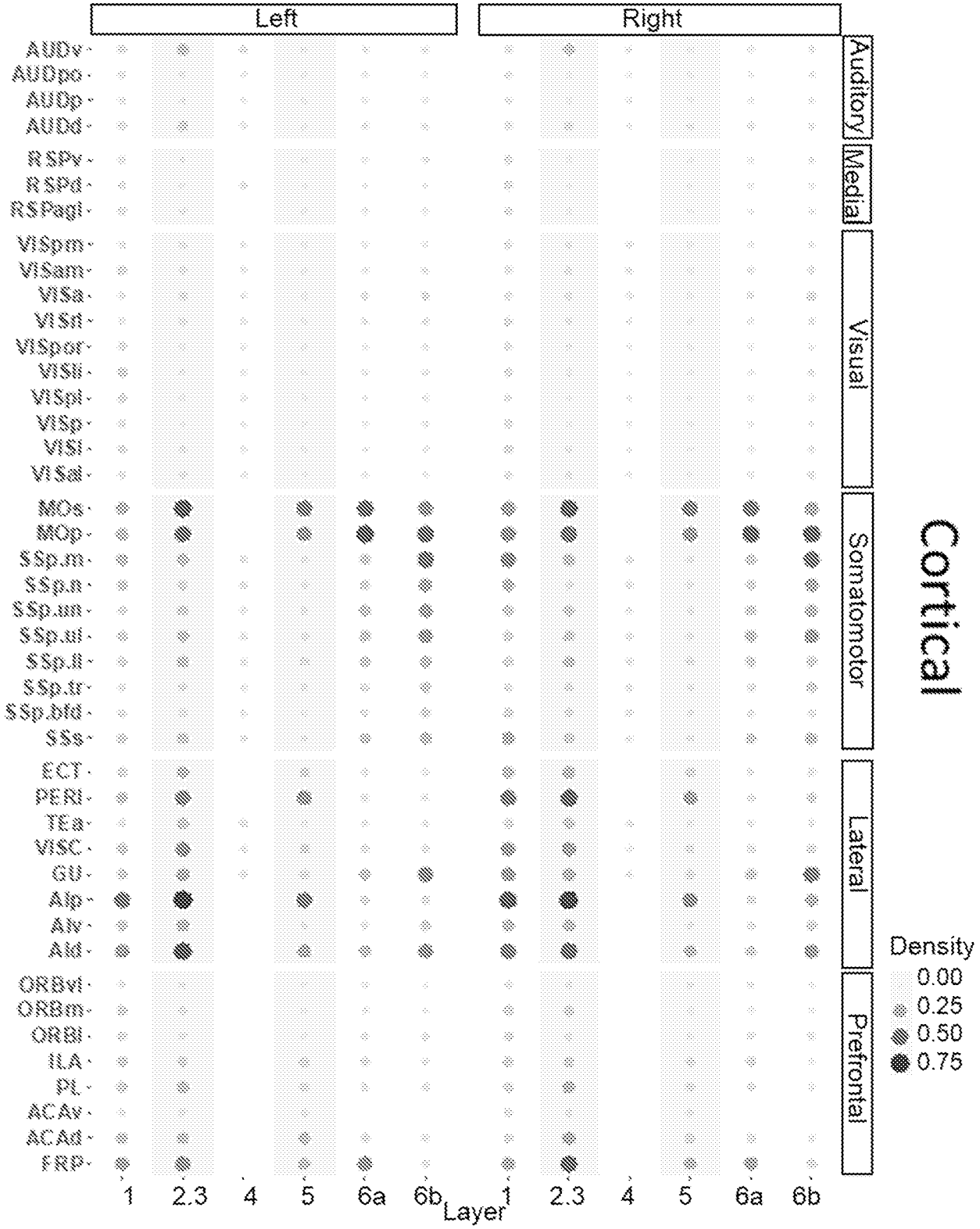

Left
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RSPv
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VISa
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VISpor
VISli
VISpl
VISp
VISl
VISal
MOs
MOp
SSp.m
SSp.n
SSp.um
SSp.ul
SSp.ll
SSp.tr
SSp.bfd
SSs
ECT
PERI
TEa
VISC
GU
AIp
AIv
AId
ORBvl
ORBm
ORBl
ILA
PL
ACAv
ACAd
FRP
Auditory
Medial
Visual
Somatomotor
Lateral
Prefrontal
Cortical
1
2.3
4
5
6a
6b
Layer
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0.50
0.75

FIG. 5G cont'd

FIG. 5G cont'd

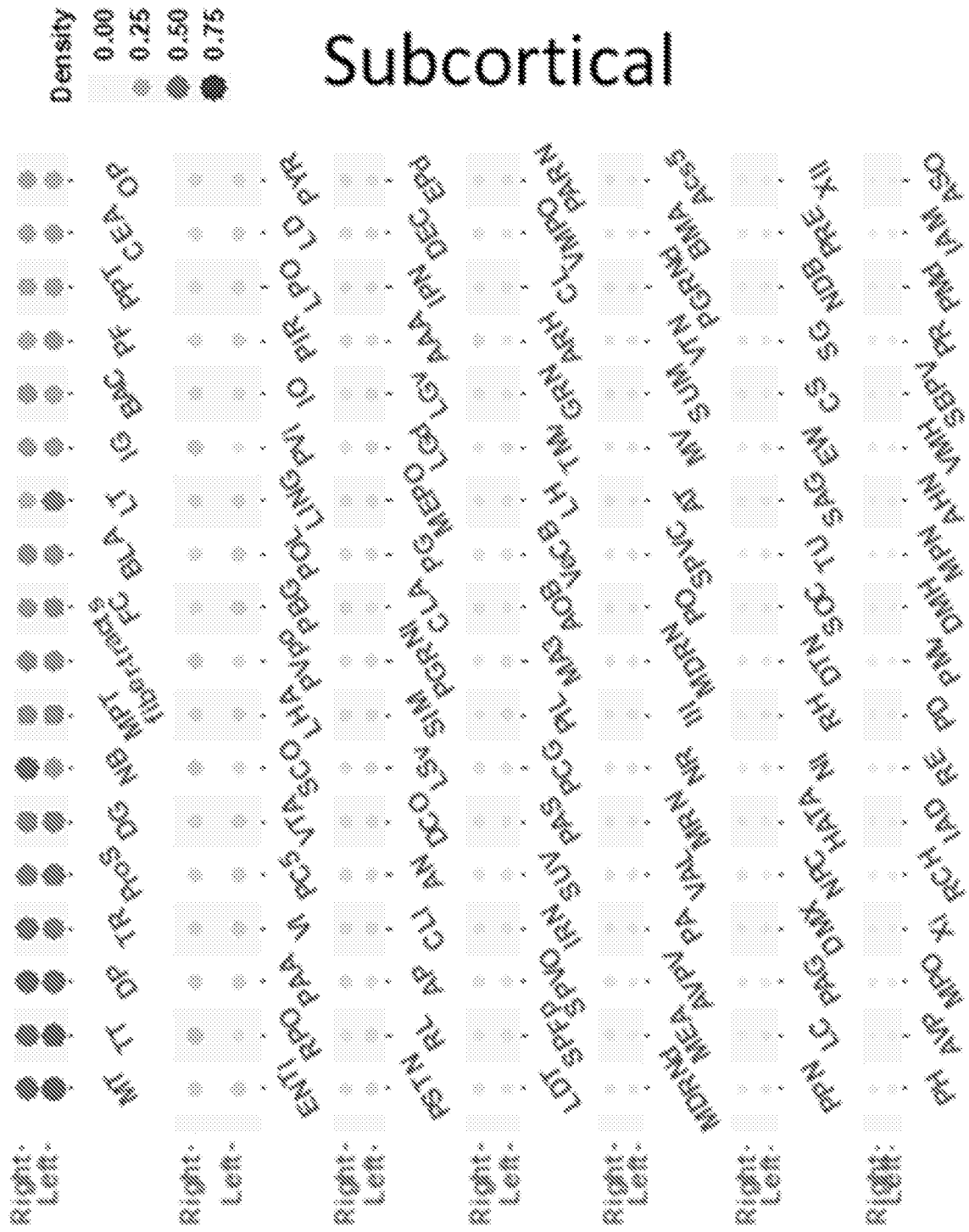

Subcortical
Density
0.00
0.25
0.50
0.75
Right
Left
Right
Left
Right
Left
Right
Left
Right
Left
Right
Left

FIG. 6A

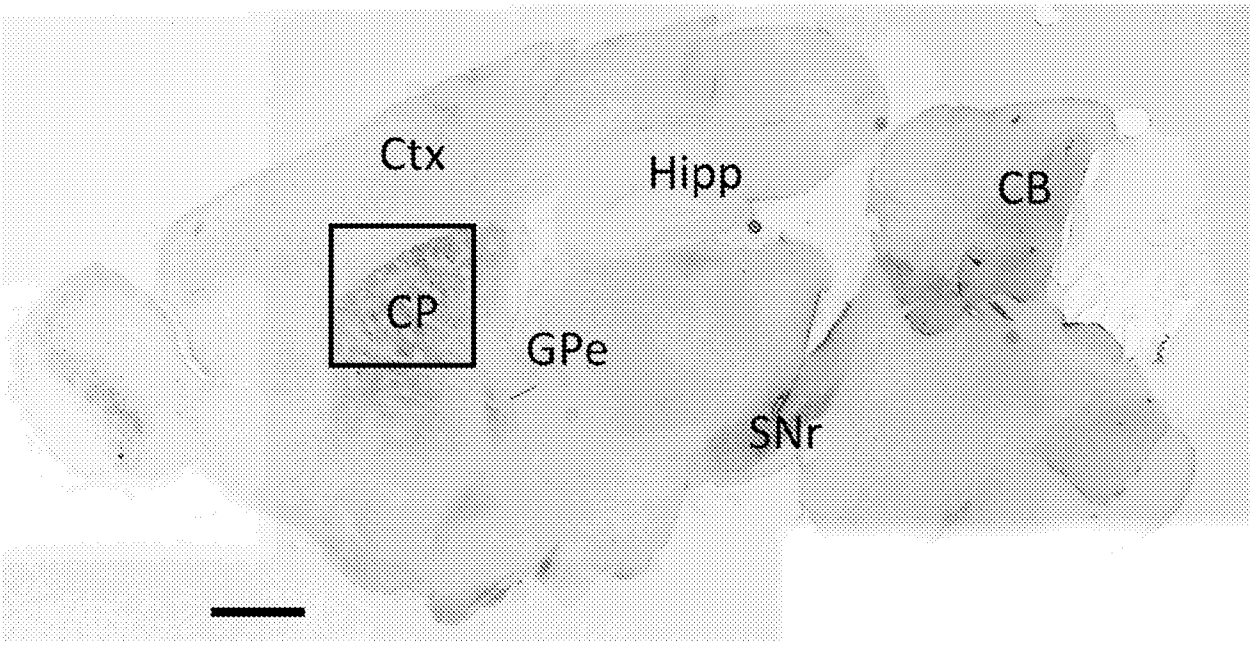


FIG. 6B

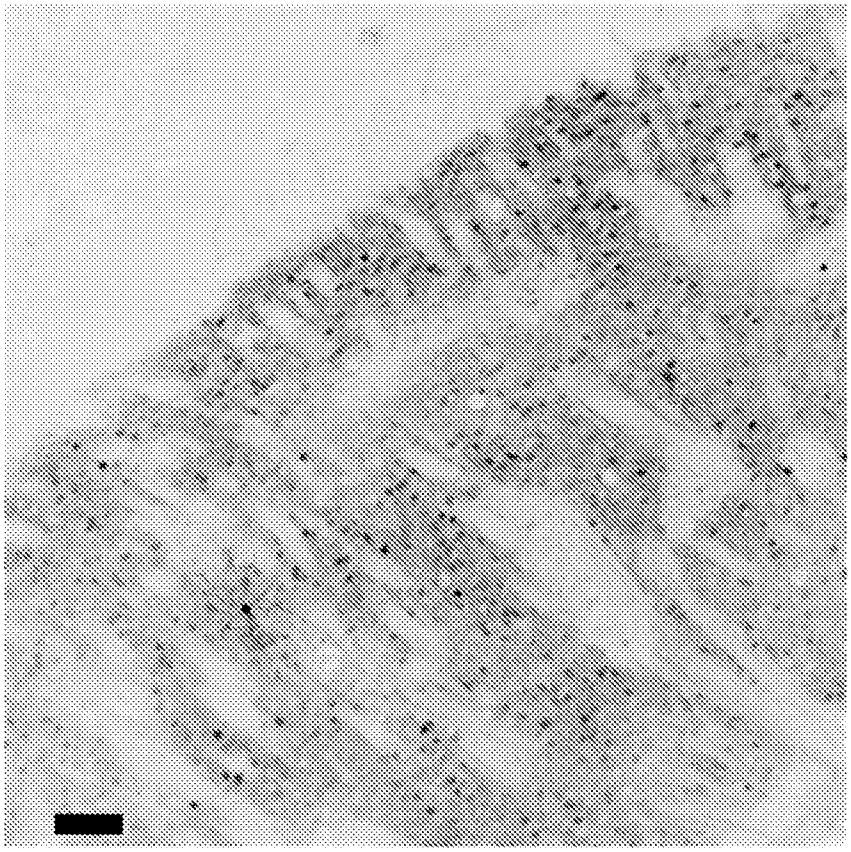


FIG. 7A

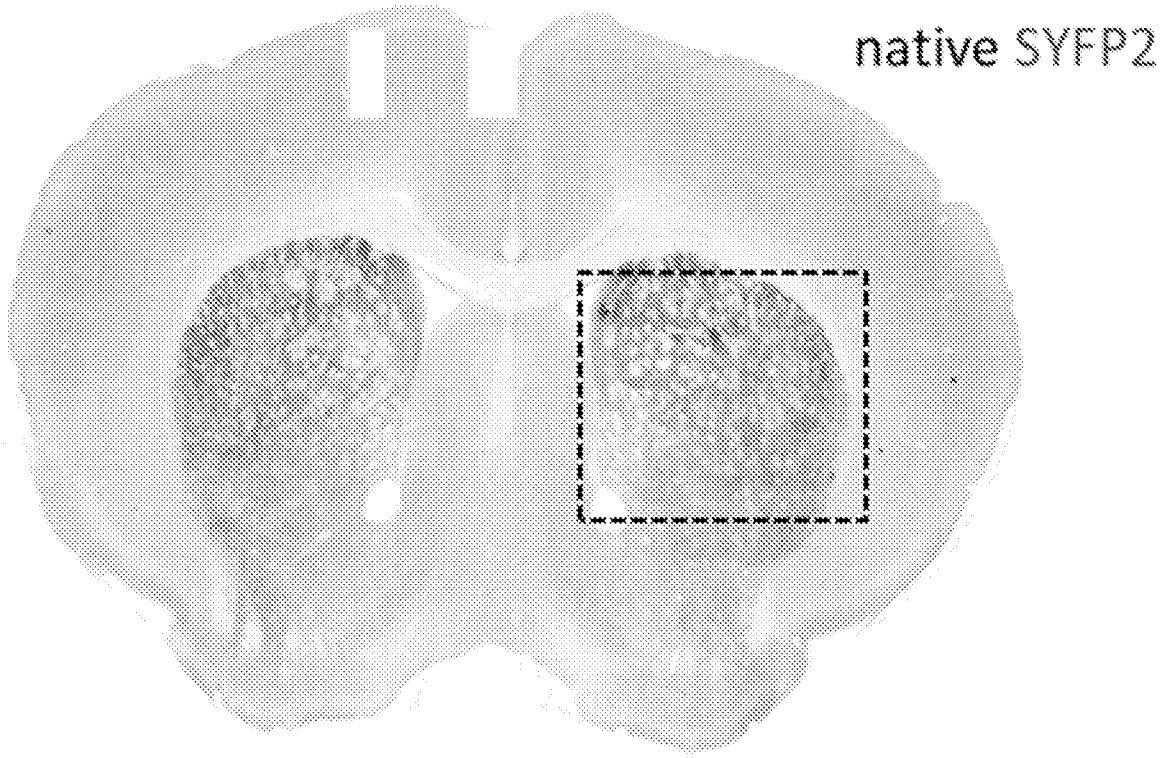


FIG. 7B

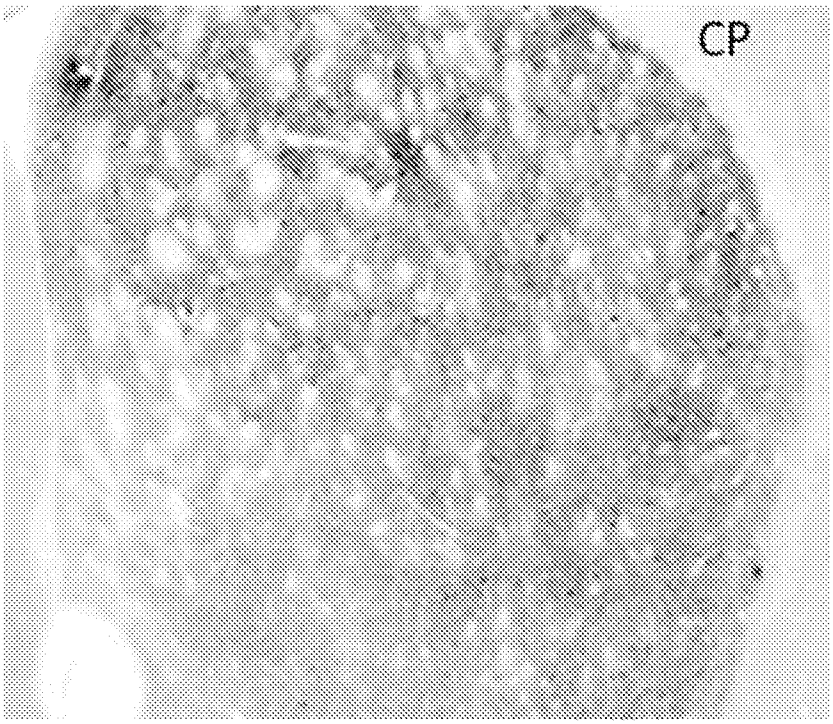


FIG. 7C

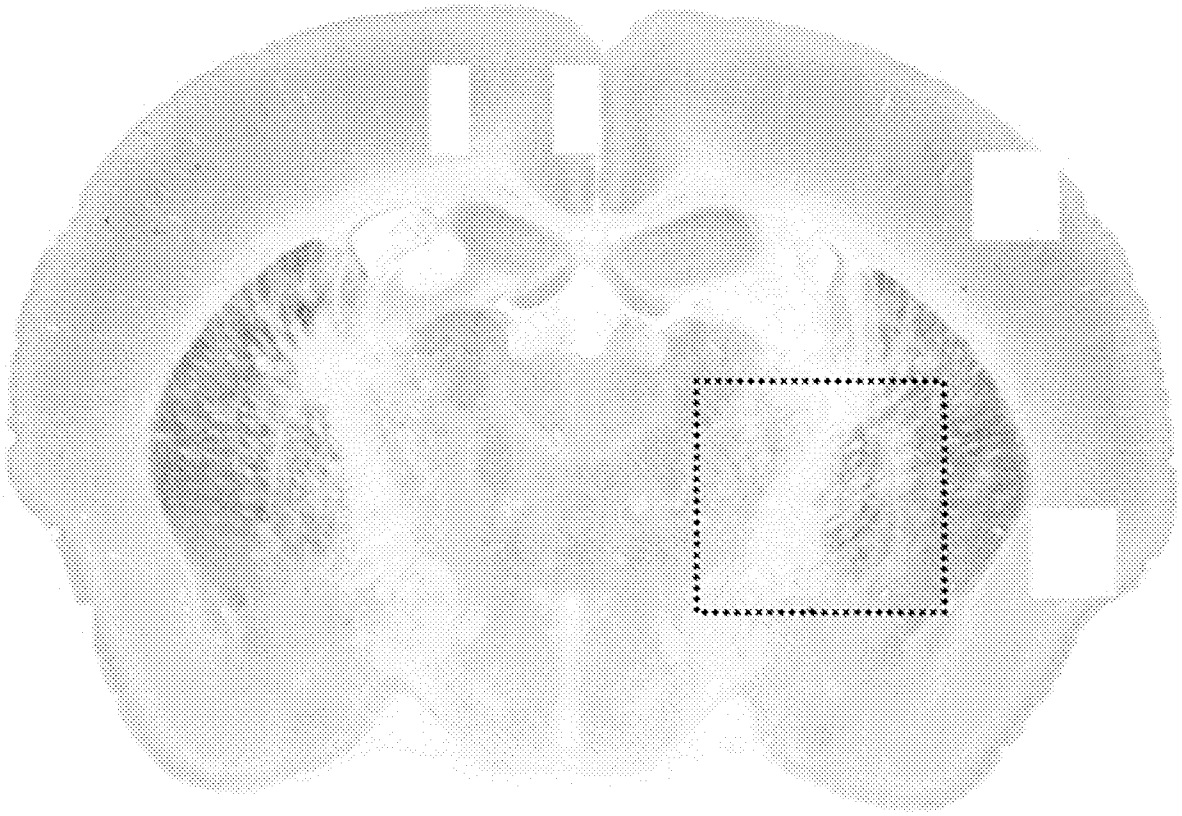


FIG. 7D

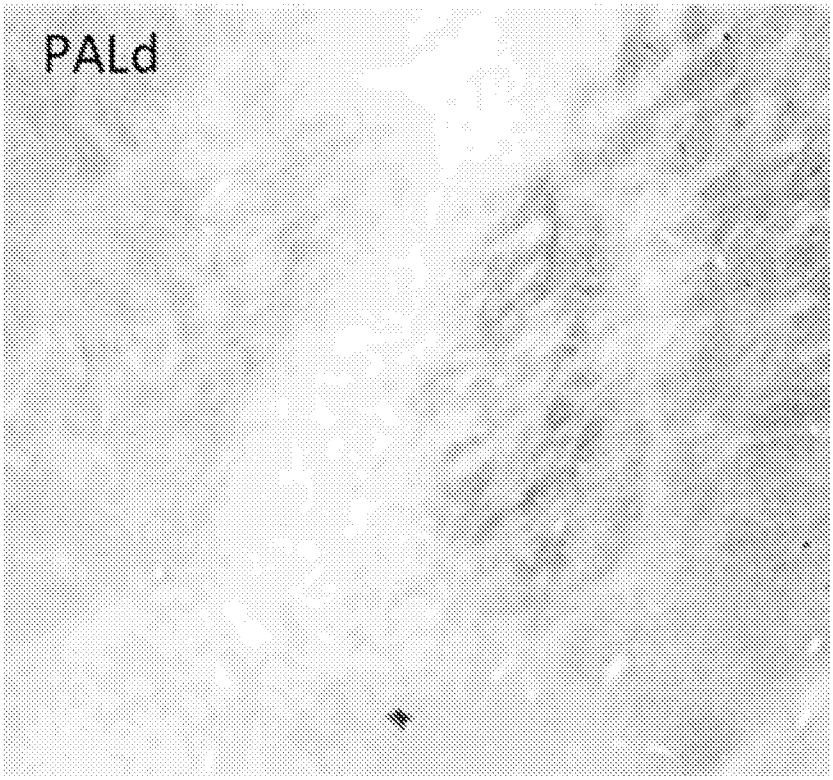


FIG. 7E

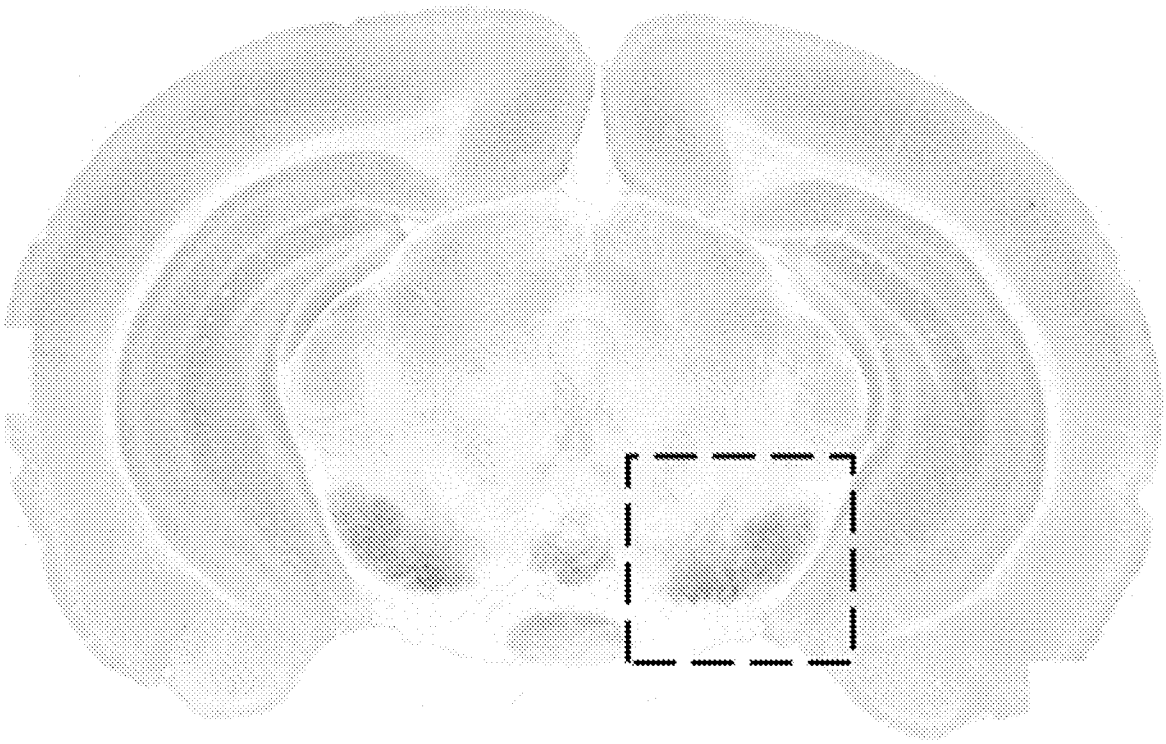


FIG. 7F

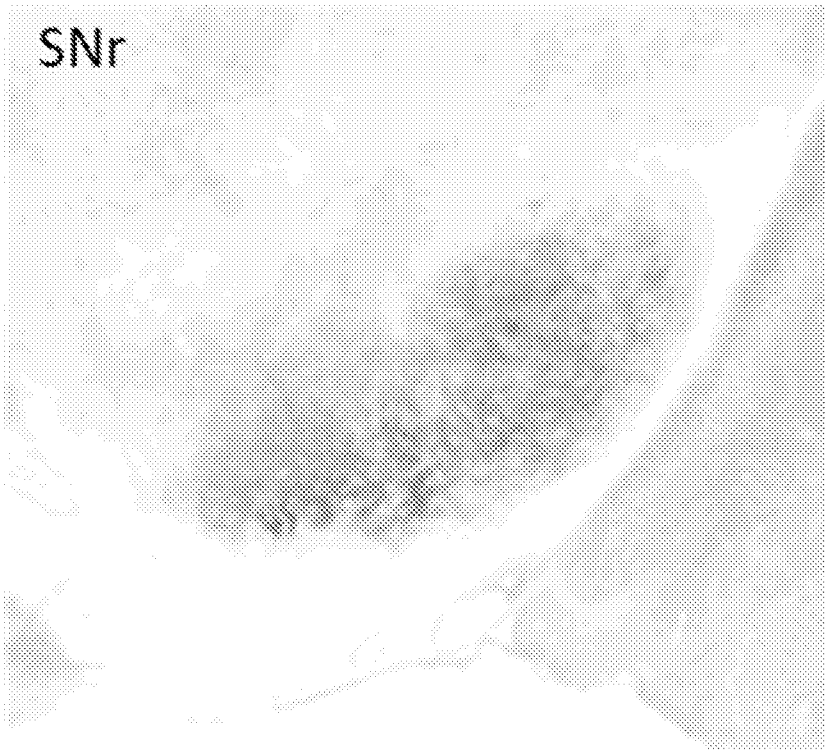


FIG. 7G

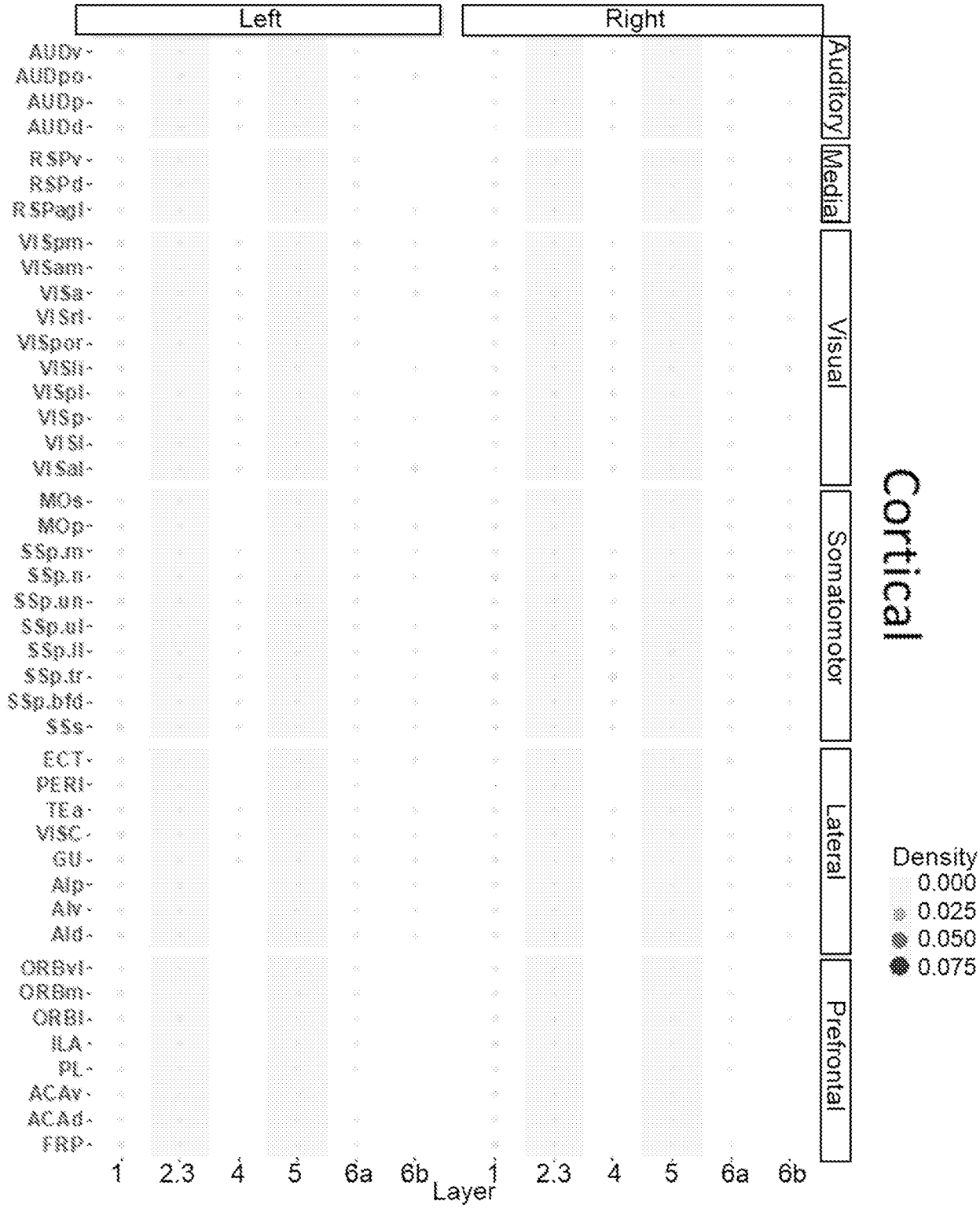

Left
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AUDv
AUDpo
AUDp
AUDd
RSPv
RSPd
RSPagl
VISpm
VISam
VISa
VISrl
VISpor
VISli
VISpl
VISp
VISl
VISal
MOs
MOp
SSp.m
SSp.n
SSp.un
SSp.ul
SSp.ll
SSp.tr
SSp.bfd
SSs
ECT
PERI
TEa
VISC
GU
AIp
AIv
AId
ORBvl
ORBm
ORBl
ILA
PL
ACAv
ACAd
FRP
1
2/3
4
5
6a
6b
Layer
Auditory
Medial
Visual
Somatomotor
Lateral
Prefrontal
Cortical
Density
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0.025
0.050
0.075

FIG. 7G cont'd



FIG. 7G cont'd

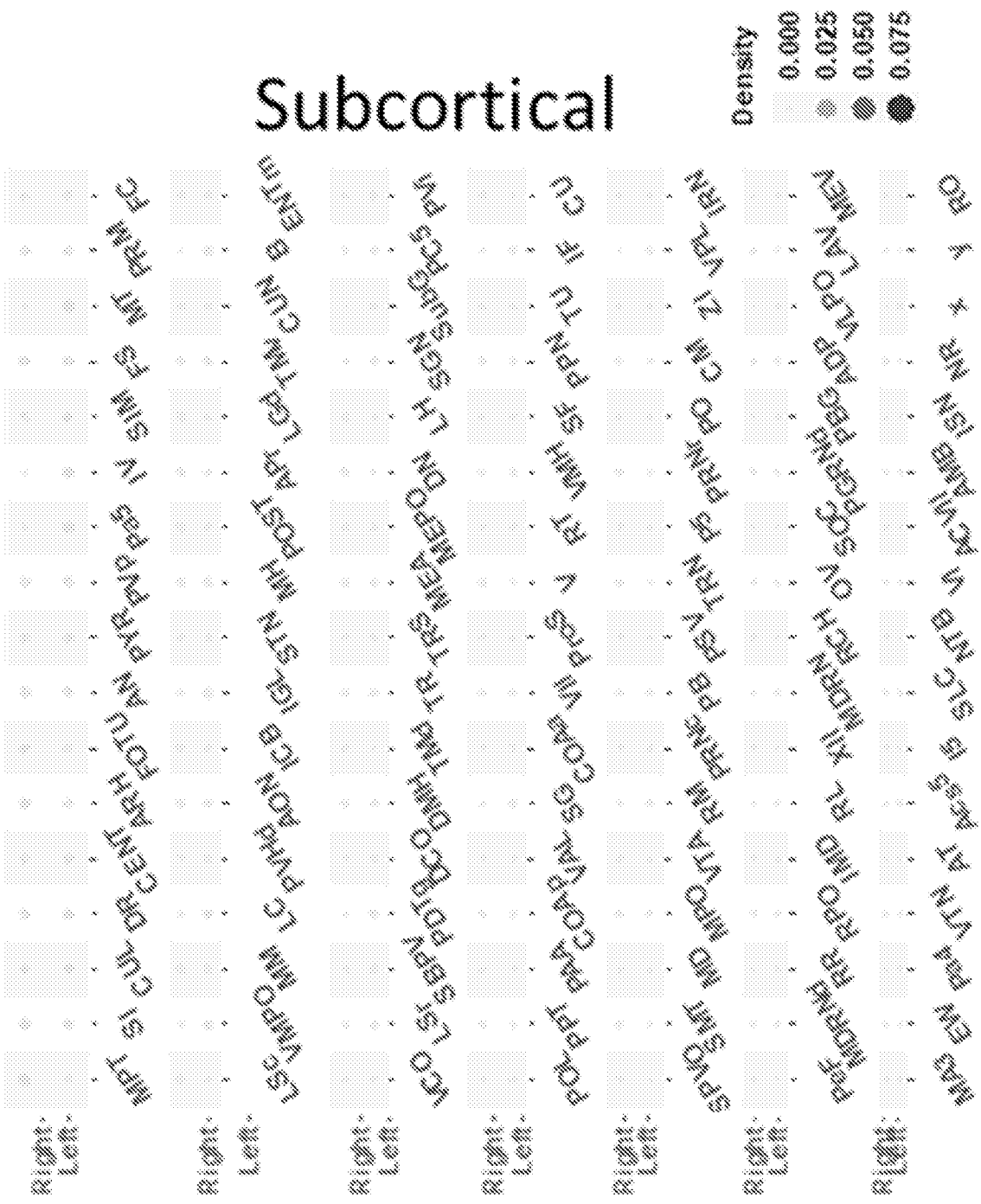


FIG. 8A

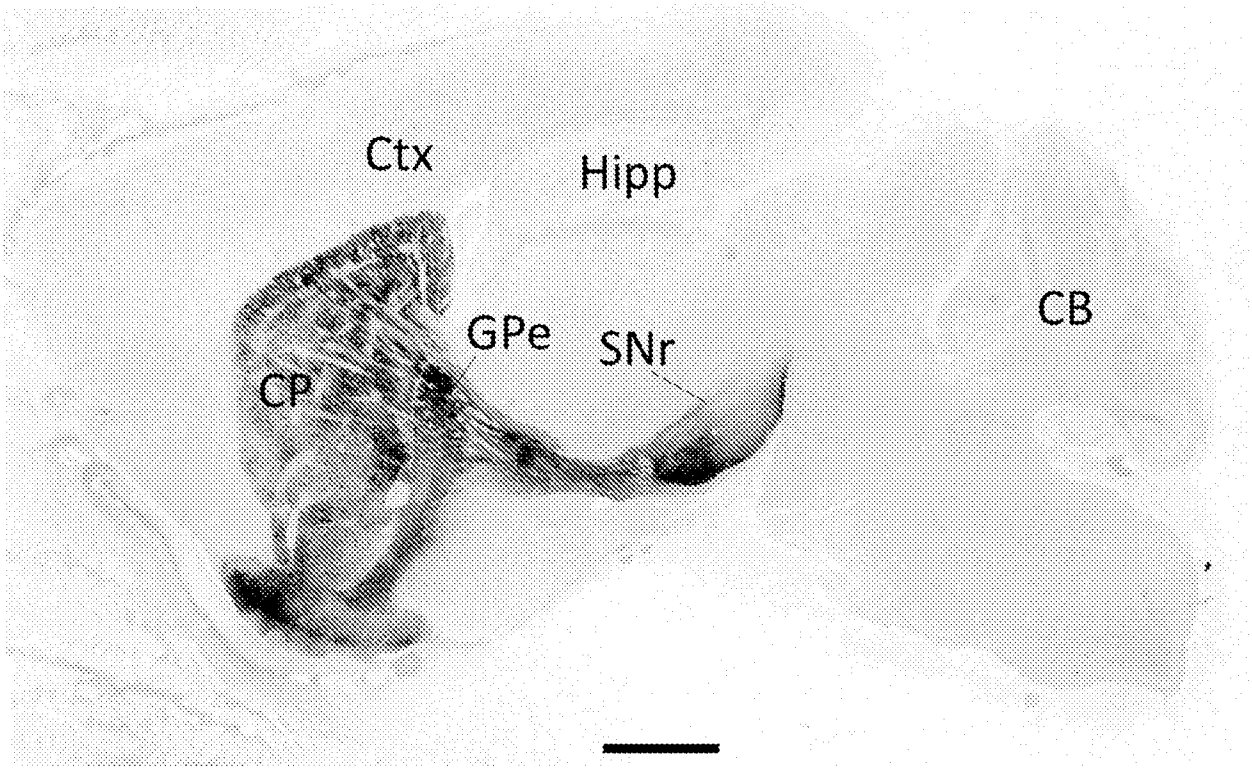
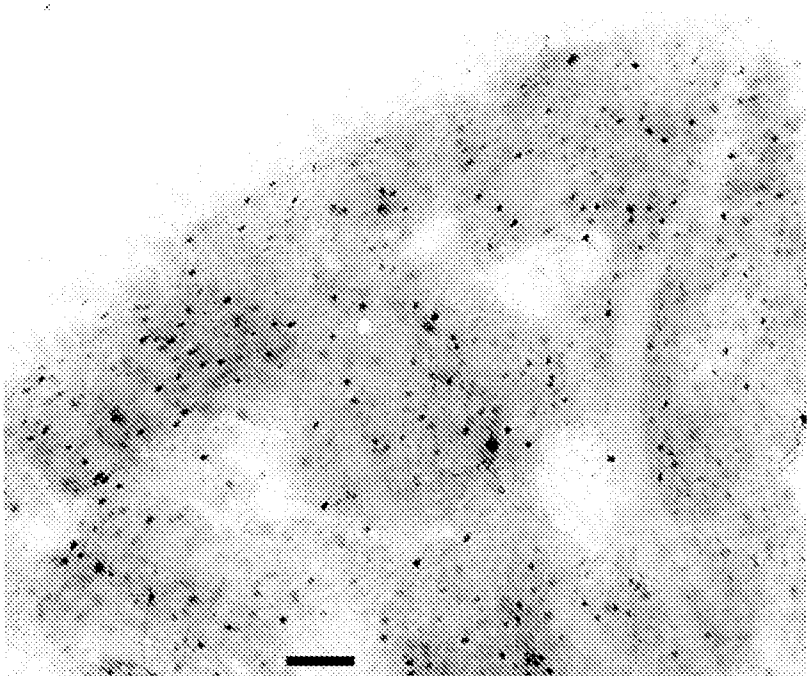


FIG.8B



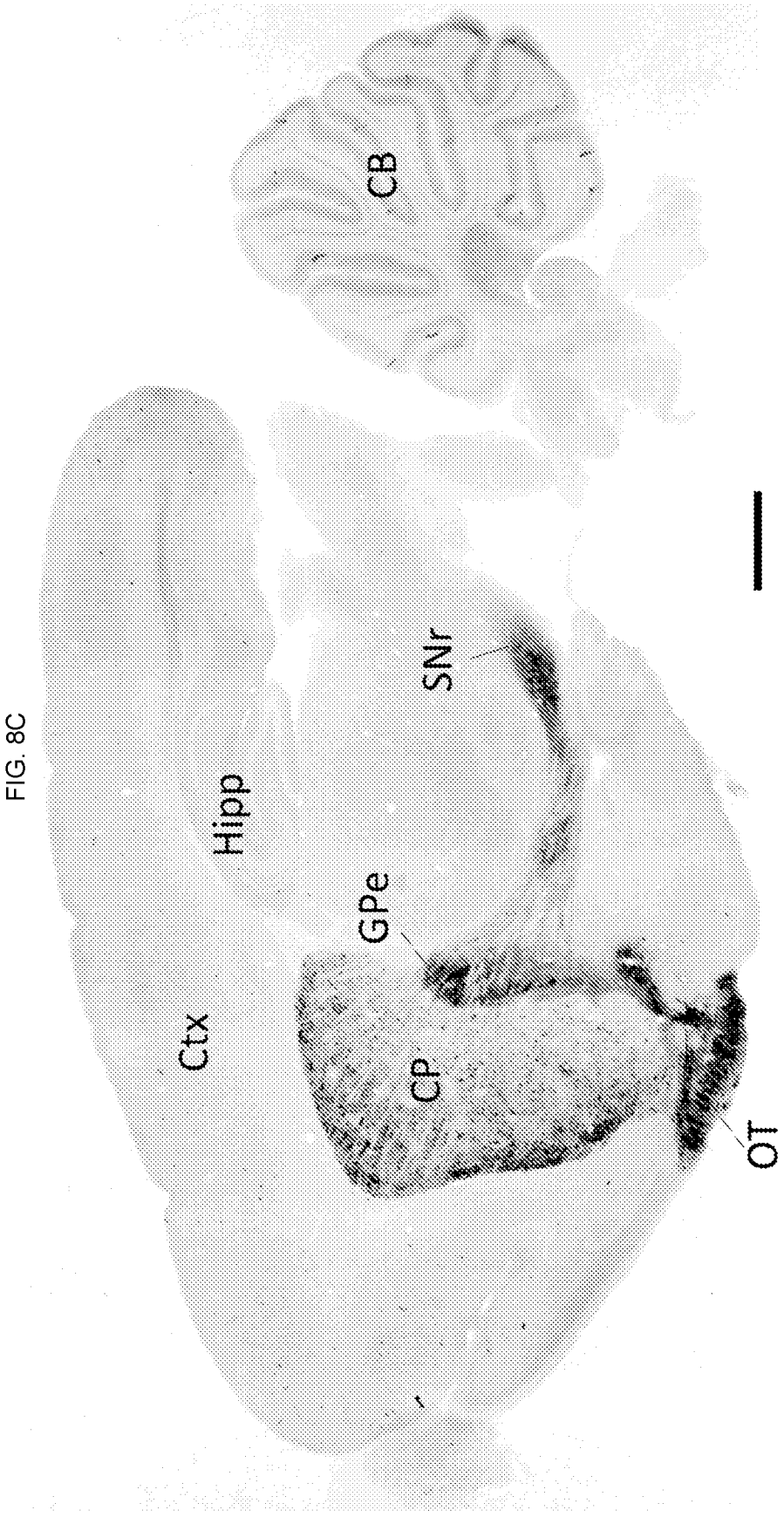


FIG. 8C

FIG. 9A

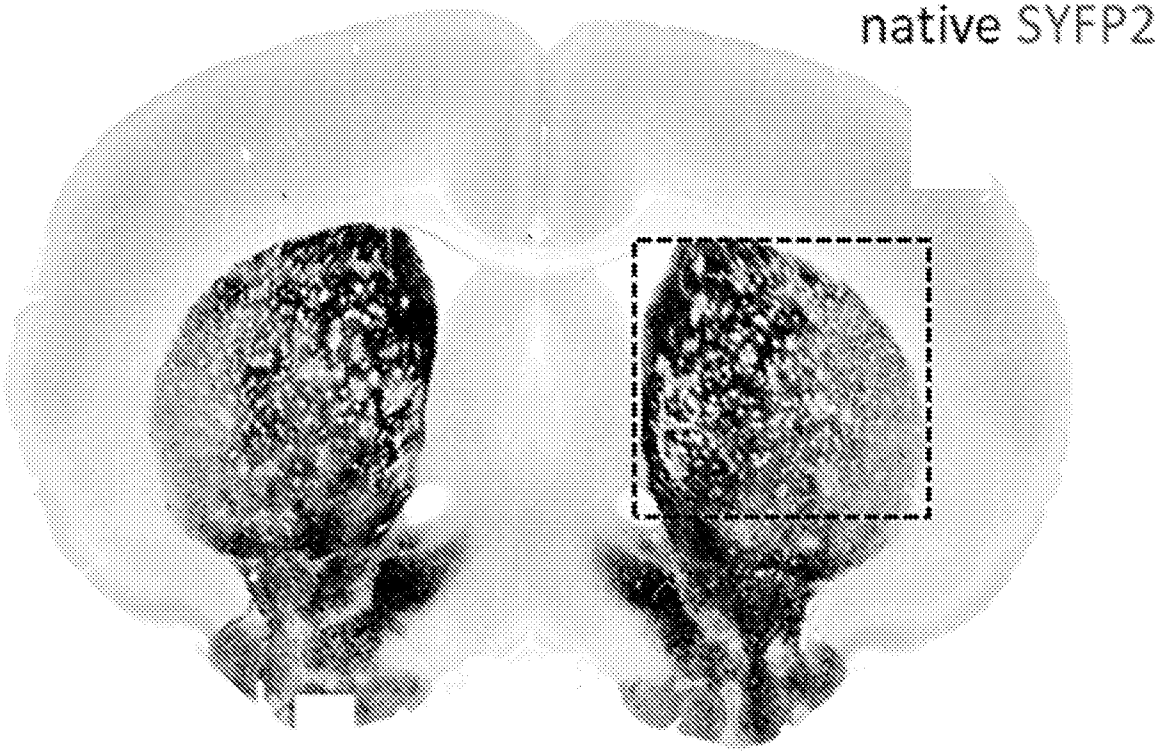


FIG. 9B

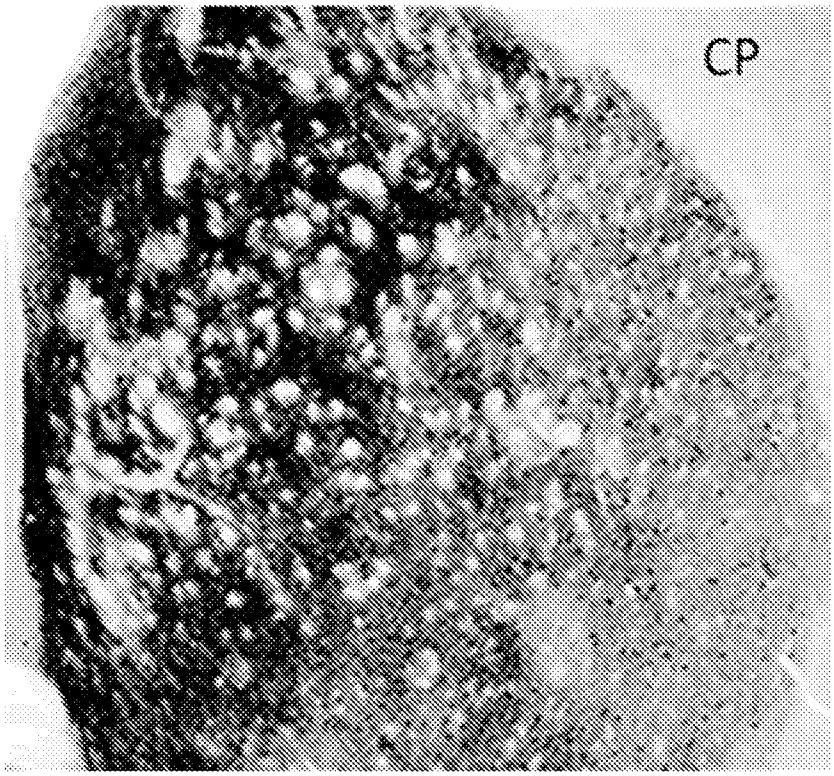


FIG. 9C

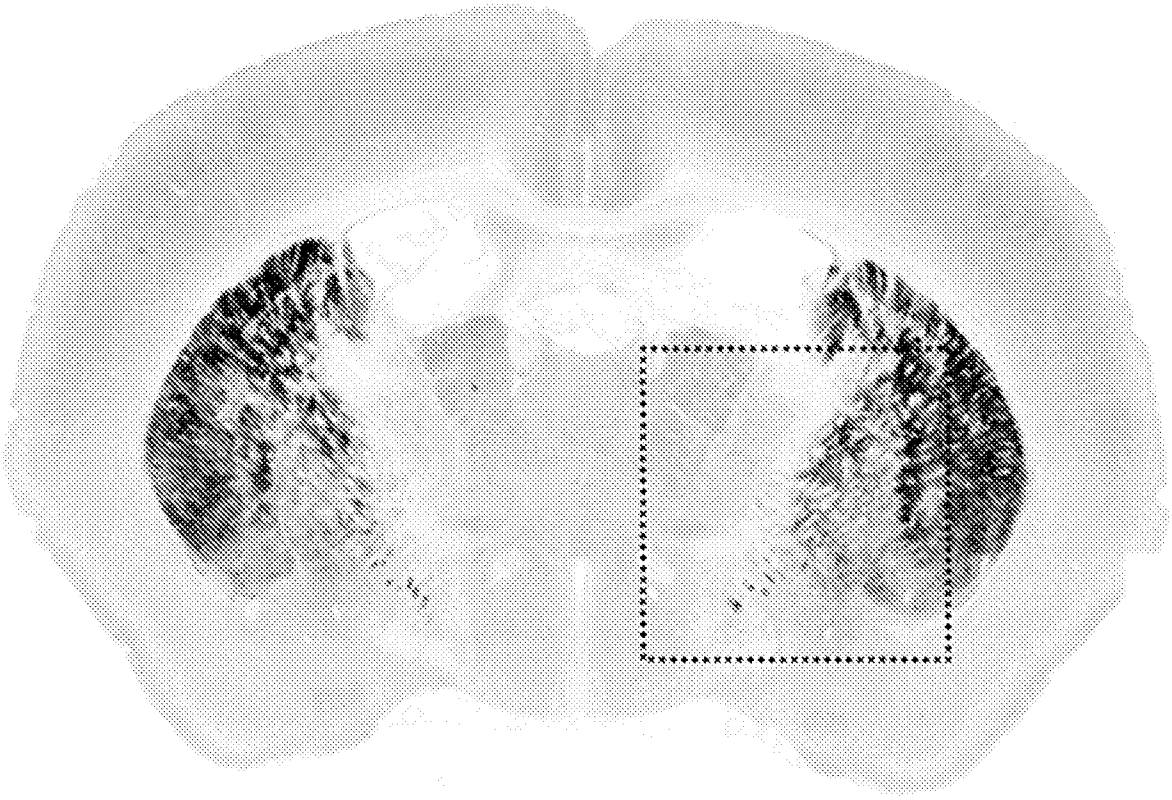


FIG. 9D

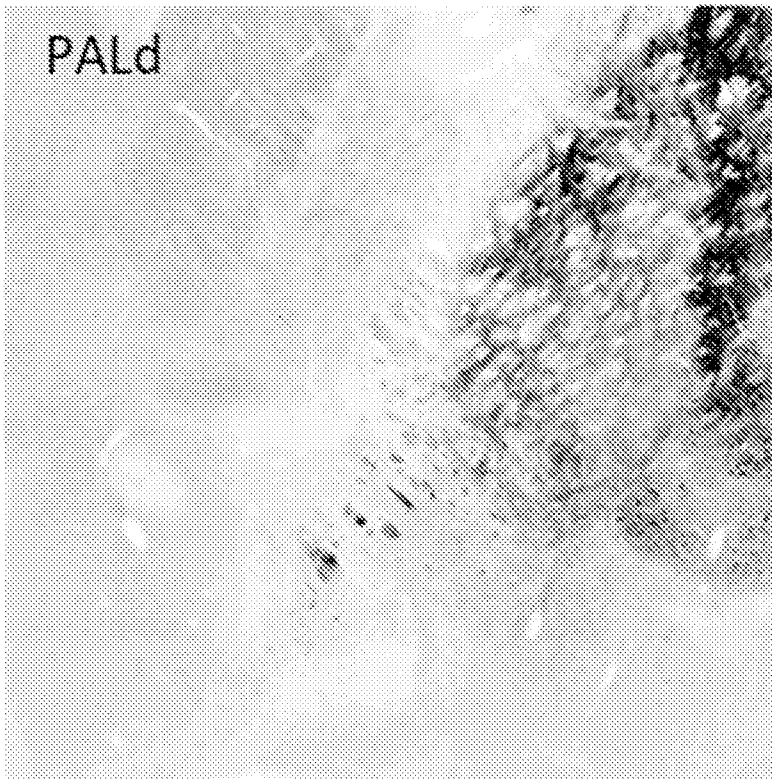


FIG. 9E

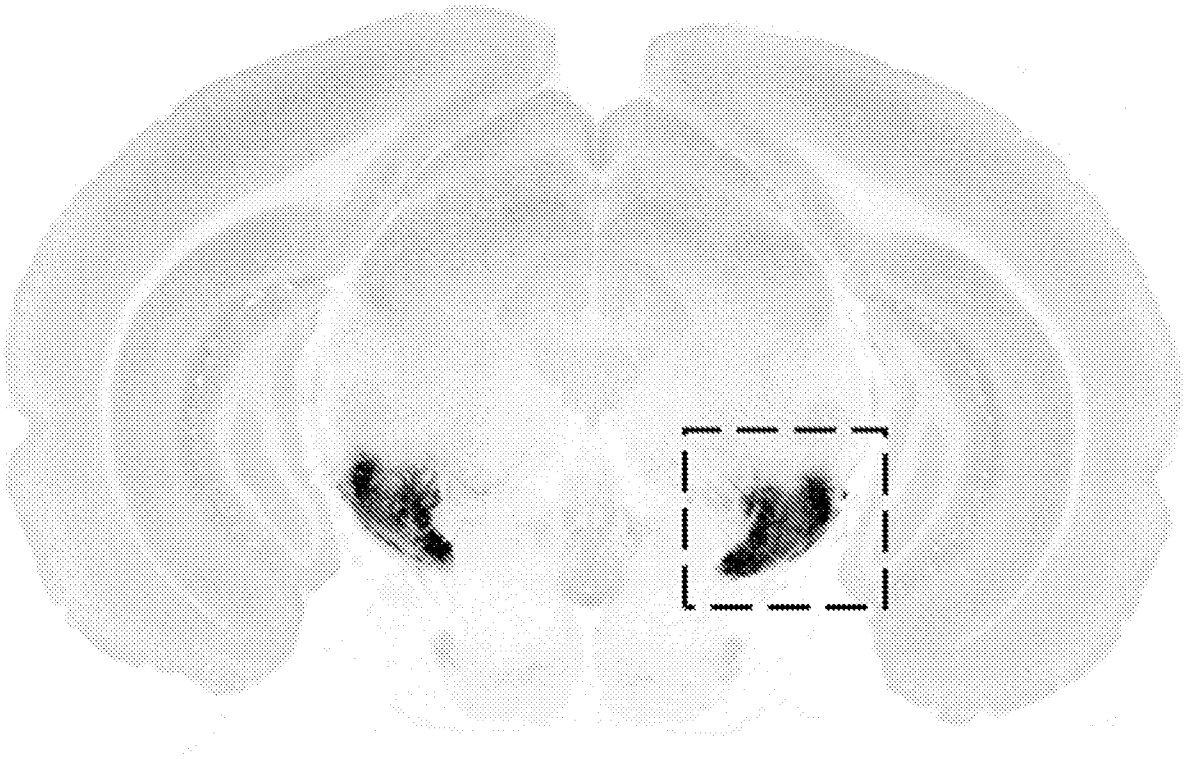


FIG. 9F

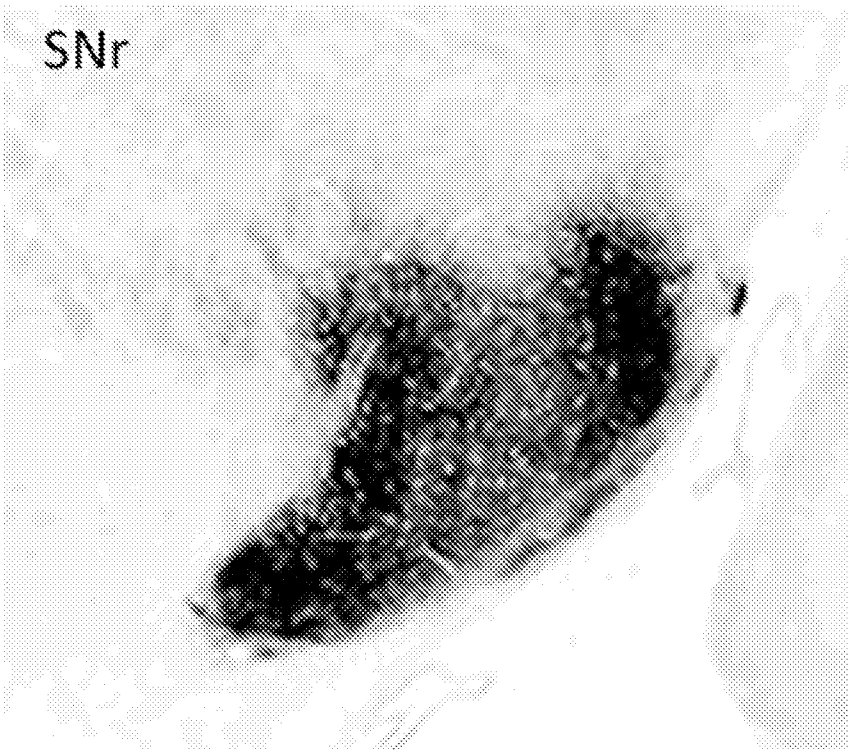


FIG. 9G

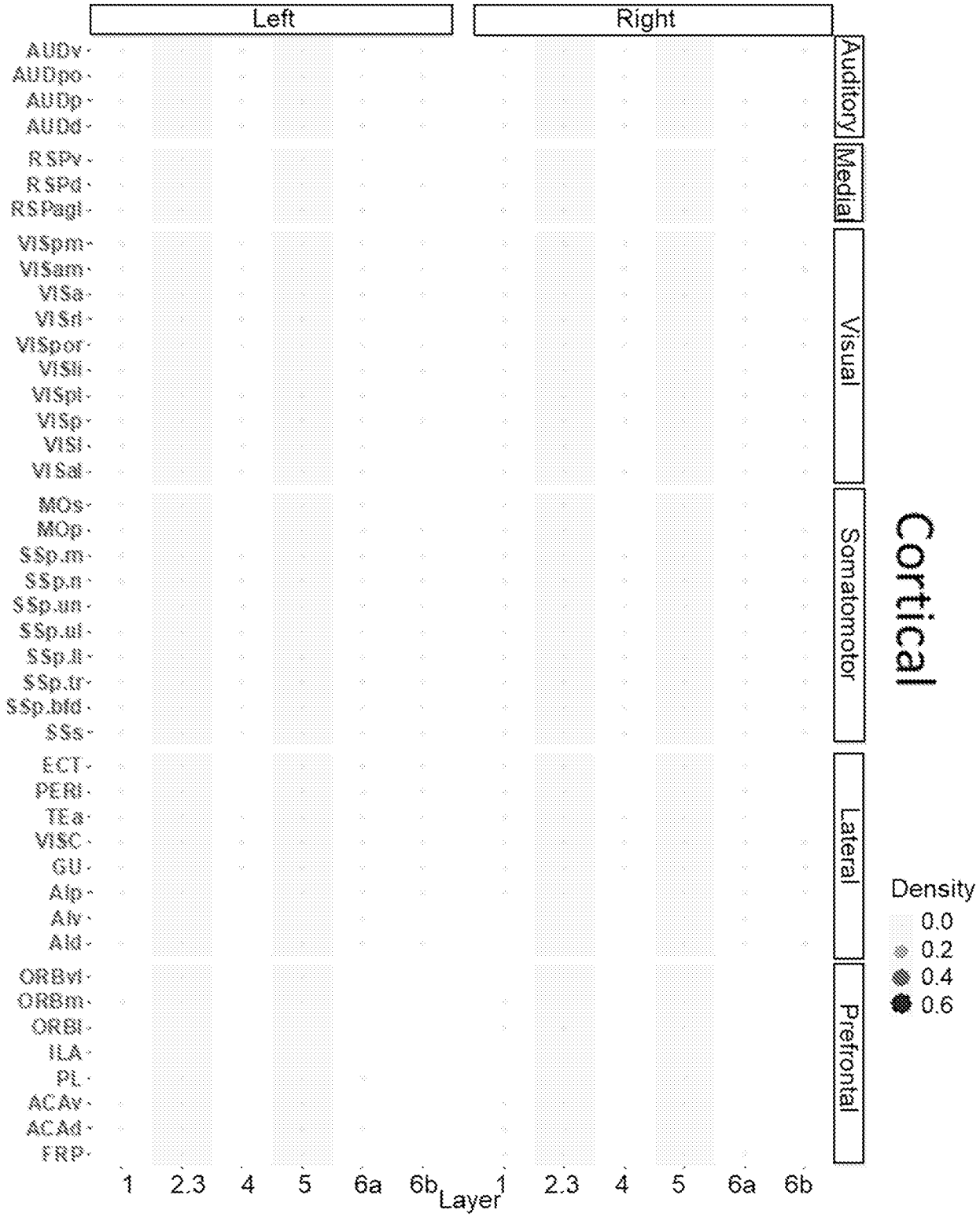

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VISal
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SSp.ul
SSp.ll
SSp.tr
SSp.bfd
SSs
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FRP
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6a
6b
Layer
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Visual
Somatomotor
Lateral
Prefrontal
Cortical
Density
0.0
0.2
0.4
0.6

FIG. 9G cont'd



FIG. 9G cont'd



FIG. 10A

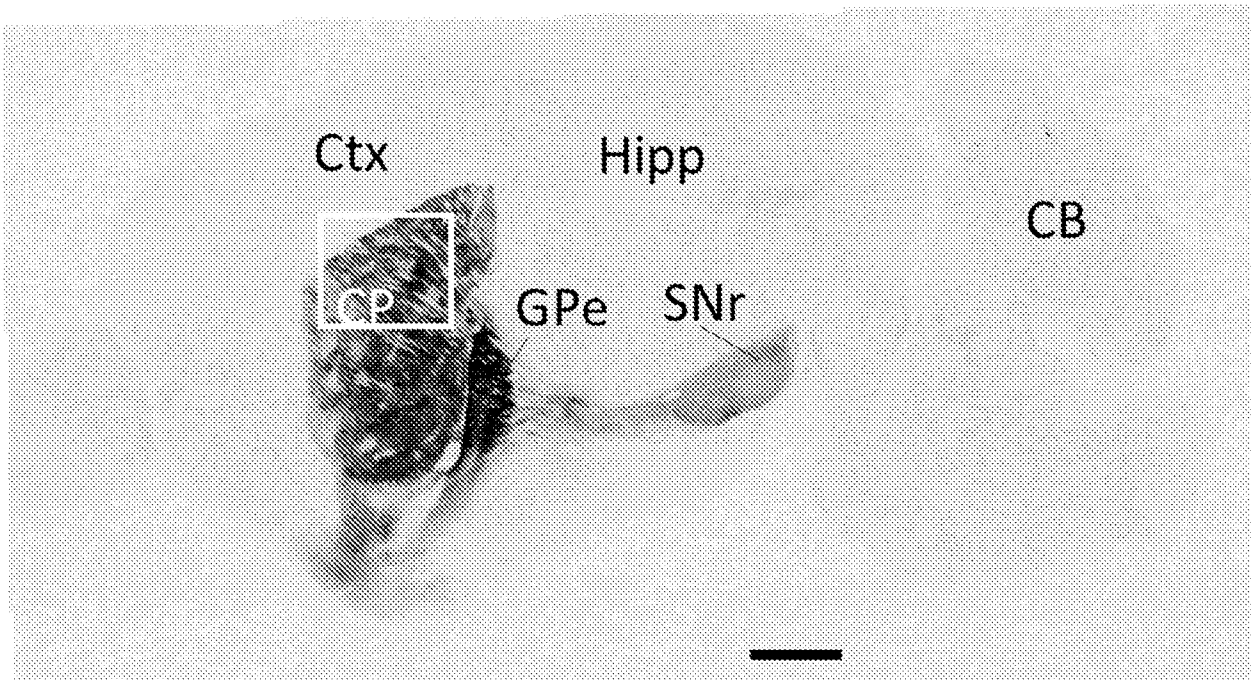


FIG. 10B

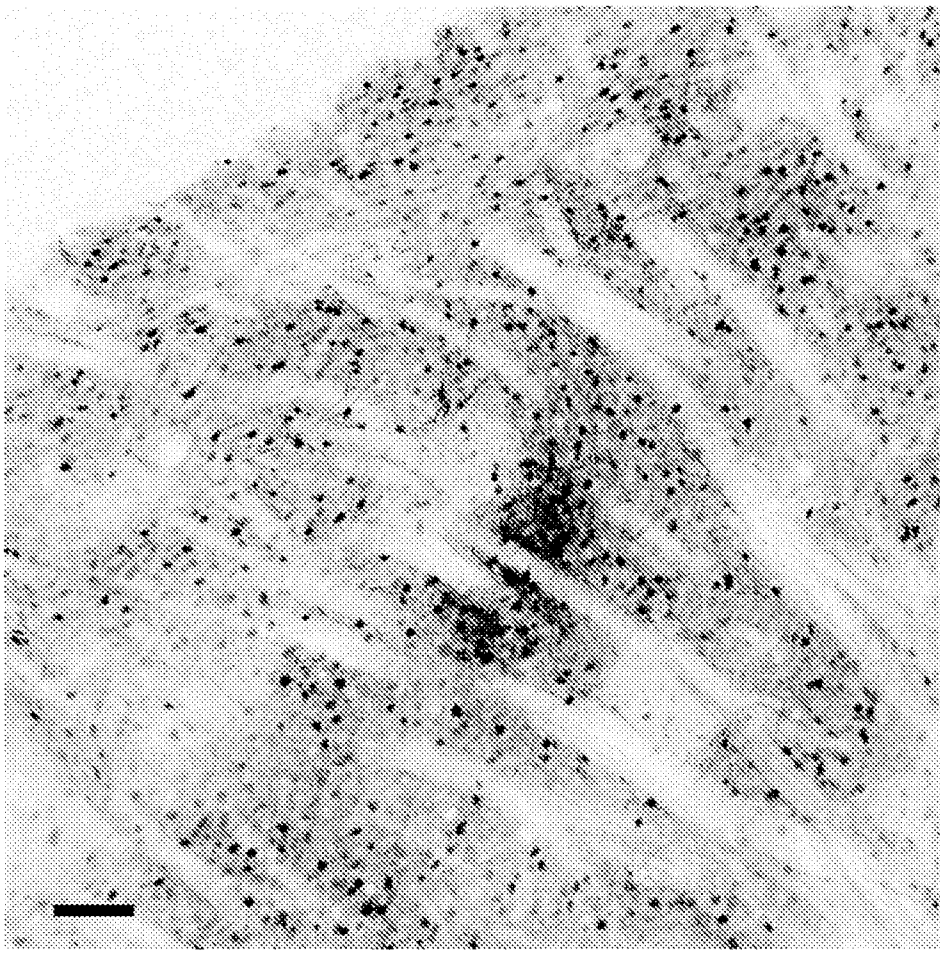


FIG. 11A

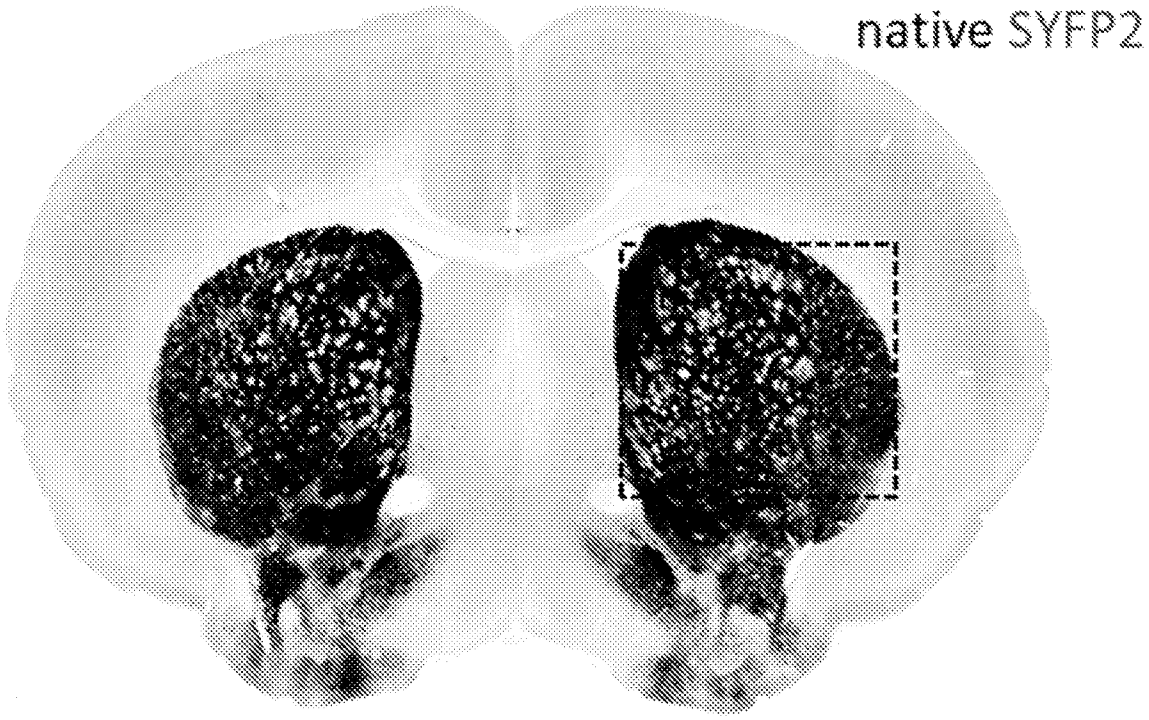


FIG. 11B

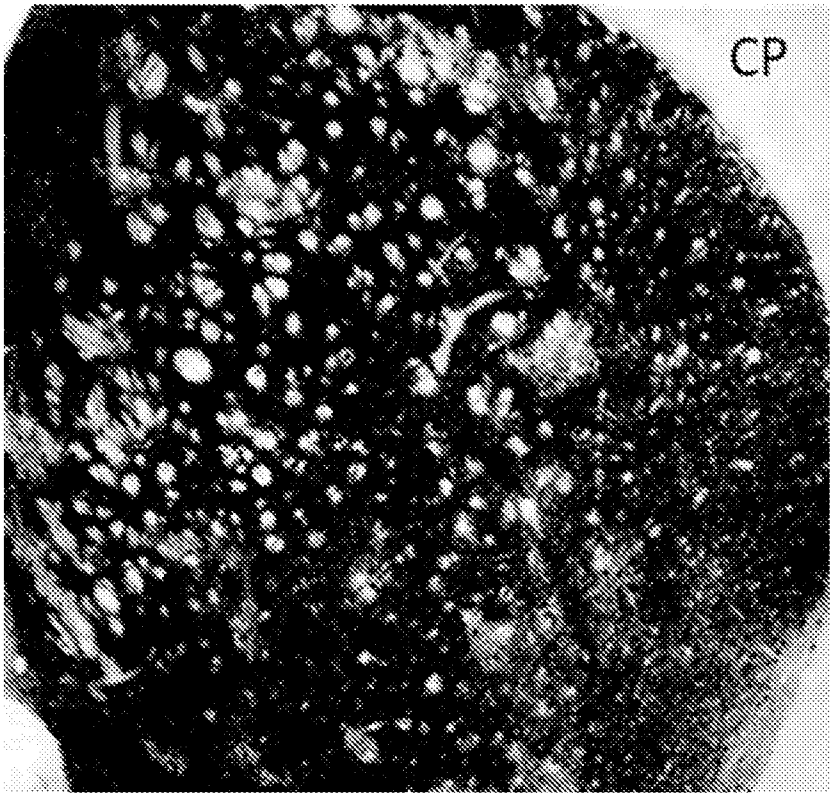


FIG. 11C

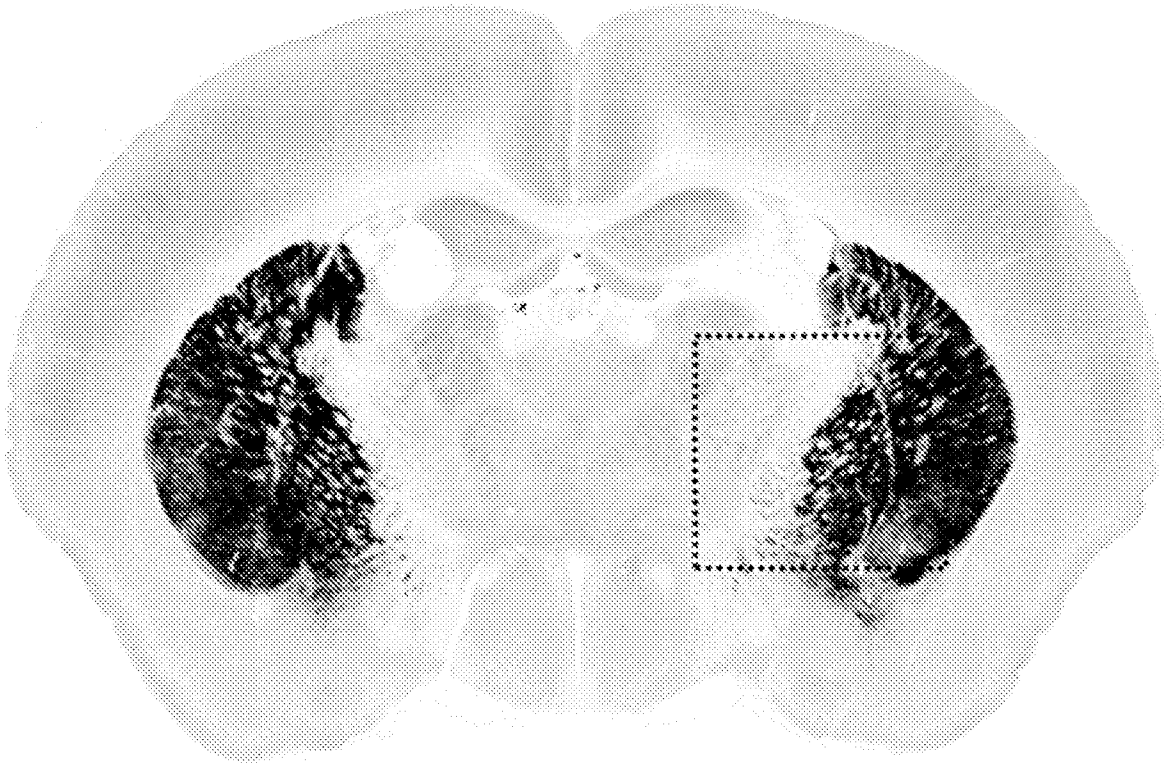


FIG. 11D

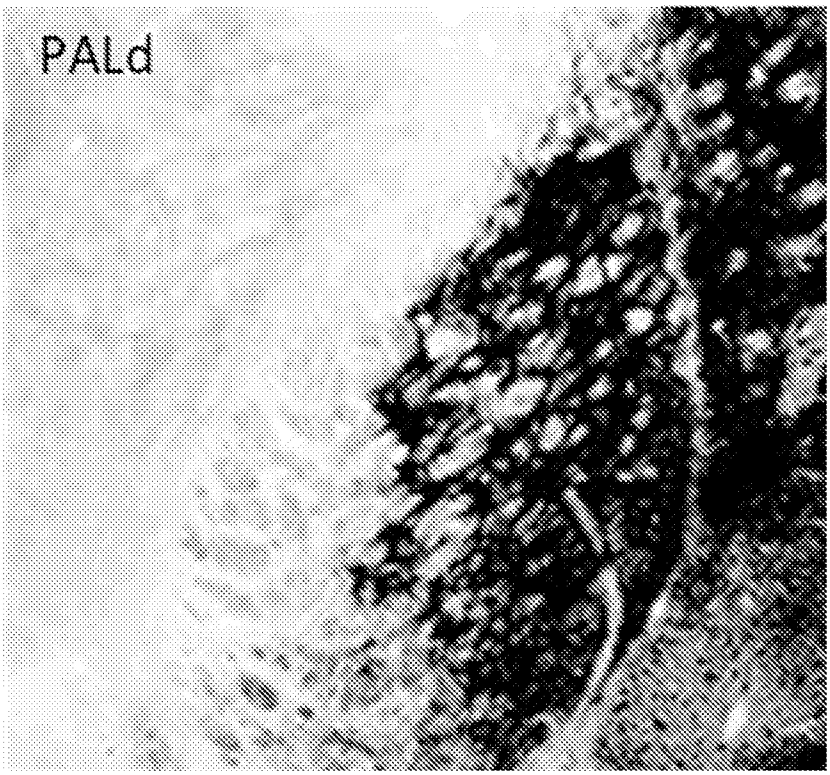


FIG. 11E

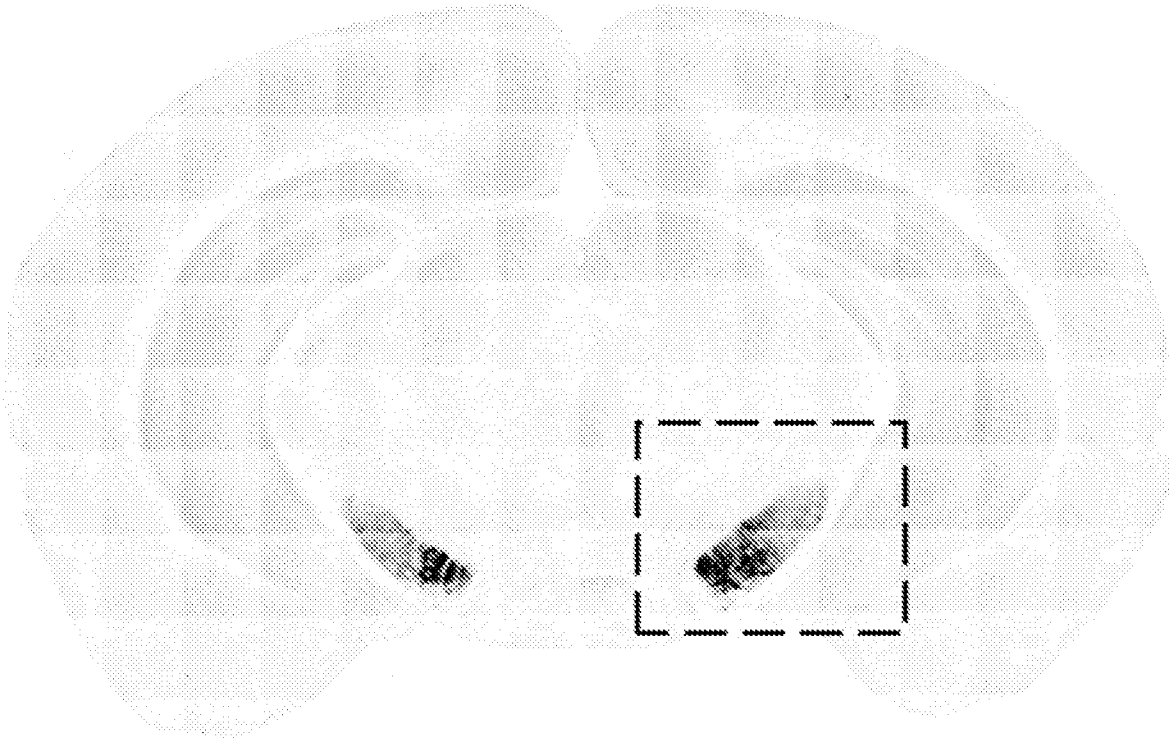


FIG. 11F

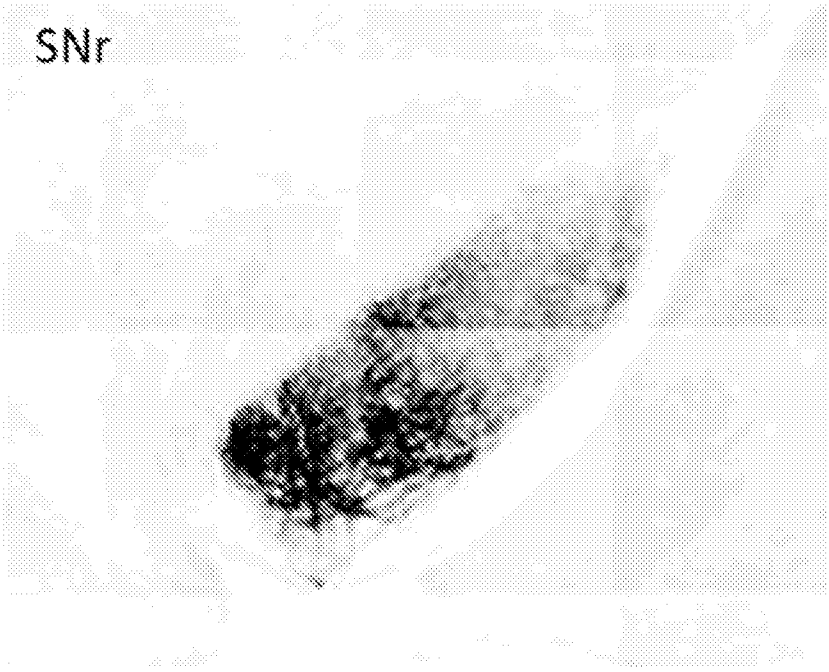


FIG. 11G

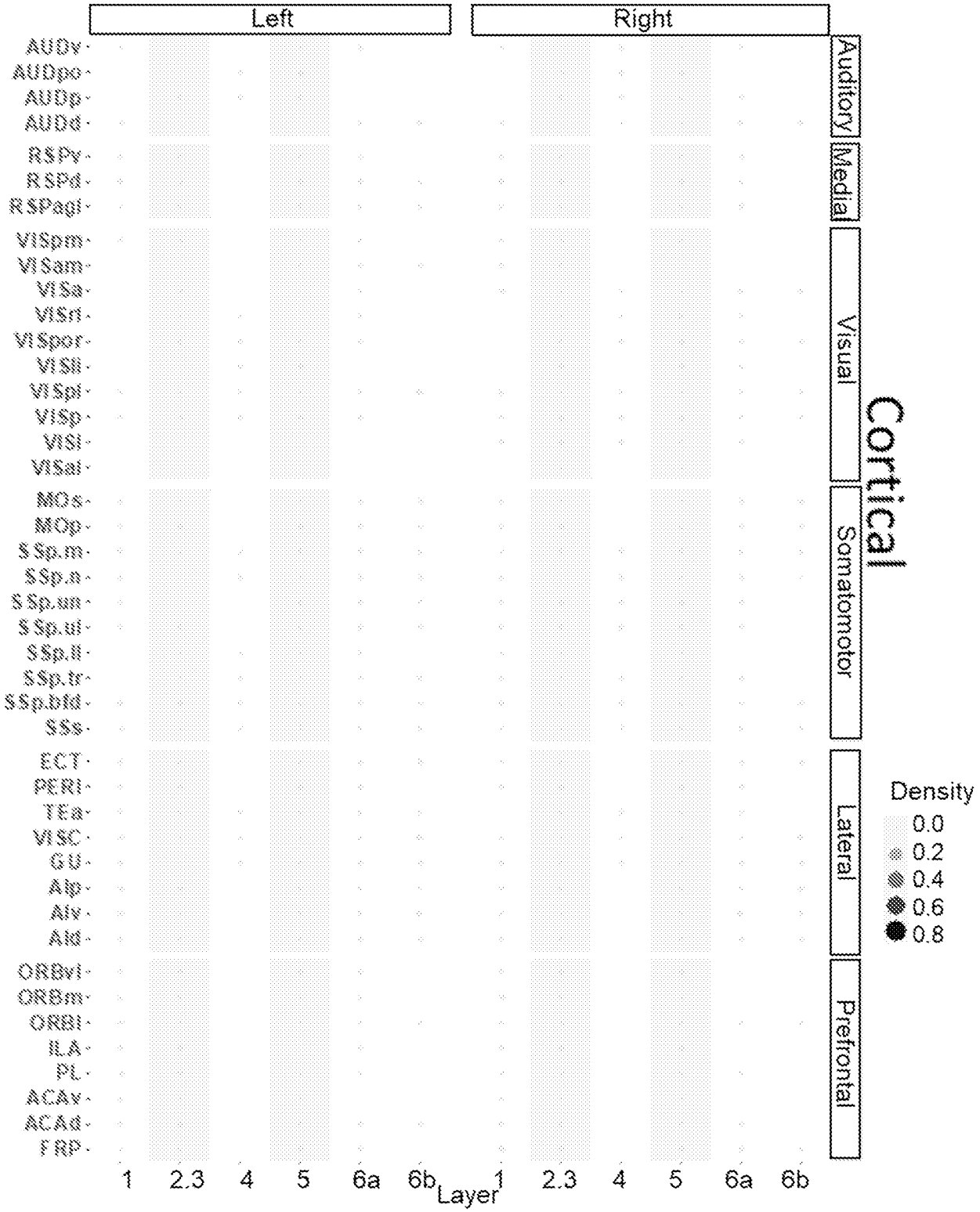

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FIG. 11G cont'd



FIG. 11G cont'd

FIG. 12A

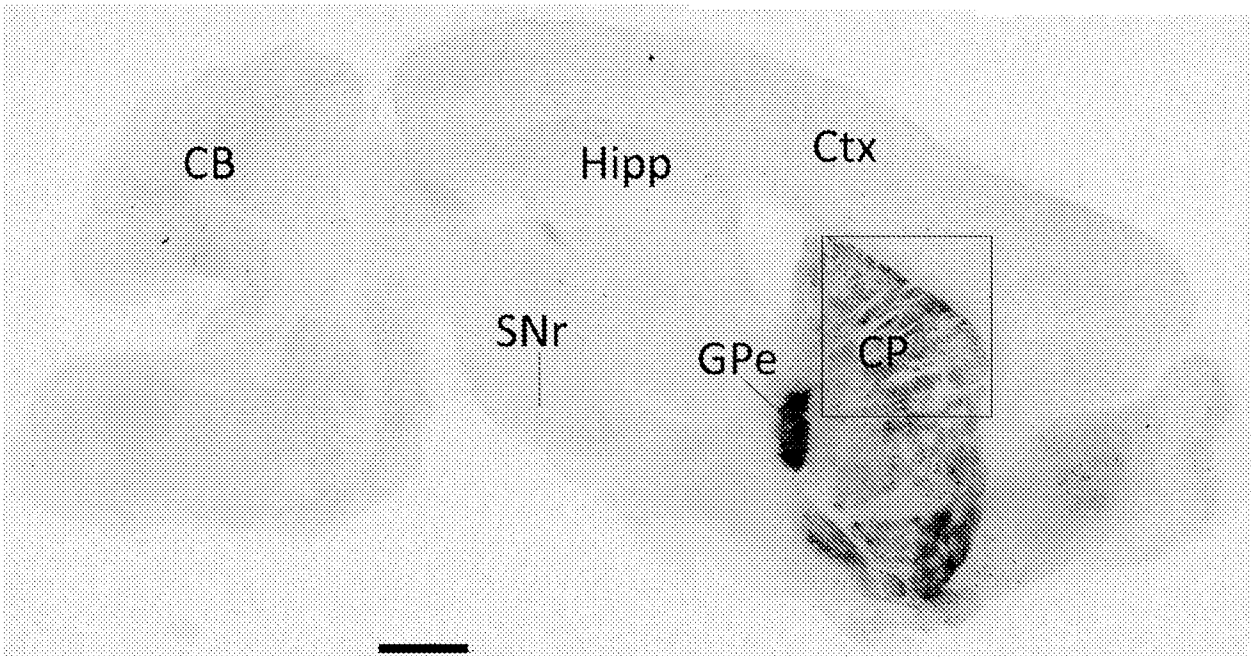


FIG. 12B

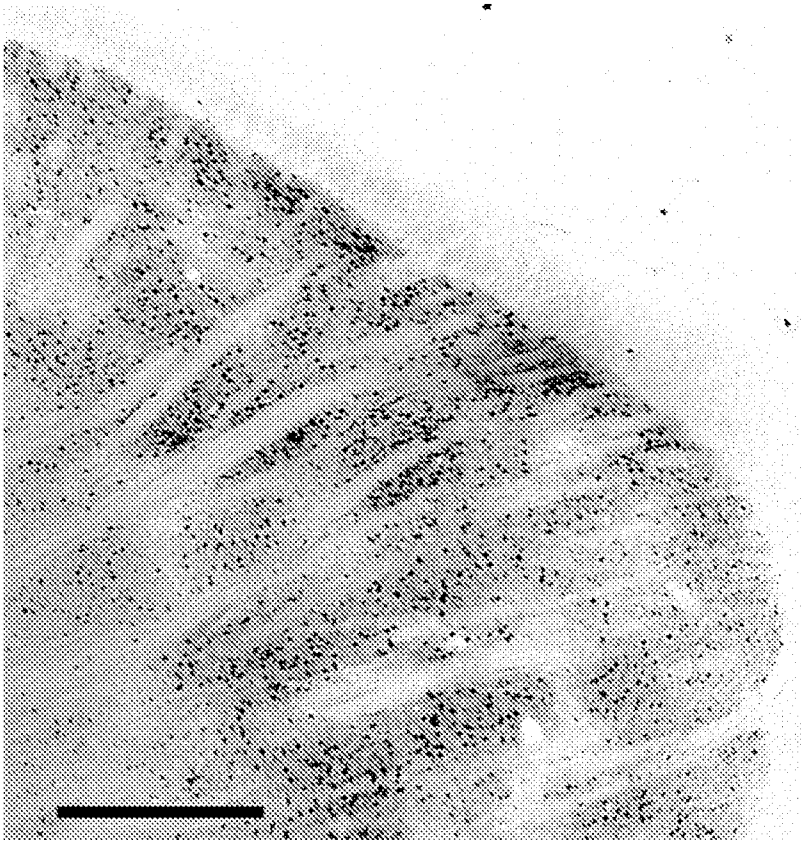


FIG. 13A

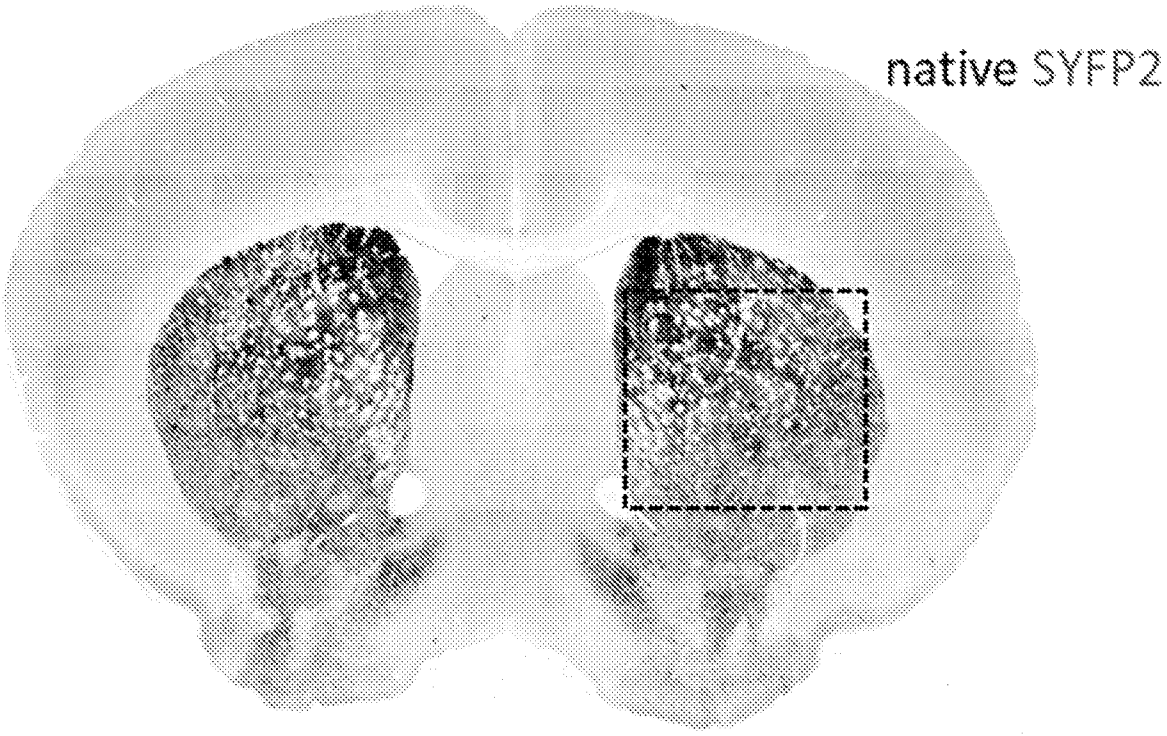


FIG. 13B

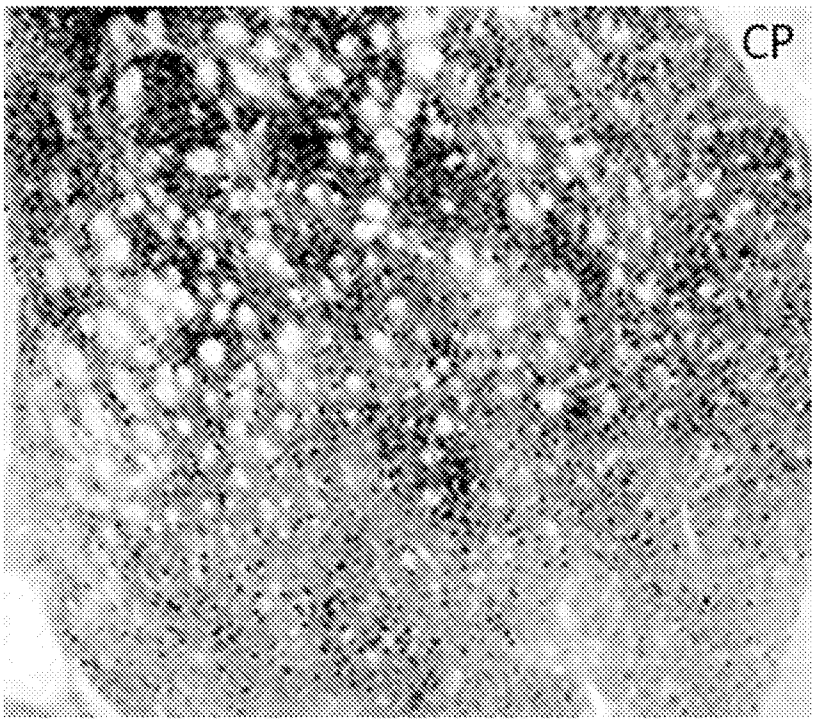


FIG. 13C

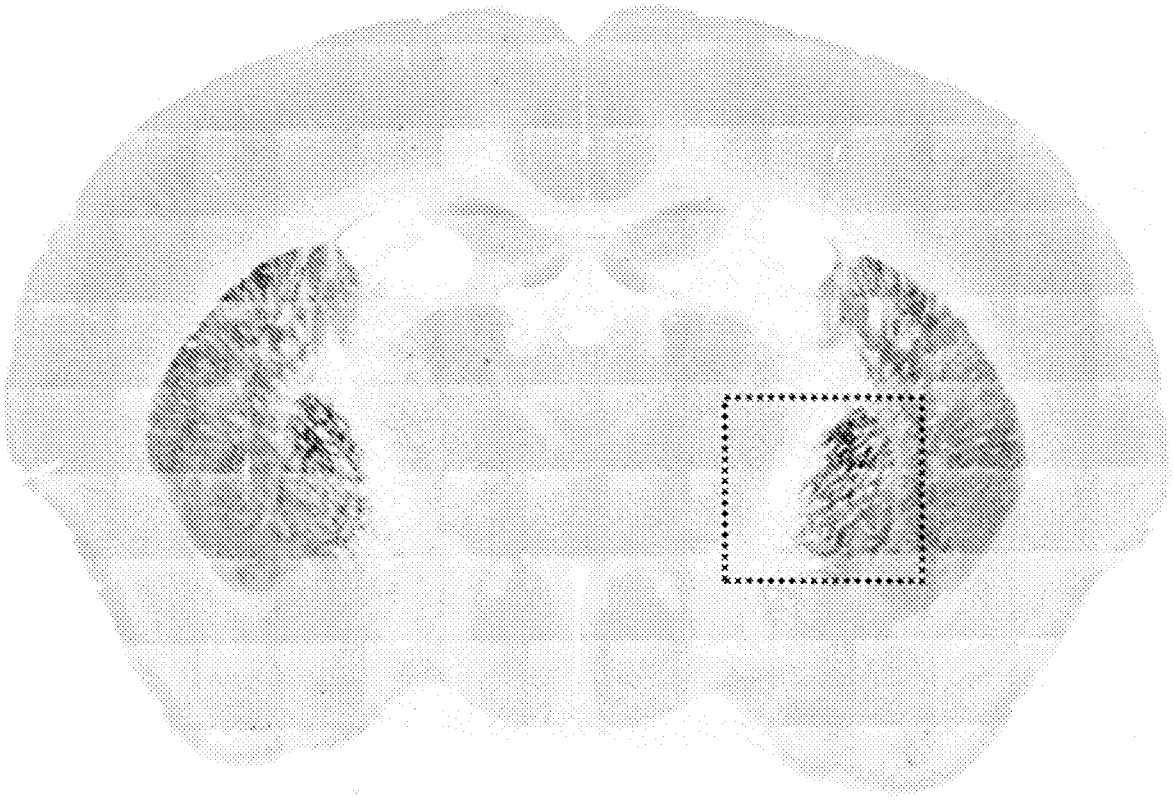


FIG. 13D

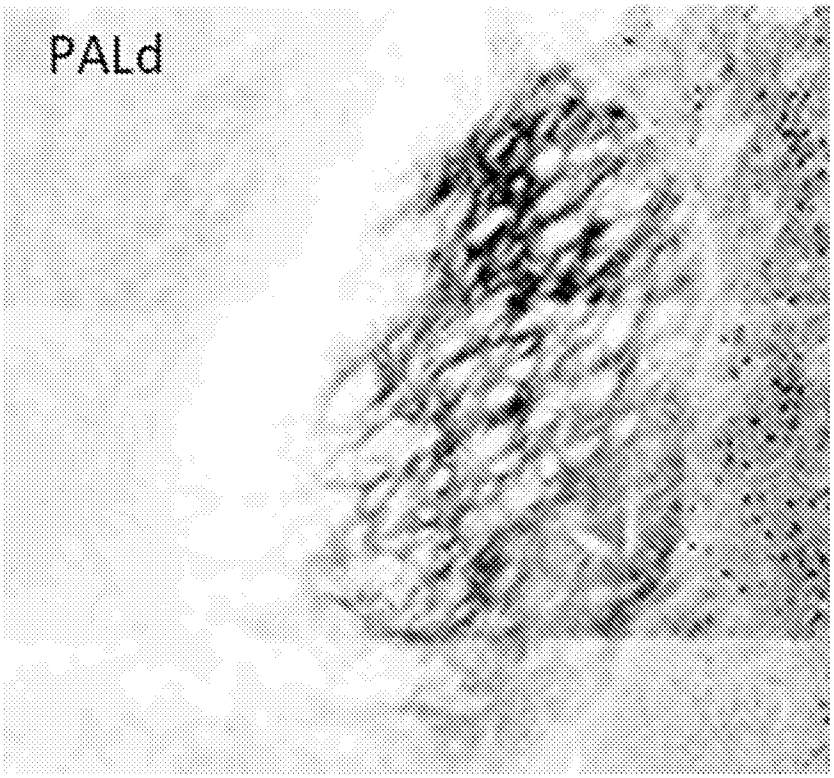


FIG. 13E



FIG. 13F

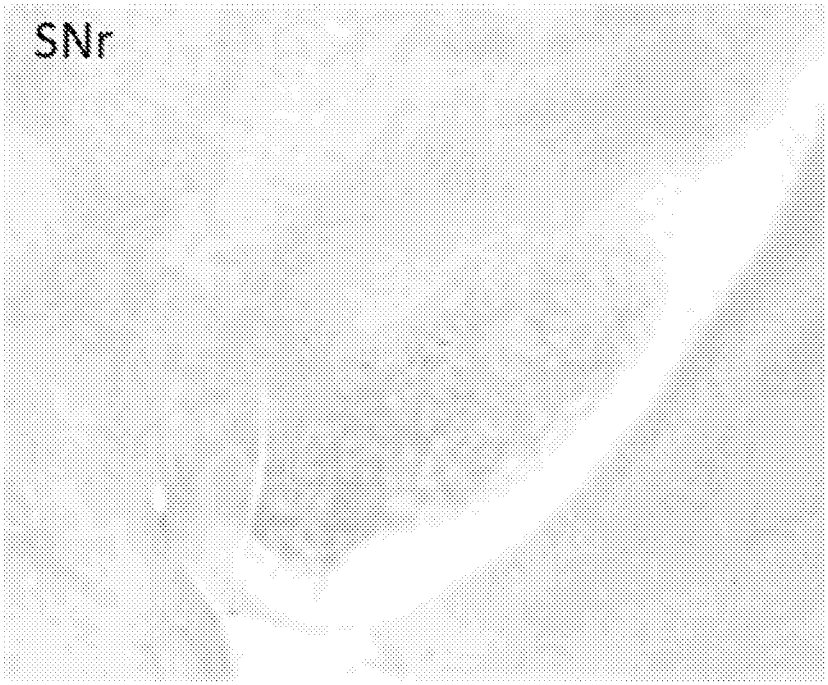


FIG. 13G

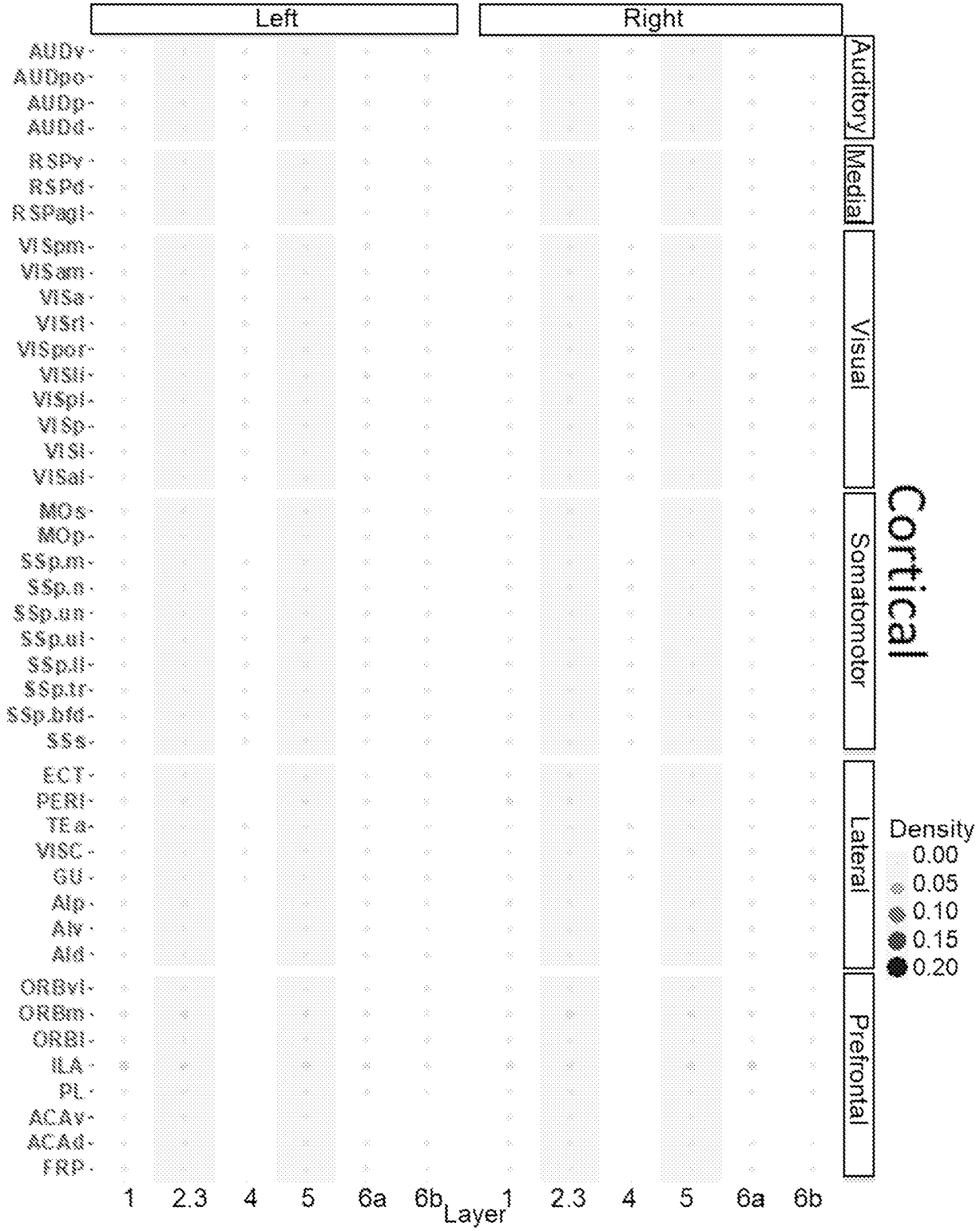

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FIG. 13G cont'd

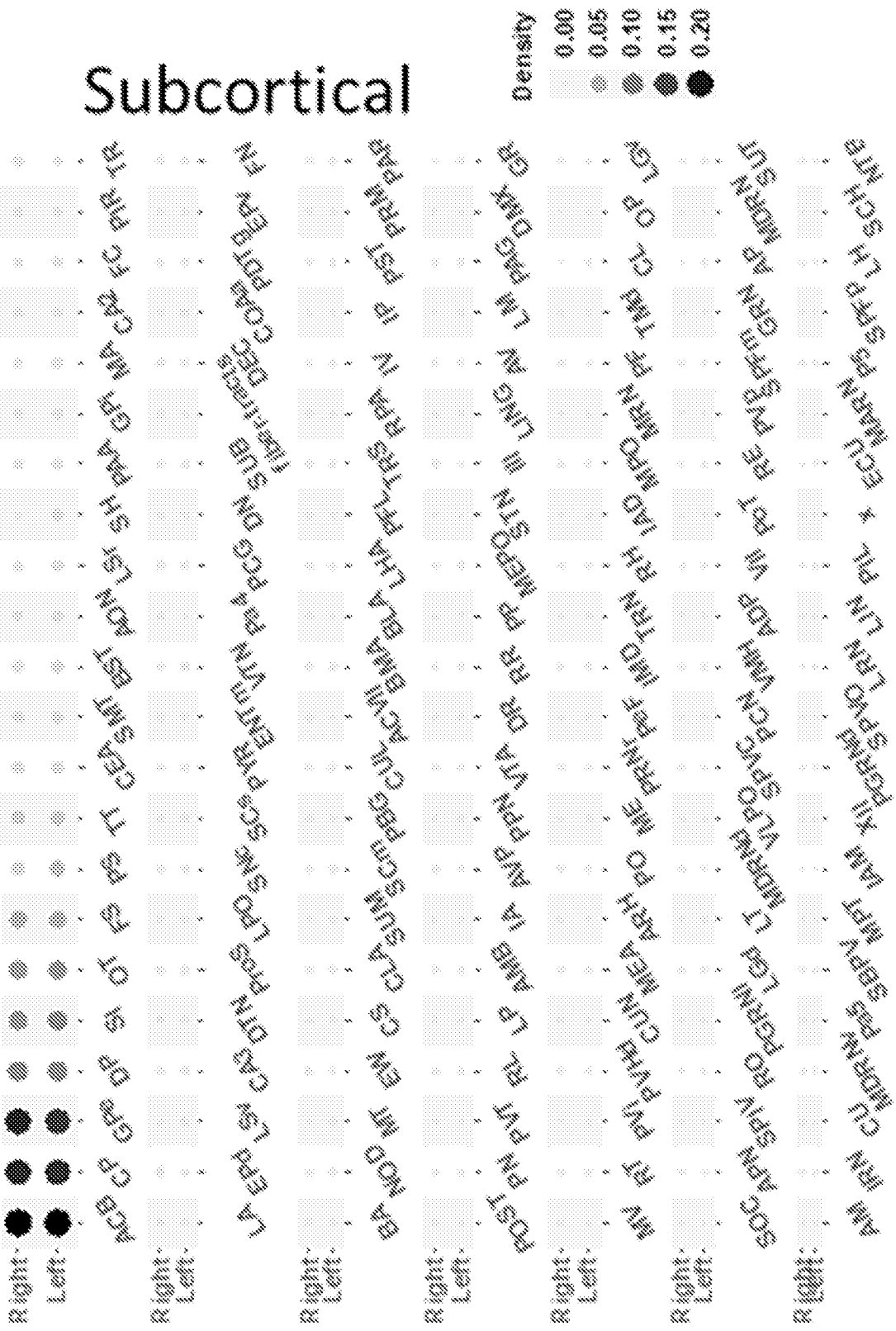


FIG. 13G cont'd

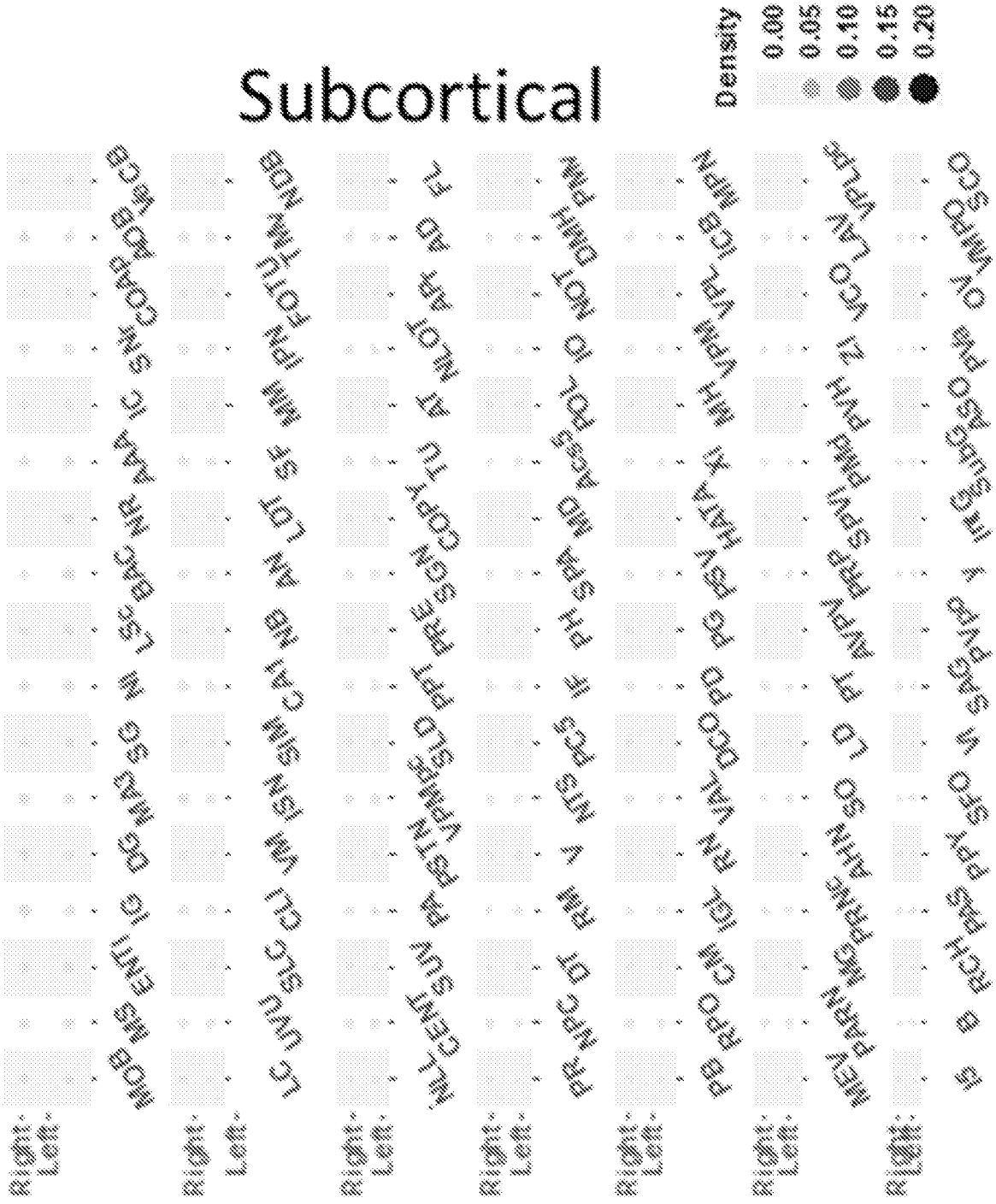


FIG. 14A

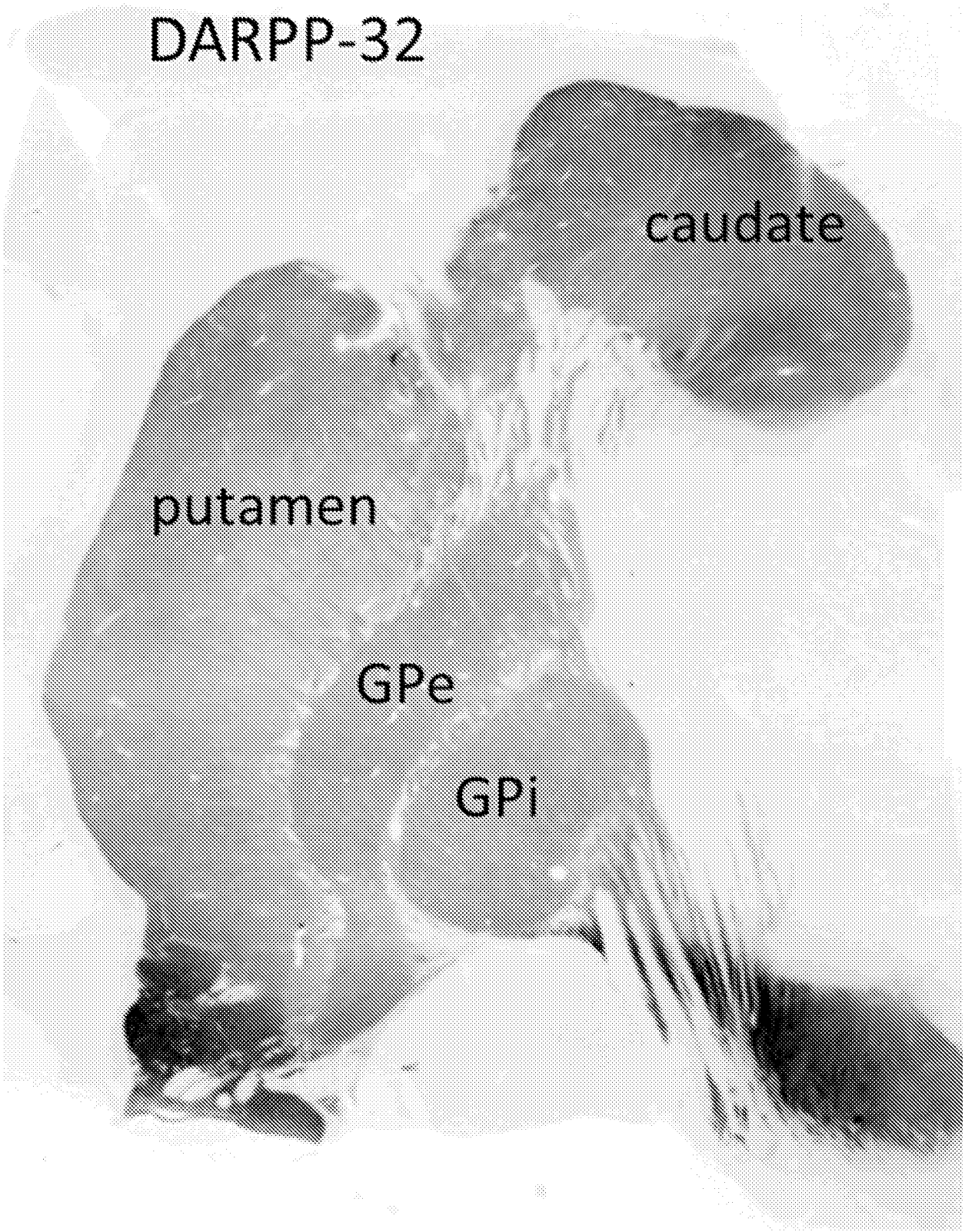


FIG. 14B

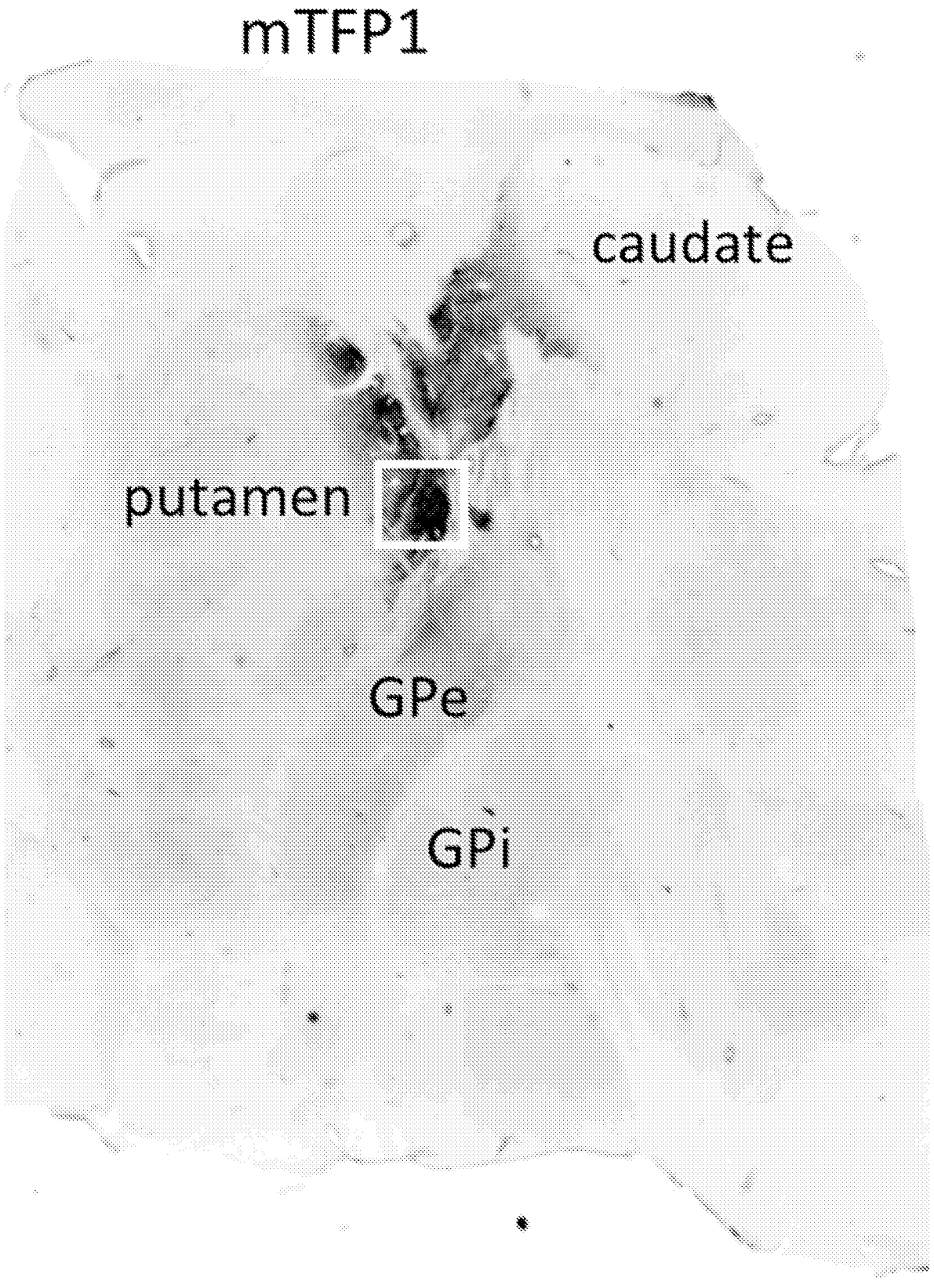


FIG. 14C

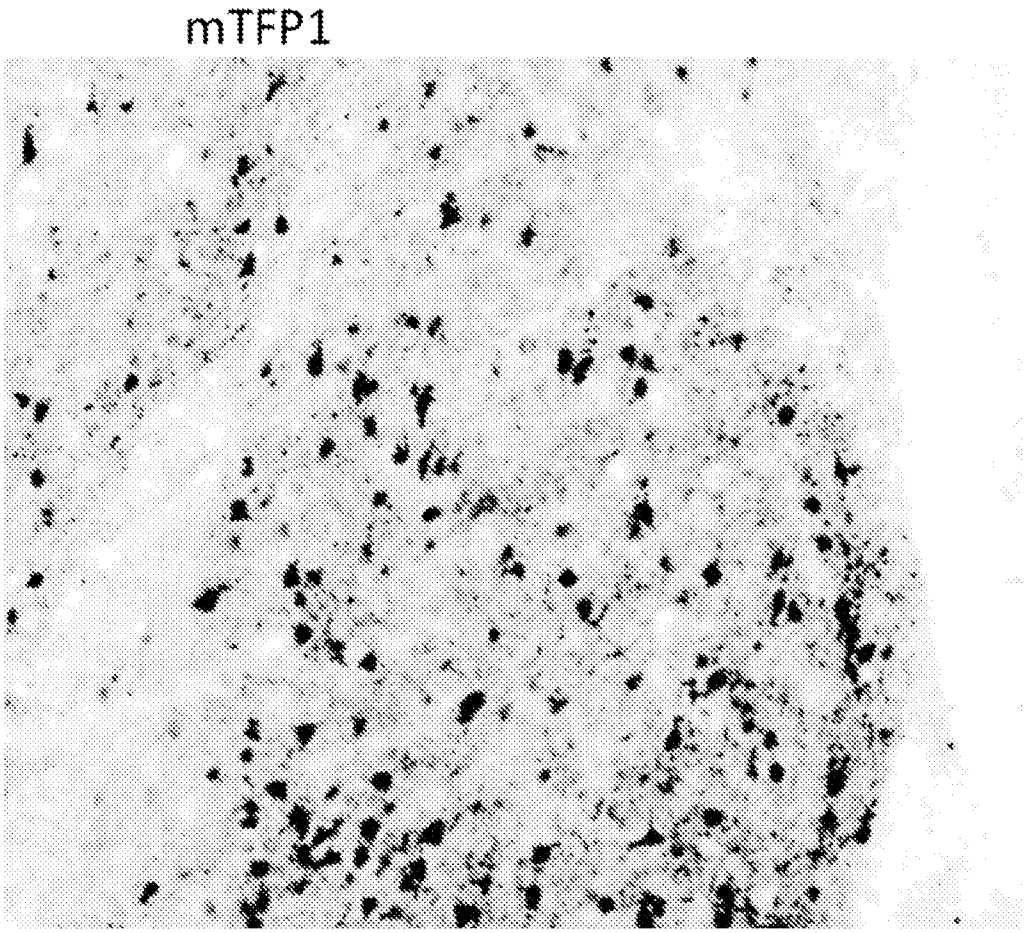


FIG. 15A

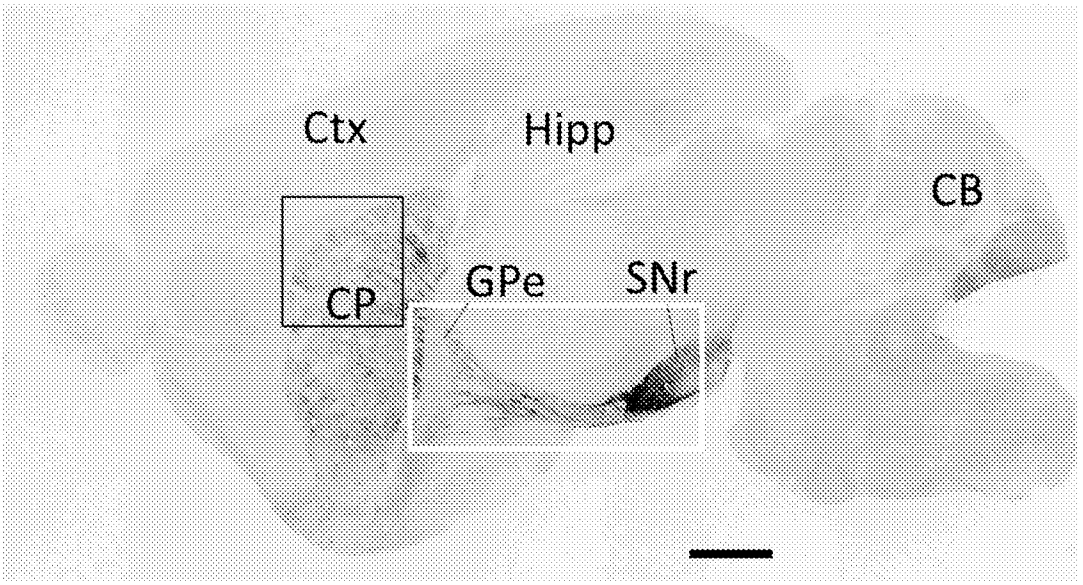


FIG. 15B

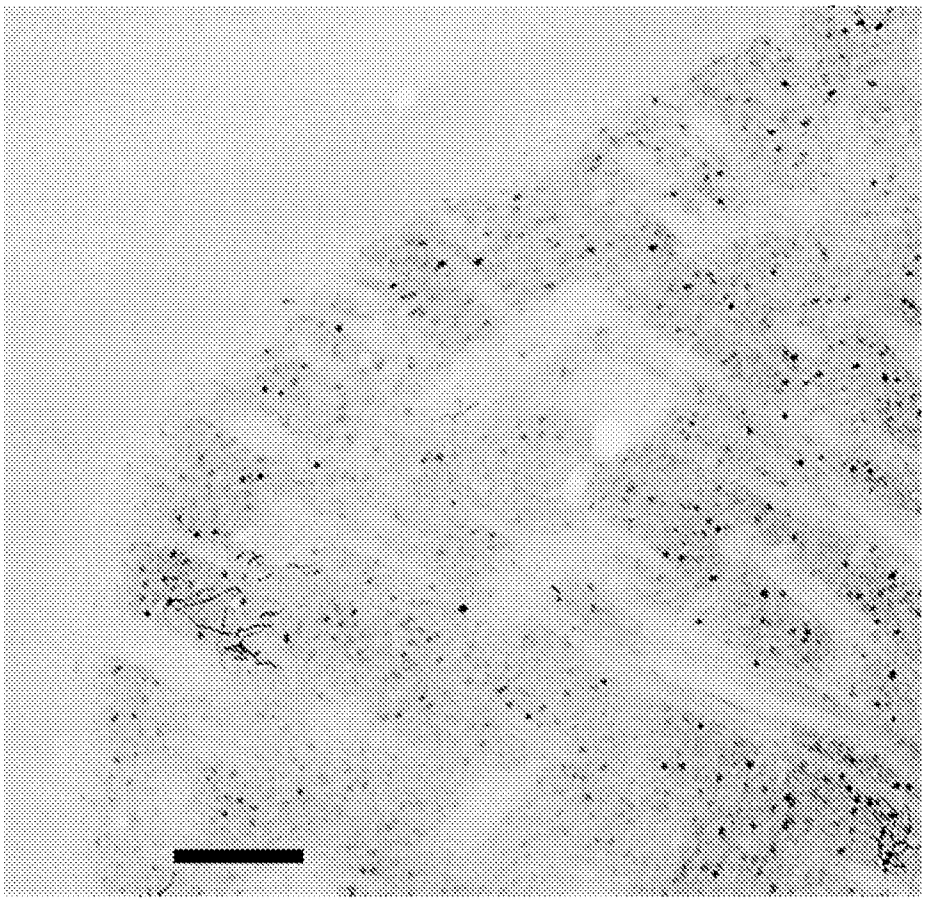


FIG. 15C

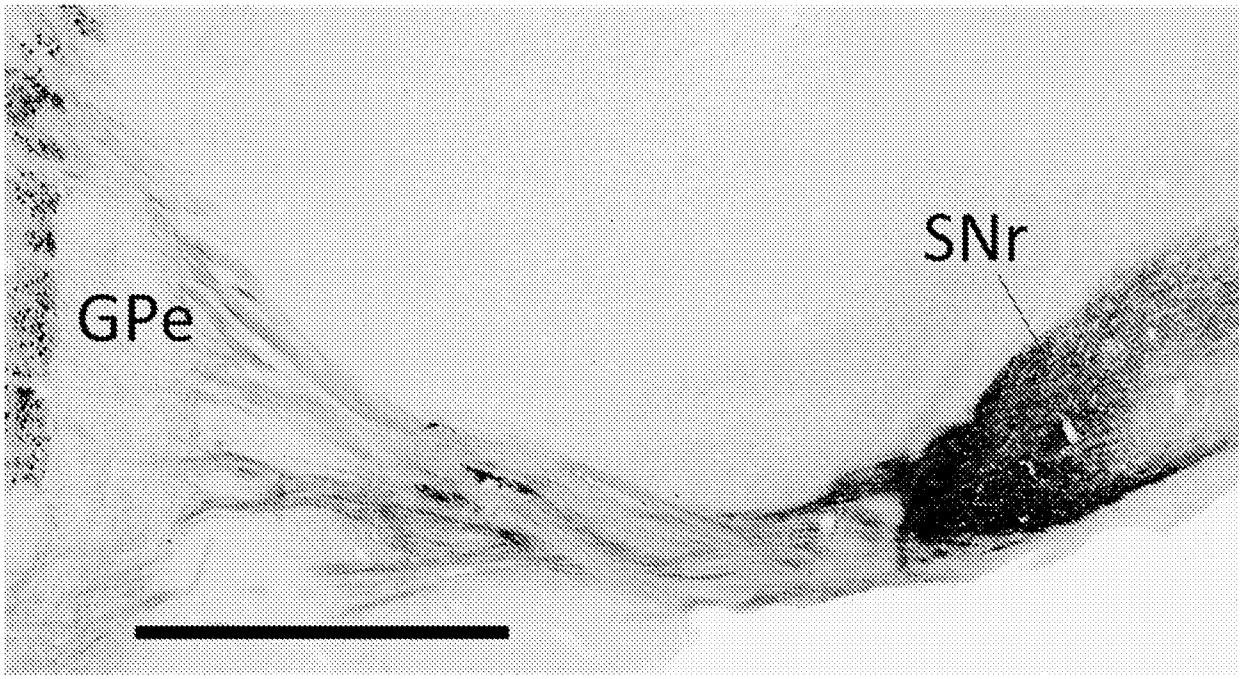


FIG. 16A

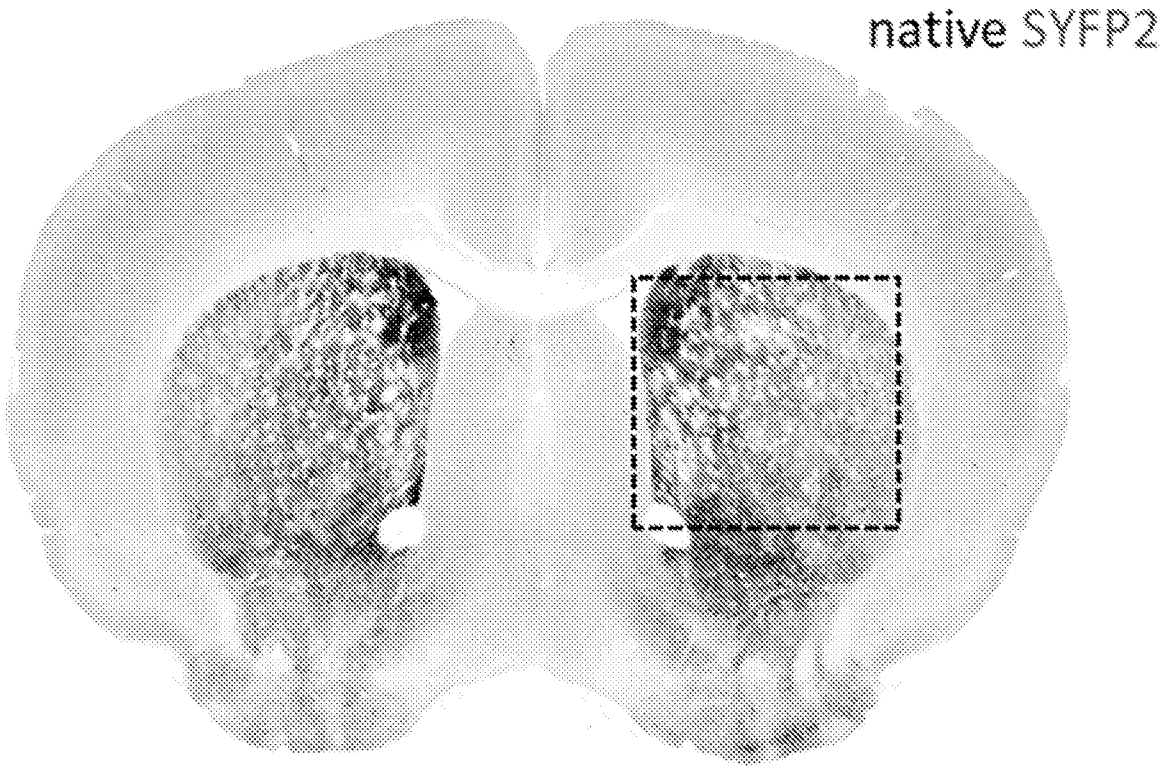


FIG. 16B

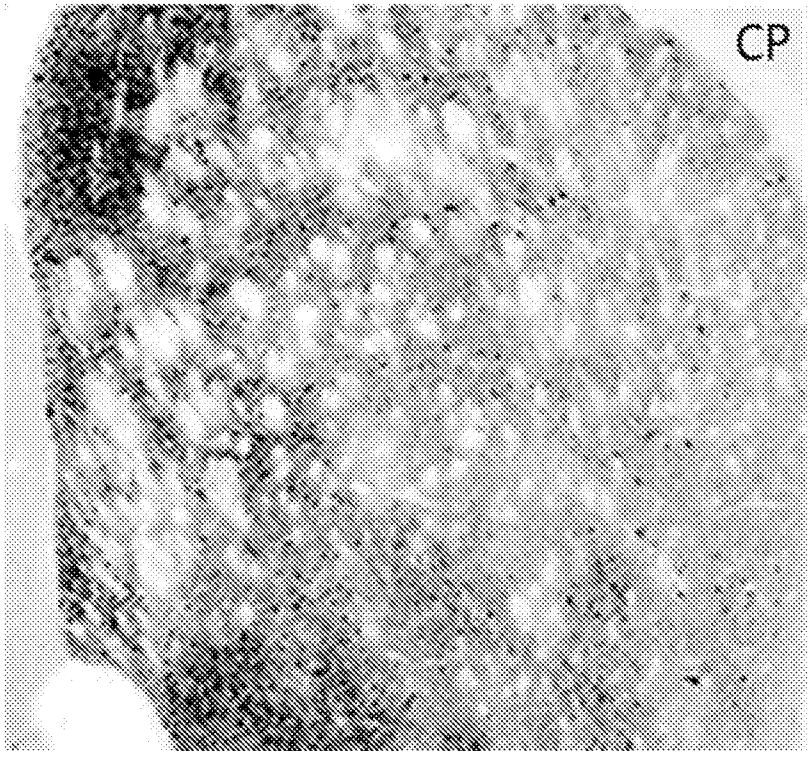


FIG. 16C

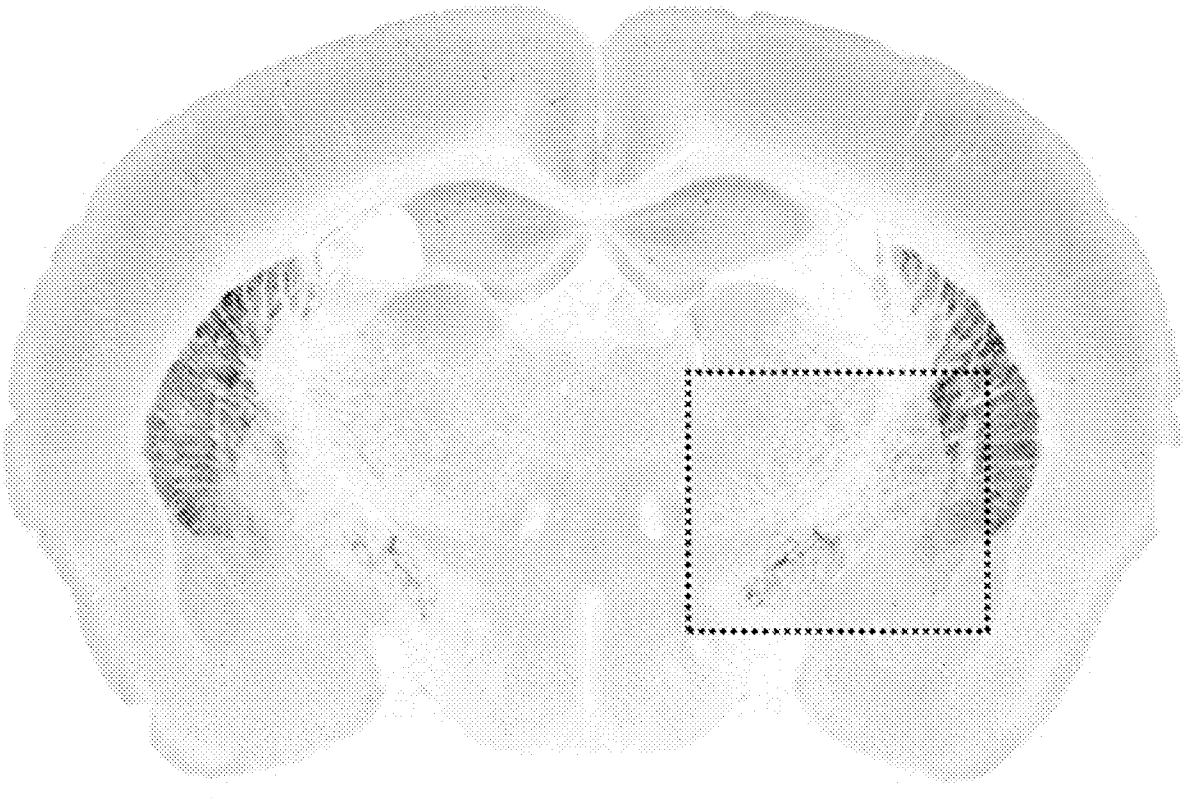


FIG. 16D

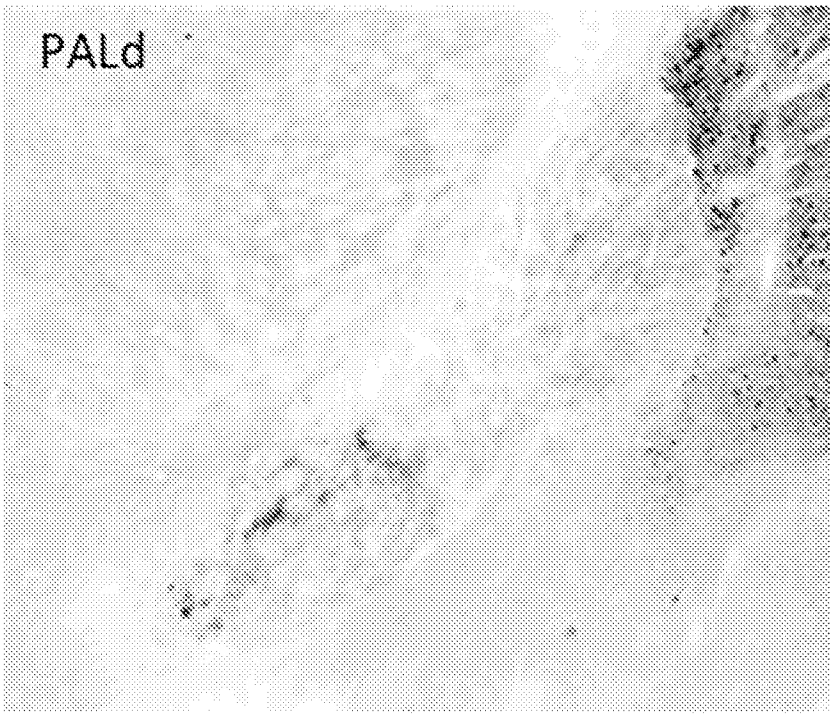


FIG. 16E

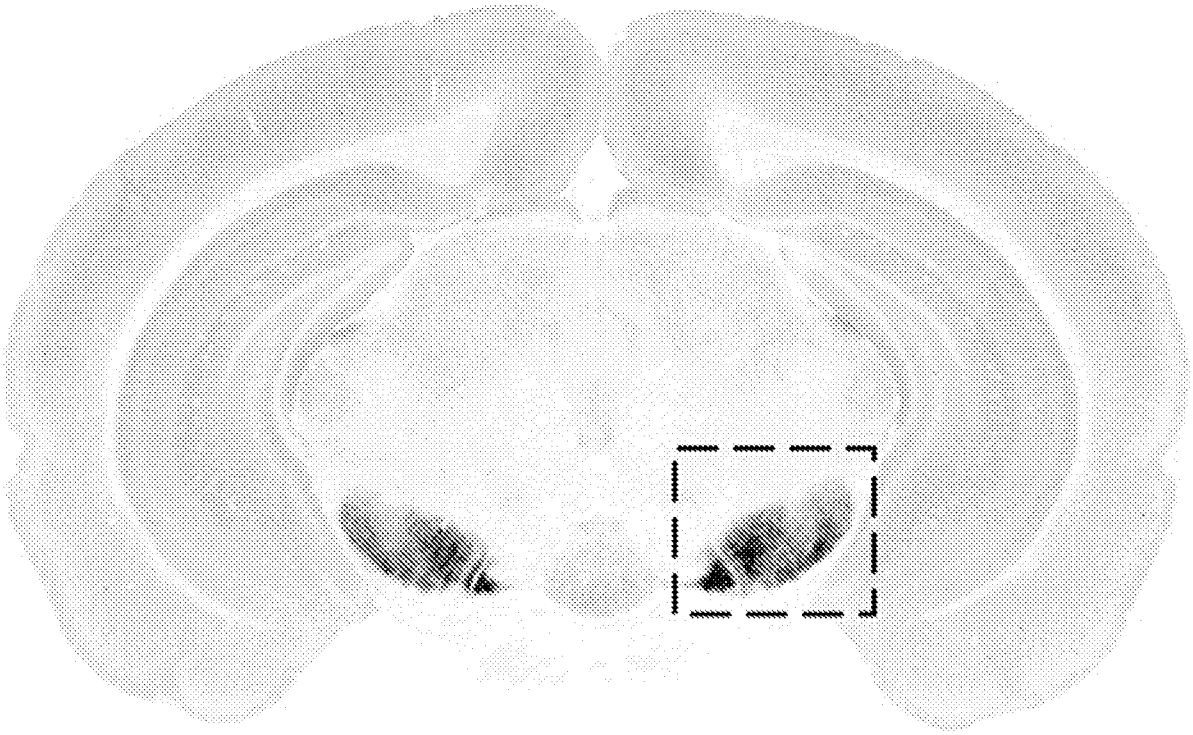


FIG. 16F

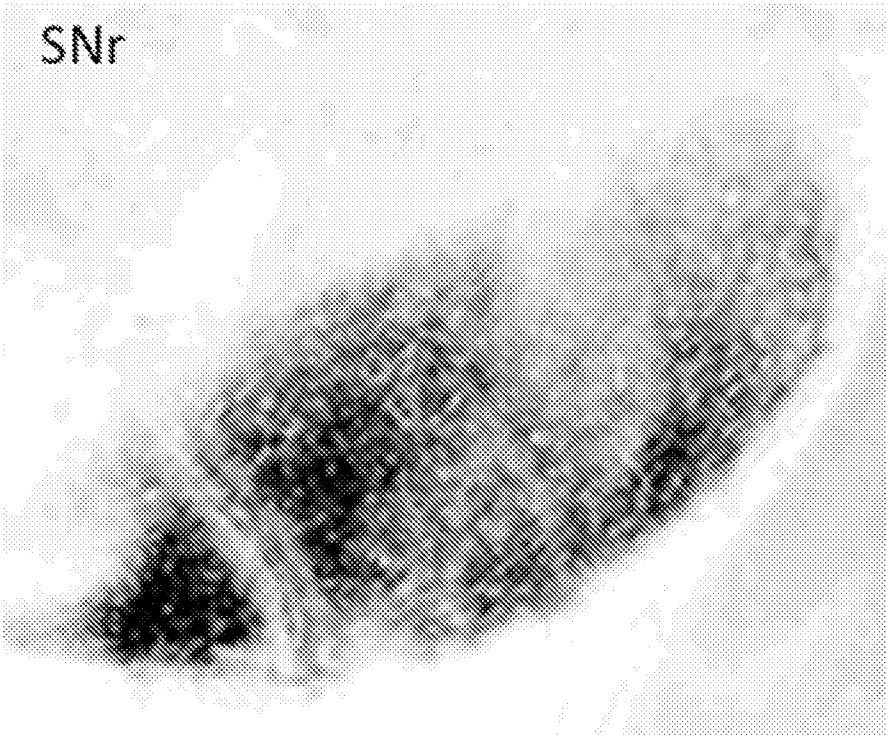


FIG. 16G

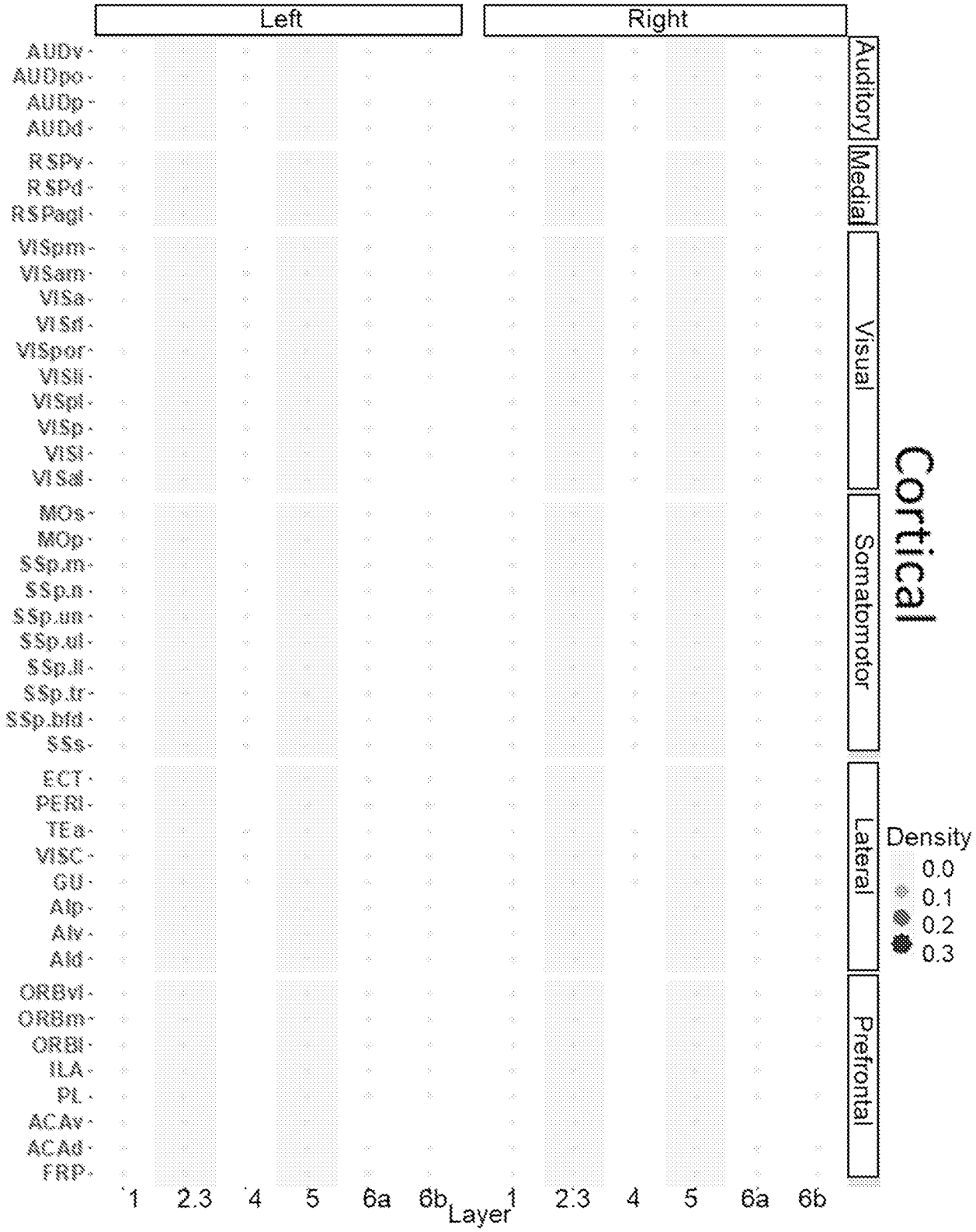

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Layer

FIG. 16G cont'd



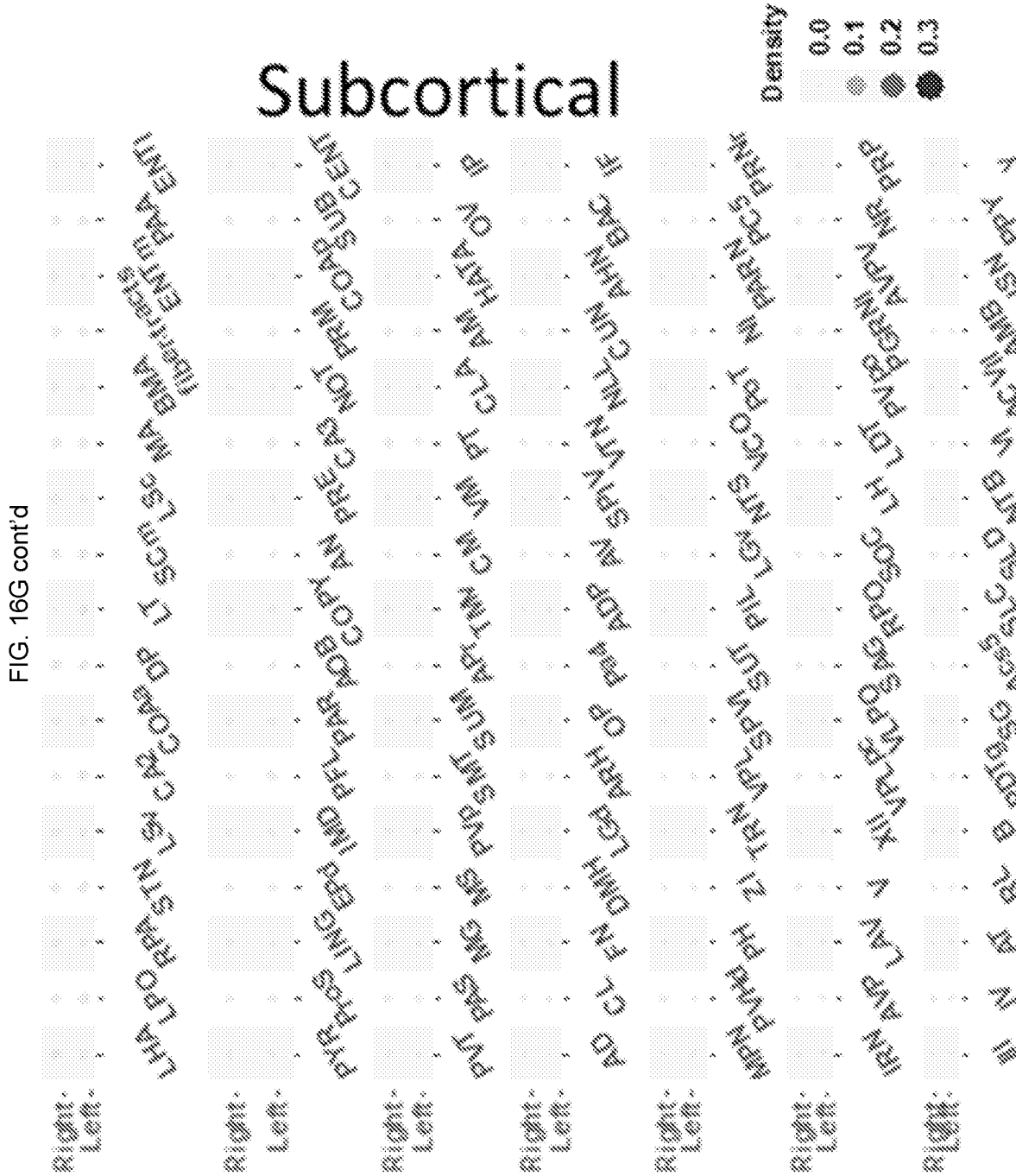


FIG. 16G cont'd

FIG. 17A

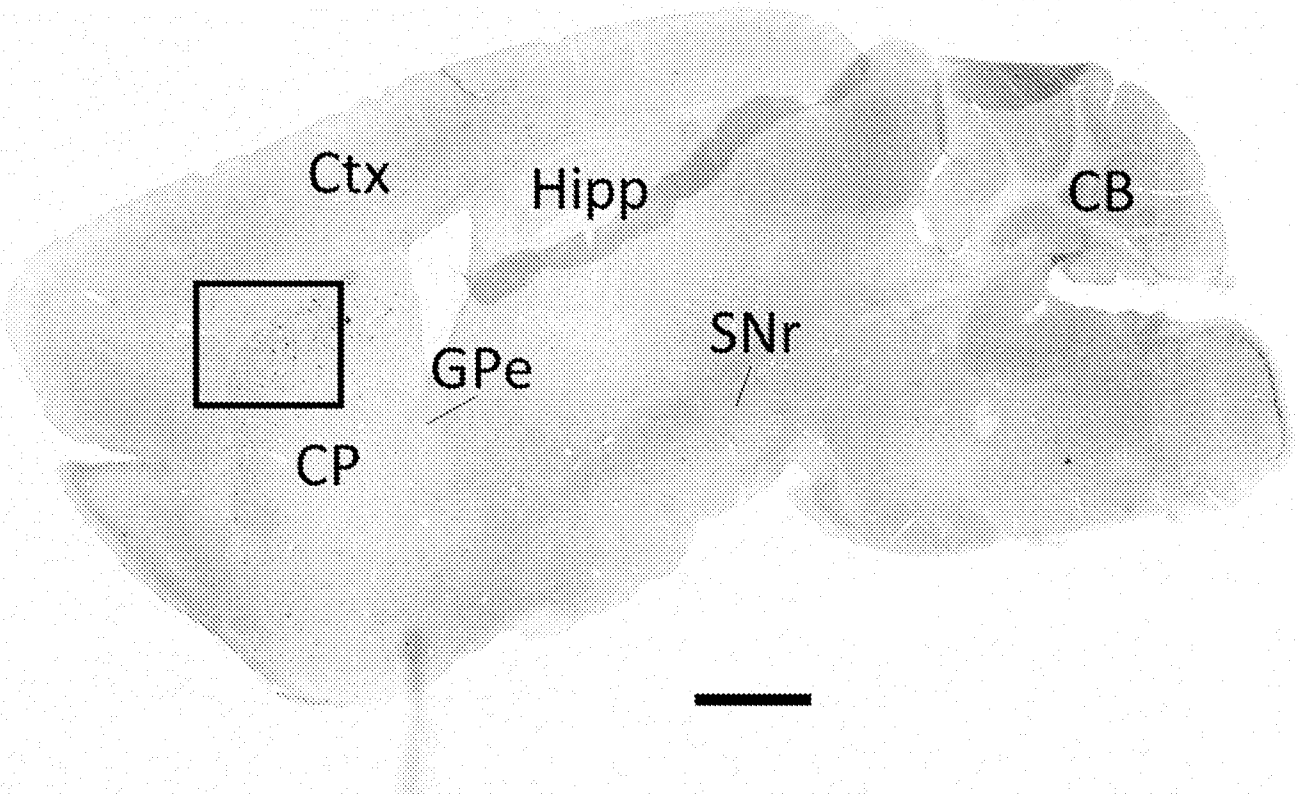


FIG. 17B

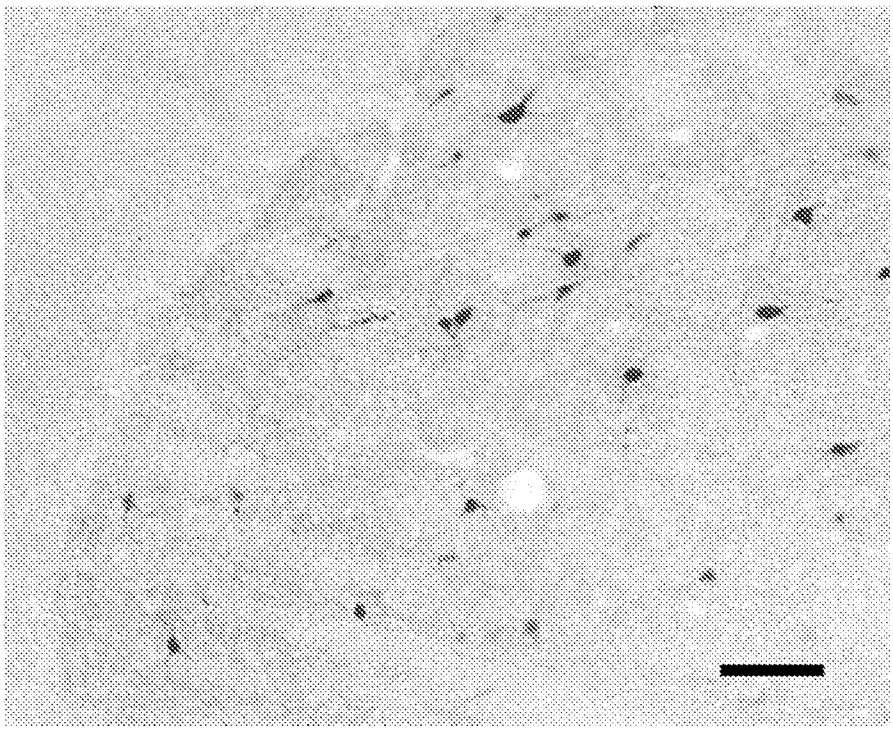


FIG. 17C

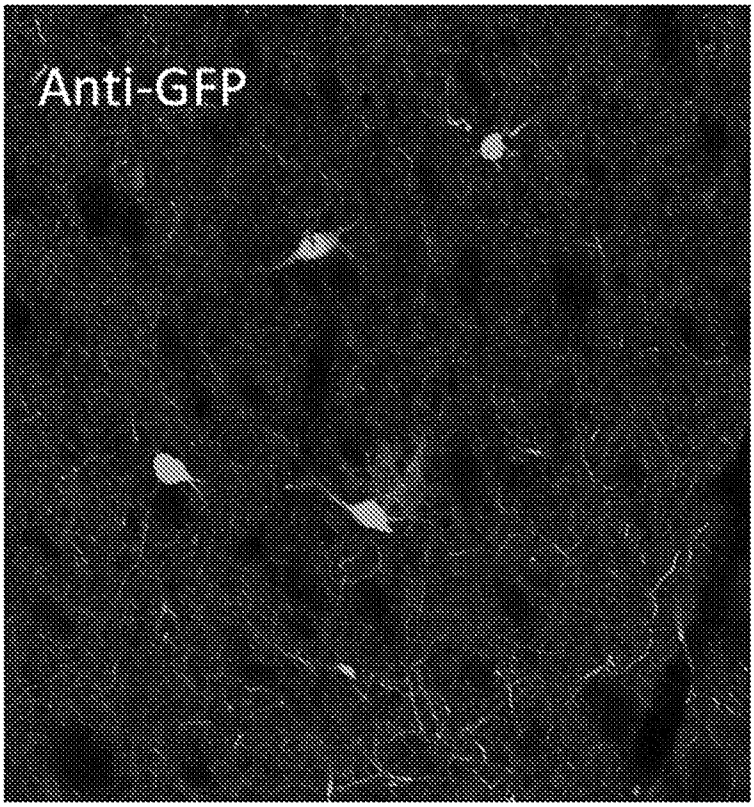


FIG. 17D

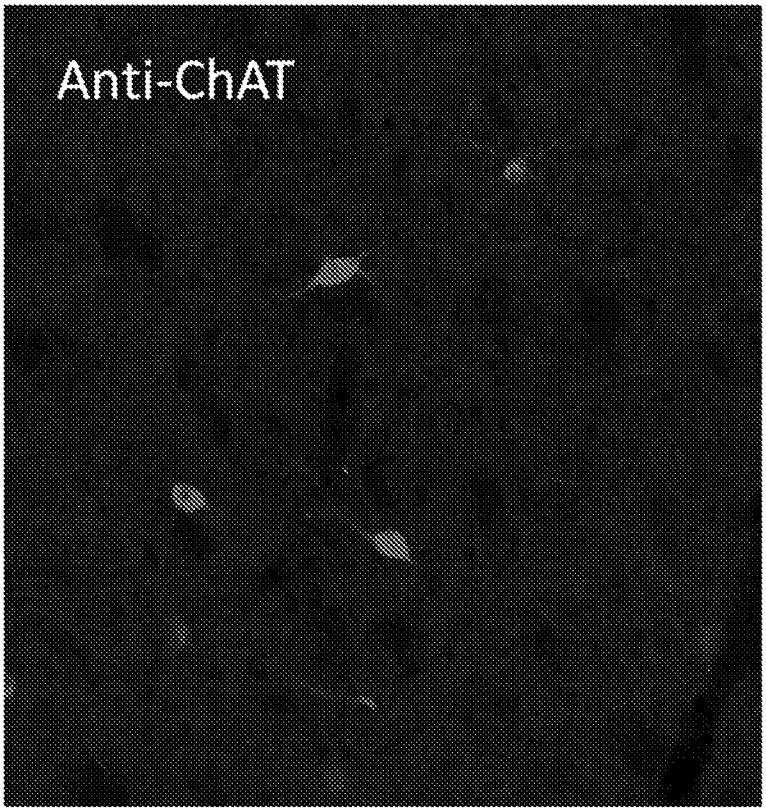
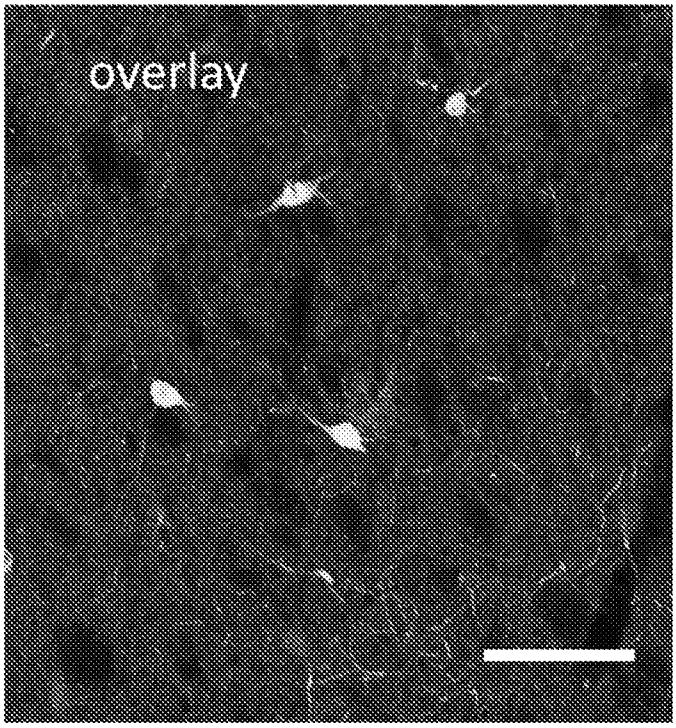


FIG. 17E



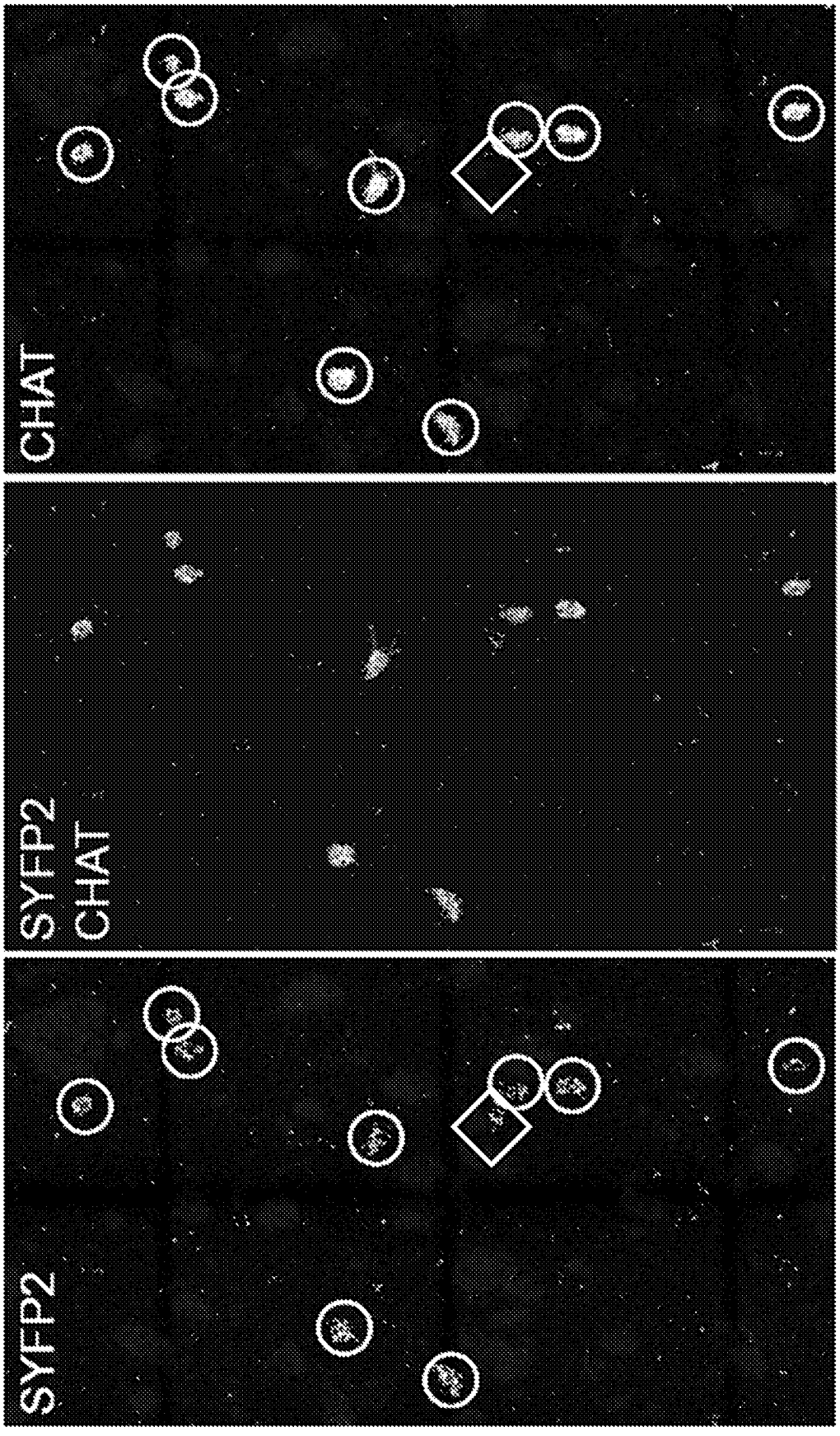


FIG. 17F FIG. 17G FIG. 17H

FIG. 18A

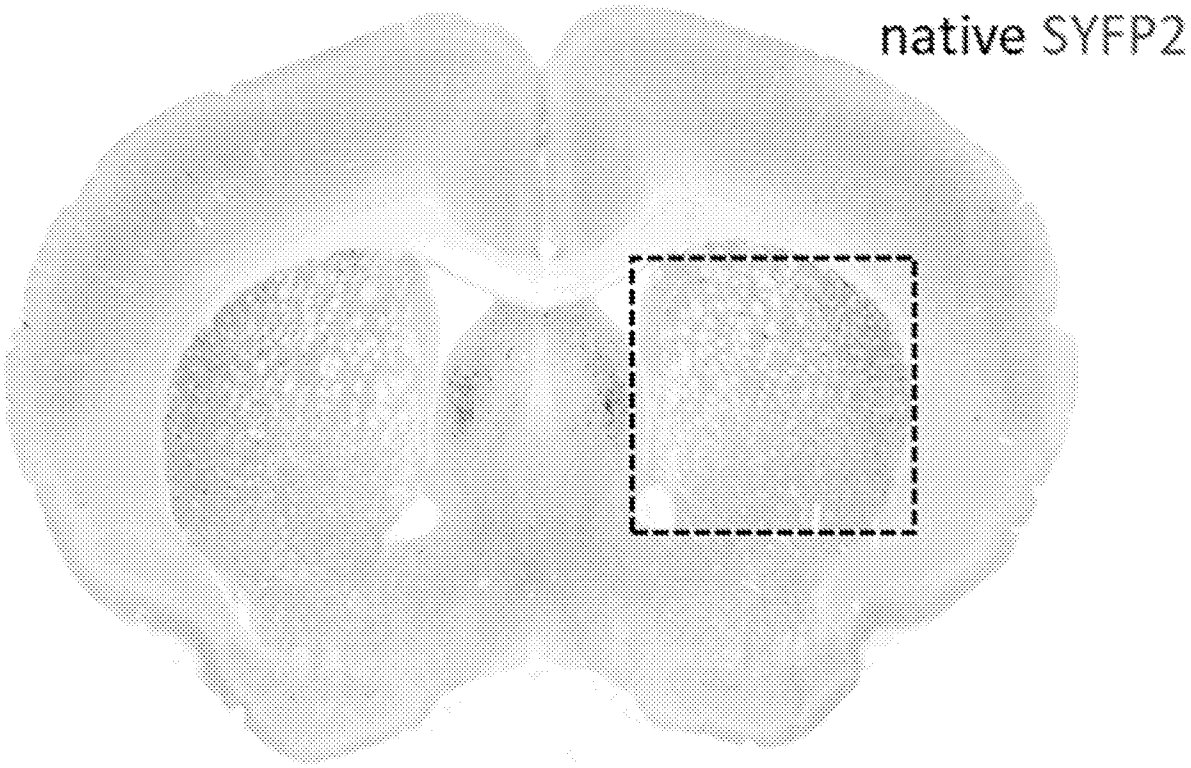


FIG. 18B

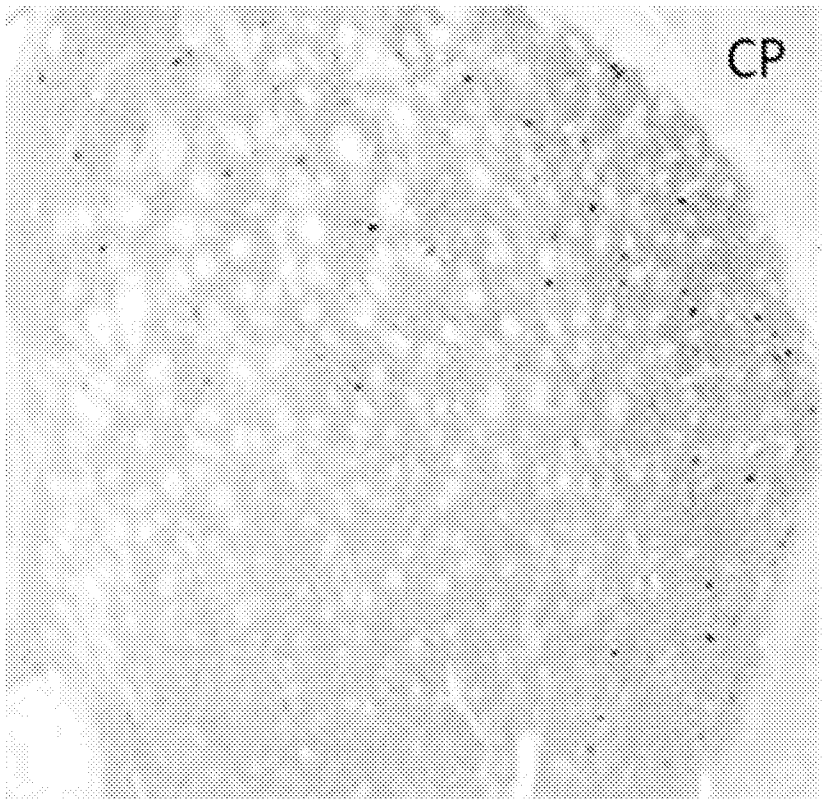


FIG. 18C

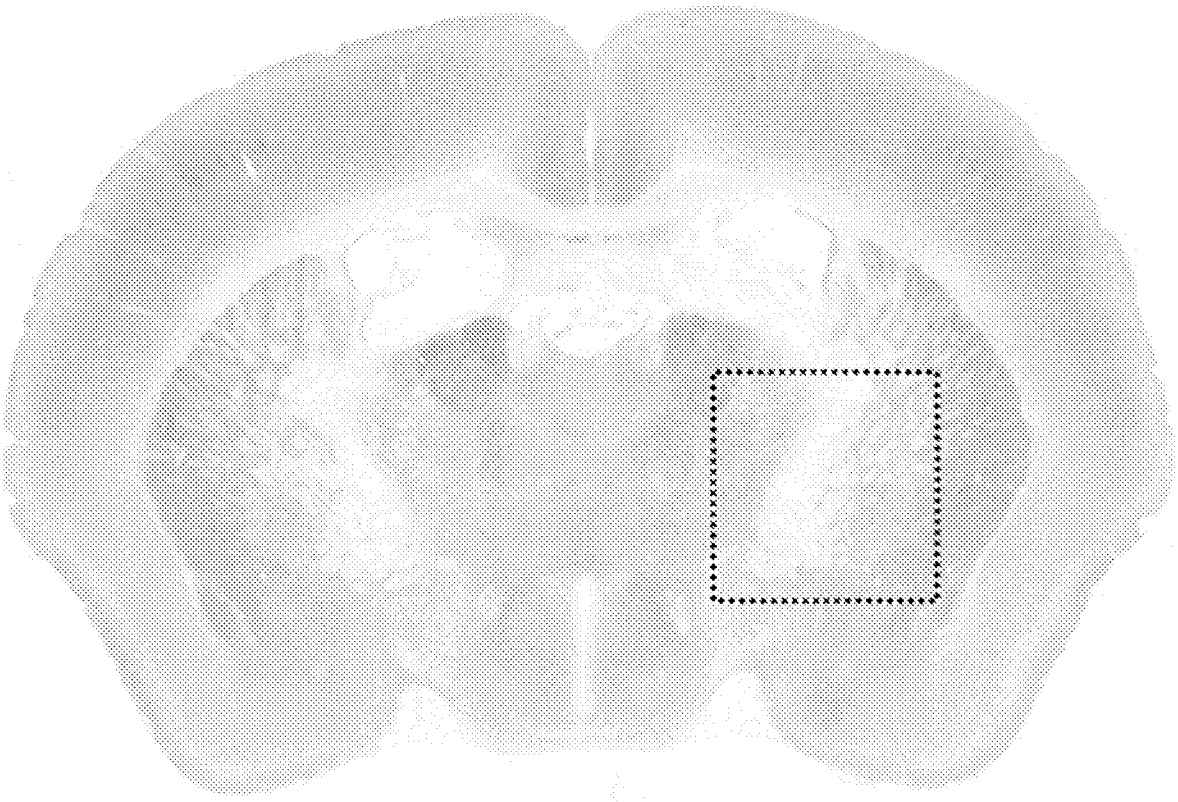


FIG. 18D

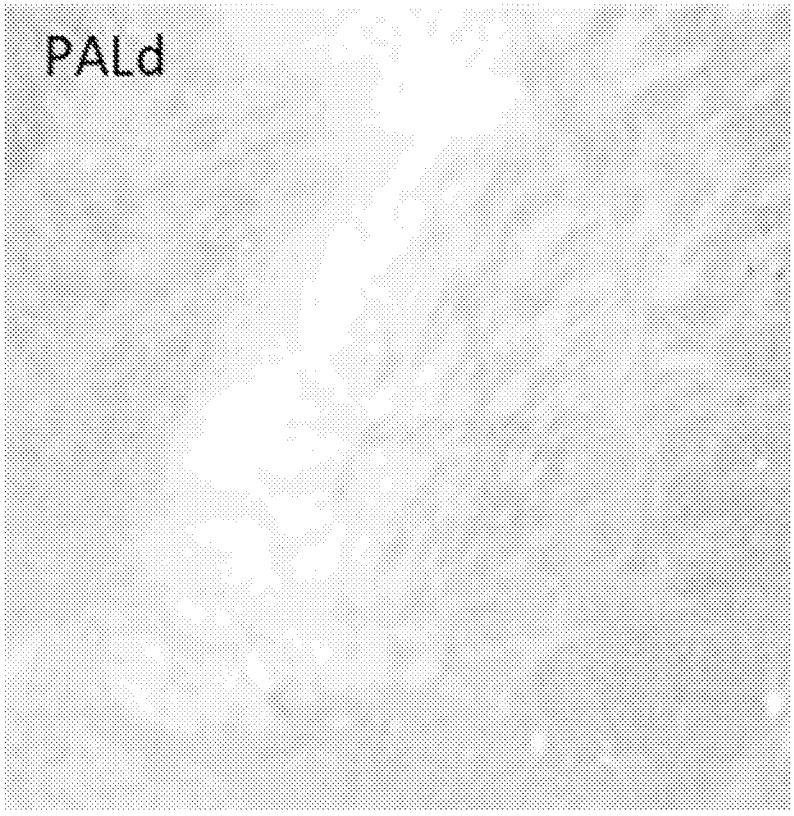


FIG. 18E

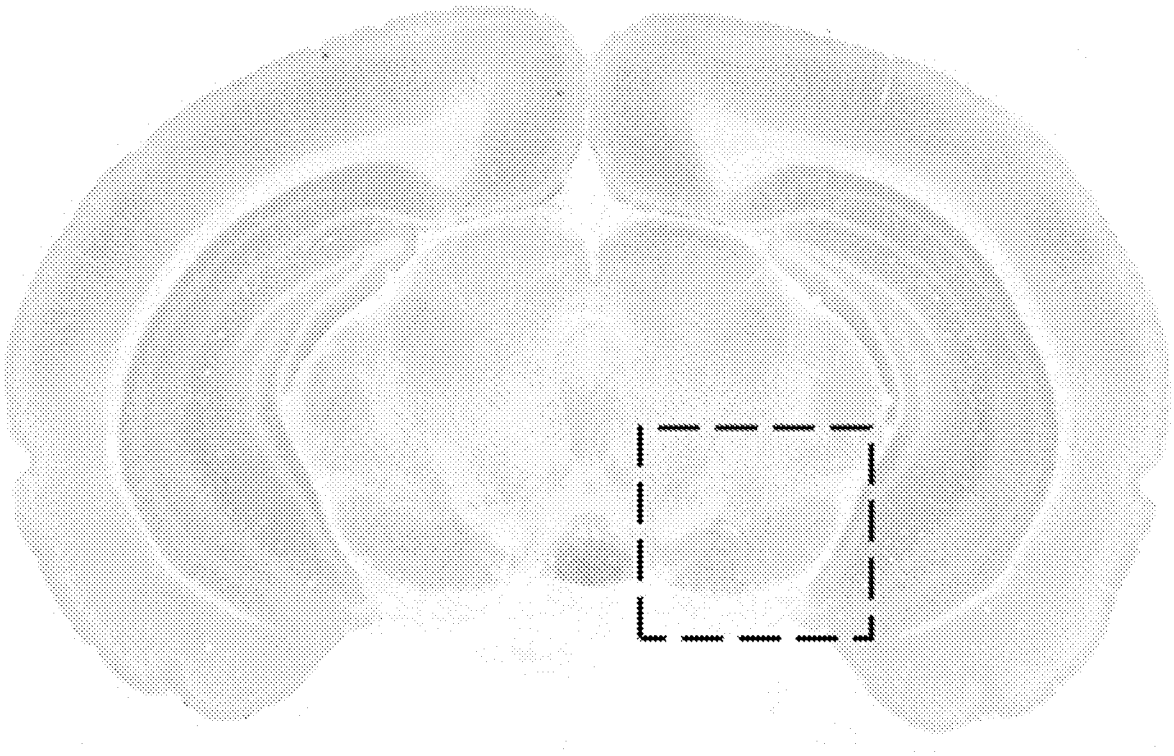


FIG. 18F

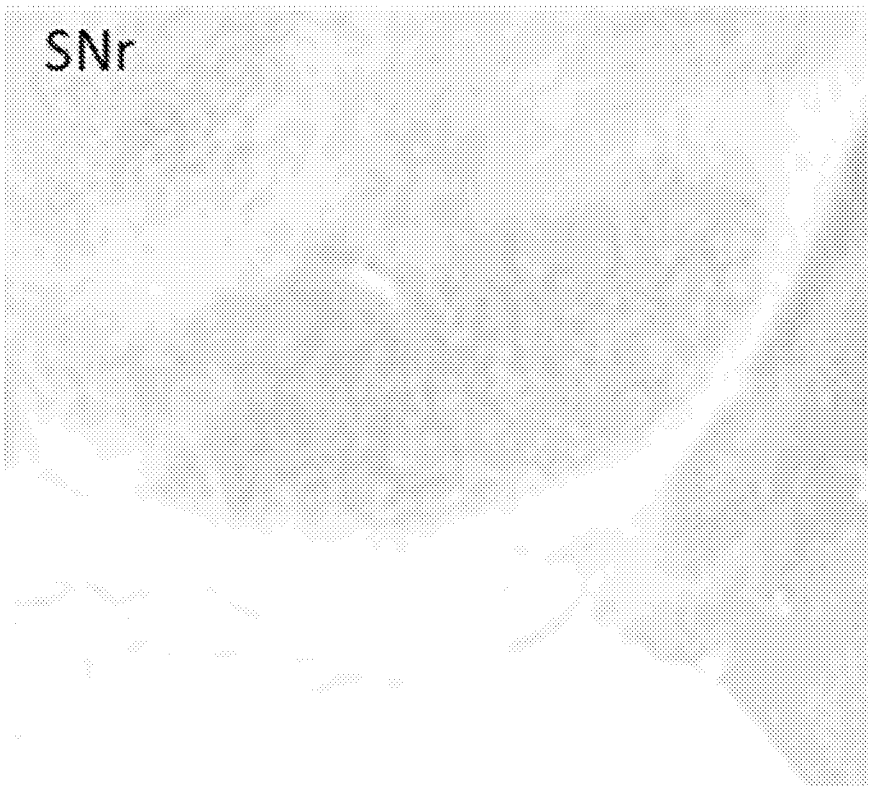


FIG. 18G

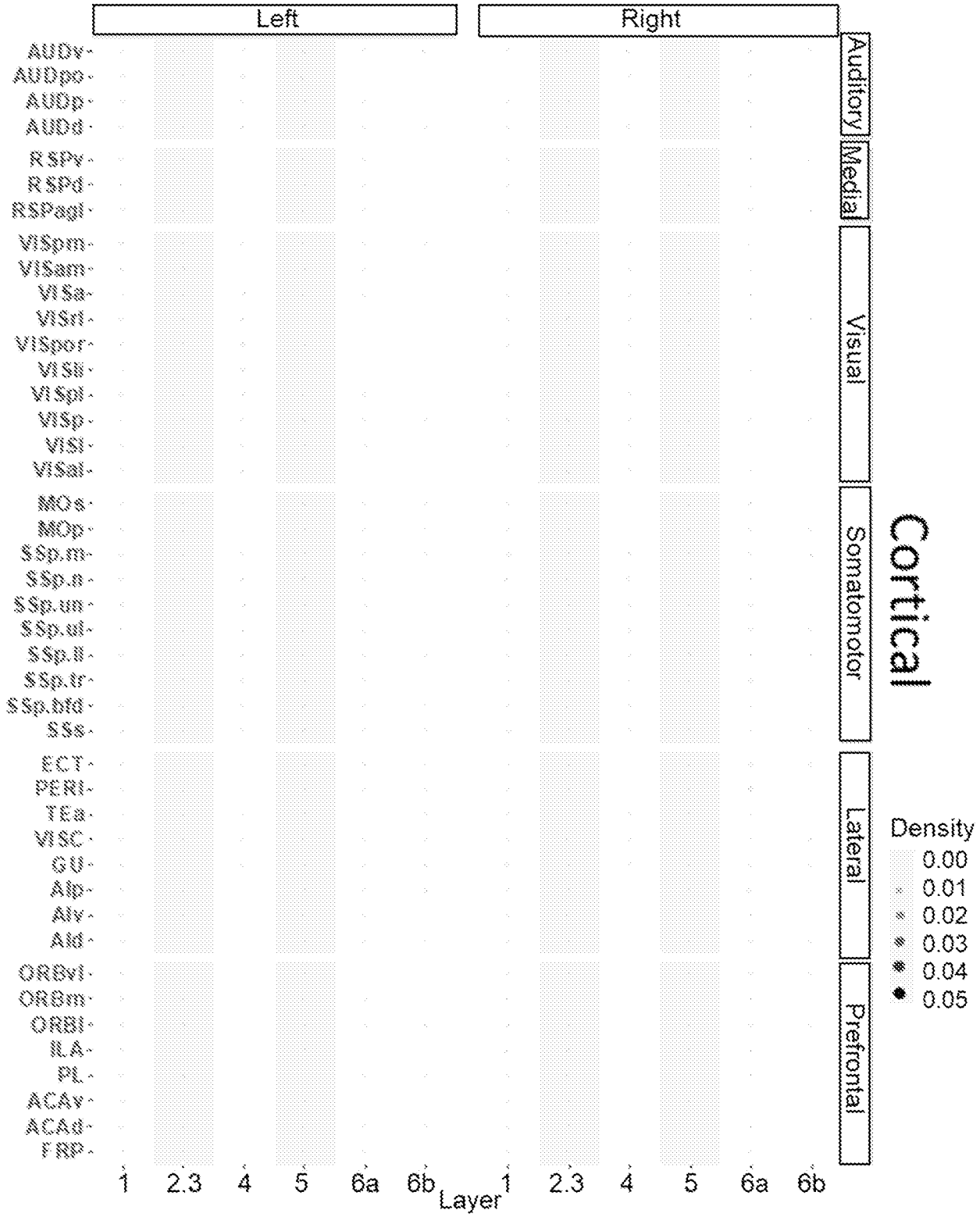

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FIG. 18G cont'd

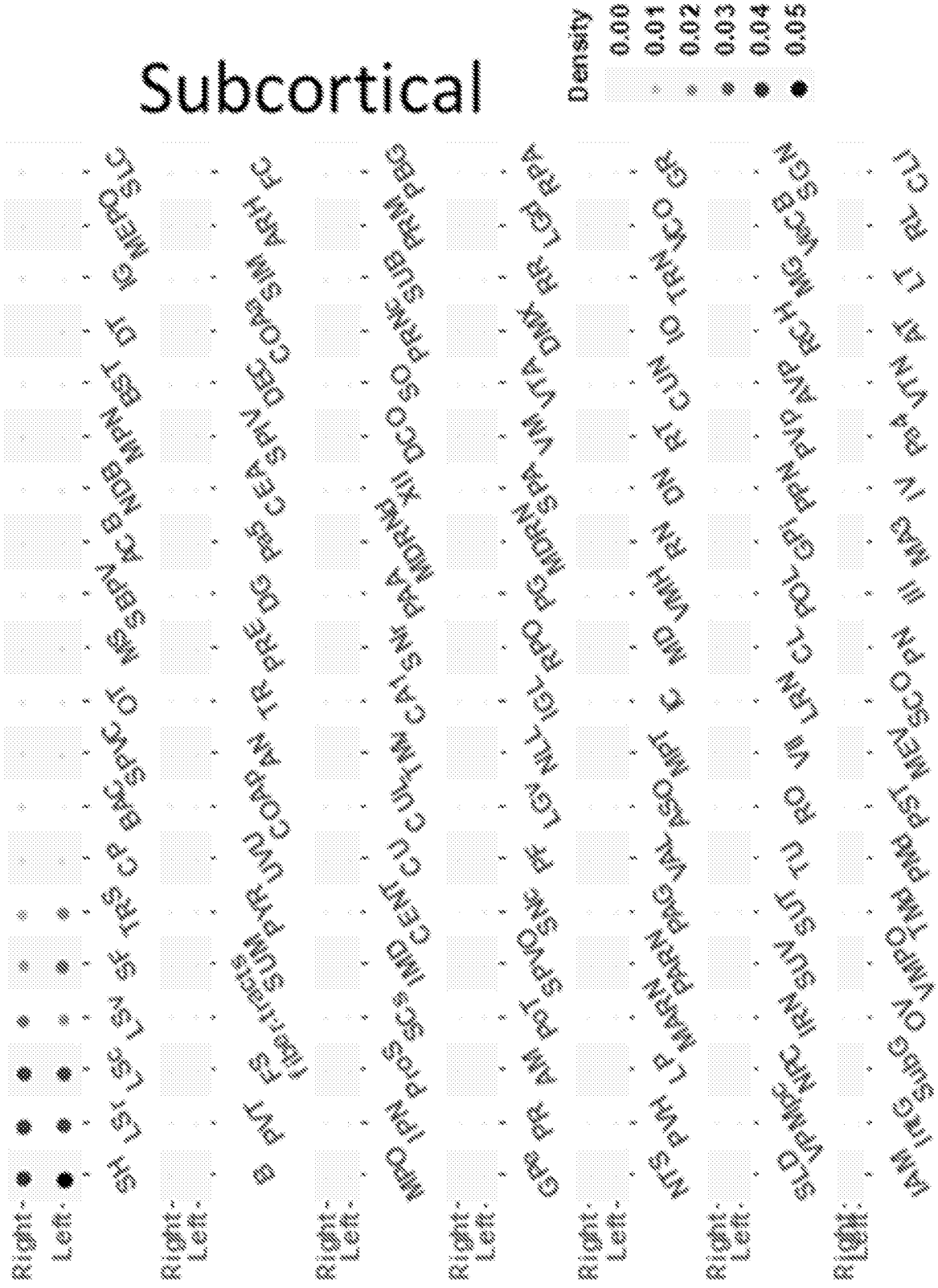


FIG. 18G cont'd



FIG. 19A

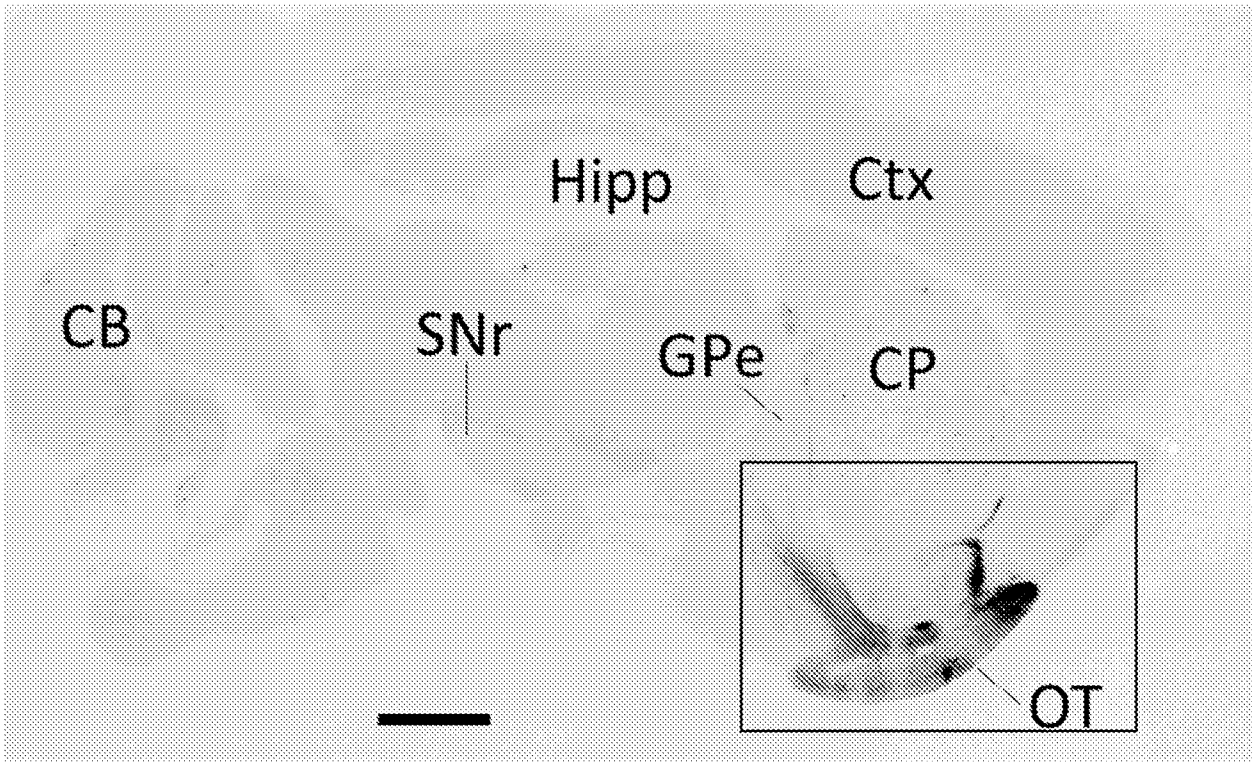


FIG. 19B

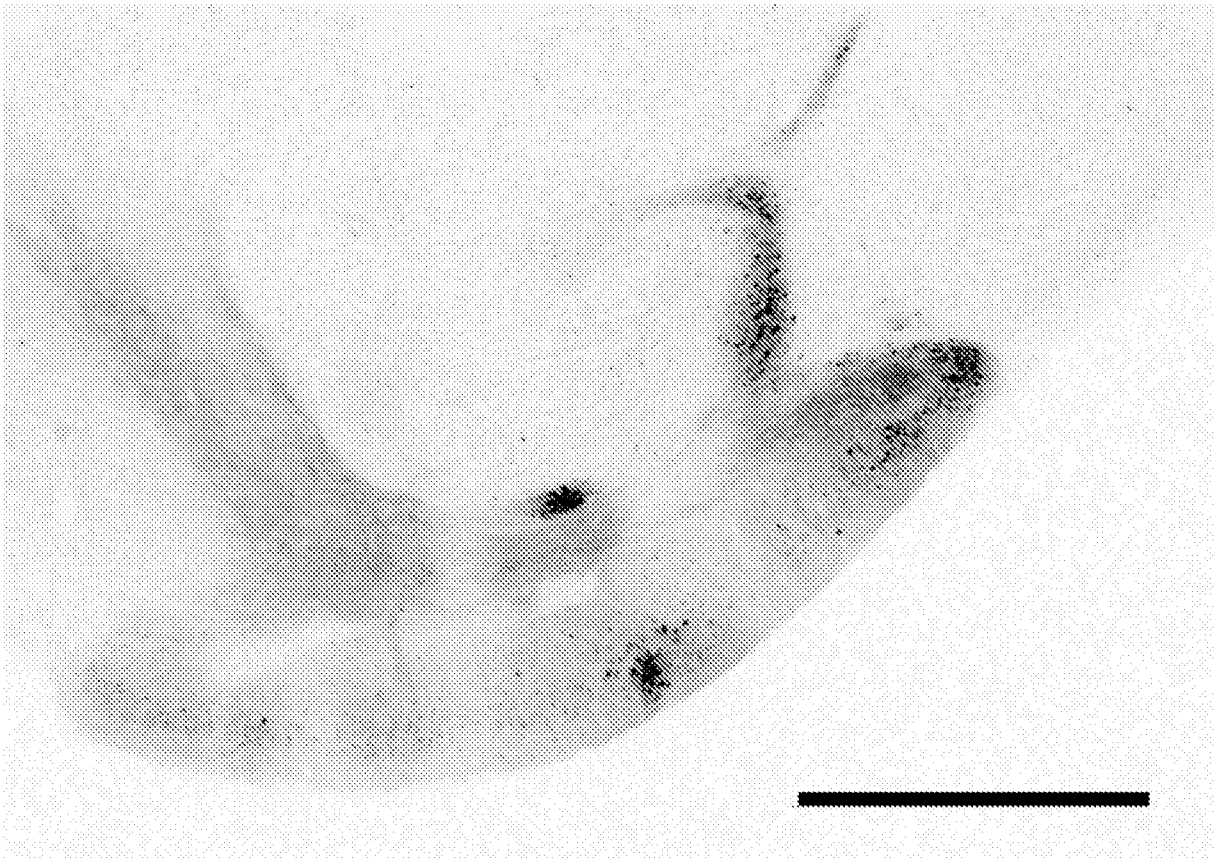
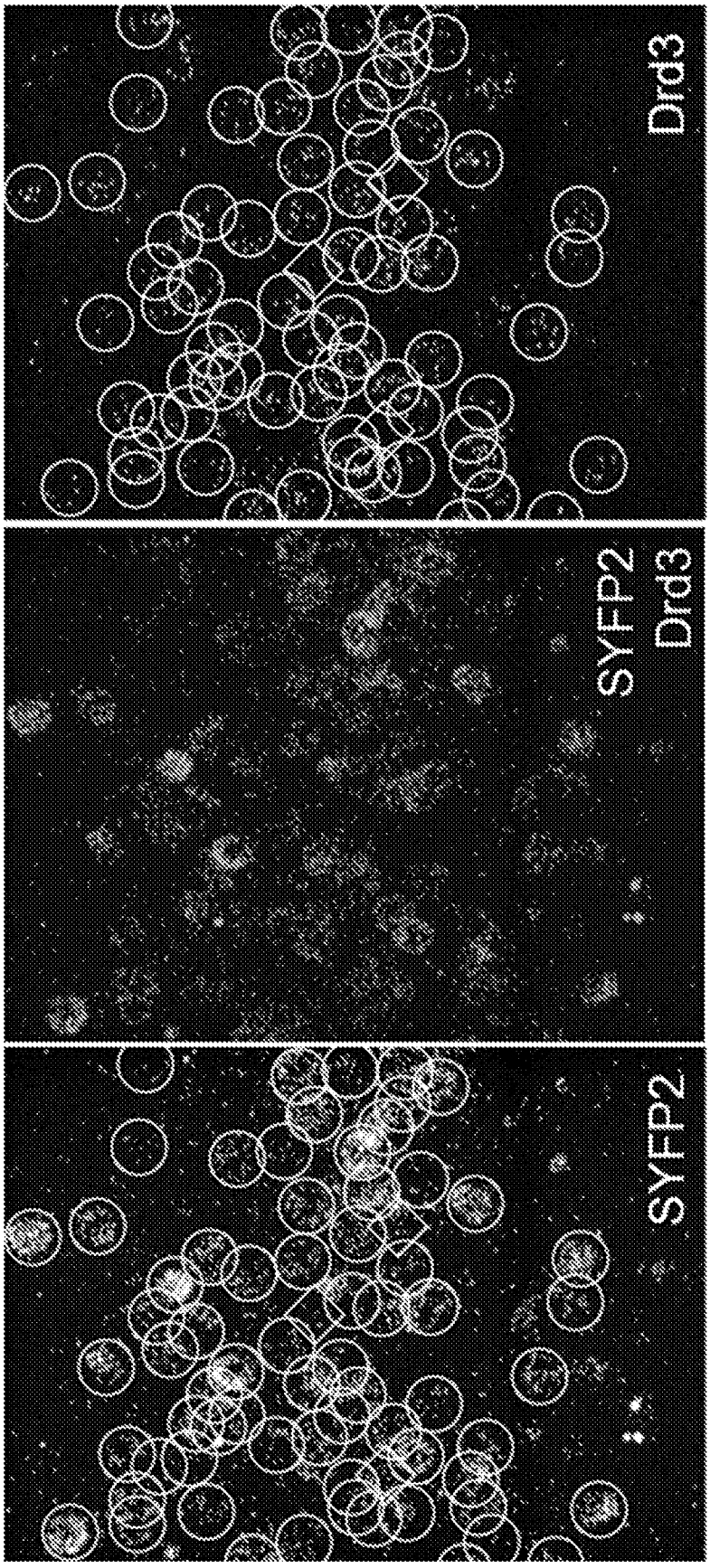


FIG. 19C

FIG. 19D

FIG. 19E



68 of 71 SYFP2+ cells are Drd3+ (96% Drd3+)

FIG. 20A

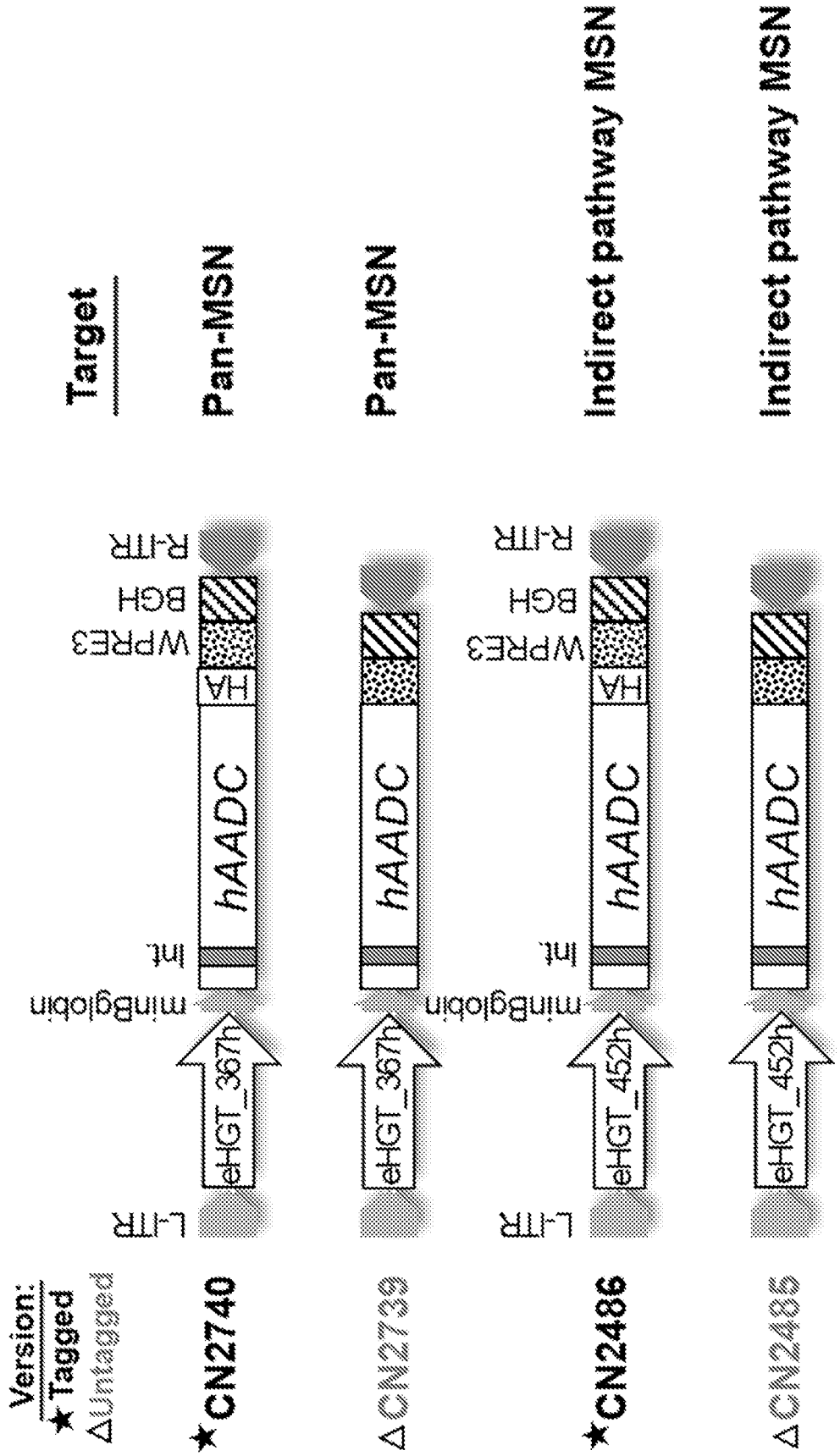

Version:
★Tagged
ΔUntagged
Target
★CN2740
ΔCN2739
★CN2486
ΔCN2485
Pan-MSN
Pan-MSN
Indirect pathway MSN
Indirect pathway MSN
L-ITR
eHGT_367h
eHGT_452h
minBglobin
Int.
hAADC
HA
WPRE3
BGH
R-ITR

FIG. 20B

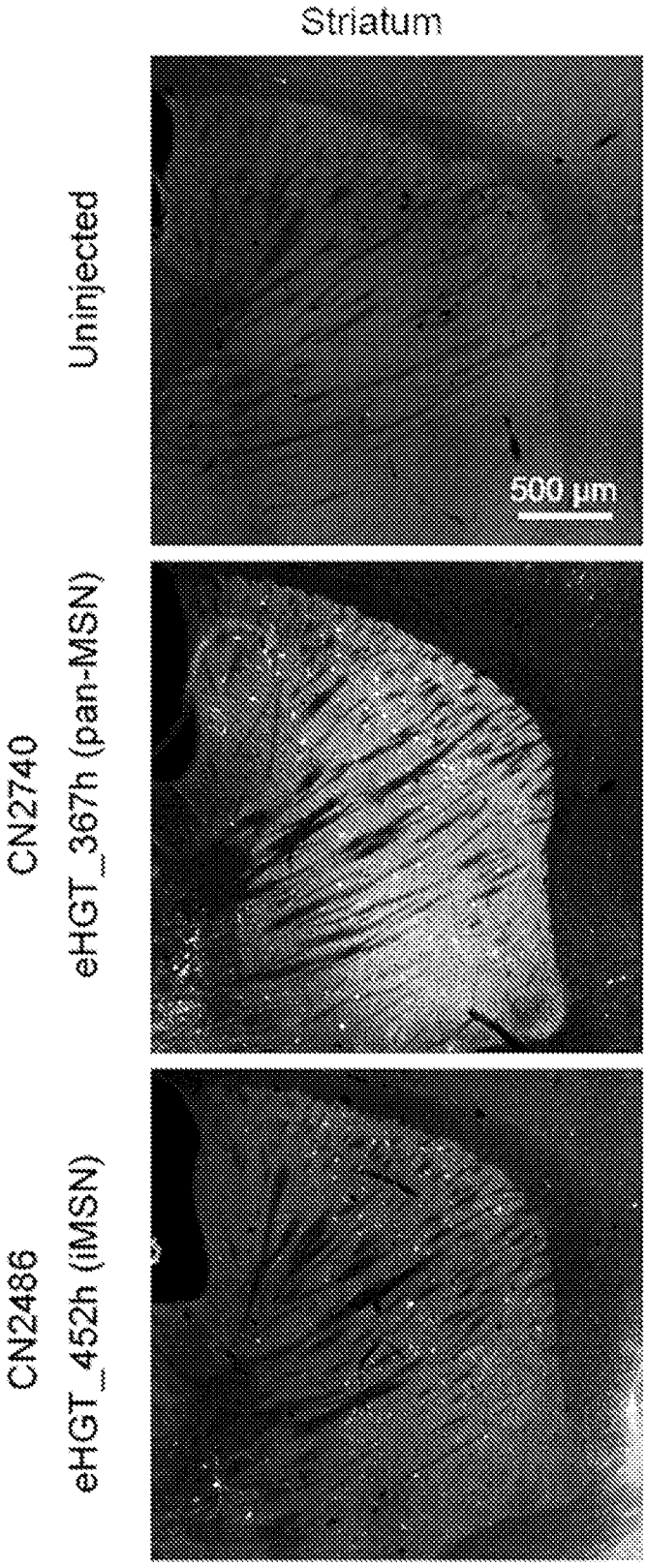

Striatum
Uninjected
500 µm
CN2740
eHGT_367h (pan-MSN)
CN2486
eHGT_452h (iMSN)

FIG. 21

Abbrev.	Full structure name
AAA	Anterior amygdalar area
ACAd	Anterior cingulate area, dorsal part
ACAv	Anterior cingulate area, ventral part
ACB	Nucleus accumbens
Acs5	Accessory trigeminal nucleus
ACVII	Accessory facial motor nucleus
AD	Anterodorsal nucleus
ADP	Anterodorsal preoptic nucleus
AHN	Anterior hypothalamic nucleus
AId	Agranular insular area, dorsal part
AIp	Agranular insular area, posterior part
AIv	Agranular insular area, ventral part
AM	Anteromedial nucleus
AMB	Nucleus ambiguus
AN	Ansiform lobule
AOB	Accessory olfactory bulb
AON	Anterior olfactory nucleus
AP	Area postrema
APN	Anterior pretectal nucleus
APr	Area prostriata
ARH	Arcuate hypothalamic nucleus
ASO	Accessory supraoptic group
AT	Anterior tegmental nucleus
AUDd	Dorsal auditory area
AUDp	Primary auditory area
AUDpo	Posterior auditory area
AUDv	Ventral auditory area
AV	Anteroventral nucleus of thalamus
AVP	Anteroventral preoptic nucleus
AVPV	Anteroventral periventricular nucleus
B	Barrington's nucleus

Abbrev.	Full structure name
BA	Bed nucleus of the accessory olfactory tract
BAC	Bed nucleus of the anterior commissure
BLA	Basolateral amygdalar nucleus
BMA	Basomedial amygdalar nucleus
BST	Bed nuclei of the stria terminalis
CA1	Field CA1
CA2	Field CA2
CA3	Field CA3
CEA	Central amygdalar nucleus
CENT	Central lobule
CL	Central lateral nucleus of the thalamus
CLA	Claustrum
CLI	Central linear nucleus raphe
CM	Central medial nucleus of the thalamus
COAa	Cortical amygdalar area, anterior part
COAp	Cortical amygdalar area, posterior part
COPY	Copula pyramidis
CP	Caudoputamen
CS	Superior central nucleus raphe
CU	Cuneate nucleus
CUL	Culmen
CUN	Cuneiform nucleus
DCO	Dorsal cochlear nucleus
DEC	Declive (VI)
DG	Dentate gyrus
DMH	Dorsomedial nucleus of the hypothalamus
DMX	Dorsal motor nucleus of the vagus nerve
DN	Dentate nucleus
DP	Dorsal peduncular area
DR	Dorsal nucleus raphe
DT	Dorsal terminal nucleus of the accessory optic tract

FIG. 21 cont'd

Abbrev.	Full structure name
DTN	Dorsal tegmental nucleus
ECT	Ectorhinal area
ECU	External cuneate nucleus
ENTl	Entorhinal area, lateral part
ENTm	Entorhinal area, medial part, dorsal zone
EPd	Endopiriform nucleus, dorsal part
EPv	Endopiriform nucleus, ventral part
EW	Edinger-Westphal nucleus
FC	Fasciola cinerea
fiber tracts	fiber tracts
FL	Flocculus
FN	Fastigial nucleus
FOTU	Folium-tuber vermis (VII)
FRP	Frontal pole, cerebral cortex
FS	Fundus of striatum
GPe	Globus pallidus, external segment
GPi	Globus pallidus, internal segment
GR	Gracile nucleus
GRN	Gigantocellular reticular nucleus
GU	Gustatory areas
HATA	Hippocampo-amygdalar transition area
I5	Intertrigeminal nucleus
IA	Intercalated amygdalar nucleus
IAD	Interanterodorsal nucleus of the thalamus
IAM	Interanteromedial nucleus of the thalamus
IC	Inferior colliculus
ICB	Infracerebellar nucleus
IF	Interfascicular nucleus raphe
IG	Induseum griseum
IGL	Intergeniculate leaflet of the lateral geniculate complex
III	Oculomotor nucleus

Abbrev.	Full structure name
ILA	Infralimbic area
IMD	Intermediodorsal nucleus of the thalamus
IntG	Intermediate geniculate nucleus
IO	Inferior olivary complex
IP	Interposed nucleus
IPN	Interpeduncular nucleus
IRN	Intermediate reticular nucleus
ISN	Inferior salivatory nucleus
IV	Trochlear nucleus
LA	Lateral amygdalar nucleus
LAV	Lateral vestibular nucleus
LC	Locus ceruleus
LD	Lateral dorsal nucleus of thalamus
LDT	Laterodorsal tegmental nucleus
LGd	Dorsal part of the lateral geniculate complex
LGv	Ventral part of the lateral geniculate complex
LH	Lateral habenula
LHA	Lateral hypothalamic area
LIN	Linear nucleus of the medulla
LING	Lingula (I)
LM	Lateral mammillary nucleus
LP	Lateral posterior nucleus of the thalamus
LPO	Lateral preoptic area
LRN	Lateral reticular nucleus
LSc	Lateral septal nucleus, caudal (caudodorsal) part
LSr	Lateral septal nucleus, rostral (rostroventral) part
LSv	Lateral septal nucleus, ventral part
LT	Lateral terminal nucleus of the accessory optic tract
MA	Magnocellular nucleus
MA3	Medial accesory oculomotor nucleus
MARN	Magnocellular reticular nucleus

FIG. 21 cont'd

Abbrev.	Full structure name
MD	Mediodorsal nucleus of thalamus
MDRN	Medullary reticular nucleus
MDRNd	Medullary reticular nucleus, dorsal part
MDRNv	Medullary reticular nucleus, ventral part
ME	Median eminence
MEA	Medial amygdalar nucleus
MEPO	Median preoptic nucleus
MEV	Midbrain trigeminal nucleus
MG	Medial geniculate complex
MH	Medial habenula
MM	Medial mammillary nucleus
MOB	Main olfactory bulb
MOp	Primary motor area
MOs	Secondary motor area
MPN	Medial preoptic nucleus
MPO	Medial preoptic area
MPT	Medial pretectal area
MRN	Midbrain reticular nucleus
MS	Medial septal nucleus
MT	Medial terminal nucleus of the accessory optic tract
MV	Medial vestibular nucleus
NB	Nucleus of the brachium of the inferior colliculus
NDB	Diagonal band nucleus
NI	Nucleus incertus
NLL	Nucleus of the lateral lemniscus
NLOT	Nucleus of the lateral olfactory tract
NOD	Nodulus (X)
NOT	Nucleus of the optic tract
NPC	Nucleus of the posterior commissure
NR	Nucleus of Roller
NTB	Nucleus of the trapezoid body
NTS	Nucleus of the solitary tract
OP	Olivary pretectal nucleus

Abbrev.	Full structure name
ORBl	Orbital area, lateral part
ORBm	Orbital area, medial part
ORBvl	Orbital area, ventrolateral part
OT	Olfactory tubercle
OV	Vascular organ of the lamina terminalis
P5	Peritrigeminal zone
Pa4	Paratrochlear nucleus
Pa5	Paratrigeminal nucleus
PAA	Piriform-amygdalar area
PAG	Periaqueductal gray
PAR	Parasubiculum
PARN	Parvicellular reticular nucleus
PAS	Parasolitary nucleus
PB	Parabrachial nucleus
PBG	Parabigeminal nucleus
PCG	Pontine central gray
PCN	Paracentral nucleus
PD	Posterodorsal preoptic nucleus
PDTg	Posterodorsal tegmental nucleus
PeF	Perifornical nucleus
PERI	Perirhinal area
PF	Parafascicular nucleus
PFL	Paraflocculus
PG	Pontine gray
PGRNd	Paragigantocellular reticular nucleus, dorsal part
PGRNl	Paragigantocellular reticular nucleus, lateral part
PH	Posterior hypothalamic nucleus
PIL	Posterior intralaminar thalamic nucleus
PIR	Piriform area
PL	Prelimbic area
PMd	Dorsal premammillary nucleus
PMv	Ventral premammillary nucleus
PN	Paranigral nucleus

FIG. 21 cont'd

Abbrev.	Full structure name
PO	Posterior complex of the thalamus
POL	Posterior limiting nucleus of the thalamus
POST	Postsubiculum
PoT	Posterior triangular thalamic nucleus
PP	Peripeduncular nucleus
PPN	Pedunculopontine nucleus
PPT	Posterior pretectal nucleus
PPY	Parapyramidal nucleus
PR	Perireunensis nucleus
PRE	Presubiculum
PRM	Paramedian lobule
PRNc	Pontine reticular nucleus, caudal part
PRNr	Pontine reticular nucleus
ProS	Prosubiculum
PRP	Nucleus prepositus
PS	Parastrial nucleus
PST	Preparasubthalamic nucleus
PSTN	Parasubthalamic nucleus
PSV	Principal sensory nucleus of the trigeminal
PT	Parataenial nucleus
PVa	Periventricular hypothalamic nucleus, anterior part
PVH	Paraventricular hypothalamic nucleus
PVHd	Paraventricular hypothalamic nucleus, descending division
PVi	Periventricular hypothalamic nucleus, intermediate part
PVp	Periventricular hypothalamic nucleus, posterior part
PVpo	Periventricular hypothalamic nucleus, preoptic part
PVT	Paraventricular nucleus of the thalamus
PYR	Pyramus (VIII)
RCH	Retrochiasmatic area

Abbrev.	Full structure name
RE	Nucleus of reuniens
RH	Rhomboid nucleus
RL	Rostral linear nucleus raphe
RM	Nucleus raphe magnus
RN	Red nucleus
RO	Nucleus raphe obscurus
RPA	Nucleus raphe pallidus
RPO	Nucleus raphe pontis
RR	Midbrain reticular nucleus, retrorubral area
RSPagl	Retrosplenial area, lateral agranular part
RSPd	Retrosplenial area, dorsal part
RSPv	Retrosplenial area, ventral part
RT	Reticular nucleus of the thalamus
SAG	Nucleus sagulum
SBPV	Subparaventricular zone
SCH	Suprachiasmatic nucleus
SCm	Superior colliculus, motor related
SCO	Subcommissural organ
SCs	Superior colliculus, sensory related
SF	Septofimbrial nucleus
SFO	Subfornical organ
SG	Supragenual nucleus
SGN	Suprageniculate nucleus
SH	Septohippocampal nucleus
SI	Substantia innominata
SIM	Simple lobule
SLC	Subceruleus nucleus
SLD	Sublaterodorsal nucleus
SMT	Submedial nucleus of the thalamus

FIG. 21 cont'd

Abbrev.	Full structure name
SNc	Substantia nigra, compact part
SNr	Substantia nigra, reticular part
SO	Supraoptic nucleus
SOC	Superior olivary complex
SPA	Subparafascicular area
SPFm	Subparafascicular nucleus, magnocellular part
SPFp	Subparafascicular nucleus, parvicellular part
SPIV	Spinal vestibular nucleus
SPVC	Spinal nucleus of the trigeminal, caudal part
SPVI	Spinal nucleus of the trigeminal, interpolar part
SPVO	Spinal nucleus of the trigeminal, oral part
SSp-bfd	Primary somatosensory area, barrel field
SSp-ll	Primary somatosensory area, lower limb
SSp-m	Primary somatosensory area, mouth
SSp-n	Primary somatosensory area, nose
SSp-tr	Primary somatosensory area, trunk
SSp-ul	Primary somatosensory area, upper limb
SSp-un	Primary somatosensory area, unassigned
SSs	Supplemental somatosensory area
STN	Subthalamic nucleus
SUB	Subiculum
SubG	Subgeniculate nucleus
SUM	Supramammillary nucleus
SUT	Supratrigeminal nucleus
SUV	Superior vestibular nucleus
TEa	Temporal association areas
TMd	Tuberomammillary nucleus, dorsal part
TMv	Tuberomammillary nucleus, ventral part

Abbrev.	Full structure name
TR	Postpiriform transition area
TRN	Tegmental reticular nucleus
TRS	Triangular nucleus of septum
TT	Taenia tecta
TU	Tuberal nucleus
UVU	Uvula (IX)
V	Motor nucleus of trigeminal
VAL	Ventral anterior-lateral complex of the thalamus
VCO	Ventral cochlear nucleus
VeCB	Vestibulocerebellar nucleus
VI	Abducens nucleus
VII	Facial motor nucleus
VISa	Anterior area
VISal	Anterolateral visual area
VISam	Anteromedial visual area
VISC	Visceral area
VISl	Lateral visual area
VISp	Primary visual area
VISpl	Posterolateral visual area
VISpm	posteromedial visual area
VISpor	Postrhinal area
VISrl	Rostrolateral visual area
VLPO	Ventrolateral preoptic nucleus
VM	Ventral medial nucleus of the thalamus
VMH	Ventromedial hypothalamic nucleus
VMPO	Ventromedial preoptic nucleus
VPL	Ventral posterolateral nucleus of the thalamus
VPLpc	Ventral posterolateral nucleus of the thalamus, parvicellular part

FIG. 21 cont'd

Abbrev.	Full structure name
VPM	Ventral posteromedial nucleus of the thalamus
VPMpc	Ventral posteromedial nucleus of the thalamus, parvicellular part
VTA	Ventral tegmental area
VTN	Ventral tegmental nucleus
x	Nucleus x
Xi	Xiphoid thalamic nucleus
XII	Hypoglossal nucleus
y	Nucleus y
ZI	Zona incerta

FIG. 22A

eHGT_608h (647 bp)
TTGAACCTCCGACTGCAACACAGATTAGGATACAGCAGTGGCTACAATTACACACTTGCTT
GGGAAGTTGGGTTGGGAGGGGGGGTGGGTGCTGCATGTGACAGGCCATGAAAGGTCCCT
GCCTATAAAACAGACTGAAAAACAAACCCTTAATTTAAATGTTAATGAAAGTGCTGTGGAGA
CATCAGAGGCTTCCCGGCTGCTCAGAGAACAGCTACACCAGCCACAGAATTTATGGCTCC
CCTTCACCCTCCCGCCTCCCTCTCTGCCTCATCACCCACTGAAATTTAAAGACAGAAAAAA
AAGAAAACTAATTTTAACATTAACTCCATGCTTCCACTTTGGGATGTGATTGCTAAATTATCT
GTTGGCAGAACGGTGATCAAAGGTGGAAAAACACAGGCACGTTGCACACACAACCCAGAA
AAGTCAGCAGCAGCTAAAGCAGGAAAATTCCCATTTCCCTTCCTGATGAGCAGAGTGGAAG
AAAGAGTGGTGCAGGTAGGGACTGGAGCCAGGAGGTGTAGGCAGTGGGAGGAAGAGAAA
GATGACTGATCCGTCCAGCGTGCTCCCAAGGCCCTGTCTCAACCTCATCTGAGAACTTACC
ACACTCTACTACCTATTTTACTTGTCGGTCTCTCCCATCA (SEQ ID NO: 1)

eHGT_609h (361 bp)
CTTATCACTTCCTAATTATTTTCTACCTTTTACTAACCTATGCTCTGGAGATTTATAACTATTA
TATCTGTGTGGTGCAAACATCATATAATGGTGTGCTACTGCACATTGCTTCCCAACTCTGCA
TGACTCTGATGTCACATTGATAGCTTGAAATTGGCCATGGTGGGTGTAGCTCTACAATGAA
AATCAGCAAATGCTACGAATCAAGACTTTTTTTCCCTCTAATGTTGAACATTTAAGAACACAT
TGTATAATATCCTAAGAAGATAGTCAAAATGCACAATGGCCTCCTTCTATCCCAAATAACCA
GCCAGATAAGCAAGCATCTGTAATGTCCCTCAGAAACCAAGTGCAGCCA (SEQ ID NO: 2)

eHGT_621h (406 bp)
TGCTGAACCAATTAAGGCCAGTGGTACCACCTGAGATTTTGAAAATAAATCAGTGGGTTTTT
ATTTCAGCTGTTTGGAAATGACTAATAGAGTAATACAATAGATTAATTTTATCTAACATTAAT
AGCTGGATGTATAAGAAACACCCACTCTCTAGAAATTAAGACATGTCACCATAGTCTTATGA
CAAGAGTGAGTCTCTTATTTTTGAACTTTCTATTGAACAGTTCTCACCATCTTAAATCACCCT
TTGTTATGAGTTTTTAAGTGTCTTAAGTAGAGAAGGTTAAGAAAATGAATACTTATACTCCTT
TAAATACTAATTAAGAGGCCCTGGTAACCATTTATCAGTAATATTAATGGCATGAAAATTGAA
AAAGTATGACTCAAAGGTGAATTCAGGGCA (SEQ ID NO: 3)

Core-eHGT_621h (200 bp)
ATACAATAGATTAATTTTATCTAACATTAATAGCTGGATGTATAAGAAACACCCACTCTCTAG
AAATTAAGACATGTCACCATAGTCTTATGACAAGAGTGAGTCTCTTATTTTTGAACTTTCTAT
TGAACAGTTCTCACCATCTTAAATCACCCTTTGTTATGAGTTTTTAAGTGTCTTAAGTAGAGA
AGGTTAAGAAA (SEQ ID NO: 202)

3xCore-eHGT_621h (600 bp)
ATACAATAGATTAATTTTATCTAACATTAATAGCTGGATGTATAAGAAACACCCACTCTCTAG
AAATTAAGACATGTCACCATAGTCTTATGACAAGAGTGAGTCTCTTATTTTTGAACTTTCTAT
TGAACAGTTCTCACCATCTTAAATCACCCTTTGTTATGAGTTTTTAAGTGTCTTAAGTAGAGA
AGGTTAAGAAAATACAATAGATTAATTTTATCTAACATTAATAGCTGGATGTATAAGAAACAC
CCACTCTCTAGAAATTAAGACATGTCACCATAGTCTTATGACAAGAGTGAGTCTCTTATTTTT
GAACTTTCTATTGAACAGTTCTCACCATCTTAAATCACCCTTTGTTATGAGTTTTTAAGTGTC
TTAAGTAGAGAAGGTTAAGAAAATACAATAGATTAATTTTATCTAACATTAATAGCTGGATGT
ATAAGAAACACCCACTCTCTAGAAATTAAGACATGTCACCATAGTCTTATGACAAGAGTGAG
TCTCTTATTTTTGAACTTTCTATTGAACAGTTCTCACCATCTTAAATCACCCTTTGTTATGAGT
TTTTAAGTGTCTTAAGTAGAGAAGGTTAAGAAA (SEQ ID NO: 203)

FIG. 22A cont'd

eHGT_633h (607 bp)

TTCTTCCACTCCTTTCCCTGCTGCAGGAATCAGTCCCCTGGACTCTGATGTGTGGCTGGGT
TGGCTGGGTTGCCCTGGGCAGACTTATTAGCTTGGACTCTTTCGCATGCAAAAGATAGCAC
CTGTGTGACTGTACATATTGAAAATGCAATTGCAGGTGTATTTGCAAATTGGATTTTGAGGG
GGAAATTTAAGCAAATCCTTTTGAAAGCAAATCCCTCCAAGGTGTGAGTAATAAAGAAACAA
GAAGAAAGGTGTCAATCAAAAACCTATTAAAATCTAGTTTCCAGAGAAGAAGCTGACTGTCT
AATGACATTTATGCTTTCATAGCTAGGCATTTAACAGTCATTTTGTGTCAGTTGCTTCCTTTA
TACATGTCACGTGGCACATTTTTCAGTTTTCTGTATTTCTGAGACCTTAATCCCAATCACTCT
TAAATGCTTGAAATGAGCCCATGTTCCTAAAAGGAGGGGGTTTTTGTCCACCTGAATTTCTC
TGCAGGAATCTACAATGATGCCTCAAGCATCAGTATATGAAGTCAACCACTGTCATTCATCC
AATTCATTCATTCCATTCATTCTTTTAGTTAGCCCTAAAACTCCATGGT (SEQ ID NO: 4)

eHGT_634h (622 bp)

CAACTCGCTTAGAGTCACCTGCTAGAGGTTTCTGGTTATTTGGAGATTTGCTGGCTCTGCC
ATGGACATGATGGCATATTCGTGGATGATATGGAGAGTGACAAAATGGCTGAGTGTCTAAT
TATTAATCAAATCACAGATTCATATCTCTCTCCCCCTCCTCCACTAGTTTCCTTGGAGACAC
AGTTTTTTGTCAATTTTTTGAATTGCATTAATATTAACTATGACTTTGAATCAGGAAGAATGC
AAAATATCTGAAGAGTAGTATTTATATCTTCCACGTGACATTTGCATCACATGGATAAACTTT
AAAAATGTTCTTGAGAACACGGGAAAATAAGGAAATAGAGTTCAAAAATAAAGTATAGAACT
TGTTAGACTAGTTTCTGTTTAAAACTCGGTGGATTATACCTCTTTGTTTTAAACCATTAGAAC
AGCAATGATTAAATATCAGATTCCTTAAAGAGTCACCAGTTCCTTTTGGAAAGTTTTGATTAA
AGCATTGTATTTATTAAACTGTTCTACCCACACATCTTTCCTTCAAGATGTTGTTTTTCCCAC
GTCTACTGTTTTATTACATGACAGTTATTGAAAGGTTAGATGTGGTTTAATTTCTCAAGGT
(SEQ ID NO: 5)

eHGT_635h (392 bp)

TGGAGAATACATTCTTGACTCAATGAATACTATCACTTTTTTGGTTAAACAGTCCAAATTTGA
CATCCAGAACATTTCTTTAAAGTCACCATTTTCCTGGAAACACTCTAATTTTGAGATGTCTAG
GGCTATATTTAGCTTTTGAACAGTAGTCTTTGAAAAAATATGGTTATGAAACAGATTGATTTA
GAGGAGCATTATAATTAGCTGCCGAATACGTTAGAAGGATAGATTATTCTACATGAATCACA
GAGCTCACTTTAAGTGTCATTCCCCATTCTAAACTGCCAGCTTAATTTCTTCTCATTTTTCAC
CACGAGAGCCTTTTTTCTATTATGCCAATAATAAAGGGTTAGTTGTCATGAAATAGGCATAC
CTTTGTGAAATAATGA (SEQ ID NO: 6)

eHGT_636h (634 bp)

ACTAAGGAATAGACAATGGGTTCTTTATGAATATGTGAGCATGCCTAAAAGCAACAAAATCA
CACTTTTGTTAAAGCATTTGTGTGTATTTTGCACAATTTTTAAAAGTTTAACCTCTGTAGATC
AATGTGCTTCCTTAAAAGACTTTAATAAATTAAAGTGCAGAGAGCTTTTTTTCACCAGGCAG
AAAAAGCTGATGAGACAGGTTTAGTTTAATCTCAGGCAATAGAAGTCATTAACCATTCTCTC
AGGGATTAAAATATAGCTTGCCCTTTTCTTCTCTCACTTATCATTAGCATCACTTTAATCTCC
TAGCGTTTCACACTGCTATTTTAATCATTACTTACTGCCTTTTGACAAGTGCAGAACATGCTT
TTTCTCATTGAGGCAATATCCTGGTTTTAGCTGACAAATGTAGGACATAATGTAAAAATATC
AAAGTGACATCTCTTAAACACACCTTCATCATAAAAACTCTAAAGTTACAATATTCCTTTGTC
TAGTATTTCCATGAAAATTATCATTTGAAAGGTTTATATCTTAAATAAAGAAAAAAGTTTCTTC
CAAATACAACAAAAACTAGTTTAGAGAAATAGTATGCTGAATAAATGAGATCTAAAAATATG
CACATACA (SEQ ID NO: 7)

FIG. 22A cont'd

eHGT_351h (427 bp)

AGACTGAGGAGACGCCTCAGAGGAATTTGTACGGGGAAAGGTCTGAGGAAAAAGGATCGG
ATCCCAATGGGCCGAACTCCTTCAAAATGTTCCCGAGGTCCACGTGACGTTCCCTCCTCCC
ACCCAGCCCTTCTTTCTGTGAAGGGTGACACACCTCCTAGAAAGAAATCTGACTCCCCTCA
TTGTGTTTTTAAAATAACTCTCATTATTCCTCCTCTGAAGGTTATTTTCAAACTCTTTATAACT
CGATTTTTTTTTAAATGCAAAGACAAGGAATCAAATCTGCCAACTTTCTATCAGAGAAACTC
GGGTTTCTAACTTTTAAAGTGGGATTATATGTCTTCTCCAATATATGGGCTCCCTGCTTTTAT
AACATGCTGCTGTTACATCTAATAAAAACCATTTTGAATGAAGGCAGCCTTTCATC (SEQ ID NO: 8)

core2_eHGT_351h (176 bp)

GCCCTTCTTTCTGTGAAGGGTGACACACCTCCTAGAAAGAAATCTGACTCCCCTCATTGTG
TTTTTAAAATAACTCTCATTATTCCTCCTCTGAAGGTTATTTTCAAACTCTTTATAACTCGATT
TTTTTTTAAATGCAAAGACAAGGAATCAAATCTGCCAACTTTCTATCAGAG (SEQ ID NO: 204)

3xcore2_eHGT_351h (528 bp)

GCCCTTCTTTCTGTGAAGGGTGACACACCTCCTAGAAAGAAATCTGACTCCCCTCATTGTG
TTTTTAAAATAACTCTCATTATTCCTCCTCTGAAGGTTATTTTCAAACTCTTTATAACTCGATT
TTTTTTTAAATGCAAAGACAAGGAATCAAATCTGCCAACTTTCTATCAGAGGCCCTTCTTTCT
GTGAAGGGTGACACACCTCCTAGAAAGAAATCTGACTCCCCTCATTGTGTTTTTAAAATAAC
TCTCATTATTCCTCCTCTGAAGGTTATTTTCAAACTCTTTATAACTCGATTTTTTTTTTAAATGC
AAAGACAAGGAATCAAATCTGCCAACTTTCTATCAGAGGCCCTTCTTTCTGTGAAGGGTGA
CACACCTCCTAGAAAGAAATCTGACTCCCCTCATTGTGTTTTTAAAATAACTCTCATTATTCC
TCCTCTGAAGGTTATTTTCAAACTCTTTATAACTCGATTTTTTTTTTAAATGCAAAGACAAGGA
ATCAAATCTGCCAACTTTCTATCAGAG (SEQ ID NO: 205)

eHGT_367h (405 bp)

TAGCAGGAGTACATCCTCCTCTGTTAGAAAAACAACTCTGCGGTTCTGGGTCACTTTTCCC
ATCTTTGTATAGAAAAGTACCGATTATTATTGTTCCCCCGGGTGCCTTCTCCAGCTTAAAGG
AAAATTCCAGCCCCAGAGATCTTCCGCAGTGAGTGACAGCTCCTTAATGTGAGGAGCAGC
GTGGGCGTGGTGGGTGGGATGTCAGAGCCATCAAAGCCCTCATTTCTGATCCCTCTGTGA
TGTCGGGGTTCCCTGGCACGCCCACTGTCATGCCTCAGCACATTGGCATCTGAGAGAGGA
AAGGTGCAGCTGACACCCTGACCCCCTTCTCCCCGACACGGGGTCAGACAGGGTCCCGC
GGTGGCCTGGTTGTGCAGCACTGACATGTTGCCTGGGAACGAA (SEQ ID NO: 9)

core2_eHGT_367h (160 bp)

TCCAGCTTAAAGGAAAATTCCAGCCCCAGAGATCTTCCGCAGTGAGTGACAGCTCCTTAAT
GTGAGGAGCAGCGTGGGCGTGGTGGGTGGGATGTCAGAGCCATCAAAGCCCTCATTTCT
GATCCCTCTGTGATGTCGGGGTTCCCTGGCACGCCCACTG (SEQ ID NO: 206)

3xcore2_eHGT_367h (480 bp)

TCCAGCTTAAAGGAAAATTCCAGCCCCAGAGATCTTCCGCAGTGAGTGACAGCTCCTTAAT
GTGAGGAGCAGCGTGGGCGTGGTGGGTGGGATGTCAGAGCCATCAAAGCCCTCATTTCT
GATCCCTCTGTGATGTCGGGGTTCCCTGGCACGCCCACTGTCCAGCTTAAAGGAAAATTC
CAGCCCCAGAGATCTTCCGCAGTGAGTGACAGCTCCTTAATGTGAGGAGCAGCGTGGGCG
TGGTGGGTGGGATGTCAGAGCCATCAAAGCCCTCATTTCTGATCCCTCTGTGATGTCGGG

FIG. 22A cont'd

GTTCCCTGGCACGCCCACTGTCCAGCTTAAAGGAAAATTCCAGCCCCAGAGATCTTCCGC
AGTGAGTGACAGCTCCTTAATGTGAGGAGCAGCGTGGGCGTGGTGGGTGGGATGTCAGA
GCCATCAAAGCCCTCATTTCTGATCCCTCTGTGATGTCGGGGTTCCCTGGCACGCCCACT
G (SEQ ID NO: 207)

eHGT_441h (450 bp)

CCCCTCCCCACTCCTTGCCCCTGCCCACCCCTCCTCCAGCTCTCAGGAGTCCCATTCCCTT
CCTCCTCTGTCGCCCACACAGCCCCCACCACCTGGCCGCCCACCTGAAAAACTTTTCCCC
AAGTTCTTGAGAAGTCGCGTAGGATCCAGGAGAGAAAAATCAAAGTAATAAAACCTCATTTA
ATTCCTAACGGAGGGCAGAGCTGCGAGCTGCAATTATCTTAATGCTGAGCTATTTTTACTCT
CTCTCCATCTCTGTCTTCTGCCTTTCTCTGTTGTGAGGTTCGCTGTCTCTCTCTCTGCCTCC
CTTTGTCTCTCCATCTCTCAACCATGTTTTCTGTCTCTCTTTGCTTTCTCCTCTCTCCCCCCA
ATCTCTCTCTCACGTCCTGTCTCTGTGCAGTCTCTTCCTCCTCCTTCATGTCTGTCCCTCTG
TCAGCCAGTCTTCCCCAC (SEQ ID NO: 10)

core_eHGT_441h (428 bp)

GCCCACCCCTCCTCCAGCTCTCAGGAGTCCCATTCCCTTCCTCCTCTGTCGCCCACACAG
CCCCCACCACCTGGCCGCCCACCTGAAAAACTTTTCCCCAAGTTCTTGAGAAGTCGCGTA
GGATCCAGGAGAGAAAAATCAAAGTAATAAAACCTCATTTAATTCCTAACGGAGGGCAGAG
CTGCGAGCTGCAATTATCTTAATGCTGAGCTATTTTTACTCTCTCTCCATCTCTGTCTTCTG
CCTTTCTCTGTTGTGAGGTTCGCTGTCTCTCTCTCTGCCTCCCTTTGTCTCTCCATCTCTCA
ACCATGTTTTCTGTCTCTCTTTGCTTTCTCCTCTCTCCCCCCAATCTCTCTCTCACGTCCTGT
CTCTGTGCAGTCTCTTCCTCCTCCTTCATGTCTGTCCCTCTGTCAGCCAGTCTTCCCCAC
(SEQ ID NO: 208)

3xcore_eHGT_441h (1284 bp)

GCCCACCCCTCCTCCAGCTCTCAGGAGTCCCATTCCCTTCCTCCTCTGTCGCCCACACAG
CCCCCACCACCTGGCCGCCCACCTGAAAAACTTTTCCCCAAGTTCTTGAGAAGTCGCGTA
GGATCCAGGAGAGAAAAATCAAAGTAATAAAACCTCATTTAATTCCTAACGGAGGGCAGAG
CTGCGAGCTGCAATTATCTTAATGCTGAGCTATTTTTACTCTCTCTCCATCTCTGTCTTCTG
CCTTTCTCTGTTGTGAGGTTCGCTGTCTCTCTCTCTGCCTCCCTTTGTCTCTCCATCTCTCA
ACCATGTTTTCTGTCTCTCTTTGCTTTCTCCTCTCTCCCCCCAATCTCTCTCTCACGTCCTGT
CTCTGTGCAGTCTCTTCCTCCTCCTTCATGTCTGTCCCTCTGTCAGCCAGTCTTCCCCACG
CCCACCCCTCCTCCAGCTCTCAGGAGTCCCATTCCCTTCCTCCTCTGTCGCCCACACAGC
CCCCACCACCTGGCCGCCCACCTGAAAAACTTTTCCCCAAGTTCTTGAGAAGTCGCGTAG
GATCCAGGAGAGAAAAATCAAAGTAATAAAACCTCATTTAATTCCTAACGGAGGGCAGAGC
TGCGAGCTGCAATTATCTTAATGCTGAGCTATTTTTACTCTCTCTCCATCTCTGTCTTCTGC
CTTTCTCTGTTGTGAGGTTCGCTGTCTCTCTCTCTGCCTCCCTTTGTCTCTCCATCTCTCAA
CCATGTTTTCTGTCTCTCTTTGCTTTCTCCTCTCTCCCCCCAATCTCTCTCTCACGTCCTGT
CTCTGTGCAGTCTCTTCCTCCTCCTTCATGTCTGTCCCTCTGTCAGCCAGTCTTCCCCACG
CCCACCCCTCCTCCAGCTCTCAGGAGTCCCATTCCCTTCCTCCTCTGTCGCCCACACAGC
CCCCACCACCTGGCCGCCCACCTGAAAAACTTTTCCCCAAGTTCTTGAGAAGTCGCGTAG
GATCCAGGAGAGAAAAATCAAAGTAATAAAACCTCATTTAATTCCTAACGGAGGGCAGAGC
TGCGAGCTGCAATTATCTTAATGCTGAGCTATTTTTACTCTCTCTCCATCTCTGTCTTCTGC
CTTTCTCTGTTGTGAGGTTCGCTGTCTCTCTCTCTGCCTCCCTTTGTCTCTCCATCTCTCAA
CCATGTTTTCTGTCTCTCTTTGCTTTCTCCTCTCTCCCCCCAATCTCTCTCTCACGTCCTGT

FIG. 22A cont'd

CTCTGTGCAGTCTCTTCCTCCTCCTTCATGTCTGTCCCTCTGTCAGCCAGTCTTCCCCAC (SEQ ID NO: 209)

eHGT_612h (279 bp)

TTCCCAGCCTTACCTTGTTGCAGGCCTCCAGGGTCTGCAGCGGGGTGAGGCAGGGTCTG
GGAGATGCAGTGAATGCAGGAAGGGGTGTCTGCCTGACAGCCCCATCCCTGCAGATTTTG
ATGGCTCCGTAAAAATGTCTCCTCATAAACTGTCAAAGTGTCACAAATTAATTAACTGTTAG
CTAGAGTGACTCAGTGTGGGGGGGGGTGGGGGAGAATGGCTCAGTGATGCTGAGCGGG
GTGGTGGCGGTGCTGTTCTCTGCGTGTGCTGCCTTTTGAT (SEQ ID NO: 11)

eHGT_613h (568 bp)

ACTTGGAGGAAAGGCAGAGGAAAATGGTCACTCCAGCAGTGCTGCCAGGACACCAGGAC
CCTGCTCCATACACCTAAACCTCAGCTTGCCCTTCCCGTGGAAATAAGGAGATGAAGCACT
CAGAAAACACAATGCAGTTTCATTTTCAGGGTGGGATTTTTTCCTTCTATGTATCTCATGAG
TCACTAGATTAGCACCTTTCCAATTACTGGGAGGCAAAAGCCCTATTATCATAGAAACCCTC
CTGCAGAGTGACGGCTCTATTCTTTCTGACGGCAGCAGCCAGTCCCACAGAGAGCTGCAG
AGCTCAGCAAGCTGGGAGCCTGAAGTTCCAGGTAACTTCATGTCCTCGTTTCAAAAGTGAA
GTTTAAAGAACTCACATCACAGCCTTAGCAGACTTCTCACACTCCACAGAACACGCCAGGA
CAGCCCAGGAAGGAAGGCTGAGGAAGGTTCAGGAGCACATCCCAGAGGCTGCACACAGG
GCCCGGGGCTGCCTCGAACACACTCTGCAAGGGTCTGCAGCACTGAACGTTCTGTCTGAG
CTGAGGGAGAACTGCATGACACA (SEQ ID NO: 12)

eHGT_614h (621 bp)

TGCCACTTGAACAATGACTGTCATTCATTATAACTTTTGCAAACCCACCAAAAGCTCCTGAT
GGCATGCATACCCATGCATCACACGTGCATACGTGCACACATGCCTTTTAAAGACCCCACA
TGGGTGATTGCAAGGGCTGTGTTTGACAGTTGTCATCTCTTAAAATGATGTAGGTTCCTGA
AGTTCCTCATGCAGGACTGTCAGCCTGACAGCCTTAGCAAGTCAGTCCTCGTTCTCAAATG
GGAAAATGACATGGGAGGGCCTTTTCCTCCCTTTTTGGTAGATCTGCCATTCATCAGCATC
ATTCTCTTCTCAGCCACTTGCTCATAAAGCCTTCCGGAGGCAATTACTCAGGTGTACATGA
CAGGCCTACATTCCTGTCAGGGGTGTGGGCTGGGTTAGAGAGGATGCGGGTGACACTCT
GTTCCAGCAGGGACCATGCCTGCCCACCAGGAAGCACATGCCGTTCTCAGTAGAATTCTC
TTTTCAGAGTTTAGGAAGCCACTAGCGCTATAATAACTGCTTGCTGTGGTTTGTGGTCAAGA
GCAATCATAGCACTGATTTTATTTTTCTAATTTCATTCTGAAATCTAGACAGGAGGTGAGACT
GCATCACGTT (SEQ ID NO: 13)

eHGT_617h (737 bp)

AAACAAGAACCCGGGGGAATCCAACTGCTCAGCATGTGGGAAGGGCTCTGCGCAGCCCG
CCCCTGCTCCTGGGGCCGCAGGGAAAAGTGGGTGAGGCCAGCACTCTGTGCCTGGGATG
CCACTGCTGTCCTGCGATGTTGTGCTGCTCCCCCGCATGGCTGCTGCTACGGGCTCTTGC
CACAGCTGGACACCCTCCCCTGAGCTCCAGTGCCGGACAACTGTTTTCTGAGCATGCTAA
GCAATGACCCTCTGCTGACGGGAGAAGTTACTTTAGAGGGGACAGAACTTAGGAAGACCC
AGGTGTGCTGTGAGGCAAGTGGCTCCCTCCCTGACCCTTACTGCTCAGTGTGCAAGGTTA
CCACCTTCTCCTCCTCCCCACACCCATCCCCCCTCTCTCCCAAGGTGCCCCTCATTGCTGC
TGTCACTCATCATTAGCAGTCACTGTCATTGTTAGGACAGCCCCTGTCAGGCTGCAGAGCC
AAGGGAGGGGGCAGGAGAATGTCAGATGACTCACACAACCTCAAAAGAGGGGGATGGAC
ACACAACACAGAACCTAGCTACAAGAAGCACCTCGTGAGACTCTGGTTCAACCCTTTCTTT
TTCCAGAGAAGAAAGAGCAGCTTAGCAGAGTTTCCTGACAAGTCCCTCTGCTTCCCACTAG
TCAGGCTTGGAGGGAGGCTGGCCTAGGAGAAAGGCCAGGCCAGGAAGTCAGCATGAGGC
TGGGCAGGTGACAGGTG (SEQ ID NO: 14)

FIG. 22A cont'd

eHGT_618h (673 bp)

AGGTTGAGTGGATTGAGGAGAAAATGGGAATTTTCATGTTTTTCAATAAATTTAGCTTTAAAT
GGAAGGAGAGAGATAGTATCTAGATGGAAATACAAAATCACAAGATAATCTTTCTCACTTTT
AGACAGAGGAGAAATCACCACATAACTGGAAACACTGAAAATAGGAGAGGGGAAAGATGG
CTGACAGAGTCAGGCTTGACAGGAGGAGGATGGGGTCCAGGACACAGTGTCAGAGGAAA
GAGGAGTATAGACAGGAGGAGGTGGGGACACAGTTCCCCTACTCTGACAGGAGGCAAGG
TGGGAATAATTGGTACTGATAGATCTAAGTTTATGGGAGGTGGGAGGAAGTTCATAGAGTT
CCTACCTGACAACCTAGATTCATCTGAAGGAGGAGTGCCAGTTAAGAGACTGTTACAAGAA
GTATCGAGAACCTGAGTTGATGACATTGGGAACAAAGCTGCATACTTGAGACACTGTAATC
ATTTAACAAAAGGTGAAGTTCACACCATACAAGCACTGCAAGAATGTAGAGCAATTAGAATT
CTCATAGACTGATGGTGGAAAAGTAAAATGGTACAAACACTTTGGAAAATCTTTAGGTGGTT
TCTCAAAAAGTTAAACAAAGTCCTAACATGTGACTCAGCCACCCACTAGTAAGTATTTACCC
A (SEQ ID NO: 15)

eHGT_619h (1125 bp)

ATTGATGGAGTTGGGGCTCTGTGAGTGTGGGGCCCTGTGATTCCTTGCACTAATTCCAGG
AGATGGGTCTCCTAACAGCATGATCATGTGGATGTCCTGTGAGCCCTGGCGGGGCTGTAC
AGAGAGAACAAACTGCCGAGCACAGTGCAGCTGCCTTATCAGATGGGGCACACAGGCTTG
CACAGTGAGCATCTCGGCAGCAGCCTTGGTAGACTGCAGACCAGAGACTCGTCCCCCACT
TTCCAGAGTTGCTAAATTCCAATGTTTTGAGAAACACAAGAGAAAGGGTTGGTGGGGGTCC
TGGAAAAATGATTTAGTGAGTAGGGGTTAAGCCGTATGTTGTTTCAGTTAGAAAAATGAAAA
GTTAAAGGCGAAAGATTTGCACGATCTGAAGAGAAACCAGAATGACGAGTTAATGGCACAT
GTTTACATACGTAACAAACCTGCATGCTGTGCACATGTACCCTAAAACTTAAAGTATAATAA
TAATAATAAGAAAAATGAAAAGTTACATTTCTTATATCTGAGCATTGTCTCATTAATATGAAG
TAGTCATAAGCACCTTGTGTTTTGGGGATTTACCTTACAAAACACTCACAATATCTTTCCTCA
TTATCTGGTCACCAAATTAATTTATTCATCATTCATATATCCATTCATCCGATATTGGAGAAT
CTGCTACAGTCATAGTGTAGAGGTGTACAATGGTGACTAAGATGTAGTTCCACGTTCTTAC
AATTCTTACTAGTGACGTGGATAGGAGATAAGGAACCGCAGTGAAAAGGATATTGACTGGG
CACAAAAAGTTTGGGGTTTTAATCCTATTTTTGTCCTTCAACTGCTGGGCAACTTTGGGCCA
ACTACACAACCTTTCTTGGCTTCCCTTTCTTCATTTGTAAAATTGGACTAAATTATCTTTAATT
TCTTACTAACTTCTAAAATACTTTACTGAAGAAAAGAGACATACACATCTGATGTAAATGCAA
GTATGTGTGTGTGTGTGTGTGTGTGTGTTTAATGGGGGCATAGCTGGCTCCTTTATTAG
GCTTTGGTTTTTCTTCATGTATCTGATTTCCAGAAATGAGAGTGAAAATACATTTTATTTTGC
TCCCACGTGTTTACT (SEQ ID NO: 16)

eHGT_620h (742 bp)

ACTGGGGTCACAAAGAAGAACCAGGGAACGCTGTTGGGGAACCCATGCAATGAAATGTGA
AGGGAAAGAGGGCGGGCAGACGTCCCCAAACCCGCTCAGCAAAGACAAGCTTCGGGCAA
ATTCACTCACGTTGACGCTGTTCGGATGGAGCAGGCCAATTGGAAAAGCCGGGTTCAGAC
ACGACTCTAGAGGGAAGAGAAGAAGGCAAGTGTGAGGAGGGCGGGCGTCGGGGAGAAG
CGGGCCCGGGTGTGCTGGCGGACGTAGGGCCTCACCGTCGCGGTCCTCAGCGTCTCTGC
GGGGTCACGGGCCAGGCTGCGGGGCTCTGAGCGCCTGCCTCGCCGTCCCGGGGCTTAA
CGGCTGCTGGAGCCACTTTATAATTAGCCCCAAACCGAAGGAGGCGCGCGCGCCCCAATC
GCCGGCGGGCTGCAGCTGACGCAGGCCCTACGCCAGCCCCGCGCCGACGCCTTCGCGG
GAGGGGTCGGTCCCCCAGCACCCGCGCGCCGCTCCCCCCGCCGAGCTCGGGTGGGGGC
CACAGGGGGCGCTCGGTGGCTCCCCACACGGCCAGGTGACAAACCCAAGGCAGTTAGGA
AGTTTGGGGAGAGTGAGATAGGATCAAGTTTCTCCGCATAAAGTCACTGAAATTGCACCGT

FIG. 22A cont'd

GGGATGCGGGCTCCAGGGAGGGAAGCGAGGTGGGGGCGTTTGGAAGGATAGATGGACT GGCTTAGACTTCTGGAATGTGCTGGAGACCCAGC (SEQ ID NO: 17)

eHGT_442h (402 bp)

CCCACTCTCACAGCCTAGGGAGAAGAGGAGGTGATGGAGGAGGAGGTGACAGGCCCCCT CCACCCCCACCCCACGCCCACCCCCACGTGGCCCCACAGCTGTCTGTCTGTGTCAAATGT TCTAAGCAGAGGTTGGGGGCTTCACTCCCCACACAAAGAGAGTTCAGAGCTGTCAGCACC TTTCCCACGGTACACTAGGTGCTGAGGAACAGGTGATAATTACAGCCCTGTCACCCTCATC ACCTCTGAGCTGGATGAGTTTTTTTCTAAAAACAAATGTTGTGCTGCCTGAAGATCAAAGTT GGAGCTTAGGTTGGGGAAATACACACATGCAGGCTGCTGCTCTTTTCCATGAAGCACAGG GAATTGGCTTGGAAAACACCTTGGAGATGGCTGTCTTGGC (SEQ ID NO: 18)

eHGT_444h (604 bp)

GACTCTACCTGCTGTAAAGGCAAATGAATGATCCTTTGATTAAAAGGCACTCTACAGAGCG GCACAGGCACAGACAGAAACCTAGGGAAAGGCAAAGAGGAGTGAAAACTGGAGGCTTCCT TTCCATCCTGTCGTCAAGAGCAAGAGACCATCGTCAGGACCTCTCTGGAGAGAGTCAGAG CCTGGGCCACCCCCTTCCACCTTGTGTTCCCGTGTCGTGTCGGGTCCTACTCCTCCCATTT CTTTGCCCCTGAAGTGCTGAGAGGGGGAGAGGGTGGAGCCCAGCCCTCCCCCTGCCCAC TCTAGCTGTCAATCTGCTGTCTGGCAGAAAGACATGAAGCCTCGTGACAACTGTGGGCAAC TTTCCCCTGCCCCGCCTCCCGCCCCTGCCCTGCCCTCTTCCCCTCTGCTCCCTGTCAATG CTCTTCTCACTCTGCTCTGGGTCTCCCTTCCGTCCCTCCCTCTCTCCCTCCCTCCCTTCCTT CTTCTTTCCTCTGCTTCTCTTTGTCATCTCTTCCAATCCTCACATCTGATAAGCCTGTATACC CTCATAAGATTCCTAATTGTGGGATATGCTTTTAAGCGTCCATCCAGGCCAAGATCT (SEQ ID NO: 19)

core2_eHGT_444h (235 bp)

GGCCACCCCCTTCCACCTTGTGTTCCCGTGTCGTGTCGGGTCCTACTCCTCCCATTTCTTT GCCCCTGAAGTGCTGAGAGGGGGAGAGGGTGGAGCCCAGCCCTCCCCCTGCCCACTCTA GCTGTCAATCTGCTGTCTGGCAGAAAGACATGAAGCCTCGTGACAACTGTGGGCAACTTTC CCCTGCCCCGCCTCCCGCCCCTGCCCTGCCCTCTTCCCCTCTGCTCCCTGTCAA (SEQ ID NO: 210)

3xcore2_eHGT_444h (705 bp)

GGCCACCCCCTTCCACCTTGTGTTCCCGTGTCGTGTCGGGTCCTACTCCTCCCATTTCTTT GCCCCTGAAGTGCTGAGAGGGGGAGAGGGTGGAGCCCAGCCCTCCCCCTGCCCACTCTA GCTGTCAATCTGCTGTCTGGCAGAAAGACATGAAGCCTCGTGACAACTGTGGGCAACTTTC CCCTGCCCCGCCTCCCGCCCCTGCCCTGCCCTCTTCCCCTCTGCTCCCTGTCAAGGCCAC CCCCTTCCACCTTGTGTTCCCGTGTCGTGTCGGGTCCTACTCCTCCCATTTCTTTGCCCCT GAAGTGCTGAGAGGGGGAGAGGGTGGAGCCCAGCCCTCCCCCTGCCCACTCTAGCTGTC AATCTGCTGTCTGGCAGAAAGACATGAAGCCTCGTGACAACTGTGGGCAACTTTCCCCTGC CCCGCCTCCCGCCCCTGCCCTGCCCTCTTCCCCTCTGCTCCCTGTCAAGGCCACCCCCTT CCACCTTGTGTTCCCGTGTCGTGTCGGGTCCTACTCCTCCCATTTCTTTGCCCCTGAAGTG CTGAGAGGGGGAGAGGGTGGAGCCCAGCCCTCCCCCTGCCCACTCTAGCTGTCAATCTG CTGTCTGGCAGAAAGACATGAAGCCTCGTGACAACTGTGGGCAACTTTCCCCTGCCCCGC CTCCCGCCCCTGCCCTGCCCTCTTCCCCTCTGCTCCCTGTCAA (SEQ ID NO: 211)

FIG. 22A cont'd

eHGT_445h (567 bp)

TAAGTCCGTTTGGGCAGCCTGAGATTTCATCAGGTGTTTTTTGGCATCTGTGTTAGACTGTT
TGCTCATTTTGTGTTTGTAAGTGGCTAAAAATCCTTAAATCTTTCTCATAGGAACCAGTTATA
AACCAGGTCTCACAATTCTGTTACTTAAGCAGAATTTCCAGCTCTAAGTGGAGGACTTTGAG
CTTAACCCTATTAAATTTAATCTAATATATTCAGCAGCCTGTCACAATCTTGTTAAATCTTTAT
TCCGTCACCCACCTTATTAGGGGGCCCTCCCACTTTAGTCATCAGCAGATTAGTAAGCATG
CCATTTAGATGTCATCTAAGTTAATGAACCTGACTGAGCCAGAGTCACATGGCAGAGTCAC
AGAAACTCCTTCTGAGCTGGCGTCCGATAATCAATAAACTTTGGTTAAAAGTATTCAGCATT
CTGGGGATTCACATTAAGTGGTGGAGCCAACCACTTAAGAGTATCTGTCTCTGGGTGGGC
AAGGAGCTAGGCTTCCTAGGAGGGCATGACAAGGCACCCTTTCTGCTTATTTCACCCGGAT
GCTGACTCCTT (SEQ ID NO: 20)

core2_eHGT_445h (222 bp)

GTGGAGGACTTTGAGCTTAACCCTATTAAATTTAATCTAATATATTCAGCAGCCTGTCACAA
TCTTGTTAAATCTTTATTCCGTCACCCACCTTATTAGGGGGCCCTCCCACTTTAGTCATCAG
CAGATTAGTAAGCATGCCATTTAGATGTCATCTAAGTTAATGAACCTGACTGAGCCAGAGTC
ACATGGCAGAGTCACAGAAACTCCTTCTGAGCTGGC (SEQ ID NO: 212)

3xcore2_eHGT_445h (666 bp)

GTGGAGGACTTTGAGCTTAACCCTATTAAATTTAATCTAATATATTCAGCAGCCTGTCACAA
TCTTGTTAAATCTTTATTCCGTCACCCACCTTATTAGGGGGCCCTCCCACTTTAGTCATCAG
CAGATTAGTAAGCATGCCATTTAGATGTCATCTAAGTTAATGAACCTGACTGAGCCAGAGTC
ACATGGCAGAGTCACAGAAACTCCTTCTGAGCTGGCGTGGAGGACTTTGAGCTTAACCCTA
TTAAATTTAATCTAATATATTCAGCAGCCTGTCACAATCTTGTTAAATCTTTATTCCGTCACC
CACCTTATTAGGGGGCCCTCCCACTTTAGTCATCAGCAGATTAGTAAGCATGCCATTTAGA
TGTCATCTAAGTTAATGAACCTGACTGAGCCAGAGTCACATGGCAGAGTCACAGAAACTCC
TTCTGAGCTGGCGTGGAGGACTTTGAGCTTAACCCTATTAAATTTAATCTAATATATTCAGC
AGCCTGTCACAATCTTGTTAAATCTTTATTCCGTCACCCACCTTATTAGGGGGCCCTCCCAC
TTTAGTCATCAGCAGATTAGTAAGCATGCCATTTAGATGTCATCTAAGTTAATGAACCTGAC
TGAGCCAGAGTCACATGGCAGAGTCACAGAAACTCCTTCTGAGCTGGC (SEQ ID NO: 213)

eHGT_450h (637 bp)

GAGACCACAGGCTGAGAGGCCAGGCAGGGTTCACCAGGACACTCTGAAAGAGCTGTCTG
GCTCCCAGGCCCACAGGCCTTCGAGGGAATAGACACATAAGCCTTGCTCCTTTTTCTCCTG
GTATCTGCCCACACCCATATCCTGGAAAGCTGCGTGATTTATGTCCACCAGAGGGGATTTG
CTCTGAGGCTGTGGCCTGCAGGAGCGCCCTTCCGCTGGAGGGTGGGAGGACTGTCTAAG
GCAGTCACAGCAAGGAGAGGCACGGTGTGGGCACTGCTGCTATTTCTAACCTGCTGGAGT
GAAGGGAACCTTGACTACTTGAAAAGCAGGCTGATTGTCAGGGGCGGAACCGAACTCAGA
GCTGTCAGGGCCGTCACATGGAAAGTGCCTGGCAGGGGGCGGCGACAGGGGGCTTGGG
CTGACAGGGCTGTGATTTTGAAAGAAACGTCTCCAAGAAAGTGATTTAAAGTAGGAGAGAA
ATATTATTATTAGATAATGGCTGTCAGGTTATTTTTTGATGTGTTTTCTGAGTATTTCATAATC
ATCTTGCGCTTAGATGGTAAGCCCTTCCTGGCTAGGGGCCGTGTCCCATCCCATGCCTCT
GTGGCTTTCACCTTCGGGTGTGCAACAGGTATCA (SEQ ID NO: 21)

core2_eHGT_450h (246 bp)

CTGCAGGAGCGCCCTTCCGCTGGAGGGTGGGAGGACTGTCTAAGGCAGTCACAGCAAGG
AGAGGCACGGTGTGGGCACTGCTGCTATTTCTAACCTGCTGGAGTGAAGGGAACCTTGAC
TACTTGAAAAGCAGGCTGATTGTCAGGGGCGGAACCGAACTCAGAGCTGTCAGGGCCGTC

FIG. 22A cont'd

ACATGGAAAGTGCCTGGCAGGGGGCGGCGACAGGGGGCTTGGGCTGACAGGGCTGTGA
TTTTGAAAG (SEQ ID NO: 214)

3xcore2_eHGT_450h (738 bp)

CTGCAGGAGCGCCCTTCCGCTGGAGGGTGGGAGGACTGTCTAAGGCAGTCACAGCAAGG
AGAGGCACGGTGTGGGCACTGCTGCTATTTCTAACCTGCTGGAGTGAAGGGAACCTTGAC
TACTTGAAAAGCAGGCTGATTGTCAGGGGCGGAACCGAACTCAGAGCTGTCAGGGCCGTC
ACATGGAAAGTGCCTGGCAGGGGGCGGCGACAGGGGGCTTGGGCTGACAGGGCTGTGA
TTTTGAAAGCTGCAGGAGCGCCCTTCCGCTGGAGGGTGGGAGGACTGTCTAAGGCAGTCA
CAGCAAGGAGAGGCACGGTGTGGGCACTGCTGCTATTTCTAACCTGCTGGAGTGAAGGGA
ACCTTGACTACTTGAAAAGCAGGCTGATTGTCAGGGGCGGAACCGAACTCAGAGCTGTCA
GGGCCGTCACATGGAAAGTGCCTGGCAGGGGGCGGCGACAGGGGGCTTGGGCTGACAG
GGCTGTGATTTTGAAAGCTGCAGGAGCGCCCTTCCGCTGGAGGGTGGGAGGACTGTCTAA
GGCAGTCACAGCAAGGAGAGGCACGGTGTGGGCACTGCTGCTATTTCTAACCTGCTGGAG
TGAAGGGAACCTTGACTACTTGAAAAGCAGGCTGATTGTCAGGGGCGGAACCGAACTCAG
AGCTGTCAGGGCCGTCACATGGAAAGTGCCTGGCAGGGGGCGGCGACAGGGGGCTTGG
GCTGACAGGGCTGTGATTTTGAAAG (SEQ ID NO: 215)

core3_eHGT_450h (245 bp)

CAGGGGGCGGCGACAGGGGGCTTGGGCTGACAGGGCTGTGATTTTGAAAGAAACGTCTC
CAAGAAAGTGATTTAAAGTAGGAGAGAAATATTATTATTAGATAATGGCTGTCAGGTTATTTT
TTGATGTGTTTTCTGAGTATTTCATAATCATCTTGCGCTTAGATGGTAAGCCCTTCCTGGCT
AGGGGCCGTGTCCCATCCCATGCCTCTGTGGCTTTCACCTTCGGGTGTGCAACAGGTATC
A (SEQ ID NO: 216)

3xcore3_eHGT_450h (735 bp)

CAGGGGGCGGCGACAGGGGGCTTGGGCTGACAGGGCTGTGATTTTGAAAGAAACGTCTC
CAAGAAAGTGATTTAAAGTAGGAGAGAAATATTATTATTAGATAATGGCTGTCAGGTTATTTT
TTGATGTGTTTTCTGAGTATTTCATAATCATCTTGCGCTTAGATGGTAAGCCCTTCCTGGCT
AGGGGCCGTGTCCCATCCCATGCCTCTGTGGCTTTCACCTTCGGGTGTGCAACAGGTATC
ACAGGGGGCGGCGACAGGGGGCTTGGGCTGACAGGGCTGTGATTTTGAAAGAAACGTCT
CCAAGAAAGTGATTTAAAGTAGGAGAGAAATATTATTATTAGATAATGGCTGTCAGGTTATT
TTTTGATGTGTTTTCTGAGTATTTCATAATCATCTTGCGCTTAGATGGTAAGCCCTTCCTGG
CTAGGGGCCGTGTCCCATCCCATGCCTCTGTGGCTTTCACCTTCGGGTGTGCAACAGGTA
TCACAGGGGGCGGCGACAGGGGGCTTGGGCTGACAGGGCTGTGATTTTGAAAGAAACGT
CTCCAAGAAAGTGATTTAAAGTAGGAGAGAAATATTATTATTAGATAATGGCTGTCAGGTTA
TTTTTTGATGTGTTTTCTGAGTATTTCATAATCATCTTGCGCTTAGATGGTAAGCCCTTCCTG
GCTAGGGGCCGTGTCCCATCCCATGCCTCTGTGGCTTTCACCTTCGGGTGTGCAACAGGT
ATCA (SEQ ID NO: 217)

eHGT_452h (586 bp)

AGGGAGGAACTAAAGTCCATTCATATGTCCATATTCTCAATTTGGGAAAAAATGTGGCTTTG
TCTTCATCCTCTTTTCCTGAGTGTATAAGGCCAGAAGCCAAAGGCAAGAGCAGGACATTCC
AGGAGCCTTTATGATTGCTCTAAGTCACATCTGCTCTCGAGCTCCCATTCCACTGTGAAAAA
TACCTAGTCTTGAACTTTGGAGTTCCAAATTCCACATGATCGACTTCCTCAAGGCTTTTCAC
TTGACGAACAAATTGCATGCCAAGAAATCGTCAAAATTCTATCAAGCTTAATTATGCAATTTC

FIG. 22A cont'd

TGTCTATAAATGACATACCTCCTGTACCCTATGACACCCACCTATGCACTAATAAGATGTGA
CAGCTGCATCACCAACAAAGCCTCCCCCGCCTGCCATTCTCTTCGGAGGTGAGCACCTCC
TGCTCGGGAGGAACTGACAGCCCCTTTCAGAAATGTGAAGGCAGTGAAGTCCCAAACCAG
AAACAGTGTGACCACCTAGGCTCACCCAAGGACCGTCCTGTGCTTCTGGGCAACCAATGG
ATGTAGGGGGTTAGGAGGCAGTGGGGATTCGTCA (SEQ ID NO: 22)

core2_eHGT_452h (228 bp)

GTGAAAAATACCTAGTCTTGAACTTTGGAGTTCCAAATTCCACATGATCGACTTCCTCAAGG
CTTTTCACTTGACGAACAAATTGCATGCCAAGAAATCGTCAAAATTCTATCAAGCTTAATTAT
GCAATTTCTGTCTATAAATGACATACCTCCTGTACCCTATGACACCCACCTATGCACTAATA
AGATGTGACAGCTGCATCACCAACAAAGCCTCCCCCGCCTG (SEQ ID NO: 218)

3xcore2_eHGT_452h (684 bp)

GTGAAAAATACCTAGTCTTGAACTTTGGAGTTCCAAATTCCACATGATCGACTTCCTCAAGG
CTTTTCACTTGACGAACAAATTGCATGCCAAGAAATCGTCAAAATTCTATCAAGCTTAATTAT
GCAATTTCTGTCTATAAATGACATACCTCCTGTACCCTATGACACCCACCTATGCACTAATA
AGATGTGACAGCTGCATCACCAACAAAGCCTCCCCCGCCTGGTGAAAAATACCTAGTCTTG
AACTTTGGAGTTCCAAATTCCACATGATCGACTTCCTCAAGGCTTTTCACTTGACGAACAAA
TTGCATGCCAAGAAATCGTCAAAATTCTATCAAGCTTAATTATGCAATTTCTGTCTATAAATG
ACATACCTCCTGTACCCTATGACACCCACCTATGCACTAATAAGATGTGACAGCTGCATCA
CCAACAAAGCCTCCCCCGCCTGGTGAAAAATACCTAGTCTTGAACTTTGGAGTTCCAAATT
CCACATGATCGACTTCCTCAAGGCTTTTCACTTGACGAACAAATTGCATGCCAAGAAATCGT
CAAAATTCTATCAAGCTTAATTATGCAATTTCTGTCTATAAATGACATACCTCCTGTACCCTA
TGACACCCACCTATGCACTAATAAGATGTGACAGCTGCATCACCAACAAAGCCTCCCCCGC
CTG (SEQ ID NO: 219)

eHGT_610h (568 bp)

CATCCCGCTGGCCATCTGCATCAGCCCGACCCCCACAGGATAGAAGACTGGCACATCCAA
GTTGCTCCTTCCACACCCTCTCCCCACTGAGGCCTCGTCTCCTCCGCCCTGTGGCCAATT
GAAGGTGAACTCCTAACGTGCATTCTGCCTGGGATCCCAGAGGTTGTGGCAGCCAGATGA
GTCACCTCACAAATACAGCACGTGTTCCTCGGGGGCGGCGGTGGGAGGAAACACGTGAA
GAGCTCTCTCTGTGATAATAGACCATTTAGAGCTTCAGATGGCGAAAACAAGCTGATCAGG
TGCAGGCCCTCCAGGAGGCTGGCAGGTGACTCCCAGCCAGCACGCCCTCCATCGCACGT
TGGGGAAGCTGGAAAGAGCCTGGTGGCTGCCGGGCCTCCCTCTGGCATCCTCTCTCCCT
CCAAGGCTGTGTGCTCCCCACCTTGTCTCTCCTTTTTTCATTCCATTGCTCTGTTCTGTTTC
TGTCTACCCATTCGTCTTTTCTTCCTCTTCTCTTTCTGTTGCCATTCTCTTTCTCTTCTCCTCT
CAACATGTCCTTCTCTCTACCCGT (SEQ ID NO: 23)

eHGT_611h (447 bp)

TGACTGTGAAGTGTCTGTCTGAACTCATAATCAGCTTTTAGCTGGTCCCAAACAGTGAGTG
CTACCAGCTCCATTAATCCCACTGACAGGGATTTATCTTTCTCAGCTGAATGAATGATGCTC
CCAGCCTTGCCCCAGAAATGTGGGCTGGGCTATTCAACACTTGTCACCAGCAAGCTCTTTT
CCTGAGGCTGCATACTCCAGCCACCCAGGTGACTGAGTACTTTGTCATCTTCTTCTCAGAG
CAGTGGCAGAACCACAAAGCAAACTCCCACCCATGACCCACCCACCCACCTTCTGACCTA
GTTTGGATGCTCCAAGCCATAATGATAAAGTAATGTTGTGAAGAGGGAAAGAGGTTTGCAG
TCAGACAGCCTGAACCCAGGTTCTGCCATGTACAGGCTGAAGCTTGGCAAGCCTCTGCAC
CTCTCTGAGGTCCATTTGCAC (SEQ ID NO: 24)

FIG. 22A cont'd

eHGT_615h (654 bp)

TCCCACATCTGTTTCTCTGGCTCTGCCTCTTCTGCCTCCTTCCATCTCTTATAGGGAGCCTT
GTGATGACATTGGGCCAACCAAATATTCCAGGATCATGCCTGCATCTCTCAAGATCCTTAA
CTTAATCATATCAGCAAAGTCCCTGCACCATGTGAGGTAACATATTCACAGTAGTAGGTGCT
CAATAAATAGATACTAAAGATAGCAGCATTTTTTATTAGACCTTCTCACAGCTTCTGGGGAT
TAGAATGAGACATCTTTGGCAGCCATTGTTCTCCCCATCATGGGTAACATGCAGTGGGCGC
TTCCAGTGCCAGGATTTCGGTGGGTTTAACTGGAGTGTGCAGATAAGTAGTTGGCGTCAAG
AACTCCTGCTGCTTCCCTTGCTGGAAAGATGGGGTGGCTTTGAATGACATCCCAGAATCTG
ATTCTTCCGTCTGCGGAATGTGCATAGGATGTCTGAATCACACTATTGTCGTGAGAAATGA
GGTAGAATATTCTCTGATGTGGCAAGCTTAGGCCAGCATCTAGCCCAATTCCTTGTATATAA
TGGAAATTCTTAAGATGTTAGGGTTCCCCTCTCCCTCTCTCTCCTTTTTCCTCGCCTACAAA
GGAAGACATCTTTTGTGAGGCCTCCACAGCATTCTTGAT (SEQ ID NO: 25)

eHGT_616h (418 bp)

TCCATTGCAGCTTCTCTCTCTCTCTCTCTCTCTCTGAGTCATCTTTACAAGCCCCTGAAACA
ATGGTATTTAAGGAGGGAGCTTTCTCAACACCTGAAATCCCTACAGAAAGGTTGAGCTTCC
TTGGTAAAGCATTTACCTGCTGGGGGAGGGTGCATGGAGTGACATGGTTTTCACATTTGAG
AAAGGTAAGTGGGAGGGAATATCAGACAACTGCAGAGTGCAGATTATCATTTAAATAAAAT
CCCCATGGGGCTCGCTGGCAGCATTAAAATTGCTCCTGCCTCTGTGGTGCTGTCACAGAA
CAGCCTCTCTCCTTTATTCTGCTTTACCATAGAAAGAGGCAGTGTGGTGCAGTGGAAATAC
CCCAGGGCTGAATCCTAGGATTCAAGTCTGATCCATCATCTCTGGGCTGTGT (SEQ ID NO:
26)

eHGT_627h (368 bp)

TGGGACTCAGCAACTTGACTAACATCACAGACACAGTTCTCAGATTTATATATCCTAATTCC
AAACCCAATATTCTTACTACTAGAATATGCTGGACCGTTTTACTCCTAACTTGGTTAAGAAG
CCAAATATAGGAGGAAATTAACAAATCAAGGTAGTTTTAGTTACTCATTGGTCTGTGGGTTC
ACAGCATTTTAATGGAGCCAACTTTGCTCTTAAGATGAGTAAGCAGTTGGTATGACTCAGG
AATCTCTAAGAATGTTTCTACCTTAAAAGGCAGGTTTTTGTTTCTTAATCCTTTAACAATTAAT
ATTTTAATTAAGGGAACATTGGATAGACATTGTAAGGTGCAAAATACCTCTAGAAGG (SEQ
ID NO: 27)

eHGT_628h (283 bp)

AGTTCTTGCTTTCTCCAATTTGTTTATTTTTATGTGACCTAGCTTTATACATTGCAATTTAAAG
GAAATGAAAAACAGTTTTGTTATTTTCTTGTGTTATCTGGGAGATTATCTTATTCTTTTAGGG
TTCAAGTGCATAGAGTTGGTGCAATCAGCCACAGTTTATGACACAGTATAATTTATGCTTCT
TGCATTCTGTTTTAAATTTATTTTCACCTTTTATTTTCCTTCCTTTTATCCCTTTGTATTATGTC
TAATATCACCTCATCTTCACCCCAATCCA (SEQ ID NO: 28)

eHGT_629h (290 bp)

TGCTCATGCACAATCACTACTTCTATCTCTTCATCAATGGTAACACGATTCTGACTTCCAAC
AGAATGGACACTTTGCAAGTTTTGAAATGTATGAAAAGGAAAAATATGTCTTTTTCTGCTTAT
GGCTTTTTTAGTCAATGTTATATTATGCACTTTATTTATGTAATTTTGTCTTGCTATAGTTTGT
TTGCCTTTATTGACGAATAATAAATATACTAGTATGTGAACACACCACTCTTTAATTATTTAG
TCTACTTTTATTTCCAGGTGTTGGATCTTTTTCATCGA (SEQ ID NO: 29)

FIG. 22A cont'd

eHGT_446h (470 bp)

CTAATTTTAAAGCCTTCATGATCTATGTCCCACAGGACCATATGTCCCATAGCAGTCAAAAT
CAAAGACAAATTCTTGGACAGAACTGGATTGATGTAATAAATTTCTAGGGCATATCTGAGGC
CAGGTGCATGTGACATTTGAGTAGGAGTCAAGGATGTAAAACTGCCTACATAGTCGTGTTA
AATGATCAGAAATTAACGTAACATGTTTTTGTTAAGATGGTTTCATTTGTCTGGGAAGCTGC
ATTCTTAGAACAAAAAGAGTCAAGGACAGAAATGTATTATGAGATAAGTTCCACCTTCAGAC
TCAACCTACGCAAGTCAAAAAAAAGTTAGATTCGCCTTGAGTTCATGAACAAGTGGTGCTT
GACATCCAAAGAAATGGCTGGAGTAAGTGATGTTGCCCTCTTTTTTATTTCTTTGGAACAGA
GAAGCAGAAATCCATACTACCTCCCATCTGGCTCCATG (SEQ ID NO: 30)

eHGT_447h (566 bp)

TATGCTGTGGCCTGGGGATGGGAGGGAGAATCCACAGGCTGTGGGGATATTTCATAGGCT
TCATCTAGGCATTAAATGAGGAAATGAATGCAAAAGTGCCCAGCACAGTGCCTGACACATA
AAAGCACCAATAAGCTTCAGCTGTCTTCCCCCTTCTTCAAACTACTTAATTTTCTGTGAAACT
AACACTTCTTTTCTAATTGCCCTTGACTTCACATTCTTTAGCCCATTCTTCGTTACTAATCCA
TTCTTGCTAGTTCCTCCTACATTCCTATTGTTCGTGTTAAAGATGACTTTTCTATTCACCTGT
GTAAGTCTTGCTGCCTCCTACACTGATTAATTTAGCTAGATTGAAAAGGAGGACTAGTGCTT
CCTCCATAAAACTCCAATTAATCAATCATTTTAGAACTTGAGCTACTTTGTGTGGTGGTATTT
GTGGAAAGAGCAGGAATATTGCTGTCAGTCCTGAGAGGTGGCATTTACTGGCAGATAGAC
CTCAGACAAGTGATTTTACTCCTGTAAGCCTGAATTTGTTTATAGTACCCCAACTCATAAGA
TTGGTGAGA (SEQ ID NO: 31)

Core-eHGT_447h (250 bp)

ACTACTTAATTTTCTGTGAAACTAACACTTCTTTTCTAATTGCCCTTGACTTCACATTCTTTAG
CCCATTCTTCGTTACTAATCCATTCTTGCTAGTTCCTCCTACATTCCTATTGTTCGTGTTAAA
GATGACTTTTCTATTCACCTGTGTAAGTCTTGCTGCCTCCTACACTGATTAATTTAGCTAGAT
TGAAAAGGAGGACTAGTGCTTCCTCCATAAAACTCCAATTAATCAATCATTTTAGAACTT
(SEQ ID NO: 220)

3xCore-eHGT_447h (750 bp)

ACTACTTAATTTTCTGTGAAACTAACACTTCTTTTCTAATTGCCCTTGACTTCACATTCTTTAG
CCCATTCTTCGTTACTAATCCATTCTTGCTAGTTCCTCCTACATTCCTATTGTTCGTGTTAAA
GATGACTTTTCTATTCACCTGTGTAAGTCTTGCTGCCTCCTACACTGATTAATTTAGCTAGAT
TGAAAAGGAGGACTAGTGCTTCCTCCATAAAACTCCAATTAATCAATCATTTTAGAACTTAC
TACTTAATTTTCTGTGAAACTAACACTTCTTTTCTAATTGCCCTTGACTTCACATTCTTTAGC
CCATTCTTCGTTACTAATCCATTCTTGCTAGTTCCTCCTACATTCCTATTGTTCGTGTTAAAG
ATGACTTTTCTATTCACCTGTGTAAGTCTTGCTGCCTCCTACACTGATTAATTTAGCTAGATT
GAAAAGGAGGACTAGTGCTTCCTCCATAAAACTCCAATTAATCAATCATTTTAGAACTTACT
ACTTAATTTTCTGTGAAACTAACACTTCTTTTCTAATTGCCCTTGACTTCACATTCTTTAGCC
CATTCTTCGTTACTAATCCATTCTTGCTAGTTCCTCCTACATTCCTATTGTTCGTGTTAAAGA
TGACTTTTCTATTCACCTGTGTAAGTCTTGCTGCCTCCTACACTGATTAATTTAGCTAGATTG
AAAAGGAGGACTAGTGCTTCCTCCATAAAACTCCAATTAATCAATCATTTTAGAACTT (SEQ
ID NO: 221)

eHGT_622h (407 bp)

ACCTCAGGTCCCACATATACTGTGGTCTATCACCTGGTTACTCTAAAATGCCCCAACTCAC
CTTCTTCCTTAAAGCAGCTCCCACTCCTAACATTTGTATCTCAGGCTGATTATTCAGGTTTA
GAAATTTCAAGGTCATCTATGACTCACTGTTTTGATCATGTCAGTCACAAAGTTCTAAAGCT

FIG. 22A cont'd

TCTGCTTTGGAATGTTTCTTGTACTGAATGCTTCCTTCCAATTCTCATTGCCAGCACCAGCC
TCCAGATCTTTATCAAGTCATAGCTGGGTTGTTGTAACAGCTTCCCAGCAGAGATGGCATG
AAGGAAGGCAACTAAACTTTTCTGAGCACCTCATATGTATGTAATGTTTTCAATGCACTATC
ATATTTAACTCTCATAACAATACCACGAAGCAGGTAT (SEQ ID NO: 32)

eHGT_623h (324 bp)
GGGGTTACCTTTGGGAAAATAAACTCTTATTAAAGTGTCACATCTTGGTGGAAAGGCTTTTA
ATTTAATGATTGCTATCTACAGGGAAAAATCACTTATAAAAATCTTACTATTTCTCCCAAAAG
ACACCAGGTTGAGAACATTAGGACATCATTCTTTCATCAATATTTCCTTTGTATTTCTTAGTA
TTTTACGGTTTTCCTTAATACTTCTTATTCCTTCAAAAGCTATACCTCCATACTATATATTTGA
ACTGAAATGTCTGATTTTAGAACAAGTCACATGTCATTTTTATTTTGTCTTTAAAAACTTCTG
ACACTGAGA (SEQ ID NO: 33)

eHGT_624h (349 bp)
CTCAGTATCTTATTTCTTAGTCACACTTTAAAACTGAAGAGATTAGTAATTTTTTCTATGTCAA
TATGTGAAATATGCAATACAAAATTGTACAAACCCATTTAATTCCATTCTCTGTCTTTTGTCA
ATCAAACATCCTCCCTGATAAGAGCTCAATTATTTGATTAATTATAAATCGCTATTTTTTGAT
ATGATATTCACAGTAGAATAATTTATAATAGACAAAATTACAAACAATAAGATCTTGGTGTTC
AGTGGGATTTATGGTGTTTTCATGCAATGGAATACCGAACTGACACAAAAGTCATGTTAGA
GAAGAATATTTATAGATGTGGGGAAAAGTTCATGA (SEQ ID NO: 34)

eHGT_625h (644 bp)
GTGGTGATGCTGGACAAGGCAAGGAGTGGGCAGAGGCGAGGACTGTGGTCCAGCTGAAT
TTTCAGAGGCCCTCTCATGTGCGCCCACTCTTTGGAATCATTCTCATAGATACCCTATGGG
AAGCCCACCCCCCAGCCTGGCCCCGCGTCACACTGAGTCATATCTAATCATAGGCTCCCA
GGGTGATTTCCTTACCTGCTTTTTTCTGTGTTTTTAAGCTCTTCATTACTTCCTAATTGTCCT
GATTTTAGTTCTTTCTCGTTCTTGTCAAACACCCATTTAGAAAATGAGTCATCATTAACTGCA
CGCCACTCTTCACTTAGAATTAGACCCATTTCACCCTTTCTCTCTCTCTTTTTTTCCTCTTCA
AAAAAACTGGGGGATTAAAAAAATTACACTTTTCTGACATCCTTTTTTTAATCTCTTTTGCTA
GCGCAAATGCTATTGGCTGCTCAACTGCCTTAAGGGTTTCTTCTGCAGCCCAAATGAACAG
CTTTGTGCTTCCAGCCTTTGATAGCTCCTGGGGGCGTTGATCACTGAGTCAAACCTCCAGG
TCTCAGCCTCCCAAGTGGCCTGCTCAGGCATGAGTCAAATCAAGACTAGACCATCAGGGG
ACAAGAAGCTACTGCTCACCTTGCAAGTGA (SEQ ID NO: 35)

eHGT_630h (304 bp)
GTGTCAGCTCCAGGACGAGCCCCGCCAGCCTCCACCCTGTCCAACCAGGCCCTACTCCTC
CCCTGCAGATCTGTGGTATCTTCTGAGCCCTAAAAACACGCCTCCAGCCAGCTTCCTGTCC
TCCACCCGGCCTCTCGGGGCTCATCCCATCTATTATTCACAGCACAAAATGGATTTTTAATT
TGAGAAATGAAATGACTCTCCCAAGTGGCCGGGGTGGCAGGGAGGGGGTGGAGGAAGGC
CGGAGCCGCCGTGGCCGCCACAGCCGCCACGGTGCTGACTCAGGTTCATCTTGGAAAGC
TCG (SEQ ID NO: 36)

eHGT_631h (445 bp)
AGAGGGATGCAAATGAGGCTGTGGGGGCTGGGGACACCCCTTCCTGTCAGGGTCTCCAT
GGCACATTGCCTGGGACTGCAAGGAAGGGCGAGCCTGGGACAGGCAGAGAAGCCTGAAT
GGCCTGGAGGGCCACTTCCTTGGCTGCCAGGGTCCTGGGCCTGCAGTCCCCTCCCCCAG
CACTCCATCATCATTTCAAGTGATTGGAGCTGAAGGGGATCGTTAGCTAATTAAAGCTGAG
GCCACTAATTGTCCCTTTTGAAGAGAGAGCAGGGCTGTGCAGGGGAGGAGACAGAGGGT
CTGGGGAGGGGGATATTGGCAGGCGGGGGGCTGGGAACAGGGCCATGGCCCCTTGTGG

FIG. 22A cont'd

GGCCTTCTTCCAGACTGTGTGTTTGAGGGGTCAGGCATTGTCAGAAGCTCCTTAAAGTGG
GTAAAGGACTAGAGAAGCAGATTTGGCGCT (SEQ ID NO: 37)

eHGT_735m (744 bp)

CACTTGGGTGCCTTGACTAAATAAAGATGGATTCCATTTTTAATGGTCAGTTCCAGTGCCTT
CCAATTCCTTTGAGGGCGTCGTTTGGCAGGCTCAAGTACAGTAGTTGAGGAGAAACCATGA
CCAGGGCAATTACTTAGGGTTCTTTTAAGCACTGGTTTAGTGGAGATTTTTTTTTTTTTTTT
TTTGCCGAGCCATTATAATTCGTGAATAATAAAGAACAAGAGTGTTCAGATTGCTTAGGGCA
TGGCACGTTCAGAAAAGATCGGGCATCCTTCCAAAGACAGCGGGGCTTCGGGAAACGATA
AAGCGCTATGATTTTTAAAAGTCATACGCAGAATTCAGAAGCAGATACTACAGAGGAGTGC
CTGCAAGTAGGTCTGCTCGCTCTGATGGGTCTGAAGCGGGAGAGTGGGGGTGGGGCGGG
GGAGTAAATGTTCCCTGCTTTGTTGCTATTAACACCTTGGCCCTTGTCACCAGGTCCTTTGT
AAATGTTGGCAGCTGTTATTAGATGCGTTATCAAGCACCGGTGTACACAGCTTACTTTACAA
ATCACCCACCCGCAGATGCCTTACAAACCTCCACAGCCATCAAAATGCACCCCAGGACTTC
CTCGAAATACCATTTCCTCCCCAAGAAGAACCAGCAGCTTCTGGCTCCACTGAGTTCTGTA
CCTAAGGGCTACTTGCCTCTCAAGGCCAGAGAACCACGAATCCAGTAGTTCACCGAGCTT
CTCTGTTCCT (SEQ ID NO: 39)

eHGT_736m (1020 bp)

GGACTTTTGGTATAGCATTGGAAATGTAAATGAGCTAAATACCTAATAAAAATGGAAAAAAA
AATAAAATAAAAGTAGCATTAACCAAAAAAAAACAAAAAAAGAATATCACTTACTGTTGCATT
TCCTTCTTTATGCAGTTCTTTCCTACATAAAGTCTTGGATAAAATGAGAAAGGCATAATGTAC
CTAAGAACTAAGCAAAGCTAATGCTAGTTAGCACCACAGGAATGCTGACCTCTCATTACAG
AACAATTCAACAAGAACTCATTCACCAACAGTCAGGGTTGAGATTCTCCCCACCTGCCTGC
AGTATATTATAGTTGAAATATGGGGCCTTGGTAGGTTAAGAGACTACTGTAAAGCTTCTAGC
ACTATTAATTGTTCACTCTACCCATGCCACATCTCCCCAGGAGATCAGGGAATATTGTATTG
TGGTGCTCCAAAAGCTCGTTATGCAACGTACAAATTATGTTATGATGAAAGGCAACAACAAA
ACCTCTGTAAGGAGTGTTATCATTTCTCTCTTTTCATTAAGTCACAATGCAGAAACTGAGTA
ATCTGAACAAGTACCTTTAAAGTAAGAGACTTAGAAAGTGGCTGGCTACATGTAAAGCCGT
TCATGTGCTTGCAGTTGTGTACAGGAGCAGGCTGCTCACCTGTTACGGAGAGCCCTTTGTT
AAGAGCCTTTGTGAGTACTAAAAGCTTTAGGTTTCCTTTTCTTTTTTAAGCTCTTGCTTTAAC
AGTGTATTTCTATGTTCACCTTTCAGGTAATGACTGTCTTTGGTCTTTTTATCAAAGAGGGAA
CAATAACACCGCATGGTATTATTTTCACAAGTATTATAGAGTATATATTTCACAAGTTTGGTA
CCCTTTTTATATCATATCTTTTTATTTTAGTTATGTACCTGATTCCAATAAAAATCAAGTAATG
TTGATTGCAAACCCCATCTGTAGTCATAGAAATATTACAATGATGGACATGTAGTTAGTTTTT
CACTTCTCAAATACTGTCCATTTC (SEQ ID NO: 40)

eHGT_737m (942 bp)

AAACAAAGAGCCGCCTTCCATTCTTCTGAGATGTCTTTAGACATCTTGCTTACCCCTGTTAC
ACAGCCCCACAGTCATTACCAAGTTCAATCATCTAATGTGGGATCCCAGGAGGTCTGCATT
AACCATGAAGCAATGAAAGGTAGAGTGATCCTGTATATGGACCAACTGTCTTCCCCACCAG
ACTGAAAGCTCCCTGGGGTCAGAGACAACTCTTACTCATCACAGAGGTACCAGTATCCAGA
CTATGCTGTCTCTTCCCAACCTCTGCTTGCTGTCAAGCCTGAAGCTAGTCAGGCATCTACC
TCTGCCTGGCTGCAGTTCTTTCTCTTGAAGAAAGGATTTTTTTTTTTTTTGGTTTCATAATGA
TTAGTTTTTTTCATTATCAAAACCTCCCTGAGTCACAGGAGGTAACCTAATATCAAAACCTC
CCTGAGTCATAAACAACCATTGCTACTGCTACATTCACCATTATGGAAAAAAAAGGCTGGTC
TGAAACTTAGCCTCAGTGTTCTTTCTGCCACCTAAGGAGGAGGTTGTTGCATTTATTTATTT
GGGGGGAGGGGTCTAGTCATAGCATACATGTTGAGGTCAGAAAACACTTTATAGGAACTG

FIG. 22A cont'd

ATTTATTCCTTCTACGGTCTGAGTCCTGGGAACGAAACTCGAGTAATCTGACTTGAGCATAA
GCACCTTTAGCTATGAGCCATCTTGCTAGCCCACAATGTGTAGGGGGCAGTGCTGATGTCA
AGGTACTGTTGCCCAATTGGTTCTTGATCTGTCAGTAAAGAAAGCCATAGGCTAATTGCTG
GGTGGAAGGTACAGTCGTGACTTCCAGGTTCCGGGAGGGAAACGGGATGCAAGGAAGGG
GGGAGGGAGTTCGACATGCTTTGGAGAGAGGAGAACAAAGCAACCATGTGAGGTAGTAAT
ACACTGTGACAACTACAGGCAGGT (SEQ ID NO: 41)

eHGT_738m (897 bp)

GAATGTATTGGATTATAACATGCACTAGTATTAAGTATAAAAGTATGTTCAAGAAAATTTAAA
GTTATTTTAAAGACTGATGTAAGGAAAGAAGGAGGAAGTTAGTCCATTAAATCACACTGAGC
AAGAGCTAACTTCTACAGAGTAGTCATTAAGAGGTAATTTTACAATCTAAATTTTTTTTTTTTA
AAGGATGCTTTCCTTTGTTGTGGTGTCAAGGTGAGAAACTATGTAGATTTGATTCCGTAAAT
ATCTATGGTAAGGCAAGTGACAGGGTGAACTCAGCTGAGCTGATGGAAATAGTTAGAACAT
AGAAACAGTCAATAACTATTCATTTTGTAAAAAAAAAAAATAATAATAAAATAGCTCCTTCAA
GTCCTGAAGCGTAATAAAATATTAGAAAACACAATGGAAAAATGAGGCACTCACAGAAGAA
ATACAGTTGGCTCTAAAGCATAGAAAGTCTCAATTATTTCAAAATAATAGAAAGGTACTTTAA
GACAGTGAACCCGGAGTGGTCTCTGGGAACAGGCAGCTTGGTCCTCAATCTGGCAGTCAG
TGCTAACTACACTGTGATCCTGGAAAAGATATGCTTTACTTCCTCATTCAAAAACTCAGAAT
TATAGTGCTGCCTGTGCCCTGATCTACCTGATGCCCCGCCCTACCTGCCTTTGGGGGTTG
CAGGTAAGGTGGTGTGGAATCAGGTGAGAAATGTCACAGCAAGCACCTCTGAAAGCTGCT
GCAAGCTCCTTTAATACGCTCACCCGTGTCCCATTGGTCCCAAGAAAGCATCTCTTCTAAG
CAGCAGTTCCTGATTGGCTGGCATTGTCTGTGTCAGCAATCCTTGGTCTCTTAGGCAGTCC
TCAATTAGGTCCTCCTGTAGAAGGTGACTTTGCC (SEQ ID NO: 42)

eHGT_739m (547 bp)

AGAATATGTCATATGCCCAGAGTCTGGTACTTATGAGGGTCATAGTATTATGGTCAATCCGA
CAACCACTCACTCTGAGTCAGGCAGAGTGTGCAAAGTGCACTCATCTGTGTCACTTATTGT
CATATGTGCACAGGTGAGTGATTAAAAGCACAAGTGTGCACCGCAGCTCCAACATGTCATA
CTGCGGCCTCAGACAAAGAAAGCAACCTCTCTAAGCCTAGGGTGTTCTTGTCTATCAAGTC
GAGGGTTATAAAGGAAAACACCATGGGGAAGAATTAAATGCAAACCTCCCCCCACACCAC
GCTTATCAAATGGCTGCTGGCATGATGCCTTGGTTTAATTCTTACACAGTCACATACCAACG
GGTAAGGCTCTCAGAGAGTGTTATATAATTAAGACAAGATTCTTGTGTTTAAGCAGGGTGG
AAAAAGAAATACTTACTGGAACACAGACGTACAAAACAAACAAGTTTCTAGGGAAGAACGA
AGCTGCAGCACTGTGTGGGAACACACAGAAGAATTAGACTGTATGCAGGAGAGGGGAT
(SEQ ID NO: 43)

eHGT_740m (598 bp)

TGACAAATGTTATGGCGAGCCCACGTTTCTTTCAGGCTGTATCTTAGTGCTATGAAATCCAT
ATTGCTTCACGATCAGCACTTATCAAGATTAAAGAAAAACAAACTCCATTTATTTTTCCTTTA
TTGACAGATTCATGGCCTACATCCCTGTGAATAAATGAGCTGGCAAGAAGGGGAATGGGA
CAGCCAGTAAGCTTGGTGACATAAATTACCCTTGATAGGGAAGGCTGATGTGGGCATGTCA
TCAAATTAATAGCTGAATGCTAAGGACCATTACATTTAGCACTGTTTGCCATATCCTTCTATA
TAATAATGCCTGAGAATAATGTGTAATTAACTCTGTGGCTGACTGACAAGGCCAAATGCAG
GGCAATCAATCATATTGTATAAACACACGTCCCTGAGTACACATGGGAGGCAAAGGGTGAC
TTAAAATGTCTCAGCACTTTCTGCCTAGATTATGGCTCTGAGCTTTTGTGAGGCCAGCAGTC
ATAGAGACTCTTATCTATAGATCTAAGCTGCCTACAGCATCTTGGTATATAGTCTTCCTTGC
TATTTATCTTGACCTTTTACTTGTGTTCTTTGAGGGGGTGACA (SEQ ID NO: 44)

FIG. 22A cont'd

eHGT_741m (686 bp)

ATCTTCAGGTGTACCAGCACTGTGTACCAGTCTGTATTCTGTGGGGTTGGCTGACTCCAGC
CCACGCTGTGTCTGTAAATGAAGTTTTATTGGAACACAGTTTAGTGCTTCCTGTTGGTGATA
TAGCACAGAGCTGAGTAGCTCCAAGAGCAATTATATAGCTCTAAAAGCTGAGGCTGTTTAC
TTTCTGACCTGCTACAGAATAAGGCTTAGACCTCCTGAGTGAGTGTTCTCAAATAGCGATG
CTGAGTGGAATTACCTCAACAGATTCAACATTGTTCCTGAAGTACATTCATTATCATTTACTG
GTGTTTTAATTGGCTTTCCTTAAAAATAAAACAGAATTAAAGCTGTTACATGTAGAATTGTTT
ATACAGCAGAACCCGTATGGTGTTCCTTGAAGGACTGTGTTTGAGAGAATCGCCTTTAGAG
TGAGAATTACAAAGACAGTGGGTCACGTAGATTAATGGTTGAGATCCTCTGACCTAAGTAA
CTGCTACTTTTAGCTTTATTCTATTTTCAACTCGGATCTTTGTTTTTGTTTTTTACTAAGCAAG
TATAAGATGGTACCAAAAAGGATGTTGGCTTTCCGAAGGAAACAGTTTGCCACCAGTTTTTT
ATATTTTCTTCTGTGCCCTGTGCGTGCCTGCCTTTTCACTGCTCTAGCTAGTAACGCCCAC
GCTTGG (SEQ ID NO: 45)

eHGT_742m (600 bp)

TCATCTGCAGTCAATGAAGGTCTTTATTATCACTAAGTACGTCTTATGAGTTTTATATATTGA
CTTTCCTTAAGTAAGCCAAGAACTTATAAAAAGATCACTCAAATAGTATTTGCTATAATCCTC
ACACAATTTTAAGAGCAGGAGGCAGGAGGTCTGTAATGTGAAAACAGGAAAGCAGAGAGA
GGCAGGAGGTGAAGCAGATCTGGGTAATTTTAGCTGTTGGTAGAGAAATCATGAACACACC
CTGGCTTTAGTCTGCTGAAGTGGAAAGCTGTATACTTATTGTTGGAGCACAAAAGCAGACA
GCATGAATTGACTATGGTGGTAAACAACTTCAGCCCTAACACAAATGAAACTGGCCAGTGA
CTCATTAGGCATTTAGTGTTTTTACTAAGTTTTAGTTTTATGAAAACTAATTCCAGTCTAGTTA
TTGAAATACTCCATGGGTTAGTTACTTAGAGTTCAATGGAAACCATTGCTTTTCTTATTTTTT
TTTTTTTTTGTAAAGCAATTAACCATTGCTTTAAAAAGATTTTTGCTGGCTAAGAAAACAGTT
GATGTTCTGGGAGAAAGGAAAACCTGACTCTCACTTCATGA (SEQ ID NO: 46)

eHGT_743m (696 bp)

TCCGTAAAGAGCACAAAACCCAAATATTTGGGTGCATGGGAGATAGATTTCAACTAAATACT
TTTAATCATGCAATTCCAATAGCACTTAAATTTTTTCAAGGCATGTATAAAGGGAGAATAGAC
TAATTCAATTTCAAAGTGCAAGAAAAACATCAAAAACTAAATTCAGAAAGTTTGCATGGGAA
GAAAAAAAAACACAAATTAATCTCACTTGTGATTATTCTAAATACATTTGAACAAGCAGCAGC
TAGTAGTACATACAAAGAAATAGAAAACATGAAGACCAGGGGAGTTTAATTATATGGTTGCA
AAAATGGTTCAACATTGCAAAGTTGTTAATACTCAGTGGATGGGGAGGGAGCTGTGCAATT
ATCTCCACAGGTACAGAAAAGGCACTTAGTAAAATGTAGCCAACTCTTTGGCTTCTAAAAAA
GGAGAAAATGGTTTACAAAAACAAGCCTCCCTGGATGCTTCCTTAATTTGTTCTTATTCATA
ATGGGGGAACATAAAGTGAACTTCTGCACACCAGAAGTCAGGTTGTTTGCTTGCTAATACC
ATTCCCACTCAATATCCCATGGAAGTTGGATGACTCGACCTGCATCCCAAGGAGTAGTTAC
CATCACTAATGAGGAGAAGCATTTGGAAGGAAGACAGAATTCTGTAGACCAAACGAAGACC
TGGAGGCTAGTGGAAA (SEQ ID NO: 47)

core2_eHGT_743m (249 bp)

AGCAGCAGCTAGTAGTACATACAAAGAAATAGAAAACATGAAGACCAGGGGAGTTTAATTA
TATGGTTGCAAAAATGGTTCAACATTGCAAAGTTGTTAATACTCAGTGGATGGGGAGGGAG
CTGTGCAATTATCTCCACAGGTACAGAAAAGGCACTTAGTAAAATGTAGCCAACTCTTTGG
CTTCTAAAAAAGGAGAAAATGGTTTACAAAAACAAGCCTCCCTGGATGCTTCCTTAATTTGT
TCTT (SEQ ID NO: 222)

FIG. 22A cont'd

3xcore2_eHGT_743m (747 bp)

AGCAGCAGCTAGTAGTACATACAAAGAAATAGAAAACATGAAGACCAGGGGAGTTTAATTA
TATGGTTGCAAAAATGGTTCAACATTGCAAAGTTGTTAATACTCAGTGGATGGGGAGGGAG
CTGTGCAATTATCTCCACAGGTACAGAAAAGGCACTTAGTAAAATGTAGCCAACTCTTTGG
CTTCTAAAAAAGGAGAAAATGGTTTACAAAAACAAGCCTCCCTGGATGCTTCCTTAATTTGT
TCTTAGCAGCAGCTAGTAGTACATACAAAGAAATAGAAAACATGAAGACCAGGGGAGTTTA
ATTATATGGTTGCAAAAATGGTTCAACATTGCAAAGTTGTTAATACTCAGTGGATGGGGAGG
GAGCTGTGCAATTATCTCCACAGGTACAGAAAAGGCACTTAGTAAAATGTAGCCAACTCTTT
GGCTTCTAAAAAAGGAGAAAATGGTTTACAAAAACAAGCCTCCCTGGATGCTTCCTTAATTT
GTTCTTAGCAGCAGCTAGTAGTACATACAAAGAAATAGAAAACATGAAGACCAGGGGAGTT
TAATTATATGGTTGCAAAAATGGTTCAACATTGCAAAGTTGTTAATACTCAGTGGATGGGGA
GGGAGCTGTGCAATTATCTCCACAGGTACAGAAAAGGCACTTAGTAAAATGTAGCCAACTC
TTTGGCTTCTAAAAAAGGAGAAAATGGTTTACAAAAACAAGCCTCCCTGGATGCTTCCTTAA
TTTGTTCTT (SEQ ID NO: 223)

eHGT_744m (518 bp)

AGGCTTCTTCTGCAATGTGGAGTTTCTAGATCCTTCCTATGATCCAACCCCTCAGACTTCAC
ATCCTCTCCATCACCAGGACAGACGATCCCATTGAGTAACATCTGGCTTTTGCCTTCTGTG
GGCATATGGCTGTAGCTATCACAGAAGCATACAGATCTGCTAGGTTCTTGTGGGCAGCACA
CCCATGGTACCTTTTAAAGGGCCTGCTGTATTCGCTCTTTAACACTCAGCGTGGCATCAAC
CCAGTGGAAATGAACTGGGAGCTCCCTGCAGGTTCTGTGCTCCCTTGGCAGGCACAGCCT
TCCCACCCCACACCTTCCCCTGGAGCATTGAGCTCTGCGGGAACACAGGCTTGCTGAAGG
AACCAGCAGGGCCATCGGGAGCACTGGGCCTGGGAGGGAGATCAACAGCACAAAGTAGA
GCCAGCACAAAGTGGAGCTGAGAGAAGCCTTGGAGCATGAACAACATATCTGCACCCCAA
GAAAAGCCCTTAACCGAAGAGCAGAGCCATGGCA (SEQ ID NO: 48)

eHGT_746m (622 bp)

AGAGAGGGAGCAATTTCTTTCAGCAACGGAAATAGGCTTTGTTGTATTTTTTAAGTCCCCAT
AAAAATGTAAAGTTCTAACATCTCAAATTACCTTATGTTCCACAGGAATATTAGGTGTTAGC
GGATACTCTGCAGGAAATGAAAAATGATTACTTGAAACCATTTAATTGGCTTTCACTCAACA
AATACCAAAGTGCAATTTGTGGCCTGATTTGAATGCTAATGCCTGAATTACAGGCATGGAAT
CAAAGTGCTAGATGCTTTCAGTGCAGAATGCCAGTGCTTAATTAAGTTTTCCAGTAACTGTG
TACAGCAATAGGATTCACAGCGAGTGCGCGGATATTTAAGGTTATTTATTTCTGCTATGTGA
AGTATTTTTCCCTTGGAATCTTTGTTGTACAAATTGACATTTACCAGGTGGTGAAAAAGTTTA
CAATCTTGACAAATTCTTTCATTCAAATTAATGTTTTCCTTATCAATCATTCCAAACTTAAATG
CCTGTATTATTAGGCACACAGTTGGCATTTAAAAGTATGGATTAAGGAACTATGAATGCATC
TGATTTGTTACTCTGTATAAGCCTATACCAAATCAAATTGGTTGTGGTTTTCCAGAATTTT
(SEQ ID NO: 49)

eHGT_747m (776 bp)

AGTTTCGTGTAGTTTTAAAAACCCTATTTATTCTTTTCTTGTGAAATGTTTCAAATGAATTCAA
AGAAAATATGATGTTTTATTTCTTTACAAAAGGTGATAAATATTATTTTTATGAATAATATTCA
CATTGGGCCCCTATGTGGACGCTGAATAGCCCTAGTGTGGAGTAAGGTACAACCTTACTG
GAGGAAGGATATCACTATGGGGCTGGGCTTTGAGGTCTCAGAAGCCCAAGTCAATTCTCT
CACTGCTGCCTGTGGTTCAAGATAAAGAACTCTCAGCTCCTTCTCTAGCATCAAGTCTGCC
TCTACACTGCCTTGTTTCCTGCCATAATAATAACAGACTAACCCTCTGAATTGTAAGCCAGC
CCCAATTAAATGTTTTCTTTATAAGAGTTGTTGTGGTAATGGTGTACTTTCACAGAAATAAAA
TCCTAACTAAGACATTTTCCAAATTGTATACCCTTGATTCTTTTTAGTTCTTGTATTGCTCTA

FIG. 22A cont'd

GGTAGAACTTCAAATACTATATTGAAAAGACATTGGTAGAGTGGGCAGCCTTCTCCTATTCC
TGATTTGAGTTGCCTCTGGTGGAGCAAGGGGTTTATGCCTGGATAGAATGACTTATTATAG
AATGACTTAGAATGAATGGGGTTCTTGGTGCTGGTATGGCCTCTGGTTGTGAAGGCTCTGG
GGAAGTATTGCTCATTCATGAGGTGGGGGCTTCTCTAAAAATCTTCATGCTAGTATAGCCT
CTCGGGGATCAGGGTCTGCTGGAAGTGTGCATAA (SEQ ID NO: 50)

eHGT_748m (518 bp)

ACTCCTCTGGTATACTGCAGAAAATCCTTCCAAAAATCTTCACAACAGTGAGGTTTTTAAAC
AGGTTGGACTCAAAGCATGGAGAACGGAAGGAGAAACACAGTGGGGGCAGAAATTCCAGA
GGCAAGCTGAGCTGGAAAACACATGGCCATAATCAGGGGGTGGGGAAACAAAGCATTCCC
ACAGGACAGTGGGAGGCACAGAGCAACCCAATGTCACTTATACACCTTATAGAAATCCTGG
CAGAGCCACCTACAGACTAGCTTATTAATATCCCAATGTTGTTTTCAGGAGAGACTAAAATT
CTAAAACGCTTTTTAAATGATGTGTTTTGTATACACAAGTTTTCACCCACACCACTTACAGTT
TTCCAATAAAAGCCTATCTAAATAAACAGTTTAAATTCGTTACACGGGGCTGCATATTTCAG
TTCTGAAATCAAAGATGGGAATCAATTTGAATTATGACTGAAATCACCATTTAGAAAATGGT
CTCATACTGGATGGGTTGTTCTCAGA (SEQ ID NO: 51)

eHGT_749m (696 bp)

TGATGTCCAGGTTGGCTGTTCACCAAGGACACCCAGAGAGACTGTATGGTCTTAGAGAGT
CTGAGTGGTAGCACATATTTGAAATAGAAAGCACCACCCTACCCCCAGATGGTCTCTGCCT
CCTCCACCTACTGAGGTGACATCTGCACTTCCTATGTAATCTTTACTCACACCTCTTACAAA
GACAGCATGTCGTCATCCTGACCCCAGCAGCCAGCCGAGCTGGGCTTTCCAGAAGTCTTC
AAGCTGGAGGAGTGGGAGGCACCATGGCCTGCTCAAGGGGAACAGAGTGAATTGATGCC
AGACGGTGGCAGGTGGCTATTTTCACTTAGCAGTTAGTGGCTAATGAAAGAGGTGTGTGG
GTATCTTTCTCCCCAGAGGCCATTCATTTCTCTCCAGCTGAAAGAGCAATGGACTGATCTG
AGGCAGGACCAAAAGTTCAAAGGAATTATGACAGATTGGCCCAGCACCCCTGAGTTTATCT
GAATAATGACGCATAAGCACCATCCAGTGTTGACAAAGCTCTGCAGGCTGTGAAGGCTTAA
GGGGAGCCTTGGAGCTAAGCACAGAGGGCAATGATGTTGCTTAAATGTGCACAGGTCTGG
ATTAAAGTGGAGTAGTTCTTAGGCTGCTCATGTCTTCTTAATCTTCAGCTAGGATTGAGACT
AGCCTCCATGACACAGGGGATCCATGACA (SEQ ID NO: 52)

eHGT_750m (684 bp)

TCCTGCGNCCGCACGCGTGCTCAGTTGCCAGCACACAAATGATGTCACATGAGCATCTATA
ACTCCAGTTCTAGGAGATCTGACACCCTCTTCTGACCTTCATTGGCACCAGGCTCTCAGTG
TTTACACATACATGCAGGCAAAAAACACTCATACACACAAAATAATAAAGAAATTTAAAATTA
AGAAAGAGAAAATCATAGTTTTAGTAGCTTTTCTCTTCCATTTGTTTGATTTCTTGCCTTATG
ACATTGTTTATTGTGTTCATTGGTGACTGTCTTTACACTGAGGATTCTATGAATGGGCAGTT
TGGAACACTTCTAACGCTTTGTACTCTGTCACTGGCATGCTCACAGTGTATACCACCTACCA
CAGAGGAACATCCATTGTTTAAAAAGCAGTTCAGGTTATTTTGAAACACTAATACAAAATAAT
TTTCAGCTGTAACGATGGGAATATAACAATTTCCTTGACTACAAAGAGAATATAACAAGTGC
CTATGATTCAAATGCAAAAGACACCGAATATCCATCAGTGCTTTTGAAAATGGCAGGACTTA
CTGTATTGACACTTAACAAGCTTTTTTTTTTTTTTGTCTGAAGCTTGTTTTTAAATGTTGGAAT
TTTAGTTGAAAAATCTATGTCACTCTTTTACTGCAGTTTTCTGCTTTCATAACATTTTCAA
(SEQ ID NO: 53)

eHGT_751m (533 bp)

GCTTATATGTGTGGGCAATATGTATATATTGTTACTTTATATGTATGTGTATAAAGAGAGACT
GTTAACATGTTTTCAGAAACTCTTAAATACATATAAAGGCATACACAAATATCTGCAGAGGT
AATTATATTAAAGTGCAGAGTTTAGCTACTATGTTTTGCATTTGTAAAATGCCATAGAAACAT

FIG. 22A cont'd

CAGCTCATTAATTTTGTTCACCTCGTAGGACTATTATTCAGAATCTTTATTCAGCCAGGGAG
GGCATTTTGTATTTAGCTATTACTTGGCTCTCTCCCTTTTGTCATACCATGGCAGGTAGTCT
ATACTTAAACCTGAAATTTTTAGTGTCAAACTTGTGGCAAACAAAGTCCCCTTGTTCCTTAG
CTAATGAGCACAAGGTTGGGGTTTACATACTATCACTAGGCTTTAAGGTGAGGACCGTTGT
CCAGCAGAGGGGCCTGTCATTTTTGAGAGGTATTTGTGTATTTTATAAACCAGCCAACTGT
CTTTCTTTTCTTTTCCACCATCACTCATTTCCTTCCA (SEQ ID NO: 54)

eHGT_779m (506 bp)

TCTCATCCTATGCCTTTCTTCTAGGTACTTCAGAAAGAATCTTTCAAATCAATAACTGTGTTC
TATCCACAGAGGTTTAATGGAGGAGCAGGAGGCTGGAACGAGATGAAGGAAATGAATTGT
TCCAGAGATGAAAAAGCTCCCAGGCATATGTCATAAGTTTGAGACAAATTAAGGAAAAGCG
GGTTGGGAGGAGTCTGAGGCTGTGGGTGGCTGCCTCGAGAGGCTGCTCACAACCTGACA
TGTTTCAGATCTTTTGACACGGTCATGCAAGCAACAGAAACTTATATGGTTTTTAGTCTCCC
AGGTAGCAGGGAAATGATGATGTGGGAGGATTAGGGGGGGGGAAAATGAGTTTCTCATTTT
TTTAATTTAAATTACTTTTGAGCTACTTCTAGACTGCAGCAGAGTTGATAAACCACCCAGTTC
ATATACTCAAACCTCCCAACTCCTCCACAGCTCAGCCAAAATTTCCCAAGGACTTGTTTTAC
CCAAATCCCAGCTCCG (SEQ ID NO: 55)

core2_eHGT_779m (194 bp)

AAGTTTGAGACAAATTAAGGAAAAGCGGGTTGGGAGGAGTCTGAGGCTGTGGGTGGCTGC
CTCGAGAGGCTGCTCACAACCTGACATGTTTCAGATCTTTTGACACGGTCATGCAAGCAAC
AGAAACTTATATGGTTTTTAGTCTCCCAGGTAGCAGGGAAATGATGATGTGGGAGGATTAG
GGGGGGGAAAAT (SEQ ID NO: 224)

3xcore2_eHGT_779m (582 bp)

AAGTTTGAGACAAATTAAGGAAAAGCGGGTTGGGAGGAGTCTGAGGCTGTGGGTGGCTGC
CTCGAGAGGCTGCTCACAACCTGACATGTTTCAGATCTTTTGACACGGTCATGCAAGCAAC
AGAAACTTATATGGTTTTTAGTCTCCCAGGTAGCAGGGAAATGATGATGTGGGAGGATTAG
GGGGGGGAAAATAAGTTTGAGACAAATTAAGGAAAAGCGGGTTGGGAGGAGTCTGAGGCT
GTGGGTGGCTGCCTCGAGAGGCTGCTCACAACCTGACATGTTTCAGATCTTTTGACACGG
TCATGCAAGCAACAGAAACTTATATGGTTTTTAGTCTCCCAGGTAGCAGGGAAATGATGAT
GTGGGAGGATTAGGGGGGGGAAAATAAGTTTGAGACAAATTAAGGAAAAGCGGGTTGGGA
GGAGTCTGAGGCTGTGGGTGGCTGCCTCGAGAGGCTGCTCACAACCTGACATGTTTCAGA
TCTTTTGACACGGTCATGCAAGCAACAGAAACTTATATGGTTTTTAGTCTCCCAGGTAGCAG
GGAAATGATGATGTGGGAGGATTAGGGGGGGGAAAAT (SEQ ID NO: 225)

eHGT_780m (534 bp)

TGTTTCACAAACTACAGGTTCACTGGAGCACAGCCATGCCAACATGGCATCTAAGGCTGGT
ATGACCTCGAGACCCCTCCAGCACTCCTTCGTTCAGCCATAGAACAAGGAGACACAGATAA
AGTCTGGAGCCGGGCCCAGGTACCTGAGGCTCAGAGATGAGCCCGCAGCGAAGCTGACA
ACTGACTCATTCCTCCGACACTCTCCCACCCTCCCAGCTAAGGAGGTGTCTGATGTGAACA
TGTTCTGCCTCTTTGTTGCCTGCTGTTGGGGGCGAGGGCTTTGGGTGGATTTTGAAGAGC
AATTATGCTTATTACTGGTTAGGATTTCTCTGTTTGCTGAGTGCATTAACTTTTAGCGCTTCC
CATCACTCATTCTTCTTCACACCCTCTTGTCAGTTACAAATGTGCAGGTGGAGAGCCACGA
AAAAACCCTGCAGCAACGGCAACAGAAATCACAGCAACAACAACAAATGAACAGAAAGGAT
AGAAAGCAGATACTCAAAGATGGAGAAAAAGATACTCCCGAGAGGCT (SEQ ID NO: 56)

FIG. 22A cont'd

Core2_eHGT_780m (200 bp)

CAGATAAAGTCTGGAGCCGGGCCCAGGTACCTGAGGCTCAGAGATGAGCCCGCAGCGAA
GCTGACAACTGACTCATTCCTCCGACACTCTCCCACCCTCCCAGCTAAGGAGGTGTCTGAT
GTGAACATGTTCTGCCTCTTTGTTGCCTGCTGTTGGGGGCGAGGGCTTTGGGTGGATTTTG
AAGAGCAATTATGCTTATT (SEQ ID NO: 226)

3xCore2_eHGT_780m (600 bp)

CAGATAAAGTCTGGAGCCGGGCCCAGGTACCTGAGGCTCAGAGATGAGCCCGCAGCGAA
GCTGACAACTGACTCATTCCTCCGACACTCTCCCACCCTCCCAGCTAAGGAGGTGTCTGAT
GTGAACATGTTCTGCCTCTTTGTTGCCTGCTGTTGGGGGCGAGGGCTTTGGGTGGATTTTG
AAGAGCAATTATGCTTATTCAGATAAAGTCTGGAGCCGGGCCCAGGTACCTGAGGCTCAG
AGATGAGCCCGCAGCGAAGCTGACAACTGACTCATTCCTCCGACACTCTCCCACCCTCCC
AGCTAAGGAGGTGTCTGATGTGAACATGTTCTGCCTCTTTGTTGCCTGCTGTTGGGGGCGA
GGGCTTTGGGTGGATTTTGAAGAGCAATTATGCTTATTCAGATAAAGTCTGGAGCCGGGCC
CAGGTACCTGAGGCTCAGAGATGAGCCCGCAGCGAAGCTGACAACTGACTCATTCCTCCG
ACACTCTCCCACCCTCCCAGCTAAGGAGGTGTCTGATGTGAACATGTTCTGCCTCTTTGTT
GCCTGCTGTTGGGGGCGAGGGCTTTGGGTGGATTTTGAAGAGCAATTATGCTTATT (SEQ
ID NO: 227)

eHGT_781m (621 bp)

AACCTCAGTGGTTTCAGCCACCATGGAAGAGAGAGAGACAGGAGTCAGAATGTAAAGGCA
TGGGGTTTGGTGGACCAGAGAGAGAGATTCTCAGTGCAGTGGGAATTGGGCTGCTGGGC
AGAATATACATCCCATAGACTACTCCCCCACCCCCTACGGTGTAAGAAAAAAGACATCTCT
ATGACTTGGCTTGCACAAACTTTCTTGTGTGCTACCTTTGCAACAGCAGATCTCAGGCAGG
TGGGTGGATGGGTGTGGAGGAGGAGAAAGCAGAAAGACAAAAGGAAGTGAGTGGGGGGA
ACTCTTGGGAACCTGTTGGCAGAGCGCTCTGAGACTCTGAAGCTAAGGGACCATGTTATGT
TAATCTATTCTCTAATTGCTCAGCAACAAACACCTCCCACCCGCTGCAAGGAAGGGCAGGA
CAAGACTATTCCAAGATCTGCTTAGAAACAATGTCAGTCACAGCAGAGGGCGCAAAAGAAA
TGGACCTCTTTTTAGCATAATTGAAAGACACTACTTACAACTGAGGGGTCTGAGTTGCTGAC
AGCAACCGCCTTAGCTAGGAGGAAAAGCTGAGGGGTAGGCTGTGCTCAATGGGAGGGTTT
GCAGGCTGACTGTTCA (SEQ ID NO: 57)

eHGT_782m (609 bp)

AGCCTGAATTCCACACTACAGCTCTTATATTAGAAAAGAAACTGGATGAAAAAAGATGGGTC
TCAGAGAAGATACTTGGAGCAATAGCCACACAAGAGTTGCTCAAGTATTTCCATCAGCCTA
AATGACTACACACCTATTTGCCACCAGCTGGCCTCAGCTCTGCTCTGAATGCCCACCATCA
ACTCTCTGAGAAAGTGCCCCTGACTACACTCAGTGAAGCTGTGAGTTGGTGGCTGCCTTTT
CCCCCTGCAAGATAACAAGGTAGGCCTTACCTCAGACTTAACTCAAGGTAAAGTTTAATTG
CTCTAACCTGCTCTTTGATGTGTGCTGAGGAGGTGGGCGCCGTGTGGGTACAAGTTGCTA
TTTATACAGACCTGACAAGCGCATCCCATCAGCACCCGCTCCTTTGTTCTCTTCCAGGCTTT
TCTGATTCTCCAAACTTAACATCCTGCACTCCCCCAAGTTGTTTAATCGTTCCAAAGTTTGT
AAGACAAGCAAGGGAATAGTGGCCTTCACATCTGCACTTGCAGCCCAAATATGGTGCACTG
TGAGAGATCCTTAATTTGGAGAGGAAAGCCTGCTGCTGACCACCTGCCTCTTAGAACT
(SEQ ID NO: 58)

FIG. 22A cont'd

eHGT_783m (679 bp)

TTCCTGGACACTGAATTCTGAGAGACAGAGGTAGGAGAGGGGAACCATGGGATGTGACGA
TTTCAAAGATTTACCCTGGGCACTGTATAAGAAAACGTTTTCCAAAGTGTCTGACACTGGGT
CTGACTGACACAAGGCACCAGCAAATGTCACCTCTCTTCCCTGTGTGTCACACAACTTCAT
TTCTCTTGAAACTAAAACTTCTCTTCTAGTTGCCCTTGACTTCCAATGTCACCGTTCTCTAGC
CCATACCCCATTACTAATCCTCCCCGCCCGGTTCCGCCTACGTCCCTTTTGTTCCCACTAA
AGATGGCTTTGCTTTTTCACCTGTTTAAGTCTTCCTGCCTCCCACACTGATGAATTCAGTTA
GACTGAAAAAAAAAAAAAGAGGCCTCTTCCTCCATAAAACCCCAATTAATCAATCATTCACG
ACTGAGCAATTTGGGGTGATGGTATTTAGTGGGAAGAACTGCTCCAGCACTGTCAGGCCT
GGGATGTGACACTAACAGCAGTGAGACCTAAGAGGAGTAATTTGGCTTTTTTCATATCTCA
GTTTGCTCACTCACAGTACCTTAACTCTTAAGACCGGTAAGAGTGAAAATTACCCCCAGAG
GAATCCTAGGGCAAAGACAGCCAGGTGATCATCAGTATAAACTAAGGATGCCTGTTCATAC
CAGCA (SEQ ID NO: 59)

eHGT_784m (490 bp)

AGGAACTGGACACACAAAGCCTTTCTCGTTTTTTCTTCCTCCCTGTGTTTCGGTCCAGGGG
TCCTAAGTGTGTAGCTCCCGGGGAGATGTGGGACTGTTCTCACCCAGAAAGAGGAACTAG
AACCACAAGAGCCTAACCCCCCCACGGTGGGAAGACACTCTGTGGCATCACCGGGAGGGG
AGGCCAGGTGTGGGCAACTGCAGCTATTTCTAATCCACCAGAGGAAAGAGAGCTTTGACT
GCTTGAAAAGCAGGCTGATTGTCAGGGGCGGAACCCAGCTCAGAGCTGTCAGGGAAGCT
CCTGGCAGGGGGTGGAGACAGGGGGCTTGGACTGACAGGCCTGTGATTTTGAAAGAAAT
GTCTTTAAGAGAGTGACTTAAAGTAGGAGAGAAATATTATTATTAGGTAATGCCTGTCAGGT
TATATTTTTTTTTGATGTGTTCTTGGTATTTCATAATCATTTTGCCTTTAGATGGTAAGCCCTT
CCTGGT (SEQ ID NO: 60)

eHGT_785m (625 bp)

TAAACCTTGGACTGAGCCCACAGGATGCTCTGGAAGGACCTTGGGAAACCGACACACAAA
GCCTGTCTCGGTTTTGTTTTGTTTTGTTTTGTCCTCCCTGTGTCGCATCCACAAGTCCCAAG
CGTGTAGCTCCTGGGAAGCTATGTGGCTGTTTTCACCAAGGATGACTTCTCAGAGACTGAC
ACCCATAAGAGAGGCCCCTCCACCCGAGGGTGGGAGGACTCTCTGTGGCATCACCGGGA
GGGGAGGCCAGGTGTGGGCACTGCAGCTATTTCTAATCCACCAGAGGAAAGAGAGCTTTG
ACTGCTTGAAAAGCAGGCTGATTGTCAGGGGCGGAACCCAGCTCAGAGCTGTCAGGGAAG
CTCCTGGCAGGGGGTGGAGACAGGGGGCTTGGACTGACAGGCCTGTGATTTTGAAAGAA
ATGTCTTTAAGAGAGTGACTTAAAGTAGGAGAGAAATATTATTATTAGGTAATGCCTGTCAG
GTTATATATTTTTTTTTGATGTGTTCTTGGTATTTCATAATCATTTTGCCTTTAGATGGTAAGC
CCTTCCTGGTCCTGGGCCATGAACTATGCCCCTCGGGTCTCACCCCAGCCTTGGACATGC
AATGGGCACCAGGAGGTA (SEQ ID NO: 61)

FIG. 22B

CN2438 (bp between ITRs: 2005)

GCGGCCGCACGCGTTTGAACCTCCGACTGCAACACAGATTAGGATACAGCAGTGGCTACA
ATTACACACTTGCTTGGGAAGTTGGGTTGGGAGGGGGGGTGGGTGCTGCATGTGACAGG
CCATGAAAGGTCCCTGCCTATAAAACAGACTGAAAAACAAACCCTTAATTTAAATGTTAATG
AAAGTGCTGTGGAGACATCAGAGGCTTCCCGGCTGCTCAGAGAACAGCTACACCAGCCAC
AGAATTTATGGCTCCCCTTCACCCTCCCGCCTCCCTCTCTGCCTCATCACCCACTGAAATTT
AAAGACAGAAAAAAAAGAAAACTAATTTTAACATTAACTCCATGCTTCCACTTTGGGATGTG
ATTGCTAAATTATCTGTTGGCAGAACGGTGATCAAAGGTGGAAAAACACAGGCACGTTGCA
CACACAACCCAGAAAAGTCAGCAGCAGCTAAAGCAGGAAAATTCCCATTTCCCTTCCTGAT
GAGCAGAGTGGAAGAAAGAGTGGTGCAGGTAGGGACTGGAGCCAGGAGGTGTAGGCAGT
GGGAGGAAGAGAAAGATGACTGATCCGTCCAGCGTGCTCCCAAGGCCCTGTCTCAACCTC
ATCTGAGAACTTACCACACTCTACTACCTATTTTACTTGTCGGTCTCTCCCATCAGAGCTCG
GGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGA
TCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCAC
CGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCG
TGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGC
ACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGT
GCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCAT
GCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGAC
CCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCA
TCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCC
ACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCC
GCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCC
ATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTG
AGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGC
CGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGC
GAATTCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTA
ACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATT
GCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGC
GGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTG
ACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTT
GCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATA
AAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTG
GGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGC
GGACCGAGCGGCCGC (SEQ ID NO: 62)

CN2439 (bp between ITRs: 1719)

GCGGCCGCACGCGTCTTATCACTTCCTAATTATTTTCTACCTTTTACTAACCTATGCTCTGG
AGATTTATAACTATTATATCTGTGTGGTGCAAACATCATATAATGGTGTGCTACTGCACATT
GCTTCCCAACTCTGCATGACTCTGATGTCACATTGATAGCTTGAAATTGGCCATGGTGGGT
GTAGCTCTACAATGAAAATCAGCAAATGCTACGAATCAAGACTTTTTTTCCCTCTAATGTTG
AACATTTAAGAACACATTGTATAATATCCTAAGAAGATAGTCAAAATGCACAATGGCCTCCT
TCTATCCCAAATAACCAGCCAGATAAGCAAGCATCTGTAATGTCCCTCAGAAACCAAGTGC
AGCCAGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTT
CTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGA
GGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCC
ACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTG
AAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCT
GGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTT

FIG. 22B cont'd

CAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGG
CAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCG
AGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTAC
AACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCC
AACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAG
CAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTA
CCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTT
CGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCG
CGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATT
GACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTT
TGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAG
TTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGG
CTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAG
CCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTG
TCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTG
GGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATG
AGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 63)

CN2451 (bp between ITRs: 1764)

GCGGCCGCACGCGTTGCTGAACCAATTAAGGCCAGTGGTACCACCTGAGATTTTGAAAAT
AAATCAGTGGGTTTTTATTTCAGCTGTTTGGAAATGACTAATAGAGTAATACAATAGATTAAT
TTTATCTAACATTAATAGCTGGATGTATAAGAAACACCCACTCTCTAGAAATTAAGACATGTC
ACCATAGTCTTATGACAAGAGTGAGTCTCTTATTTTTGAACTTTCTATTGAACAGTTCTCACC
ATCTTAAATCACCCTTTGTTATGAGTTTTTAAGTGTCTTAAGTAGAGAAGGTTAAGAAAATGA
ATACTTATACTCCTTTAAATACTAATTAAGAGGCCCTGGTAACCATTTATCAGTAATATTAAT
GGCATGAAAATTGAAAAAGTATGACTCAAAGGTGAATTCAGGGCAGAGCTCGGGCTGGGC
ATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAA
GCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGG
TGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGC
GAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGG
CAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCT
TCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAG
GCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCG
AGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCA
AGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCT
ATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACA
TCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGAC
GGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGAC
CCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCAC
TCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGAT
ATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTG
CTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGT
ATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCAT
CGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCG
TGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCC
CCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGA
AATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGGTGGGGTGGGGCAGGA
CAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAG
CGGCCGC (SEQ ID NO: 64)

FIG. 22B cont'd

CN2463 (bp between ITRs: 1965)

GCGGCCGCACGCGTTTCTTCCACTCCTTTCCCTGCTGCAGGAATCAGTCCCCTGGACTCT
GATGTGTGGCTGGGTTGGCTGGGTTGCCCTGGGCAGACTTATTAGCTTGGACTCTTTCGC
ATGCAAAAGATAGCACCTGTGTGACTGTACATATTGAAAATGCAATTGCAGGTGTATTTGCA
AATTGGATTTTGAGGGGGAAATTTAAGCAAATCCTTTTGAAAGCAAATCCCTCCAAGGTGTG
AGTAATAAAGAAACAAGAAGAAAGGTGTCAATCAAAAACCTATTAAAATCTAGTTTCCAGAG
AAGAAGCTGACTGTCTAATGACATTTATGCTTTCATAGCTAGGCATTTAACAGTCATTTTGT
GTCAGTTGCTTCCTTTATACATGTCACGTGGCACATTTTTCAGTTTTCTGTATTTCTGAGACC
TTAATCCCAATCACTCTTAAATGCTTGAAATGAGCCCATGTTCCTAAAAGGAGGGGGTTTTT
GTCCACCTGAATTTCTCTGCAGGAATCTACAATGATGCCTCAAGCATCAGTATATGAAGTCA
ACCACTGTCATTCATCCAATTCATTCATTCCATTCATTCTTTTAGTTAGCCCTAAAACTCCAT
GGTGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCT
GGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAG
GAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCA
CAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGA
AGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTG
GGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTC
AAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGC
AACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGA
GCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACA
ACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCA
ACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAG
CAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTA
CCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTT
CGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCG
CGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATT
GACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTT
TGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAG
TTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGG
CTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAG
CCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTG
TCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTG
GGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATG
AGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 65)

CN2464 (bp between ITRs: 1980)

GCGGCCGCACGCGTCAACTCGCTTAGAGTCACCTGCTAGAGGTTTCTGGTTATTTGGAGA
TTTGCTGGCTCTGCCATGGACATGATGGCATATTCGTGGATGATATGGAGAGTGACAAAAT
GGCTGAGTGTCTAATTATTAATCAAATCACAGATTCATATCTCTCTCCCCCTCCTCCACTAG
TTTCCTTGGAGACACAGTTTTTTGTCAATTTTTTGAATTGCATTAATATTAACTATGACTTTGA
ATCAGGAAGAATGCAAAATATCTGAAGAGTAGTATTTATATCTTCCACGTGACATTTGCATC
ACATGGATAAACTTTAAAAATGTTCTTGAGAACACGGGAAAATAAGGAAATAGAGTTCAAAA
ATAAAGTATAGAACTTGTTAGACTAGTTTCTGTTTAAAACTCGGTGGATTATACCTCTTTGTT
TTAAACCATTAGAACAGCAATGATTAAATATCAGATTCCTTAAAGAGTCACCAGTTCCTTTTG
GAAAGTTTTGATTAAAGCATTGTATTTATTAAACTGTTCTACCCACACATCTTTCCTTCAAGA
TGTTGTTTTTCCCACGTCTACTGTTTTATTACATGACAGTTATTGAAAGGTTAGATGTGGTTT
AATTTCTCAAGGTGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTAC
ATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCA

FIG. 22B cont'd

AGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTA
AACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCT
GACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGA
CCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCAC
GACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAG
GACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAA
CCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGC
TGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCA
TCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGAC
CACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTA
CCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCT
GCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGT
CGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATTACAAAATTTGT
GAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTT
AATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATC
CTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGG
GGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTA
GTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCA
CTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCAT
TCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAG
CAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 66)

CN2465 (bp between ITRs: 1750)

GCGGCCGCACGCGTTGGAGAATACATTCTTGACTCAATGAATACTATCACTTTTTTGGTTAA
ACAGTCCAAATTTGACATCCAGAACATTTCTTTAAAGTCACCATTTTCCTGGAAACACTCTAA
TTTTGAGATGTCTAGGGCTATATTTAGCTTTTGAACAGTAGTCTTTGAAAAAATATGGTTATG
AAACAGATTGATTTAGAGGAGCATTATAATTAGCTGCCGAATACGTTAGAAGGATAGATTAT
TCTACATGAATCACAGAGCTCACTTTAAGTGTCATTCCCCATTCTAAACTGCCAGCTTAATT
TCTTCTCATTTTTCACCACGAGAGCCTTTTTTCTATTATGCCAATAATAAAGGGTTAGTTGTC
ATGAAATAGGCATACCTTTGTGAAATAATGAGAGCTCGGGCTGGGCATAAAAGTCAGGGCA
GAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGG
TCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTC
GAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCG
ATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGC
CCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCC
GACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAG
CGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAG
GGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAA
CATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGA
CAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGG
CGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGC
TGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGC
GCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGAC
GAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCT
CTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTA
TGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTT
CTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTT
GCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGAT
CTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTT

FIG. 22B cont'd

GACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCAT
TGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGA
GGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ
ID NO: 67)

CN2466 (bp between ITRs: 1992)

GCGGCCGCACGCGTACTAAGGAATAGACAATGGGTTCTTTATGAATATGTGAGCATGCCTA
AAAGCAACAAAATCACACTTTTGTTAAAGCATTTGTGTGTATTTTGCACAATTTTTAAAAGTT
TAACCTCTGTAGATCAATGTGCTTCCTTAAAAGACTTTAATAAATTAAAGTGCAGAGAGCTTT
TTTTCACCAGGCAGAAAAAGCTGATGAGACAGGTTTAGTTTAATCTCAGGCAATAGAAGTC
ATTAACCATTCTCTCAGGGATTAAAATATAGCTTGCCCTTTTCTTCTCTCACTTATCATTAGC
ATCACTTTAATCTCCTAGCGTTTCACACTGCTATTTTAATCATTACTTACTGCCTTTTGACAA
GTGCAGAACATGCTTTTTCTCATTGAGGCAATATCCTGGTTTTAGCTGACAAATGTAGGACA
TAATGTAAAAATATCAAAGTGACATCTCTTAAACACACCTTCATCATAAAAACTCTAAAGTTA
CAATATTCCTTTGTCTAGTATTTCCATGAAAATTATCATTTGAAAGGTTTATATCTTAAATAAA
GAAAAAAGTTTCTTCCAAATACAACAAAAACTAGTTTAGAGAAATAGTATGCTGAATAAATGA
GATCTAAAAATATGCACATACAGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATC
TATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACC
ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGA
CGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCT
ACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCC
ACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACAT
GAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCAT
CTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACA
CCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTG
GGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAG
AAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCA
GCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCG
ACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATC
ACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGT
ACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATT
ACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGAT
ACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCT
TGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTG
CTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTG
TGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGA
AGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTA
GGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAA
GACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 68)

CN2013 (bp between ITRs: 2015)

GCGGCCGCACGCGCCGGTACCGAAGCTACCCCTAACACACTATTCTACACACAGAAAATG
CTCTTCACTAGGAAGCTACCCCTAACACACTATTCTACACACAGAAAATGCTCTTCACTAGG
AAGCTACCCCTAACACACTATTCTACACACAGAAAATGCTCTTCACTAGACGCGTAGACTG
AGGAGACGCCTCAGAGGAATTTGTACGGGGAAAGGTCTGAGGAAAAAGGATCGGATCCCA
ATGGGCCGAACTCCTTCAAAATGTTCCCGAGGTCCACGTGACGTTCCCTCCTCCCACCCA
GCCCTTCTTTCTGTGAAGGGTGACACACCTCCTAGAAAGAAATCTGACTCCCCTCATTGTG
TTTTTAAAATAACTCTCATTATTCCTCCTCTGAAGGTTATTTTCAAACTCTTTATAACTCGATT
TTTTTTTAAATGCAAAGACAAGGAATCAAATCTGCCAACTTTCTATCAGAGAAACTCGGGTT

FIG. 22B cont'd

TCTAACTTTTAAAGTGGGATTATATGTCTTCTCCAATATATGGGCTCCCTGCTTTTATAACAT
GCTGCTGTTACATCTAATAAAAACCATTTTGAATGAAGGCAGCCTTTCATCGAGCTCGATTC
AGCCGGGAGCTTAGGGAGGGGAGGTCACTTCATAAGGGCTTGGGGGGGGAGTTGGAGCC
ACGAGTCGTCCAGCCGGAGCCCCGTGTGGCTGTGCTCCGGCCTCAGAAGCATCCCCGGA
TCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCT
GTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGT
TCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTG
ATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTA
CGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTC
CGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTA
CAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGA
AGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACA
ACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCA
AGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAAC
ACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTC
CAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGAC
CGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGC
GGCCGCGAATTCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGT
ATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCAT
GCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCC
ACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGG
CACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGT
TGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCC
TAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTG
GGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCA
CGTGCGGACCGAGCGGCCGC (SEQ ID NO: 69)

CN2025 (bp between ITRs: 1993)

GCGGCCGCACGCGCCGGTACCGAAGCTACCCCTAACACACTATTCTACACACAGAAAATG
CTCTTCACTAGGAAGCTACCCCTAACACACTATTCTACACACAGAAAATGCTCTTCACTAGG
AAGCTACCCCTAACACACTATTCTACACACAGAAAATGCTCTTCACTAGACGCGTTAGCAG
GAGTACATCCTCCTCTGTTAGAAAAACAACTCTGCGGTTCTGGGTCACTTTTCCCATCTTTG
TATAGAAAAGTACCGATTATTATTGTTCCCCCGGGTGCCTTCTCCAGCTTAAAGGAAAATTC
CAGCCCCAGAGATCTTCCGCAGTGAGTGACAGCTCCTTAATGTGAGGAGCAGCGTGGGCG
TGGTGGGTGGGATGTCAGAGCCATCAAAGCCCTCATTTCTGATCCCTCTGTGATGTCGGG
GTTCCCTGGCACGCCCACTGTCATGCCTCAGCACATTGGCATCTGAGAGAGGAAAGGTGC
AGCTGACACCCTGACCCCCTTCTCCCCGACACGGGGTCAGACAGGGTCCCGCGGTGGCC
TGGTTGTGCAGCACTGACATGTTGCCTGGGAACGAAGAGCTCGATTCAGCCGGGAGCTTA
GGGAGGGGAGGTCACTTCATAAGGGCTTGGGGGGGGAGTTGGAGCCACGAGTCGTCCAG
CCGGAGCCCCGTGTGGCTGTGCTCCGGCCTCAGAAGCATCCCCGGATCCAGATCTTTCGA
AGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTG
GTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGG
CGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCG
GCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGC
TTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAA
GGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCC
GAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTT
CAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGT
CTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAA

FIG. 22B cont'd

CATCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCG
ACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAG
ACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATC
ACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCG
ATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGT
TGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCC
GTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTC
ATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTC
CGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTC
CCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAG
GAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAG
GACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCG
AGCGGCCGC (SEQ ID NO: 70)

CN2229 (bp between ITRs: 1786)

GCGGCCGCACGCGTGCCCACCCCTCCTCCAGCTCTCAGGAGTCCCATTCCCTTCCTCCTC
TGTCGCCCACACAGCCCCCACCACCTGGCCGCCCACCTGAAAAACTTTTCCCCAAGTTCTT
GAGAAGTCGCGTAGGATCCAGGAGAGAAAAATCAAAGTAATAAAACCTCATTTAATTCCTAA
CGGAGGGCAGAGCTGCGAGCTGCAATTATCTTAATGCTGAGCTATTTTTACTCTCTCTCCA
TCTCTGTCTTCTGCCTTTCTCTGTTGTGAGGTTCGCTGTCTCTCTCTCTGCCTCCCTTTGTC
TCTCCATCTCTCAACCATGTTTTCTGTCTCTCTTTGCTTTCTCCTCTCTCCCCCCAATCTCTC
TCTCACGTCCTGTCTCTGTGCAGTCTCTTCCTCCTCCTTCATGTCTGTCCCTCTGTCAGCCA
GTCTTCCCCACGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACA
TTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAA
GGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAA
ACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTG
ACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGAC
CACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACG
ACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGG
ACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAAC
CGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCT
GGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCAT
CAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGACC
ACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTAC
CTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTG
CTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTC
GACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATTACAAAATTTGTG
AAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTA
ATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCC
TGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGG
GCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAG
TTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACT
CCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTC
TATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCA
GGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 71)

CN2442 (bp between ITRs: 1637)

GCGGCCGCACGCGTTTCCCAGCCTTACCTTGTTGCAGGCCTCCAGGGTCTGCAGCGGGG
TGAGGCAGGGTCTGGGAGATGCAGTGAATGCAGGAAGGGGTGTCTGCCTGACAGCCCCA

FIG. 22B cont'd

TCCCTGCAGATTTTGATGGCTCCGTAAAAATGTCTCCTCATAAACTGTCAAAGTGTCACAAA
TTAATTAACTGTTAGCTAGAGTGACTCAGTGTGGGGGGGGGTGGGGGAGAATGGCTCAGT
GATGCTGAGCGGGGTGGTGGCGGTGCTGTTCTCTGCGTGTGCTGCCTTTTGATGAGCTCG
GGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGA
TCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCAC
CGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCG
TGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGC
ACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGT
GCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCAT
GCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGAC
CCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCA
TCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCC
ACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCC
GCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCC
ATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTG
AGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGC
CGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGC
GAATTCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTA
ACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATT
GCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGC
GGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTG
ACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTT
GCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATA
AAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTG
GGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGC
GGACCGAGCGGCCGC (SEQ ID NO: 72)

CN2443 (bp between ITRs: 1926)

GCGGCCGCACGCGTACTTGGAGGAAAGGCAGAGGAAAATGGTCACTCCAGCAGTGCTGC
CAGGACACCAGGACCCTGCTCCATACACCTAAACCTCAGCTTGCCCTTCCCGTGGAAATAA
GGAGATGAAGCACTCAGAAAACACAATGCAGTTTCATTTTCAGGGTGGGATTTTTTCCTTCT
ATGTATCTCATGAGTCACTAGATTAGCACCTTTCCAATTACTGGGAGGCAAAAGCCCTATTA
TCATAGAAACCCTCCTGCAGAGTGACGGCTCTATTCTTTCTGACGGCAGCAGCCAGTCCCA
CAGAGAGCTGCAGAGCTCAGCAAGCTGGGAGCCTGAAGTTCCAGGTAACTTCATGTCCTC
GTTTCAAAAGTGAAGTTTAAAGAACTCACATCACAGCCTTAGCAGACTTCTCACACTCCACA
GAACACGCCAGGACAGCCCAGGAAGGAAGGCTGAGGAAGGTTCAGGAGCACATCCCAGA
GGCTGCACACAGGGCCCGGGGCTGCCTCGAACACACTCTGCAAGGGTCTGCAGCACTGA
ACGTTCTGTCTGAGCTGAGGGAGAACTGCATGACACAGAGCTCGGGCTGGGCATAAAAGT
CAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCG
CTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCAT
CCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCG
AGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTG
CCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCG
CTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGT
CCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAA
GTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGG
ACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCA
CCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGG
ACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCC

FIG. 22B cont'd

GTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAAC
GAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGG
CATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAA
TCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTT
TACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTT
TCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCC
TGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCG
AGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCC
TTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCAT
CGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAG
GGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC
(SEQ ID NO: 73)

CN2444 (bp between ITRs: 1979)

GCGGCCGCACGCGTTGCCACTTGAACAATGACTGTCATTCATTATAACTTTTGCAAACCCA
CCAAAAGCTCCTGATGGCATGCATACCCATGCATCACACGTGCATACGTGCACACATGCCT
TTTAAAGACCCCACATGGGTGATTGCAAGGGCTGTGTTTGACAGTTGTCATCTCTTAAAATG
ATGTAGGTTCCTGAAGTTCCTCATGCAGGACTGTCAGCCTGACAGCCTTAGCAAGTCAGTC
CTCGTTCTCAAATGGGAAAATGACATGGGAGGGCCTTTTCCTCCCTTTTTGGTAGATCTGC
CATTCATCAGCATCATTCTCTTCTCAGCCACTTGCTCATAAAGCCTTCCGGAGGCAATTACT
CAGGTGTACATGACAGGCCTACATTCCTGTCAGGGGTGTGGGCTGGGTTAGAGAGGATGC
GGGTGACACTCTGTTCCAGCAGGGACCATGCCTGCCCACCAGGAAGCACATGCCGTTCTC
AGTAGAATTCTCTTTTCAGAGTTTAGGAAGCCACTAGCGCTATAATAACTGCTTGCTGTGGT
TTGTGGTCAAGAGCAATCATAGCACTGATTTTATTTTTCTAATTTCATTCTGAAATCTAGACA
GGAGGTGAGACTGCATCACGTTGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCAT
CTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCAC
CATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGG
ACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACC
TACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCC
CACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACAT
GAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCAT
CTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACA
CCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTG
GGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAG
AAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCA
GCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCG
ACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATC
ACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGT
ACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATT
ACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGAT
ACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCT
TGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTG
CTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTG
TGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGA
AGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTA
GGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAA
GACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 74)

FIG. 22B cont'd

CN2447 (bp between ITRs: 2095)

GCGGCCGCACGCGTAAACAAGAACCCGGGGGAATCCAACTGCTCAGCATGTGGGAAGGG
CTCTGCGCAGCCCGCCCCTGCTCCTGGGGCCGCAGGGAAAAGTGGGTGAGGCCAGCACT
CTGTGCCTGGGATGCCACTGCTGTCCTGCGATGTTGTGCTGCTCCCCCGCATGGCTGCTG
CTACGGGCTCTTGCCACAGCTGGACACCCTCCCCTGAGCTCCAGTGCCGGACAACTGTTT
TCTGAGCATGCTAAGCAATGACCCTCTGCTGACGGGAGAAGTTACTTTAGAGGGGACAGA
ACTTAGGAAGACCCAGGTGTGCTGTGAGGCAAGTGGCTCCCTCCCTGACCCTTACTGCTC
AGTGTGCAAGGTTACCACCTTCTCCTCCTCCCCACACCCATCCCCCCTCTCTCCCAAGGTG
CCCCTCATTGCTGCTGTCACTCATCATTAGCAGTCACTGTCATTGTTAGGACAGCCCCTGT
CAGGCTGCAGAGCCAAGGGAGGGGGCAGGAGAATGTCAGATGACTCACACAACCTCAAA
AGAGGGGGATGGACACACAACACAGAACCTAGCTACAAGAAGCACCTCGTGAGACTCTGG
TTCAACCCTTTCTTTTTCCAGAGAAGAAAGAGCAGCTTAGCAGAGTTTCCTGACAAGTCCCT
CTGCTTCCCACTAGTCAGGCTTGGAGGGAGGCTGGCCTAGGAGAAAGGCCAGGCCAGGA
AGTCAGCATGAGGCTGGGCAGGTGACAGGTGGAGCTCGGGCTGGGCATAAAAGTCAGGG
CAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACC
GGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGG
TCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGC
GATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTG
CCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCC
CGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGA
GCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGA
GGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCA
ACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCG
ACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCG
GCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTG
CTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAG
CGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGA
CGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACC
TCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCT
ATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTT
CTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTT
GCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGAT
CTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTT
GACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCAT
TGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGA
GGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ
ID NO: 75)

CN2448 (bp between ITRs: 2031)

GCGGCCGCACGCGTAGGTTGAGTGGATTGAGGAGAAAATGGGAATTTTCATGTTTTTCAAT
AAATTTAGCTTTAAATGGAAGGAGAGAGATAGTATCTAGATGGAAATACAAAATCACAAGAT
AATCTTTCTCACTTTTAGACAGAGGAGAAATCACCACATAACTGGAAACACTGAAAATAGGA
GAGGGGAAAGATGGCTGACAGAGTCAGGCTTGACAGGAGGAGGATGGGGTCCAGGACAC
AGTGTCAGAGGAAAGAGGAGTATAGACAGGAGGAGGTGGGGACACAGTTCCCCTACTCTG
ACAGGAGGCAAGGTGGGAATAATTGGTACTGATAGATCTAAGTTTATGGGAGGTGGGAGG
AAGTTCATAGAGTTCCTACCTGACAACCTAGATTCATCTGAAGGAGGAGTGCCAGTTAAGA
GACTGTTACAAGAAGTATCGAGAACCTGAGTTGATGACATTGGGAACAAAGCTGCATACTT
GAGACACTGTAATCATTTAACAAAAGGTGAAGTTCACACCATACAAGCACTGCAAGAATGTA
GAGCAATTAGAATTCTCATAGACTGATGGTGGAAAAGTAAAATGGTACAAACACTTTGGAAA

FIG. 22B cont'd

ATCTTTAGGTGGTTTCTCAAAAAGTTAAACAAAGTCCTAACATGTGACTCAGCCACCCACTA
GTAAGTATTTACCCAGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTT
ACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAG
CAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACG
TAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAG
CTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGT
GACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGC
ACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAA
GGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGA
ACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAG
CTGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGC
ATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGA
CCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACT
ACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCC
TGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAG
TCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATTACAAAATTTG
TGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTT
TAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAAT
CCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAG
GGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCT
AGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCC
ACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCA
TTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATA
GCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 76)

CN2449 (bp between ITRs: 2483)

GCGGCCGCACGCGTATTGATGGAGTTGGGGCTCTGTGAGTGTGGGGCCCTGTGATTCCTT
GCACTAATTCCAGGAGATGGGTCTCCTAACAGCATGATCATGTGGATGTCCTGTGAGCCCT
GGCGGGGCTGTACAGAGAGAACAAACTGCCGAGCACAGTGCAGCTGCCTTATCAGATGG
GGCACACAGGCTTGCACAGTGAGCATCTCGGCAGCAGCCTTGGTAGACTGCAGACCAGA
GACTCGTCCCCCACTTTCCAGAGTTGCTAAATTCCAATGTTTTGAGAAACACAAGAGAAAG
GGTTGGTGGGGGTCCTGGAAAAATGATTTAGTGAGTAGGGGTTAAGCCGTATGTTGTTTCA
GTTAGAAAAATGAAAAGTTAAAGGCGAAAGATTTGCACGATCTGAAGAGAAACCAGAATGA
CGAGTTAATGGCACATGTTTACATACGTAACAAACCTGCATGCTGTGCACATGTACCCTAAA
ACTTAAAGTATAATAATAATAATAAGAAAAATGAAAAGTTACATTTCTTATATCTGAGCATTGT
CTCATTAATATGAAGTAGTCATAAGCACCTTGTGTTTTGGGGATTTACCTTACAAAACACTC
ACAATATCTTTCCTCATTATCTGGTCACCAAATTAATTTATTCATCATTCATATATCCATTCAT
CCGATATTGGAGAATCTGCTACAGTCATAGTGTAGAGGTGTACAATGGTGACTAAGATGTA
GTTCCACGTTCTTACAATTCTTACTAGTGACGTGGATAGGAGATAAGGAACCGCAGTGAAA
AGGATATTGACTGGGCACAAAAAGTTTGGGGTTTTAATCCTATTTTTGTCCTTCAACTGCTG
GGCAACTTTGGGCCAACTACACAACCTTTCTTGGCTTCCCTTTCTTCATTTGTAAAATTGGA
CTAAATTATCTTTAATTTCTTACTAACTTCTAAAATACTTTACTGAAGAAAAGAGACATACACA
TCTGATGTAAATGCAAGTATGTGTGTGTGTGTGTGTGTGTGTGTTTAATGGGGGCATAG
CTGGCTCCTTTATTAGGCTTTGGTTTTTCTTCATGTATCTGATTTCCAGAAATGAGAGTGAA
AATACATTTTATTTTGCTCCCACGTGTTTACTGAGCTCGGGCTGGGCATAAAAGTCAGGGC
AGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCG
GTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGT
CGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGC
GATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTG

FIG. 22B cont'd

CCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCC
CGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGA
GCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGA
GGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCA
ACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCG
ACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCG
GCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTG
CTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAG
CGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGA
CGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACC
TCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCT
ATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTT
CTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTT
GCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGAT
CTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTT
GACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCAT
TGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGA
GGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ
ID NO: 77)

CN2450 (bp between ITRs: 2100)

GCGGCCGCACGCGTACTGGGGTCACAAAGAAGAACCAGGGAACGCTGTTGGGGAACCCA
TGCAATGAAATGTGAAGGGAAAGAGGGCGGGCAGACGTCCCCAAACCCGCTCAGCAAAG
ACAAGCTTCGGGCAAATTCACTCACGTTGACGCTGTTCGGATGGAGCAGGCCAATTGGAA
AAGCCGGGTTCAGACACGACTCTAGAGGGAAGAGAAGAAGGCAAGTGTGAGGAGGGCGG
GCGTCGGGGAGAAGCGGGCCCGGGTGTGCTGGCGGACGTAGGGCCTCACCGTCGCGGT
CCTCAGCGTCTCTGCGGGGTCACGGGCCAGGCTGCGGGGCTCTGAGCGCCTGCCTCGCC
GTCCCGGGGCTTAACGGCTGCTGGAGCCACTTTATAATTAGCCCCAAACCGAAGGAGGCG
CGCGCGCCCCAATCGCCGGCGGGCTGCAGCTGACGCAGGCCCTACGCCAGCCCCGCGC
CGACGCCTTCGCGGGAGGGGTCGGTCCCCCAGCACCCGCGCGCCGCTCCCCCCGCCGA
GCTCGGGTGGGGGCCACAGGGGGCGCTCGGTGGCTCCCCACACGGCCAGGTGACAAAC
CCAAGGCAGTTAGGAAGTTTGGGGAGAGTGAGATAGGATCAAGTTTCTCCGCATAAAGTCA
CTGAAATTGCACCGTGGGATGCGGGCTCCAGGGAGGGAAGCGAGGTGGGGGCGTTTGGA
AGGATAGATGGACTGGCTTAGACTTCTGGAATGTGCTGGAGACCCAGCGAGCTCGGGCTG
GGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTT
CGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGG
GTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTC
CGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCA
CCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAG
TGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCC
GAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGC
GCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGA
CTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAA
CGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCA
CAACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCG
GCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGC
AAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGG
GATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAA
TTCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACT

FIG. 22B cont'd

ATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTT
CCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAA
CTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAA
TTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCC
CTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAAT
GAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGG
CAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGA
CCGAGCGGCCGC (SEQ ID NO: 78)

CN2467 (bp between ITRs: 1760)

GCGGCCGCACGCGTCCCACTCTCACAGCCTAGGGAGAAGAGGAGGTGATGGAGGAGGAG
GTGACAGGCCCCCTCCACCCCCACCCCACGCCCACCCCCACGTGGCCCCACAGCTGTCT
GTCTGTGTCAAATGTTCTAAGCAGAGGTTGGGGGCTTCACTCCCCACACAAAGAGAGTTCA
GAGCTGTCAGCACCTTTCCCACGGTACACTAGGTGCTGAGGAACAGGTGATAATTACAGC
CCTGTCACCCTCATCACCTCTGAGCTGGATGAGTTTTTTTCTAAAAACAAATGTTGTGCTGC
CTGAAGATCAAAGTTGGAGCTTAGGTTGGGGAAATACACACATGCAGGCTGCTGCTCTTTT
CCATGAAGCACAGGGAATTGGCTTGGAAAACACCTTGGAGATGGCTGTCTTGGCGAGCTC
GGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAG
ATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCA
CCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGC
GTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTG
CACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCG
TGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCA
TGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGA
CCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGC
ATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGC
CACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATC
CGCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCC
CATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCT
GAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCG
CCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCG
CGAATTCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTT
AACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATT
GCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGC
GGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTG
ACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTT
GCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATA
AAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTG
GGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGC
GGACCGAGCGGCCGC (SEQ ID NO: 79)

CN2421 (bp between ITRs: 1962)

GCGGCCGCACGCGTGACTCTACCTGCTGTAAAGGCAAATGAATGATCCTTTGATTAAAAGG
CACTCTACAGAGCGGCACAGGCACAGACAGAAACCTAGGGAAAGGCAAAGAGGAGTGAAA
ACTGGAGGCTTCCTTTCCATCCTGTCGTCAAGAGCAAGAGACCATCGTCAGGACCTCTCTG
GAGAGAGTCAGAGCCTGGGCCACCCCCTTCCACCTTGTGTTCCCGTGTCGTGTCGGGTCC
TACTCCTCCCATTTCTTTGCCCCTGAAGTGCTGAGAGGGGGAGAGGGTGGAGCCCAGCCC
TCCCCCTGCCCACTCTAGCTGTCAATCTGCTGTCTGGCAGAAAGACATGAAGCCTCGTGAC
AACTGTGGGCAACTTTCCCCTGCCCCGCCTCCCGCCCCTGCCCTGCCCTCTTCCCCTCTG

FIG. 22B cont'd

CTCCCTGTCAATGCTCTTCTCACTCTGCTCTGGGTCTCCCTTCCGTCCCTCCCTCTCTCCC
TCCCTCCCTTCCTTCTTCTTTCCTCTGCTTCTCTTTGTCATCTCTTCCAATCCTCACATCTGA
TAAGCCTGTATACCCTCATAAGATTCCTAATTGTGGGATATGCTTTTAAGCGTCCATCCAGG
CCAAGATCTGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTT
GCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGG
GCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAAC
GGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGAC
CCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCA
CCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGAC
TTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGAC
GACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCG
CATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGG
AGTACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAA
GGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACT
ACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTG
AGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTG
GAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGAC
GGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAA
GATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATG
CCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGG
TTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCT
CGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTG
CCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCC
CACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTA
TTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAG
GCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 80)

CN2231 (bp between ITRs: 2074)

GCGGCCGCACGCGTGTGGAGGTTGGGTGTTTCCATCACCTGGCTAACAGAGATCACAATC
TCCTTTTGTTCATCTTAGGGATAAGGTTTGTCCATAGCTCGACTTGTCTGGATTTCTCTGTC
CATCACATGCCTATGTACGCTCCCCACACCTCTCTCCTAGTGGCTCCTTGGTTTAAAATGC
CCCAGATCTGCAGCTCACAGAAGAACATTTGGCTACTCCCGTTTTTAATCTACTACTTCTGT
AATGGGGCTCGGGAGCTGGGCTGGGTCCCCCGAACCTGTGGGCAGCTGGCAGCCTGACC
CTGGGCTGAGTACCAGGCATGGGGAGGCCAGAAGGAAGGGGCAGATTGAGCCAGAGAG
GTAAGACTGCAGAGAGCCAAATAGGAGGGGAGGAGGCCAGAGCCTGAGGGTCCAGATGG
GGCTGGCTGGGCACAGGAGGGCATCTGATGCAATCCGCCAGGAGAGATGCCAGCCGGCC
GGGTGCTGCAGAGGCTCTGTTCTTGAAGAGTCTAGTGCCTGCTCTATTAATTCTGGCTCTG
TGGGAATTGGGGAAGATTTCCCTATGAGGTCTCCTGAGCCCCAGCAACCTCCCCAAAGGC
CTTAGCTCATAAAAGCACCTGTGTCTGAACAAGCAGGGGGTGGGGACATAGAACACCTGG
GTTGGTGGCTGCCTGGGGAAGGGCAAGCTGAAGTATCTTGTCAGTATAAACACAGTACCT
CAGCCCTGCGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATT
TGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAG
GGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAA
CGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGA
CCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACC
ACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGA
CTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGA
CGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACC
GCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTG

FIG. 22B cont'd

GAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCATC
AAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGACCA
CTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCT
GAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCT
GGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGA
CGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAA
AGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAAT
GCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTG
GTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGG
CTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTT
GCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTC
CCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCT
ATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCA
GGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 81)

CN2236 (bp between ITRs: 2182)

GCGGCCGCACGCGTGGGAAGAATAGTGAGTTCTGGGGTGGAGGGTTTTGATTTTTTAAAG
TGGAAAGTCAAGAAATGCACCACGGAGAAGGTGGCATTGAGTGAAAACCTCAAAGTGGTTT
GAGAGAAAGTGGTGCAGATATGCGGACAGCGCTTCAGGCAGAGAAAATAACCTGGGATGT
CTGAGAAAAGCAAAGAAGCTGGGGCTACTGCAGTAAGAGCAAGAGAGTTAAGAATAGGTG
TAGCCAGAGAGTTATCAGAATATAAGATTGCATAGGGCATTTTTAGGCCAATATAAGGACTG
GCATTTTTAGGTCATGATGAGAACTGGCATTTACTCTGCCTAAAATAGGAAACCACTGGAG
CATTTTGAGCAGAGGAGTTGAACTGTCTGATTTAAAATTTTAAAAGGTTCTGGCTACCTTGT
GAGAAGAGACTGAAGTAAGATATGCATGGAAGTAGGTCATCAGTTATTAGGTTATTGCAAT
AATCTAGGCAAGAGAGATGGATCAGGGTGATAACAGTAAACTTCATGAGAGCATTTCAGTT
GCAAATATATTCCAGATTTGCTGACCAGATTTGATAAGGAATATAGAAAAAGAGGAAAGAAC
AAGAGATAACAGAGTGTAGGCAGAAAAGAGAAAAGGTTCAAAGACTGAGCCCTGCAGTATT
TCAACATTAAGAGCTTGAATTGCAGAATAGGAACCATCTCAAGGCTTTAAATACAAGTGCTG
AACACTCTCAAATTTATATTTGTATCCCAGACTTCTCTAAAATTCAAGTTCTAAAATCCAGTT
GGTTACTTTATGTCTCCACTTGGAAACAAGTCTTGAAGCAGTGAGCTCGGGCTGGGCATAA
AAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCT
AGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGC
CCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAG
GGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAA
GCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCG
CCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCT
ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAG
GTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAG
GAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTAT
ATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATC
GAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGG
CCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCC
CAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCT
CGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATC
ATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTC
CTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATG
GCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGC
CGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGG
CTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCG

FIG. 22B cont'd

TGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAAT
TGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAG
CAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGG
CCGC (SEQ ID NO: 82)

CN2237 (bp between ITRs: 2278)

GCGGCCGCACGCGTTGAGGCTCTCCCAGATTCTGAAGCTGACCGGCTCACAGACGGCAG
TAGTTCTTTGTCGAATGGGGAGCACAGAGCTGGATATGCAGCAGTAAATCATGACACAATT
ATTGAAGCCCAGCCAGTGCCCCCTGGCACATCAGCACAAAAGGCTAAAATCATTGATCTTA
CTCAAGCATTAATGTTGGGACAAGGGAAAAAACTTAACATCTATACAGATTCTAAATATGCA
TTCCTTGTGGTTCATGCTCATACCGCCATCAGGAAAGAAAGGGGATTACTTACTAGCAAGC
ACTCCCCTATAGAGCATGGACCTGAAATTCTGCAGCTATTGAAGGCAATACACCTGCCAAA
GGCCATAGCTATCATTCATTGTAGGGGGCATCAAAGGGACTTAACCCCTATAGCACAAGGG
AATGGAAAGGCTGACGGAAGCCAAAGCAAAAGCCCTCAGCGTGCAATCCCAACAGATCCT
AGCACTGCTTCCTTTCTACAATTCCCCAGTAGAACCCAAATACACACCACAGGAAGAACAG
CTAATAAAAAAAGCAAGGGAGACAAAAACAAGGATCCTGGTGGCATATGGAGCCAAAAATA
TATCTCCCTCAGGCAGCCCAGTGGAGAGTTATAAAAGCCCTGCATGACTCTTTCCATGTGG
GGAGGGATGCGGCTCTGGCCATGGTAAACAAGTTCTTTACTGGGTTTAACTCAGCTTCAAT
GGCTAAGCAGGTCTGTCAAGCCTGCTCACTGTGTGCATTTAACAATCCAGGCATCAAAATG
CCCCCTCTAATAAAACCAGTCCAAAGGAGGGGAACTTATCCAGGGGAAGACTGGCAGTTA
GACGTCATCCATATGCCAGCTTGCAGAGGATACAAGCTTTTGTTAATACTAATAGATACTTT
TAGGTTGGGTCAAAGGTTACCGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCT
ATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCA
TGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGAC
GGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTA
CGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCA
CCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATG
AAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATC
TTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACAC
CCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGG
GGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGA
AGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCAG
CTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGA
CAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCA
CATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTA
CAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATTA
CAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATA
CGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTT
GTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTG
CTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTG
TGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGA
AGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTA
GGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAA
GACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 83)

CN2440 (bp between ITRs: 1926)

GCGGCCGCACGCGTCATCCCGCTGGCCATCTGCATCAGCCCGACCCCCACAGGATAGAA
GACTGGCACATCCAAGTTGCTCCTTCCACACCCTCTCCCCACTGAGGCCTCGTCTCCTCC
GCCCTGTGGCCAATTGAAGGTGAACTCCTAACGTGCATTCTGCCTGGGATCCCAGAGGTT

FIG. 22B cont'd

GTGGCAGCCAGATGAGTCACCTCACAAATACAGCACGTGTTCCTCGGGGGCGGCGGTGG
GAGGAAACACGTGAAGAGCTCTCTCTGTGATAATAGACCATTTAGAGCTTCAGATGGCGAA
AACAAGCTGATCAGGTGCAGGCCCTCCAGGAGGCTGGCAGGTGACTCCCAGCCAGCACG
CCCTCCATCGCACGTTGGGGAAGCTGGAAAGAGCCTGGTGGCTGCCGGGCCTCCCTCTG
GCATCCTCTCTCCCTCCAAGGCTGTGTGCTCCCCACCTTGTCTCTCCTTTTTTCATTCCATT
GCTCTGTTCTGTTTCTGTCTACCCATTCGTCTTTTCTTCCTCTTCTCTTTCTGTTGCCATTCT
CTTTCTCTTCTCCTCTCAACATGTCCTTCTCTCTACCCGTGAGCTCGGGCTGGGCATAAAA
GTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAG
CGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCC
ATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGG
CGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGC
TGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCC
CGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTAC
GTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGT
GAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGG
AGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATA
TCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCG
AGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGC
CCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCC
AACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTC
GGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCA
TAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCC
TTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGG
CTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCC
GCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGC
TCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGT
GCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATT
GCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGC
AAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGC
CGC (SEQ ID NO: 84)

CN2441 (bp between ITRs: 1805)

GCGGCCGCACGCGTTGACTGTGAAGTGTCTGTCTGAACTCATAATCAGCTTTTAGCTGGTC
CCAAACAGTGAGTGCTACCAGCTCCATTAATCCCACTGACAGGGATTTATCTTTCTCAGCT
GAATGAATGATGCTCCCAGCCTTGCCCCAGAAATGTGGGCTGGGCTATTCAACACTTGTCA
CCAGCAAGCTCTTTTCCTGAGGCTGCATACTCCAGCCACCCAGGTGACTGAGTACTTTGTC
ATCTTCTTCTCAGAGCAGTGGCAGAACCACAAAGCAAACTCCCACCCATGACCCACCCACC
CACCTTCTGACCTAGTTTGGATGCTCCAAGCCATAATGATAAAGTAATGTTGTGAAGAGGG
AAAGAGGTTTGCAGTCAGACAGCCTGAACCCAGGTTCTGCCATGTACAGGCTGAAGCTTG
GCAAGCCTCTGCACCTCTCTGAGGTCCATTTGCACGAGCTCGGGCTGGGCATAAAAGTCA
GGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCT
ACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCC
TGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAG
GGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCC
CGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCT
ACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCC
AGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGT
TCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGAC
GGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCACC

FIG. 22B cont'd

GCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGAC
GGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGT
GCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGA
GAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCAT
GGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCA
ACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTAC
GCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCA
TTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTG
CCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAG
AGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTT
CCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATC
GCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGG
GGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC
(SEQ ID NO: 85)

CN2445 (bp between ITRs: 2012)

GCGGCCGCACGCGTTCCCACATCTGTTTCTCTGGCTCTGCCTCTTCTGCCTCCTTCCATCT
CTTATAGGGAGCCTTGTGATGACATTGGGCCAACCAAATATTCCAGGATCATGCCTGCATC
TCTCAAGATCCTTAACTTAATCATATCAGCAAAGTCCCTGCACCATGTGAGGTAACATATTC
ACAGTAGTAGGTGCTCAATAAATAGATACTAAAGATAGCAGCATTTTTTATTAGACCTTCTC
ACAGCTTCTGGGGATTAGAATGAGACATCTTTGGCAGCCATTGTTCTCCCCATCATGGGTA
ACATGCAGTGGGCGCTTCCAGTGCCAGGATTTCGGTGGGTTTAACTGGAGTGTGCAGATA
AGTAGTTGGCGTCAAGAACTCCTGCTGCTTCCCTTGCTGGAAAGATGGGGTGGCTTTGAAT
GACATCCCAGAATCTGATTCTTCCGTCTGCGGAATGTGCATAGGATGTCTGAATCACACTA
TTGTCGTGAGAAATGAGGTAGAATATTCTCTGATGTGGCAAGCTTAGGCCAGCATCTAGCC
CAATTCCTTGTATATAATGGAAATTCTTAAGATGTTAGGGTTCCCCTCTCCCTCTCTCTCCTT
TTTCCTCGCCTACAAAGGAAGACATCTTTTGTGAGGCCTCCACAGCATTCTTGATGAGCTC
GGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAG
ATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCA
CCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGC
GTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTG
CACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCG
TGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCA
TGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGA
CCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGC
ATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGC
CACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATC
CGCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCC
CATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCT
GAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCG
CCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCG
CGAATTCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTT
AACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATT
GCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGC
GGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTG
ACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTT
GCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATA
AAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTG

FIG. 22B cont'd

GGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGC
GGACCGAGCGGCCGC (SEQ ID NO: 86)

CN2446 (bp between ITRs: 1776)

GCGGCCGCACGCGTTCCATTGCAGCTTCTCTCTCTCTCTCTCTCTCTCTGAGTCATCTTTA
CAAGCCCCTGAAACAATGGTATTTAAGGAGGGAGCTTTCTCAACACCTGAAATCCCTACAG
AAAGGTTGAGCTTCCTTGGTAAAGCATTTACCTGCTGGGGGAGGGTGCATGGAGTGACAT
GGTTTTCACATTTGAGAAAGGTAAGTGGGAGGGAATATCAGACAACTGCAGAGTGCAGATT
ATCATTTAAATAAAATCCCCATGGGGCTCGCTGGCAGCATTAAAATTGCTCCTGCCTCTGT
GGTGCTGTCACAGAACAGCCTCTCTCCTTTATTCTGCTTTACCATAGAAAGAGGCAGTGTG
GTGCAGTGGAAATACCCCAGGGCTGAATCCTAGGATTCAAGTCTGATCCATCATCTCTGGG
CTGTGTGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCT
TCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCG
AGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGC
CACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCT
GAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCC
TGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCT
TCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACG
GCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATC
GAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTA
CAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGC
CAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCA
GCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCT
ACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGT
TCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGC
GCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGAT
TGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCT
TTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTA
GTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCG
GCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCA
GCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACT
GTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCT
GGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCAT
GAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 87)

CN2457 (bp between ITRs: 1726)

GCGGCCGCACGCGTTGGGACTCAGCAACTTGACTAACATCACAGACACAGTTCTCAGATTT
ATATATCCTAATTCCAAACCCAATATTCTTACTACTAGAATATGCTGGACCGTTTTACTCCTA
ACTTGGTTAAGAAGCCAAATATAGGAGGAAATTAACAAATCAAGGTAGTTTTAGTTACTCAT
TGGTCTGTGGGTTCACAGCATTTTAATGGAGCCAACTTTGCTCTTAAGATGAGTAAGCAGTT
GGTATGACTCAGGAATCTCTAAGAATGTTTCTACCTTAAAAGGCAGGTTTTTGTTTCTTAAT
CCTTTAACAATTAATATTTTAATTAAGGGAACATTGGATAGACATTGTAAGGTGCAAAATACC
TCTAGAAGGGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTT
GCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGG
GCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAAC
GGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGAC
CCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCA
CCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGAC
TTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGAC

FIG. 22B cont'd

GACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCG
CATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGG
AGTACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAA
GGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACT
ACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTG
AGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTG
GAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGAC
GGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAA
GATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATG
CCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGG
TTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCT
CGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTG
CCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCC
CACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTA
TTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAG
GCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 88)

CN2458 (bp between ITRs: 1641)

GCGGCCGCACGCGTAGTTCTTGCTTTCTCCAATTTGTTTATTTTTATGTGACCTAGCTTTAT
ACATTGCAATTTAAAGGAAATGAAAAACAGTTTTGTTATTTTCTTGTGTTATCTGGGAGATTA
TCTTATTCTTTTAGGGTTCAAGTGCATAGAGTTGGTGCAATCAGCCACAGTTTATGACACAG
TATAATTTATGCTTCTTGCATTCTGTTTTAAATTTATTTTCACCTTTTATTTTCCTTCCTTTTAT
CCCTTTGTATTATGTCTAATATCACCTCATCTTCACCCCAATCCAGAGCTCGGGCTGGGCAT
AAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAG
CTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGT
GCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCG
AGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGC
AAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTT
CGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGG
CTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGA
GGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAA
GGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTA
TATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACAT
CGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACG
GCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACC
CCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACT
CTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATA
TCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGC
TCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTA
TGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATC
GCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGT
GGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCC
CGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAA
ATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGAC
AGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGC
GGCCGC (SEQ ID NO: 89)

FIG. 22B cont'd

CN2459 (bp between ITRs: 1648)

GCGGCCGCACGCGTTGCTCATGCACAATCACTACTTCTATCTCTTCATCAATGGTAACACG
ATTCTGACTTCCAACAGAATGGACACTTTGCAAGTTTTGAAATGTATGAAAAGGAAAAATAT
GTCTTTTTCTGCTTATGGCTTTTTTAGTCAATGTTATATTATGCACTTTATTTATGTAATTTTG
TCTTGCTATAGTTTGTTTGCCTTTATTGACGAATAATAAATATACTAGTATGTGAACACACCA
CTCTTTAATTATTTAGTCTACTTTTATTTCCAGGTGTTGGATCTTTTTCATCGAGAGCTCGGG
CTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATC
TTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACC
GGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGT
GTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCA
CCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTG
CAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATG
CCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACC
CGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCAT
CGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCA
CAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCG
CCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCA
TCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGA
GCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCC
GGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCG
AATTCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAA
CTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTG
CTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCG
GAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGA
CAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTG
CCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAA
AATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTG
GGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGC
GGACCGAGCGGCCGC (SEQ ID NO: 90)

CN2232 (bp between ITRs: 1729)

GCGGCCGCACGCGTGGATGCCCAAGCCAACATGGAGGGAAGGGGGGGGGGGGGGGGTG
CGGACTGAATCCCAAAGGCCCCAAGACGGGTGGTTACTCACTGCCTTCTGTTTGGGACTG
GCTAAGGCCGCCAAGTTCACTCAGCCCACTCAGTAGAAGCAAGATGAGCCACATGGCCTG
GCCTCCTGGACCCCGCCCCGGGGAATGGCAGTTGGCCCTCTACAGGGCAGTTGGGGGCG
CGAGGTGGGGGCTGTGGGCAGCGCAGCTGTGTGCCGGGAAGCGTTTGTGCTGCTCGGTG
AAAGCTTTGAAACTGTGAAAGGTTTGAAGGACTTGCTGGGGTTTGAAATCTGAGACCAAAG
AAGGGAAAAGGGAGGACAGGCAGTTGAGGGAGCTCGGGCTGGGCATAAAAGTCAGGGCA
GAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGG
TCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTC
GAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCG
ATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGC
CCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCC
GACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAG
CGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAG
GGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAA
CATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGA
CAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGG
CGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGC

FIG. 22B cont'd

TGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGC
GCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGAC
GAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCT
CTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTA
TGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTT
CTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTT
GCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGAT
CTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTT
GACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCAT
TGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGA
GGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ
ID NO: 91)

CN2233 (bp between ITRs: 1866)

GCGGCCGCACGCGTTGTCTCATCAGTGGTCCTTCTGTATCATTACGCCTGGGAACAGCCA
AAGTGACATCTCTGCAGACCCTTCCAGTTTTAATTCTATTTAAGTTTTACACGGCTTGGGAA
GTCCCCTCTATGACTGTGGAGAAGCCAGGATAGATTGGGCCACGCTGCTGCTGAAGACTT
CAAGGGAGCAGTTAAATCTGGGGCTGTCACACTGAATTGGTGGCTTCTGTTTGAGCCATCT
GTTCCTGCCACGGAGCATCCCATCCCATCCTGCCTGCCTGGCAGGGTCCCACTCCCATCA
TTATCCTTCAAAGAGCTTTGGATGAGAATTCTGAACATCCTCAATTGATGCACAGGGGGGG
AGGGTATTGGTGAGTGAATGGTTCCAGATGACAAGTTTCACCCCTGGCATGGTTAATAAGT
GAGGGAGGGCACATGAAATATAATGACATGATCTTTCAGAGTTTTTCCCAGTTGAGCTCTG
TGGGCAGTTATTCCTCTGTCACAGAGCGATCTCTATGAGCTCGGGCTGGGCATAAAAGTCA
GGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCT
ACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCC
TGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAG
GGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCC
CGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCT
ACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCC
AGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGT
TCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGAC
GGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCACC
GCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGAC
GGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGT
GCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGA
GAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCAT
GGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCA
ACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTAC
GCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCA
TTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTG
CCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAG
AGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTT
CCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATC
GCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGG
GGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC
(SEQ ID NO: 92)

FIG. 22B cont'd

CN2452 (bp between ITRs: 1765)

GCGGCCGCACGCGTACCTCAGGTCCCACATATACTGTGGTCTATCACCTGGTTACTCTAAA
ATGCCCCAACTCACCTTCTTCCTTAAAGCAGCTCCCACTCCTAACATTTGTATCTCAGGCTG
ATTATTCAGGTTTAGAAATTTCAAGGTCATCTATGACTCACTGTTTTGATCATGTCAGTCACA
AAGTTCTAAAGCTTCTGCTTTGGAATGTTTCTTGTACTGAATGCTTCCTTCCAATTCTCATTG
CCAGCACCAGCCTCCAGATCTTTATCAAGTCATAGCTGGGTTGTTGTAACAGCTTCCCAGC
AGAGATGGCATGAAGGAAGGCAACTAAACTTTTCTGAGCACCTCATATGTATGTAATGTTTT
CAATGCACTATCATATTTAACTCTCATAACAATACCACGAAGCAGGTATGAGCTCGGGCTG
GGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTT
CGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGG
GTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTC
CGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCA
CCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAG
TGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCC
GAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGC
GCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGA
CTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAA
CGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCA
CAACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCG
GCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGC
AAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGG
GATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAA
TTCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACT
ATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTT
CCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAA
CTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAA
TTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCC
CTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAAT
GAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGG
CAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGA
CCGAGCGGCCGC (SEQ ID NO: 93)

CN2453 (bp between ITRs: 1682)

GCGGCCGCACGCGTGGGGTTACCTTTGGGAAAATAAACTCTTATTAAAGTGTCACATCTTG
GTGGAAAGGCTTTTAATTTAATGATTGCTATCTACAGGGAAAAATCACTTATAAAAATCTTAC
TATTTCTCCCAAAAGACACCAGGTTGAGAACATTAGGACATCATTCTTTCATCAATATTTCCT
TTGTATTTCTTAGTATTTTACGGTTTTCCTTAATACTTCTTATTCCTTCAAAAGCTATACCTCC
ATACTATATATTTGAACTGAAATGTCTGATTTTAGAACAAGTCACATGTCATTTTTATTTTGTC
TTTAAAAACTTCTGACACTGAGAGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCAT
CTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCAC
CATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGG
ACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACC
TACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCC
CACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACAT
GAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCAT
CTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACA
CCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTG
GGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAG
AAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCA

FIG. 22B cont'd

GCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCG
ACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATC
ACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGT
ACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATT
ACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGAT
ACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCT
TGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTG
CTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTG
TGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGA
AGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTA
GGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAA
GACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 94)

CN2454 (bp between ITRs: 1707)
GCGGCCGCACGCGTCTCAGTATCTTATTTCTTAGTCACACTTTAAAACTGAAGAGATTAGTA
ATTTTTTCTATGTCAATATGTGAAATATGCAATACAAAATTGTACAAACCCATTTAATTCCATT
CTCTGTCTTTTGTCAATCAAACATCCTCCCTGATAAGAGCTCAATTATTTGATTAATTATAAA
TCGCTATTTTTTGATATGATATTCACAGTAGAATAATTTATAATAGACAAAATTACAAACAATA
AGATCTTGGTGTTCAGTGGGATTTATGGTGTTTTCATGCAATGGAATACCGAACTGACACAA
AAGTCATGTTAGAGAAGAATATTTATAGATGTGGGGAAAAGTTCATGAGAGCTCGGGCTGG
GCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTC
GAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGG
TGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCC
GGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCAC
CGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGT
GCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCG
AAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCG
CCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGAC
TTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAAC
GTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCAC
AACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGG
CGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAA
AGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGA
TCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATT
CGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTAT
GTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTC
CCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAAC
TCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATT
CCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCT
CCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGA
GGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCA
GGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACC
GAGCGGCCGC (SEQ ID NO: 95)

CN2455 (bp between ITRs: 2002)
GCGGCCGCACGCGTGTGGTGATGCTGGACAAGGCAAGGAGTGGGCAGAGGCGAGGACT
GTGGTCCAGCTGAATTTTCAGAGGCCCTCTCATGTGCGCCCACTCTTTGGAATCATTCTCA
TAGATACCCTATGGGAAGCCCACCCCCCAGCCTGGCCCCGCGTCACACTGAGTCATATCT
AATCATAGGCTCCCAGGGTGATTTCCTTACCTGCTTTTTTCTGTGTTTTTAAGCTCTTCATTA

FIG. 22B cont'd

CTTCCTAATTGTCCTGATTTTAGTTCTTTCTCGTTCTTGTCAAACACCCATTTAGAAAATGAG
TCATCATTAACTGCACGCCACTCTTCACTTAGAATTAGACCCATTTCACCCTTTCTCTCTCTC
TTTTTTTCCTCTTCAAAAAAACTGGGGGATTAAAAAAATTACACTTTTCTGACATCCTTTTTTT
AATCTCTTTTGCTAGCGCAAATGCTATTGGCTGCTCAACTGCCTTAAGGGTTTCTTCTGCAG
CCCAAATGAACAGCTTTGTGCTTCCAGCCTTTGATAGCTCCTGGGGGCGTTGATCACTGAG
TCAAACCTCCAGGTCTCAGCCTCCCAAGTGGCCTGCTCAGGCATGAGTCAAATCAAGACTA
GACCATCAGGGGACAAGAAGCTACTGCTCACCTTGCAAGTGAGAGCTCGGGCTGGGCATA
AAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGC
TAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTG
CCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGA
GGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCA
AGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTC
GCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGC
TACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAG
GTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAG
GAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTAT
ATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATC
GAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGG
CCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCC
CAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCT
CGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATC
ATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTC
CTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATG
GCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGC
CGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGG
CTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCG
TGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAAT
TGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAG
CAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGG
CCGC (SEQ ID NO: 96)

CN2460 (bp between ITRs: 1622)

GCGGCCGCACGCGTGTGTCAGCTCCAGGACGAGCCCCGCCAGCCTCCACCCTGTCCAAC
CAGGCCCTACTCCTCCCCTGCAGATCTGTGGTATCTTCTGAGCCCTAAAAACACGCCTCCA
GCCAGCTTCCTGTCCTCCACCCGGCCTCTCGGGGCTCATCCCATCTATTATTCACAGCACA
AAATGGATTTTTAATTTGAGAAATGAAATGACTCTCCCAAGTGGCCGGGGTGGCAGGGAGG
GGGTGGAGGAAGGCCGGAGCCGCCGTGGCCGCCACAGCCGCCACGGTGCTGACTCAGG
TTCATCTTGGAAAGCTCGGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATT
GCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGG
TGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGC
GACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGG
CAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCT
CGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGC
AGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCT
TCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTG
GTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCA
CAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAA
CGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCG
CCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAAC

FIG. 22B cont'd

CACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATG
GTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAA
GTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATTACAA
AATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACG
CTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGT
ATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCT
GGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTG
CCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAG
GTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAG
GTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAG
ACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 97)

CN2461 (bp between ITRs: 1803)

GCGGCCGCACGCGTAGAGGGATGCAAATGAGGCTGTGGGGGCTGGGGACACCCCTTCCT
GTCAGGGTCTCCATGGCACATTGCCTGGGACTGCAAGGAAGGGCGAGCCTGGGACAGGC
AGAGAAGCCTGAATGGCCTGGAGGGCCACTTCCTTGGCTGCCAGGGTCCTGGGCCTGCA
GTCCCCTCCCCCAGCACTCCATCATCATTTCAAGTGATTGGAGCTGAAGGGGATCGTTAGC
TAATTAAAGCTGAGGCCACTAATTGTCCCTTTTGAAGAGAGAGCAGGGCTGTGCAGGGGA
GGAGACAGAGGGTCTGGGGAGGGGGATATTGGCAGGCGGGGGGCTGGGAACAGGGCCA
TGGCCCCTTGTGGGGCCTTCTTCCAGACTGTGTGTTTGAGGGGTCAGGCATTGTCAGAAG
CTCCTTAAAGTGGGTAAAGGACTAGAGAAGCAGATTTGGCGCTGAGCTCGGGCTGGGCAT
AAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAG
CTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGT
GCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCG
AGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGC
AAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTT
CGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGG
CTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGA
GGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAA
GGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTA
TATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACAT
CGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACG
GCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACC
CCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACT
CTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATA
TCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGC
TCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTA
TGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATC
GCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGT
GGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCC
CGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAA
ATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGAC
AGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGC
GGCCGC (SEQ ID NO: 98)

CN2628 (bp between ITRs: 2102)

GCGGCCGCACGCGTCACTTGGGTGCCTTGACTAAATAAAGATGGATTCCATTTTTAATGGT
CAGTTCCAGTGCCTTCCAATTCCTTTGAGGGCGTCGTTTGGCAGGCTCAAGTACAGTAGTT
GAGGAGAAACCATGACCAGGGCAATTACTTAGGGTTCTTTTAAGCACTGGTTTAGTGGAGA

FIG. 22B cont'd

TTTTTTTTTTTTTTTTTTTTGCCGAGCCATTATAATTCGTGAATAATAAAGAACAAGAGTGTTC
AGATTGCTTAGGGCATGGCACGTTCAGAAAAGATCGGGCATCCTTCCAAAGACAGCGGGG
CTTCGGGAAACGATAAAGCGCTATGATTTTTAAAAGTCATACGCAGAATTCAGAAGCAGATA
CTACAGAGGAGTGCCTGCAAGTAGGTCTGCTCGCTCTGATGGGTCTGAAGCGGGAGAGTG
GGGGTGGGGCGGGGGAGTAAATGTTCCCTGCTTTGTTGCTATTAACACCTTGGCCCTTGT
CACCAGGTCCTTTGTAAATGTTGGCAGCTGTTATTAGATGCGTTATCAAGCACCGGTGTAC
ACAGCTTACTTTACAAATCACCCACCCGCAGATGCCTTACAAACCTCCACAGCCATCAAAAT
GCACCCCAGGACTTCCTCGAAATACCATTTCCTCCCCAAGAAGAACCAGCAGCTTCTGGCT
CCACTGAGTTCTGTACCTAAGGGCTACTTGCCTCTCAAGGCCAGAGAACCACGAATCCAGT
AGTTCACCGAGCTTCTCTGTTCCTGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCA
TCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCA
CCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTG
GACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCAC
CTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGC
CCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCAC
ATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACC
ATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGAC
ACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTG
GGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAG
AAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCA
GCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCG
ACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATC
ACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGT
ACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATT
ACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGAT
ACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCT
TGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTG
CTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTG
TGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGA
AGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTA
GGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAA
GACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 100)

CN2641 (bp between ITRs: 2378)

GCGGCCGCACGCGTGGACTTTTGGTATAGCATTGGAAATGTAAATGAGCTAAATACCTAAT
AAAAATGGAAAAAAAAATAAAATAAAAGTAGCATTAACCAAAAAAAAACAAAAAAAGAATATC
ACTTACTGTTGCATTTCCTTCTTTATGCAGTTCTTTCCTACATAAAGTCTTGGATAAAATGAG
AAAGGCATAATGTACCTAAGAACTAAGCAAAGCTAATGCTAGTTAGCACCACAGGAATGCT
GACCTCTCATTACAGAACAATTCAACAAGAACTCATTCACCAACAGTCAGGGTTGAGATTCT
CCCCACCTGCCTGCAGTATATTATAGTTGAAATATGGGGCCTTGGTAGGTTAAGAGACTAC
TGTAAAGCTTCTAGCACTATTAATTGTTCACTCTACCCATGCCACATCTCCCCAGGAGATCA
GGGAATATTGTATTGTGGTGCTCCAAAAGCTCGTTATGCAACGTACAAATTATGTTATGATG
AAAGGCAACAACAAAACCTCTGTAAGGAGTGTTATCATTTCTCTCTTTTCATTAAGTCACAAT
GCAGAAACTGAGTAATCTGAACAAGTACCTTTAAAGTAAGAGACTTAGAAAGTGGCTGGCT
ACATGTAAAGCCGTTCATGTGCTTGCAGTTGTGTACAGGAGCAGGCTGCTCACCTGTTACG
GAGAGCCCTTTGTTAAGAGCCTTTGTGAGTACTAAAAGCTTTAGGTTTCCTTTTCTTTTTTAA
GCTCTTGCTTTAACAGTGTATTTCTATGTTCACCTTTCAGGTAATGACTGTCTTTGGTCTTTT
TATCAAAGAGGGAACAATAACACCGCATGGTATTATTTTCACAAGTATTATAGAGTATATATT
TCACAAGTTTGGTACCCTTTTTATATCATATCTTTTTATTTTAGTTATGTACCTGATTCCAATA

FIG. 22B cont'd

AAAATCAAGTAATGTTGATTGCAAACCCCATCTGTAGTCATAGAAATATTACAATGATGGAC
ATGTAGTTAGTTTTTCACTTCTCAAATACTGTCCATTTCGAGCTCGGGCTGGGCATAAAAGT
CAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCG
CTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCAT
CCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCG
AGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTG
CCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCG
CTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGT
CCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAA
GTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGG
ACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCA
CCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGG
ACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCC
GTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAAC
GAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGG
CATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAA
TCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTT
TACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTT
TCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCC
TGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCG
AGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCC
TTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCAT
CGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAG
GGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC
(SEQ ID NO: 101)

CN2642 (bp between ITRs: 2300)

GCGGCCGCACGCGTAAACAAAGAGCCGCCTTCCATTCTTCTGAGATGTCTTTAGACATCTT
GCTTACCCCTGTTACACAGCCCCACAGTCATTACCAAGTTCAATCATCTAATGTGGGATCC
CAGGAGGTCTGCATTAACCATGAAGCAATGAAAGGTAGAGTGATCCTGTATATGGACCAAC
TGTCTTCCCCACCAGACTGAAAGCTCCCTGGGGTCAGAGACAACTCTTACTCATCACAGAG
GTACCAGTATCCAGACTATGCTGTCTCTTCCCAACCTCTGCTTGCTGTCAAGCCTGAAGCT
AGTCAGGCATCTACCTCTGCCTGGCTGCAGTTCTTTCTCTTGAAGAAAGGATTTTTTTTTTT
TTTGGTTTCATAATGATTAGTTTTTTTCATTATCAAAACCTCCCTGAGTCACAGGAGGTAACC
TAATATCAAAACCTCCCTGAGTCATAAACAACCATTGCTACTGCTACATTCACCATTATGGA
AAAAAAAGGCTGGTCTGAAACTTAGCCTCAGTGTTCTTTCTGCCACCTAAGGAGGAGGTTG
TTGCATTTATTTATTTGGGGGGAGGGGTCTAGTCATAGCATACATGTTGAGGTCAGAAAAC
ACTTTATAGGAACTGATTTATTCCTTCTACGGTCTGAGTCCTGGGAACGAAACTCGAGTAAT
CTGACTTGAGCATAAGCACCTTTAGCTATGAGCCATCTTGCTAGCCCACAATGTGTAGGGG
GCAGTGCTGATGTCAAGGTACTGTTGCCCAATTGGTTCTTGATCTGTCAGTAAAGAAAGCC
ATAGGCTAATTGCTGGGTGGAAGGTACAGTCGTGACTTCCAGGTTCCGGGAGGGAAACGG
GATGCAAGGAAGGGGGGAGGGAGTTCGACATGCTTTGGAGAGAGGAGAACAAAGCAACC
ATGTGAGGTAGTAATACACTGTGACAACTACAGGCAGGTGAGCTCGGGCTGGGCATAAAA
GTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAG
CGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCC
ATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGG
CGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGC
TGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCC
CGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTAC

FIG. 22B cont'd

GTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGT
GAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGG
AGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATA
TCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCG
AGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGC
CCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCC
AACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTC
GGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCA
TAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCC
TTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGG
CTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCC
GCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGC
TCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGT
GCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATT
GCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGC
AAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGC
CGC (SEQ ID NO: 102)

CN2643 (bp between ITRs: 2255)

GCGGCCGCACGCGTGAATGTATTGGATTATAACATGCACTAGTATTAAGTATAAAAGTATGT
TCAAGAAAATTTAAAGTTATTTTAAAGACTGATGTAAGGAAAGAAGGAGGAAGTTAGTCCAT
TAAATCACACTGAGCAAGAGCTAACTTCTACAGAGTAGTCATTAAGAGGTAATTTTACAATC
TAAATTTTTTTTTTTTAAAGGATGCTTTCCTTTGTTGTGGTGTCAAGGTGAGAAACTATGTAG
ATTTGATTCCGTAAATATCTATGGTAAGGCAAGTGACAGGGTGAACTCAGCTGAGCTGATG
GAAATAGTTAGAACATAGAAACAGTCAATAACTATTCATTTTGTAAAAAAAAAAAATAATAAT
AAAATAGCTCCTTCAAGTCCTGAAGCGTAATAAAATATTAGAAAACACAATGGAAAAATGAG
GCACTCACAGAAGAAATACAGTTGGCTCTAAAGCATAGAAAGTCTCAATTATTTCAAAATAA
TAGAAAGGTACTTTAAGACAGTGAACCCGGAGTGGTCTCTGGGAACAGGCAGCTTGGTCC
TCAATCTGGCAGTCAGTGCTAACTACACTGTGATCCTGGAAAAGATATGCTTTACTTCCTCA
TTCAAAAACTCAGAATTATAGTGCTGCCTGTGCCCTGATCTACCTGATGCCCCGCCCTACC
TGCCTTTGGGGGTTGCAGGTAAGGTGGTGTGGAATCAGGTGAGAAATGTCACAGCAAGCA
CCTCTGAAAGCTGCTGCAAGCTCCTTTAATACGCTCACCCGTGTCCCATTGGTCCCAAGAA
AGCATCTCTTCTAAGCAGCAGTTCCTGATTGGCTGGCATTGTCTGTGTCAGCAATCCTTGG
TCTCTTAGGCAGTCCTCAATTAGGTCCTCCTGTAGAAGGTGACTTTGCCGAGCTCGGGCTG
GGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTT
CGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGG
GTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTC
CGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCA
CCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAG
TGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCC
GAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGC
GCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGA
CTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAA
CGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCA
CAACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCG
GCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGC
AAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGG
GATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAA
TTCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACT

FIG. 22B cont'd

ATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTT
CCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAA
CTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAA
TTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCC
CTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAAT
GAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGG
CAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGA
CCGAGCGGCCGC (SEQ ID NO: 103)

CN2629 (bp between ITRs: 1905)

GCGGCCGCACGCGTAGAATATGTCATATGCCCAGAGTCTGGTACTTATGAGGGTCATAGT
ATTATGGTCAATCCGACAACCACTCACTCTGAGTCAGGCAGAGTGTGCAAAGTGCACTCAT
CTGTGTCACTTATTGTCATATGTGCACAGGTGAGTGATTAAAAGCACAAGTGTGCACCGCA
GCTCCAACATGTCATACTGCGGCCTCAGACAAAGAAAGCAACCTCTCTAAGCCTAGGGTGT
TCTTGTCTATCAAGTCGAGGGTTATAAAGGAAAACACCATGGGGAAGAATTAAATGCAAAC
CTCCCCCCACACCACGCTTATCAAATGGCTGCTGGCATGATGCCTTGGTTTAATTCTTACA
CAGTCACATACCAACGGGTAAGGCTCTCAGAGAGTGTTATATAATTAAGACAAGATTCTTGT
GTTTAAGCAGGGTGGAAAAAGAAATACTTACTGGAACACAGACGTACAAAACAAACAAGTT
TCTAGGGAAGAACGAAGCTGCAGCACTGTGTGGGAACACACAGAAGAATTAGACTGTATG
CAGGAGAGGGGATGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTA
CATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAG
CAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACG
TAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAG
CTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGT
GACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGC
ACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAA
GGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGA
ACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAG
CTGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGC
ATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGA
CCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACT
ACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCC
TGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAG
TCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATTACAAAATTTG
TGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTT
TAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAAT
CCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAG
GGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCT
AGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCC
ACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCA
TTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATA
GCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 104)

CN2630 (bp between ITRs: 1956)

GCGGCCGCACGCGTTGACAAATGTTATGGCGAGCCCACGTTTCTTTCAGGCTGTATCTTAG
TGCTATGAAATCCATATTGCTTCACGATCAGCACTTATCAAGATTAAAGAAAAACAAACTCC
ATTTATTTTTCCTTTATTGACAGATTCATGGCCTACATCCCTGTGAATAAATGAGCTGGCAA
GAAGGGGAATGGGACAGCCAGTAAGCTTGGTGACATAAATTACCCTTGATAGGGAAGGCT
GATGTGGGCATGTCATCAAATTAATAGCTGAATGCTAAGGACCATTACATTTAGCACTGTTT

FIG. 22B cont'd

GCCATATCCTTCTATATAATAATGCCTGAGAATAATGTGTAATTAACTCTGTGGCTGACTGA
CAAGGCCAAATGCAGGGCAATCAATCATATTGTATAAACACACGTCCCTGAGTACACATGG
GAGGCAAAGGGTGACTTAAAATGTCTCAGCACTTTCTGCCTAGATTATGGCTCTGAGCTTT
TGTGAGGCCAGCAGTCATAGAGACTCTTATCTATAGATCTAAGCTGCCTACAGCATCTTGG
TATATAGTCTTCCTTGCTATTTATCTTGACCTTTTACTTGTGTTCTTTGAGGGGGTGACAGA
GCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGAT
CCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCT
GTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGT
TCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTG
ATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTA
CGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTC
CGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTA
CAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGA
AGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACA
ACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCA
AGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAAC
ACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTC
CAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGAC
CGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGC
GGCCGCGAATTCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGT
ATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCAT
GCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCC
ACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGG
CACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGT
TGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCC
TAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTG
GGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCA
CGTGCGGACCGAGCGGCCGC (SEQ ID NO: 105)

CN2745 (bp between ITRs: 2044)

GCGGCCGCACGCGTATCTTCAGGTGTACCAGCACTGTGTACCAGTCTGTATTCTGTGGGG
TTGGCTGACTCCAGCCCACGCTGTGTCTGTAAATGAAGTTTTATTGGAACACAGTTTAGTG
CTTCCTGTTGGTGATATAGCACAGAGCTGAGTAGCTCCAAGAGCAATTATATAGCTCTAAAA
GCTGAGGCTGTTTACTTTCTGACCTGCTACAGAATAAGGCTTAGACCTCCTGAGTGAGTGT
TCTCAAATAGCGATGCTGAGTGGAATTACCTCAACAGATTCAACATTGTTCCTGAAGTACAT
TCATTATCATTTACTGGTGTTTTAATTGGCTTTCCTTAAAAATAAAACAGAATTAAAGCTGTT
ACATGTAGAATTGTTTATACAGCAGAACCCGTATGGTGTTCCTTGAAGGACTGTGTTTGAGA
GAATCGCCTTTAGAGTGAGAATTACAAAGACAGTGGGTCACGTAGATTAATGGTTGAGATC
CTCTGACCTAAGTAACTGCTACTTTTAGCTTTATTCTATTTTCAACTCGGATCTTTGTTTTTG
TTTTTTACTAAGCAAGTATAAGATGGTACCAAAAAGGATGTTGGCTTTCCGAAGGAAACAGT
TTGCCACCAGTTTTTTATATTTTCTTCTGTGCCCTGTGCGTGCCTGCCTTTTCACTGCTCTA
GCTAGTAACGCCCACGCTTGGGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATC
TATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACC
ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGA
CGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCT
ACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCC
ACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACAT
GAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCAT
CTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACA

FIG. 22B cont'd

CCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTG
GGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAG
AAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCA
GCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCG
ACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATC
ACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGT
ACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATT
ACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGAT
ACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCT
TGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTG
CTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTG
TGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGA
AGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTA
GGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAA
GACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 106)

CN2746 (bp between ITRs: 1958)

GCGGCCGCACGCGTTCATCTGCAGTCAATGAAGGTCTTTATTATCACTAAGTACGTCTTAT
GAGTTTTATATATTGACTTTCCTTAAGTAAGCCAAGAACTTATAAAAAGATCACTCAAATAGT
ATTTGCTATAATCCTCACACAATTTTAAGAGCAGGAGGCAGGAGGTCTGTAATGTGAAAAC
AGGAAAGCAGAGAGAGGCAGGAGGTGAAGCAGATCTGGGTAATTTTAGCTGTTGGTAGAG
AAATCATGAACACACCCTGGCTTTAGTCTGCTGAAGTGGAAAGCTGTATACTTATTGTTGGA
GCACAAAAGCAGACAGCATGAATTGACTATGGTGGTAAACAACTTCAGCCCTAACACAAAT
GAAACTGGCCAGTGACTCATTAGGCATTTAGTGTTTTTACTAAGTTTTAGTTTTATGAAAACT
AATTCCAGTCTAGTTATTGAAATACTCCATGGGTTAGTTACTTAGAGTTCAATGGAAACCAT
TGCTTTTCTTATTTTTTTTTTTTTTTGTAAAGCAATTAACCATTGCTTTAAAAAGATTTTTGCTG
GCTAAGAAAACAGTTGATGTTCTGGGAGAAAGGAAAACCTGACTCTCACTTCATGAGAGCT
CGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCA
GATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTC
ACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAG
CGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCT
GCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGC
GTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCC
ATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAG
ACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGG
CATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAG
CCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGAT
CCGCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCC
CCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAG
CTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCC
GCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCC
GCGAATTCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTC
TTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTA
TTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACG
GCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCAC
TGACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGT
TTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAA
TAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGG

FIG. 22B cont'd

TGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGT
GCGGACCGAGCGGCCGC (SEQ ID NO: 107)

CN2631 (bp between ITRs: 2054)

GCGGCCGCACGCGTTCCGTAAAGAGCACAAAACCCAAATATTTGGGTGCATGGGAGATAG
ATTTCAACTAAATACTTTTAATCATGCAATTCCAATAGCACTTAAATTTTTTCAAGGCATGTAT
AAAGGGAGAATAGACTAATTCAATTTCAAAGTGCAAGAAAAACATCAAAAACTAAATTCAGA
AAGTTTGCATGGGAAGAAAAAAAAACACAAATTAATCTCACTTGTGATTATTCTAAATACATT
TGAACAAGCAGCAGCTAGTAGTACATACAAAGAAATAGAAAACATGAAGACCAGGGGAGTT
TAATTATATGGTTGCAAAAATGGTTCAACATTGCAAAGTTGTTAATACTCAGTGGATGGGGA
GGGAGCTGTGCAATTATCTCCACAGGTACAGAAAAGGCACTTAGTAAAATGTAGCCAACTC
TTTGGCTTCTAAAAAAGGAGAAAATGGTTTACAAAAACAAGCCTCCCTGGATGCTTCCTTAA
TTTGTTCTTATTCATAATGGGGGAACATAAAGTGAACTTCTGCACACCAGAAGTCAGGTTGT
TTGCTTGCTAATACCATTCCCACTCAATATCCCATGGAAGTTGGATGACTCGACCTGCATCC
CAAGGAGTAGTTACCATCACTAATGAGGAGAAGCATTTGGAAGGAAGACAGAATTCTGTAG
ACCAAACGAAGACCTGGAGGCTAGTGGAAAGAGCTCGGGCTGGGCATAAAAGTCAGGGC
AGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCG
GTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGT
CGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGC
GATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTG
CCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCC
CGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGA
GCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGA
GGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCA
ACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCG
ACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCG
GCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTG
CTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAG
CGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGA
CGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACC
TCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCT
ATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTT
CTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTT
GCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGAT
CTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTT
GACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCAT
TGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGA
GGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ
ID NO: 108)

CN2747 (bp between ITRs: 2112)

GCGGCCGCACGCGCCGGTACCGAAGCTACCCCTAACACACTATTCTACACACAGAAAATG
CTCTTCACTAGGAAGCTACCCCTAACACACTATTCTACACACAGAAAATGCTCTTCACTAGG
AAGCTACCCCTAACACACTATTCTACACACAGAAAATGCTCTTCACTAGACGCGTAGGCTT
CTTCTGCAATGTGGAGTTTCTAGATCCTTCCTATGATCCAACCCCTCAGACTTCACATCCTC
TCCATCACCAGGACAGACGATCCCATTGAGTAACATCTGGCTTTTGCCTTCTGTGGGCATA
TGGCTGTAGCTATCACAGAAGCATACAGATCTGCTAGGTTCTTGTGGGCAGCACACCCATG
GTACCTTTTAAAGGGCCTGCTGTATTCGCTCTTTAACACTCAGCGTGGCATCAACCCAGTG
GAAATGAACTGGGAGCTCCCTGCAGGTTCTGTGCTCCCTTGGCAGGCACAGCCTTCCCAC

FIG. 22B cont'd

CCCACACCTTCCCCTGGAGCATTGAGCTCTGCGGGAACACAGGCTTGCTGAAGGAACCAG
CAGGGCCATCGGGAGCACTGGGCCTGGGAGGGAGATCAACAGCACAAAGTAGAGCCAGC
ACAAAGTGGAGCTGAGAGAAGCCTTGGAGCATGAACAACATATCTGCACCCCAAGAAAAG
CCCTTAACCGAAGAGCAGAGCCATGGCACTTAAGGAGCTCGATTCAGCCGGGAGCTTAGG
GAGGGGAGGTCACTTCATAAGGGCTTGGGGGGGGAGTTGGAGCCACGAGTCGTCCAGCC
GGAGCCCCGTGTGGCTGTGCTCCGGCCTCAGAAGCATCCCCGGATCCAGATCTTTCGAAG
CTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGT
GCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCG
AGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGC
AAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTT
CGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGG
CTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGA
GGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAA
GGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTA
TATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACAT
CGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACG
GCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACC
CCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACT
CTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATA
TCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGC
TCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTA
TGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATC
GCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGT
GGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCC
CGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAA
ATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGAC
AGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGC
GGCCGC (SEQ ID NO: 109)

CN2632 (bp between ITRs: 1980)

GCGGCCGCACGCGTAGAGAGGGAGCAATTTCTTTCAGCAACGGAAATAGGCTTTGTTGTA
TTTTTTAAGTCCCCATAAAAATGTAAAGTTCTAACATCTCAAATTACCTTATGTTCCACAGGA
ATATTAGGTGTTAGCGGATACTCTGCAGGAAATGAAAAATGATTACTTGAAACCATTTAATT
GGCTTTCACTCAACAAATACCAAAGTGCAATTTGTGGCCTGATTTGAATGCTAATGCCTGAA
TTACAGGCATGGAATCAAAGTGCTAGATGCTTTCAGTGCAGAATGCCAGTGCTTAATTAAG
TTTTCCAGTAACTGTGTACAGCAATAGGATTCACAGCGAGTGCGCGGATATTTAAGGTTATT
TATTTCTGCTATGTGAAGTATTTTTCCCTTGGAATCTTTGTTGTACAAATTGACATTTACCAG
GTGGTGAAAAAGTTTACAATCTTGACAAATTCTTTCATTCAAATTAATGTTTTCCTTATCAAT
CATTCCAAACTTAAATGCCTGTATTATTAGGCACACAGTTGGCATTTAAAAGTATGGATTAA
GGAACTATGAATGCATCTGATTTGTTACTCTGTATAAGCCTATACCAAATCAAATTGGTTGT
GGTTTTCCAGAATTTTGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCT
TACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGA
GCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGAC
GTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAA
GCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCG
TGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAG
CACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTC
AAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGT
GAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACA

FIG. 22B cont'd

AGCTGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACG
GCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCGCC
GACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCA
CTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGT
CCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTA
AGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATTACAAAATT
TGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGC
TTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAA
ATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGAC
AGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTT
CTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGC
CACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTC
ATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAAT
AGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 110)

CN2644 (bp between ITRs: 2134)

GCGGCCGCACGCGTAGTTTCGTGTAGTTTTAAAAACCCTATTTATTCTTTTCTTGTGAAATG
TTTCAAATGAATTCAAAGAAAATATGATGTTTTATTTCTTTACAAAAGGTGATAAATATTATTT
TTATGAATAATATTCACATTGGGCCCCTATGTGGACGCTGAATAGCCCTAGTGTGGAGTAA
GGTACAACCTTACTGGAGGAAGGATATCACTATGGGGCTGGGCTTTGAGGTCTCAGAAGC
CCAAGTCAATTCTCTCACTGCTGCCTGTGGTTCAAGATAAAGAACTCTCAGCTCCTTCTCTA
GCATCAAGTCTGCCTCTACACTGCCTTGTTTCCTGCCATAATAATAACAGACTAACCCTCTG
AATTGTAAGCCAGCCCCAATTAAATGTTTTCTTTATAAGAGTTGTTGTGGTAATGGTGTACTT
TCACAGAAATAAAATCCTAACTAAGACATTTTCCAAATTGTATACCCTTGATTCTTTTTAGTT
CTTGTATTGCTCTAGGTAGAACTTCAAATACTATATTGAAAAGACATTGGTAGAGTGGGCAG
CCTTCTCCTATTCCTGATTTGAGTTGCCTCTGGTGGAGCAAGGGGTTTATGCCTGGATAGA
ATGACTTATTATAGAATGACTTAGAATGAATGGGGTTCTTGGTGCTGGTATGGCCTCTGGTT
GTGAAGGCTCTGGGGAAGTATTGCTCATTCATGAGGTGGGGGCTTCTCTAAAAATCTTCAT
GCTAGTATAGCCTCTCGGGGATCAGGGTCTGCTGGAAGTGTGCATAAGAGCTCGGGCTGG
GCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTC
GAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGG
TGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCC
GGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCAC
CGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGT
GCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCG
AAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCG
CCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGAC
TTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAAC
GTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCAC
AACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGG
CGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAA
AGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGA
TCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATT
CGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTAT
GTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTC
CCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAAC
TCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATT
CCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCT
CCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGA

FIG. 22B cont'd

GGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCA
GGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACC
GAGCGGCCGC (SEQ ID NO: 111)

CN2748 (bp between ITRs: 1876)

GCGGCCGCACGCGTACTCCTCTGGTATACTGCAGAAAATCCTTCCAAAAATCTTCACAACA
GTGAGGTTTTTAAACAGGTTGGACTCAAAGCATGGAGAACGGAAGGAGAAACACAGTGGG
GGCAGAAATTCCAGAGGCAAGCTGAGCTGGAAAACACATGGCCATAATCAGGGGGTGGG
GAAACAAAGCATTCCCACAGGACAGTGGGAGGCACAGAGCAACCCAATGTCACTTATACA
CCTTATAGAAATCCTGGCAGAGCCACCTACAGACTAGCTTATTAATATCCCAATGTTGTTTT
CAGGAGAGACTAAAATTCTAAAACGCTTTTTAAATGATGTGTTTTGTATACACAAGTTTTCAC
CCACACCACTTACAGTTTTCCAATAAAAGCCTATCTAAATAAACAGTTTAAATTCGTTACACG
GGGCTGCATATTTCAGTTCTGAAATCAAAGATGGGAATCAATTTGAATTATGACTGAAATCA
CCATTTAGAAAATGGTCTCATACTGGATGGGTTGTTCTCAGAGAGCTCGGGCTGGGCATAA
AAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCT
AGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGC
CCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAG
GGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAA
GCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCG
CCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCT
ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAG
GTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAG
GAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTAT
ATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATC
GAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGG
CCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCC
CAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCT
CGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATC
ATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTC
CTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATG
GCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGC
CGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGG
CTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCG
TGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAAT
TGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAG
CAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGG
CCGC (SEQ ID NO: 112)

CN2633 (bp between ITRs: 2054)

GCGGCCGCACGCGTTGATGTCCAGGTTGGCTGTTCACCAAGGACACCCAGAGAGACTGTA
TGGTCTTAGAGAGTCTGAGTGGTAGCACATATTTGAAATAGAAAGCACCACCCTACCCCCA
GATGGTCTCTGCCTCCTCCACCTACTGAGGTGACATCTGCACTTCCTATGTAATCTTTACTC
ACACCTCTTACAAAGACAGCATGTCGTCATCCTGACCCCAGCAGCCAGCCGAGCTGGGCT
TTCCAGAAGTCTTCAAGCTGGAGGAGTGGGAGGCACCATGGCCTGCTCAAGGGGAACAGA
GTGAATTGATGCCAGACGGTGGCAGGTGGCTATTTTCACTTAGCAGTTAGTGGCTAATGAA
AGAGGTGTGTGGGTATCTTTCTCCCCAGAGGCCATTCATTTCTCTCCAGCTGAAAGAGCAA
TGGACTGATCTGAGGCAGGACCAAAAGTTCAAAGGAATTATGACAGATTGGCCCAGCACC
CCTGAGTTTATCTGAATAATGACGCATAAGCACCATCCAGTGTTGACAAAGCTCTGCAGGC
TGTGAAGGCTTAAGGGGAGCCTTGGAGCTAAGCACAGAGGGCAATGATGTTGCTTAAATG

FIG. 22B cont'd

TGCACAGGTCTGGATTAAAGTGGAGTAGTTCTTAGGCTGCTCATGTCTTCTTAATCTTCAGC
TAGGATTGAGACTAGCCTCCATGACACAGGGGATCCATGACAGAGCTCGGGCTGGGCATA
AAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGC
TAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTG
CCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGA
GGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCA
AGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTC
GCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGC
TACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAG
GTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAG
GAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTAT
ATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATC
GAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGG
CCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCC
CAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCT
CGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATC
ATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTC
CTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATG
GCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGC
CGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGG
CTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCG
TGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAAT
TGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAG
CAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGG
CCGC (SEQ ID NO: 113)

CN2634 (bp between ITRs: 2042)

GCGGCCGCACGCGTTCCTGCGNCCGCACGCGTGCTCAGTTGCCAGCACACAAATGATGT
CACATGAGCATCTATAACTCCAGTTCTAGGAGATCTGACACCCTCTTCTGACCTTCATTGGC
ACCAGGCTCTCAGTGTTTACACATACATGCAGGCAAAAAACACTCATACACACAAAATAATA
AAGAAATTTAAAATTAAGAAAGAGAAAATCATAGTTTTAGTAGCTTTTCTCTTCCATTTGTTT
GATTTCTTGCCTTATGACATTGTTTATTGTGTTCATTGGTGACTGTCTTTACACTGAGGATTC
TATGAATGGGCAGTTTGGAACACTTCTAACGCTTTGTACTCTGTCACTGGCATGCTCACAG
TGTATACCACCTACCACAGAGGAACATCCATTGTTTAAAAAGCAGTTCAGGTTATTTTGAAA
CACTAATACAAAATAATTTTCAGCTGTAACGATGGGAATATAACAATTTCCTTGACTACAAAG
AGAATATAACAAGTGCCTATGATTCAAATGCAAAAGACACCGAATATCCATCAGTGCTTTTG
AAAATGGCAGGACTTACTGTATTGACACTTAACAAGCTTTTTTTTTTTTTTTGTCTGAAGCTTG
TTTTTAAATGTTGGAATTTTAGTTGAAAAATCTATGTCACTCTTTTACTGCAGTTTTCTGCTTT
CATAACATTTTCAAGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTA
CATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAG
CAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACG
TAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAG
CTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGT
GACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGC
ACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAA
GGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGA
ACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAG
CTGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGC
ATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGA

FIG. 22B cont'd

CCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACT
ACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCC
TGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAG
TCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATTACAAAATTTG
TGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTT
TAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAAT
CCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAG
GGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCT
AGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCC
ACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCA
TTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATA
GCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 114)

CN2635 (bp between ITRs: 1891)

GCGGCCGCACGCGTGCTTATATGTGTGGGCAATATGTATATATTGTTACTTTATATGTATGT
GTATAAAGAGAGACTGTTAACATGTTTTCAGAAACTCTTAAATACATATAAAGGCATACACA
AATATCTGCAGAGGTAATTATATTAAAGTGCAGAGTTTAGCTACTATGTTTTGCATTTGTAAA
ATGCCATAGAAACATCAGCTCATTAATTTTGTTCACCTCGTAGGACTATTATTCAGAATCTTT
ATTCAGCCAGGGAGGGCATTTTGTATTTAGCTATTACTTGGCTCTCTCCCTTTTGTCATACC
ATGGCAGGTAGTCTATACTTAAACCTGAAATTTTTAGTGTCAAACTTGTGGCAAACAAAGTC
CCCTTGTTCCTTAGCTAATGAGCACAAGGTTGGGGTTTACATACTATCACTAGGCTTTAAGG
TGAGGACCGTTGTCCAGCAGAGGGGCCTGTCATTTTTGAGAGGTATTTGTGTATTTTATAA
ACCAGCCAACTGTCTTTCTTTTCTTTTCCACCATCACTCATTTCCTTCCAGAGCTCGGGCTG
GGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTT
CGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGG
GTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTC
CGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCA
CCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAG
TGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCC
GAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGC
GCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGA
CTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAA
CGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCA
CAACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCG
GCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGC
AAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGG
GATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAA
TTCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACT
ATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTT
CCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAA
CTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAA
TTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCC
CTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAAT
GAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGG
CAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGA
CCGAGCGGCCGC (SEQ ID NO: 115)

FIG. 22B cont'd

CN2609 (bp between ITRs: 1864)

GCGGCCGCACGCGTTCTCATCCTATGCCTTTCTTCTAGGTACTTCAGAAAGAATCTTTCAAA
TCAATAACTGTGTTCTATCCACAGAGGTTTAATGGAGGAGCAGGAGGCTGGAACGAGATGA
AGGAAATGAATTGTTCCAGAGATGAAAAAGCTCCCAGGCATATGTCATAAGTTTGAGACAA
ATTAAGGAAAAGCGGGTTGGGAGGAGTCTGAGGCTGTGGGTGGCTGCCTCGAGAGGCTG
CTCACAACCTGACATGTTTCAGATCTTTTGACACGGTCATGCAAGCAACAGAAACTTATATG
GTTTTTAGTCTCCCAGGTAGCAGGGAAATGATGATGTGGGAGGATTAGGGGGGGGAAAAT
GAGTTTCTCATTTTTTTAATTTAAATTACTTTTGAGCTACTTCTAGACTGCAGCAGAGTTGAT
AAACCACCCAGTTCATATACTCAAACCTCCCAACTCCTCCACAGCTCAGCCAAAATTTCCCA
AGGACTTGTTTTACCCAAATCCCAGCTCCGGAGCTCGGGCTGGGCATAAAAGTCAGGGCA
GAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGG
TCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTC
GAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCG
ATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGC
CCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCC
GACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAG
CGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAG
GGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAA
CATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGA
CAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGG
CGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGC
TGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGC
GCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGAC
GAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCT
CTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTA
TGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTT
CTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTT
GCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGAT
CTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTT
GACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCAT
TGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGA
GGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ
ID NO: 116)

CN2610 (bp between ITRs: 1892)

GCGGCCGCACGCGTTGTTTCACAAACTACAGGTTCACTGGAGCACAGCCATGCCAACATG
GCATCTAAGGCTGGTATGACCTCGAGACCCCTCCAGCACTCCTTCGTTCAGCCATAGAACA
AGGAGACACAGATAAAGTCTGGAGCCGGGCCCAGGTACCTGAGGCTCAGAGATGAGCCC
GCAGCGAAGCTGACAACTGACTCATTCCTCCGACACTCTCCCACCCTCCCAGCTAAGGAG
GTGTCTGATGTGAACATGTTCTGCCTCTTTGTTGCCTGCTGTTGGGGGCGAGGGCTTTGG
GTGGATTTTGAAGAGCAATTATGCTTATTACTGGTTAGGATTTCTCTGTTTGCTGAGTGCAT
TAACTTTTAGCGCTTCCCATCACTCATTCTTCTTCACACCCTCTTGTCAGTTACAAATGTGCA
GGTGGAGAGCCACGAAAAAACCCTGCAGCAACGGCAACAGAAATCACAGCAACAACAACA
AATGAACAGAAAGGATAGAAAGCAGATACTCAAAGATGGAGAAAAAGATACTCCCGAGAGG
CTGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTG
GGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGG
AGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCAC
AAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAA
GCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGG

FIG. 22B cont'd

GCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCA
AGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCA
ACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAG
CTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAAC
TACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAAC
TTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCA
GAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACC
AGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCG
TGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCG
CCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGA
CTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGT
ATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTC
TTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTG
TTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCA
TCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCC
TTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGG
GGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGAT
CTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 117)

CN2749 (bp between ITRs: 1979)

GCGGCCGCACGCGTAACCTCAGTGGTTTCAGCCACCATGGAAGAGAGAGAGACAGGAGT
CAGAATGTAAAGGCATGGGGTTTGGTGGACCAGAGAGAGAGATTCTCAGTGCAGTGGGAA
TTGGGCTGCTGGGCAGAATATACATCCCATAGACTACTCCCCCACCCCCTACGGTGTAAGA
AAAAAGACATCTCTATGACTTGGCTTGCACAAACTTTCTTGTGTGCTACCTTTGCAACAGCA
GATCTCAGGCAGGTGGGTGGATGGGTGTGGAGGAGGAGAAAGCAGAAAGACAAAAGGAA
GTGAGTGGGGGGAACTCTTGGGAACCTGTTGGCAGAGCGCTCTGAGACTCTGAAGCTAAG
GGACCATGTTATGTTAATCTATTCTCTAATTGCTCAGCAACAAACACCTCCCACCCGCTGCA
AGGAAGGGCAGGACAAGACTATTCCAAGATCTGCTTAGAAACAATGTCAGTCACAGCAGA
GGGCGCAAAAGAAATGGACCTCTTTTTAGCATAATTGAAAGACACTACTTACAACTGAGGG
GTCTGAGTTGCTGACAGCAACCGCCTTAGCTAGGAGGAAAAGCTGAGGGGTAGGCTGTGC
TCAATGGGAGGGTTTGCAGGCTGACTGTTCAGAGCTCGGGCTGGGCATAAAAGTCAGGGC
AGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCG
GTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGT
CGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGC
GATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTG
CCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCC
CGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGA
GCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGA
GGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCA
ACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCG
ACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCG
GCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTG
CTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAG
CGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGA
CGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACC
TCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCT
ATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTT
CTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTT
GCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGAT

FIG. 22B cont'd

CTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTT
GACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCAT
TGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGA
GGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ
ID NO: 118)

CN2626 (bp between ITRs: 1967)

GCGGCCGCACGCGTAGCCTGAATTCCACACTACAGCTCTTATATTAGAAAAGAAACTGGAT
GAAAAAAGATGGGTCTCAGAGAAGATACTTGGAGCAATAGCCACACAAGAGTTGCTCAAGT
ATTTCCATCAGCCTAAATGACTACACACCTATTTGCCACCAGCTGGCCTCAGCTCTGCTCT
GAATGCCCACCATCAACTCTCTGAGAAAGTGCCCCTGACTACACTCAGTGAAGCTGTGAGT
TGGTGGCTGCCTTTTCCCCCTGCAAGATAACAAGGTAGGCCTTACCTCAGACTTAACTCAA
GGTAAAGTTTAATTGCTCTAACCTGCTCTTTGATGTGTGCTGAGGAGGTGGGCGCCGTGTG
GGTACAAGTTGCTATTTATACAGACCTGACAAGCGCATCCCATCAGCACCCGCTCCTTTGT
TCTCTTCCAGGCTTTTCTGATTCTCCAAACTTAACATCCTGCACTCCCCCAAGTTGTTTAAT
CGTTCCAAAGTTTGTAAGACAAGCAAGGGAATAGTGGCCTTCACATCTGCACTTGCAGCCC
AAATATGGTGCACTGTGAGAGATCCTTAATTTGGAGAGGAAAGCCTGCTGCTGACCACCTG
CCTCTTAGAACTGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACA
TTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAA
GGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAA
ACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTG
ACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGAC
CACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACG
ACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGG
ACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAAC
CGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCT
GGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCAT
CAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGACC
ACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTAC
CTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTG
CTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTC
GACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATTACAAAATTTGTG
AAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTA
ATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCC
TGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGG
GCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAG
TTGCCAGCCATCTGTTGTttgcccctcccccgtgccttccttgaccctggaaggtgccacTCCCACTGTCCTTTC
CTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGT
GGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTC
ACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 119)

CN2611 (bp between ITRs: 2037)

GCGGCCGCACGCGTTTCCTGGACACTGAATTCTGAGAGACAGAGGTAGGAGAGGGGAAC
CATGGGATGTGACGATTTCAAAGATTTACCCTGGGCACTGTATAAGAAAACGTTTTCCAAA
GTGTCTGACACTGGGTCTGACTGACACAAGGCACCAGCAAATGTCACCTCTCTTCCCTGTG
TGTCACACAACTTCATTTCTCTTGAAACTAAAACTTCTCTTCTAGTTGCCCTTGACTTCCAAT
GTCACCGTTCTCTAGCCCATACCCCATTACTAATCCTCCCCGCCCGGTTCCGCCTACGTCC
CTTTTGTTCCCACTAAAGATGGCTTTGCTTTTTCACCTGTTTAAGTCTTCCTGCCTCCCACA
CTGATGAATTCAGTTAGACTGAAAAAAAAAAAAAGAGGCCTCTTCCTCCATAAAACCCCAAT

FIG. 22B cont'd

TAATCAATCATTCACGACTGAGCAATTTGGGGTGATGGTATTTAGTGGGAAGAACTGCTCC
AGCACTGTCAGGCCTGGGATGTGACACTAACAGCAGTGAGACCTAAGAGGAGTAATTTGG
CTTTTTTCATATCTCAGTTTGCTCACTCACAGTACCTTAACTCTTAAGACCGGTAAGAGTGA
AAATTACCCCCAGAGGAATCCTAGGGCAAAGACAGCCAGGTGATCATCAGTATAAACTAAG
GATGCCTGTTCATACCAGCAGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTA
TTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCAT
GGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACG
GCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTAC
GGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCAC
CCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAA
GCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTT
CTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCC
TGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGG
CACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAG
AACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTC
GCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAA
CCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACAT
GGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACA
AGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATTACA
AAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATAC
GCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTG
TATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCT
GGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTG
CCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAG
GTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAG
GTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAG
ACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 120)

CN2750 (bp between ITRs: 1848)

GCGGCCGCACGCGTAGGAACTGGACACACAAAGCCTTTCTCGTTTTTTCTTCCTCCCTGTG
TTTCGGTCCAGGGGTCCTAAGTGTGTAGCTCCCGGGGAGATGTGGGACTGTTCTCACCCA
GAAAGAGGAACTAGAACCACAAGAGCCTAACCCCCCACGGTGGGAAGACACTCTGTGGCA
TCACCGGGAGGGGAGGCCAGGTGTGGGCAACTGCAGCTATTTCTAATCCACCAGAGGAAA
GAGAGCTTTGACTGCTTGAAAAGCAGGCTGATTGTCAGGGGCGGAACCCAGCTCAGAGCT
GTCAGGGAAGCTCCTGGCAGGGGGTGGAGACAGGGGGCTTGGACTGACAGGCCTGTGAT
TTTGAAAGAAATGTCTTTAAGAGAGTGACTTAAAGTAGGAGAGAAATATTATTATTAGGTAAT
GCCTGTCAGGTTATATTTTTTTTTGATGTGTTCTTGGTATTTCATAATCATTTTGCCTTTAGAT
GGTAAGCCCTTCCTGGTGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTG
CTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGT
GAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGC
GACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGG
CAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCT
CGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGC
AGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCT
TCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTG
GTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCA
CAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAA
CGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCG
CCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAAC

FIG. 22B cont'd

CACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATG
GTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAA
GTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATTACAA
AATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACG
CTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGT
ATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCT
GGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTG
CCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAG
GTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAG
GTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAG
ACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 121)

CN2614 (bp between ITRs: 1983)

GCGGCCGCACGCGTTAAACCTTGGACTGAGCCCACAGGATGCTCTGGAAGGACCTTGGG
AAACCGACACACAAAGCCTGTCTCGGTTTTGTTTTGTTTTGTTTTGTCCTCCCTGTGTCGCA
TCCACAAGTCCCAAGCGTGTAGCTCCTGGGAAGCTATGTGGCTGTTTTCACCAAGGATGAC
TTCTCAGAGACTGACACCCATAAGAGAGGCCCCTCCACCCGAGGGTGGGAGGACTCTCTG
TGGCATCACCGGGAGGGGAGGCCAGGTGTGGGCACTGCAGCTATTTCTAATCCACCAGA
GGAAAGAGAGCTTTGACTGCTTGAAAAGCAGGCTGATTGTCAGGGGCGGAACCCAGCTCA
GAGCTGTCAGGGAAGCTCCTGGCAGGGGGTGGAGACAGGGGGCTTGGACTGACAGGCCT
GTGATTTTGAAAGAAATGTCTTTAAGAGAGTGACTTAAAGTAGGAGAGAAATATTATTATTA
GGTAATGCCTGTCAGGTTATATATTTTTTTTTGATGTGTTCTTGGTATTTCATAATCATTTTG
CCTTTAGATGGTAAGCCCTTCCTGGTCCTGGGCCATGAACTATGCCCCTCGGGTCTCACC
CCAGCCTTGGACATGCAATGGGCACCAGGAGGTAGAGCTCGGGCTGGGCATAAAAGTCA
GGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCT
ACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCC
TGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAG
GGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCC
CGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCT
ACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCC
AGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGT
TCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGAC
GGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCACC
GCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGAC
GGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGT
GCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGA
GAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCAT
GGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCA
ACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTAC
GCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCA
TTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTG
CCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAG
AGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTT
CCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATC
GCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGG
GGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC
(SEQ ID NO: 122)

FIG. 22B cont'd

CN2485 (bp between ITR: 2769)

GCGGCCGCACGCGTAGGGAGGAACTAAAGTCCATTCATATGTCCATATTCTCAATTTGGGA
AAAAATGTGGCTTTGTCTTCATCCTCTTTTCCTGAGTGTATAAGGCCAGAAGCCAAAGGCAA
GAGCAGGACATTCCAGGAGCCTTTATGATTGCTCTAAGTCACATCTGCTCTCGAGCTCCCA
TTCCACTGTGAAAAATACCTAGTCTTGAACTTTGGAGTTCCAAATTCCACATGATCGACTTC
CTCAAGGCTTTTCACTTGACGAACAAATTGCATGCCAAGAAATCGTCAAAATTCTATCAAGC
TTAATTATGCAATTTCTGTCTATAAATGACATACCTCCTGTACCCTATGACACCCACCTATGC
ACTAATAAGATGTGACAGCTGCATCACCAACAAAGCCTCCCCCGCCTGCCATTCTCTTCGG
AGGTGAGCACCTCCTGCTCGGGAGGAACTGACAGCCCCTTTCAGAAATGTGAAGGCAGTG
AAGTCCCAAACCAGAAACAGTGTGACCACCTAGGCTCACCCAAGGACCGTCCTGTGCTTC
TGGGCAACCAATGGATGTAGGGGGTTAGGAGGCAGTGGGGATTCGTCAGAGCTCGGGCT
GGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTT
TCGAAGCTAGCCACCATGAATGCCTCAGAGTTCCGCAGGAGGGGAAAAGAGATGGTTGAC
TACATGGCAAACTATATGGAAGGCATAGAAGGGAGGCAAGTTTATCCAGATGTAGAACCGG
GGTACTTGCGACCTTTGATTCCAGCAGCAGCTCCTCAGGTAAGTACTAGCAGCTACAATCC
AGCTACCATTCTGCTTTTATTTTATGGTTGGGATAAGGCTGGATTATTCTGAGTCCAAGCTA
GGCCCTTTTGCTAATCATGTTCATACCTCTTATCTTCCTCCCACAGGAACCAGATACATTTG
AAGACATAATAAATGATGTTGAAAAGATAATCATGCCCGGGGTTACACATTGGCATAGCCC
ATACTTCTTTGCTTACTTTCCTACTGCTTCCTCTTACCCTGCAATGCTAGCAGATATGCTGT
GTGGAGCTATAGGGTGTATTGGGTTCTCTTGGGCTGCTAGCCCTGCTTGTACTGAGCTGG
AGACCGTGATGATGGATTGGCTTGGAAAAATGCTGGAGCTGCCCAAAGCATTCCTGAATGA
GAAAGCAGGAGAGGGTGGAGGTGTAATTCAAGGATCAGCTAGTGAAGCTACCCTTGTAGC
ATTGCTGGCAGCACGGACTAAAGTCATCCATCGCCTTCAAGCAGCTTCCCCTGAGCTCACT
CAGGCTGCGATAATGGAAAAGCTGGTTGCCTACTCTTCTGATCAAGCACACTCCTCAGTTG
AACGAGCAGGGCTCATTGGAGGCGTTAAGCTGAAGGCTATCCCTTCTGATGGGAATTTTG
CTATGAGAGCCTCAGCTCTGCAGGAAGCACTGGAACGTGATAAAGCTGCTGGCTTGATCC
CTTTCTTCATGGTGGCAACGTTGGGAACCACCACATGCTGTTCCTTTGATAATCTTCTGGA
GGTGGGCCCCATCTGCAATAAAGAGGACATCTGGCTTCATGTTGACGCAGCCTATGCTGG
ATCTGCTTTTATTTGTCCTGAATTTAGGCATTTGCTCAATGGTGTGGAGTTCGCTGATAGTT
TCAATTTCAATCCGCATAAATGGCTGCTTGTCAATTTTGATTGTTCCGCCATGTGGGTTAAG
AAACGCACTGATCTTACAGGAGCTTTTCGCCTGGACCCTACCTATTTGAAGCATTCCCACC
AAGACTCTGGACTGATTACGGACTATAGACACTGGCAGATTCCTCTGGGTAGACGATTCCG
CTCCCTCAAGATGTGGTTTGTTTTCCGAATGTATGGAGTCAAGGGTCTGCAAGCATACATC
CGGAAACATGTTCAGCTTTCACATGAATTTGAATCACTTGTCCGACAAGACCCCCGCTTCG
AGATCTGTGTAGAGGTCATATTGGGCCTTGTGTGTTTCCGACTGAAAGGGAGTAATAAAGT
CAATGAGGCCCTCTTGCAGAGAATCAATTCAGCGAAAAAGATACACTTGGTACCCTGCCAT
CTGAGAGATAAATTCGTCCTGAGATTCGCAATTTGCAGCCGGACCGTAGAATCTGCTCATG
TGCAGCGGGCCTGGGAACACATCAAAGAGTTGGCGGCAGATGTTCTCCGAGCTGAGAGG
GAGTAGTGAGGCGCGCCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTG
ACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTT
GTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGT
TCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGC
TGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGC
CATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGT
CCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGG

FIG. 22B cont'd

GGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGA
GATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 228)

CN2486 (bp between ITR: 2871)

GCGGCCGCACGCGTAGGGAGGAACTAAAGTCCATTCATATGTCCATATTCTCAATTTGGGA
AAAAATGTGGCTTTGTCTTCATCCTCTTTTCCTGAGTGTATAAGGCCAGAAGCCAAAGGCAA
GAGCAGGACATTCCAGGAGCCTTTATGATTGCTCTAAGTCACATCTGCTCTCGAGCTCCCA
TTCCACTGTGAAAAATACCTAGTCTTGAACTTTGGAGTTCCAAATTCCACATGATCGACTTC
CTCAAGGCTTTTCACTTGACGAACAAATTGCATGCCAAGAAATCGTCAAAATTCTATCAAGC
TTAATTATGCAATTTCTGTCTATAAATGACATACCTCCTGTACCCTATGACACCCACCTATGC
ACTAATAAGATGTGACAGCTGCATCACCAACAAAGCCTCCCCCGCCTGCCATTCTCTTCGG
AGGTGAGCACCTCCTGCTCGGGAGGAACTGACAGCCCCTTTCAGAAATGTGAAGGCAGTG
AAGTCCCAAACCAGAAACAGTGTGACCACCTAGGCTCACCCAAGGACCGTCCTGTGCTTC
TGGGCAACCAATGGATGTAGGGGGTTAGGAGGCAGTGGGGATTCGTCAGAGCTCGGGCT
GGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTT
TCGAAGCTAGCCACCATGAATGCCTCAGAGTTCCGCAGGAGGGGAAAAGAGATGGTTGAC
TACATGGCAAACTATATGGAAGGCATAGAAGGGAGGCAAGTTTATCCAGATGTAGAACCGG
GGTACTTGCGACCTTTGATTCCAGCAGCAGCTCCTCAGGTAAGTACTAGCAGCTACAATCC
AGCTACCATTCTGCTTTTATTTTATGGTTGGGATAAGGCTGGATTATTCTGAGTCCAAGCTA
GGCCCTTTTGCTAATCATGTTCATACCTCTTATCTTCCTCCCACAGGAACCAGATACATTTG
AAGACATAATAAATGATGTTGAAAAGATAATCATGCCCGGGGTTACACATTGGCATAGCCC
ATACTTCTTTGCTTACTTTCCTACTGCTTCCTCTTACCCTGCAATGCTAGCAGATATGCTGT
GTGGAGCTATAGGGTGTATTGGGTTCTCTTGGGCTGCTAGCCCTGCTTGTACTGAGCTGG
AGACCGTGATGATGGATTGGCTTGGAAAAATGCTGGAGCTGCCCAAAGCATTCCTGAATGA
GAAAGCAGGAGAGGGTGGAGGTGTAATTCAAGGATCAGCTAGTGAAGCTACCCTTGTAGC
ATTGCTGGCAGCACGGACTAAAGTCATCCATCGCCTTCAAGCAGCTTCCCCTGAGCTCACT
CAGGCTGCGATAATGGAAAAGCTGGTTGCCTACTCTTCTGATCAAGCACACTCCTCAGTTG
AACGAGCAGGGCTCATTGGAGGCGTTAAGCTGAAGGCTATCCCTTCTGATGGGAATTTTG
CTATGAGAGCCTCAGCTCTGCAGGAAGCACTGGAACGTGATAAAGCTGCTGGCTTGATCC
CTTTCTTCATGGTGGCAACGTTGGGAACCACCACATGCTGTTCCTTTGATAATCTTCTGGA
GGTGGGCCCCATCTGCAATAAAGAGGACATCTGGCTTCATGTTGACGCAGCCTATGCTGG
ATCTGCTTTTATTTGTCCTGAATTTAGGCATTTGCTCAATGGTGTGGAGTTCGCTGATAGTT
TCAATTTCAATCCGCATAAATGGCTGCTTGTCAATTTTGATTGTTCCGCCATGTGGGTTAAG
AAACGCACTGATCTTACAGGAGCTTTTCGCCTGGACCCTACCTATTTGAAGCATTCCCACC
AAGACTCTGGACTGATTACGGACTATAGACACTGGCAGATTCCTCTGGGTAGACGATTCCG
CTCCCTCAAGATGTGGTTTGTTTTCCGAATGTATGGAGTCAAGGGTCTGCAAGCATACATC
CGGAAACATGTTCAGCTTTCACATGAATTTGAATCACTTGTCCGACAAGACCCCCGCTTCG
AGATCTGTGTAGAGGTCATATTGGGCCTTGTGTGTTTCCGACTGAAAGGGAGTAATAAAGT
CAATGAGGCCCTCTTGCAGAGAATCAATTCAGCGAAAAAGATACACTTGGTACCCTGCCAT
CTGAGAGATAAATTCGTCCTGAGATTCGCAATTTGCAGCCGGACCGTAGAATCTGCTCATG
TGCAGCGGGCCTGGGAACACATCAAAGAGTTGGCGGCAGATGTTCTCCGAGCTGAGAGG
GAGGGTTCAGGTTACCCGTATGATGTCCCGGATTACGCTGGCAGCTACCCATACGATGTA
CCCGACTATGCCGGCAGTTATCCCTACGACGTCCCTGACTACGCATAGTGAGGCGCGCCG
ATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGT
TGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCC
GTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTC

FIG. 22B cont'd

ATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTC
CGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTC
CCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAG
GAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAG
GACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCG
AGCGGCCGC (SEQ ID NO: 229)

CN2739 (bp between ITR: 2818)

GCGGCCGCACGCGCCGGTACCGAAGCTACCCCTAACACACTATTCTACACACAGAAAATG
CTCTTCACTAGGAAGCTACCCCTAACACACTATTCTACACACAGAAAATGCTCTTCACTAGG
AAGCTACCCCTAACACACTATTCTACACACAGAAAATGCTCTTCACTAGACGCGTTAGCAG
GAGTACATCCTCCTCTGTTAGAAAAACAACTCTGCGGTTCTGGGTCACTTTTCCCATCTTTG
TATAGAAAAGTACCGATTATTATTGTTCCCCCGGGTGCCTTCTCCAGCTTAAAGGAAAATTC
CAGCCCCAGAGATCTTCCGCAGTGAGTGACAGCTCCTTAATGTGAGGAGCAGCGTGGGCG
TGGTGGGTGGGATGTCAGAGCCATCAAAGCCCTCATTTCTGATCCCTCTGTGATGTCGGG
GTTCCCTGGCACGCCCACTGTCATGCCTCAGCACATTGGCATCTGAGAGAGGAAAGGTGC
AGCTGACACCCTGACCCCCTTCTCCCCGACACGGGGTCAGACAGGGTCCCGCGGTGGCC
TGGTTGTGCAGCACTGACATGTTGCCTGGGAACGAAGAGCTCGATTCAGCCGGGAGCTTA
GGGAGGGGAGGTCACTTCATAAGGGCTTGGGGGGGGAGTTGGAGCCACGAGTCGTCCAG
CCGGAGCCCCGTGTGGCTGTGCTCCGGCCTCAGAAGCATCCCCGGATCCAGATCTTTCGA
AGCTAGCCACCATGAATGCCTCAGAGTTCCGCAGGAGGGGAAAAGAGATGGTTGACTACA
TGGCAAACTATATGGAAGGCATAGAAGGGAGGCAAGTTTATCCAGATGTAGAACCGGGGT
ACTTGCGACCTTTGATTCCAGCAGCAGCTCCTCAGGTAAGTACTAGCAGCTACAATCCAGC
TACCATTCTGCTTTTATTTTATGGTTGGGATAAGGCTGGATTATTCTGAGTCCAAGCTAGGC
CCTTTTGCTAATCATGTTCATACCTCTTATCTTCCTCCCACAGGAACCAGATACATTTGAAG
ACATAATAAATGATGTTGAAAAGATAATCATGCCCGGGGTTACACATTGGCATAGCCCATAC
TTCTTTGCTTACTTTCCTACTGCTTCCTCTTACCCTGCAATGCTAGCAGATATGCTGTGTGG
AGCTATAGGGTGTATTGGGTTCTCTTGGGCTGCTAGCCCTGCTTGTACTGAGCTGGAGAC
CGTGATGATGGATTGGCTTGGAAAAATGCTGGAGCTGCCCAAAGCATTCCTGAATGAGAAA
GCAGGAGAGGGTGGAGGTGTAATTCAAGGATCAGCTAGTGAAGCTACCCTTGTAGCATTG
CTGGCAGCACGGACTAAAGTCATCCATCGCCTTCAAGCAGCTTCCCCTGAGCTCACTCAG
GCTGCGATAATGGAAAAGCTGGTTGCCTACTCTTCTGATCAAGCACACTCCTCAGTTGAAC
GAGCAGGGCTCATTGGAGGCGTTAAGCTGAAGGCTATCCCTTCTGATGGGAATTTTGCTAT
GAGAGCCTCAGCTCTGCAGGAAGCACTGGAACGTGATAAAGCTGCTGGCTTGATCCCTTT
CTTCATGGTGGCAACGTTGGGAACCACCACATGCTGTTCCTTTGATAATCTTCTGGAGGTG
GGCCCCATCTGCAATAAAGAGGACATCTGGCTTCATGTTGACGCAGCCTATGCTGGATCTG
CTTTTATTTGTCCTGAATTTAGGCATTTGCTCAATGGTGTGGAGTTCGCTGATAGTTTCAATT
TCAATCCGCATAAATGGCTGCTTGTCAATTTTGATTGTTCCGCCATGTGGGTTAAGAAACGC
ACTGATCTTACAGGAGCTTTTCGCCTGGACCCTACCTATTTGAAGCATTCCCACCAAGACT
CTGGACTGATTACGGACTATAGACACTGGCAGATTCCTCTGGGTAGACGATTCCGCTCCCT
CAAGATGTGGTTTGTTTTCCGAATGTATGGAGTCAAGGGTCTGCAAGCATACATCCGGAAA
CATGTTCAGCTTTCACATGAATTTGAATCACTTGTCCGACAAGACCCCCGCTTCGAGATCT
GTGTAGAGGTCATATTGGGCCTTGTGTGTTTCCGACTGAAAGGGAGTAATAAAGTCAATGA
GGCCCTCTTGCAGAGAATCAATTCAGCGAAAAAGATACACTTGGTACCCTGCCATCTGAGA
GATAAATTCGTCCTGAGATTCGCAATTTGCAGCCGGACCGTAGAATCTGCTCATGTGCAGC
GGGCCTGGGAACACATCAAAGAGTTGGCGGCAGATGTTCTCCGAGCTGAGAGGGAGTAG

FIG. 22B cont'd

TGAGGCGCGCCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGT
ATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCAT
GCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCC
ACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGG
CACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGT
TGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCC
TAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTG
GGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCA
CGTGCGGACCGAGCGGCCGC (SEQ ID NO: 230)

CN2740 (bp between ITR: 2920)

GCGGCCGCACGCGCCGGTACCGAAGCTACCCCTAACACACTATTCTACACACAGAAAATG
CTCTTCACTAGGAAGCTACCCCTAACACACTATTCTACACACAGAAAATGCTCTTCACTAGG
AAGCTACCCCTAACACACTATTCTACACACAGAAAATGCTCTTCACTAGACGCGTTAGCAG
GAGTACATCCTCCTCTGTTAGAAAAACAACTCTGCGGTTCTGGGTCACTTTTCCCATCTTTG
TATAGAAAAGTACCGATTATTATTGTTCCCCCGGGTGCCTTCTCCAGCTTAAAGGAAAATTC
CAGCCCCAGAGATCTTCCGCAGTGAGTGACAGCTCCTTAATGTGAGGAGCAGCGTGGGCG
TGGTGGGTGGGATGTCAGAGCCATCAAAGCCCTCATTTCTGATCCCTCTGTGATGTCGGG
GTTCCCTGGCACGCCCACTGTCATGCCTCAGCACATTGGCATCTGAGAGAGGAAAGGTGC
AGCTGACACCCTGACCCCCTTCTCCCCGACACGGGGTCAGACAGGGTCCCGCGGTGGCC
TGGTTGTGCAGCACTGACATGTTGCCTGGGAACGAAGAGCTCGATTCAGCCGGGAGCTTA
GGGAGGGGAGGTCACTTCATAAGGGCTTGGGGGGGGAGTTGGAGCCACGAGTCGTCCAG
CCGGAGCCCCGTGTGGCTGTGCTCCGGCCTCAGAAGCATCCCCGGATCCAGATCTTTCGA
AGCTAGCCACCATGAATGCCTCAGAGTTCCGCAGGAGGGGAAAAGAGATGGTTGACTACA
TGGCAAACTATATGGAAGGCATAGAAGGGAGGCAAGTTTATCCAGATGTAGAACCGGGGT
ACTTGCGACCTTTGATTCCAGCAGCAGCTCCTCAGGTAAGTACTAGCAGCTACAATCCAGC
TACCATTCTGCTTTTATTTTATGGTTGGGATAAGGCTGGATTATTCTGAGTCCAAGCTAGGC
CCTTTTGCTAATCATGTTCATACCTCTTATCTTCCTCCCACAGGAACCAGATACATTTGAAG
ACATAATAAATGATGTTGAAAAGATAATCATGCCCGGGGTTACACATTGGCATAGCCCATAC
TTCTTTGCTTACTTTCCTACTGCTTCCTCTTACCCTGCAATGCTAGCAGATATGCTGTGTGG
AGCTATAGGGTGTATTGGGTTCTCTTGGGCTGCTAGCCCTGCTTGTACTGAGCTGGAGAC
CGTGATGATGGATTGGCTTGGAAAAATGCTGGAGCTGCCCAAAGCATTCCTGAATGAGAAA
GCAGGAGAGGGTGGAGGTGTAATTCAAGGATCAGCTAGTGAAGCTACCCTTGTAGCATTG
CTGGCAGCACGGACTAAAGTCATCCATCGCCTTCAAGCAGCTTCCCCTGAGCTCACTCAG
GCTGCGATAATGGAAAAGCTGGTTGCCTACTCTTCTGATCAAGCACACTCCTCAGTTGAAC
GAGCAGGGCTCATTGGAGGCGTTAAGCTGAAGGCTATCCCTTCTGATGGGAATTTTGCTAT
GAGAGCCTCAGCTCTGCAGGAAGCACTGGAACGTGATAAAGCTGCTGGCTTGATCCCTTT
CTTCATGGTGGCAACGTTGGGAACCACCACATGCTGTTCCTTTGATAATCTTCTGGAGGTG
GGCCCCATCTGCAATAAAGAGGACATCTGGCTTCATGTTGACGCAGCCTATGCTGGATCTG
CTTTTATTTGTCCTGAATTTAGGCATTTGCTCAATGGTGTGGAGTTCGCTGATAGTTTCAATT
TCAATCCGCATAAATGGCTGCTTGTCAATTTTGATTGTTCCGCCATGTGGGTTAAGAAACGC
ACTGATCTTACAGGAGCTTTTCGCCTGGACCCTACCTATTTGAAGCATTCCCACCAAGACT
CTGGACTGATTACGGACTATAGACACTGGCAGATTCCTCTGGGTAGACGATTCCGCTCCCT
CAAGATGTGGTTTGTTTTCCGAATGTATGGAGTCAAGGGTCTGCAAGCATACATCCGGAAA
CATGTTCAGCTTTCACATGAATTTGAATCACTTGTCCGACAAGACCCCCGCTTCGAGATCT
GTGTAGAGGTCATATTGGGCCTTGTGTGTTTCCGACTGAAAGGGAGTAATAAAGTCAATGA

FIG. 22B cont'd

GGCCCTCTTGCAGAGAATCAATTCAGCGAAAAAGATACACTTGGTACCCTGCCATCTGAGA
GATAAATTCGTCCTGAGATTCGCAATTTGCAGCCGGACCGTAGAATCTGCTCATGTGCAGC
GGGCCTGGGAACACATCAAAGAGTTGGCGGCAGATGTTCTCCGAGCTGAGAGGGAGGGT
TCAGGTTACCCGTATGATGTCCCGGATTACGCTGGCAGCTACCCATACGATGTACCCGACT
ATGCCGGCAGTTATCCCTACGACGTCCCTGACTACGCATAGTGAGGCGCGCCGATATCAT
AATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCT
TTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGC
TTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCG
CCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCT
CGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTG
CCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTG
CATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCA
AGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCC
GC (SEQ ID NO: 231)

CN2765 (bp between ITR: 2751)

GCGGCCGCACGCGCCGGTACCGAAGCTACCCCTAACACACTATTCTACACACAGAAAATG
CTCTTCACTAGGAAGCTACCCCTAACACACTATTCTACACACAGAAAATGCTCTTCACTAGG
AAGCTACCCCTAACACACTATTCTACACACAGAAAATGCTCTTCACTAGACGCGTTAGCAG
GAGTACATCCTCCTCTGTTAGAAAAACAACTCTGCGGTTCTGGGTCACTTTTCCCATCTTTG
TATAGAAAAGTACCGATTATTATTGTTCCCCCGGGTGCCTTCTCCAGCTTAAAGGAAAATTC
CAGCCCCAGAGATCTTCCGCAGTGAGTGACAGCTCCTTAATGTGAGGAGCAGCGTGGGCG
TGGTGGGTGGGATGTCAGAGCCATCAAAGCCCTCATTTCTGATCCCTCTGTGATGTCGGG
GTTCCCTGGCACGCCCACTGTCATGCCTCAGCACATTGGCATCTGAGAGAGGAAAGGTGC
AGCTGACACCCTGACCCCCTTCTCCCCGACACGGGGTCAGACAGGGTCCCGCGGTGGCC
TGGTTGTGCAGCACTGACATGTTGCCTGGGAACGAAGAGCTCGGGCTGGGCATAAAAGTC
AGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCCA
CCATGAATGCCTCAGAGTTCCGCAGGAGGGGAAAAGAGATGGTTGACTACATGGCAAACT
ATATGGAAGGCATAGAAGGGAGGCAAGTTTATCCAGATGTAGAACCGGGGTACTTGCGAC
CTTTGATTCCAGCAGCAGCTCCTCAGGTAAGTACTAGCAGCTACAATCCAGCTACCATTCT
GCTTTTATTTTATGGTTGGGATAAGGCTGGATTATTCTGAGTCCAAGCTAGGCCCTTTTGCT
AATCATGTTCATACCTCTTATCTTCCTCCCACAGGAACCAGATACATTTGAAGACATAATAA
ATGATGTTGAAAAGATAATCATGCCCGGGGTTACACATTGGCATAGCCCATACTTCTTTGCT
TACTTTCCTACTGCTTCCTCTTACCCTGCAATGCTAGCAGATATGCTGTGTGGAGCTATAGG
GTGTATTGGGTTCTCTTGGGCTGCTAGCCCTGCTTGTACTGAGCTGGAGACCGTGATGAT
GGATTGGCTTGGAAAAATGCTGGAGCTGCCCAAAGCATTCCTGAATGAGAAAGCAGGAGA
GGGTGGAGGTGTAATTCAAGGATCAGCTAGTGAAGCTACCCTTGTAGCATTGCTGGCAGC
ACGGACTAAAGTCATCCATCGCCTTCAAGCAGCTTCCCCTGAGCTCACTCAGGCTGCGATA
ATGGAAAAGCTGGTTGCCTACTCTTCTGATCAAGCACACTCCTCAGTTGAACGAGCAGGGC
TCATTGGAGGCGTTAAGCTGAAGGCTATCCCTTCTGATGGGAATTTTGCTATGAGAGCCTC
AGCTCTGCAGGAAGCACTGGAACGTGATAAAGCTGCTGGCTTGATCCCTTTCTTCATGGTG
GCAACGTTGGGAACCACCACATGCTGTTCCTTTGATAATCTTCTGGAGGTGGGCCCCATCT
GCAATAAAGAGGACATCTGGCTTCATGTTGACGCAGCCTATGCTGGATCTGCTTTTATTTGT
CCTGAATTTAGGCATTTGCTCAATGGTGTGGAGTTCGCTGATAGTTTCAATTTCAATCCGCA
TAAATGGCTGCTTGTCAATTTTGATTGTTCCGCCATGTGGGTTAAGAAACGCACTGATCTTA
CAGGAGCTTTTCGCCTGGACCCTACCTATTTGAAGCATTCCCACCAAGACTCTGGACTGAT

FIG. 22B cont'd

TACGGACTATAGACACTGGCAGATTCCTCTGGGTAGACGATTCCGCTCCCTCAAGATGTGG
TTTGTTTTCCGAATGTATGGAGTCAAGGGTCTGCAAGCATACATCCGGAAACATGTTCAGC
TTTCACATGAATTTGAATCACTTGTCCGACAAGACCCCCGCTTCGAGATCTGTGTAGAGGT
CATATTGGGCCTTGTGTGTTTCCGACTGAAAGGGAGTAATAAAGTCAATGAGGCCCTCTTG
CAGAGAATCAATTCAGCGAAAAAGATACACTTGGTACCCTGCCATCTGAGAGATAAATTCG
TCCTGAGATTCGCAATTTGCAGCCGGACCGTAGAATCTGCTCATGTGCAGCGGGCCTGGG
AACACATCAAAGAGTTGGCGGCAGATGTTCTCCGAGCTGAGAGGGAGTAGTGAGGCGCG
CCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTA
TGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTT
CCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAA
CTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAA
TTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCC
CTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAAT
GAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGG
CAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGA
CCGAGCGGCCGC (SEQ ID NO: 232)

CN2766 (bp between ITR: 2853)

GCGGCCGCACGCGCCGGTACCGAAGCTACCCCTAACACACTATTCTACACACAGAAAATG
CTCTTCACTAGGAAGCTACCCCTAACACACTATTCTACACACAGAAAATGCTCTTCACTAGG
AAGCTACCCCTAACACACTATTCTACACACAGAAAATGCTCTTCACTAGACGCGTTAGCAG
GAGTACATCCTCCTCTGTTAGAAAAACAACTCTGCGGTTCTGGGTCACTTTTCCCATCTTTG
TATAGAAAAGTACCGATTATTATTGTTCCCCCGGGTGCCTTCTCCAGCTTAAAGGAAAATTC
CAGCCCCAGAGATCTTCCGCAGTGAGTGACAGCTCCTTAATGTGAGGAGCAGCGTGGGCG
TGGTGGGTGGGATGTCAGAGCCATCAAAGCCCTCATTTCTGATCCCTCTGTGATGTCGGG
GTTCCCTGGCACGCCCACTGTCATGCCTCAGCACATTGGCATCTGAGAGAGGAAAGGTGC
AGCTGACACCCTGACCCCCTTCTCCCCGACACGGGGTCAGACAGGGTCCCGCGGTGGCC
TGGTTGTGCAGCACTGACATGTTGCCTGGGAACGAAGAGCTCGGGCTGGGCATAAAAGTC
AGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCCA
CCATGAATGCCTCAGAGTTCCGCAGGAGGGGAAAAGAGATGGTTGACTACATGGCAAACT
ATATGGAAGGCATAGAAGGGAGGCAAGTTTATCCAGATGTAGAACCGGGGTACTTGCGAC
CTTTGATTCCAGCAGCAGCTCCTCAGGTAAGTACTAGCAGCTACAATCCAGCTACCATTCT
GCTTTTATTTTATGGTTGGGATAAGGCTGGATTATTCTGAGTCCAAGCTAGGCCCTTTTGCT
AATCATGTTCATACCTCTTATCTTCCTCCCACAGGAACCAGATACATTTGAAGACATAATAA
ATGATGTTGAAAAGATAATCATGCCCGGGGTTACACATTGGCATAGCCCATACTTCTTTGCT
TACTTTCCTACTGCTTCCTCTTACCCTGCAATGCTAGCAGATATGCTGTGTGGAGCTATAGG
GTGTATTGGGTTCTCTTGGGCTGCTAGCCCTGCTTGTACTGAGCTGGAGACCGTGATGAT
GGATTGGCTTGGAAAAATGCTGGAGCTGCCCAAAGCATTCCTGAATGAGAAAGCAGGAGA
GGGTGGAGGTGTAATTCAAGGATCAGCTAGTGAAGCTACCCTTGTAGCATTGCTGGCAGC
ACGGACTAAAGTCATCCATCGCCTTCAAGCAGCTTCCCCTGAGCTCACTCAGGCTGCGATA
ATGGAAAAGCTGGTTGCCTACTCTTCTGATCAAGCACACTCCTCAGTTGAACGAGCAGGGC
TCATTGGAGGCGTTAAGCTGAAGGCTATCCCTTCTGATGGGAATTTTGCTATGAGAGCCTC
AGCTCTGCAGGAAGCACTGGAACGTGATAAAGCTGCTGGCTTGATCCCTTTCTTCATGGTG
GCAACGTTGGGAACCACCACATGCTGTTCCTTTGATAATCTTCTGGAGGTGGGCCCCATCT
GCAATAAAGAGGACATCTGGCTTCATGTTGACGCAGCCTATGCTGGATCTGCTTTTATTTGT
CCTGAATTTAGGCATTTGCTCAATGGTGTGGAGTTCGCTGATAGTTTCAATTTCAATCCGCA

FIG. 22B cont'd

TAAATGGCTGCTTGTCAATTTTGATTGTTCCGCCATGTGGGTTAAGAAACGCACTGATCTTA
CAGGAGCTTTTCGCCTGGACCCTACCTATTTGAAGCATTCCCACCAAGACTCTGGACTGAT
TACGGACTATAGACACTGGCAGATTCCTCTGGGTAGACGATTCCGCTCCCTCAAGATGTGG
TTTGTTTTCCGAATGTATGGAGTCAAGGGTCTGCAAGCATACATCCGGAAACATGTTCAGC
TTTCACATGAATTTGAATCACTTGTCCGACAAGACCCCCGCTTCGAGATCTGTGTAGAGGT
CATATTGGGCCTTGTGTGTTTCCGACTGAAAGGGAGTAATAAAGTCAATGAGGCCCTCTTG
CAGAGAATCAATTCAGCGAAAAAGATACACTTGGTACCCTGCCATCTGAGAGATAAATTCG
TCCTGAGATTCGCAATTTGCAGCCGGACCGTAGAATCTGCTCATGTGCAGCGGGCCTGGG
AACACATCAAAGAGTTGGCGGCAGATGTTCTCCGAGCTGAGAGGGAGGGTTCAGGTTACC
CGTATGATGTCCCGGATTACGCTGGCAGCTACCCATACGATGTACCCGACTATGCCGGCA
GTTATCCCTACGACGTCCCTGACTACGCATAGTGAGGCGCGCCGATATCATAATCAACCTC
TGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTAT
GTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTC
TCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTG
CCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATC
TTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTG
ACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATT
GTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAG
GATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID
NO: 233)

CN2514 (bp between ITR: 1748)

GCGGCCGCACGCGCCGGTACCGAAGCTACCCCTAACACACTATTCTACACACAGAAAATG
CTCTTCACTAGGAAGCTACCCCTAACACACTATTCTACACACAGAAAATGCTCTTCACTAGG
AAGCTACCCCTAACACACTATTCTACACACAGAAAATGCTCTTCACTAGACGCGTTCCAGCT
TAAAGGAAAATTCCAGCCCCAGAGATCTTCCGCAGTGAGTGACAGCTCCTTAATGTGAGGA
GCAGCGTGGGCGTGGTGGGTGGGATGTCAGAGCCATCAAAGCCCTCATTTCTGATCCCTC
TGTGATGTCGGGGTTCCCTGGCACGCCCACTGGAGCTCGATTCAGCCGGGAGCTTAGGG
AGGGGAGGTCACTTCATAAGGGCTTGGGGGGGGAGTTGGAGCCACGAGTCGTCCAGCCG
GAGCCCCGTGTGGCTGTGCTCCGGCCTCAGAAGCATCCCCGGATCCAGATCTTTCGAAGC
TAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTG
CCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGA
GGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCA
AGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTC
GCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGC
TACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAG
GTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAG
GAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTAT
ATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATC
GAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGG
CCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCC
CAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCT
CGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATC
ATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTC
CTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATG
GCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGC

FIG. 22B cont'd

CGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGG
CTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCG
TGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAAT
TGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAG
CAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGG
CCGC (SEQ ID NO: 234)

CN2555 (bp between ITR: 2068)

GCGGCCGCACGCGCCGGTACCGAAGCTACCCCTAACACACTATTCTACACACAGAAAATG
CTCTTCACTAGGAAGCTACCCCTAACACACTATTCTACACACAGAAAATGCTCTTCACTAGG
AAGCTACCCCTAACACACTATTCTACACACAGAAAATGCTCTTCACTAGACGCGTTCCAGCT
TAAAGGAAAATTCCAGCCCCAGAGATCTTCCGCAGTGAGTGACAGCTCCTTAATGTGAGGA
GCAGCGTGGGCGTGGTGGGTGGGATGTCAGAGCCATCAAAGCCCTCATTTCTGATCCCTC
TGTGATGTCGGGGTTCCCTGGCACGCCCACTGTCCAGCTTAAAGGAAAATTCCAGCCCCA
GAGATCTTCCGCAGTGAGTGACAGCTCCTTAATGTGAGGAGCAGCGTGGGCGTGGTGGGT
GGGATGTCAGAGCCATCAAAGCCCTCATTTCTGATCCCTCTGTGATGTCGGGGTTCCCTG
GCACGCCCACTGTCCAGCTTAAAGGAAAATTCCAGCCCCAGAGATCTTCCGCAGTGAGTG
ACAGCTCCTTAATGTGAGGAGCAGCGTGGGCGTGGTGGGTGGGATGTCAGAGCCATCAAA
GCCCTCATTTCTGATCCCTCTGTGATGTCGGGGTTCCCTGGCACGCCCACTGGAGCTCGA
TTCAGCCGGGAGCTTAGGGAGGGGAGGTCACTTCATAAGGGCTTGGGGGGGGAGTTGGA
GCCACGAGTCGTCCAGCCGGAGCCCCGTGTGGCTGTGCTCCGGCCTCAGAAGCATCCCC
GGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGG
AGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCAC
AAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAA
GCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGG
GCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCA
AGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCA
ACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAG
CTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAAC
TACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAAC
TTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCA
GAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACC
AGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCG
TGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCG
CCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGA
CTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGT
ATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTC
TTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTG
TTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCA
TCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCC
TTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGG
GGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGAT
CTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 235)

FIG. 22B cont'd

CN2907 (bp between ITR: 2636)

GCGGCCGCACGCGTGCCCACCCCTCCTCCAGCTCTCAGGAGTCCCATTCCCTTCCTCCTC
TGTCGCCCACACAGCCCCCACCACCTGGCCGCCCACCTGAAAAACTTTTCCCCAAGTTCTT
GAGAAGTCGCGTAGGATCCAGGAGAGAAAAATCAAAGTAATAAAACCTCATTTAATTCCTAA
CGGAGGGCAGAGCTGCGAGCTGCAATTATCTTAATGCTGAGCTATTTTTACTCTCTCTCCA
TCTCTGTCTTCTGCCTTTCTCTGTTGTGAGGTTCGCTGTCTCTCTCTCTGCCTCCCTTTGTC
TCTCCATCTCTCAACCATGTTTTCTGTCTCTCTTTGCTTTCTCCTCTCTCCCCCCAATCTCTC
TCTCACGTCCTGTCTCTGTGCAGTCTCTTCCTCCTCCTTCATGTCTGTCCCTCTGTCAGCCA
GTCTTCCCCACGCCCACCCCTCCTCCAGCTCTCAGGAGTCCCATTCCCTTCCTCCTCTGTC
GCCCACACAGCCCCCACCACCTGGCCGCCCACCTGAAAAACTTTTCCCCAAGTTCTTGAG
AAGTCGCGTAGGATCCAGGAGAGAAAAATCAAAGTAATAAAACCTCATTTAATTCCTAACG
GAGGGCAGAGCTGCGAGCTGCAATTATCTTAATGCTGAGCTATTTTTACTCTCTCTCCATCT
CTGTCTTCTGCCTTTCTCTGTTGTGAGGTTCGCTGTCTCTCTCTCTGCCTCCCTTTGTCTCT
CCATCTCTCAACCATGTTTTCTGTCTCTCTTTGCTTTCTCCTCTCTCCCCCCAATCTCTCTCT
CACGTCCTGTCTCTGTGCAGTCTCTTCCTCCTCCTTCATGTCTGTCCCTCTGTCAGCCAGT
CTTCCCCACGCCCACCCCTCCTCCAGCTCTCAGGAGTCCCATTCCCTTCCTCCTCTGTCGC
CCACACAGCCCCCACCACCTGGCCGCCCACCTGAAAAACTTTTCCCCAAGTTCTTGAGAA
GTCGCGTAGGATCCAGGAGAGAAAAATCAAAGTAATAAAACCTCATTTAATTCCTAACGGA
GGGCAGAGCTGCGAGCTGCAATTATCTTAATGCTGAGCTATTTTTACTCTCTCTCCATCTCT
GTCTTCTGCCTTTCTCTGTTGTGAGGTTCGCTGTCTCTCTCTCTGCCTCCCTTTGTCTCTCC
ATCTCTCAACCATGTTTTCTGTCTCTCTTTGCTTTCTCCTCTCTCCCCCCAATCTCTCTCTCA
CGTCCTGTCTCTGTGCAGTCTCTTCCTCCTCCTTCATGTCTGTCCCTCTGTCAGCCAGTCTT
CCCCACGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGC
TTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGC
GAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGG
CCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCC
TGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACC
CTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTC
TTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGAC
GGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCAT
CGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGT
ACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGG
CCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACC
AGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGC
TACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAG
TTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGC
GCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGAT
TGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCT
TTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTA
GTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCG
GCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCA
GCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACT
GTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCT
GGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCAT
GCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 236)

FIG. 22B cont'd

CN2909 (bp between ITR: 2018)

GCGGCCGCACGCGTGTGGAGGACTTTGAGCTTAACCCTATTAAATTTAATCTAATATATTCA
GCAGCCTGTCACAATCTTGTTAAATCTTTATTCCGTCACCCACCTTATTAGGGGGCCCTCC
CACTTTAGTCATCAGCAGATTAGTAAGCATGCCATTTAGATGTCATCTAAGTTAATGAACCT
GACTGAGCCAGAGTCACATGGCAGAGTCACAGAAACTCCTTCTGAGCTGGCGTGGAGGAC
TTTGAGCTTAACCCTATTAAATTTAATCTAATATATTCAGCAGCCTGTCACAATCTTGTTAAA
TCTTTATTCCGTCACCCACCTTATTAGGGGGCCCTCCCACTTTAGTCATCAGCAGATTAGTA
AGCATGCCATTTAGATGTCATCTAAGTTAATGAACCTGACTGAGCCAGAGTCACATGGCAG
AGTCACAGAAACTCCTTCTGAGCTGGCGTGGAGGACTTTGAGCTTAACCCTATTAAATTTAA
TCTAATATATTCAGCAGCCTGTCACAATCTTGTTAAATCTTTATTCCGTCACCCACCTTATTA
GGGGGCCCTCCCACTTTAGTCATCAGCAGATTAGTAAGCATGCCATTTAGATGTCATCTAA
GTTAATGAACCTGACTGAGCCAGAGTCACATGGCAGAGTCACAGAAACTCCTTCTGAGCTG
GCGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCT
GGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAG
GAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCA
CAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGA
AGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTG
GGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTC
AAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGC
AACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGA
GCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACA
ACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCA
ACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAG
CAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTA
CCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTT
CGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCG
CGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATT
GACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTT
TGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAG
TTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGG
CTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAG
CCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTG
TCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTG
GGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATG
CACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 237)

CN2921 (bp between ITR: 2057)

GCGGCCGCACGCGTGGCCACCCCCTTCCACCTTGTGTTCCCGTGTCGTGTCGGGTCCTAC
TCCTCCCATTTCTTTGCCCCTGAAGTGCTGAGAGGGGGAGAGGGTGGAGCCCAGCCCTCC
CCCTGCCCACTCTAGCTGTCAATCTGCTGTCTGGCAGAAAGACATGAAGCCTCGTGACAAC
TGTGGGCAACTTTCCCCTGCCCCGCCTCCCGCCCCTGCCCTGCCCTCTTCCCCTCTGCTC
CCTGTCAAGGCCACCCCCTTCCACCTTGTGTTCCCGTGTCGTGTCGGGTCCTACTCCTCC
CATTTCTTTGCCCCTGAAGTGCTGAGAGGGGGAGAGGGTGGAGCCCAGCCCTCCCCCTG
CCCACTCTAGCTGTCAATCTGCTGTCTGGCAGAAAGACATGAAGCCTCGTGACAACTGTGG
GCAACTTTCCCCTGCCCCGCCTCCCGCCCCTGCCCTGCCCTCTTCCCCTCTGCTCCCTGT
CAAGGCCACCCCCTTCCACCTTGTGTTCCCGTGTCGTGTCGGGTCCTACTCCTCCCATTTC

FIG. 22B cont'd

TTTGCCCCTGAAGTGCTGAGAGGGGGAGAGGGTGGAGCCCAGCCCTCCCCCTGCCCACT
CTAGCTGTCAATCTGCTGTCTGGCAGAAAGACATGAAGCCTCGTGACAACTGTGGGCAACT
TTCCCCTGCCCCGCCTCCCGCCCCTGCCCTGCCCTCTTCCCCTCTGCTCCCTGTCAAGAG
CTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATC
CAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGT
TCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTC
AGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGAT
CTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACG
GCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCG
CCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACA
AGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAG
GGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAAC
AGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAG
ATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACAC
CCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAA
GCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGC
CGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGC
CGCGAATTCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATT
CTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCT
ATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCAC
GGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCA
CTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTG
TTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTA
ATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGG
GTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCACGTGCGGA
CCGAGCGGCCGC (SEQ ID NO: 238)

CN2982 (bp between ITR: 2036)

GCGGCCGCACGCGTGTGAAAAATACCTAGTCTTGAACTTTGGAGTTCCAAATTCCACATGA
TCGACTTCCTCAAGGCTTTTCACTTGACGAACAAATTGCATGCCAAGAAATCGTCAAAATTC
TATCAAGCTTAATTATGCAATTTCTGTCTATAAATGACATACCTCCTGTACCCTATGACACCC
ACCTATGCACTAATAAGATGTGACAGCTGCATCACCAACAAAGCCTCCCCCGCCTGGTGAA
AAATACCTAGTCTTGAACTTTGGAGTTCCAAATTCCACATGATCGACTTCCTCAAGGCTTTT
CACTTGACGAACAAATTGCATGCCAAGAAATCGTCAAAATTCTATCAAGCTTAATTATGCAA
TTTCTGTCTATAAATGACATACCTCCTGTACCCTATGACACCCACCTATGCACTAATAAGAT
GTGACAGCTGCATCACCAACAAAGCCTCCCCCGCCTGGTGAAAAATACCTAGTCTTGAACT
TTGGAGTTCCAAATTCCACATGATCGACTTCCTCAAGGCTTTTCACTTGACGAACAAATTGC
ATGCCAAGAAATCGTCAAAATTCTATCAAGCTTAATTATGCAATTTCTGTCTATAAATGACAT
ACCTCCTGTACCCTATGACACCCACCTATGCACTAATAAGATGTGACAGCTGCATCACCAA
CAAAGCCTCCCCCGCCTGGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATT
GCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGG
TGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGC
GACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGG
CAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCT
CGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGC
AGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCT

FIG. 22B cont'd

TCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTG
GTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCA
CAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAA
CGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCG
CCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAAC
CACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATG
GTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAA
GTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATTACAA
AATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACG
CTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGT
ATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCT
GGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTG
CCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAG
GTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAG
GTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAG
ACAATAGCAGGCATGCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 239)

CN3044 (bp between ITR: 1934)

GCGGCCGCACGCGTAAGTTTGAGACAAATTAAGGAAAAGCGGGTTGGGAGGAGTCTGAG
GCTGTGGGTGGCTGCCTCGAGAGGCTGCTCACAACCTGACATGTTTCAGATCTTTTGACAC
GGTCATGCAAGCAACAGAAACTTATATGGTTTTTAGTCTCCCAGGTAGCAGGGAAATGATG
ATGTGGGAGGATTAGGGGGGGGAAAATAAGTTTGAGACAAATTAAGGAAAAGCGGGTTGG
GAGGAGTCTGAGGCTGTGGGTGGCTGCCTCGAGAGGCTGCTCACAACCTGACATGTTTCA
GATCTTTTGACACGGTCATGCAAGCAACAGAAACTTATATGGTTTTTAGTCTCCCAGGTAGC
AGGGAAATGATGATGTGGGAGGATTAGGGGGGGGAAAATAAGTTTGAGACAAATTAAGGA
AAAGCGGGTTGGGAGGAGTCTGAGGCTGTGGGTGGCTGCCTCGAGAGGCTGCTCACAAC
CTGACATGTTTCAGATCTTTTGACACGGTCATGCAAGCAACAGAAACTTATATGGTTTTTAG
TCTCCCAGGTAGCAGGGAAATGATGATGTGGGAGGATTAGGGGGGGGAAAATGAGCTCG
GGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGA
TCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCAC
CGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCG
TGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGC
ACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGT
GCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCAT
GCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGAC
CCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCA
TCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCC
ACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCC
GCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCC
ATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTG
AGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGC
CGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGC
GAATTCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTA
ACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATT
GCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGC
GGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTG

FIG. 22B cont'd

ACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTT
GCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATA
AAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTG
GGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCACGTGCGGACC
GAGCGGCCGC (SEQ ID NO: 240)

CN3038 (bp between ITR: 2099)

GCGGCCGCACGCGTAGCAGCAGCTAGTAGTACATACAAAGAAATAGAAAACATGAAGACC
AGGGGAGTTTAATTATATGGTTGCAAAAATGGTTCAACATTGCAAAGTTGTTAATACTCAGT
GGATGGGGAGGGAGCTGTGCAATTATCTCCACAGGTACAGAAAAGGCACTTAGTAAAATG
TAGCCAACTCTTTGGCTTCTAAAAAAGGAGAAAATGGTTTACAAAAACAAGCCTCCCTGGAT
GCTTCCTTAATTTGTTCTTAGCAGCAGCTAGTAGTACATACAAAGAAATAGAAAACATGAAG
ACCAGGGGAGTTTAATTATATGGTTGCAAAAATGGTTCAACATTGCAAAGTTGTTAATACTC
AGTGGATGGGGAGGGAGCTGTGCAATTATCTCCACAGGTACAGAAAAGGCACTTAGTAAA
ATGTAGCCAACTCTTTGGCTTCTAAAAAAGGAGAAAATGGTTTACAAAAACAAGCCTCCCTG
GATGCTTCCTTAATTTGTTCTTAGCAGCAGCTAGTAGTACATACAAAGAAATAGAAAACATG
AAGACCAGGGGAGTTTAATTATATGGTTGCAAAAATGGTTCAACATTGCAAAGTTGTTAATA
CTCAGTGGATGGGGAGGGAGCTGTGCAATTATCTCCACAGGTACAGAAAAGGCACTTAGT
AAAATGTAGCCAACTCTTTGGCTTCTAAAAAAGGAGAAAATGGTTTACAAAAACAAGCCTCC
CTGGATGCTTCCTTAATTTGTTCTTGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCA
TCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCA
CCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTG
GACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCAC
CTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGC
CCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCAC
ATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACC
ATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGAC
ACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTG
GGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAG
AAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCA
GCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCG
ACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATC
ACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGT
ACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATT
ACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGAT
ACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCT
TGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTG
CTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTG
TGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGA
AGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTA
GGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAA
GACAATAGCAGGCATGCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 241)

CN3344 (bp between ITR: 1958)

GCGGCCGCACGCGTATACAATAGATTAATTTTATCTAACATTAATAGCTGGATGTATAAGAA
ACACCCACTCTCTAGAAATTAAGACATGTCACCATAGTCTTATGACAAGAGTGAGTCTCTTA

FIG. 22B cont'd

TTTTTGAACTTTCTATTGAACAGTTCTCACCATCTTAAATCACCCTTTGTTATGAGTTTTTAAG
TGTCTTAAGTAGAGAAGGTTAAGAAAATACAATAGATTAATTTTATCTAACATTAATAGCTGG
ATGTATAAGAAACACCCACTCTCTAGAAATTAAGACATGTCACCATAGTCTTATGACAAGAG
TGAGTCTCTTATTTTTGAACTTTCTATTGAACAGTTCTCACCATCTTAAATCACCCTTTGTTAT
GAGTTTTTAAGTGTCTTAAGTAGAGAAGGTTAAGAAAATACAATAGATTAATTTTATCTAACA
TTAATAGCTGGATGTATAAGAAACACCCACTCTCTAGAAATTAAGACATGTCACCATAGTCT
TATGACAAGAGTGAGTCTCTTATTTTTGAACTTTCTATTGAACAGTTCTCACCATCTTAAATC
ACCCTTTGTTATGAGTTTTTAAGTGTCTTAAGTAGAGAAGGTTAAGAAAGAGCTCGGGCTG
GGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTT
CGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGG
GTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTC
CGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCA
CCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAG
TGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCC
GAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGC
GCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGA
CTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAA
CGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCA
CAACATCGAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCG
GCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGC
AAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGG
GATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAA
TTCGATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACT
ATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTT
CCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAA
CTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAA
TTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCC
CTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAAT
GAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGG
CAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGA
CCGAGCGGCCGC (SEQ ID NO: 242)

CN3281 (bp between ITR: 1958)

GCGGCCGCACGCGTCAGATAAAGTCTGGAGCCGGGCCCAGGTACCTGAGGCTCAGAGAT
GAGCCCGCAGCGAAGCTGACAACTGACTCATTCCTCCGACACTCTCCCACCCTCCCAGCT
AAGGAGGTGTCTGATGTGAACATGTTCTGCCTCTTTGTTGCCTGCTGTTGGGGGCGAGGG
CTTTGGGTGGATTTTGAAGAGCAATTATGCTTATTCAGATAAAGTCTGGAGCCGGGCCCAG
GTACCTGAGGCTCAGAGATGAGCCCGCAGCGAAGCTGACAACTGACTCATTCCTCCGACA
CTCTCCCACCCTCCCAGCTAAGGAGGTGTCTGATGTGAACATGTTCTGCCTCTTTGTTGCC
TGCTGTTGGGGGCGAGGGCTTTGGGTGGATTTTGAAGAGCAATTATGCTTATTCAGATAAA
GTCTGGAGCCGGGCCCAGGTACCTGAGGCTCAGAGATGAGCCCGCAGCGAAGCTGACAA
CTGACTCATTCCTCCGACACTCTCCCACCCTCCCAGCTAAGGAGGTGTCTGATGTGAACAT
GTTCTGCCTCTTTGTTGCCTGCTGTTGGGGGCGAGGGCTTTGGGTGGATTTTGAAGAGCA
ATTATGCTTATTGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACA
TTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCAA
GGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAA

FIG. 22B cont'd

ACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTG
ACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGAC
CACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACG
ACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGG
ACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAAC
CGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCT
GGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCAT
CAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGACC
ACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTAC
CTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTG
CTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGTC
GACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATTACAAAATTTGTG
AAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTA
ATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCC
TGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGG
GCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAG
TTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACT
CCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTC
TATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCA
GGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 243)

CN3346 (bp between ITR: 2108)

GCGGCCGCACGCGTACTACTTAATTTTCTGTGAAACTAACACTTCTTTTCTAATTGCCCTTG
ACTTCACATTCTTTAGCCCATTCTTCGTTACTAATCCATTCTTGCTAGTTCCTCCTACATTCC
TATTGTTCGTGTTAAAGATGACTTTTCTATTCACCTGTGTAAGTCTTGCTGCCTCCTACACT
GATTAATTTAGCTAGATTGAAAAGGAGGACTAGTGCTTCCTCCATAAAACTCCAATTAATCA
ATCATTTTAGAACTTACTACTTAATTTTCTGTGAAACTAACACTTCTTTTCTAATTGCCCTTGA
CTTCACATTCTTTAGCCCATTCTTCGTTACTAATCCATTCTTGCTAGTTCCTCCTACATTCCT
ATTGTTCGTGTTAAAGATGACTTTTCTATTCACCTGTGTAAGTCTTGCTGCCTCCTACACTG
ATTAATTTAGCTAGATTGAAAAGGAGGACTAGTGCTTCCTCCATAAAACTCCAATTAATCAA
TCATTTTAGAACTTACTACTTAATTTTCTGTGAAACTAACACTTCTTTTCTAATTGCCCTTGAC
TTCACATTCTTTAGCCCATTCTTCGTTACTAATCCATTCTTGCTAGTTCCTCCTACATTCCTA
TTGTTCGTGTTAAAGATGACTTTTCTATTCACCTGTGTAAGTCTTGCTGCCTCCTACACTGA
TTAATTTAGCTAGATTGAAAAGGAGGACTAGTGCTTCCTCCATAAAACTCCAATTAATCAAT
CATTTTAGAACTTGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTAC
ATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGTGAGCA
AGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTA
AACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCT
GACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGA
CCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCAC
GACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAG
GACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAA
CCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGC
TGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCA
TCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCGCCGAC
CACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTA

FIG. 22B cont'd

CCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCT
GCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAGT
CGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATTACAAAATTTGT
GAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTT
AATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATC
CTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGG
GGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTGCCTTCTA
GTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCA
CTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCAT
TCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAG
CAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 244)

CN3566 (bp between ITR: 2116)

GCGGCCGCACGCGCCGGTACCGAAGCTACCCCTAACACACTATTCTACACACAGAAAATG
CTCTTCACTAGGAAGCTACCCCTAACACACTATTCTACACACAGAAAATGCTCTTCACTAGG
AAGCTACCCCTAACACACTATTCTACACACAGAAAATGCTCTTCACTAGACGCGTGCCCTT
CTTTCTGTGAAGGGTGACACACCTCCTAGAAAGAAATCTGACTCCCCTCATTGTGTTTTTAA
AATAACTCTCATTATTCCTCCTCTGAAGGTTATTTTCAAACTCTTTATAACTCGATTTTTTTTT
AAATGCAAAGACAAGGAATCAAATCTGCCAACTTTCTATCAGAGGCCCTTCTTTCTGTGAAG
GGTGACACACCTCCTAGAAAGAAATCTGACTCCCCTCATTGTGTTTTTAAAATAACTCTCAT
TATTCCTCCTCTGAAGGTTATTTTCAAACTCTTTATAACTCGATTTTTTTTTTAAATGCAAAGAC
AAGGAATCAAATCTGCCAACTTTCTATCAGAGGCCCTTCTTTCTGTGAAGGGTGACACACC
TCCTAGAAAGAAATCTGACTCCCCTCATTGTGTTTTTAAAATAACTCTCATTATTCCTCCTCT
GAAGGTTATTTTCAAACTCTTTATAACTCGATTTTTTTTTTAAATGCAAAGACAAGGAATCAAA
TCTGCCAACTTTCTATCAGAGGAGCTCGATTCAGCCGGGAGCTTAGGGAGGGGAGGTCAC
TTCATAAGGGCTTGGGGGGGGAGTTGGAGCCACGAGTCGTCCAGCCGGAGCCCCGTGTG
GCTGTGCTCCGGCCTCAGAAGCATCCCCGGATCCAGATCTTTCGAAGCTAGCGCTACCGG
TCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTC
GAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCG
ATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGC
CCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCC
GACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAG
CGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAG
GGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAA
CATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGA
CAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGG
CGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGC
TGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGC
GCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGAC
GAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCT
CTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTA
TGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTT
CTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTT
GCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGAT
CTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTT
GACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCAT

FIG. 22B cont'd

TGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGA GGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 245)

CN2912 (bp between ITR: 2090)

GCGGCCGCACGCGTCTGCAGGAGCGCCCTTCCGCTGGAGGGTGGGAGGACTGTCTAAG GCAGTCACAGCAAGGAGAGGCACGGTGTGGGCACTGCTGCTATTTCTAACCTGCTGGAGT GAAGGGAACCTTGACTACTTGAAAAGCAGGCTGATTGTCAGGGGCGGAACCGAACTCAGA GCTGTCAGGGCCGTCACATGGAAAGTGCCTGGCAGGGGGCGGCGACAGGGGGCTTGGG CTGACAGGGCTGTGATTTTGAAAGCTGCAGGAGCGCCCTTCCGCTGGAGGGTGGGAGGA CTGTCTAAGGCAGTCACAGCAAGGAGAGGCACGGTGTGGGCACTGCTGCTATTTCTAACC TGCTGGAGTGAAGGGAACCTTGACTACTTGAAAAGCAGGCTGATTGTCAGGGGCGGAACC GAACTCAGAGCTGTCAGGGCCGTCACATGGAAAGTGCCTGGCAGGGGGCGGCGACAGGG GGCTTGGGCTGACAGGGCTGTGATTTTGAAAGCTGCAGGAGCGCCCTTCCGCTGGAGGG TGGGAGGACTGTCTAAGGCAGTCACAGCAAGGAGAGGCACGGTGTGGGCACTGCTGCTA TTTCTAACCTGCTGGAGTGAAGGGAACCTTGACTACTTGAAAAGCAGGCTGATTGTCAGGG GCGGAACCGAACTCAGAGCTGTCAGGGCCGTCACATGGAAAGTGCCTGGCAGGGGGCGG CGACAGGGGGCTTGGGCTGACAGGGCTGTGATTTTGAAAGGAGCTCGGGCTGGGCATAA AAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCT AGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGC CCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAG GGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAA GCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCG CCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCT ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAG GTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAG GAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTAT ATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATC GAGGACGGCGGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGG CCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCC CAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCT CGGCATGGACGAGCTGTACAAGTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATC ATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTC CTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATG GCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGC CGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGG CTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCG TGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAAT TGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAG CAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 246)

CN2913 (bp between ITR: 2087)

GCGGCCGCACGCGTCAGGGGGCGGCGACAGGGGGCTTGGGCTGACAGGGCTGTGATTT TGAAAGAAACGTCTCCAAGAAAGTGATTTAAAGTAGGAGAGAAATATTATTATTAGATAATG GCTGTCAGGTTATTTTTTGATGTGTTTTCTGAGTATTTCATAATCATCTTGCGCTTAGATGGT

FIG. 22B cont'd

AAGCCCTTCCTGGCTAGGGGCCGTGTCCCATCCCATGCCTCTGTGGCTTTCACCTTCGGG
TGTGCAACAGGTATCACAGGGGGCGGCGACAGGGGGCTTGGGCTGACAGGGCTGTGATT
TTGAAAGAAACGTCTCCAAGAAAGTGATTTAAAGTAGGAGAGAAATATTATTATTAGATAAT
GGCTGTCAGGTTATTTTTTGATGTGTTTTCTGAGTATTTCATAATCATCTTGCGCTTAGATGG
TAAGCCCTTCCTGGCTAGGGGCCGTGTCCCATCCCATGCCTCTGTGGCTTTCACCTTCGG
GTGTGCAACAGGTATCACAGGGGGCGGCGACAGGGGGCTTGGGCTGACAGGGCTGTGAT
TTTGAAAGAAACGTCTCCAAGAAAGTGATTTAAAGTAGGAGAGAAATATTATTATTAGATAAT
GGCTGTCAGGTTATTTTTTGATGTGTTTTCTGAGTATTTCATAATCATCTTGCGCTTAGATGG
TAAGCCCTTCCTGGCTAGGGGCCGTGTCCCATCCCATGCCTCTGTGGCTTTCACCTTCGG
GTGTGCAACAGGTATCAGAGCTCGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTG
CTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCGCTACCGGTCGCCACCATGGT
GAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGC
GACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGG
CAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCT
CGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGC
AGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCT
TCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTG
GTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCA
CAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAA
CGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCAGCTCG
CCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAAC
CACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATG
GTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAA
GTAAGTCGACGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGGATTACAA
AATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACG
CTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGT
ATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCT
GGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGACTGTG
CCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAG
GTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAG
GTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAG
ACAATAGCAGGCATGCACGTGCGGACCGAGCGGCCGC (SEQ ID NO: 247)

CN2966 (bp between ITR: 2374)

GCGGCCGCACGCGTTCCGTAAAGAGCACAAAACCCAAATATTTGGGTGCATGGGAGATAG
ATTTCAACTAAATACTTTTAATCATGCAATTCCAATAGCACTTAAATTTTTTCAAGGCATGTAT
AAAGGGAGAATAGACTAATTCAATTTCAAAGTGCAAGAAAAACATCAAAAACTAAATTCAGA
AAGTTTGCATGGGAAGAAAAAAAAACACAAATTAATCTCACTTGTGATTATTCTAAATACATT
TGAACAAGCAGCAGCTAGTAGTACATACAAAGAAATAGAAAACATGAAGACCAGGGGAGTT
TAATTATATGGTTGCAAAAATGGTTCAACATTGCAAAGTTGTTAATACTCAGTGGATGGGGA
GGGAGCTGTGCAATTATCTCCACAGGTACAGAAAAGGCACTTAGTAAAATGTAGCCAACTC
TTTGGCTTCTAAAAAAGGAGAAAATGGTTTACAAAAACAAGCCTCCCTGGATGCTTCCTTAA
TTTGTTCTTATTCATAATGGGGGAACATAAAGTGAACTTCTGCACACCAGAAGTCAGGTTGT
TTGCTTGCTAATACCATTCCCACTCAATATCCCATGGAAGTTGGATGACTCGACCTGCATCC
CAAGGAGTAGTTACCATCACTAATGAGGAGAAGCATTTGGAAGGAAGACAGAATTCTGTAG
ACCAAACGAAGACCTGGAGGCTAGTGGAAAGAGCTCGGGCTGGGCATAAAAGTCAGGGC

FIG. 22B cont'd

AGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTTTCGAAGCTAGCACCATGGT
GCCCAAGAAGAAGAGGAAAGTCTCCAACCTGCTGACTGTGCACCAAAACCTGCCTGCCCT
CCCTGTGGATGCCACCTCTGATGAAGTCAGGAAGAACCTGATGGACATGTTCAGGGACAG
GCAGGCCTTCTCTGAACACACCTGGAAGATGCTCCTGTCTGTGTGCAGATCCTGGGCTGC
CTGGTGCAAGCTGAACAACAGGAAATGGTTCCCTGCTGAACCTGAGGATGTGAGGGACTA
CCTCCTGTACCTGCAAGCCAGAGGCCTGGCTGTGAAGACCATCCAACAGCACCTGGGCCA
GCTCAACATGCTGCACAGGAGATCTGGCCTGCCTCGCCCTTCTGACTCCAATGCTGTGTC
CCTGGTGATGAGGAGAATCAGAAAGGAGAATGTGGATGCTGGGGAGAGAGCCAAGCAGG
CCCTGGCCTTTGAACGCACTGACTTTGACCAAGTCAGATCCCTGATGGAGAACTCTGACAG
ATGCCAGGACATCAGGAACCTGGCCTTCCTGGGCATTGCCTACAACACCCTGCTGCGCAT
TGCCGAAATTGCCAGAATCAGAGTGAAGGACATCTCCCGCACCGATGGTGGGAGAATGCT
GATCCACATTGGCAGGACCAAGACCCTGGTGTCCACAGCTGGTGTGGAGAAGGCCCTGTC
CCTGGGGGTTACCAAGCTGGTGGAGAGATGGATCTCTGTGTCTGGTGTGGCTGATGACCC
CAACAACTACCTGTTCTGCCGGGTCAGAAAGAATGGTGTGGCTGCCCCTTCTGCCACCTC
CCAACTGTCCACCCGGGCCCTGGAAGGGATCTTTGAGGCCACCCACCGCCTGATCTATGG
TGCCAAGGATGACTCTGGGCAGAGATACCTGGCCTGGTCTGGCCACTCTGCCAGAGTGG
GTGCTGCCAGGGACATGGCCAGGGCTGGTGTGTCCATCCCTGAAATCATGCAGGCTGGT
GGCTGGACCAATGTGAACATTGTGATGAACTACATCAGAAACCTGGACTCTGAGACTGGG
GCCATGGTGAGGCTGCTCGAGGATGGGGACTAATGAGGCGCGCCGCGGCCGCGAATTCG
ATATCATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGT
TGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCC
GTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTC
ATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTC
CGTGGCTCGAGAGATCTTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTC
CCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAG
GAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAG
GACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCG
AGCGGCCGC (SEQ ID NO: 248)

CN2203 (bp between ITR: 2279)

GCGGCCGCACGCGCCGGTACCGAAGCTACCCCTAACACACTATTCTACACACAGAAAATG
CTCTTCACTAGGAAGCTACCCCTAACACACTATTCTACACACAGAAAATGCTCTTCACTAGG
AAGCTACCCCTAACACACTATTCTACACACAGAAAATGCTCTTCACTAGACGCGTTAGCAG
GAGTACATCCTCCTCTGTTAGAAAAACAACTCTGCGGTTCTGGGTCACTTTTCCCATCTTTG
TATAGAAAAGTACCGATTATTATTGTTCCCCCGGGTGCCTTCTCCAGCTTAAAGGAAAATTC
CAGCCCCAGAGATCTTCCGCAGTGAGTGACAGCTCCTTAATGTGAGGAGCAGCGTGGGCG
TGGTGGGTGGGATGTCAGAGCCATCAAAGCCCTCATTTCTGATCCCTCTGTGATGTCGGG
GTTCCCTGGCACGCCCACTGTCATGCCTCAGCACATTGGCATCTGAGAGAGGAAAGGTGC
AGCTGACACCCTGACCCCCTTCTCCCCGACACGGGGTCAGACAGGGTCCCGCGGTGGCC
TGGTTGTGCAGCACTGACATGTTGCCTGGGAACGAAGAGCTCGATTCAGCCGGGAGCTTA
GGGAGGGGAGGTCACTTCATAAGGGCTTGGGGGGGGAGTTGGAGCCACGAGTCGTCCAG
CCGGAGCCCCGTGTGGCTGTGCTCCGGCCTCAGAAGCATCCCCGGATCCGCCACCATGG
TGCCCAAGAAGAAGAGGAAAGTCTCCAACCTGCTGACTGTGCACCAAAACCTGCCTGCCC
TCCCTGTGGATGCCACCTCTGATGAAGTCAGGAAGAACCTGATGGACATGTTCAGGGACA
GGCAGGCCTTCTCTGAACACACCTGGAAGATGCTCCTGTCTGTGTGCAGATCCTGGGCTG
CCTGGTGCAAGCTGAACAACAGGAAATGGTTCCCTGCTGAACCTGAGGATGTGAGGGACT

FIG. 22B cont'd

ACCTCCTGTACCTGCAAGCCAGAGGCCTGGCTGTGAAGACCATCCAACAGCACCTGGGCC
AGCTCAACATGCTGCACAGGAGATCTGGCCTGCCTCGCCCTTCTGACTCCAATGCTGTGT
CCCTGGTGATGAGGAGAATCAGAAAGGAGAATGTGGATGCTGGGGAGAGAGCCAAGCAG
GCCCTGGCCTTTGAACGCACTGACTTTGACCAAGTCAGATCCCTGATGGAGAACTCTGACA
GATGCCAGGACATCAGGAACCTGGCCTTCCTGGGCATTGCCTACAACACCCTGCTGCGCA
TTGCCGAAATTGCCAGAATCAGAGTGAAGGACATCTCCCGCACCGATGGTGGGAGAATGC
TGATCCACATTGGCAGGACCAAGACCCTGGTGTCCACAGCTGGTGTGGAGAAGGCCCTGT
CCCTGGGGGTTACCAAGCTGGTGGAGAGATGGATCTCTGTGTCTGGTGTGGCTGATGACC
CCAACAACTACCTGTTCTGCCGGGTCAGAAAGAATGGTGTGGCTGCCCCTTCTGCCACCT
CCCAACTGTCCACCCGGGCCCTGGAAGGGATCTTTGAGGCCACCCACCGCCTGATCTATG
GTGCCAAGGATGACTCTGGGCAGAGATACCTGGCCTGGTCTGGCCACTCTGCCAGAGTG
GGTGCTGCCAGGGACATGGCCAGGGCTGGTGTGTCCATCCCTGAAATCATGCAGGCTGG
TGGCTGGACCAATGTGAACATTGTGATGAACTACATCAGAAACCTGGACTCTGAGACTGGG
GCCATGGTGAGGCTGCTCGAGGATGGGGACTAAGAATTCGATATCATAATCAACCTCTGG
ATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTG
GATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCT
CCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCG
CTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGA
CTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCT
GGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTG
AGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTG
GGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO:
249)

CN2700 (bp between ITR: 1922)

GCGGCCGCACGCGTAGGGAGGAACTAAAGTCCATTCATATGTCCATATTCTCAATTTGGGA
AAAAATGTGGCTTTGTCTTCATCCTCTTTTCCTGAGTGTATAAGGCCAGAAGCCAAAGGCAA
GAGCAGGACATTCCAGGAGCCTTTATGATTGCTCTAAGTCACATCTGCTCTCGAGCTCCCA
TTCCACTGTGAAAAATACCTAGTCTTGAACTTTGGAGTTCCAAATTCCACATGATCGACTTC
CTCAAGGCTTTTCACTTGACGAACAAATTGCATGCCAAGAAATCGTCAAAATTCTATCAAGC
TTAATTATGCAATTTCTGTCTATAAATGACATACCTCCTGTACCCTATGACACCCACCTATGC
ACTAATAAGATGTGACAGCTGCATCACCAACAAAGCCTCCCCCGCCTGCCATTCTCTTCGG
AGGTGAGCACCTCCTGCTCGGGAGGAACTGACAGCCCCTTTCAGAAATGTGAAGGCAGTG
AAGTCCCAAACCAGAAACAGTGTGACCACCTAGGCTCACCCAAGGACCGTCCTGTGCTTC
TGGGCAACCAATGGATGTAGGGGGTTAGGAGGCAGTGGGGATTCGTCAGAGCTCGGGCT
GGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGGGATCCAGATCTT
TCGAAGCTAGCGCCACCATGGTGAGCAAGGGCGAGGAGACCACAATGGGCGTAATCAAG
CCCGACATGAAGATCAAGCTGAAGATGGAGGGCAACGTGAATGGCCACGCCTTCGTGATC
GAGGGCGAGGGCGAGGGCAAGCCCTACGACGGCACCAACACCATCAACCTGGAGGTGAA
GGAGGGAGCCCCCCTGCCCTTCTCCTACGACATTCTGACCACCGCGTTCGCCTACGGCAA
CAGGGCCTTCACCAAGTACCCCGACGACATCCCCAACTACTTCAAGCAGTCCTTCCCCGA
GGGCTACTCTTGGGAGCGCACCATGACCTTCGAGGACAAGGGCATCGTGAAGGTGAAGTC
CGACATCTCCATGGAGGAGGACTCCTTCATCTACGAGATACACCTCAAGGGCGAGAACTT
CCCCCCCAACGGCCCCGTGATGCAGAAGAAGACCACCGGCTGGGACGCCTCCACCGAGA
GGATGTACGTGCGCGACGGCGTGCTGAAGGGCGACGTCAAGCACAAGCTGCTGCTGGAG
GGCGGCGGCCACCACCGCGTTGACTTCAAGACCATCTACAGGGCCAAGAAGGCGGTGAA

FIG. 22B cont'd

GCTGCCCGACTATCACTTTGTGGACCACCGCATCGAGATCCTGAACCACGACAAGGACTA
CAACAAGGTGACCGTTTACGAGAGCGCCGTGGCCCGCAACTCCACCGACGGCATGGACG
AGCTGTACAAGTAATGAGGCGCGCCGCGGCCGCGAATTCGATATCATAATCAACCTCTGG
ATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTG
GATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCT
CCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCG
CTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGCTCGAGAGATCTTCGA
CTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCT
GGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTG
AGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTG
GGAAGACAATAGCAGGCATGAGATCTCACGTGCGGACCGAGCGGCCGC (SEQ ID NO:
250)

FIG. 22C

Beta-Globin Minimal Promoter (pBGmin/minBGlobin/minBGprom):
GGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTG (SEQ ID NO: 123)

minCMV Promoter:
GAGGTAGGCGTGTACGGTGGGAGGCCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGA TCGCCTGG (SEQ ID NO: 124)

Mutated minCMV Promoter (SacI RE site removed):
GAGGTAGGCGTGTACGGTGGGAGGCCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGA TCGCCTGG (SEQ ID NO: 125)

minRho Promoter:
GATTCAGCCGGGAGCTTAGGGAGGGGAGGTCACTTCATAAGGGCCTGGGGGGGGAGTTG GAGCCACGAGTCGTCCAGCCGGAGCCCCGTGTGGCTGAGCTCCGGCCTCAGAAGCATCC CC (SEQ ID NO: 126)

minRho* Promoter:
GATTCAGCCGGGAGCTTAGGGAGGGGAGGTCACTTCATAAGGGCTTGGGGGGGGAGTTG GAGCCACGAGTCGTCCAGCCGGAGCCCCGTGTGGCTGTGCTCCGGCCTCAGAAGCATCC CC (SEQ ID NO:127

Hsp68 minimal Promoter (proHsp68):
CAGGAACATCCAAACTGAGCAGCCGGGGTCCCCCCCACCCCCCACCCCGCCCCACGCGG CAACTTTGAGCCTGTGCTGGGACAGAGCCTCTAGTTCCTAAATTAGTCCATGAGGTCAGAG GCAGCACTGCCATTGTAACGCGATTGGAGAGGATCACGTCACCGGACACGCCCCCAGGC ATCTCCCTGGGTCTCCTAAACTTGGCGGGGAGAAGTTTTAGCCCTTAAGTTTTAGCCTTTAA CCCCCATATTCAGAACTGTGCGAGTTGGCGAAACCCCACAAATCACAACAAACTGTACACA ACACCGAGCTAGAGGTGATCTTTCTTGTCCATTCCACACAGGCCTTAGTAATGCGTCGCCA TAGCAACAGTGTCACTAGTAGCACCAGCACTTCCCCACACCCTCCCCCTCAGGAATCCGTA CTCTCCAGTGAACCCCAGAAACCTCTGGAGAGTTCTGGACAAGGGCGGAACCCACAACTC CGATTACTCAAGGGAGGCGGGGAAGCTCCACCAGACGCGAAACTGCTGGAAGATTCCTG GCCCCAAGGCCTCCTCCGGCTCGCTGATTGGCCCAGCGGAGAGTGGGCGGGGCCGGTG AAGACTCCTTAAAGGCGCAGGGCGGCGAGCAGGTCACCAGACGCTGACAGCTACTCAGA ACCAAATCTGGTTCCATCCAGAGACAAGCGAAGACAAGAGAAGCAGAGCGAGCGGCGCGT TCCCGATCCTCGGCCAGGACCAGCCTTCCCCAGAGCATCCCTGCCGCGGAGCGCAACCT TCCCAGGAGCATCCCTGCCGCGGAGCGCAACTTTCCCCGGAGCATCCACGCCGCGGAGC GCAGCCTTCCAGAAGCAGAGCGCGGCGCC (SEQ ID NO: 128)

SYFP2:
ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGA CGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCT ACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCC ACCCTCGTGACCACCCTGGGCTACGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACAT GAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCAT

FIG. 22C cont'd

CTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACA
CCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTG
GGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCACCGCCGACAAGCAG
AAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCGGCGTGCA
GCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCG
ACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATC
ACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGT
ACAAGTAA (SEQ ID NO: 129)

EGFP:

ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGA
CGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCT
ACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCA
CCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTCAGCCGCTACCCCGACCACATGA
AGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCT
TCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACC
CTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGG
GCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAA
GAACGGCATCAAGGTGAACTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCT
CGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACA
ACCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACA
TGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACA
AGTAA (SEQ ID NO: 130)

Optimized Flp recombinase (FlpO):

ATGGCTCCTAAGAAGAAGAGGAAGGTGATGAGCCAGTTCGACATCCTGTGCAAGACCCCC
CCCAAGGTGCTGGTGCGGCAGTTCGTGGAGAGATTCGAGAGGCCCAGCGGCGAGAAGAT
CGCCAGCTGTGCCGCCGAGCTGACCTACCTGTGCTGGATGATCACCCACAACGGCACCG
CCATCAAGAGGGCCACCTTCATGAGCTACAACACCATCATCAGCAACAGCCTGAGCTTCGA
CATCGTGAACAAGAGCCTGCAGTTCAAGTACAAGACCCAGAAGGCCACCATCCTGGAGGC
CAGCCTGAAGAAGCTGATCCCCGCCTGGGAGTTCACCATCATCCCTTACAACGGCCAGAA
GCACCAGAGCGACATCACCGACATCGTGTCCAGCCTGCAGCTGCAGTTCGAGAGCAGCG
AGGAGGCCGACAAGGGCAACAGCCACAGCAAGAAGATGCTGAAGGCCCTGCTGTCCGAG
GGCGAGAGCATCTGGGAGATCACCGAGAAGATCCTGAACAGCTTCGAGTACACCAGCAGG
TTCACCAAGACCAAGACCCTGTACCAGTTCCTGTTCCTGGCCACATTCATCAACTGCGGCA
GGTTCAGCGACATCAAGAACGTGGACCCCAAGAGCTTCAAGCTGGTGCAGAACAAGTACC
TGGGCGTGATCATTCAGTGCCTGGTGACCGAGACCAAGACAAGCGTGTCCAGGCACATCT
ACTTTTTCAGCGCCAGAGGCAGGATCGACCCCCTGGTGTACCTGGACGAGTTCCTGAGGA
ACAGCGAGCCCGTGCTGAAGAGAGTGAACAGGACCGGCAACAGCAGCAGCAACAAGCAG
GAGTACCAGCTGCTGAAGGACAACCTGGTGCGCAGCTACAACAAGGCCCTGAAGAAGAAC
GCCCCCTACCCCATCTTCGCTATCAAGAACGGCCCTAAGAGCCACATCGGCAGGCACCTG
ATGACCAGCTTTCTGAGCATGAAGGGCCTGACCGAGCTGACAAACGTGGTGGGCAACTGG
AGCGACAAGAGGGCCTCCGCCGTGGCCAGGACCACCTACACCCACCAGATCACCGCCAT
CCCCGACCACTACTTCGCCCTGGTGTCCAGGTACTACGCCTACGACCCCATCAGCAAGGA
GATGATCGCCCTGAAGGACGAGACCAACCCCATCGAGGAGTGGCAGCACATCGAGCAGC

FIG. 22C cont'd

TGAAGGGCAGCGCCGAGGGCAGCATCAGATACCCCGCCTGGAACGGCATCATCAGCCAG
GAGGTGCTGGACTACCTGAGCAGCTACATCAACAGGCGGATCTGA (SEQ ID NO: 131)

Improved Cre recombinase (iCre):

ATGGTGCCCAAGAAGAAGAGGAAAGTCTCCAACCTGCTGACTGTGCACCAAAACCTGCCT
GCCCTCCCTGTGGATGCCACCTCTGATGAAGTCAGGAAGAACCTGATGGACATGTTCAGG
GACAGGCAGGCCTTCTCTGAACACACCTGGAAGATGCTCCTGTCTGTGTGCAGATCCTGG
GCTGCCTGGTGCAAGCTGAACAACAGGAAATGGTTCCCTGCTGAACCTGAGGATGTGAGG
GACTACCTCCTGTACCTGCAAGCCAGAGGCCTGGCTGTGAAGACCATCCAACAGCACCTG
GGCCAGCTCAACATGCTGCACAGGAGATCTGGCCTGCCTCGCCCTTCTGACTCCAATGCT
GTGTCCCTGGTGATGAGGAGAATCAGAAAGGAGAATGTGGATGCTGGGGAGAGAGCCAA
GCAGGCCCTGGCCTTTGAACGCACTGACTTTGACCAAGTCAGATCCCTGATGGAGAACTC
TGACAGATGCCAGGACATCAGGAACCTGGCCTTCCTGGGCATTGCCTACAACACCCTGCT
GCGCATTGCCGAAATTGCCAGAATCAGAGTGAAGGACATCTCCCGCACCGATGGTGGGAG
AATGCTGATCCACATTGGCAGGACCAAGACCCTGGTGTCCACAGCTGGTGTGGAGAAGGC
CCTGTCCCTGGGGGTTACCAAGCTGGTGGAGAGATGGATCTCTGTGTCTGGTGTGGCTGA
TGACCCCAACAACTACCTGTTCTGCCGGGTCAGAAAGAATGGTGTGGCTGCCCCTTCTGC
CACCTCCCAACTGTCCACCCGGGCCCTGGAAGGGATCTTTGAGGCCACCCACCGCCTGAT
CTATGGTGCCAAGGATGACTCTGGGCAGAGATACCTGGCCTGGTCTGGCCACTCTGCCAG
AGTGGGTGCTGCCAGGGACATGGCCAGGGCTGGTGTGTCCATCCCTGAAATCATGCAGG
CTGGTGGCTGGACCAATGTGAACATTGTGATGAACTACATCAGAAACCTGGACTCTGAGAC
TGGGGCCATGGTGAGGCTGCTCGAGGATGGGGACTAA (SEQ ID NO: 132)

SP10 insulator (SP10ins):

GAAGCTACCCCTAACACACTATTCTACACACAGAAAATGCTCTTCACTAG (SEQ ID NO: 133)

3xSP10ins:

GAAGCTACCCCTAACACACTATTCTACACACAGAAAATGCTCTTCACTAGGAAGCTACCCC
TAACACACTATTCTACACACAGAAAATGCTCTTCACTAGGAAGCTACCCCTAACACACTATT
CTACACACAGAAAATGCTCTTCACTAG (SEQ ID NO: 134)

3xHA tag (DNA):

TACCCGTATGATGTCCCGGATTACGCTGGCAGCTACCCATACGATGTACCCGACTATGCC
GGCAGTTATCCCTACGACGTCCCTGACTACGCA (SEQ ID NO: 251)

WPRE3:

ATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTC
CTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATG
GCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCACGGCGGAACTCATCGC
CGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGG
(SEQ ID NO: 135)

WPRE:

GCTTATCGATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTA
TGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTT
CCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGTCTCTTTATGAGGAG

FIG. 22C cont'd

TTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTGTGCACTGTGTTTGCTGACGCAACCCCC
ACTGGTTGGGGCATTGCCACCACCTGTCAGCTCCTTTCCGGGACTTTCGCTTTCCCCCTCC
CTATTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGG
CTGTTGGGCACTGACAATTCCGTGGTGTTGTCGGGGAAATCATCGTCCTTTCCTTGGCTGC
TCGCCTATGTTGCCACCTGGATTCTGCGCGGGACGTCCTTCTGCTACGTCCCTTCGGCCC
TCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTGCCGGCTCTGCGGCCTCTTCCGCGTC
TTCGCCTTCGCCCTCAGACGAGTCGGATCTCCCTTTGGGCCGCCTCCCCGCATCGATACC
G (SEQ ID NO: 136)

BGHpA:
CGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGAC
CCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGT
CTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGA
TTGGGAAGACAATAGCAGGCATG (SEQ ID NO: 137)

HGHpA:
ACGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGGCCCTGGAAGTTGCCACTC
CAGTGCCCACCAGCCTTGTCCTAATAAAATTAAGTTGCATCATTTTGTCTGACTAGGTGTCC
TTCTATAATATTATGGGGTGGAGGGGGGTGGTATGGAGCAAGGGGCAAGTTGGGAAGACA
ACCTGTAGGGCCTGCGGGGTCTATTGGGAACCAAGCTGGAGTGCAGTGGCACAATCTTGG
CTCACTGCAATCTCCGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCGAGTTGT
TGGGATTCCAGGCATGCATGACCAGGCTCAGCTAATTTTTGTTTTTTTGGTAGAGACGGGG
TTTCACCATATTGGCCAGGCTGGTCTCCAACTCCTAATCTCAGGTGATCTACCCACCTTGG
CCTCCCAAATTGCTGGGATTACAGGCGTGAACCACTGCTCCCTTCCCTGTCCTT (SEQ ID
NO: 138)

P2A:
GGCAGCGGCGCCACCAACTTCAGCCTGCTGAAGCAGGCCGGCGACGTGGAGGAGAACCC
CGGCCCCGGAGCTAGCGGA (SEQ ID NO: 139)

T2A:
(GSG)EGRGSLLTCGDVEENPGP (SEQ ID NO: 140)

E2A:
(GSG)QCTNYALLKLAGDVESNPGPP (SEQ ID NO: 141)

F2A:
(GSG)VKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 142)

Exemplary Plasmid Backbone 1 – Left ITR:
CCTGCAGGCAGCTGCGCGCTCGCTCGCTCACTGAGGCCGCCCGGGCGTCGGGCGACCTT
TGGTCGCCCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTGGCCAACTCCATCA
CTAGGGGTTCCT (SEQ ID NO: 143)

Exemplary Plasmid Backbone 1 – Right ITR:
CCTGCAGGCAGCTGCGCGCTCGCTCGCTCACTGAGGCCGCCCGGGCAAAGCCCGGGCG

FIG. 22C cont'd

TCGGGCGACCTTTGGTCGCCCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG
GCCAACTCCATCACTAGGGGTTCCT (SEQ ID NO: 144)

Exemplary Plasmid Backbone 2 – Left ITR:

CATGTCCTGCAGGCAGCTGCGCGCTCGCTCGCTCACTGAGGCCGCCCGGGCAAAGCCCG
GGCGTCGGGCGACCTTTGGTCGCCCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGG
AGTGGCCAACTCCATCACTAGGGGTTCCT (SEQ ID NO: 145)

Exemplary Plasmid Backbone 2 – Right ITR:

AGGAACCCCTAGTGATGGAGTTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGG
CCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGA
GCGAGCGCGCAGCTGCCTGCAGGGGCGCCTG (SEQ ID NO: 146)

PHP.eB capsid:

MAADGYLPDWLEDNLSEGIREWWALKPGAPQPKANQQHQDNARGLVLPGYKYLGPGNGLDK
GEPVNAADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKK
RLLEPLGLVEEAAKTAPGKKRPVEQSPQEPDSSAGIGKSGAQPAKKRLNFGQTGDTESVPDP
QPIGEPPAAPSGVGSLTMASGGGAPVADNNEGADGVGSSSGNWHCDSQWLGDRVITTSTRT
WALPTYNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWG
FRPKRLNFKLFNIQVKEVTDNNGVKTIANNLTSTVQVFTDSDYQLPYVLGSAHEGCLPPFPADV
FMIPQYGYLTLNDGSQAVGRSSFYCLEYFPSQMLRTGNNFQFSYEFENVPFHSSYAHSQSLD
RLMNPLIDQYLYYLSKTINGSGQNQQTLKFSVAGPSNMAVQGRNYIPGPSYRQQRVSTTVTQN
NNSEFAWPGASSWALNGRNSLMNPGPAMASHKEGEDRFFPLSGSLIFGKQGTGRDNVDADK
VMITNEEEIKTTNPVATESYGQVATNHQSDGTLAVPFKAQAQTGWVQNQGILPGMVWQDRDV
YLQGPIWAKIPHTDGNFHPSPLMGGFGMKHPPPQILIKNTPVPADPPTAFNKDKLNSFITQYST
GQVSVEIEWELQKENSKRWNPEIQYTSNYYKSNNVEFAVNTEGVYSEPRPIGTRYLTRNL
(SEQ ID NO: 147)

AAV9 VP1 capsid protein:

MAADGYLPDWLEDNLSEGIREWWALKPGAPQPKANQQHQDNARGLVLPGYKYLGPGNGLDK
GEPVNAADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKK
RLLEPLGLVEEAAKTAPGKKRPVEQSPQEPDSSAGIGKSGAQPAKKRLNFGQTGDTESVPDP
QPIGEPPAAPSGVGSLTMASGGGAPVADNNEGADGVGSSSGNWHCDSQWLGDRVITTSTRT
WALPTYNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWG
FRPKRLNFKLFNIQVKEVTDNNGVKTIANNLTSTVQVFTDSDYQLPYVLGSAHEGCLPPFPADV
FMIPQYGYLTLNDGSQAVGRSSFYCLEYFPSQMLRTGNNFQFSYEFENVPFHSSYAHSQSLD
RLMNPLIDQYLYYLSKTINGSGQNQQTLKFSVAGPSNMAVQGRNYIPGPSYRQQRVSTTVTQN
NNSEFAWPGASSWALNGRNSLMNPGPAMASHKEGEDRFFPLSGSLIFGKQGTGRDNVDADK
VMITNEEEIKTTNPVATESYGQVATNHQSAQAQAQTGWVQNQGILPGMVWQDRDVYLQGPIW
AKIPHTDGNFHPSPLMGGFGMKHPPPQILIKNTPVPADPPTAFNKDKLNSFITQYSTGQVSVEIE
WELQKENSKRWNPEIQYTSNYYKSNNVEFAVNTEGVYSEPRPIGTRYLTRNL (SEQ ID NO:
148)

tet-Transactivator version 2 (tTA2):

ATGTCTAGACTGGACAAGAGCAAAGTCATAAACTCTGCTCTGGAATTACTCAATGAAGTCG
GTATCGAAGGCCTGACGACAAGGAAACTCGCTCAAAAGCTGGGAGTTGAGCAGCCTACCC

FIG. 22C cont'd

TGTACTGGCACGTGAAGAACAAGCGGGCCCTGCTCGATGCCCTGGCAATCGAGATGCTGG
ACAGGCATCATACCCACTTCTGCCCCCTGGAAGGCGAGTCATGGCAAGACTTTCTGCGGA
ACAACGCCAAGTCATTCCGCTGTGCTCTCCTCTCACATCGCGACGGGGCTAAAGTGCATCT
CGGCACCCGCCCAACAGAGAAACAGTACGAAACCCTGGAAAATCAGCTCGCGTTCCTGTG
TCAGCAAGGCTTCTCCCTGGAGAACGCACTGTACGCTCTGTCCGCCGTGGGCCACTTTAC
ACTGGGCTGCGTATTGGAGGATCAGGAGCATCAAGTAGCAAAAGAGGAAAGAGAGACACC
TACCACCGATTCTATGCCCCCACTTCTGAGACAAGCAATTGAGCTGTTCGACCATCAGGGA
GCCGAACCTGCCTTCCTTTTCGGCCTGGAACTAATCATATGTGGCCTGGAGAAACAGCTAA
AGTGCGAAAGCGGCGGGCCGGCCGACGCCCTTGACGATTTTGACTTAGACATGCTCCCAG
CCGATGCCCTTGACGACTTTGACCTTGATATGCTGCCTGCTGACGCTCTTGACGATTTTGA
CCTTGACATGCTCCCCGGGTAA (SEQ ID NO: 149)

Aromatic L-amino acid decarboxylase (AADC) mRNA, [Homo sapiens], Accession No. M76180.1

GGAGAGAGAGAGGACAGAGAGCAAGTCACTCCCGGCTGCCTTTTTCACCTCTGACAGAGC
CCAGACACCATGAACGCAAGTGAATTCCGAAGGAGAGGGAAGGAGATGGTGGATTACGTG
GCCAACTACATGGAAGGCATTGAGGGACGCCAGGTCTACCCTGACGTGGAGCCCGGGTA
CCTGCGGCCGCTGATCCCTGCCGCTGCCCCTCAGGAGCCAGACACGTTTGAGGACATCAT
CAACGACGTTGAGAAGATAATCATGCCTGGGGTGACGCACTGGCACAGCCCCTACTTCTT
CGCCTACTTCCCCACTGCCAGCTCGTACCCGGCCATGCTTGCGGACATGCTGTGCGGGG
CCATTGGCTGCATCGGCTTCTCCTGGGCGGCAAGCCCAGCATGCACAGAGCTGGAGACT
GTGATGATGGACTGGCTCGGGAAGATGCTGGAACTACCAAAGGCATTTTTGAATGAGAAA
GCTGGAGAAGGGGGAGGAGTGATCCAGGGAAGTGCCAGTGAAGCCACCCTGGTGGCCCT
GCTGGCCGCTCGGACCAAAGTGATCCATCGGCTGCAGGCAGCGTCCCCAGAGCTCACAC
AGGCCGCTATCATGGAGAAGCTGGTGGCTTACTCATCCGATCAGGCACACTCCTCAGTGG
AAAGAGCTGGGTTAATTGGTGGAGTGAAATTAAAAGCCATCCCCTCAGATGGCAACTTCGC
CATGCGTGCGTCTGCCCTGCAGGAAGCCCTGGAGAGAGACAAAGCGGCTGGCCTGATTC
CTTTCTTTATGGTTGCCACCCTGGGGACCACAACATGCTGCTCCTTTGACAATCTCTTAGAA
GTCGGTCCTATCTGCAACAAGGAAGACATATGGCTGCACGTTGATGCAGCCTACGCAGGC
AGTGCATTCATCTGCCCTGAGTTCCGGCACCTTCTGAATGGAGTGGAGTTTGCAGATTCAT
TCAACTTTAATCCCCACAAATGGCTATTGGTGAATTTTGACTGTTCTGCCATGTGGGTGAAA
AAGAGAACAGACTTAACGGGAGCCTTTAGACTGGACCCCACTTACCTGAAGCACAGCCAT
CAGGATTCAGGGCTTATCACTGACTACCGGCATTGGCAGATACCACTGGGCAGAAGATTTC
GCTCTTTGAAAATGTGGTTTGTATTTAGGATGTATGGAGTCAAAGGACTGCAGGCTTATATC
CGCAAGCATGTCCAGCTGTCCCATGAGTTTGAGTCACTGGTGCGCCAGGATCCCCGCTTT
GAAATCTGTGTGGAAGTCATTCTGGGGCTTGTCTGCTTTCGGCTAAAGGGTTCCAACAAAG
TGAATGAAGCTCTTCTGCAAAGAATAAACAGTGCCAAAAAAATCCACTTGGTTCCATGTCAC
CTCAGGGACAAGTTTGTCCTGCGCTTTGCCATCTGTTCTCGCACGGTGGAATCTGCCCATG
TGCAGCGGGCCTGGGAACACATCAAAGAGCTGGCGGCCGACGTGCTGCGAGCAGAGAGG
GAGTAGGAGTGAAGCCAGCTGCAGGAATCAAAAATTGAAGAGAGATATATCTGAAAACTGG
AATAAGAAGCAAATAAATATCATCCTGCCTTCATGGAACTCAGCTGTCTGTGGCTTCCCATG
TCTTTCTCCAAAGCCATCCAGAGGGTTGTGATTTTGTCTGCTTAGTATCTCATCAACAAAGA
AATATTATTTGCTAATTAAAAAGTTAATCTTCATGGCCATAGCTTTTATTCATTAGCTGTGATT
TTTGTTGATTAAAACATTATAGATTTTCATGTTCTTGCAGTCATCAGAAGTGGTAGGAAAGC
CTCACTGATATATTTTCCAGGGCAATCAATGTTCACGCAACTTGAAATTATATCTGTGGTCT

FIG. 22C cont'd

TCAAATTGTCTTTTGTCATGTGGCTAAATGCCTAATAAACAATTCAAGTGA (SEQ ID NO: 150)

rAAV-hAADC-vector gene insert

TCTGCGCGCTCGCTCGCTCACTGAGGCCGCCCGGGCGTCGGGCGACCTTTGGTCGCCCG
GCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTC
CTTGTAGTTAATGATTAACCCGCCATGCTACTTATCTACGTAGCCATGCTCTAGAGCGGCC
GCACGCGTACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATG
GAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCC
CGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATT
GACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCA
TATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCC
CAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTAT
TACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACG
GGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAA
CGGGACTTTCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGT
GTACGGTGGGAGGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGA
CGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGCCTCCGCGGA
TTCGAATCCCGGCCGGGAACGGTGCATTGGAACGCGGATTCCCCGTGCCAAGAGTGACG
TAAGTACCGCCTATAGAGTCTATAGGCCCACAAAAAATGCTTTCTTCTTTTAATATACTTTTT
TGTTTATCTTATTTCTAATACTTTCCCTAATCTCTTTCTTTCAGGGCAATAATGATACAATGTA
TCATGCCTCTTTGCACCATTCTAAAGAATAACAGTGATAATTTCTGGGTTAAGGCAATAGCA
ATATTTCTGCATATAAATATTTCTGCATATAAATTGTAACTGATGTAAGAGGTTTCATATTGC
TAATAGCAGCTACAATCCAGCTACCATTCTGGTTTTATTTTATGGTTGGGATAAGGCTGGAT
TATTCTGAGTCCAAGCTAGGCCCTTTTGCTAATCATGTTCATACCTCTTATCTTCCTCCCAC
AGCTCCTGGGCAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATTGGGAT
TCGAACATCGATTGAATTCCCCGGGGATCCACCATGAACGCAAGTGAATTCCGAAGGAGA
GGGAAGGAGATGGTGGATTACGTGGCCAACTACATGGAAGGCATTGAGGGACGCCAGGT
CTACCCTGACGTGGAGCCCGGGTACCTGCGGCCGCTGATCCCTGCCGCTGCCCCTCAGG
AGCCAGACACGTTTGAGGACATCATCAACGACGTTGAGAAGATAATCATGCCTGGGGTGA
CGCACTGGCACAGCCCCTACTTCTTCGCCTACTTCCCCACTGCCAGCTCGTACCCGGCCA
TGCTTGCGGACATGCTGTGCGGGGCCATTGGCTGCATCGGCTTCTCCTGGGCGGCAAGC
CCAGCATGCACAGAGCTGGAGACTGTGATGATGGACTGGCTCGGGAAGATGCTGGAACTA
CCAAAGGCATTTTTGAATGAGAAAGCTGGAGAAGGGGGAGGAGTGATCCAGGGAAGTGCC
AGTGAAGCCACCCTGGTGGCCCTGCTGGCCGCTCGGACCAAAGTGATCCATCGGCTGCA
GGCAGCGTCCCCAGAGCTCACACAGGCCGCTATCATGGAGAAGCTGGTGGCTTACTCATC
CGATCAGGCACACTCCTCAGTGGAAAGAGCTGGGTTAATTGGTGGAGTGAAATTAAAAGC
CATCCCCTCAGATGGCAACTTCGCCATGCGTGCGTCTGCCCTGCAGGAAGCCCTGGAGAG
AGACAAAGCGGCTGGCCTGATTCCTTTCTTTATGGTTGCCACCCTGGGGACCACAACATGC
TGCTCCTTTGACAATCTCTTAGAAGTCGGTCCTATCTGCAACAAGGAAGACATATGGCTGC
ACGTTGATGCAGCCTACGCAGGCAGTGCATTCATCTGCCCTGAGTTCCGGCACCTTCTGA
ATGGAGTGGAGTTTGCAGATTCATTCAACTTTAATCCCCACAAATGGCTATTGGTGAATTTT
GACTGTTCTGCCATGTGGGTGAAAAAGAGAACAGACTTAACGGGAGCCTTTAGACTGGAC
CCCACTTACCTGAAGCACAGCCATCAGGATTCAGGGCTTATCACTGACTACCGGCATTGGC
AGATACCACTGGGCAGAAGATTTCGCTCTTTGAAAATGTGGTTTGTATTTAGGATGTATGGA
GTCAAAGGACTGCAGGCTTATATCCGCAAGCATGTCCAGCTGTCCCATGAGTTTGAGTCAC

FIG. 22C cont'd

TGGTGCGCCAGGATCCCCGCTTTGAAATCTGTGTGGAAGTCATTCTGGGGCTTGTCTGCTT
TCGGCTAAAGGGTTCCAACAAAGTGAATGAAGCTCTTCTGCAAAGAATAAACAGTGCCAAA
AAAATCCACTTGGTTCCATGTCACCTCAGGGACAAGTTTGTCCTGCGCTTTGCCATCTGTT
CTCGCACGGTGGAATCTGCCCATGTGCAGCGGGCCTGGGAACACATCAAAGAGCTGGCG
GCCGACGTGCTGCGAGCAGAGAGGGAGTAGGAGTGAAGCCAGCTGCAGGAATCAAAAAT
TGAAGAGAGATATATCTGAAAACTGGAATAAGAAGCAAATAAATATCATCCTGCCTTCATGG
AACTCAGCTGTCTGTGGCTTCCCATGTCTTTCTCCAAAGTTATCCAGAGGGTTGTGATTTTG
TCTGCTTAGTATCTCATCAACAAAGAAATATTATTTGCTAATTAAAAAGTTAATCTTCATGGC
CATAGCTTTTATTCATTAGCTGTGATTTTTGTTGATTAAAACATTATAGATTTTCATGTTCTTG
CAGTCATCAGAAGTGGTAGGAAAGCCTCACTGATATATTTTCCAGGGCAATCAATGTTCAC
GCAACTTGAAATTATATCTGTGGTCTTCAAATTGTCTTTTGTCATGTGGCTAAATGCCTAATA
AGGAATTAATTCGATATCAAGCTATCCAACACACTGGTAGGGATAACAGGGTAATCTCGAG
GCAAGCTTGGGCCCGGTACCCAATTCGCCCTATAGTGAGTCGTATTACGCGCGCAGCGGC
CGACCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCAC
AAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAA
TGTATCTTATCATGTCTGGATCTCCGGACACGTGCGGACCGAGCGGCCGCTCTAGAGCAT
GGCTACGTAGATAAGTAGCATGGCGGGTTAATCATTAACTACAAGGAACCCCTAGTGATGG
AGTTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTC
GCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAT
(SEQ ID NO: 151)

Tyrosine hydroxylase (TH) mRNA, [Homo sapiens], Accession No. X05290.1

CGGACCTCCACACTGAGCCATGCCCACCCCCGACGCCACCACGCCACAGGCCAAGGGCT
TCCGCAGGGCCGTGTCTGAGCTGGACGCCAAGCAGGCAGAGGCCATCATGTCCCCGCGG
TTCATTGGGCGCAGGCAGAGCCTCATCGAGGACGCCCGCAAGGAGCGGGAGGCGGCGG
TGGCAGCAGCGGCCGCTGCAGTCCCCTCGGAGCCCGGGGACCCCCTGGAGGCTGTGGC
CTTTGAGGAGAAGGAGGGGAAGGCCGTGCTAAACCTGCTCTTCTCCCCGAGGGCCACCAA
GCCCTCGGCGCTGTCCCGAGCTGTGAAGGTGTTTGAGACGTTTGAAGCCAAAATCCACCA
TCTAGAGACCCGGCCCGCCCAGAGGCCGCGAGCTGGGGGCCCCCACCTGGAGTACTTCG
TGCGCCTCGAGGTGCGCCGAGGGGACCTGGCCGCCCTGCTCAGTGGTGTGCGCCAGGT
GTCAGAGGACGTGCGCAGCCCCGCGGGGCCCAAGGTCCCCTGGTTCCCAAGAAAAGTGT
CAGAGCTGGACAAGTGTCATCACCTGGTCACCAAGTTCGACCCTGACCTGGACTTGGACC
ACCCGGGCTTCTCGGACCAGGTGTACCGCCAGCGCAGGAAGCTGATTGCTGAGATCGCC
TTCCAGTACAGGCACGGCGACCCGATTCCCCGTGTGGAGTACACCGCCGAGGAGATTGC
CACCTGGAAGGAGGTCTACACCACGCTGAAGGGCCTCTACGCCACGCACGCCTGCGGGG
AGCACCTGGAGGCCTTTGCTTTGCTGGAGCGCTTCAGCGGCTACCGGGAAGACAATATCC
CCCAGCTGGAGGACGTCTCCCGCTTCCTGAAGGAGCGCACGGGCTTCCAGCTGCGGCCT
GTGGCCGGCCTGCTGTCCGCCCGGGACTTCCTGGCCAGCCTGGCCTTCCGCGTGTTCCA
GTGCACCCAGTATATCCGCCACGCGTCCTCGCCCATGCACTCCCCTGAGCCGGACTGCTG
CCACGAGCTGCTGGGGCACGTGCCCATGCTGGCCGACCGCACCTTCGCGCAGTTCTCGC
AGGACATTGGCCTGGCGTCCCTGGGGGCCTCGGATGAGGAAATTGAGAAGCTGTCCACG
CTGTCATGGTTCACGGTGGAGTTCGGGCTGTGTAAGCAGAACGGGGAGGTGAAGGCCTAT
GGTGCCGGGCTGCTGTCCTCCTACGGGGAGCTCCTGCACTGCCTGTCTGAGGAGCCTGA
GATTCGGGCCTTCGACCCTGAGGCTGCGGCCGTGCAGCCCTACCAAGACCAGACGTACC
AGTCAGTCTACTTCGTGTCTGAGAGCTTCAGTGACGCCAAGGACAAGCTCAGGAGCTATG
CCTCACGCATCCAGCGCCCCTTCTCCGTGAAGTTCGACCCGTACACGCTGGCCATCGACG

FIG. 22C cont'd

TGCTGGACAGCCCCCAGGCCGTGCGGCGCTCCCTGGAGGGTGTCCAGGATGAGCTGGAC
ACCCTTGCCCATGCGCTGAGTGCCATTGGCTAGGTGCACGGCGTCCCTGAGGGCCCTTCC
CAACCTCCCCTGGTCCTGCACTGTCCCGGAGCTCAGGCCCTGGTGAGGGGCTGGGTCCC
GGGTGCCCCCCATGCCCTCCCTGCTGCCAGGCTCCCACTGCCCCTGCACCTGCTTCTCAG
CGCAACAGCTGTGTGTGCCCGTGGTGAGGTTGTGCTGCCTGTGGTGAGGTCCTGTCCTGG
CTCCCAGGGTCCTGGGGGCTGCTGCACTGCCCTCCGCCCTTCCCTGACACTGTCTGCTGC
CCCAATCACCGTCACAATAAAAGAAACTGTGGTCTCT (SEQ ID NO: 152)

GTP cyclohydrolase I (CH1) mRNA, [Homo sapiens], Accession No. U19523.1

CCGGCTCGGAGTGTGATCTAAGCAGGTCGCGTACCTTCCTCAGGTGACTCCGGCCACAGC
CCATTGTCCGCGGCCACCGGCGGAGTTTAGCCGCAGACCTCGAAGCGCCCCGGGGTCCT
TCCCGAACGGCAGCGGCTGCGGCGGGTCCATGGAGAAGGGCCCTGTGCGGGCACCGGC
GGAGAAGCCGCGGGGCGCCAGGTGCAGCAATGGGTTCCCCGAGCGGGATCCGCCGCGG
CCCGGGCCCAGCAGGCCGGCGGAGAAGCCCCCGCGGCCCGAGGCCAAGAGCGCGCAG
CCCGCGGACGGCTGGAAGGGCGAGCGGCCCCGCAGCGAGGAGGATAACGAGCTGAACC
TCCCTAACCTGGCAGCCGCCTACTCGTCCATCCTGAGCTCGCTGGGCGAGAACCCCCAGC
GGCAAGGGCTGCTCAAGACGCCCTGGAGGGCGGCCTCGGCCATGCAGTTCTTCACCAAG
GGCTACCAGGAGACCATCTCAGATGTCCTAAACGATGCTATATTTGATGAAGATCATGATG
AGATGGTGATTGTGAAGGACATAGACATGTTTTCCATGTGTGAGCATCACTTGGTTCCATTT
GTTGGAAAGGTCCATATTGGTTATCTTCCTAACAAGCAAGTCCTTGGCCTCAGCAAACTTG
CGAGGATTGTAGAAATCTATAGTAGAAGACTACAAGTTCAGGAGCGCCTTACAAAACAAAT
TGCTGTAGCAATCACGGAAGCCTTGCGGCCTGCTGGAGTCGGGGTAGTGGTTGAAGCAAC
ACACATGTGTATGGTAATGCGAGGTGTACAGAAAATGAACAGCAAAACTGTGACCAGCACA
ATGTTGGGTGTGTTCCGGGAGGATCCAAAGACTCGGGAAGAGTTCCTGACTCTCATTAGG
AGCTGAGCTTCATTCAGTGTGTGTGCGTTGGTTGCCGATCGTACTGCCAGTAGCATTGTCT
GTCTGTCCGGTCTTGTTTGTACATTCCATTTTCAATTGTTACAGATGTGAACTTTATTCCTTG
TCACTAATTATATTTAAAATTATTTCTAGGAAGTCAAATAAATATAATAAAGGGTTGAGCCTC
TACTTTCTTCTTGCCACCTTTTTGTGGCAATATTAAAGTGAACTGCTAATAGTGTAAGTATGT
GCACAAAACCACTGCCAGATAACCAGAGGGGCCTGGGAAGGGAGAAGAATTAGTGTATTT
TTTTCAAATAGTACAGTAATTTGCCTCATAAGCATAGGAGCATTGGGAATGAGAGGGAACT
GTGCCCAGTATACTGTTTTTTTTCTTCCTCCAATAAAAGTGGTGTAGTGCCGAAAGTGCTAA
AATATTTAGTGCGGTATTGCTCTGTGAATTCAAGTTCAACAGACTTCACTTTGGTCATGTTTA
TTAAACCACCAGTGACATTTAAAAATATATTTTTAGCAGTCGTAATGTTAGTCACCAAGGGA
AGGTGGTGGAATGTCTATGTTTTTGATTTTACTGTGAGTTAAAAAGGCACATTTCTACCTTC
TATTGTTTTTAAATTCAAGAATAGGGAATTAGTTCCTGGTGTTGTTTACGAGTGTATTCTCGT
GTCAACATACAGGGATTTAGACATTTAACTCTCTGTGCCTTGATAAGAATATCATTTAGAGT
GTAGATACTTTTGCCTTTTTAAAAAAGCCATTATTTTATGAGACTTAGTACTCACACTGCAAA
TAACTAGTCAGCTCAGTTTTAACTTTATAGGTTTATTGAGTTTCCTTTGTGTGATCCATGTAG
ATGCCTCAAAATGTTTCTTCTTCTTCTTTTTTTTAATCTTATAAGATATTTTTCTAAGTATTTCC
AGAAACATTTGAGAGTGCCCATCATTTTCAGGTCTGCAGAACCATAGCTTCCACGCACCTG
AACGAGCACAGAATGAACTGACGGTGGAAGACATTATGAGCTGTGTCCAACGTTTTAACCA
AAGCGTATCGTACCAACGATCTGTGAAAATGCACTGGAAGCTTCTGGTCCCGGTTTCCTTT
GTGGTCTATGTGGGTCTTGTCCTCATTGTAACTCCGTATAGATGGTATAGGTATTTTAATCC
TGGAAGCTGTTGCCTTATTAATGATTATCTTAAAATTTCCTCCATTGGGGCAGCGTGGGCCA
AATTAAAACAAACAAAACCGCAACTCCTCCACAGAAACACAAACACAGTTATTCCATGAAGT
TTAGTATTTGGTTGACATAGTGCTCTTCAAATTCATCCCATTACCCTAAAAGTAATAACTTTG

FIG. 22C cont'd

ATGCTTGCTTTAACTTTAGTCCCATCTCTGCCACTTTGATGCTATTTGGGTTATGATGGGGC
AAGATGGCAGAGGTATTGGGTTTTTTTGTTTTTTTCCATTCCTCTCTACTTCTGTTTCCTAGC
TTTTTCTTTCTGGAGTTTAAGTACAGTGATGGTTGGCTTGAGTACCTTTTTAAATCTAGCCCA
GTATAAACATTAGCCTGCTTAATATTTAGACATTTATAGGTAGAATTCTGAGCACTCAACTCA
TGTTTGGCATTTTAAAGTAAAAACAAGTGTGACTTCGAGGACCAAAGAAATTGTCAGCTATA
CATTTATCTTTATGAACTCATTTATATTCCTTTTTAATGACTCGTTGTTCTAACATTTCCTAGA
AGTGTTCTTATAAAGGTCTAATGTATCCACAGGCTGTTGTCTTATTAGTAAATGCAAAGTAAT
GACTTTGTCTGTTTTACTCTAGTCTTTAGTACTTCAAAATTACCTTTTCATATCCATGATCTTG
AGTCCATTTGGGGGATTTTTAAGAATTTGATGTATTTCAATACACTGTTCAAAATTAAATTGT
TTAATTTTATGTATGAGTATGTATGTTCCTGAAGTTGGTCCTATTTAAATTATTAAACTATTGT
AACTTTAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO: 153)

Glucocerebrosidase (GCase, lysosomal acid gluocsylceramidase isoform 1 precursor), [Homo sapiens], NP_000148.2

MEFSSPSREECPKPLSRVSIMAGSLTGLLLLQAVSWASGARPCIPKSFGYSSVVCVCNATYCD
SFDPPTFPALGTFSRYESTRSGRRMELSMGPIQANHTGTGLLLTLQPEQKFQKVKGFGGAMT
DAAALNILALSPPAQNLLLKSYFSEEGIGYNIIRVPMASCDFSIRTYTYADTPDDFQLHNFSLPEE
DTKLKIPLIHRALQLAQRPVSLLASPWTSPTWLKTNGAVNGKGSLKGQPGDIYHQTWARYFVK
FLDAYAEHKLQFWAVTAENEPSAGLLSGYPFQCLGFTPEHQRDFIARDLGPTLANSTHHNVRL
LMLDDQRLLLPHWAKVVLTDPEAAKYVHGIAVHWYLDFLAPAKATLGETHRLFPNTMLFASEA
CVGSKFWEQSVRLGSWDRGMQYSHSIITNLLYHVVGWTDWNLALNPEGGPNWVRNFVDSPII
VDITKDTFYKQPMFYHLGHFSKFIPEGSQRVGLVASQKNDLDAVALMHPDGSAVVVVLNRSSK
DVPLTIKDPAVGFLETISPGYSIHTYLWRRQ (SEQ ID NO: 154)

GBA1 gene product Isoform 2, NP_001165282.1

MELSMGPIQANHTGTGLLLTLQPEQKFQKVKGFGGAMTDAAALNILALSPPAQNLLLKSYFSEE
GIGYNIIRVPMASCDFSIRTYTYADTPDDFQLHNFSLPEEDTKLKIPLIHRALQLAQRPVSLLASP
WTSPTWLKTNGAVNGKGSLKGQPGDIYHQTWARYFVKFLDAYAEHKLQFWAVTAENEPSAGL
LSGYPFQCLGFTPEHQRDFIARDLGPTLANSTHHNVRLLMLDDQRLLLPHWAKVVLTDPEAAK
YVHGIAVHWYLDFLAPAKATLGETHRLFPNTMLFASEACVGSKFWEQSVRLGSWDRGMQYSH
SIITNLLYHVVGWTDWNLALNPEGGPNWVRNFVDSPIIVDITKDTFYKQPMFYHLGHFSKFIPEG
SQRVGLVASQKNDLDAVALMHPDGSAVVVVLNRSSKDVPLTIKDPAVGFLETISPGYSIHTYLW
RRQ (SEQ ID NO: 155)

GBA1 gene product Isoform 3, NP_001165283.1

MEFSSPSREECPKPLSRVSIMAGSLTGLLLLQAVSWASGARPCIPKSFGYSSVVCVCNATYCD
SFDPPTFPALGTFSRYESTRSGRRMELSMGPIQANHTGTGIGYNIIRVPMASCDFSIRTYTYADT
PDDFQLHNFSLPEEDTKLKIPLIHRALQLAQRPVSLLASPWTSPTWLKTNGAVNGKGSLKGQP
GDIYHQTWARYFVKFLDAYAEHKLQFWAVTAENEPSAGLLSGYPFQCLGFTPEHQRDFIARDL
GPTLANSTHHNVRLLMLDDQRLLLPHWAKVVLTDPEAAKYVHGIAVHWYLDFLAPAKATLGET
HRLFPNTMLFASEACVGSKFWEQSVRLGSWDRGMQYSHSIITNLLYHVVGWTDWNLALNPEG
GPNWVRNFVDSPIIVDITKDTFYKQPMFYHLGHFSKFIPEGSQRVGLVASQKNDLDAVALMHPD
GSAVVVVLNRSSKDVPLTIKDPAVGFLETISPGYSIHTYLWRRQ (SEQ ID NO: 156)

FIG. 22C cont'd

Human Huntingtin gene of exon 1

UUGCUGUGUGAGGCAGAACCUGCGGGGGGCAGGGGCGGGCUGGUUCCCUGGCCAGCCA
UUGGCAGAGUCCGCAGGCUAGGGCUGUCAAUCAUGCUGGCCGGGCGUGGCCCCGCCUC
CGCCGGCGCGGCCCCGCCUCCGCCGGCGCACGUCUGGGACGCAAGGCGCCGUGGGGG
CUGCCGGGACGGGUCCAAGAUGGACGGCCGCUCAGGUUCUGCUUUUACCUGCGGCCCA
GAGCCCCAUUCAUUGCCCCGGUGCUGAGCGGCGCCGCGAGUCGGCCCGAGGCCUCCG
GGGACUGCCGUGCCGGGCGGGAGACCGCCAUGGCGACCCUGGAAAAGCUGAUGAAGG
CCUUCGAGUCCCUCAAGUCCUUCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA
GCAGCAGCAGCAGCAGCAGCAGCAGCAGCAACAGCCGCCACCGCCGCCGCCGCCGCCG
CCGCCUCCUCAGCUUCCUCAGCCGCCGCCGCAGGCACAGCCGCUGCUGCCUCAGCCGC
AGCCGCCCCCCGCCGCCGCCCCCCGCCGCCACCCGGCCCGGCUGUGGCUGAGGAGCCGC
UGCACCGACCGUGAGUUUGGGCCCGCUGCAGCUCCCUGUC (SEQ ID NO: 157)

Target sequence of human huntingtin gene of exon 1

CUUCGAGUCCCUCAAGUCCUU (SEQ ID NO: 158)

GTPase HRas [Homo sapiens]:

MTEYKLVVVGAGGVGKSALTIQLIQNHFVDEYDPTIEDSYRKQVVIDGETCLLDILDTAGQEEYS
AMRDQYMRTGEGFLCVFAINNTKSFEDIHQYREQIKRVKDSDDVPMVLVGNKCDLAARTVESR
QAQDLARSYGIPYIETSAKTRQGVEDAFYTLVREIRQHKLRKLNPPDESGPGCMSCKCVLS
(SEQ ID NO: 159)

GCaMP6m

ATGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAAATGG
GTCGGGATCTGTACGACGATGACGATAAGGATCTCGCCACCATGGTCGACTCATCACGTC
GTAAGTGGAATAAGACAGGTCACGCAGTCAGAGCTATAGGTCGGCTGAGCTCACTCGAGA
ACGTCTATATCAAGGCCGACAAGCAGAAGAACGGCATCAAGGCGAACTTCAAGATCCGCC
ACAACATCGAGGACGGCGGCGTGCAGCTCGCCTACCACTACCAGCAGAACACCCCCATC
GGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCGTGCAGTCCAAACTTTCG
AAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGG
GATCACTCTCGGCATGGACGAGCTGTACAAGGGCGGTACCGGAGGGAGCATGGTGAGCA
AGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTA
AACGGCCACAAGTTCAGCGTGTCCGGCGAGGGTGAGGGCGATGCCACCTACGGCAAGCT
GACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGAC
CACCCTGACCTACGGCGTGCAGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGA
CTTCTTCAAGTCCGCCATGCCCGAAGGCTACATCCAGGAGCGCACCATCTTCTTCAAGGAC
GACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCG
CATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGG
AGTACAACCTGCCGGACCAACTGACTGAAGAGCAGATCGCAGAATTTAAAGAGGCTTTCTC
CCTATTTGACAAGGACGGGGATGGGACAATAACAACCAAGGAGCTGGGGACGGTGATGC
GGTCTCTGGGGCAGAACCCCACAGAAGCAGAGCTGCAGGACATGATCAATGAAGTAGATG
CCGACGGTGACGGCACAATCGACTTCCCTGAGTTCCTGACAATGATGGCAAGAAAAGGGA
GCTACAGGGACACGGAAGAAGAAATTAGAGAAGCGTTCGGTGTGTTTGATAAGGATGGCA
ATGGCTACATCAGTGCAGCAGAGCTTCGCCACGTGATGACAAACCTTGGAGAGAAGTTAA
CAGATGAAGAGGTTGATGAAATGATCAGGGAAGCAGACATCGATGGGGATGGTCAGGTAA
ACTACGAAGAGTTTGTACAAATGATGACAGCGAAGTGA (SEQ ID NO: 160)

FIG. 22C cont'd

GCaMP6s

ATGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAAATGG
GTCGGGATCTGTACGACGATGACGATAAGGATCTCGCCACCATGGTCGACTCATCACGTC
GTAAGTGGAATAAGACAGGTCACGCAGTCAGAGCTATAGGTCGGCTGAGCTCACTCGAGA
ACGTCTATATCAAGGCCGACAAGCAGAAGAACGGCATCAAGGCGAACTTCCACATCCGCC
ACAACATCGAGGACGGCGGCGTGCAGCTCGCCTACCACTACCAGCAGAACACCCCCATC
GGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCGTGCAGTCCAAACTTTCG
AAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGG
GATCACTCTCGGCATGGACGAGCTGTACAAGGGCGGTACCGGAGGGAGCATGGTGAGCA
AGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTA
AACGGCCACAAGTTCAGCGTGTCCGGCGAGGGTGAGGGCGATGCCACCTACGGCAAGCT
GACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGAC
CACCCTGACCTACGGCGTGCAGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGA
CTTCTTCAAGTCCGCCATGCCCGAAGGCTACATCCAGGAGCGCACCATCTTCTTCAAGGAC
GACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCG
CATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGG
AGTACAACCTGCCGGACCAACTGACTGAAGAGCAGATCGCAGAATTTAAAGAGGCTTTCTC
CCTATTTGACAAGGACGGGGATGGGACAATAACAACCAAGGAGCTGGGGACGGTGATGC
GGTCTCTGGGGCAGAACCCCACAGAAGCAGAGCTGCAGGACATGATCAATGAAGTAGATG
CCGACGGTGACGGCACAATCGACTTCCCTGAGTTCCTGACAATGATGGCAAGAAAAATGA
AATACAGGGACACGGAAGAAGAAATTAGAGAAGCGTTCGGTGTGTTTGATAAGGATGGCA
ATGGCTACATCAGTGCAGCAGAGCTTCGCCACGTGATGACAAACCTTGGAGAGAAGTTAA
CAGATGAAGAGGTTGATGAAATGATCAGGGAAGCAGACATCGATGGGGATGGTCAGGTAA
ACTACGAAGAGTTTGTACAAATGATGACAGCGAAGTGA (SEQ ID NO: 161)

GCaMP6f

ATGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAAATGG
GTCGGGATCTGTACGACGATGACGATAAGGATCTCGCCACCATGGTCGACTCATCACGTC
GTAAGTGGAATAAGACAGGTCACGCAGTCAGAGCTATAGGTCGGCTGAGCTCACTCGAGA
ACGTCTATATCAAGGCCGACAAGCAGAAGAACGGCATCAAGGCGAACTTCAAGATCCGCC
ACAACATCGAGGACGGCGGCGTGCAGCTCGCCTACCACTACCAGCAGAACACCCCCATC
GGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCGTGCAGTCCAAACTTTCG
AAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGG
GATCACTCTCGGCATGGACGAGCTGTACAAGGGCGGTACCGGAGGGAGCATGGTGAGCA
AGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTA
AACGGCCACAAGTTCAGCGTGTCCGGCGAGGGTGAGGGCGATGCCACCTACGGCAAGCT
GACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGAC
CACCCTGACCTACGGCGTGCAGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGA
CTTCTTCAAGTCCGCCATGCCCGAAGGCTACATCCAGGAGCGCACCATCTTCTTCAAGGAC
GACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCG
CATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGG
AGTACAACCTGCCGGACCAACTGACTGAAGAGCAGATCGCAGAATTTAAAGAGGAATTCTC
CCTATTTGACAAGGACGGGGATGGGACAATAACAACCAAGGAGCTGGGGACGGTGATGC
GGTCTCTGGGGCAGAACCCCACAGAAGCAGAGCTGCAGGACATGATCAATGAAGTAGATG
CCGACGGTGACGGCACAATCGACTTCCCTGAGTTCCTGACAATGATGGCAAGAAAAATGA

FIG. 22C cont'd

AATACAGGGACACGGAAGAAGAAATTAGAGAAGCGTTCGGTGTGTTTGATAAGGATGGCA
ATGGCTACATCAGTGCAGCAGAGCTTCGCCACGTGATGACAAACCTTGGAGAGAAGTTAA
CAGATGAAGAGGTTGATGAAATGATCAGGGAAGCAGACATCGATGGGGATGGTCAGGTAA
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SEQUENCE LISTING

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<130> A166-0027PCT / 20-05PCT

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<151> 2020-08-14

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agggggaaat ttaagcaaat ccttttgaaa gcaaatccct ccaaggtgtg agtaataaag 240

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<211> 279
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<212> DNA
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<212> DNA
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<212> DNA
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<211> 368
<212> DNA
<213> Homo sapiens

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actcaggaat ctctaagaat gtttctacct taaaaggcag gtttttgttt cttaatcctt 300

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<212> DNA
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<211> 290
<212> DNA
<213> Homo sapiens

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ttaattattt agtctacttt tatttccagg tgttggatct ttttcatcga 290

<210> 30
<211> 470
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<213> Homo sapiens

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<211> 566
<212> DNA
<213> Homo sapiens

<400> 31
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aaaagcacca ataagcttca gctgtcttcc cccttcttca aactacttaa ttttctgtga 180

aactaacact tcttttctaa ttgcccttga cttcacattc tttagcccat tcttcgttac 240

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taccccaact cataagattg gtgaga 566

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<211> 407
<212> DNA
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atgcactatc atatttaact ctcataacaa taccacgaag caggtat 407

<210> 33
<211> 324
<212> DNA
<213> Homo sapiens

<400> 33
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tcttagtatt ttacggtttt ccttaatact tcttattcct tcaaaagcta tacctccata 240

ctatatattt gaactgaaat gtctgatttt agaacaagtc acatgtcatt tttattttgt 300

ctttaaaaac ttctgacact gaga 324

<210> 34
<211> 349
<212> DNA
<213> Homo sapiens

<400> 34
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atttttgat atgatattca cagtagaata atttataata gacaaaatta caaacaataa 240

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aaagtcatgt tagagaagaa tatttataga tgtggggaaa agttcatga 349

<210> 35
<211> 644
<212> DNA
<213> Homo sapiens

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gggtgatttc cttacctgct tttttctgtg tttttaagct cttcattact tcctaattgt 240

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tctcttttgc tagcgcaaat gctattggct gctcaactgc cttaagggtt tcttctgcag 480

cccaaatgaa cagctttgtg cttccagcct ttgatagctc ctgggggcgt tgatcactga 540

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<210> 36
<211> 304
<212> DNA
<213> Homo sapiens

<400> 36
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atttgagaaa tgaaatgact ctcccaagtg gccggggtgg cagggagggg gtggaggaag 240

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ctcg 304

<210> 37
<211> 445
<212> DNA
<213> Homo sapiens

<400> 37
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ggactagaga agcagatttg gcgct 445

<210> 38

<400> 38
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<210> 39
<211> 744
<212> DNA
<213> Mus musculus

<400> 39
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<212> DNA
<213> Mus musculus

<400> 40
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aaagcttcta gcactattaa ttgttcactc tacccatgcc acatctcccc aggagatcag 420

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gaaaggcaac aacaaaacct ctgtaaggag tgttatcatt tctctctttt cattaagtca 540

caatgcagaa actgagtaat ctgaacaagt acctttaaag taagagactt agaaagtggc 600

tggctacatg taaagccgtt catgtgcttg cagttgtgta caggagcagg ctgctcacct 660

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tatgtacctg attccaataa aaatcaagta atgttgattg caaaccccat ctgtagtcat 960

agaaatatta caatgatgga catgtagtta gtttttcact tctcaaatac tgtccatttc 1020

<210> 41
<211> 942
<212> DNA
<213> Mus musculus

<400> 41
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acacagcccc acagtcatta ccaagttcaa tcatctaatg tgggatccca ggaggtctgc 120

attaaccatg aagcaatgaa aggtagagtg atcctgtata tggaccaact gtcttcccca 180

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tctacctctg cctggctgca gttctttctc ttgaagaaag gatttttttt ttttttggtt 360

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<211> 897
<212> DNA
<213> Mus musculus

<400> 42
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aaatagctcc ttcaagtcct gaagcgtaat aaaatattag aaaacacaat ggaaaaatga 420

ggcactcaca gaagaaatac agttggctct aaagcataga aagtctcaat tatttcaaaa 480

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ccaagaaagc atctcttcta agcagcagtt cctgattggc tggcattgtc tgtgtcagca 840

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<210> 43
<211> 547
<212> DNA

<213> Mus musculus

<400> 43
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cagggtggaa aaagaaatac ttactggaac acagacgtac aaaacaaaca agtttctagg 480

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<210> 44
<211> 598
<212> DNA
<213> Mus musculus

<400> 44
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<210> 45
<211> 686
<212> DNA
<213> Mus musculus

<400> 45
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tcgcctttag agtgagaatt acaaagacag tgggtcacgt agattaatgg ttgagatcct 480

ctgacctaag taactgctac ttttagcttt attctatttt caactcggat ctttgttttt 540

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<210> 46
<211> 600
<212> DNA
<213> Mus musculus

<400> 46
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<210> 47
<211> 696
<212> DNA
<213> Mus musculus

<400> 47
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<210> 48
<211> 518
<212> DNA
<213> Mus musculus

<400> 48
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<210> 49
<211> 622
<212> DNA
<213> Mus musculus

<400> 49
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atcattccaa acttaaatgc ctgtattatt aggcacacag ttggcattta aaagtatgga 540

ttaaggaact atgaatgcat ctgatttgtt actctgtata agcctatacc aaatcaaatt 600

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<210> 50
<211> 776
<212> DNA
<213> Mus musculus

<400> 50
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<212> DNA
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<211> 533
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<213> Mus musculus

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agaaacatca gctcattaat tttgttcacc tcgtaggact attattcaga atctttattc 240

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ggtgaggacc gttgtccagc agaggggcct gtcatttttg agaggtattt gtgtatttta 480

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<212> DNA
<213> Mus musculus

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<212> DNA
<213> Mus musculus

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<212> DNA
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<213> Mus musculus

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<223> EGFP

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<400> 132
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<223> WPRE3

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<210> 139
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<212> DNA
<213> Artificial Sequence

<220>
<223> P2A

<400> 139
ggcagcggcg ccaccaactt cagcctgctg aagcaggccg gcgacgtgga ggagaacccc 60

ggccccggag ctagcgga 78

<210> 140

<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> T2A

<220>
<221> MISC_FEATURE
<222> (1)..(3)
<223> (GlySerGly) residues can be added to 5' end to improve cleavage
       efficiency

<400> 140

Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
1   5   10   15

Glu Asn Pro Gly Pro
            20

<210> 141
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> E2A

<220>
<221> MISC_FEATURE
<222> (1)..(3)
<223> (GlySerGly) residues can be added to 5' end to improve cleavage
       efficiency

<400> 141

Gly Ser Gly Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp
1   5   10   15

Val Glu Ser Asn Pro Gly Pro Pro
            20

<210> 142
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> F2A

<220>
<221> MISC_FEATURE
<222> (1)..(3)
<223> (GlySerGly) residues can be added to 5' end to improve cleavage
       efficiency

<400> 142

Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala
1   5   10   15

Gly Asp Val Glu Ser Asn Pro Gly Pro
            20   25

<210> 143
<211> 130
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary Plasmid Backbone 1, Left ITR

<400> 143
cctgcaggca gctgcgcgct cgctcgctca ctgaggccgc ccgggcgtcg ggcgaccttt 60

ggtcgcccgg cctcagtgag cgagcgagcg cgcagagagg gagtggccaa ctccatcact 120

aggggttcct   130

<210> 144
<211> 141
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary Plasmid Backbone 1, Right ITR

<400> 144
cctgcaggca gctgcgcgct cgctcgctca ctgaggccgc ccgggcaaag cccgggcgtc 60

gggcgacctt tggtcgcccg gcctcagtga gcgagcgagc gcgcagagag ggagtggcca 120

actccatcac taggggttcc t   141

<210> 145
<211> 146
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary Plasmid Backbone 2, Left ITR

<400> 145
catgtcctgc aggcagctgc gcgctcgctc gctcactgag gccgcccggg caaagcccgg 60

gcgtcgggcg acctttggtc gcccggcctc agtgagcgag cgagcgcgca gagagggagt 120

ggccaactcc atcactaggg gttcct   146

<210> 146
<211> 149
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary Plasmid Backbone 2, Right ITR

<400> 146
aggaacccct agtgatggag ttggccactc cctctctgcg cgctcgctcg ctcactgagg 60

ccgggcgacc aaaggtcgcc cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc 120

gagcgcgcag ctgcctgcag gggcgcctg   149

<210> 147
<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<223> PHP.eB capsid

<400> 147

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145   150   155   160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180   185   190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195   200   205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210   215   220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225   230   235   240

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Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510
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Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Asp Gly Thr Leu Ala Val
            580                 585                 590


Pro Phe Lys Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595                 600                 605


Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610                 615                 620


Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625                 630                 635                 640


Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
                645                 650                 655


Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
            660                 665                 670


Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
        675                 680                 685


Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
    690                 695                 700


Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
705                 710                 715                 720


Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
                725                 730                 735


Arg Tyr Leu Thr Arg Asn Leu
            740


<210>  148
<211>  736
<212>  PRT
<213>  Adeno-associated virus

<400>  148

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15
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Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285
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Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560
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Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  149
<211>  747
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  tet-Transactivator version 2

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ggtatcgaag gcctgacgac aaggaaactc gctcaaaagc tgggagttga gcagcctacc      120

ctgtactggc acgtgaagaa caagcgggcc ctgctcgatg ccctggcaat cgagatgctg      180

gacaggcatc atacccactt ctgccccctg gaaggcgagt catggcaaga ctttctgcgg      240

aacaacgcca agtcattccg ctgtgctctc ctctcacatc gcgacggggc taaagtgcat      300

ctcggcaccc gcccaacaga gaaacagtac gaaaccctgg aaaatcagct cgcgttcctg      360

tgtcagcaag gcttctccct ggagaacgca ctgtacgctc tgtccgccgt gggccacttt      420

acactgggct gcgtattgga ggatcaggag catcaagtag caaaagagga aagagagaca      480
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cctaccaccg attctatgcc cccacttctg agacaagcaa ttgagctgtt cgaccatcag 540

ggagccgaac ctgccttcct tttcggcctg gaactaatca tatgtggcct ggagaaacag 600

ctaaagtgcg aaagcggcgg gccggccgac gcccttgacg attttgactt agacatgctc 660

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tttgaccttg acatgctccc cgggtaa 747

<210> 150
<211> 1930
<212> DNA
<213> Homo sapiens

<400> 150
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aacgacgttg agaagataat catgcctggg gtgacgcact ggcacagccc ctacttcttc 300

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atgatggact ggctcgggaa gatgctggaa ctaccaaagg catttttgaa tgagaaagct 480

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gcattcatct gccctgagtt ccggcacctt ctgaatggag tggagtttgc agattcattc 960

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agaagtggta ggaaagcctc actgatatat tttccagggc aatcaatgtt cacgcaactt 1860

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<210> 151
<211> 3703
<212> DNA
<213> Artificial Sequence

<220>
<223> rAAV-hAADC-vector gene insert

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cacgcgtact agttattaat agtaatcaat tacggggtca ttagttcata gcccatatat 240

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ctcacgggga tttccaagtc tccaccccat tgacgtcaat gggagtttgt tttggcacca 660

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caagtttgtc ctgcgctttg ccatctgttc tcgcacggtg gaatctgccc atgtgcagcg 2760

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ggtcttcaaa ttgtcttttg tcatgtggct aaatgcctaa taaggaatta attcgatatc 3240

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gtttattgca gcttataatg gttacaaata aagcaatagc atcacaaatt tcacaaataa 3420

agcatttttt tcactgcatt ctagttgtgg tttgtccaaa ctcatcaatg tatcttatca 3480

tgtctggatc tccggacacg tgcggaccga gcggccgctc tagagcatgg ctacgtagat 3540

aagtagcatg gcgggttaat cattaactac aaggaacccc tagtgatgga gttggccact 3600

ccctctctgc gcgctcgctc gctcactgag gccgggcgac caaaggtcgc ccgacgcccg 3660

ggctttgccc gggcggcctc agtgagcgag cgagcgcgca gat 3703

<210> 152
<211> 1816
<212> DNA
<213> Homo sapiens

<400> 152
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gctcaagacg ccctggaggg cggcctcggc catgcagttc ttcaccaagg gctaccagga 480

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gatcttgagt ccatttgggg gatttttaag aatttgatgt atttcaatac actgttcaaa 2820

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tattaaacta ttgtaacttt aaaaaaaaaa aaaaaaaaaa a 2921

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<212> PRT
<213> Homo sapiens

<400> 154

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Arg Val Ser Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln
20 25 30

Ala Val Ser Trp Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe
35 40 45

Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser
50 55 60

```
Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu
65                  70                  75                  80

Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln
                85                  90                  95

Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
            100                 105                 110

Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala
        115                 120                 125

Ala Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu
    130                 135                 140

Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val
145                 150                 155                 160

Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp
                165                 170                 175

Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp
            180                 185                 190

Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln
        195                 200                 205

Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu
    210                 215                 220

Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro
225                 230                 235                 240

Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu
                245                 250                 255

Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu
            260                 265                 270

Asn Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu
        275                 280                 285

Gly Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly
    290                 295                 300

Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu
305                 310                 315                 320

Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr
                325                 330                 335
```

```
Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr
            340                 345                 350

Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg
        355                 360                 365

Leu Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser
    370                 375                 380

Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met
385                 390                 395                 400

Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly
                405                 410                 415

Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp
            420                 425                 430

Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp
        435                 440                 445

Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
    450                 455                 460

Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys
465                 470                 475                 480

Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val
                485                 490                 495

Val Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys
            500                 505                 510

Asp Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile
        515                 520                 525

His Thr Tyr Leu Trp Arg Arg Gln
    530                 535


<210>  155
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<212>  PRT
<213>  Homo sapiens

<400>  155

Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly
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Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly
            20                  25                  30

Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu
        35                  40                  45
```

```
Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser Glu Glu
    50                  55                  60

Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe
65                  70                  75                  80

Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu
                85                  90                  95

His Asn Phe Ser Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu
            100                 105                 110

Ile His Arg Ala Leu Gln Leu Ala Gln Arg Pro Val Ser Leu Leu Ala
        115                 120                 125

Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys Thr Asn Gly Ala Val Asn
    130                 135                 140

Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile Tyr His Gln Thr
145                 150                 155                 160

Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu His Lys
                165                 170                 175

Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu
            180                 185                 190

Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln
        195                 200                 205

Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr
    210                 215                 220

His His Asn Val Arg Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu
225                 230                 235                 240

Pro His Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr
                245                 250                 255

Val His Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro Ala
            260                 265                 270

Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu
        275                 280                 285

Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val
    290                 295                 300

Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile
305                 310                 315                 320
```

```
Thr Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala
                325                 330                 335

Leu Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser
            340                 345                 350

Pro Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met
        355                 360                 365

Phe Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln
    370                 375                 380

Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala
385                 390                 395                 400

Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn Arg Ser
                405                 410                 415

Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu
            420                 425                 430

Glu Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp Arg Arg
        435                 440                 445

Gln
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<210> 156
<211> 487
<212> PRT
<213> Homo sapiens

<400> 156

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Arg Val Ser Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln
            20                  25                  30

Ala Val Ser Trp Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe
        35                  40                  45

Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser
    50                  55                  60

Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu
65                  70                  75                  80

Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln
                85                  90                  95

Ala Asn His Thr Gly Thr Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro
```

```
            100                 105                 110

Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr
        115                 120                 125

Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp Thr
    130                 135                 140

Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln Arg
145                 150                 155                 160

Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys
                165                 170                 175

Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly
            180                 185                 190

Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp
        195                 200                 205

Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn
    210                 215                 220

Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly
225                 230                 235                 240

Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro
                245                 250                 255

Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu Asp
            260                 265                 270

Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr Asp
        275                 280                 285

Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu
    290                 295                 300

Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu
305                 310                 315                 320

Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys
                325                 330                 335

Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln
            340                 345                 350

Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly Trp
        355                 360                 365

Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp Val
    370                 375                 380
```

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Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp Thr
385                 390                 395                 400

Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys Phe
                405                 410                 415

Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn
            420                 425                 430

Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val
        435                 440                 445

Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp
    450                 455                 460

Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile His
465                 470                 475                 480

Thr Tyr Leu Trp Arg Arg Gln
                485
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<211> 614
<212> RNA
<213> Homo sapiens

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cgcggccccg ccuccgccgg cgcacgucug ggacgcaagg cgccgugggg gcugccggga 180

cggguccaag auggacggcc gcucagguuc ugcuuuuacc ugcggcccag agccccauuc 240

auugccccgg ugcugagcgg cgccgcgagu cggcccgagg ccuccgggga cugccgugcc 300

gggcgggaga ccgccauggc gacccuggaa aagcugauga aggccuucga gucccucaag 360

uccuuccagc agcagcagca gcagcagcag cagcagcagc agcagcagca gcagcagcag 420

cagcagcagc aacagccgcc accgccgccg ccgccgccgc cgccuccuca gcuuccucag 480

ccgccgccgc aggcacagcc gcugcugccu cagccgcagc cgcccccgcc gccgcccccg 540

ccgccacccg gcccggcugu ggcugaggag ccgcugcacc gaccgugagu uugggcccgc 600

ugcagcuccc uguc   614

<210> 158
<211> 21
<212> RNA
<213> Homo sapiens

<400> 158
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<210> 159

<211> 189
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<213> Homo sapiens

<400> 159

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys
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Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
            20   25   30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
        35   40   45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
    50   55   60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
65   70   75   80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr
                85   90   95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val
            100   105   110

Leu Val Gly Asn Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg
        115   120   125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr
    130   135   140

Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val
145   150   155   160

Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu
                165   170   175

Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser
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cgtaagtgga ataagacagg tcacgcagtc agagctatag gtcggctgag ctcactcgag   180

aacgtctata tcaaggccga caagcagaag aacggcatca aggcgaactt caagatccgc 240

cacaacatcg aggacggcgg cgtgcagctc gcctaccact accagcagaa cacccccatc 300

ggcgacggcc ccgtgctgct gcccgacaac cactacctga gcgtgcagtc caaactttcg 360

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<213> Artificial Sequence

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<400> 161
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aacgtctata tcaaggccga caagcagaag aacggcatca aggcgaactt ccacatccgc 240

cacaacatcg aggacggcgg cgtgcagctc gcctaccact accagcagaa cacccccatc 300

ggcgacggcc ccgtgctgct gcccgacaac cactacctga gcgtgcagtc caaactttcg 360

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ggtgacggca caatcgactt ccctgagttc ctgacaatga tggcaagaaa aatgaaatac 1140

agggacacgg aagaagaaat tagagaagcg ttcggtgtgt ttgataagga tggcaatggc 1200

tacatcagtg cagcagagct tcgccacgtg atgacaaacc ttggagagaa gttaacagat 1260

gaagaggttg atgaaatgat cagggaagca gacatcgatg gggatggtca ggtaaactac 1320

gaagagtttg tacaaatgat gacagcgaag tga 1353

<210> 162
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> GCaMP6f

<400> 162
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cgtaagtgga ataagacagg tcacgcagtc agagctatag gtcggctgag ctcactcgag 180

aacgtctata tcaaggccga caagcagaag aacggcatca aggcgaactt caagatccgc 240

cacaacatcg aggacggcgg cgtgcagctc gcctaccact accagcagaa cacccccatc 300

ggcgacggcc ccgtgctgct gcccgacaac cactacctga gcgtgcagtc caaactttcg 360

aaagacccca acgagaagcg cgatcacatg gtcctgctgg agttcgtgac cgccgccggg 420

atcactctcg gcatggacga gctgtacaag ggcggtaccg gagggagcat ggtgagcaag 480

ggcgaggagc tgttcaccgg ggtggtgccc atcctggtcg agctggacgg cgacgtaaac 540

ggccacaagt tcagcgtgtc cggcgagggt gagggcgatg ccacctacgg caagctgacc 600

ctgaagttca tctgcaccac cggcaagctg cccgtgccct ggcccaccct cgtgaccacc 660

ctgacctacg gcgtgcagtg cttcagccgc taccccgacc acatgaagca gcacgacttc 720

ttcaagtccg ccatgcccga aggctacatc caggagcgca ccatcttctt caaggacgac 780

ggcaactaca agacccgcgc cgaggtgaag ttcgagggcg acaccctggt gaaccgcatc 840

gagctgaagg gcatcgactt caaggaggac ggcaacatcc tggggcacaa gctggagtac 900

aacctgccgg accaactgac tgaagagcag atcgcagaat ttaaagagga attctcccta 960

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ctggggcaga accccacaga agcagagctg caggacatga tcaatgaagt agatgccgac 1080

ggtgacggca caatcgactt ccctgagttc ctgacaatga tggcaagaaa aatgaaatac 1140

agggacacgg aagaagaaat tagagaagcg ttcggtgtgt ttgataagga tggcaatggc 1200

tacatcagtg cagcagagct tcgccacgtg atgacaaacc ttggagagaa gttaacagat 1260

gaagaggttg atgaaatgat cagggaagca gacatcgatg gggatggtca ggtaaactac 1320

gaagagtttg tacaaatgat gacagcgaag tga 1353

<210> 163
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> First RNA sequence for targeting huntingtin gene

<400> 163
aaggacuuga gggacucga 19

<210> 164
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> First RNA sequence for targeting huntingtin gene

<400> 164
aaggacuuga gggacucgaa 20

<210> 165
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> First RNA sequence for targeting huntingtin gene

<400> 165
aaggacuuga gggacucgaa g 21

<210> 166
<211> 22
<212> RNA
<213> Artificial Sequence

<220>
<223> First RNA sequence for targeting huntingtin gene

<400> 166
aaggacuuga gggacucgaa gg 22

<210> 167
<211> 23
<212> RNA
<213> Artificial Sequence

<220>

<223> First RNA sequence for targeting huntingtin gene

<400> 167
aaggacuuga gggacucgaa ggc 23

<210> 168
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Second RNA sequence for targeting huntingtin gene

<400> 168
ucgagucccu caaguccuu 19

<210> 169
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> Second RNA sequence for targeting huntingtin gene

<400> 169
uucgaguccc ucaaguccuu 20

<210> 170
<211> 21
<212> RNA
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<220>
<223> Second RNA sequence for targeting huntingtin gene

<400> 170
cuucgagucc cucaaguccu u 21

<210> 171
<211> 22
<212> RNA
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<220>
<223> Second RNA sequence for targeting huntingtin gene

<400> 171
ccuucgaguc ccucaagucc uu 22

<210> 172
<211> 23
<212> RNA
<213> Artificial Sequence

<220>
<223> Second RNA sequence for targeting huntingtin gene

<400> 172
gccuucgagu cccucaaguc cuu 23

<210> 173
<211> 19
<212> RNA

<213> Artificial Sequence

<220>
<223> Second RNA sequence for targeting huntingtin gene

<400> 173
cuucgagucu caaguccuu 19

<210> 174
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Second RNA sequence for targeting huntingtin gene

<400> 174
acgagucccu caaguccuc 19

<210> 175
<211> 72
<212> RNA
<213> Artificial Sequence

<220>
<223> pre-miR451a

<400> 175
cuuggggaaug gcaaggaagg acuugaggga cucgaagacg agucccucaa guccucucuu 60

gcuauaccca ga 72

<210> 176
<211> 69
<212> RNA
<213> Artificial Sequence

<220>
<223> Pre-miR155

<400> 176
ugcugaagga cuugagggac ucgaagguuu uggccacuga cugaccuucg agucucaagu 60

ccuucagga 69

<210> 177
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Double stranded RNA for targeting human hungtingtin gene of exon 1

<400> 177
augaaggccu ucgagucccu c 21

<210> 178
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Double stranded RNA for targeting human hungtingtin gene of exon

1

<400> 178
ggcgacccug gaaaagcuga u 21

<210> 179
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Double stranded RNA for targeting human hungtingtin gene of exon 1

<400> 179
uggcgacccu ggaaaagcug a 21

<210> 180
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Double stranded RNA for targeting human hungtingtin gene of exon 1

<400> 180
auggcgaccc uggaaaagcu g 21

<210> 181
<211> 18
<212> RNA
<213> Artificial Sequence

<220>
<223> Double stranded RNA for targeting human hungtingtin gene of exon 1

<400> 181
cgaccaugcg agccagca 18

<210> 182
<211> 18
<212> RNA
<213> Artificial Sequence

<220>
<223> Double stranded RNA for targeting human hungtingtin gene of exon 1

<400> 182
agucgcugau gaccggga 18

<210> 183
<211> 18
<212> RNA
<213> Artificial Sequence

<220>
<223> Double stranded RNA for targeting human hungtingtin gene of exon 1

<400> 183
acgucguaaa caagagga 18

<210> 184
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Double stranded RNA for targeting human hungtingtin gene of exon 1

<400> 184
gucgaccaug cgagccagca c 21

<210> 185
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Double stranded RNA for targeting human hungtingtin gene of exon 1

<400> 185
auagucgcug augaccggga u 21

<210> 186
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> Double stranded RNA for targeting human hungtingtin gene of exon 1

<400> 186
uuacgucgua aacaagagga a 21

<210> 187
<211> 75
<212> RNA
<213> Artificial Sequence

<220>
<223> Double stranded RNA for targeting human hungtingtin gene of exon 1

<400> 187
aaaacucgag ugagcgcuga aggccuucga gucccucaug agggacucga aggccuucau 60

cgccuacuag uaaaa 75

<210> 188
<211> 75
<212> RNA
<213> Artificial Sequence

<220>
<223> Double stranded RNA for targeting human hungtingtin gene of exon 1

<400> 188
aaaacucgag ugagcgcuga aggccuucga gucuuuuaug agggacucga aggccuucau 60

cgccuacuag uaaaa 75

<210> 189
<211> 75
<212> RNA
<213> Artificial Sequence

<220>
<223> Double stranded RNA for targeting human hungtingtin gene of exon 1

<400> 189
aaaacucgag ugagcgcaug aaggccuucg agucccucga gggacucgaa ggccuucauc 60

cgccuacuag uaaaa 75

<210> 190
<211> 75
<212> RNA
<213> Artificial Sequence

<220>
<223> Double stranded RNA for targeting human hungtingtin gene of exon 1

<400> 190
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cgccuacuag uaaaa 75

<210> 191
<211> 85
<212> RNA
<213> Artificial Sequence

<220>
<223> Double stranded RNA for targeting human hungtingtin gene of exon 1

<400> 191
cucgagugag cgcucccggu caucagcgac uauuccguaa agccacagau ggggauaguc 60

gcugaugacc gggaucgccu acuag 85

<210> 192
<211> 86
<212> RNA
<213> Artificial Sequence

<220>
<223> Double stranded RNA for targeting human hungtingtin gene of exon 1

<400> 192
cucgagugag cgaugcuggc ucgcaugguc gauacuguaa agccacagau gggugucgac 60

caugcgagcc agcaccgccu acuaga 86

<210> 193
<211> 86
<212> RNA
<213> Artificial Sequence

<220>
<223> Double stranded RNA for targeting human hungtingtin gene of exon

1

<400> 193
cucgagugag cgcuccucuu guuuacgacg ugaucuguaa agccacagau gggauuacgu 60

cguaaacaag aggaacgccu acuagu 86

<210> 194
<211> 163
<212> RNA
<213> Artificial Sequence

<220>
<223> Double stranded RNA for targeting human hungtingtin gene of exon 1

<400> 194
gcguuuagug aaccgucaga ugguaccguu uaaacucgag ugagcgaugc uggcucgcau 60

ggucgauacu guaaagccac agaugggugu cgaccaugcg agccagcacc gccuacuaga 120

gcggccgcca cagcggggag auccagacau gauaagauac auu 163

<210> 195
<211> 163
<212> RNA
<213> Artificial Sequence

<220>
<223> Double stranded RNA for targeting human hungtingtin gene of exon 1

<400> 195
gcguuuagug aaccgucaga ugguaccguu uaaacucgag ugagcgcucc cggucaucag 60

cgacuauucc guaaagccac agauggggau agucgcugau gaccgggauc gccuacuaga 120

gcggccgcca cagcggggag auccagacau gauaagauac auu 163

<210> 196
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Change from AAV9 to PHP.eB

<400> 196

Ser Ala Gln Ala
1

<210> 197
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Change from AAV9 to PHP.eB

<400> 197

Ser Asp Gly Thr Leu Ala Val Pro Phe Lys Ala
1 5 10

<210> 198
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> AAV-BR1

<400> 198

Asn Arg Gly Thr Glu Trp Asp
1   5

<210> 199
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> AAV-PHP.S

<400> 199

Gln Ala Val Arg Thr Ser Leu
1   5

<210> 200
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> AAV-PHP.B

<400> 200

Thr Leu Ala Val Pro Phe Lys
1   5

<210> 201
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> AAV-PPS

<400> 201

Asp Ser Pro Ala His Pro Ser
1   5

<210> 202
<211> 200
<212> DNA
<213> Artificial Sequence

<220>
<223> Core-eHGT_621h

<400> 202
atacaataga ttaattttat ctaacattaa tagctggatg tataagaaac acccactctc   60

tagaaattaa gacatgtcac catagtctta tgacaagagt gagtctctta tttttgaact   120

ttctattgaa cagttctcac catcttaaat cacccttttgt tatgagtttt taagtgtctt 180

aagtagagaa ggttaagaaa 200

<210> 203
<211> 600
<212> DNA
<213> Artificial Sequence

<220>
<223> 3xCore-eHGT_621h

<400> 203
atacaataga ttaattttat ctaacattaa tagctggatg tataagaaac acccactctc 60

tagaaattaa gacatgtcac catagtctta tgacaagagt gagtctctta tttttgaact 120

ttctattgaa cagttctcac catcttaaat cacccttttgt tatgagtttt taagtgtctt 180

aagtagagaa ggttaagaaa atacaataga ttaattttat ctaacattaa tagctggatg 240

tataagaaac acccactctc tagaaattaa gacatgtcac catagtctta tgacaagagt 300

gagtctctta tttttgaact ttctattgaa cagttctcac catcttaaat cacccttttgt 360

tatgagtttt taagtgtctt aagtagagaa ggttaagaaa atacaataga ttaattttat 420

ctaacattaa tagctggatg tataagaaac acccactctc tagaaattaa gacatgtcac 480

catagtctta tgacaagagt gagtctctta tttttgaact ttctattgaa cagttctcac 540

catcttaaat cacccttttgt tatgagtttt taagtgtctt aagtagagaa ggttaagaaa 600

<210> 204
<211> 176
<212> DNA
<213> Artificial Sequence

<220>
<223> core2_eHGT_351h

<400> 204
gcccttcttt ctgtgaaggg tgacacacct cctagaaaga aatctgactc ccctcattgt 60

gtttttaaaa taactctcat tattcctcct ctgaaggtta ttttcaaact ctttataact 120

cgatttttt ttaaatgcaa agacaaggaa tcaaatctgc caactttcta tcagag 176

<210> 205
<211> 528
<212> DNA
<213> Artificial Sequence

<220>
<223> 3xcore2_eHGT_351h

<400> 205
gcccttcttt ctgtgaaggg tgacacacct cctagaaaga aatctgactc ccctcattgt 60

gtttttaaaa taactctcat tattcctcct ctgaaggtta ttttcaaact ctttataact 120

cgatttttt ttaaatgcaa agacaaggaa tcaaatctgc caactttcta tcagaggccc 180

ttctttctgt gaagggtgac acacctccta gaaagaaatc tgactcccct cattgtgttt 240

ttaaaataac tctcattatt cctcctctga aggttatttt caaactcttt ataactcgat 300

ttttttttaa atgcaaagac aaggaatcaa atctgccaac tttctatcag aggcccttct 360

ttctgtgaag ggtgacacac ctcctagaaa gaaatctgac tcccctcatt gtgtttttaa 420

aataactctc attattcctc ctctgaaggt tattttcaaa ctctttataa ctcgattttt 480

ttttaaatgc aaagacaagg aatcaaatct gccaactttc tatcagag 528

<210> 206
<211> 160
<212> DNA
<213> Artificial Sequence

<220>
<223> core2_eHGT_367h

<400> 206
tccagcttaa aggaaaattc cagccccaga gatcttccgc agtgagtgac agctccttaa 60

tgtgaggagc agcgtgggcg tggtgggtgg gatgtcagag ccatcaaagc cctcatttct 120

gatccctctg tgatgtcggg gttccctggc acgcccactg 160

<210> 207
<211> 480
<212> DNA
<213> Artificial Sequence

<220>
<223> 3xcore2_eHGT_367h

<400> 207
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tgtgaggagc agcgtgggcg tggtgggtgg gatgtcagag ccatcaaagc cctcatttct 120

gatccctctg tgatgtcggg gttccctggc acgcccactg tccagcttaa aggaaaattc 180

cagccccaga gatcttccgc agtgagtgac agctccttaa tgtgaggagc agcgtgggcg 240

tggtgggtgg gatgtcagag ccatcaaagc cctcatttct gatccctctg tgatgtcggg 300

gttccctggc acgcccactg tccagcttaa aggaaaattc cagccccaga gatcttccgc 360

agtgagtgac agctccttaa tgtgaggagc agcgtgggcg tggtgggtgg gatgtcagag 420

ccatcaaagc cctcatttct gatccctctg tgatgtcggg gttccctggc acgcccactg 480

<210> 208
<211> 428
<212> DNA
<213> Artificial Sequence

<220>
<223> core_eHGT_441h

<400> 208
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cccccaccac ctggccgccc acctgaaaaa cttttcccca agttcttgag aagtcgcgta 120

ggatccagga gagaaaaatc aaagtaataa aacctcattt aattcctaac ggagggcaga 180

gctgcgagct gcaattatct taatgctgag ctatttttac tctctctcca tctctgtctt 240

ctgcctttct ctgttgtgag gttcgctgtc tctctctctg cctccctttg tctctccatc 300

tctcaaccat gttttctgtc tctctttgct ttctcctctc tccccccaat ctctctctca 360

cgtcctgtct ctgtgcagtc tcttcctcct ccttcatgtc tgtccctctg tcagccagtc 420

ttccccac 428

<210> 209
<211> 1284
<212> DNA
<213> Artificial Sequence

<220>
<223> 3xcore_eHGT_441h

<400> 209
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cccccaccac ctggccgccc acctgaaaaa cttttcccca agttcttgag aagtcgcgta 120

ggatccagga gagaaaaatc aaagtaataa aacctcattt aattcctaac ggagggcaga 180

gctgcgagct gcaattatct taatgctgag ctatttttac tctctctcca tctctgtctt 240

ctgcctttct ctgttgtgag gttcgctgtc tctctctctg cctccctttg tctctccatc 300

tctcaaccat gttttctgtc tctctttgct ttctcctctc tccccccaat ctctctctca 360

cgtcctgtct ctgtgcagtc tcttcctcct ccttcatgtc tgtccctctg tcagccagtc 420

ttccccacgc ccacccctcc tccagctctc aggagtccca ttcccttcct cctctgtcgc 480

ccacacagcc cccaccacct ggccgcccac ctgaaaaact tttccccaag ttcttgagaa 540

gtcgcgtagg atccaggaga gaaaaatcaa agtaataaaa cctcatttaa ttcctaacgg 600

agggcagagc tgcgagctgc aattatctta atgctgagct atttttactc tctctccatc 660

tctgtcttct gcctttctct gttgtgaggt tcgctgtctc tctctctgcc tccctttgtc 720

tctccatctc tcaaccatgt tttctgtctc tctttgcttt ctcctctctc cccccaatct 780

ctctctcacg tcctgtctct gtgcagtctc ttcctcctcc ttcatgtctg tccctctgtc 840

agccagtctt ccccacgccc acccctcctc cagctctcag gagtcccatt cccttcctcc 900

tctgtcgccc acacagcccc caccacctgg ccgcccacct gaaaaacttt tccccaagtt 960

cttgagaagt cgcgtaggat ccaggagaga aaaatcaaag taataaaacc tcatttaatt 1020

cctaacggag ggcagagctg cgagctgcaa ttatcttaat gctgagctat ttttactctc 1080

tctccatctc tgtcttctgc ctttctctgt tgtgaggttc gctgtctctc tctctgcctc 1140

cctttgtctc tccatctctc aaccatgttt tctgtctctc tttgctttct cctctctccc 1200

cccaatctct ctctcacgtc ctgtctctgt gcagtctctt cctcctcctt catgtctgtc 1260

cctctgtcag ccagtcttcc ccac 1284

<210> 210
<211> 235
<212> DNA
<213> Artificial Sequence

<220>
<223> core2_eHGT_444h

<400> 210
ggccaccccc ttccaccttg tgttcccgtg tcgtgtcggg tcctactcct cccatttctt 60

tgcccctgaa gtgctgagag ggggagaggg tggagcccag ccctcccccc gcccactcta 120

gctgtcaatc tgctgtctgg cagaaagaca tgaagcctcg tgacaactgt gggcaacttt 180

cccctgcccc gcctcccgcc cctgccctgc cctcttcccc tctgctccct gtcaa 235

<210> 211
<211> 705
<212> DNA
<213> Artificial Sequence

<220>
<223> 3xcore2_eHGT_444h

<400> 211
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tgcccctgaa gtgctgagag ggggagaggg tggagcccag ccctcccccc gcccactcta 120

gctgtcaatc tgctgtctgg cagaaagaca tgaagcctcg tgacaactgt gggcaacttt 180

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ctgaagtgct gagaggggga gagggtggag cccagccctc cccctgccca ctctagctgt 360

caatctgctg tctggcagaa agacatgaag cctcgtgaca actgtgggca actttccccct 420

gccccgcctc ccgcccctgc cctgccctct tcccctctgc tccctgtcaa ggccaccccc 480

ttccaccttg tgttcccgtg tcgtgtcggg tcctactcct cccatttctt tgcccctgaa 540

gtgctgagag ggggagaggg tggagcccag ccctcccccc gcccactcta gctgtcaatc 600

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gcctcccgcc cctgccctgc cctcttcccc tctgctccct gtcaa 705

<210> 212
<211> 222
<212> DNA
<213> Artificial Sequence

<220>
<223> core2_eHGT_445h

<400> 212
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aatcttgtta aatctttatt ccgtcaccca ccttattagg gggccctccc actttagtca 120

tcagcagatt agtaagcatg ccatttagat gtcatctaag ttaatgaacc tgactgagcc 180

agagtcacat ggcagagtca cagaaactcc ttctgagctg gc 222

<210> 213
<211> 666
<212> DNA
<213> Artificial Sequence

<220>
<223> 3xcore2_eHGT_445h

<400> 213
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aatcttgtta aatctttatt ccgtcaccca ccttattagg gggccctccc actttagtca 120

tcagcagatt agtaagcatg ccatttagat gtcatctaag ttaatgaacc tgactgagcc 180

agagtcacat ggcagagtca cagaaactcc ttctgagctg gcgtggagga ctttgagctt 240

aaccctatta aatttaatct aatatattca gcagcctgtc acaatcttgt taaatcttta 300

ttccgtcacc caccttatta gggggccctc ccactttagt catcagcaga ttagtaagca 360

tgccatttag atgtcatcta agttaatgaa cctgactgag ccagagtcac atggcagagt 420

cacagaaact ccttctgagc tggcgtggag gactttgagc ttaaccctat taaatttaat 480

ctaatatatt cagcagcctg tcacaatctt gttaaatctt tattccgtca cccaccttat 540

taggggggccc tcccacttta gtcatcagca gattagtaag catgccattt agatgtcatc 600

taagttaatg aacctgactg agccagagtc acatggcaga gtcacagaaa ctccttctga 660

gctggc 666

<210> 214
<211> 246
<212> DNA
<213> Artificial Sequence

<220>
<223> core2_eHGT_450h

<400> 214
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gaggcacggt gtgggcactg ctgctatttc taacctgctg gagtgaaggg aaccttgact 120

acttgaaaag caggctgatt gtcaggggcg gaaccgaact cagagctgtc agggccgtca 180

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ccgtcacatg gaaagtgcct ggcaggggggc ggcgacaggg ggcttgggct gacagggctg 480

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attatgcaat ttctgtctat aaatgacata cctcctgtac cctatgacac ccacctatgc 180

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tgttaaagat gacttttcta ttcacctgtg taagtcttgc tgcctcctac actgattaat 180

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tggcttctaa aaaaggagaa aatggtttac aaaaacaagc ctccctggat gcttccttaa 240

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