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(71) Applicant(s)
Wuhan Neurophth Biotechnology Limited Company

(72) Inventor(s)
LI, Bin

(74) Agent / Attorney
Pizzeys Patent and Trade Mark Attorneys Pty Ltd, GPO Box 1374, Brisbane, QLD, 4001, AU

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(71) Applicant: WUHAN NEUROPHTH BIOLOGICAL TECHNOLOGY LIMITED COMPANY [CN/CN]; C270-271 B1, No. 666 Ave Gaoxin, Wuhan, Hubei 430060 (CN).

(72) Inventor: LI, Bin; C270-271 B1, No. 666 Ave Gaoxin, Wuhan, Hubei 430060 (CN).

(74) Agent: METIS IP (CHENGDU) LLC; Room 808, 8th Floor, Building B7, Block D, Tianfu Jingrong Center, No. 99 West Section of Hupan Road, Tianfu New District, Chengdu, Sichuan 610213 (CN).

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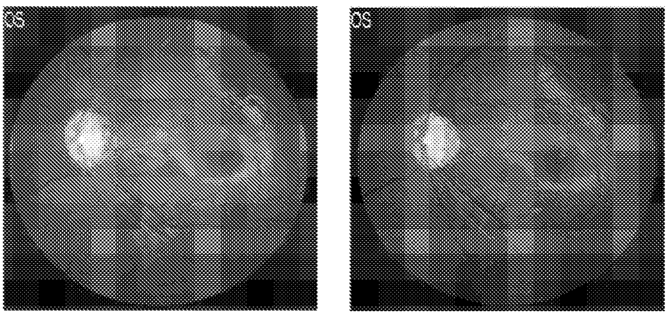

FIG. 5

(57) Abstract: Disclosed herein is a recombinant nucleic acid, comprising: a mitochondrial targeting sequence; a mitochondrial protein coding sequence, wherein said mitochondrial protein coding sequence encodes a polypeptide comprising a mitochondrial protein; and a 3'UTR nucleic acid sequence. Also disclosed is a pharmaceutical composition comprising the recombinant nucleic acid and a method of treating Leber's hereditary optic neuropathy (LHON) using the pharmaceutical composition.

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COMPOSITIONS AND METHODS FOR TREATING LEBER'S HEREDITARY OPTIC NEUROPATHY

CROSS-REFERENCE

[0001] This application claims the benefit of PCT Application No. PCT/CN2018/095023, filed on July 9, 2018; PCT Application No. PCT/CN2018/103937, filed on September 4, 2018; Chinese Application Nos. CN201810703168.7 and CN201810702492.7, both filed on June 29, 2018; PCT Application No. PCT/CN2018/113799, filed on November 2, 2018; Chinese Application No. CN201811230856.2, filed on October 22, 2018; PCT Application No. PCT/CN2018/118662, filed on November 30, 2018; Chinese Application No. CN201811221305.X, filed on October 19, 2018; PCT Application No. PCT/CN2019/070461, filed on January 4, 2019; Chinese Application No. CN201810948193.1, filed on August 20, 2018; all of which are incorporated herein by reference in their entirety.

REFERENCE TO A SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted in ASCII format via EFS-Web and is hereby incorporated by reference in its entirety. Said ASCII copy, created on June 30, 2019, is named 207298476_1.txt and is 304,914 bytes in size.

BACKGROUND OF THE INVENTION

[0003] Leber's hereditary optic neuropathy (LHON) is a mitochondrially inherited (transmitted from mother to offspring) degeneration of retinal ganglion cells (RGCs) and their axons that leads to an acute or subacute loss of central vision; this affects predominantly young adult males. LHON is only transmitted through the mother, as it is primarily due to mutations in the mitochondrial (not nuclear) genome, and only the egg contributes mitochondria to the embryo. LHON is usually due to one of three pathogenic mitochondrial DNA (mtDNA) point mutations. These mutations are at nucleotide positions 11778 G to A (G11778A), 3460 G to A (G3460A) and 14484 T to C (T14484C), respectively in the NADH dehydrogenase subunit-4 protein (ND4), NADH dehydrogenase subunit-1 protein (ND1) and NADH dehydrogenase subunit-6 protein (ND6) subunit genes of complex I of the oxidative phosphorylation chain in mitochondria. Each mutation is believed to have significant risk of permanent loss of vision. It typically progresses within several weeks to several months without pain, until the binocular vision deteriorate to below 0.1, which seriously affects the quality of life of the patient. Two LHON mutants, G3460A and T14484C, results in the reduction of the patient's platelets isolated mitochondrial NADH dehydrogenase activity by 80%. Ninety percent of the Chinese LHON patients carry the G11778A mutation. The G11778A mutation changes an arginine into histidine in the ND4 protein, resulting the dysfunction and optic nerve damage in LHON patients. There is a need for developing compositions and methods for treating LHON with higher transfection efficiency and treatment efficacy.

SUMMARY OF THE INVENTION

[0004] Disclosed here recombinant nucleic acids, pharmaceutical compositions, and methods for treating LHON. In one aspect, disclosed herein is a recombinant nucleic acid, comprising: a mitochondrial targeting sequence; a mitochondrial protein coding sequence comprising a sequence that is at least 99% identical to a sequence selected from the group consisting of SEQ ID NO: 7, 8, 10, and 12; and a 3'UTR nucleic acid sequence.

[0005] In some cases, the mitochondrial targeting sequence encodes a polypeptide comprising a peptide sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence selected from the group consisting of SEQ ID NO: 129-159. In some cases, the mitochondrial targeting sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 2. In some cases, the mitochondrial targeting sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 3. In some cases, the mitochondrial targeting sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 4. In some cases, the mitochondrial targeting sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 5.

[0006] In some cases, the mitochondrial protein coding sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 7 or 8. In some cases, the mitochondrial protein coding sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 10. In some cases, the mitochondrial protein coding sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 12.

[0007] In some cases, the 3'UTR nucleic acid sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence selected from the group consisting of SEQ ID NO: 111-125. In some cases, the 3'UTR nucleic acid sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 13 or SEQ ID NO: 14.

[0008] In some cases, the recombinant nucleic acid comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence selected from the group consisting of SEQ ID NO: 17-20, 23-24, 27-28, 31-34, 37-38, 41-42, 45-48, 51-52, 55-56, 59-62, 65-66, 69-70, 73-76, 79-80, and 83-84.

[0009] In another aspect, disclosed herein is a recombinant nucleic acid, comprising: a mitochondrial targeting sequence comprising a sequence that is at least 90% identical to a sequence selected from the group consisting of SEQ ID NO: 2, 3, 4, and 5; a mitochondrial protein coding sequence, wherein the mitochondrial protein coding sequence encodes a polypeptide comprising a mitochondrial protein; and a 3'UTR nucleic acid sequence.

[0010] In some cases, the mitochondrial targeting sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 2. In some cases, the mitochondrial targeting sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 3. In some cases, the mitochondrial targeting sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 4. In some cases, the mitochondrial targeting sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 5.

[0011] In some cases, the mitochondrial protein is selected from a group consisting of NADH dehydrogenase 4 (ND4), NADH dehydrogenase 6 (ND6), NADH dehydrogenase 1 (ND1), and a variant thereof. In some cases, the mitochondrial protein comprises NADH dehydrogenase 4 (ND4), or a variant thereof. In some cases, the mitochondrial protein comprises a peptide sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 160. In some cases, the mitochondrial protein coding sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 6, 7, or 8. In some cases, the mitochondrial protein comprises NADH dehydrogenase 6 (ND6), or a variant thereof. In some cases, the mitochondrial protein comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 161. In some cases, the mitochondrial protein coding sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 9 or 10. In some cases, the mitochondrial protein comprises NADH dehydrogenase 1 (ND1), or a variant thereof. In some cases, the mitochondrial protein comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 162. In some cases, the mitochondrial protein coding sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 11 or 12.

[0012] In some cases, the 3'UTR nucleic acid sequence is located at 3' of the mitochondrial targeting sequence. In some cases, the 3'UTR nucleic acid sequence comprises a sequence selected from the group consisting of hsACO2, hsATP5B, hsAK2, hsALDH2, hsCOX10, hsUQCRFS1, hsNDUFV1, hsNDUFV2, hsSOD2, hsCOX6c, hsIRP1, hsMRPS12, hsATP5J2, rnSOD2, and hsOXA1L. In some cases, the 3'UTR nucleic acid sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence selected from the group consisting of SEQ ID NO: 111-125. In some cases, the 3'UTR nucleic acid sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 13 or SEQ ID NO: 14.

[0013] In some cases, the mitochondrial targeting sequence is located at 5' of the 3'UTR nucleic acid sequence. In some cases, the mitochondrial targeting sequence is located at 3' of the mitochondrial targeting sequence.

[0014] In some cases, the recombinant nucleic acid comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence selected from the group consisting of SEQ ID NO: 29-84.

[0015] In another aspect, disclosed herein is a recombinant nucleic acid, comprising: a mitochondrial targeting sequence; a mitochondrial protein coding sequence comprising a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence selected from the group consisting of SEQ ID NO: 7, 8, 10, and 12; and a 3'UTR nucleic acid sequence.

[0016] In some cases, the mitochondrial targeting sequence comprises a sequence encodes a polypeptide selected from the group consisting of hsCOX10, hsCOX8, scRPM2, lcSirt5, tbNDUS7, ncQCR2, hsATP5G2, hsLACTB, spilv1, gmCOX2, crATP6, hsOPA1, hsSDHD, hsADCK3, osP0644B06.24-2, Neurospora crassa ATP9 (ncATP9), hsGHITM, hsNDUFAB1, hsATP5G3, crATP6 _hsADCK3, ncATP9_ncATP9, zmLOC100282174, ncATP9_zmLOC100282174_spilv1_ncATP9, zmLOC100282174_hsADCK3_crATP6 _hsATP5G3, zmLOC100282174_hsADCK3_hsATP5G3, ncATP9_zmLOC100282174, hsADCK3_zmLOC100282174_crATP6 _hsATP5G3, crATP6_hsADCK3_zmLOC100282174_hsATP5G3, hsADCK3_zmLOC100282174, hsADCK3_zmLOC100282174_crATP6, ncATP9_zmLOC100282174_spilv1_GNFP_ncATP9, and ncATP9_zmLOC100282174_spilv1_lcSirt5_osP0644B06.24-2_hsATP5G2_ncATP9. In some cases, the mitochondrial targeting sequence encodes a polypeptide comprising a peptide sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence selected from the group consisting of SEQ ID NO: 129-159. In some cases, the mitochondrial targeting sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 2 or 3. In some cases, the mitochondrial targeting sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 4. In some cases, the mitochondrial targeting sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 5.

[0017] In some cases, the mitochondrial protein coding sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 7 or 8. In some cases, the mitochondrial protein coding sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 10. In some cases, the mitochondrial protein coding sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 12.

[0018] In some cases, the 3'UTR nucleic acid sequence is located at 3' of the mitochondrial targeting sequence. In some cases, the 3'UTR nucleic acid sequence comprises a sequence selected from the group consisting of hsACO2, hsATP5B, hsAK2, hsALDH2, hsCOX10, hsUQCRFS1, hsNDUFV1, hsNDUFV2, hsSOD2, hsCOX6c, hsIRP1, hsMRPS12, hsATP5J2, rnSOD2, and hsOXA1L. In some cases, the 3'UTR nucleic acid sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence selected from the group consisting of SEQ ID NO: 111-125. In some cases, the 3'UTR nucleic acid sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 13 or SEQ ID NO: 14.

[0019] In some cases, the mitochondrial targeting sequence is located at 5' of the 3'UTR nucleic acid sequence. In some cases, the mitochondrial targeting sequence is located at 3' of the mitochondrial targeting sequence.

[0020] In some cases, the recombinant nucleic acid comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence selected from the group consisting of SEQ ID NO: 17-20, 23-24, 27-28, 31-34, 37-38, 41-42, 45-48, 51-52, 55-56, 59-62, 65-66, 69-70, 73-76, 79-80, and 83-84.

[0021] In another aspect, disclosed herein is a recombinant nucleic acid, comprising a mitochondrial targeting sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence selected from the group consisting of SEQ ID NO: 2, 3, and 4. In some cases, the mitochondrial targeting sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 2. In some cases, the mitochondrial targeting sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 3. In some cases, the mitochondrial targeting sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 4.

[0022] In some cases, the recombinant nucleic acid further comprises a mitochondrial protein coding sequence, wherein the mitochondrial protein coding sequence encodes a polypeptide comprising a mitochondrial protein. In some cases, the mitochondrial protein is selected from a group consisting of NADH dehydrogenase 4 (ND4), NADH dehydrogenase 6 (ND6), NADH dehydrogenase 1 (ND1), and a variant thereof. In some cases, the mitochondrial protein comprises NADH dehydrogenase 4 (ND4), or a variant thereof. In some cases, the mitochondrial protein comprises a peptide sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 160. In some cases, the mitochondrial protein coding sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 6, 7, or 8. In some cases, the mitochondrial protein comprises NADH dehydrogenase 6 (ND6), or a variant thereof. In some cases, the mitochondrial protein comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 161. In some cases, the mitochondrial protein coding sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 9 or 10. In some cases, the mitochondrial protein comprises NADH dehydrogenase 1 (ND1), or a variant thereof. In some cases, the mitochondrial protein comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 162. In some cases, the mitochondrial protein coding sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 11 or 12.

[0023] In some cases, the recombinant nucleic acid further comprises a 3'UTR nucleic acid sequence. In some cases, the 3'UTR nucleic acid sequence is located at 3' of the mitochondrial targeting sequence. In some cases, the 3'UTR nucleic acid sequence comprises a sequence selected from the group consisting of hsACO2, hsATP5B, hsAK2, hsALDH2, hsCOX10, hsUQCRFS1, hsNDUFV1, hsNDUFV2, hsSOD2, hsCOX6c, hsIRP1, hsMRPS12, hsATP5J2, rnSOD2, and hsOXA1L. In some cases, the 3'UTR nucleic acid sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence selected from the group consisting of SEQ ID NO: 111-125. In some cases, the 3'UTR nucleic acid sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 13 or SEQ ID NO: 14. In some cases, the mitochondrial targeting sequence is located at 5' of the 3'UTR nucleic acid sequence. In some cases, the mitochondrial targeting sequence is located at 3' of the mitochondrial targeting sequence.

[0024] In some cases, the recombinant nucleic acid comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence selected from the group consisting of SEQ ID NO: 29-70.

[0025] In another aspect, disclosed herein is a recombinant nucleic acid, comprising a mitochondrial protein coding sequence, wherein the mitochondrial protein coding sequence encodes a polypeptide comprising a mitochondrial protein, wherein the mitochondrial protein coding sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence selected from the group consisting of SEQ ID NO: 7, 8, 10, and 12.

[0026] In some cases, the recombinant nucleic acid further comprises a mitochondrial targeting sequence. In some cases, the mitochondrial targeting sequence comprises a sequence encodes a polypeptide selected from the group consisting of hsCOX10, hsCOX8, scRPM2, lcSirt5, tbNDUS7, ncQCR2, hsATP5G2, hsLACTB, spilv1, gmCOX2, crATP6, hsOPA1, hsSDHD, hsADCK3, osP0644B06.24-2, Neurospora crassa ATP9 (ncATP9), hsGHITM, hsNDUFAB1, hsATP5G3, crATP6 _hsADCK3, ncATP9_ncATP9, zmLOC100282174, ncATP9_zmLOC100282174_spilv1_ncATP9, zmLOC100282174_hsADCK3_crATP6 _hsATP5G3, zmLOC100282174_hsADCK3_hsATP5G3, ncATP9_zmLOC100282174, hsADCK3_zmLOC100282174_crATP6 _hsATP5G3, crATP6_hsADCK3_zmLOC100282174_hsATP5G3, hsADCK3_zmLOC100282174, hsADCK3_zmLOC100282174_crATP6, ncATP9_zmLOC100282174_spilv1_GNFP_ncATP9, and ncATP9_zmLOC100282174_spilv1_lcSirt5_osP0644B06.24-2_hsATP5G2_ncATP9. In some cases, the mitochondrial targeting sequence encodes a polypeptide comprising a peptide sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence selected from the group consisting of SEQ ID NO: 129-159. In some cases, the mitochondrial targeting sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 2. In some cases, the mitochondrial targeting sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 3. In some cases, the mitochondrial targeting sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 4. In some cases, the mitochondrial targeting sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 5.

[0027] In some cases, the mitochondrial protein coding sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 7 or 8. In some cases, the mitochondrial protein coding sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 10. In some cases, the mitochondrial protein coding sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 12.

[0028] In some cases, the recombinant nucleic acid further comprises a3'UTR nucleic acid sequence. In some cases, the 3'UTR nucleic acid sequence is located at 3' of the mitochondrial targeting sequence. In some cases, the 3'UTR nucleic acid sequence comprises a sequence selected from the group consisting of hsACO2, hsATP5B, hsAK2, hsALDH2, hsCOX10, hsUQCRFS1, hsNDUFV1, hsNDUFV2, hsSOD2, hsCOX6c, hsIRP1, hsMRPS12, hsATP5J2, rnSOD2, and hsOXA1L. In some cases, the 3'UTR nucleic acid sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence selected from the group consisting of SEQ ID NO: 111-125. In some cases, the 3'UTR nucleic acid sequence comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 13 or SEQ ID NO: 14. In some cases, the mitochondrial targeting sequence is located at 5' of the 3'UTR nucleic acid sequence. In some cases, the mitochondrial targeting sequence is located at 3' of the mitochondrial targeting sequence.

[0029] In some cases, the recombinant nucleic acid comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence selected from the group consisting of SEQ ID NO: 17-20, 23-24, 27-28, 31-34, 37-38, 41-42, 45-48, 51-52, 55-56, 59-62, 65-66, 69-70, 73-76, 79-80, and 83-84.

[0030] In another aspect, disclosed herein is a viral vector comprising the recombinant nucleic acid disclosed herein. In some cases, the viral vector is an adeno-associated virus (AAV) vector. In some cases, the AAV vector is selected from the group consisting of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, AAV13, AAV14, AAV15, and AAV16 vectors. In some cases, the AAV vector is a recombinant AAV (rAAV) vector. In some cases, the rAAV vector is rAAV2 vector.

[0031] In another aspect, disclosed herein is a pharmaceutical composition, comprising an adeno-associated virus (AAV) comprising any recombinant nucleic acid disclosed herein. In some cases, the pharmaceutical composition further comprises a pharmaceutically acceptable excipient thereof. Also disclosed is a pharmaceutical composition, comprising the viral vector disclosed herein, and a pharmaceutically acceptable excipient thereof, wherein the viral vector comprises any recombinant nucleic acid disclosed herein. Also disclosed is a pharmaceutical composition, comprising: an adeno-associated virus (AAV) comprising any recombinant nucleic acid disclosed herein, wherein the recombinant nucleic acid comprises a sequence that is at least 90%, at least 95%, at least 97%, at least 99%, or 100% identical to a sequence as set forth in SEQ ID NO: 15; and a pharmaceutically acceptable excipient.

[0032] In some cases, the pharmaceutically acceptable excipient comprises phosphate-buffered saline (PBS), α,α-trehalose dehydrate, L-histidine monohydrochloride monohydrate, polysorbate 20, NaCl, NaH_2PO_4, Na_2HPO_4, KH_2PO_4, K_2HPO_4, poloxamer 188, or any combination thereof. In some cases, the pharmaceutically acceptable excipient is selected from phosphate-buffered saline (PBS), α,α-trehalose dehydrate, L-histidine monohydrochloride monohydrate, polysorbate 20, NaCl, NaH_2PO_4, Na_2HPO_4, KH_2PO_4, K_2HPO_4, poloxamer 188, and any combination thereof. In some cases, the pharmaceutically acceptable excipient comprises poloxamer 188. In some cases, the pharmaceutically acceptable excipient comprises 0.0001%-0.01% poloxamer 188. In some cases, the pharmaceutically acceptable excipient comprises 0.001% poloxamer 188. In some cases, the pharmaceutically acceptable excipient further comprises one or more salts. In some cases, the one or more salts comprises NaCl, NaH_2PO_4, Na_2HPO_4, and KH_2PO_4. In some cases, the one or more salts comprises 80 mM NaCl, 5 mM NaH_2PO_4, 40 mM Na_2HPO_4, and 5 mM KH_2PO_4. In some cases, the pharmaceutical composition has a pH of 6-8. In some cases, the pharmaceutical composition has a pH of 7.2-7.4. In some cases, the pharmaceutical composition has a pH of 7.3. In some cases, the pharmaceutical composition has a viral titer of at least 1.0×10^{10} vg/mL. In some cases, the pharmaceutical composition has a viral titer of at least 5.0×10^{10} vg/mL.

[0033] In some cases, the pharmaceutical composition is subject to five freeze/thaw cycles, the pharmaceutical composition retains at least 60%, 70%, 80%, or 90% of a viral titer as compared to the viral titer prior to the five freeze/thaw cycles. In some cases, the pharmaceutical composition, when administered to a patient with Leber's hereditary optic neuropathy, generates a higher average recovery of vision than a comparable pharmaceutical composition without the recombinant nucleic acid. In some cases, the pharmaceutical composition, when administered to a patient with Leber's hereditary optic neuropathy, generates a higher average recovery of vision than a comparable pharmaceutical composition comprising a recombinant nucleic acid as set forth in SEQ ID NO: 15.

[0034] In another aspect, disclosed herein is a method of treating an eye disorder, comprising administering any pharmaceutical composition disclosed herein to a patient in need thereof. In some cases, the eye disorder is Leber's hereditary optic neuropathy (LHON). In some cases, the method comprises administering the pharmaceutical composition to one or both eyes of the patient. In some cases, the pharmaceutical composition is administered via intraocular or intravitreal injection. In some cases, the pharmaceutical composition is administered via intravitreal injection. In some cases, about 0.01-0.1 mL of the pharmaceutical composition is administered via intravitreal injection. In some cases, about 0.05 mL of the pharmaceutical composition is administered via intravitreal injection.

[0035] In some cases, the method further comprises administering methylprednisolone to the patient. In some cases, the methylprednisolone is administered prior to the intravitreal injection of the pharmaceutical composition. In some cases, the methylprednisolone is administered orally In some cases, the methylprednisolone is administered daily for at least 1, 2, 3, 4, 5, 6, or 7 days prior to the intravitreal injection of the pharmaceutical composition. In some cases, the methylprednisolone is administered daily. In some cases, the a daily dosage of about 32 mg/60 kg methylprednisolone is administered. In some cases, the methylprednisolone is administered after the intravitreal injection of the pharmaceutical composition. In some cases, the method further comprises administering creatine phosphate sodium to the patient. In some cases, the creatine phosphate sodium is administered intravenously. In some cases, the methylprednisolone is administered intravenously or orally. In some cases, the method comprises administering methylprednisolone intravenously for at least one day, which is followed by administering methylprednisolone orally for at least a week. In some cases, the method comprises administering methylprednisolone intravenously for about 3 days, which is followed by administering methylprednisolone orally for at least about 6 weeks. In some cases, the methylprednisolone is administered intravenously at a daily dose of about 80 mg/60 kg. In some cases, the administering the pharmaceutical composition generates a higher average recovery of vision than a comparable pharmaceutical composition without the recombinant nucleic acid. In some cases, the administering the pharmaceutical composition generates a higher average recovery of vision than a comparable pharmaceutical composition comprising a recombinant nucleic acid as set forth in SEQ ID NO: 15.

INCORPORATION BY REFERENCE

[0036] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference.

BRIEF DESCRIPTION OF THE DRAWINGS

[0037] The novel features of the invention are set forth with particularity in the appended claims. A better understanding of the features and advantages of the present invention will be obtained by reference to the following detailed description that sets forth illustrative embodiments, in which the principles of the invention are utilized, and the accompanying drawings of which:

[0038] **FIG. 1** shows the PCR nucleic acid electrophoresis verification of ND4 (lane A) and optimized ND4 (lane B) gene cloning results.

[0039] **FIG. 2** shows the relative expression level comparison using qPCR between the rAAV2-opt_ND4 (left black column) and rAAV2-ND4 (right black column). β-actin is the internal reference gene (white column).

[0040] **FIG. 3** shows the relative expression level comparison using immunoblotting between the rAAV2-opt_ND4 (left black column) and rAAV2-ND4 (right black column). β-actin is the internal reference gene (white column).

[0041] **FIG. 4** shows the fundus photographic results for rabbits injected with rAAV2-opt_ND4 (right) and rAAV2-ND4 (left), respectively.

[0042] **FIG. 5** shows the fundus photographic results for a patient before (left) and after (right) the injection with rAAV2-optimized ND4.

[0043] **FIG. 6** shows EGFP expression levels of rAAV2-ND4 (left) and rAAV2-opt_ND4* (right).

[0044] **FIG. 7** shows the ND4 expression in 293T cells: rAAV2-ND4 (left) and rAAV2-opt_ND4* (right).

[0045] **FIG. 8** shows the relative ND4 expression in 293T cells: rAAV2-ND4 (left) and rAAV2-opt_ND4* (right).

[0046] **FIG. 9** shows the ND4 expression in rabbit optic nerve cells: rAAV2-ND4 (left) and rAAV2-opt_ND4* (right).

[0047] **FIG. 10** shows the relative ND4 expression in rabbit optic nerve cells: rAAV2-ND4 (left) and rAAV2-opt_ND4* (right).

[0048] FIG. 11 shows the fundus photographic results for rAAV2-ND4 (left) and rAAV2-opt_ND4* (right).

[0049] FIG. 12 shows the microscope inspection (HE staining) results for rAAV2-ND4 (left) and rAAV2-opt_ND4* (right).

[0050] FIG. 13 shows the fundus photographic results for rabbits injected with rAAV2-ND6 (A), rAAV-GFP (B) and PBS, respectively.

[0051] FIG. 14 shows the fundus photographic results for rabbits injected with rAAV2-opt_ND6 (A), rAAV2-ND6 (B), rAAV-EGFP (C), respectively.

[0052] FIG. 15 shows the relative ND6 expression in rabbit optic nerve cells: rAAV2-opt_ND6 (A), rAAV2-ND6 (B), and rAAV-EGFP (C).

[0053] FIG. 16 shows the relative ND6 expression by western blot: rAAV2-opt_ND6 (A), rAAV2-ND6 (B), and rAAV-EGFP (C).

[0054] FIG. 17 shows the relative ND1 expression in rabbit optic nerve cells: rAAV2-opt_ND1 (A), rAAV2-ND1 (B), and rAAV-EGFP (C).

[0055] FIG. 18 shows the relative ND1 expression by western blot: rAAV2-opt_ND1 (A), rAAV2-ND1 (B), and rAAV-EGFP (C).

DETAILED DESCRIPTION OF THE INVENTION

Definitions

[0056] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of the ordinary skill in the art to which this disclosure belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the formulations or unit doses herein, some methods and materials are now described. Unless mentioned otherwise, the techniques employed or contemplated herein are standard methodologies. The materials, methods and examples are illustrative only and not limiting.

[0057] As used herein and in the appended claims, the singular forms “a,” “and,” and “the” include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to “a compound” includes a plurality of such agents, and reference to “the salt” includes reference to one or more salts (or to a plurality of salts) and equivalents thereof known to those skilled in the art, and so forth.

[0058] As used herein, unless otherwise indicated, the term "or" can be conjunctive or disjunctive. As used herein, unless otherwise indicated, any embodiment can be combined with any other embodiment.

[0059] As used herein, unless otherwise indicated, some inventive embodiments herein contemplate numerical ranges. When ranges are present, the ranges include the range endpoints. Additionally, every subrange and value within the range is present as if explicitly written out.

[0060] The term "about" and its grammatical equivalents in relation to a reference numerical value and its grammatical equivalents as used herein can include a range of values plus or minus 10% from that value, such as a range of values plus or minus 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, or 1% from that value. For example, the amount "about 10" includes amounts from 9 to 11.

[0061] The term "comprising" (and related terms such as "comprise" or "comprises" or "having" or "including") is not intended to exclude that in other certain embodiments, for example, an embodiment of any composition of matter, composition, method, or process, or the like, described herein, may "consist of" or "consist essentially of" the described features.

[0062] The term "subject" refers to a mammal that has been or will be the object of treatment, observation or experiment. The term "mammal" is intended to have its standard meaning, and encompasses humans, dogs, cats, sheep, and cows, for example. The methods described herein can be useful in both human therapy and veterinary applications. In some embodiments, the subject is a human.

[0063] The term "treating" or "treatment" encompasses administration of at least one compound disclosed herein, or a pharmaceutically acceptable salt thereof, to a mammalian subject, particularly a human subject, in need of such an administration and includes (i) arresting the development of clinical symptoms of the disease, such as cancer, (ii) bringing about a regression in the clinical symptoms of the disease, such as cancer, and/or (iii) prophylactic treatment for preventing the onset of the disease, such as cancer.

[0064] The term "therapeutically effective amount" of a chemical entity described herein refers to an amount effective, when administered to a human or non-human subject, to provide a therapeutic benefit such as amelioration of symptoms, slowing of disease progression, or prevention of disease.

[0065] As used herein, unless otherwise indicated, the terms "nucleic acid" and "polynucleotide" can be used interchangeably.

Nucleic acid and polypeptide sequences

[0066] Table 1 discloses all the nucleic acid and polypeptide sequences disclosed herein. The first column shows the SEQ ID NO of each sequence. The second column describes the nucleic acid or polypeptide construct. For example, the construct COX10-ND6-3'UTR is a nucleic acid combining the nucleic acid sequences of COX10 (**SEQ ID NO: 1**), ND6 (**SEQ ID NO: 9**), and 3'UTR (**SEQ ID NO: 13**) (from 5' to 3' without linker between the nucleic acid sequences.

Table 1 - nucleic acid and polypeptide sequences and SEQ ID NOs

SEQ	description	sequence
1	COX10	ATGGCCGCATCTCCGCACACTCTCTCCTCACGCCTCCTGACAGGTTGCGTAGGAGGCTCTGTCTGGTATCTTGAAAGAAGAACT
2	opt_COX10	ATGGCCGCCTCTCCACACACACTGAGTAGCAGACTGCTGACCGGCTGTGTTGGCGGCTCTGTGTGGTATCTGGAACGGCGGACA
3	opt_COX10*	ATGGCCGCCAGCCCCCACACCCTGAGCAGCCGCCTGCTGACCGGCTGCGTGGGCGGCAGCGTGTGGTACCTGGAGCGCCGCACC
4	COX8	ATGTCCGTCCTGACGCGCCTGCTGCTGCGGGGCTTGACACGGCTCGGCTCGGCGGCTCCAGTGCGGCGCGCCAGAATCCATTCGTTG
5	OPA1	GTGCTGCCCGCCTAGAAAGGGTGAAGTGGTTGTTTCCGTGACGGACTGAGTACGGGTGCCTGTCAGGCTCTTGCGGAAGTCCATGCGCCATTGGGAGGGCCTCGGCCGCGGCTCTGTGCCCTTGCTGCTGAGGGCCACTTCCTGGGTCATTCCTGGACCGGGAGCCGGGCTGGGGCTCACACGGGGGCTCCCGCGTGGCCGTCTCGGCGCCTGCGTGACCTCCCCGCCGGCGGGATGTGGCGACTACGTCGGGCCGCTGTGGCCTG
6	ND4	ATGCTAAAACTAATCGTCCCAACAATTATGTTACTACCACTGACATGGCTTTCCAAAAAACACATGATTTGGATCAACACAACCACCCACAGCCTAATTATTAGCATCATCCCTCTACTATTTTTTAACCAAATCAACAACAACCTATTTAGCTGTTCCCCAACCTTTTCCTCCGACCCCCTAACAACCCCCCTCCTAATGCTAACTACCTGGCTCCTACCCCTCACAATCATGGCAAGCCAACGCCACTTATCCAGTGAACCACTATCACGAAAAAAACTCTACCTCTCTATGCTAATCTCCCTACAAATCTCCTTAATTATGACATTCACAGCCACAGAACTAATCATGTTTTATATCTTCTTCGAAACCACACTTATCCCCACCTTGGCTATCATCACCCGATGGGGCAACCAGCCAGAACGCCTGAACGCAGGCACATACTTCCTATTCTACACCCTAGTAGGCTCCCTTCCCCTACTCATCGCACTAATTTACACTCACAACACCCTAGGCTCACTAAACATTCTACTACTCACTCTCACTGCCCAAGAACTATCAAACTCCTGGGCCAACAACTTAATGTGGCTAGCTTACACAATGGCTTTTATGGTAAAGATGCCTCTTTACGGACTCCACTTATGGCTCCCTAAAGCCCATGTCGAAGCCCCCATCGCTGGGTCAATGGTACTTGCCGCAGTACTCTTAAAACTAGGCGGCTATGGTATGATGCGCCTCACACTCATTCTCAACCCCCTGACAAAACACATGGCCTACCCCTTCCTTGTACTATCCCTATGGGGCATGATTATGACAAGCTCCATCTGCCTACGACAAACAGACCTAAAATCGCTCATTGCATACTCTTCAATCAGCCACATGGCCCTCGTAGTAACAGCCATTCTCATCCAAACCCCCTGGAGCTTCACCGGCGCAGTCATTCTCATGATCGCCCACGGGCTTACATCCTCATTACTATTCTGCCTAGCAAACTCAAACTACGAACGCACTCACAGTCGCATCATGATCCTCTCTCAAGGACTTCAAACTCTACTCCCACTAATGGCTTTTTGGTGGCTTCTAGCAAGCCTCGCTAACCTCGCCTTACCCCCCACTATTAACCTACTGGGAGAACTCTCTGTGCTAGTAACCACGTTCTCCTGGTCAAATATCACTCTCCTACTTACAGGACTCAACATGCTAGTCACAGCCCTATACTCCCTCTACATGTTTACCACAACACAATGGGGCTCACTCACCCACCACATTAACAACATGAAACCCTCATTCACACGAGAAAACACCCTCATGTTCATGCACCTATCCCCCATTCTCCTCCTATCCCTCAACCCCGACATCATTACCGGGTTTTCCTCTTAA
7	opt_ND4	ATGCTGAAGCTGATCGTGCCCACCATCATGCTGCTGCCTCTGACCTGGCTGAGCAAGAAACACATGATCTGGATCAACACCACCACGCACAGCCTGATCATCAGCATCATCCCTCTGCTGTTCTTCAACCAGATCAACAACAACCTGTTCAGCTGCAGCCCCACCTTCAGCAGCGACCCTCTGACAACACCTCTGCTGATGCTGACCACCTGGCTGCTGCCCCTCACAATCATGGCCTCTCAGAGACACCTGAGCAGCGAGCCCCTGAGCCGGAAGAAACTGTACCTGAGCATGCTGATCTCCCTGCAGATCTCTCTGATCATGACCTTCACCGCCACCGAGCTGATCATGTTCTACATCTTTTTCGAGACAACGCTGATCCCCACACTGGCCATCATCACCAGATGGGGCAACCAGCCTGAGAGACTGAACGCCGGCACCTACTTTCTGTTCTACACCCTCGTGGGCAGCCTGCCACTGCTGATTGCCCTGATCTACACCCACAACACCCTGGGCTCCCTGAACATCCTGCTGCTGACACTGACAGCCCAAGAGCTGAGCAACAGCTGGGCCAACAATCTGATGTGGCTGGCCTACACAATGGCCTTCATGGTCAAGATGCCCCTGTACGGCCTGCACCTGTGGCTGCCTAAAGCTCATGTGGAAGCCCCTATCGCCGGCTCTATGGTGCTGGCTGCAGTGCTGCTGAAACTCGGCGGCTACGGCATGATGCGGCTGACCCTGATTCTGAATCCCCTGACCAAGCACATGGCCTATCCATTTCTGGTGCTGAGCCTGTGGGGCATGATTATGACCAGCAGCATCTGCCTGCGGCAGACCGATCTGAAGTCCCTGATCGCCTACAGCTCCATCAGCCACATGGCCCTGGTGGTCACCGCCATCCTGATTCAGACCCCTTGGAGCTTTACAGGCGCCGTGATCCTGATGATTGCCCACGGCCTGACAAGCAGCCTGCTGTTTTGTCTGGCCAACAGCAACTACGAGCGGACCCACAGCAGAATCATGATCCTGTCTCAGGGCCTGCAGACCCTCCTGCCTCTTATGGCTTTTTGGTGGCTGCTGGCCTCTCTGGCCAATCTGGCACTGCCTCCTACCATCAATCTGCTGGGCGAGCTGAGCGTGCTGGTCACCACATTCAGCTGGTCCAATATCACCCTGCTGCTCACCGGCCTGAACATGCTGGTTACAGCCCTGTACTCCCTGTACATGTTCACCACCACACAGTGGGGAAGCCTGACACACCACATCAACAATATGAAGCCCAGCTTCACCCGCGAGAACACCCTGATGTTCATGCATCTGAGCCCCATTCTGCTGCTGTCCCTGAATCCTGATATCATCACCGGCTTCTCCAGCTGA

8	opt_ND4*	ATGCTGAAGCTGATCGTGCCCACCATCATGCTGCTGCCCCTGACCTGGCTGAGCAAGAAGCACATGATCTGGATCAACACCACCACCCACAGCCTGATCATCAGCATCATCCCCCTGCTGTTCTTCAACCAGATCAACAACAACCTGTTCAGCTGCAGCCCCACCTTCAGCAGCGACCCCCTGACCACCCCCCTGCTGATGCTGACCACCTGGCTGCTGCCCCTGACCATCATGGCCAGCCAGCGCCACCTGAGCAGCGAGCCCCTGAGCCGCAAGAAGCTGTACCTGAGCATGCTGATCAGCCTGCAGATCAGCCTGATCATGACCTTCACCGCCACCGAGCTGATCATGTTCTACATCTTCTTCGAGACCACCCTGATCCCCACCCTGGCCATCATCACCCGCTGGGGCAACCAGCCCGAGCGCCTGAACGCCGGCACCTACTTCCTGTTCTACACCCTGGTGGGCAGCCTGCCCCTGCTGATCGCCCTGATCTACACCCACAACACCCTGGGCAGCCTGAACATCCTGCTGCTGACCCTGACCGCCCAGGAGCTGAGCAACAGCTGGGCCAACAACCTGATGTGGCTGGCCTACACCATGGCCTTCATGGTGAAGATGCCCCTGTACGGCCTGCACCTGTGGCTGCCCAAGGCCCACGTGGAGGCCCCCATCGCCGGCAGCATGGTGCTGGCCGCCGTGCTGCTGAAGCTGGGCGGCTACGGCATGATGCGCCTGACCCTGATCCTGAACCCCCTGACCAAGCACATGGCCTACCCCTTCCTGGTGCTGAGCCTGTGGGGCATGATCATGACCAGCAGCATCTGCCTGCGCCAGACCGACCTGAAGAGCCTGATCGCCTACAGCAGCATCAGCCACATGGCCCTGGTGGTGACCGCCATCCTGATCCAGACCCCCTGGAGCTTCACCGGCGCCGTGATCCTGATGATCGCCCACGGCCTGACCAGCAGCCTGCTGTTCTGCCTGGCCAACAGCAACTACGAGCGCACCCACAGCCGCATCATGATCCTGAGCCAGGGCCTGCAGACCCTGCTGCCCCTGATGGCCTTCTGGTGGCTGCTGGCCAGCCTGGCCAACCTGGCCCTGCCCCCCACCATCAACCTGCTGGGCGAGCTGAGCGTGCTGGTGACCACCTTCAGCTGGAGCAACATCACCCTGCTGCTGACCGGCCTGAACATGCTGGTGACCGCCCTGTACAGCCTGTACATGTTCACCACCACCCAGTGGGGCAGCCTGACCCACCACATCAACAACATGAAGCCCAGCTTCACCCGCGAGAACACCCTGATGTTCATGCACCTGAGCCCCATCCTGCTGCTGAGCCTGAACCCCGACATCATCACCGGCTTCAGCAGCTAA
9	ND6	ATGATGTATGCTTTGTTTCTGTTGAGTGTGGGTTTAGTAATGGGGTTTGTGGGGTTTTCTTCTAAGCCTTCTCCTATTTATGGGGGTTTAGTATTGATTGTTAGCGGTGTGGTCGGGTGTGTTATTATTCTGAATTTTGGGGGAGGTTATATGGGTTTAATGGTTTTTTTAATTTATTTAGGGGGAATGATGGTTGTCTTTGGATATACTACAGCGATGGCTATTGAGGAGTATCCTGAGGCATGGGGGTCAGGGGTTGAGGTCTTGGTGAGTGTTTTAGTGGGGTTAGCGATGGAGGTAGGATTGGTGCTGTGGGTGAAAGAGTATGATGGGGTGGTGGTTGTGGTAAACTTTAATAGTGTAGGAAGCTGGATGATTTATGAAGGAGAGGGGTCAGGGTTGATTCGGGAGGATCCTATTGGTGCGGGGGCTTTGTATGATTATGGGCGTTGGTTAGTAGTAGTTACTGGTTGGACATTGTTTGTTGGTGTATATATTGTAATTGAGATTGCTCGGGGGAATTAG
10	opt_ND6	ATGATGTACGCCCTGTTCCTGCTGAGCGTGGGCCTGGTGATGGGCTTCGTGGGCTTCAGCAGCAAGCCCAGCCCCATCTACGGCGGCCTGGTGCTGATCGTGAGCGGCGTGGTGGGCTGCGTGATCATCCTGAACTTCGGCGGCGGCTACATGGGCCTGATGGTGTTCCTGATCTACCTGGGCGGCATGATGGTGGTGTTCGGCTACACCACCGCCATGGCCATCGAGGAGTACCCCGAGGCCTGGGGCAGCGGCGTGGAGGTGCTGGTGAGCGTGCTGGTGGGCCTGGCCATGGAGGTGGGCCTGGTGCTGTGGGTGAAGGAGTACGACGGCGTGGTGGTGGTGGTGAACTTCAACAGCGTGGGCAGCTGGATGATCTACGAGGGCGAGGGCAGCGGCCTGATCCGCGAGGACCCCATCGGCGCCGGCGCCCTGTACGACTACGGCCGCTGGCTGGTGGTGGTGACCGGCTGGACCCTGTTCGTGGGCGTGTACATCGTGATCGAGATCGCCCGCGGCAACTAA
11	ND1	ATGGCCAACCTCCTACTCCTCATTGTACCCATTCTAATCGCAATGGCATTCCTAATGCTTACCGAACGAAAAATTCTAGGCTATATGCAACTACGCAAAGGCCCCAACGTTGTAGGCCCCTACGGGCTACTACAACCCTTCGCTGACGCCATAAAACTCTTCACCAAAGAGCCCCTAAAACCCGCCACATCTACCATCACCCTCTACATCACCGCCCCGACCTTAGCTCTCACCATCGCTCTTCTACTATGGACCCCCCTCCCCATGCCCAACCCCCTGGTCAACCTCAACCTAGGCCTCCTATTTATTCTAGCCACCTCTAGCCTAGCCGTTTACTCAATCCTCTGGTCAGGGTGGGCATCAAACTCAAACTACGCCCTGATCGGCGCACTGCGAGCAGTAGCCCAAACAATCTCATATGAAGTCACCCTAGCCATCATTCTACTATCAACATTACTAATGAGTGGCTCCTTTAACCTCTCCACCCTTATCACAACACAAGAACACCTCTGGTTACTCCTGCCATCATGGCCCTTGGCCATGATGTGGTTTATCTCCACACTAGCAGAGACCAACCGAACCCCCTTCGACCTTGCCGAAGGGGAGTCCGAACTAGTCTCAGGCTTCAACATCGAATACGCCGCAGGCCCCTTCGCCCTATTCTTCATGGCCGAATACACAAACATTATTATGATGAACACCCTCACCACTACAATCTTCCTAGGAACAACATATGACGCACTCTCCCCTGAACTCTACACAACATATTTTGTCACCAAGACCCTACTTCTAACCTCCCTGTTCTTATGGATTCGAACAGCATACCCCCGATTCCGCTACGACCAACTCATGCACCTCCTATGGAAAAACTTCCTACCACTCACCCTAGCATTACTTATGTGGTATGTCTCCATGCCCATTACAATCTCCAGCATTCCCCCTCAAACCTAA
12	opt_ND1	ATGGCCAACCTGCTGCTGCTGATCGTGCCCATCCTGATCGCCATGGCCTTCCTGATGCTGACCGAGCGCAAGATCCTGGGCTACATGCAGCTGCGCAAGGGCCCCAACGTGGTGGGCCCCTACGGCCTGCTGCAGCCCTTCGCCGACGCCATCAAGCTGTTCACCAAGGAGCCCCTGAAGCCCGCCACCAGCACCATCACCCTGTACATCACCGCCCCCACCCTGGCCCTGACCATCGCCCTGCTGCTGTGGACCCCCCTGCCCATGCCCAACCCCCTGGTGAACCTGAACCTGGGCCTGCTGTTCATCCTGGCCACCAGCAGCCTGGCCGTGTACAGCATCCTGTGGAGCGGCTGGGCCAGCAACAGCAACTACGCCCTGATCGGCGCCCTGCGCGCCGTGGCCCAGACCATCAGCTACGAGGTGACCCTGGCCATCATCCTGCTGAGCACCCTGCTGATGAGCGGCAGCTTCAACCTGAGCACCCTGATCACCACCCAGGAGCACCTGTGGCTGCTGCTGCCCAGCTGGCCCCTGGCCATGATGTGGTTCATCAGCACCCTGGCCGAGACCAACCGCACCCCCTTCGACCTGGCCGAGGGCGAGAGCGAGCTGGTGAGCGGCTTCAACATCGAGTACGCCGCCGGCCCCTTCGCCCTGTTCTTCATGGCCGAGTACACCAACATCATCATGATGAACACCCTGACCACCACCATCTTCCTGGGCACCACCTACGACGCCCTGAGCCCCGAGCTGTACACCACCTACTTCGTGACCAAGACCCTGCTGCTGACCAGCCTGTTCCTGTGGATCCGCACCGCCTACCCCCGCTTCCGCTACGACCAGCTGATGCACCTGCTGTGGAAGAACTTCCTGCCCCTGACCCTGGCCCTGCTGATGTGGTACGTGAGCATGCCCATCACCATCAGCAGCATCCCCCCCCAGACCTAA

13	3'UTR	GAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAA CACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGAC AGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAAT ACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCT GTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACAC CACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCT GCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAG CCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAAT AGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCT GGACTGCCAGCCCCTGTCCTCCCTTCACCCCCATTGCGTATGAGCATTTCAGAACTCCAAGGAGTCAC AGGCATCTTTATAGTTCACGTTAACATATAGACACTGTTGGAAGCAGTTCCTTCTAAAAGGGTAGCCCT GGACTTAATACCAGCCGGATACCTCTGGCCCCCACCCCATTACTGTACCTCTGGAGTCACTACTGTGG GTCGCCACTCCTCTGCTACACAGCACGGCTTTTTCAAGGCTGTATTGAGAAGGGAAGTTAGGAAGAAG GGTGTGCTGGGCTAACCAGCCCACAGAGCTCACATTCCTGTCCCTTGGGTGAAAAATACATGTCCATC CTGATATCTCCTGAATTCAGAAATTAGCCTCCACATGTGCAATGGCTTTAAGAGCCAGAAGCAGGGTT CTGGGAATTTTGCAAGTTACCTGTGGCCAGGTGTGGTCTCGGTTACCAAATACGGTTACCTGCAGCTT TTTAGTCCTTTGTGCTCCCACGGGTCTACAGAGTCCCATCTGCCCAAAGGTCTTGAAGCTTGACAGGA TGTTTTCGATTACTCAGTCTCCCAGGGCACTACTGGTCCGTAGGATTCGATTGGTCGGGGTAGGAGAG TTAAACAACATTTAAACAGAGTTCTCTCAAAAATGTCTAAAGGGATTGTAGGTAGATAACATCCAATCAC TGTTTGCACTTATCTGAAATCTTCCCTCTTGGCTGCCCCCAGGTATTTACTGTGGAGAACATTGCATAG GAATGTCTGGAAAAAGCTTCTACAACTTGTTACAGCCTTCACATTTGTAGAAGCTTT
14	3'UTR*	GAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAA CACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGAC AGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAAT ACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCT GTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACAC CACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCT GCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAG CCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAAT AGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCT GGACTGCCA
15	COX10-ND4-3'UTR	ATGGCCGCATCTCCGCACACTCTCTCCTCACGCCTCCTGACAGGTTGCGTAGGAGGCTCTGTCTGGT ATCTTGAAAGAAGAACTATGCTAAAACTAATCGTCCCAACAATTATGTTACTACCACTGACATGGCTTTC CAAAAAACACATGATTTGGATCAACACAACCACCCACAGCCTAATTATTAGCATCATCCCTCTACTATTT TTTAACCAAATCAACAACAACCTATTTAGCTGTTCCCCAACCTTTTCCTCCGACCCCCTAACAACCCCC CTCCTAATGCTAACTACCTGGCTCCTACCCCTCACAATCATGGCAAGCCAACGCCACTTATCCAGTGA ACCACTATCACGAAAAAAACTCTACCTCTCTATGCTAATCTCCCTACAAATCTCCTTAATTATGACATTC ACAGCCACAGAACTAATCATGTTTTATATCTTCTTCGAAACCACACTTATCCCCACCTTGGCTATCATCA CCCGATGGGGCAACCAGCCAGAACGCCTGAACGCAGGCACATACTTCCTATTCTACACCCTAGTAGG CTCCCTTCCCCTACTCATCGCACTAATTTACACTCACAACACCCTAGGCTCACTAAACATTCTACTACT CACTCTCACTGCCCAAGAACTATCAAACTCCTGGGCCAACAACTTAATGTGGCTAGCTTACACAATGG CTTTTATGGTAAAGATGCCTCTTTACGGACTCCACTTATGGCTCCCTAAAGCCCATGTCGAAGCCCCCA TCGCTGGGTCAATGGTACTTGCCGCAGTACTCTTAAAACTAGGCGGCTATGGTATGATGCGCCTCACA CTCATTCTCAACCCCCTGACAAAACACATGGCCTACCCCTTCCTTGTACTATCCCTATGGGGCATGATT ATGACAAGCTCCATCTGCCTACGACAAACAGACCTAAAATCGCTCATTGCATACTCTTCAATCAGCCAC ATGGCCCTCGTAGTAACAGCCATTCTCATCCAAACCCCCTGGAGCTTCACCGGCGCAGTCATTCTCAT GATCGCCCACGGGCTTACATCCTCATTACTATTCTGCCTAGCAAACTCAAACTACGAACGCACTCACA GTCGCATCATGATCCTCTCTCAAGGACTTCAAACTCTACTCCCACTAATGGCTTTTTGGTGGCTTCTAG CAAGCCTCGCTAACCTCGCCTTACCCCCCACTATTAACCTACTGGGAGAACTCTCTGTGCTAGTAACC ACGTTCTCCTGGTCAAATATCACTCTCCTACTTACAGGACTCAACATGCTAGTCACAGCCCTATACTCC CTCTACATGTTTACCACAACACAATGGGGCTCACTCACCCACCACATTAACAACATGAAACCCTCATTC ACACGAGAAAACACCCTCATGTTCATGCACCTATCCCCCATTCTCCTCCTATCCCTCAACCCCGACATC ATTACCGGGTTTTCCTCTTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAG CATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTC GGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAA TGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTC CTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTT GGTTCCATCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCA GAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGC ACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCAT AGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTT TGCCTTGGGAGTCTCAAGCTGGACTGCCAGCCCCTGTCCTCCCTTCACCCCCATTGCGTATGAGCATT TCAGAACTCCAAGGAGTCACAGGCATCTTTATAGTTCACGTTAACATATAGACACTGTTGGAAGCAGTT CCTTCTAAAAGGGTAGCCCTGGACTTAATACCAGCCGGATACCTCTGGCCCCCACCCCATTACTGTAC CTCTGGAGTCACTACTGTGGGTCGCCACTCCTCTGCTACACAGCACGGCTTTTTCAAGGCTGTATTGA GAAGGGAAGTTAGGAAGAAGGGTGTGCTGGGCTAACCAGCCCACAGAGCTCACATTCCTGTCCCTTG GGTGAAAAATACATGTCCATCCTGATATCTCCTGAATTCAGAAATTAGCCTCCACATGTGCAATGGCTT TAAGAGCCAGAAGCAGGGTTCTGGGAATTTTGCAAGTTACCTGTGGCCAGGTGTGGTCTCGGTTACCA AATACGGTTACCTGCAGCTTTTTAGTCCTTTGTGCTCCCACGGGTCTACAGAGTCCCATCTGCCCAAA GGTCTTGAAGCTTGACAGGATGTTTTCGATTACTCAGTCTCCCAGGGCACTACTGGTCCGTAGGATTC GATTGGTCGGGGTAGGAGAGTTAAACAACATTTAAACAGAGTTCTCTCAAAAATGTCTAAAGGGATTGT AGGTAGATAACATCCAATCACTGTTTGCACTTATCTGAAATCTTCCCTCTTGGCTGCCCCCAGGTATTT ACTGTGGAGAACATTGCATAGGAATGTCTGGAAAAAGCTTCTACAACTTGTTACAGCCTTCACATTTGT AGAAGCTTT

16	COX10-ND4-3'UTR*	ATGGCCGCATCTCCGCACACTCTCTCCTCACGCCTCCTGACAGGTTGCGTAGGAGGCTCTGTCTGGT ATCTTGAAAGAAGAACTATGCTAAAACTAATCGTCCCAACAATTATGTTACTACCACTGACATGGCTTTC CAAAAAACACATGATTTGGATCAACACAACCACCCACAGCCTAATTATTAGCATCATCCCTCTACTATTT TTTAACCAAATCAACAACAACCTATTTAGCTGTTCCCCAACCTTTTCCTCCGACCCCCTAACAACCCCC CTCCTAATGCTAACTACCTGGCTCCTACCCCTCACAATCATGGCAAGCCAACGCCACTTATCCAGTGA ACCACTATCACGAAAAAAACTCTACCTCTCTATGCTAATCTCCCTACAAATCTCCTTAATTATGACATTC ACAGCCACAGAACTAATCATGTTTTATATCTTCTTCGAAACCACACTTATCCCCACCTTGGCTATCATCA CCCGATGGGGCAACCAGCCAGAACGCCTGAACGCAGGCACATACTTCCTATTCTACACCCTAGTAGG CTCCCTTCCCCTACTCATCGCACTAATTTACACTCACAACACCCTAGGCTCACTAAACATTCTACTACT CACTCTCACTGCCCAAGAACTATCAAACTCCTGGGCCAACAACTTAATGTGGCTAGCTTACACAATGG CTTTTATGGTAAAGATGCCTCTTTACGGACTCCACTTATGGCTCCCTAAAGCCCATGTCGAAGCCCCCA TCGCTGGGTCAATGGTACTTGCCGCAGTACTCTTAAAACTAGGCGGCTATGGTATGATGCGCCTCACA CTCATTCTCAACCCCCTGACAAAACACATGGCCTACCCCTTCCTTGTACTATCCCTATGGGGCATGATT ATGACAAGCTCCATCTGCCTACGACAAACAGACCTAAAATCGCTCATTGCATACTCTTCAATCAGCCAC ATGGCCCTCGTAGTAACAGCCATTCTCATCCAAACCCCCTGGAGCTTCACCGGCGCAGTCATTCTCAT GATCGCCCACGGGCTTACATCCTCATTACTATTCTGCCTAGCAAACTCAAACTACGAACGCACTCACA GTCGCATCATGATCCTCTCTCAAGGACTTCAAACTCTACTCCCACTAATGGCTTTTTGGTGGCTTCTAG CAAGCCTCGCTAACCTCGCCTTACCCCCCACTATTAACCTACTGGGAGAACTCTCTGTGCTAGTAACC ACGTTCTCCTGGTCAAATATCACTCTCCTACTTACAGGACTCAACATGCTAGTCACAGCCCTATACTCC CTCTACATGTTTACCACAACACAATGGGGCTCACTCACCCACCACATTAACAACATGAAACCCTCATTC ACACGAGAAAACACCCTCATGTTCATGCACCTATCCCCCATTCTCCTCCTATCCCTCAACCCCGACATC ATTACCGGGTTTTCCTCTTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAG CATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTC GGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAA TGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTC CTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTT GGTTCCATCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCA GAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGC ACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCAT AGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTT TGCCTTGGGAGTCTCAAGCTGGACTGCCA
17	COX10-opt_ND4-3'UTR	ATGGCCGCATCTCCGCACACTCTCTCCTCACGCCTCCTGACAGGTTGCGTAGGAGGCTCTGTCTGGT ATCTTGAAAGAAGAACTATGCTGAAGCTGATCGTGCCCACCATCATGCTGCTGCCTCTGACCTGGCTG AGCAAGAAACACATGATCTGGATCAACACCACCACGCACAGCCTGATCATCAGCATCATCCCTCTGCT GTTCTTCAACCAGATCAACAACAACCTGTTCAGCTGCAGCCCCACCTTCAGCAGCGACCCTCTGACAA CACCTCTGCTGATGCTGACCACCTGGCTGCTGCCCCTCACAATCATGGCCTCTCAGAGACACCTGAG CAGCGAGCCCCTGAGCCGGAAGAAACTGTACCTGAGCATGCTGATCTCCCTGCAGATCTCTCTGATC ATGACCTTCACCGCCACCGAGCTGATCATGTTCTACATCTTTTTCGAGACAACGCTGATCCCCACACT GGCCATCATCACCAGATGGGGCAACCAGCCTGAGAGACTGAACGCCGGCACCTACTTTCTGTTCTAC ACCCTCGTGGGCAGCCTGCCACTGCTGATTGCCCTGATCTACACCCACAACACCCTGGGCTCCCTGA ACATCCTGCTGCTGACACTGACAGCCCAAGAGCTGAGCAACAGCTGGGCCAACAATCTGATGTGGCT GGCCTACACAATGGCCTTCATGGTCAAGATGCCCCTGTACGGCCTGCACCTGTGGCTGCCTAAAGCT CATGTGGAAGCCCCTATCGCCGGCTCTATGGTGCTGGCTGCAGTGCTGCTGAAACTCGGCGGCTACG GCATGATGCGGCTGACCCTGATTCTGAATCCCCTGACCAAGCACATGGCCTATCCATTTCTGGTGCTG AGCCTGTGGGGCATGATTATGACCAGCAGCATCTGCCTGCGGCAGACCGATCTGAAGTCCCTGATCG CCTACAGCTCCATCAGCCACATGGCCCTGGTGGTCACCGCCATCCTGATTCAGACCCCTTGGAGCTTT ACAGGCGCCGTGATCCTGATGATTGCCCACGGCCTGACAAGCAGCCTGCTGTTTTGTCTGGCCAACA GCAACTACGAGCGGACCCACAGCAGAATCATGATCCTGTCTCAGGGCCTGCAGACCCTCCTGCCTCT TATGGCTTTTTGGTGGCTGCTGGCCTCTCTGGCCAATCTGGCACTGCCTCCTACCATCAATCTGCTGG GCGAGCTGAGCGTGCTGGTCACCACATTCAGCTGGTCCAATATCACCCTGCTGCTCACCGGCCTGAA CATGCTGGTTACAGCCCTGTACTCCCTGTACATGTTCACCACCACACAGTGGGGAAGCCTGACACACC ACATCAACAATATGAAGCCCAGCTTCACCCGCGAGAACACCCTGATGTTCATGCATCTGAGCCCCATT CTGCTGCTGTCCCTGAATCCTGATATCATCACCGGCTTCTCCAGCTGAGAGCACTGGGACGCCCACC GCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTG GGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTTAAATAT TACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTT CCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGG GGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACTCCACATG CCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGA GCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGG TTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTG TGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCAGCCCCTGTCC TCCCTTCACCCCCATTGCGTATGAGCATTTCAGAACTCCAAGGAGTCACAGGCATCTTTATAGTTCACG TTAACATATAGACACTGTTGGAAGCAGTTCCTTCTAAAAGGGTAGCCCTGGACTTAATACCAGCCGGAT ACCTCTGGCCCCCACCCCATTACTGTACCTCTGGAGTCACTACTGTGGGTCGCCACTCCTCTGCTACA CAGCACGGCTTTTTCAAGGCTGTATTGAGAAGGGAAGTTAGGAAGAAGGGTGTGCTGGGCTAACCAG CCCACAGAGCTCACATTCCTGTCCCTTGGGTGAAAAATACATGTCCATCCTGATATCTCCTGAATTCAG AAATTAGCCTCCACATGTGCAATGGCTTTAAGAGCCAGAAGCAGGGTTCTGGGAATTTTGCAAGTTAC CTGTGGCCAGGTGTGGTCTCGGTTACCAAATACGGTTACCTGCAGCTTTTTAGTCCTTTGTGCTCCCA CGGGTCTACAGAGTCCCATCTGCCCAAAGGTCTTGAAGCTTGACAGGATGTTTTCGATTACTCAGTCT CCCAGGGCACTACTGGTCCGTAGGATTCGATTGGTCGGGGTAGGAGAGTTAAACAACATTTAAACAGA GTTCTCTCAAAAATGTCTAAAGGGATTGTAGGTAGATAACATCCAATCACTGTTTGCACTTATCTGAAAT CTTCCCTCTTGGCTGCCCCCAGGTATTTACTGTGGAGAACATTGCATAGGAATGTCTGGAAAAAGCTT CTACAACTTGTTACAGCCTTCACATTTGTAGAAGCTTT

18	COX10-opt_ND4-3'UTR*	ATGGCCGCATCTCCGCACACTCTCTCCTCACGCCTCCTGACAGGTTGCGTAGGAGGCTCTGTCTGGT ATCTTGAAAGAAGAACTATGCTGAAGCTGATCGTGCCCACCATCATGCTGCTGCCTCTGACCTGGCTG AGCAAGAAACACATGATCTGGATCAACACCACCACGCACAGCCTGATCATCAGCATCATCCCTCTGCT GTTCTTCAACCAGATCAACAACAACCTGTTCAGCTGCAGCCCCACCTTCAGCAGCGACCCTCTGACAA CACCTCTGCTGATGCTGACCACCTGGCTGCTGCCCCTCACAATCATGGCCTCTCAGAGACACCTGAG CAGCGAGCCCCTGAGCCGGAAGAAACTGTACCTGAGCATGCTGATCTCCCTGCAGATCTCTCTGATC ATGACCTTCACCGCCACCGAGCTGATCATGTTCTACATCTTTTTCGAGACAACGCTGATCCCCACACT GGCCATCATCACCAGATGGGGCAACCAGCCTGAGAGACTGAACGCCGGCACCTACTTTCTGTTCTAC ACCCTCGTGGGCAGCCTGCCACTGCTGATTGCCCTGATCTACACCCACAACACCCTGGGCTCCCTGA ACATCCTGCTGCTGACACTGACAGCCCAAGAGCTGAGCAACAGCTGGGCCAACAATCTGATGTGGCT GGCCTACACAATGGCCTTCATGGTCAAGATGCCCCTGTACGGCCTGCACCTGTGGCTGCCTAAAGCT CATGTGGAAGCCCCTATCGCCGGCTCTATGGTGCTGGCTGCAGTGCTGCTGAAACTCGGCGGCTACG GCATGATGCGGCTGACCCTGATTCTGAATCCCCTGACCAAGCACATGGCCTATCCATTTCTGGTGCTG AGCCTGTGGGGCATGATTATGACCAGCAGCATCTGCCTGCGGCAGACCGATCTGAAGTCCCTGATCG CCTACAGCTCCATCAGCCACATGGCCCTGGTGGTCACCGCCATCCTGATTCAGACCCCTTGGAGCTTT ACAGGCGCCGTGATCCTGATGATTGCCCACGGCCTGACAAGCAGCCTGCTGTTTTGTCTGGCCAACA GCAACTACGAGCGGACCCACAGCAGAATCATGATCCTGTCTCAGGGCCTGCAGACCCTCCTGCCTCT TATGGCTTTTTGGTGGCTGCTGGCCTCTCTGGCCAATCTGGCACTGCCTCCTACCATCAATCTGCTGG GCGAGCTGAGCGTGCTGGTCACCACATTCAGCTGGTCCAATATCACCCTGCTGCTCACCGGCCTGAA CATGCTGGTTACAGCCCTGTACTCCCTGTACATGTTCACCACCACACAGTGGGGAAGCCTGACACACC ACATCAACAATATGAAGCCCAGCTTCACCCGCGAGAACACCCTGATGTTCATGCATCTGAGCCCCATT CTGCTGCTGTCCCTGAATCCTGATATCATCACCGGCTTCTCCAGCTGAGAGCACTGGGACGCCCACC GCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTG GGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTAAATAT TACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTT CCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGG GGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACTCCACATG CCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGA GCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGG TTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTG TGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCA
19	COX10-opt_ND4*-3'UTR	ATGGCCGCATCTCCGCACACTCTCTCCTCACGCCTCCTGACAGGTTGCGTAGGAGGCTCTGTCTGGT ATCTTGAAAGAAGAACTATGCTGAAGCTGATCGTGCCCACCATCATGCTGCTGCCCCTGACCTGGCTG AGCAAGAAGCACATGATCTGGATCAACACCACCACCCACAGCCTGATCATCAGCATCATCCCCCTGCT GTTCTTCAACCAGATCAACAACAACCTGTTCAGCTGCAGCCCCACCTTCAGCAGCGACCCCCTGACCA CCCCCCTGCTGATGCTGACCACCTGGCTGCTGCCCCTGACCATCATGGCCAGCCAGCGCCACCTGAG CAGCGAGCCCCTGAGCCGCAAGAAGCTGTACCTGAGCATGCTGATCAGCCTGCAGATCAGCCTGATC ATGACCTTCACCGCCACCGAGCTGATCATGTTCTACATCTTCTTCGAGACCACCCTGATCCCCACCCT GGCCATCATCACCCGCTGGGGCAACCAGCCCGAGCGCCTGAACGCCGGCACCTACTTCCTGTTCTAC ACCCTGGTGGGCAGCCTGCCCCTGCTGATCGCCCTGATCTACACCCACAACACCCTGGGCAGCCTGA ACATCCTGCTGCTGACCCTGACCGCCCAGGAGCTGAGCAACAGCTGGGCCAACAACCTGATGTGGCT GGCCTACACCATGGCCTTCATGGTGAAGATGCCCCTGTACGGCCTGCACCTGTGGCTGCCCAAGGCC CACGTGGAGGCCCCCATCGCCGGCAGCATGGTGCTGGCCGCCGTGCTGCTGAAGCTGGGCGGCTAC GGCATGATGCGCCTGACCCTGATCCTGAACCCCCTGACCAAGCACATGGCCTACCCCTTCCTGGTGC TGAGCCTGTGGGGCATGATCATGACCAGCAGCATCTGCCTGCGCCAGACCGACCTGAAGAGCCTGAT CGCCTACAGCAGCATCAGCCACATGGCCCTGGTGGTGACCGCCATCCTGATCCAGACCCCCTGGAGC TTCACCGGCGCCGTGATCCTGATGATCGCCCACGGCCTGACCAGCAGCCTGCTGTTCTGCCTGGCCA ACAGCAACTACGAGCGCACCCACAGCCGCATCATGATCCTGAGCCAGGGCCTGCAGACCCTGCTGCC CCTGATGGCCTTCTGGTGGCTGCTGGCCAGCCTGGCCAACCTGGCCCTGCCCCCCACCATCAACCTG CTGGGCGAGCTGAGCGTGCTGGTGACCACCTTCAGCTGGAGCAACATCACCCTGCTGCTGACCGGC CTGAACATGCTGGTGACCGCCCTGTACAGCCTGTACATGTTCACCACCACCCAGTGGGGCAGCCTGA CCCACCACATCAACAACATGAAGCCCAGCTTCACCCGCGAGAACACCCTGATGTTCATGCACCTGAGC CCCATCCTGCTGCTGAGCCTGAACCCCGACATCATCACCGGCTTCAGCAGCTAAGAGCACTGGGACG CCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAA ATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTT TTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAA TTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCT CACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACT CCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGT TCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCA TTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCG GCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCAGCC CCTGTCCTCCCTTCACCCCCATTGCGTATGAGCATTTCAGAACTCCAAGGAGTCACAGGCATCTTTATA GTTCACGTTAACATATAGACACTGTTGGAAGCAGTTCCTTCTAAAAGGGTAGCCCTGGACTTAATACCA GCCGGATACCTCTGGCCCCCACCCCATTACTGTACCTCTGGAGTCACTACTGTGGGTCGCCACTCCT CTGCTACACAGCACGGCTTTTTCAAGGCTGTATTGAGAAGGGAAGTTAGGAAGAAGGGTGTGCTGGG CTAACCAGCCCACAGAGCTCACATTCCTGTCCCTTGGGTGAAAAATACATGTCCATCCTGATATCTCCT GAATTCAGAAATTAGCCTCCACATGTGCAATGGCTTTAAGAGCCAGAAGCAGGGTTCTGGGAATTTTG CAAGTTACCTGTGGCCAGGTGTGGTCTCGGTTACCAAATACGGTTACCTGCAGCTTTTTAGTCCTTTGT GCTCCCACGGGTCTACAGAGTCCCATCTGCCCAAAGGTCTTGAAGCTTGACAGGATGTTTTCGATTAC TCAGTCTCCCAGGGCACTACTGGTCCGTAGGATTCGATTGGTCGGGGTAGGAGAGTTAAACAACATTT AAACAGAGTTCTCTCAAAAATGTCTAAAGGGATTGTAGGTAGATAACATCCAATCACTGTTTGCACTTAT CTGAAATCTTCCCTCTTGGCTGCCCCCAGGTATTTACTGTGGAGAACATTGCATAGGAATGTCTGGAA AAAGCTTCTACAACTTGTTACAGCCTTCACATTTGTAGAAGCTTT

20	COX10-opt_ND4*-3'UTR*	ATGGCCGCATCTCCGCACACTCTCTCCTCACGCCTCCTGACAGGTTGCGTAGGAGGCTCTGTCTGGT ATCTTGAAAGAAGAACTATGCTGAAGCTGATCGTGCCCACCATCATGCTGCTGCCCCTGACCTGGCTG AGCAAGAAGCACATGATCTGGATCAACACCACCACCCACAGCCTGATCATCAGCATCATCCCCCTGCT GTTCTTCAACCAGATCAACAACAACCTGTTCAGCTGCAGCCCCACCTTCAGCAGCGACCCCCTGACCA CCCCCCTGCTGATGCTGACCACCTGGCTGCTGCCCCTGACCATCATGGCCAGCCAGCGCCACCTGAG CAGCGAGCCCCTGAGCCGCAAGAAGCTGTACCTGAGCATGCTGATCAGCCTGCAGATCAGCCTGATC ATGACCTTCACCGCCACCGAGCTGATCATGTTCTACATCTTCTTCGAGACCACCCTGATCCCCACCCT GGCCATCATCACCCGCTGGGGCAACCAGCCCGAGCGCCTGAACGCCGGCACCTACTTCCTGTTCTAC ACCCTGGTGGGCAGCCTGCCCCTGCTGATCGCCCTGATCTACACCCACAACACCCTGGGCAGCCTGA ACATCCTGCTGCTGACCCTGACCGCCCAGGAGCTGAGCAACAGCTGGGCCAACAACCTGATGTGGCT GGCCTACACCATGGCCTTCATGGTGAAGATGCCCCTGTACGGCCTGCACCTGTGGCTGCCCAAGGCC CACGTGGAGGCCCCCATCGCCGGCAGCATGGTGCTGGCCGCCGTGCTGCTGAAGCTGGGCGGCTAC GGCATGATGCGCCTGACCCTGATCCTGAACCCCCTGACCAAGCACATGGCCTACCCCTTCCTGGTGC TGAGCCTGTGGGGCATGATCATGACCAGCAGCATCTGCCTGCGCCAGACCGACCTGAAGAGCCTGAT CGCCTACAGCAGCATCAGCCACATGGCCCTGGTGGTGACCGCCATCCTGATCCAGACCCCCTGGAGC TTCACCGGCGCCGTGATCCTGATGATCGCCCACGGCCTGACCAGCAGCCTGCTGTTCTGCCTGGCCA ACAGCAACTACGAGCGCACCCACAGCCGCATCATGATCCTGAGCCAGGGCCTGCAGACCCTGCTGCC CCTGATGGCCTTCTGGTGGCTGCTGGCCAGCCTGGCCAACCTGGCCCTGCCCCCCACCATCAACCTG CTGGGCGAGCTGAGCGTGCTGGTGACCACCTTCAGCTGGAGCAACATCACCCTGCTGCTGACCGGC CTGAACATGCTGGTGACCGCCCTGTACAGCCTGTACATGTTCACCACCACCCAGTGGGGCAGCCTGA CCCACCACATCAACAACATGAAGCCCAGCTTCACCCGCGAGAACACCCTGATGTTCATGCACCTGAGC CCCATCCTGCTGCTGAGCCTGAACCCCGACATCATCACCGGCTTCAGCAGCTAAGAGCACTGGGACG CCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAA ATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTT TTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAA TTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCT CACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACT CCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGT TCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCA TTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCG GCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCA
21	COX10-ND6-3'UTR	ATGGCCGCATCTCCGCACACTCTCTCCTCACGCCTCCTGACAGGTTGCGTAGGAGGCTCTGTCTGGT ATCTTGAAAGAAGAACTATGATGTATGCTTTGTTTCTGTTGAGTGTGGGTTTAGTAATGGGGTTTGTGG GGTTTTCTTCTAAGCCTTCTCCTATTTATGGGGGTTTAGTATTGATTGTTAGCGGTGTGGTCGGGTGTG TTATTATTCTGAATTTTGGGGGAGGTTATATGGGTTTAATGGTTTTTTTAATTTATTTAGGGGGAATGAT GGTTGTCTTTGGATATACTACAGCGATGGCTATTGAGGAGTATCCTGAGGCATGGGGGTCAGGGGTT GAGGTCTTGGTGAGTGTTTTAGTGGGGTTAGCGATGGAGGTAGGATTGGTGCTGTGGGTGAAAGAGT ATGATGGGGTGGTGGTTGTGGTAAACTTTAATAGTGTAGGAAGCTGGATGATTTATGAAGGAGAGGGG TCAGGGTTGATTCGGGAGGATCCTATTGGTGCGGGGGCTTTGTATGATTATGGGCGTTGGTTAGTAGT AGTTACTGGTTGGACATTGTTTGTTGGTGTATATATTGTAATTGAGATTGCTCGGGGGAATTAGGAGCA CTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAA GAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTT TTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAA AAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTT CTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACA CGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTG TCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAG GGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCT AGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGAC TGCCAGCCCCTGTCCTCCCTTCACCCCCATTGCGTATGAGCATTTCAGAACTCCAAGGAGTCACAGGC ATCTTTATAGTTCACGTTAACATATAGACACTGTTGGAAGCAGTTCCTTCTAAAAGGGTAGCCCTGGAC TTAATACCAGCCGGATACCTCTGGCCCCCACCCCATTACTGTACCTCTGGAGTCACTACTGTGGGTCG CCACTCCTCTGCTACACAGCACGGCTTTTTCAAGGCTGTATTGAGAAGGGAAGTTAGGAAGAAGGGTG TGCTGGGCTAACCAGCCCACAGAGCTCACATTCCTGTCCCTTGGGTGAAAAATACATGTCCATCCTGA TATCTCCTGAATTCAGAAATTAGCCTCCACATGTGCAATGGCTTTAAGAGCCAGAAGCAGGGTTCTGG GAATTTTGCAAGTTACCTGTGGCCAGGTGTGGTCTCGGTTACCAAATACGGTTACCTGCAGCTTTTTAG TCCTTTGTGCTCCCACGGGTCTACAGAGTCCCATCTGCCCAAAGGTCTTGAAGCTTGACAGGATGTTT TCGATTACTCAGTCTCCCAGGGCACTACTGGTCCGTAGGATTCGATTGGTCGGGGTAGGAGAGTTAAA CAACATTTAAACAGAGTTCTCTCAAAAATGTCTAAAGGGATTGTAGGTAGATAACATCCAATCACTGTTT GCACTTATCTGAAATCTTCCCTCTTGGCTGCCCCCAGGTATTTACTGTGGAGAACATTGCATAGGAATG TCTGGAAAAAGCTTCTACAACTTGTTACAGCCTTCACATTTGTAGAAGCTTT
22	COX10-ND6-3'UTR*	ATGGCCGCATCTCCGCACACTCTCTCCTCACGCCTCCTGACAGGTTGCGTAGGAGGCTCTGTCTGGT ATCTTGAAAGAAGAACTATGATGTATGCTTTGTTTCTGTTGAGTGTGGGTTTAGTAATGGGGTTTGTGG GGTTTTCTTCTAAGCCTTCTCCTATTTATGGGGGTTTAGTATTGATTGTTAGCGGTGTGGTCGGGTGTG TTATTATTCTGAATTTTGGGGGAGGTTATATGGGTTTAATGGTTTTTTTAATTTATTTAGGGGGAATGAT GGTTGTCTTTGGATATACTACAGCGATGGCTATTGAGGAGTATCCTGAGGCATGGGGGTCAGGGGTT GAGGTCTTGGTGAGTGTTTTAGTGGGGTTAGCGATGGAGGTAGGATTGGTGCTGTGGGTGAAAGAGT ATGATGGGGTGGTGGTTGTGGTAAACTTTAATAGTGTAGGAAGCTGGATGATTTATGAAGGAGAGGGG TCAGGGTTGATTCGGGAGGATCCTATTGGTGCGGGGGCTTTGTATGATTATGGGCGTTGGTTAGTAGT AGTTACTGGTTGGACATTGTTTGTTGGTGTATATATTGTAATTGAGATTGCTCGGGGGAATTAGGAGCA CTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAA GAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTT TTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAA AAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTT

		CTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACA CGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTG TCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAG GGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCT AGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGAC TGCCA
23	COX10-opt_ND6-3'UTR	ATGGCCGCATCTCCGCACACTCTCTCCTCACGCCTCCTGACAGGTTGCGTAGGAGGCTCTGTCTGGT ATCTTGAAAGAAGAACTATGATGTACGCCCTGTTCCTGCTGAGCGTGGGCCTGGTGATGGGCTTCGTG GGCTTCAGCAGCAAGCCCAGCCCCATCTACGGCGGCCTGGTGCTGATCGTGAGCGGCGTGGTGGGC TGCGTGATCATCCTGAACTTCGGCGGCGGCTACATGGGCCTGATGGTGTTCCTGATCTACCTGGGCG GCATGATGGTGGTGTTCGGCTACACCACCGCCATGGCCATCGAGGAGTACCCCGAGGCCTGGGGCA GCGGCGTGGAGGTGCTGGTGAGCGTGCTGGTGGGCCTGGCCATGGAGGTGGGCCTGGTGCTGTGG GTGAAGGAGTACGACGGCGTGGTGGTGGTGGTGAACTTCAACAGCGTGGGCAGCTGGATGATCTAC GAGGGCGAGGGCAGCGGCCTGATCCGCGAGGACCCCATCGGCGCCGGCGCCCTGTACGACTACGG CCGCTGGCTGGTGGTGGTGACCGGCTGGACCCTGTTCGTGGGCGTGTACATCGTGATCGAGATCGC CCGCGGCAACTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTG TGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTC AGTGATCACTTGACAGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAG CTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACC CCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCAT CCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGT GAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTT CCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTC TAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGG GAGTCTCAAGCTGGACTGCCAGCCCCTGTCCTCCCTTCACCCCCATTGCGTATGAGCATTTCAGAACT CCAAGGAGTCACAGGCATCTTTATAGTTCACGTTAACATATAGACACTGTTGGAAGCAGTTCCTTCTAA AAGGGTAGCCCTGGACTTAATACCAGCCGGATACCTCTGGCCCCCACCCCATTACTGTACCTCTGGA GTCACTACTGTGGGTCGCCACTCCTCTGCTACACAGCACGGCTTTTTCAAGGCTGTATTGAGAAGGGA AGTTAGGAAGAAGGGTGTGCTGGGCTAACCAGCCCACAGAGCTCACATTCCTGTCCCTTGGGTGAAA AATACATGTCCATCCTGATATCTCCTGAATTCAGAAATTAGCCTCCACATGTGCAATGGCTTTAAGAGC CAGAAGCAGGGTTCTGGGAATTTTGCAAGTTACCTGTGGCCAGGTGTGGTCTCGGTTACCAAATACGG TTACCTGCAGCTTTTTAGTCCTTTGTGCTCCCACGGGTCTACAGAGTCCCATCTGCCCAAAGGTCTTGA AGCTTGACAGGATGTTTTCGATTACTCAGTCTCCCAGGGCACTACTGGTCCGTAGGATTCGATTGGTC GGGGTAGGAGAGTTAAACAACATTTAAACAGAGTTCTCTCAAAAATGTCTAAAGGGATTGTAGGTAGAT AACATCCAATCACTGTTTGCACTTATCTGAAATCTTCCCTCTTGGCTGCCCCCAGGTATTTACTGTGGA GAACATTGCATAGGAATGTCTGGAAAAAGCTTCTACAACTTGTTACAGCCTTCACATTTGTAGAAGCTT T
24	COX10-opt_ND6-3'UTR*	ATGGCCGCATCTCCGCACACTCTCTCCTCACGCCTCCTGACAGGTTGCGTAGGAGGCTCTGTCTGGT ATCTTGAAAGAAGAACTATGATGTACGCCCTGTTCCTGCTGAGCGTGGGCCTGGTGATGGGCTTCGTG GGCTTCAGCAGCAAGCCCAGCCCCATCTACGGCGGCCTGGTGCTGATCGTGAGCGGCGTGGTGGGC TGCGTGATCATCCTGAACTTCGGCGGCGGCTACATGGGCCTGATGGTGTTCCTGATCTACCTGGGCG GCATGATGGTGGTGTTCGGCTACACCACCGCCATGGCCATCGAGGAGTACCCCGAGGCCTGGGGCA GCGGCGTGGAGGTGCTGGTGAGCGTGCTGGTGGGCCTGGCCATGGAGGTGGGCCTGGTGCTGTGG GTGAAGGAGTACGACGGCGTGGTGGTGGTGGTGAACTTCAACAGCGTGGGCAGCTGGATGATCTAC GAGGGCGAGGGCAGCGGCCTGATCCGCGAGGACCCCATCGGCGCCGGCGCCCTGTACGACTACGG CCGCTGGCTGGTGGTGGTGACCGGCTGGACCCTGTTCGTGGGCGTGTACATCGTGATCGAGATCGC CCGCGGCAACTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTG TGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTC AGTGATCACTTGACAGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAG CTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACC CCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCAT CCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGT GAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTT CCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTC TAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGG GAGTCTCAAGCTGGACTGCCA

25	COX10-ND1-3'UTR	ATGGCCGCATCTCCGCACACTCTCTCCTCACGCCTCCTGACAGGTTGCGTAGGAGGCTCTGTCTGGT ATCTTGAAAGAAGAACTATGGCCAACCTCCTACTCCTCATTGTACCCATTCTAATCGCAATGGCATTCC TAATGCTTACCGAACGAAAAATTCTAGGCTATATGCAACTACGCAAAGGCCCCAACGTTGTAGGCCCC TACGGGCTACTACAACCCTTCGCTGACGCCATAAAACTCTTCACCAAAGAGCCCCTAAAACCCGCCAC ATCTACCATCACCCTCTACATCACCGCCCCGACCTTAGCTCTCACCATCGCTCTTCTACTATGGACCCC CCTCCCCATGCCCAACCCCCTGGTCAACCTCAACCTAGGCCTCCTATTTATTCTAGCCACCTCTAGCC TAGCCGTTTACTCAATCCTCTGGTCAGGGTGGGCATCAAACTCAAACTACGCCCTGATCGGCGCACTG CGAGCAGTAGCCCAAACAATCTCATATGAAGTCACCCTAGCCATCATTCTACTATCAACATTACTAATG AGTGGCTCCTTTAACCTCTCCACCCTTATCACAACACAAGAACACCTCTGGTTACTCCTGCCATCATGG CCCTTGGCCATGATGTGGTTTATCTCCACACTAGCAGAGACCAACCGAACCCCCTTCGACCTTGCCGA AGGGGAGTCCGAACTAGTCTCAGGCTTCAACATCGAATACGCCGCAGGCCCCTTCGCCCTATTCTTCA TGGCCGAATACACAAACATTATTATGATGAACACCCTCACCACTACAATCTTCCTAGGAACAACATATG ACGCACTCTCCCCTGAACTCTACACAACATATTTTGTCACCAAGACCCTACTTCTAACCTCCCTGTTCT TATGGATTCGAACAGCATACCCCCGATTCCGCTACGACCAACTCATGCACCTCCTATGGAAAAACTTC CTACCACTCACCCTAGCATTACTTATGTGGTATGTCTCCATGCCCATTACAATCTCCAGCATTCCCCCT CAAACCTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTA ATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGA TCACTTGACAGTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAG TCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACC CTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTAC CACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCT CATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGT GACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAA TACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTC TCAAGCTGGACTGCCAGCCCCTGTCCTCCCTTCACCCCCATTGCGTATGAGCATTTCAGAACTCCAAG GAGTCACAGGCATCTTTATAGTTCACGTTAACATATAGACACTGTTGGAAGCAGTTCCTTCTAAAAGGG TAGCCCTGGACTTAATACCAGCCGGATACCTCTGGCCCCCACCCCATTACTGTACCTCTGGAGTCACT ACTGTGGGTCGCCACTCCTCTGCTACACAGCACGGCTTTTTCAAGGCTGTATTGAGAAGGGAAGTTAG GAAGAAGGGTGTGCTGGGCTAACCAGCCCACAGAGCTCACATTCCTGTCCCTTGGGTGAAAAATACAT GTCCATCCTGATATCTCCTGAATTCAGAAATTAGCCTCCACATGTGCAATGGCTTTAAGAGCCAGAAGC AGGGTTCTGGGAATTTTGCAAGTTACCTGTGGCCAGGTGTGGTCTCGGTTACCAAATACGGTTACCTG CAGCTTTTTAGTCCTTTGTGCTCCCACGGGTCTACAGAGTCCCATCTGCCCAAAGGTCTTGAAGCTTG ACAGGATGTTTTCGATTACTCAGTCTCCCAGGGCACTACTGGTCCGTAGGATTCGATTGGTCGGGGTA GGAGAGTTAAACAACATTTAAACAGAGTTCTCTCAAAAATGTCTAAAGGGATTGTAGGTAGATAACATC CAATCACTGTTTGCACTTATCTGAAATCTTCCCTCTTGGCTGCCCCCAGGTATTTACTGTGGAGAACAT TGCATAGGAATGTCTGGAAAAAGCTTCTACAACTTGTTACAGCCTTCACATTTGTAGAAGCTTT
26	COX10-ND1-3'UTR*	ATGGCCGCATCTCCGCACACTCTCTCCTCACGCCTCCTGACAGGTTGCGTAGGAGGCTCTGTCTGGT ATCTTGAAAGAAGAACTATGGCCAACCTCCTACTCCTCATTGTACCCATTCTAATCGCAATGGCATTCC TAATGCTTACCGAACGAAAAATTCTAGGCTATATGCAACTACGCAAAGGCCCCAACGTTGTAGGCCCC TACGGGCTACTACAACCCTTCGCTGACGCCATAAAACTCTTCACCAAAGAGCCCCTAAAACCCGCCAC ATCTACCATCACCCTCTACATCACCGCCCCGACCTTAGCTCTCACCATCGCTCTTCTACTATGGACCCC CCTCCCCATGCCCAACCCCCTGGTCAACCTCAACCTAGGCCTCCTATTTATTCTAGCCACCTCTAGCC TAGCCGTTTACTCAATCCTCTGGTCAGGGTGGGCATCAAACTCAAACTACGCCCTGATCGGCGCACTG CGAGCAGTAGCCCAAACAATCTCATATGAAGTCACCCTAGCCATCATTCTACTATCAACATTACTAATG AGTGGCTCCTTTAACCTCTCCACCCTTATCACAACACAAGAACACCTCTGGTTACTCCTGCCATCATGG CCCTTGGCCATGATGTGGTTTATCTCCACACTAGCAGAGACCAACCGAACCCCCTTCGACCTTGCCGA AGGGGAGTCCGAACTAGTCTCAGGCTTCAACATCGAATACGCCGCAGGCCCCTTCGCCCTATTCTTCA TGGCCGAATACACAAACATTATTATGATGAACACCCTCACCACTACAATCTTCCTAGGAACAACATATG ACGCACTCTCCCCTGAACTCTACACAACATATTTTGTCACCAAGACCCTACTTCTAACCTCCCTGTTCT TATGGATTCGAACAGCATACCCCCGATTCCGCTACGACCAACTCATGCACCTCCTATGGAAAAACTTC CTACCACTCACCCTAGCATTACTTATGTGGTATGTCTCCATGCCCATTACAATCTCCAGCATTCCCCCT CAAACCTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTA ATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGA TCACTTGACAGTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAG TCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACC CTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTAC CACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCT CATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGT GACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAA TACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTC TCAAGCTGGACTGCCA

27	COX10-opt_ND1-3'UTR	ATGGCCGCATCTCCGCACACTCTCTCCTCACGCCTCCTGACAGGTTGCGTAGGAGGCTCTGTCTGGT ATCTTGAAAGAAGAACTATGGCCAACCTGCTGCTGCTGATCGTGCCCATCCTGATCGCCATGGCCTTC CTGATGCTGACCGAGCGCAAGATCCTGGGCTACATGCAGCTGCGCAAGGGCCCCAACGTGGTGGGC CCCTACGGCCTGCTGCAGCCCTTCGCCGACGCCATCAAGCTGTTCACCAAGGAGCCCCTGAAGCCCG CCACCAGCACCATCACCCTGTACATCACCGCCCCCACCCTGGCCCTGACCATCGCCCTGCTGCTGTG GACCCCCCTGCCCATGCCCAACCCCCTGGTGAACCTGAACCTGGGCCTGCTGTTCATCCTGGCCACC AGCAGCCTGGCCGTGTACAGCATCCTGTGGAGCGGCTGGGCCAGCAACAGCAACTACGCCCTGATC GGCGCCCTGCGCGCCGTGGCCCAGACCATCAGCTACGAGGTGACCCTGGCCATCATCCTGCTGAGC ACCCTGCTGATGAGCGGCAGCTTCAACCTGAGCACCCTGATCACCACCCAGGAGCACCTGTGGCTGC TGCTGCCCAGCTGGCCCCTGGCCATGATGTGGTTCATCAGCACCCTGGCCGAGACCAACCGCACCCC CTTCGACCTGGCCGAGGGCGAGAGCGAGCTGGTGAGCGGCTTCAACATCGAGTACGCCGCCGGCCC CTTCGCCCTGTTCTTCATGGCCGAGTACACCAACATCATCATGATGAACACCCTGACCACCACCATCTT CCTGGGCACCACCTACGACGCCCTGAGCCCCGAGCTGTACACCACCTACTTCGTGACCAAGACCCTG CTGCTGACCAGCCTGTTCCTGTGGATCCGCACCGCCTACCCCCGCTTCCGCTACGACCAGCTGATGC ACCTGCTGTGGAAGAACTTCCTGCCCCTGACCCTGGCCCTGCTGATGTGGTACGTGAGCATGCCCAT CACCATCAGCAGCATCCCCCCCCAGACCTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCT GCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTA TAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCC CAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTT ATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAG CTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCAC TTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAG GCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACA TTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGA TTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCAGCCCCTGTCCTCCCTTCACCCCCATTGC GTATGAGCATTTCAGAACTCCAAGGAGTCACAGGCATCTTTATAGTTCACGTTAACATATAGACACTGT TGGAAGCAGTTCCTTCTAAAAGGGTAGCCCTGGACTTAATACCAGCCGGATACCTCTGGCCCCCACCC CATTACTGTACCTCTGGAGTCACTACTGTGGGTCGCCACTCCTCTGCTACACAGCACGGCTTTTTCAA GGCTGTATTGAGAAGGGAAGTTAGGAAGAAGGGTGTGCTGGGCTAACCAGCCCACAGAGCTCACATT CCTGTCCCTTGGGTGAAAAATACATGTCCATCCTGATATCTCCTGAATTCAGAAATTAGCCTCCACATG TGCAATGGCTTTAAGAGCCAGAAGCAGGGTTCTGGGAATTTTGCAAGTTACCTGTGGCCAGGTGTGGT CTCGGTTACCAAATACGGTTACCTGCAGCTTTTTAGTCCTTTGTGCTCCCACGGGTCTACAGAGTCCC ATCTGCCCAAAGGTCTTGAAGCTTGACAGGATGTTTTCGATTACTCAGTCTCCCAGGGCACTACTGGT CCGTAGGATTCGATTGGTCGGGGTAGGAGAGTTAAACAACATTTAAACAGAGTTCTCTCAAAAATGTCT AAAGGGATTGTAGGTAGATAACATCCAATCACTGTTTGCACTTATCTGAAATCTTCCCTCTTGGCTGCC CCCAGGTATTTACTGTGGAGAACATTGCATAGGAATGTCTGGAAAAAGCTTCTACAACTTGTTACAGCC TTCACATTTGTAGAAGCTTT
28	COX10-opt_ND1-3'UTR*	ATGGCCGCATCTCCGCACACTCTCTCCTCACGCCTCCTGACAGGTTGCGTAGGAGGCTCTGTCTGGT ATCTTGAAAGAAGAACTATGGCCAACCTGCTGCTGCTGATCGTGCCCATCCTGATCGCCATGGCCTTC CTGATGCTGACCGAGCGCAAGATCCTGGGCTACATGCAGCTGCGCAAGGGCCCCAACGTGGTGGGC CCCTACGGCCTGCTGCAGCCCTTCGCCGACGCCATCAAGCTGTTCACCAAGGAGCCCCTGAAGCCCG CCACCAGCACCATCACCCTGTACATCACCGCCCCCACCCTGGCCCTGACCATCGCCCTGCTGCTGTG GACCCCCCTGCCCATGCCCAACCCCCTGGTGAACCTGAACCTGGGCCTGCTGTTCATCCTGGCCACC AGCAGCCTGGCCGTGTACAGCATCCTGTGGAGCGGCTGGGCCAGCAACAGCAACTACGCCCTGATC GGCGCCCTGCGCGCCGTGGCCCAGACCATCAGCTACGAGGTGACCCTGGCCATCATCCTGCTGAGC ACCCTGCTGATGAGCGGCAGCTTCAACCTGAGCACCCTGATCACCACCCAGGAGCACCTGTGGCTGC TGCTGCCCAGCTGGCCCCTGGCCATGATGTGGTTCATCAGCACCCTGGCCGAGACCAACCGCACCCC CTTCGACCTGGCCGAGGGCGAGAGCGAGCTGGTGAGCGGCTTCAACATCGAGTACGCCGCCGGCCC CTTCGCCCTGTTCTTCATGGCCGAGTACACCAACATCATCATGATGAACACCCTGACCACCACCATCTT CCTGGGCACCACCTACGACGCCCTGAGCCCCGAGCTGTACACCACCTACTTCGTGACCAAGACCCTG CTGCTGACCAGCCTGTTCCTGTGGATCCGCACCGCCTACCCCCGCTTCCGCTACGACCAGCTGATGC ACCTGCTGTGGAAGAACTTCCTGCCCCTGACCCTGGCCCTGCTGATGTGGTACGTGAGCATGCCCAT CACCATCAGCAGCATCCCCCCCCAGACCTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCT GCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTA TAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCC CAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTT ATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAG CTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCAC TTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAG GCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACA TTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGA TTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCA

29	opt_COX10-ND4-3'UTR	ATGGCCGCCTCTCCACACACACTGAGTAGCAGACTGCTGACCGGCTGTGTTGGCGGCTCTGTGTGGT ATCTGGAACGGCGGACAATGCTAAAACTAATCGTCCCAACAATTATGTTACTACCACTGACATGGCTTT CCAAAAAACACATGATTTGGATCAACACAACCACCCACAGCCTAATTATTAGCATCATCCCTCTACTATT TTTTAACCAAATCAACAACAACCTATTTAGCTGTTCCCCAACCTTTTCCTCCGACCCCCTAACAACCCC CCTCCTAATGCTAACTACCTGGCTCCTACCCCTCACAATCATGGCAAGCCAACGCCACTTATCCAGTG AACCACTATCACGAAAAAAACTCTACCTCTCTATGCTAATCTCCCTACAAATCTCCTTAATTATGACATT CACAGCCACAGAACTAATCATGTTTTATATCTTCTTCGAAACCACACTTATCCCCACCTTGGCTATCATC ACCCGATGGGGCAACCAGCCAGAACGCCTGAACGCAGGCACATACTTCCTATTCTACACCCTAGTAG GCTCCCTTCCCCTACTCATCGCACTAATTTACACTCACAACACCCTAGGCTCACTAAACATTCTACTAC TCACTCTCACTGCCCAAGAACTATCAAACTCCTGGGCCAACAACTTAATGTGGCTAGCTTACACAATGG CTTTTATGGTAAAGATGCCTCTTTACGGACTCCACTTATGGCTCCCTAAAGCCCATGTCGAAGCCCCCA TCGCTGGGTCAATGGTACTTGCCGCAGTACTCTTAAAACTAGGCGGCTATGGTATGATGCGCCTCACA CTCATTCTCAACCCCCTGACAAAACACATGGCCTACCCCTTCCTTGTACTATCCCTATGGGGCATGATT ATGACAAGCTCCATCTGCCTACGACAAACAGACCTAAAATCGCTCATTGCATACTCTTCAATCAGCCAC ATGGCCCTCGTAGTAACAGCCATTCTCATCCAAACCCCCTGGAGCTTCACCGGCGCAGTCATTCTCAT GATCGCCCACGGGCTTACATCCTCATTACTATTCTGCCTAGCAAACTCAAACTACGAACGCACTCACA GTCGCATCATGATCCTCTCTCAAGGACTTCAAACTCTACTCCCACTAATGGCTTTTTGGTGGCTTCTAG CAAGCCTCGCTAACCTCGCCTTACCCCCCACTATTAACCTACTGGGAGAACTCTCTGTGCTAGTAACC ACGTTCTCCTGGTCAAATATCACTCTCCTACTTACAGGACTCAACATGCTAGTCACAGCCCTATACTCC CTCTACATGTTTACCACAACACAATGGGGCTCACTCACCCACCACATTAACAACATGAAACCCTCATTC ACACGAGAAAACACCCTCATGTTCATGCACCTATCCCCCATTCTCCTCCTATCCCTCAACCCCGACATC ATTACCGGGTTTTCCTCTTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAG CATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTC GGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAA TGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTC CTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTT GGTTCCATCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCA GAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGC ACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCAT AGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTT TGCCTTGGGAGTCTCAAGCTGGACTGCCAGCCCCTGTCCTCCCTTCACCCCCATTGCGTATGAGCATT TCAGAACTCCAAGGAGTCACAGGCATCTTTATAGTTCACGTTAACATATAGACACTGTTGGAAGCAGTT CCTTCTAAAAGGGTAGCCCTGGACTTAATACCAGCCGGATACCTCTGGCCCCCACCCCATTACTGTAC CTCTGGAGTCACTACTGTGGGTCGCCACTCCTCTGCTACACAGCACGGCTTTTTCAAGGCTGTATTGA GAAGGGAAGTTAGGAAGAAGGGTGTGCTGGGCTAACCAGCCCACAGAGCTCACATTCCTGTCCCTTG GGTGAAAAATACATGTCCATCCTGATATCTCCTGAATTCAGAAATTAGCCTCCACATGTGCAATGGCTT TAAGAGCCAGAAGCAGGGTTCTGGGAATTTTGCAAGTTACCTGTGGCCAGGTGTGGTCTCGGTTACCA AATACGGTTACCTGCAGCTTTTTAGTCCTTTGTGCTCCCACGGGTCTACAGAGTCCCATCTGCCCAAA GGTCTTGAAGCTTGACAGGATGTTTTCGATTACTCAGTCTCCCAGGGCACTACTGGTCCGTAGGATTC GATTGGTCGGGGTAGGAGAGTTAAACAACATTTAAACAGAGTTCTCTCAAAAATGTCTAAAGGGATTGT AGGTAGATAACATCCAATCACTGTTTGCACTTATCTGAAATCTTCCCTCTTGGCTGCCCCCAGGTATTT ACTGTGGAGAACATTGCATAGGAATGTCTGGAAAAAGCTTCTACAACTTGTTACAGCCTTCACATTTGT AGAAGCTTT
30	opt_COX10-ND4-3'UTR*	ATGGCCGCCTCTCCACACACACTGAGTAGCAGACTGCTGACCGGCTGTGTTGGCGGCTCTGTGTGGT ATCTGGAACGGCGGACAATGCTAAAACTAATCGTCCCAACAATTATGTTACTACCACTGACATGGCTTT CCAAAAAACACATGATTTGGATCAACACAACCACCCACAGCCTAATTATTAGCATCATCCCTCTACTATT TTTTAACCAAATCAACAACAACCTATTTAGCTGTTCCCCAACCTTTTCCTCCGACCCCCTAACAACCCC CCTCCTAATGCTAACTACCTGGCTCCTACCCCTCACAATCATGGCAAGCCAACGCCACTTATCCAGTG AACCACTATCACGAAAAAAACTCTACCTCTCTATGCTAATCTCCCTACAAATCTCCTTAATTATGACATT CACAGCCACAGAACTAATCATGTTTTATATCTTCTTCGAAACCACACTTATCCCCACCTTGGCTATCATC ACCCGATGGGGCAACCAGCCAGAACGCCTGAACGCAGGCACATACTTCCTATTCTACACCCTAGTAG GCTCCCTTCCCCTACTCATCGCACTAATTTACACTCACAACACCCTAGGCTCACTAAACATTCTACTAC TCACTCTCACTGCCCAAGAACTATCAAACTCCTGGGCCAACAACTTAATGTGGCTAGCTTACACAATGG CTTTTATGGTAAAGATGCCTCTTTACGGACTCCACTTATGGCTCCCTAAAGCCCATGTCGAAGCCCCCA TCGCTGGGTCAATGGTACTTGCCGCAGTACTCTTAAAACTAGGCGGCTATGGTATGATGCGCCTCACA CTCATTCTCAACCCCCTGACAAAACACATGGCCTACCCCTTCCTTGTACTATCCCTATGGGGCATGATT ATGACAAGCTCCATCTGCCTACGACAAACAGACCTAAAATCGCTCATTGCATACTCTTCAATCAGCCAC ATGGCCCTCGTAGTAACAGCCATTCTCATCCAAACCCCCTGGAGCTTCACCGGCGCAGTCATTCTCAT GATCGCCCACGGGCTTACATCCTCATTACTATTCTGCCTAGCAAACTCAAACTACGAACGCACTCACA GTCGCATCATGATCCTCTCTCAAGGACTTCAAACTCTACTCCCACTAATGGCTTTTTGGTGGCTTCTAG CAAGCCTCGCTAACCTCGCCTTACCCCCCACTATTAACCTACTGGGAGAACTCTCTGTGCTAGTAACC ACGTTCTCCTGGTCAAATATCACTCTCCTACTTACAGGACTCAACATGCTAGTCACAGCCCTATACTCC CTCTACATGTTTACCACAACACAATGGGGCTCACTCACCCACCACATTAACAACATGAAACCCTCATTC ACACGAGAAAACACCCTCATGTTCATGCACCTATCCCCCATTCTCCTCCTATCCCTCAACCCCGACATC ATTACCGGGTTTTCCTCTTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAG CATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTC GGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAA TGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTC CTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTT GGTTCCATCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCA GAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGC ACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCAT AGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTT TGCCTTGGGAGTCTCAAGCTGGACTGCCA

31	opt_COX10-opt_ND4-3'UTR	ATGGCCGCCTCTCCACACACACTGAGTAGCAGACTGCTGACCGGCTGTGTTGGCGGCTCTGTGTGGT ATCTGGAACGGCGGACAATGCTGAAGCTGATCGTGCCCACCATCATGCTGCTGCCTCTGACCTGGCT GAGCAAGAAACACATGATCTGGATCAACACCACCACGCACAGCCTGATCATCAGCATCATCCCTCTGC TGTTCTTCAACCAGATCAACAACAACCTGTTCAGCTGCAGCCCCACCTTCAGCAGCGACCCTCTGACA ACACCTCTGCTGATGCTGACCACCTGGCTGCTGCCCCTCACAATCATGGCCTCTCAGAGACACCTGA GCAGCGAGCCCCTGAGCCGGAAGAAACTGTACCTGAGCATGCTGATCTCCCTGCAGATCTCTCTGAT CATGACCTTCACCGCCACCGAGCTGATCATGTTCTACATCTTTTTCGAGACAACGCTGATCCCCACACT GGCCATCATCACCAGATGGGGCAACCAGCCTGAGAGACTGAACGCCGGCACCTACTTTCTGTTCTAC ACCCTCGTGGGCAGCCTGCCACTGCTGATTGCCCTGATCTACACCCACAACACCCTGGGCTCCCTGA ACATCCTGCTGCTGACACTGACAGCCCAAGAGCTGAGCAACAGCTGGGCCAACAATCTGATGTGGCT GGCCTACACAATGGCCTTCATGGTCAAGATGCCCCTGTACGGCCTGCACCTGTGGCTGCCTAAAGCT CATGTGGAAGCCCCTATCGCCGGCTCTATGGTGCTGGCTGCAGTGCTGCTGAAACTCGGCGGCTACG GCATGATGCGGCTGACCCTGATTCTGAATCCCCTGACCAAGCACATGGCCTATCCATTTCTGGTGCTG AGCCTGTGGGGCATGATTATGACCAGCAGCATCTGCCTGCGGCAGACCGATCTGAAGTCCCTGATCG CCTACAGCTCCATCAGCCACATGGCCCTGGTGGTCACCGCCATCCTGATTCAGACCCCTTGGAGCTTT ACAGGCGCCGTGATCCTGATGATTGCCCACGGCCTGACAAGCAGCCTGCTGTTTTGTCTGGCCAACA GCAACTACGAGCGGACCCACAGCAGAATCATGATCCTGTCTCAGGGCCTGCAGACCCTCCTGCCTCT TATGGCTTTTTGGTGGCTGCTGGCCTCTCTGGCCAATCTGGCACTGCCTCCTACCATCAATCTGCTGG GCGAGCTGAGCGTGCTGGTCACCACATTCAGCTGGTCCAATATCACCCTGCTGCTCACCGGCCTGAA CATGCTGGTTACAGCCCTGTACTCCCTGTACATGTTCACCACCACACAGTGGGGAAGCCTGACACACC ACATCAACAATATGAAGCCCAGCTTCACCCGCGAGAACACCCTGATGTTCATGCATCTGAGCCCCATT CTGCTGCTGTCCCTGAATCCTGATATCATCACCGGCTTCTCCAGCTGAGAGCACTGGGACGCCCACC GCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTG GGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTAAATAT TACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTT CCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGG GGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACTCCACATG CCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGA GCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGG TTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTG TGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCAGCCCCTGTCC TCCCTTCACCCCCATTGCGTATGAGCATTTCAGAACTCCAAGGAGTCACAGGCATCTTTATAGTTCACG TTAACATATAGACACTGTTGGAAGCAGTTCCTTCTAAAAGGGTAGCCCTGGACTTAATACCAGCCGGAT ACCTCTGGCCCCCACCCCATTACTGTACCTCTGGAGTCACTACTGTGGGTCGCCACTCCTCTGCTACA CAGCACGGCTTTTTCAAGGCTGTATTGAGAAGGGAAGTTAGGAAGAAGGGTGTGCTGGGCTAACCAG CCCACAGAGCTCACATTCCTGTCCCTTGGGTGAAAAATACATGTCCATCCTGATATCTCCTGAATTCAG AAATTAGCCTCCACATGTGCAATGGCTTTAAGAGCCAGAAGCAGGGTTCTGGGAATTTTGCAAGTTAC CTGTGGCCAGGTGTGGTCTCGGTTACCAAATACGGTTACCTGCAGCTTTTTAGTCCTTTGTGCTCCCA CGGGTCTACAGAGTCCCATCTGCCCAAAGGTCTTGAAGCTTGACAGGATGTTTTCGATTACTCAGTCT CCCAGGGCACTACTGGTCCGTAGGATTCGATTGGTCGGGGTAGGAGAGTTAAACAACATTTAAACAGA GTTCTCTCAAAAATGTCTAAAGGGATTGTAGGTAGATAACATCCAATCACTGTTTGCACTTATCTGAAAT CTTCCCTCTTGGCTGCCCCCAGGTATTTACTGTGGAGAACATTGCATAGGAATGTCTGGAAAAAGCTT CTACAACTTGTTACAGCCTTCACATTTGTAGAAGCTTT
32	opt_COX10-opt_ND4-3'UTR*	ATGGCCGCCTCTCCACACACACTGAGTAGCAGACTGCTGACCGGCTGTGTTGGCGGCTCTGTGTGGT ATCTGGAACGGCGGACAATGCTGAAGCTGATCGTGCCCACCATCATGCTGCTGCCTCTGACCTGGCT GAGCAAGAAACACATGATCTGGATCAACACCACCACGCACAGCCTGATCATCAGCATCATCCCTCTGC TGTTCTTCAACCAGATCAACAACAACCTGTTCAGCTGCAGCCCCACCTTCAGCAGCGACCCTCTGACA ACACCTCTGCTGATGCTGACCACCTGGCTGCTGCCCCTCACAATCATGGCCTCTCAGAGACACCTGA GCAGCGAGCCCCTGAGCCGGAAGAAACTGTACCTGAGCATGCTGATCTCCCTGCAGATCTCTCTGAT CATGACCTTCACCGCCACCGAGCTGATCATGTTCTACATCTTTTTCGAGACAACGCTGATCCCCACACT GGCCATCATCACCAGATGGGGCAACCAGCCTGAGAGACTGAACGCCGGCACCTACTTTCTGTTCTAC ACCCTCGTGGGCAGCCTGCCACTGCTGATTGCCCTGATCTACACCCACAACACCCTGGGCTCCCTGA ACATCCTGCTGCTGACACTGACAGCCCAAGAGCTGAGCAACAGCTGGGCCAACAATCTGATGTGGCT GGCCTACACAATGGCCTTCATGGTCAAGATGCCCCTGTACGGCCTGCACCTGTGGCTGCCTAAAGCT CATGTGGAAGCCCCTATCGCCGGCTCTATGGTGCTGGCTGCAGTGCTGCTGAAACTCGGCGGCTACG GCATGATGCGGCTGACCCTGATTCTGAATCCCCTGACCAAGCACATGGCCTATCCATTTCTGGTGCTG AGCCTGTGGGGCATGATTATGACCAGCAGCATCTGCCTGCGGCAGACCGATCTGAAGTCCCTGATCG CCTACAGCTCCATCAGCCACATGGCCCTGGTGGTCACCGCCATCCTGATTCAGACCCCTTGGAGCTTT ACAGGCGCCGTGATCCTGATGATTGCCCACGGCCTGACAAGCAGCCTGCTGTTTTGTCTGGCCAACA GCAACTACGAGCGGACCCACAGCAGAATCATGATCCTGTCTCAGGGCCTGCAGACCCTCCTGCCTCT TATGGCTTTTTGGTGGCTGCTGGCCTCTCTGGCCAATCTGGCACTGCCTCCTACCATCAATCTGCTGG GCGAGCTGAGCGTGCTGGTCACCACATTCAGCTGGTCCAATATCACCCTGCTGCTCACCGGCCTGAA CATGCTGGTTACAGCCCTGTACTCCCTGTACATGTTCACCACCACACAGTGGGGAAGCCTGACACACC ACATCAACAATATGAAGCCCAGCTTCACCCGCGAGAACACCCTGATGTTCATGCATCTGAGCCCCATT CTGCTGCTGTCCCTGAATCCTGATATCATCACCGGCTTCTCCAGCTGAGAGCACTGGGACGCCCACC GCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTG GGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTAAATAT TACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTT CCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGG GGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACTCCACATG CCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGA GCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGG TTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTG TGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCA

33	opt_COX10-opt_ND4*-3'UTR	ATGGCCGCCTCTCCACACACACTGAGTAGCAGACTGCTGACCGGCTGTGTTGGCGGCTCTGTGTGGT ATCTGGAACGGCGGACAATGCTGAAGCTGATCGTGCCCACCATCATGCTGCTGCCCCTGACCTGGCT GAGCAAGAAGCACATGATCTGGATCAACACCACCACCCACAGCCTGATCATCAGCATCATCCCCCTGC TGTTCTTCAACCAGATCAACAACAACCTGTTCAGCTGCAGCCCCACCTTCAGCAGCGACCCCCTGACC ACCCCCCTGCTGATGCTGACCACCTGGCTGCTGCCCCTGACCATCATGGCCAGCCAGCGCCACCTGA GCAGCGAGCCCCTGAGCCGCAAGAAGCTGTACCTGAGCATGCTGATCAGCCTGCAGATCAGCCTGAT CATGACCTTCACCGCCACCGAGCTGATCATGTTCTACATCTTCTTCGAGACCACCCTGATCCCCACCC TGGCCATCATCACCCGCTGGGGCAACCAGCCCGAGCGCCTGAACGCCGGCACCTACTTCCTGTTCTA CACCCTGGTGGGCAGCCTGCCCCTGCTGATCGCCCTGATCTACACCCACAACACCCTGGGCAGCCTG AACATCCTGCTGCTGACCCTGACCGCCCAGGAGCTGAGCAACAGCTGGGCCAACAACCTGATGTGGC TGGCCTACACCATGGCCTTCATGGTGAAGATGCCCCTGTACGGCCTGCACCTGTGGCTGCCCAAGGC CCACGTGGAGGCCCCCATCGCCGGCAGCATGGTGCTGGCCGCCGTGCTGCTGAAGCTGGGCGGCTA CGGCATGATGCGCCTGACCCTGATCCTGAACCCCCTGACCAAGCACATGGCCTACCCCTTCCTGGTG CTGAGCCTGTGGGGCATGATCATGACCAGCAGCATCTGCCTGCGCCAGACCGACCTGAAGAGCCTGA TCGCCTACAGCAGCATCAGCCACATGGCCCTGGTGGTGACCGCCATCCTGATCCAGACCCCCTGGAG CTTCACCGGCGCCGTGATCCTGATGATCGCCCACGGCCTGACCAGCAGCCTGCTGTTCTGCCTGGCC AACAGCAACTACGAGCGCACCCACAGCCGCATCATGATCCTGAGCCAGGGCCTGCAGACCCTGCTGC CCCTGATGGCCTTCTGGTGGCTGCTGGCCAGCCTGGCCAACCTGGCCCTGCCCCCCACCATCAACCT GCTGGGCGAGCTGAGCGTGCTGGTGACCACCTTCAGCTGGAGCAACATCACCCTGCTGCTGACCGG CCTGAACATGCTGGTGACCGCCCTGTACAGCCTGTACATGTTCACCACCACCCAGTGGGGCAGCCTG ACCCACCACATCAACAACATGAAGCCCAGCTTCACCCGCGAGAACACCCTGATGTTCATGCACCTGAG CCCCATCCTGCTGCTGAGCCTGAACCCCGACATCATCACCGGCTTCAGCAGCTAAGAGCACTGGGAC GCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGA AATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTT TTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGA ATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCC TCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACT CCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGT TCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCA TTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCG GCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCAGCC CCTGTCCTCCCTTCACCCCCATTGCGTATGAGCATTTCAGAACTCCAAGGAGTCACAGGCATCTTTATA GTTCACGTTAACATATAGACACTGTTGGAAGCAGTTCCTTCTAAAAGGGTAGCCCTGGACTTAATACCA GCCGGATACCTCTGGCCCCCACCCCATTACTGTACCTCTGGAGTCACTACTGTGGGTCGCCACTCCT CTGCTACACAGCACGGCTTTTTCAAGGCTGTATTGAGAAGGGAAGTTAGGAAGAAGGGTGTGCTGGG CTAACCAGCCCACAGAGCTCACATTCCTGTCCCTTGGGTGAAAAATACATGTCCATCCTGATATCTCCT GAATTCAGAAATTAGCCTCCACATGTGCAATGGCTTTAAGAGCCAGAAGCAGGGTTCTGGGAATTTTG CAAGTTACCTGTGGCCAGGTGTGGTCTCGGTTACCAAATACGGTTACCTGCAGCTTTTTAGTCCTTTGT GCTCCCACGGGTCTACAGAGTCCCATCTGCCCAAAGGTCTTGAAGCTTGACAGGATGTTTTCGATTAC TCAGTCTCCCAGGGCACTACTGGTCCGTAGGATTCGATTGGTCGGGGTAGGAGAGTTAAACAACATTT AAACAGAGTTCTCTCAAAAATGTCTAAAGGGATTGTAGGTAGATAACATCCAATCACTGTTTGCACTTAT CTGAAATCTTCCCTCTTGGCTGCCCCCAGGTATTTACTGTGGAGAACATTGCATAGGAATGTCTGGAA AAAGCTTCTACAACTTGTTACAGCCTTCACATTTGTAGAAGCTTT
34	opt_COX10-opt_ND4*-3'UTR*	ATGGCCGCCTCTCCACACACACTGAGTAGCAGACTGCTGACCGGCTGTGTTGGCGGCTCTGTGTGGT ATCTGGAACGGCGGACAATGCTGAAGCTGATCGTGCCCACCATCATGCTGCTGCCCCTGACCTGGCT GAGCAAGAAGCACATGATCTGGATCAACACCACCACCCACAGCCTGATCATCAGCATCATCCCCCTGC TGTTCTTCAACCAGATCAACAACAACCTGTTCAGCTGCAGCCCCACCTTCAGCAGCGACCCCCTGACC ACCCCCCTGCTGATGCTGACCACCTGGCTGCTGCCCCTGACCATCATGGCCAGCCAGCGCCACCTGA GCAGCGAGCCCCTGAGCCGCAAGAAGCTGTACCTGAGCATGCTGATCAGCCTGCAGATCAGCCTGAT CATGACCTTCACCGCCACCGAGCTGATCATGTTCTACATCTTCTTCGAGACCACCCTGATCCCCACCC TGGCCATCATCACCCGCTGGGGCAACCAGCCCGAGCGCCTGAACGCCGGCACCTACTTCCTGTTCTA CACCCTGGTGGGCAGCCTGCCCCTGCTGATCGCCCTGATCTACACCCACAACACCCTGGGCAGCCTG AACATCCTGCTGCTGACCCTGACCGCCCAGGAGCTGAGCAACAGCTGGGCCAACAACCTGATGTGGC TGGCCTACACCATGGCCTTCATGGTGAAGATGCCCCTGTACGGCCTGCACCTGTGGCTGCCCAAGGC CCACGTGGAGGCCCCCATCGCCGGCAGCATGGTGCTGGCCGCCGTGCTGCTGAAGCTGGGCGGCTA CGGCATGATGCGCCTGACCCTGATCCTGAACCCCCTGACCAAGCACATGGCCTACCCCTTCCTGGTG CTGAGCCTGTGGGGCATGATCATGACCAGCAGCATCTGCCTGCGCCAGACCGACCTGAAGAGCCTGA TCGCCTACAGCAGCATCAGCCACATGGCCCTGGTGGTGACCGCCATCCTGATCCAGACCCCCTGGAG CTTCACCGGCGCCGTGATCCTGATGATCGCCCACGGCCTGACCAGCAGCCTGCTGTTCTGCCTGGCC AACAGCAACTACGAGCGCACCCACAGCCGCATCATGATCCTGAGCCAGGGCCTGCAGACCCTGCTGC CCCTGATGGCCTTCTGGTGGCTGCTGGCCAGCCTGGCCAACCTGGCCCTGCCCCCCACCATCAACCT GCTGGGCGAGCTGAGCGTGCTGGTGACCACCTTCAGCTGGAGCAACATCACCCTGCTGCTGACCGG CCTGAACATGCTGGTGACCGCCCTGTACAGCCTGTACATGTTCACCACCACCCAGTGGGGCAGCCTG ACCCACCACATCAACAACATGAAGCCCAGCTTCACCCGCGAGAACACCCTGATGTTCATGCACCTGAG CCCCATCCTGCTGCTGAGCCTGAACCCCGACATCATCACCGGCTTCAGCAGCTAAGAGCACTGGGAC GCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGA AATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTT TTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGA ATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCC TCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACT CCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGT TCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCA TTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCG GCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCA

35	opt_COX10-ND6-3'UTR	ATGGCCGCCTCTCCACACACACTGAGTAGCAGACTGCTGACCGGCTGTGTTGGCGGCTCTGTGTGGT ATCTGGAACGGCGGACAATGATGTATGCTTTGTTTCTGTTGAGTGTGGGTTTAGTAATGGGGTTTGTG GGGTTTTCTTCTAAGCCTTCTCCTATTTATGGGGGTTTAGTATTGATTGTTAGCGGTGTGGTCGGGTGT GTTATTATTCTGAATTTTGGGGGAGGTTATATGGGTTTAATGGTTTTTTTAATTTATTTAGGGGGAATGA TGGTTGTCTTTGGATATACTACAGCGATGGCTATTGAGGAGTATCCTGAGGCATGGGGGTCAGGGGTT GAGGTCTTGGTGAGTGTTTTAGTGGGGTTAGCGATGGAGGTAGGATTGGTGCTGTGGGTGAAAGAGT ATGATGGGGTGGTGGTTGTGGTAAACTTTAATAGTGTAGGAAGCTGGATGATTTATGAAGGAGAGGGG TCAGGGTTGATTCGGGAGGATCCTATTGGTGCGGGGGCTTTGTATGATTATGGGCGTTGGTTAGTAGT AGTTACTGGTTGGACATTGTTTGTTGGTGTATATATTGTAATTGAGATTGCTCGGGGGAATTAGGAGCA CTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAA GAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTT TTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAA AAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTT CTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACA CGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTG TCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAG GGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCT AGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGAC TGCCAGCCCCTGTCCTCCCTTCACCCCCATTGCGTATGAGCATTTCAGAACTCCAAGGAGTCACAGGC ATCTTTATAGTTCACGTTAACATATAGACACTGTTGGAAGCAGTTCCTTCTAAAAGGGTAGCCCTGGAC TTAATACCAGCCGGATACCTCTGGCCCCCACCCCATTACTGTACCTCTGGAGTCACTACTGTGGGTCG CCACTCCTCTGCTACACAGCACGGCTTTTTCAAGGCTGTATTGAGAAGGGAAGTTAGGAAGAAGGGTG TGCTGGGCTAACCAGCCCACAGAGCTCACATTCCTGTCCCTTGGGTGAAAAATACATGTCCATCCTGA TATCTCCTGAATTCAGAAATTAGCCTCCACATGTGCAATGGCTTTAAGAGCCAGAAGCAGGGTTCTGG GAATTTTGCAAGTTACCTGTGGCCAGGTGTGGTCTCGGTTACCAAATACGGTTACCTGCAGCTTTTTAG TCCTTTGTGCTCCCACGGGTCTACAGAGTCCCATCTGCCCAAAGGTCTTGAAGCTTGACAGGATGTTT TCGATTACTCAGTCTCCCAGGGCACTACTGGTCCGTAGGATTCGATTGGTCGGGGTAGGAGAGTTAAA CAACATTTAAACAGAGTTCTCTCAAAAATGTCTAAAGGGATTGTAGGTAGATAACATCCAATCACTGTTT GCACTTATCTGAAATCTTCCCTCTTGGCTGCCCCCAGGTATTTACTGTGGAGAACATTGCATAGGAATG TCTGGAAAAAGCTTCTACAACTTGTTACAGCCTTCACATTTGTAGAAGCTTT
36	opt_COX10-ND6-3'UTR*	ATGGCCGCCTCTCCACACACACTGAGTAGCAGACTGCTGACCGGCTGTGTTGGCGGCTCTGTGTGGT ATCTGGAACGGCGGACAATGATGTATGCTTTGTTTCTGTTGAGTGTGGGTTTAGTAATGGGGTTTGTG GGGTTTTCTTCTAAGCCTTCTCCTATTTATGGGGGTTTAGTATTGATTGTTAGCGGTGTGGTCGGGTGT GTTATTATTCTGAATTTTGGGGGAGGTTATATGGGTTTAATGGTTTTTTTAATTTATTTAGGGGGAATGA TGGTTGTCTTTGGATATACTACAGCGATGGCTATTGAGGAGTATCCTGAGGCATGGGGGTCAGGGGTT GAGGTCTTGGTGAGTGTTTTAGTGGGGTTAGCGATGGAGGTAGGATTGGTGCTGTGGGTGAAAGAGT ATGATGGGGTGGTGGTTGTGGTAAACTTTAATAGTGTAGGAAGCTGGATGATTTATGAAGGAGAGGGG TCAGGGTTGATTCGGGAGGATCCTATTGGTGCGGGGGCTTTGTATGATTATGGGCGTTGGTTAGTAGT AGTTACTGGTTGGACATTGTTTGTTGGTGTATATATTGTAATTGAGATTGCTCGGGGGAATTAGGAGCA CTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAA GAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTT TTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAA AAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTT CTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACA CGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTG TCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAG GGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCT AGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGAC TGCCA
37	opt_COX10-opt_ND6-3'UTR	ATGGCCGCCTCTCCACACACACTGAGTAGCAGACTGCTGACCGGCTGTGTTGGCGGCTCTGTGTGGT ATCTGGAACGGCGGACAATGATGTACGCCCTGTTCCTGCTGAGCGTGGGCCTGGTGATGGGCTTCGT GGGCTTCAGCAGCAAGCCCAGCCCCATCTACGGCGGCCTGGTGCTGATCGTGAGCGGCGTGGTGGG CTGCGTGATCATCCTGAACTTCGGCGGCGGCTACATGGGCCTGATGGTGTTCCTGATCTACCTGGGC GGCATGATGGTGGTGTTCGGCTACACCACCGCCATGGCCATCGAGGAGTACCCCGAGGCCTGGGGC AGCGGCGTGGAGGTGCTGGTGAGCGTGCTGGTGGGCCTGGCCATGGAGGTGGGCCTGGTGCTGTG GGTGAAGGAGTACGACGGCGTGGTGGTGGTGGTGAACTTCAACAGCGTGGGCAGCTGGATGATCTA CGAGGGCGAGGGCAGCGGCCTGATCCGCGAGGACCCCATCGGCGCCGGCGCCCTGTACGACTACG GCCGCTGGCTGGTGGTGGTGACCGGCTGGACCCTGTTCGTGGGCGTGTACATCGTGATCGAGATCG CCCGCGGCAACTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTT GTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCT CAGTGATCACTTGACAGTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCA GCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAAC CCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCA TCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTG TGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCT TCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTT CTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTG GGAGTCTCAAGCTGGACTGCCAGCCCCTGTCCTCCCTTCACCCCCATTGCGTATGAGCATTTCAGAAC TCCAAGGAGTCACAGGCATCTTTATAGTTCACGTTAACATATAGACACTGTTGGAAGCAGTTCCTTCTA AAAGGGTAGCCCTGGACTTAATACCAGCCGGATACCTCTGGCCCCCACCCCATTACTGTACCTCTGGA GTCACTACTGTGGGTCGCCACTCCTCTGCTACACAGCACGGCTTTTTCAAGGCTGTATTGAGAAGGGA AGTTAGGAAGAAGGGTGTGCTGGGCTAACCAGCCCACAGAGCTCACATTCCTGTCCCTTGGGTGAAA AATACATGTCCATCCTGATATCTCCTGAATTCAGAAATTAGCCTCCACATGTGCAATGGCTTTAAGAGC CAGAAGCAGGGTTCTGGGAATTTTGCAAGTTACCTGTGGCCAGGTGTGGTCTCGGTTACCAAATACGG

		TTACCTGCAGCTTTTTAGTCCTTTGTGCTCCCACGGGTCTACAGAGTCCCATCTGCCCAAAGGTCTTGA AGCTTGACAGGATGTTTTCGATTACTCAGTCTCCCAGGGCACTACTGGTCCGTAGGATTCGATTGGTC GGGGTAGGAGAGTTAAACAACATTTAAACAGAGTTCTCTCAAAAATGTCTAAAGGGATTGTAGGTAGAT AACATCCAATCACTGTTTGCACTTATCTGAAATCTTCCCTCTTGGCTGCCCCCAGGTATTTACTGTGGA GAACATTGCATAGGAATGTCTGGAAAAAGCTTCTACAACTTGTTACAGCCTTCACATTTGTAGAAGCTT T
38	opt_COX10- opt_ND6- 3'UTR*	ATGGCCGCCTCTCCACACACACTGAGTAGCAGACTGCTGACCGGCTGTGTTGGCGGCTCTGTGTGGT ATCTGGAACGGCGGACAATGATGTACGCCCTGTTCCTGCTGAGCGTGGGCCTGGTGATGGGCTTCGT GGGCTTCAGCAGCAAGCCCAGCCCCATCTACGGCGGCCTGGTGCTGATCGTGAGCGGCGTGGTGGG CTGCGTGATCATCCTGAACTTCGGCGGCGGCTACATGGGCCTGATGGTGTTCCTGATCTACCTGGGC GGCATGATGGTGGTGTTCGGCTACACCACCGCCATGGCCATCGAGGAGTACCCCGAGGCCTGGGGC AGCGGCGTGGAGGTGCTGGTGAGCGTGCTGGTGGGCCTGGCCATGGAGGTGGGCCTGGTGCTGTG GGTGAAGGAGTACGACGGCGTGGTGGTGGTGGTGAACTTCAACAGCGTGGGCAGCTGGATGATCTA CGAGGGCGAGGGCAGCGGCCTGATCCGCGAGGACCCCATCGGCGCCGGCGCCCTGTACGACTACG GCCGCTGGCTGGTGGTGGTGACCGGCTGGACCCTGTTCGTGGGCGTGTACATCGTGATCGAGATCG CCCGCGGCAACTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTT GTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCT CAGTGATCACTTGACAGTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCA GCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAAC CCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCA TCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTG TGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCT TCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTT CTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTG GGAGTCTCAAGCTGGACTGCCA
39	opt_COX10- ND1-3'UTR	ATGGCCGCCTCTCCACACACACTGAGTAGCAGACTGCTGACCGGCTGTGTTGGCGGCTCTGTGTGGT ATCTGGAACGGCGGACAATGGCCAACCTCCTACTCCTCATTGTACCCATTCTAATCGCAATGGCATTC CTAATGCTTACCGAACGAAAAATTCTAGGCTATATGCAACTACGCAAAGGCCCCAACGTTGTAGGCCC CTACGGGCTACTACAACCCTTCGCTGACGCCATAAAACTCTTCACCAAAGAGCCCCTAAAACCCGCCA CATCTACCATCACCCTCTACATCACCGCCCCGACCTTAGCTCTCACCATCGCTCTTCTACTATGGACCC CCCTCCCCATGCCCAACCCCCTGGTCAACCTCAACCTAGGCCTCCTATTTATTCTAGCCACCTCTAGC CTAGCCGTTTACTCAATCCTCTGGTCAGGGTGGGCATCAAACTCAAACTACGCCCTGATCGGCGCACT GCGAGCAGTAGCCCAAACAATCTCATATGAAGTCACCCTAGCCATCATTCTACTATCAACATTACTAAT GAGTGGCTCCTTTAACCTCTCCACCCTTATCACAACACAAGAACACCTCTGGTTACTCCTGCCATCATG GCCCTTGGCCATGATGTGGTTTATCTCCACACTAGCAGAGACCAACCGAACCCCCTTCGACCTTGCCG AAGGGGAGTCCGAACTAGTCTCAGGCTTCAACATCGAATACGCCGCAGGCCCCTTCGCCCTATTCTTC ATGGCCGAATACACAAACATTATTATGATGAACACCCTCACCACTACAATCTTCCTAGGAACAACATAT GACGCACTCTCCCCTGAACTCTACACAACATATTTTGTCACCAAGACCCTACTTCTAACCTCCCTGTTC TTATGGATTCGAACAGCATACCCCCGATTCCGCTACGACCAACTCATGCACCTCCTATGGAAAAACTTC CTACCACTCACCCTAGCATTACTTATGTGGTATGTCTCCATGCCCATTACAATCTCCAGCATTCCCCCT CAAACCTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTA ATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGA TCACTTGACAGTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAG TCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACC CTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTAC CACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCT CATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGT GACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAA TACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTC TCAAGCTGGACTGCCAGCCCCTGTCCTCCCTTCACCCCCATTGCGTATGAGCATTTCAGAACTCCAAG GAGTCACAGGCATCTTTATAGTTCACGTTAACATATAGACACTGTTGGAAGCAGTTCCTTCTAAAAGGG TAGCCCTGGACTTAATACCAGCCGGATACCTCTGGCCCCCACCCCATTACTGTACCTCTGGAGTCACT ACTGTGGGTCGCCACTCCTCTGCTACACAGCACGGCTTTTTCAAGGCTGTATTGAGAAGGGAAGTTAG GAAGAAGGGTGTGCTGGGCTAACCAGCCCACAGAGCTCACATTCCTGTCCCTTGGGTGAAAAATACAT GTCCATCCTGATATCTCCTGAATTCAGAAATTAGCCTCCACATGTGCAATGGCTTTAAGAGCCAGAAGC AGGGTTCTGGGAATTTTGCAAGTTACCTGTGGCCAGGTGTGGTCTCGGTTACCAAATACGGTTACCTG CAGCTTTTTAGTCCTTTGTGCTCCCACGGGTCTACAGAGTCCCATCTGCCCAAAGGTCTTGAAGCTTG ACAGGATGTTTTCGATTACTCAGTCTCCCAGGGCACTACTGGTCCGTAGGATTCGATTGGTCGGGGTA GGAGAGTTAAACAACATTTAAACAGAGTTCTCTCAAAAATGTCTAAAGGGATTGTAGGTAGATAACATC CAATCACTGTTTGCACTTATCTGAAATCTTCCCTCTTGGCTGCCCCCAGGTATTTACTGTGGAGAACAT TGCATAGGAATGTCTGGAAAAAGCTTCTACAACTTGTTACAGCCTTCACATTTGTAGAAGCTTT

40	opt_COX10-ND1-3'UTR*	ATGGCCGCCTCTCCACACACACTGAGTAGCAGACTGCTGACCGGCTGTGTTGGCGGCTCTGTGTGGT ATCTGGAACGGCGGACAATGGCCAACCTCCTACTCCTCATTGTACCCATTCTAATCGCAATGGCATTC CTAATGCTTACCGAACGAAAAATTCTAGGCTATATGCAACTACGCAAAGGCCCCAACGTTGTAGGCCC CTACGGGCTACTACAACCCTTCGCTGACGCCATAAAACTCTTCACCAAAGAGCCCCTAAAACCCGCCA CATCTACCATCACCCTCTACATCACCGCCCCGACCTTAGCTCTCACCATCGCTCTTCTACTATGGACCC CCCTCCCCATGCCCAACCCCCTGGTCAACCTCAACCTAGGCCTCCTATTTATTCTAGCCACCTCTAGC CTAGCCGTTTACTCAATCCTCTGGTCAGGGTGGGCATCAAACTCAAACTACGCCCTGATCGGCGCACT GCGAGCAGTAGCCCAAACAATCTCATATGAAGTCACCCTAGCCATCATTCTACTATCAACATTACTAAT GAGTGGCTCCTTTAACCTCTCCACCCTTATCACAACACAAGAACACCTCTGGTTACTCCTGCCATCATG GCCCTTGGCCATGATGTGGTTTATCTCCACACTAGCAGAGACCAACCGAACCCCCTTCGACCTTGCCG AAGGGGAGTCCGAACTAGTCTCAGGCTTCAACATCGAATACGCCGCAGGCCCCTTCGCCCTATTCTTC ATGGCCGAATACACAAACATTATTATGATGAACACCCTCACCACTACAATCTTCCTAGGAACAACATAT GACGCACTCTCCCCTGAACTCTACACAACATATTTTGTCACCAAGACCCTACTTCTAACCTCCCTGTTC TTATGGATTCGAACAGCATACCCCCGATTCCGCTACGACCAACTCATGCACCTCCTATGGAAAAACTTC CTACCACTCACCCTAGCATTACTTATGTGGTATGTCTCCATGCCCATTACAATCTCCAGCATTCCCCCT CAAACCTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTA ATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGA TCACTTGACAGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAG TCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACC CTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTAC CACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCT CATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGT GACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAA TACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTC TCAAGCTGGACTGCCA
41	opt_COX10-opt_ND1-3'UTR	ATGGCCGCCTCTCCACACACACTGAGTAGCAGACTGCTGACCGGCTGTGTTGGCGGCTCTGTGTGGT ATCTGGAACGGCGGACAATGGCCAACCTGCTGCTGCTGATCGTGCCCATCCTGATCGCCATGGCCTT CCTGATGCTGACCGAGCGCAAGATCCTGGGCTACATGCAGCTGCGCAAGGGCCCCAACGTGGTGGG CCCCTACGGCCTGCTGCAGCCCTTCGCCGACGCCATCAAGCTGTTCACCAAGGAGCCCCTGAAGCCC GCCACCAGCACCATCACCCTGTACATCACCGCCCCCACCCTGGCCCTGACCATCGCCCTGCTGCTGT GGACCCCCCTGCCCATGCCCAACCCCCTGGTGAACCTGAACCTGGGCCTGCTGTTCATCCTGGCCAC CAGCAGCCTGGCCGTGTACAGCATCCTGTGGAGCGGCTGGGCCAGCAACAGCAACTACGCCCTGAT CGGCGCCCTGCGCGCCGTGGCCCAGACCATCAGCTACGAGGTGACCCTGGCCATCATCCTGCTGAG CACCCTGCTGATGAGCGGCAGCTTCAACCTGAGCACCCTGATCACCACCCAGGAGCACCTGTGGCTG CTGCTGCCCAGCTGGCCCCTGGCCATGATGTGGTTCATCAGCACCCTGGCCGAGACCAACCGCACCC CCTTCGACCTGGCCGAGGGCGAGAGCGAGCTGGTGAGCGGCTTCAACATCGAGTACGCCGCCGGCC CCTTCGCCCTGTTCTTCATGGCCGAGTACACCAACATCATCATGATGAACACCCTGACCACCACCATC TTCCTGGGCACCACCTACGACGCCCTGAGCCCCGAGCTGTACACCACCTACTTCGTGACCAAGACCC TGCTGCTGACCAGCCTGTTCCTGTGGATCCGCACCGCCTACCCCCGCTTCCGCTACGACCAGCTGAT GCACCTGCTGTGGAAGAACTTCCTGCCCCTGACCCTGGCCCTGCTGATGTGGTACGTGAGCATGCCC ATCACCATCAGCAGCATCCCCCCCCAGACCTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCG CTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGAT TATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCC CCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTT TATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACA GCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCA CTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAA GGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACA CATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGG GATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCAGCCCCTGTCCTCCCTTCACCCCCATT GCGTATGAGCATTTCAGAACTCCAAGGAGTCACAGGCATCTTTATAGTTCACGTTAACATATAGACACT GTTGGAAGCAGTTCCTTCTAAAAGGGTAGCCCTGGACTTAATACCAGCCGGATACCTCTGGCCCCCAC CCCATTACTGTACCTCTGGAGTCACTACTGTGGGTCGCCACTCCTCTGCTACACAGCACGGCTTTTTC AAGGCTGTATTGAGAAGGGAAGTTAGGAAGAAGGGTGTGCTGGGCTAACCAGCCCACAGAGCTCACA TTCCTGTCCCTTGGGTGAAAAATACATGTCCATCCTGATATCTCCTGAATTCAGAAATTAGCCTCCACA TGTGCAATGGCTTTAAGAGCCAGAAGCAGGGTTCTGGGAATTTTGCAAGTTACCTGTGGCCAGGTGTG GTCTCGGTTACCAAATACGGTTACCTGCAGCTTTTTAGTCCTTTGTGCTCCCACGGGTCTACAGAGTC CCATCTGCCCAAAGGTCTTGAAGCTTGACAGGATGTTTTCGATTACTCAGTCTCCCAGGGCACTACTG GTCCGTAGGATTCGATTGGTCGGGGTAGGAGAGTTAAACAACATTTAAACAGAGTTCTCTCAAAAATGT CTAAAGGGATTGTAGGTAGATAACATCCAATCACTGTTTGCACTTATCTGAAATCTTCCCTCTTGGCTG CCCCCAGGTATTTACTGTGGAGAACATTGCATAGGAATGTCTGGAAAAAGCTTCTACAACTTGTTACAG CCTTCACATTTGTAGAAGCTTT

42	opt_COX10-opt_ND1-3'UTR*	ATGGCCGCCTCTCCACACACACTGAGTAGCAGACTGCTGACCGGCTGTGTTGGCGGCTCTGTGTGGT ATCTGGAACGGCGGACAATGGCCAACCTGCTGCTGCTGATCGTGCCCATCCTGATCGCCATGGCCTT CCTGATGCTGACCGAGCGCAAGATCCTGGGCTACATGCAGCTGCGCAAGGGCCCCAACGTGGTGGG CCCCTACGGCCTGCTGCAGCCCTTCGCCGACGCCATCAAGCTGTTCACCAAGGAGCCCCTGAAGCCC GCCACCAGCACCATCACCCTGTACATCACCGCCCCCACCCTGGCCCTGACCATCGCCCTGCTGCTGT GGACCCCCCTGCCCATGCCCAACCCCCTGGTGAACCTGAACCTGGGCCTGCTGTTCATCCTGGCCAC CAGCAGCCTGGCCGTGTACAGCATCCTGTGGAGCGGCTGGGCCAGCAACAGCAACTACGCCCTGAT CGGCGCCCTGCGCGCCGTGGCCCAGACCATCAGCTACGAGGTGACCCTGGCCATCATCCTGCTGAG CACCCTGCTGATGAGCGGCAGCTTCAACCTGAGCACCCTGATCACCACCCAGGAGCACCTGTGGCTG CTGCTGCCCAGCTGGCCCCTGGCCATGATGTGGTTCATCAGCACCCTGGCCGAGACCAACCGCACCC CCTTCGACCTGGCCGAGGGCGAGAGCGAGCTGGTGAGCGGCTTCAACATCGAGTACGCCGCCGGCC CCTTCGCCCTGTTCTTCATGGCCGAGTACACCAACATCATCATGATGAACACCCTGACCACCACCATC TTCCTGGGCACCACCTACGACGCCCTGAGCCCCGAGCTGTACACCACCTACTTCGTGACCAAGACCC TGCTGCTGACCAGCCTGTTCCTGTGGATCCGCACCGCCTACCCCCGCTTCCGCTACGACCAGCTGAT GCACCTGCTGTGGAAGAACTTCCTGCCCCTGACCCTGGCCCTGCTGATGTGGTACGTGAGCATGCCC ATCACCATCAGCAGCATCCCCCCCCAGACCTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCG CTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGAT TATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCC CCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTT TATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACA GCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCA CTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAA GGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACA CATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGG GATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCA
43	opt_COX10*-ND4-3'UTR	ATGGCCGCCAGCCCCCACACCCTGAGCAGCCGCCTGCTGACCGGCTGCGTGGGCGGCAGCGTGTG GTACCTGGAGCGCCGCACCATGCTAAAACTAATCGTCCCAACAATTATGTTACTACCACTGACATGGC TTTCCAAAAAACACATGATTTGGATCAACACAACCACCCACAGCCTAATTATTAGCATCATCCCTCTACT ATTTTTTAACCAAATCAACAACAACCTATTTAGCTGTTCCCCAACCTTTTCCTCCGACCCCCTAACAACC CCCCTCCTAATGCTAACTACCTGGCTCCTACCCCTCACAATCATGGCAAGCCAACGCCACTTATCCAG TGAACCACTATCACGAAAAAAACTCTACCTCTCTATGCTAATCTCCCTACAAATCTCCTTAATTATGACA TTCACAGCCACAGAACTAATCATGTTTTATATCTTCTTCGAAACCACACTTATCCCCACCTTGGCTATCA TCACCCGATGGGGCAACCAGCCAGAACGCCTGAACGCAGGCACATACTTCCTATTCTACACCCTAGTA GGCTCCCTTCCCCTACTCATCGCACTAATTTACACTCACAACACCCTAGGCTCACTAAACATTCTACTA CTCACTCTCACTGCCCAAGAACTATCAAACTCCTGGGCCAACAACTTAATGTGGCTAGCTTACACAATG GCTTTTATGGTAAAGATGCCTCTTTACGGACTCCACTTATGGCTCCCTAAAGCCCATGTCGAAGCCCC CATCGCTGGGTCAATGGTACTTGCCGCAGTACTCTTAAAACTAGGCGGCTATGGTATGATGCGCCTCA CACTCATTCTCAACCCCCTGACAAAACACATGGCCTACCCCTTCCTTGTACTATCCCTATGGGGCATGA TTATGACAAGCTCCATCTGCCTACGACAAACAGACCTAAAATCGCTCATTGCATACTCTTCAATCAGCC ACATGGCCCTCGTAGTAACAGCCATTCTCATCCAAACCCCCTGGAGCTTCACCGGCGCAGTCATTCTC ATGATCGCCCACGGGCTTACATCCTCATTACTATTCTGCCTAGCAAACTCAAACTACGAACGCACTCAC AGTCGCATCATGATCCTCTCTCAAGGACTTCAAACTCTACTCCCACTAATGGCTTTTTGGTGGCTTCTA GCAAGCCTCGCTAACCTCGCCTTACCCCCCACTATTAACCTACTGGGAGAACTCTCTGTGCTAGTAAC CACGTTCTCCTGGTCAAATATCACTCTCCTACTTACAGGACTCAACATGCTAGTCACAGCCCTATACTC CCTCTACATGTTTACCACAACACAATGGGGCTCACTCACCCACCACATTAACAACATGAAACCCTCATT CACACGAGAAAACACCCTCATGTTCATGCACCTATCCCCCATTCTCCTCCTATCCCTCAACCCCGACAT CATTACCGGGTTTTCCTCTTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGA GCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATT CGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAA ATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCT CCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTT TGGTTCCATCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCC AGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAG CACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACC ATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATG TTTGCCTTGGGAGTCTCAAGCTGGACTGCCAGCCCCTGTCCTCCCTTCACCCCCATTGCGTATGAGCA TTTCAGAACTCCAAGGAGTCACAGGCATCTTTATAGTTCACGTTAACATATAGACACTGTTGGAAGCAG TTCCTTCTAAAAGGGTAGCCCTGGACTTAATACCAGCCGGATACCTCTGGCCCCCACCCCATTACTGT ACCTCTGGAGTCACTACTGTGGGTCGCCACTCCTCTGCTACACAGCACGGCTTTTTCAAGGCTGTATT GAGAAGGGAAGTTAGGAAGAAGGGTGTGCTGGGCTAACCAGCCCACAGAGCTCACATTCCTGTCCCT TGGGTGAAAAATACATGTCCATCCTGATATCTCCTGAATTCAGAAATTAGCCTCCACATGTGCAATGGC TTTAAGAGCCAGAAGCAGGGTTCTGGGAATTTTGCAAGTTACCTGTGGCCAGGTGTGGTCTCGGTTAC CAAATACGGTTACCTGCAGCTTTTTAGTCCTTTGTGCTCCCACGGGTCTACAGAGTCCCATCTGCCCA AAGGTCTTGAAGCTTGACAGGATGTTTTCGATTACTCAGTCTCCCAGGGCACTACTGGTCCGTAGGAT TCGATTGGTCGGGGTAGGAGAGTTAAACAACATTTAAACAGAGTTCTCTCAAAAATGTCTAAAGGGATT GTAGGTAGATAACATCCAATCACTGTTTGCACTTATCTGAAATCTTCCCTCTTGGCTGCCCCCAGGTAT TTACTGTGGAGAACATTGCATAGGAATGTCTGGAAAAAGCTTCTACAACTTGTTACAGCCTTCACATTT GTAGAAGCTTT

44	opt_COX10*- ND4-3'UTR*	ATGGCCGCCAGCCCCCACACCCTGAGCAGCCGCCTGCTGACCGGCTGCGTGGGCGGCAGCGTGTG GTACCTGGAGCGCCGCACCATGCTAAAACTAATCGTCCCAACAATTATGTTACTACCACTGACATGGC TTTCCAAAAAACACATGATTTGGATCAACACAACCACCCACAGCCTAATTATTAGCATCATCCCTCTACT ATTTTTTAACCAAATCAACAACAACCTATTTAGCTGTTCCCCAACCTTTTCCTCCGACCCCCTAACAACC CCCCTCCTAATGCTAACTACCTGGCTCCTACCCCTCACAATCATGGCAAGCCAACGCCACTTATCCAG TGAACCACTATCACGAAAAAAACTCTACCTCTCTATGCTAATCTCCCTACAAATCTCCTTAATTATGACA TTCACAGCCACAGAACTAATCATGTTTTATATCTTCTTCGAAACCACACTTATCCCCACCTTGGCTATCA TCACCCGATGGGGCAACCAGCCAGAACGCCTGAACGCAGGCACATACTTCCTATTCTACACCCTAGTA GGCTCCCTTCCCCTACTCATCGCACTAATTTACACTCACAACACCCTAGGCTCACTAAACATTCTACTA CTCACTCTCACTGCCCAAGAACTATCAAACTCCTGGGCCAACAACTTAATGTGGCTAGCTTACACAATG GCTTTTATGGTAAAGATGCCTCTTTACGGACTCCACTTATGGCTCCCTAAAGCCCATGTCGAAGCCCC CATCGCTGGGTCAATGGTACTTGCCGCAGTACTCTTAAAACTAGGCGGCTATGGTATGATGCGCCTCA CACTCATTCTCAACCCCCTGACAAAACACATGGCCTACCCCTTCCTTGTACTATCCCTATGGGGCATGA TTATGACAAGCTCCATCTGCCTACGACAAACAGACCTAAAATCGCTCATTGCATACTCTTCAATCAGCC ACATGGCCCTCGTAGTAACAGCCATTCTCATCCAAACCCCCTGGAGCTTCACCGGCGCAGTCATTCTC ATGATCGCCCACGGGCTTACATCCTCATTACTATTCTGCCTAGCAAACTCAAACTACGAACGCACTCAC AGTCGCATCATGATCCTCTCTCAAGGACTTCAAACTCTACTCCCACTAATGGCTTTTTGGTGGCTTCTA GCAAGCCTCGCTAACCTCGCCTTACCCCCCACTATTAACCTACTGGGAGAACTCTCTGTGCTAGTAAC CACGTTCTCCTGGTCAAATATCACTCTCCTACTTACAGGACTCAACATGCTAGTCACAGCCCTATACTC CCTCTACATGTTTACCACAACACAATGGGGCTCACTCACCCACCACATTAACAACATGAAACCCTCATT CACACGAGAAAACACCCTCATGTTCATGCACCTATCCCCCATTCTCCTCCTATCCCTCAACCCCGACAT CATTACCGGGTTTTCCTCTTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGA GCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATT CGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAA ATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCT CCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTT TGGTTCCATCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCC AGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAG CACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACC ATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATG TTTGCCTTGGGAGTCTCAAGCTGGACTGCCA
45	opt_COX10*- opt_ND4- 3'UTR	ATGGCCGCCAGCCCCCACACCCTGAGCAGCCGCCTGCTGACCGGCTGCGTGGGCGGCAGCGTGTG GTACCTGGAGCGCCGCACCATGCTGAAGCTGATCGTGCCCACCATCATGCTGCTGCCTCTGACCTGG CTGAGCAAGAAACACATGATCTGGATCAACACCACCACGCACAGCCTGATCATCAGCATCATCCCTCT GCTGTTCTTCAACCAGATCAACAACAACCTGTTCAGCTGCAGCCCCACCTTCAGCAGCGACCCTCTGA CAACACCTCTGCTGATGCTGACCACCTGGCTGCTGCCCCTCACAATCATGGCCTCTCAGAGACACCTG AGCAGCGAGCCCCTGAGCCGGAAGAAACTGTACCTGAGCATGCTGATCTCCCTGCAGATCTCTCTGA TCATGACCTTCACCGCCACCGAGCTGATCATGTTCTACATCTTTTTCGAGACAACGCTGATCCCCACAC TGGCCATCATCACCAGATGGGGCAACCAGCCTGAGAGACTGAACGCCGGCACCTACTTTCTGTTCTA CACCCTCGTGGGCAGCCTGCCACTGCTGATTGCCCTGATCTACACCCACAACACCCTGGGCTCCCTG AACATCCTGCTGCTGACACTGACAGCCCAAGAGCTGAGCAACAGCTGGGCCAACAATCTGATGTGGC TGGCCTACACAATGGCCTTCATGGTCAAGATGCCCCTGTACGGCCTGCACCTGTGGCTGCCTAAAGC TCATGTGGAAGCCCCTATCGCCGGCTCTATGGTGCTGGCTGCAGTGCTGCTGAAACTCGGCGGCTAC GGCATGATGCGGCTGACCCTGATTCTGAATCCCCTGACCAAGCACATGGCCTATCCATTTCTGGTGCT GAGCCTGTGGGGCATGATTATGACCAGCAGCATCTGCCTGCGGCAGACCGATCTGAAGTCCCTGATC GCCTACAGCTCCATCAGCCACATGGCCCTGGTGGTCACCGCCATCCTGATTCAGACCCCTTGGAGCT TTACAGGCGCCGTGATCCTGATGATTGCCCACGGCCTGACAAGCAGCCTGCTGTTTTGTCTGGCCAA CAGCAACTACGAGCGGACCCACAGCAGAATCATGATCCTGTCTCAGGGCCTGCAGACCCTCCTGCCT CTTATGGCTTTTTGGTGGCTGCTGGCCTCTCTGGCCAATCTGGCACTGCCTCCTACCATCAATCTGCT GGGCGAGCTGAGCGTGCTGGTCACCACATTCAGCTGGTCCAATATCACCCTGCTGCTCACCGGCCTG AACATGCTGGTTACAGCCCTGTACTCCCTGTACATGTTCACCACCACACAGTGGGGAAGCCTGACACA CCACATCAACAATATGAAGCCCAGCTTCACCCGCGAGAACACCCTGATGTTCATGCATCTGAGCCCCA TTCTGCTGCTGTCCCTGAATCCTGATATCATCACCGGCTTCTCCAGCTGAGAGCACTGGGACGCCCAC CGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCT GGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTTAAAT ATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTT TCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATG GGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACTCCACAT GCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTG AGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTG GTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCT GTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCAGCCCCTGTC CTCCCTTCACCCCCATTGCGTATGAGCATTTCAGAACTCCAAGGAGTCACAGGCATCTTTATAGTTCAC GTTAACATATAGACACTGTTGGAAGCAGTTCCTTCTAAAAGGGTAGCCCTGGACTTAATACCAGCCGG ATACCTCTGGCCCCCACCCCATTACTGTACCTCTGGAGTCACTACTGTGGGTCGCCACTCCTCTGCTA CACAGCACGGCTTTTTCAAGGCTGTATTGAGAAGGGAAGTTAGGAAGAAGGGTGTGCTGGGCTAACC AGCCCACAGAGCTCACATTCCTGTCCCTTGGGTGAAAAATACATGTCCATCCTGATATCTCCTGAATTC AGAAATTAGCCTCCACATGTGCAATGGCTTTAAGAGCCAGAAGCAGGGTTCTGGGAATTTTGCAAGTT ACCTGTGGCCAGGTGTGGTCTCGGTTACCAAATACGGTTACCTGCAGCTTTTTAGTCCTTTGTGCTCC CACGGGTCTACAGAGTCCCATCTGCCCAAAGGTCTTGAAGCTTGACAGGATGTTTTCGATTACTCAGT CTCCCAGGGCACTACTGGTCCGTAGGATTCGATTGGTCGGGGTAGGAGAGTTAAACAACATTTAAACA GAGTTCTCTCAAAAATGTCTAAAGGGATTGTAGGTAGATAACATCCAATCACTGTTTGCACTTATCTGA AATCTTCCCTCTTGGCTGCCCCCAGGTATTTACTGTGGAGAACATTGCATAGGAATGTCTGGAAAAAG CTTCTACAACTTGTTACAGCCTTCACATTTGTAGAAGCTTT

46	opt_COX10*-opt_ND4-3'UTR*	ATGGCCGCCAGCCCCCACACCCTGAGCAGCCGCCTGCTGACCGGCTGCGTGGGCGGCAGCGTGTG GTACCTGGAGCGCCGCACCATGCTGAAGCTGATCGTGCCCACCATCATGCTGCTGCCTCTGACCTGG CTGAGCAAGAAACACATGATCTGGATCAACACCACCACGCACAGCCTGATCATCAGCATCATCCCTCT GCTGTTCTTCAACCAGATCAACAACAACCTGTTCAGCTGCAGCCCCACCTTCAGCAGCGACCCTCTGA CAACACCTCTGCTGATGCTGACCACCTGGCTGCTGCCCCTCACAATCATGGCCTCTCAGAGACACCTG AGCAGCGAGCCCCTGAGCCGGAAGAAACTGTACCTGAGCATGCTGATCTCCCTGCAGATCTCTCTGA TCATGACCTTCACCGCCACCGAGCTGATCATGTTCTACATCTTTTTCGAGACAACGCTGATCCCCACAC TGGCCATCATCACCAGATGGGGCAACCAGCCTGAGAGACTGAACGCCGGCACCTACTTTCTGTTCTA CACCCTCGTGGGCAGCCTGCCACTGCTGATTGCCCTGATCTACACCCACAACACCCTGGGCTCCCTG AACATCCTGCTGCTGACACTGACAGCCCAAGAGCTGAGCAACAGCTGGGCCAACAATCTGATGTGGC TGGCCTACACAATGGCCTTCATGGTCAAGATGCCCCTGTACGGCCTGCACCTGTGGCTGCCTAAAGC TCATGTGGAAGCCCCTATCGCCGGCTCTATGGTGCTGGCTGCAGTGCTGCTGAAACTCGGCGGCTAC GGCATGATGCGGCTGACCCTGATTCTGAATCCCCTGACCAAGCACATGGCCTATCCATTTCTGGTGCT GAGCCTGTGGGGCATGATTATGACCAGCAGCATCTGCCTGCGGCAGACCGATCTGAAGTCCCTGATC GCCTACAGCTCCATCAGCCACATGGCCCTGGTGGTCACCGCCATCCTGATTCAGACCCCTTGGAGCT TTACAGGCGCCGTGATCCTGATGATTGCCCACGGCCTGACAAGCAGCCTGCTGTTTTGTCTGGCCAA CAGCAACTACGAGCGGACCCACAGCAGAATCATGATCCTGTCTCAGGGCCTGCAGACCCTCCTGCCT CTTATGGCTTTTTGGTGGCTGCTGGCCTCTCTGGCCAATCTGGCACTGCCTCCTACCATCAATCTGCT GGGCGAGCTGAGCGTGCTGGTCACCACATTCAGCTGGTCCAATATCACCCTGCTGCTCACCGGCCTG AACATGCTGGTTACAGCCCTGTACTCCCTGTACATGTTCACCACCACACAGTGGGGAAGCCTGACACA CCACATCAACAATATGAAGCCCAGCTTCACCCGCGAGAACACCCTGATGTTCATGCATCTGAGCCCCA TTCTGCTGCTGTCCCTGAATCCTGATATCATCACCGGCTTCTCCAGCTGAGAGCACTGGGACGCCCAC CGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCT GGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTAAAT ATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTT TCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATG GGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACTCCACAT GCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTG AGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTG GTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCT GTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCA
47	opt_COX10*-opt_ND4*-3'UTR	ATGGCCGCCAGCCCCCACACCCTGAGCAGCCGCCTGCTGACCGGCTGCGTGGGCGGCAGCGTGTG GTACCTGGAGCGCCGCACCATGCTGAAGCTGATCGTGCCCACCATCATGCTGCTGCCCCTGACCTGG CTGAGCAAGAAGCACATGATCTGGATCAACACCACCACCCACAGCCTGATCATCAGCATCATCCCCCT GCTGTTCTTCAACCAGATCAACAACAACCTGTTCAGCTGCAGCCCCACCTTCAGCAGCGACCCCCTGA CCACCCCCCTGCTGATGCTGACCACCTGGCTGCTGCCCCTGACCATCATGGCCAGCCAGCGCCACCT GAGCAGCGAGCCCCTGAGCCGCAAGAAGCTGTACCTGAGCATGCTGATCAGCCTGCAGATCAGCCTG ATCATGACCTTCACCGCCACCGAGCTGATCATGTTCTACATCTTCTTCGAGACCACCCTGATCCCCAC CCTGGCCATCATCACCCGCTGGGGCAACCAGCCCGAGCGCCTGAACGCCGGCACCTACTTCCTGTTC TACACCCTGGTGGGCAGCCTGCCCCTGCTGATCGCCCTGATCTACACCCACAACACCCTGGGCAGCC TGAACATCCTGCTGCTGACCCTGACCGCCCAGGAGCTGAGCAACAGCTGGGCCAACAACCTGATGTG GCTGGCCTACACCATGGCCTTCATGGTGAAGATGCCCCTGTACGGCCTGCACCTGTGGCTGCCCAAG GCCCACGTGGAGGCCCCCATCGCCGGCAGCATGGTGCTGGCCGCCGTGCTGCTGAAGCTGGGCGG CTACGGCATGATGCGCCTGACCCTGATCCTGAACCCCCTGACCAAGCACATGGCCTACCCCTTCCTG GTGCTGAGCCTGTGGGGCATGATCATGACCAGCAGCATCTGCCTGCGCCAGACCGACCTGAAGAGC CTGATCGCCTACAGCAGCATCAGCCACATGGCCCTGGTGGTGACCGCCATCCTGATCCAGACCCCCT GGAGCTTCACCGGCGCCGTGATCCTGATGATCGCCCACGGCCTGACCAGCAGCCTGCTGTTCTGCCT GGCCAACAGCAACTACGAGCGCACCCACAGCCGCATCATGATCCTGAGCCAGGGCCTGCAGACCCT GCTGCCCCTGATGGCCTTCTGGTGGCTGCTGGCCAGCCTGGCCAACCTGGCCCTGCCCCCCACCAT CAACCTGCTGGGCGAGCTGAGCGTGCTGGTGACCACCTTCAGCTGGAGCAACATCACCCTGCTGCTG ACCGGCCTGAACATGCTGGTGACCGCCCTGTACAGCCTGTACATGTTCACCACCACCCAGTGGGGCA GCCTGACCCACCACATCAACAACATGAAGCCCAGCTTCACCCGCGAGAACACCCTGATGTTCATGCAC CTGAGCCCCATCCTGCTGCTGAGCCTGAACCCCGACATCATCACCGGCTTCAGCAGCTAAGAGCACT GGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGA AGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTT TTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAA AAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCT TCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACG CACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTC TGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGG CCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAG GACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTG CCAGCCCCTGTCCTCCCTTCACCCCCATTGCGTATGAGCATTTCAGAACTCCAAGGAGTCACAGGCAT CTTTATAGTTCACGTTAACATATAGACACTGTTGGAAGCAGTTCCTTCTAAAAGGGTAGCCCTGGACTT AATACCAGCCGGATACCTCTGGCCCCCACCCCATTACTGTACCTCTGGAGTCACTACTGTGGGTCGCC ACTCCTCTGCTACACAGCACGGCTTTTTCAAGGCTGTATTGAGAAGGGAAGTTAGGAAGAAGGGTGTG CTGGGCTAACCAGCCCACAGAGCTCACATTCCTGTCCCTTGGGTGAAAAATACATGTCCATCCTGATA TCTCCTGAATTCAGAAATTAGCCTCCACATGTGCAATGGCTTTAAGAGCCAGAAGCAGGGTTCTGGGA ATTTTGCAAGTTACCTGTGGCCAGGTGTGGTCTCGGTTACCAAATACGGTTACCTGCAGCTTTTTAGTC CTTTGTGCTCCCACGGGTCTACAGAGTCCCATCTGCCCAAAGGTCTTGAAGCTTGACAGGATGTTTTC GATTACTCAGTCTCCCAGGGCACTACTGGTCCGTAGGATTCGATTGGTCGGGGTAGGAGAGTTAAACA ACATTTAAACAGAGTTCTCTCAAAAATGTCTAAAGGGATTGTAGGTAGATAACATCCAATCACTGTTTGC ACTTATCTGAAATCTTCCCTCTTGGCTGCCCCCAGGTATTTACTGTGGAGAACATTGCATAGGAATGTC TGGAAAAAGCTTCTACAACTTGTTACAGCCTTCACATTTGTAGAAGCTTT

48	opt_COX10*- opt_ND4*- 3'UTR*	ATGGCCGCCAGCCCCCACACCCTGAGCAGCCGCCTGCTGACCGGCTGCGTGGGCGGCAGCGTGTG GTACCTGGAGCGCCGCACCATGCTGAAGCTGATCGTGCCCACCATCATGCTGCTGCCCCTGACCTGG CTGAGCAAGAAGCACATGATCTGGATCAACACCACCACCCACAGCCTGATCATCAGCATCATCCCCCT GCTGTTCTTCAACCAGATCAACAACAACCTGTTCAGCTGCAGCCCCACCTTCAGCAGCGACCCCCTGA CCACCCCCCTGCTGATGCTGACCACCTGGCTGCTGCCCCTGACCATCATGGCCAGCCAGCGCCACCT GAGCAGCGAGCCCCTGAGCCGCAAGAAGCTGTACCTGAGCATGCTGATCAGCCTGCAGATCAGCCTG ATCATGACCTTCACCGCCACCGAGCTGATCATGTTCTACATCTTCTTCGAGACCACCCTGATCCCCAC CCTGGCCATCATCACCCGCTGGGGCAACCAGCCCGAGCGCCTGAACGCCGGCACCTACTTCCTGTTC TACACCCTGGTGGGCAGCCTGCCCCTGCTGATCGCCCTGATCTACACCCACAACACCCTGGGCAGCC TGAACATCCTGCTGCTGACCCTGACCGCCCAGGAGCTGAGCAACAGCTGGGCCAACAACCTGATGTG GCTGGCCTACACCATGGCCTTCATGGTGAAGATGCCCCTGTACGGCCTGCACCTGTGGCTGCCCAAG GCCCACGTGGAGGCCCCCATCGCCGGCAGCATGGTGCTGGCCGCCGTGCTGCTGAAGCTGGGCGG CTACGGCATGATGCGCCTGACCCTGATCCTGAACCCCCTGACCAAGCACATGGCCTACCCCTTCCTG GTGCTGAGCCTGTGGGGCATGATCATGACCAGCAGCATCTGCCTGCGCCAGACCGACCTGAAGAGC CTGATCGCCTACAGCAGCATCAGCCACATGGCCCTGGTGGTGACCGCCATCCTGATCCAGACCCCCT GGAGCTTCACCGGCGCCGTGATCCTGATGATCGCCCACGGCCTGACCAGCAGCCTGCTGTTCTGCCT GGCCAACAGCAACTACGAGCGCACCCACAGCCGCATCATGATCCTGAGCCAGGGCCTGCAGACCCT GCTGCCCCTGATGGCCTTCTGGTGGCTGCTGGCCAGCCTGGCCAACCTGGCCCTGCCCCCCACCAT CAACCTGCTGGGCGAGCTGAGCGTGCTGGTGACCACCTTCAGCTGGAGCAACATCACCCTGCTGCTG ACCGGCCTGAACATGCTGGTGACCGCCCTGTACAGCCTGTACATGTTCACCACCACCCAGTGGGGCA GCCTGACCCACCACATCAACAACATGAAGCCCAGCTTCACCCGCGAGAACACCCTGATGTTCATGCAC CTGAGCCCCATCCTGCTGCTGAGCCTGAACCCCGACATCATCACCGGCTTCAGCAGCTAAGAGCACT GGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGA AGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTT TTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAA AAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCT TCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACG CACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTC TGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGG CCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAG GACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTG CCA
49	opt_COX10*- ND6-3'UTR	ATGGCCGCCAGCCCCCACACCCTGAGCAGCCGCCTGCTGACCGGCTGCGTGGGCGGCAGCGTGTG GTACCTGGAGCGCCGCACCATGATGTATGCTTTGTTTCTGTTGAGTGTGGGTTTAGTAATGGGGTTTG TGGGGTTTTCTTCTAAGCCTTCTCCTATTTATGGGGGTTTAGTATTGATTGTTAGCGGTGTGGTCGGGT GTGTTATTATTCTGAATTTTGGGGGAGGTTATATGGGTTTAATGGTTTTTTTAATTTATTTAGGGGGAAT GATGGTTGTCTTTGGATATACTACAGCGATGGCTATTGAGGAGTATCCTGAGGCATGGGGGTCAGGG GTTGAGGTCTTGGTGAGTGTTTTAGTGGGGTTAGCGATGGAGGTAGGATTGGTGCTGTGGGTGAAAG AGTATGATGGGGTGGTGGTTGTGGTAAACTTTAATAGTGTAGGAAGCTGGATGATTTATGAAGGAGAG GGGTCAGGGTTGATTCGGGAGGATCCTATTGGTGCGGGGGCTTTGTATGATTATGGGCGTTGGTTAG TAGTAGTTACTGGTTGGACATTGTTTGTTGGTGTATATATTGTAATTGAGATTGCTCGGGGGAATTAGG AGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAAC ACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACA GTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATA CAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTG TTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACC ACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTG CTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCC AGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAG CTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGG ACTGCCAGCCCCTGTCCTCCCTTCACCCCCATTGCGTATGAGCATTTCAGAACTCCAAGGAGTCACAG GCATCTTTATAGTTCACGTTAACATATAGACACTGTTGGAAGCAGTTCCTTCTAAAAGGGTAGCCCTGG ACTTAATACCAGCCGGATACCTCTGGCCCCCACCCCATTACTGTACCTCTGGAGTCACTACTGTGGGT CGCCACTCCTCTGCTACACAGCACGGCTTTTTCAAGGCTGTATTGAGAAGGGAAGTTAGGAAGAAGG GTGTGCTGGGCTAACCAGCCCACAGAGCTCACATTCCTGTCCCTTGGGTGAAAAATACATGTCCATCC TGATATCTCCTGAATTCAGAAATTAGCCTCCACATGTGCAATGGCTTTAAGAGCCAGAAGCAGGGTTCT GGGAATTTTGCAAGTTACCTGTGGCCAGGTGTGGTCTCGGTTACCAAATACGGTTACCTGCAGCTTTT TAGTCCTTTGTGCTCCCACGGGTCTACAGAGTCCCATCTGCCCAAAGGTCTTGAAGCTTGACAGGATG TTTTCGATTACTCAGTCTCCCAGGGCACTACTGGTCCGTAGGATTCGATTGGTCGGGGTAGGAGAGTT AAACAACATTTAAACAGAGTTCTCTCAAAAATGTCTAAAGGGATTGTAGGTAGATAACATCCAATCACT GTTTGCACTTATCTGAAATCTTCCCTCTTGGCTGCCCCCAGGTATTTACTGTGGAGAACATTGCATAGG AATGTCTGGAAAAAGCTTCTACAACTTGTTACAGCCTTCACATTTGTAGAAGCTTT
50	opt_COX10*- ND6-3'UTR*	ATGGCCGCCAGCCCCCACACCCTGAGCAGCCGCCTGCTGACCGGCTGCGTGGGCGGCAGCGTGTG GTACCTGGAGCGCCGCACCATGATGTATGCTTTGTTTCTGTTGAGTGTGGGTTTAGTAATGGGGTTTG TGGGGTTTTCTTCTAAGCCTTCTCCTATTTATGGGGGTTTAGTATTGATTGTTAGCGGTGTGGTCGGGT GTGTTATTATTCTGAATTTTGGGGGAGGTTATATGGGTTTAATGGTTTTTTTAATTTATTTAGGGGGAAT GATGGTTGTCTTTGGATATACTACAGCGATGGCTATTGAGGAGTATCCTGAGGCATGGGGGTCAGGG GTTGAGGTCTTGGTGAGTGTTTTAGTGGGGTTAGCGATGGAGGTAGGATTGGTGCTGTGGGTGAAAG AGTATGATGGGGTGGTGGTTGTGGTAAACTTTAATAGTGTAGGAAGCTGGATGATTTATGAAGGAGAG GGGTCAGGGTTGATTCGGGAGGATCCTATTGGTGCGGGGGCTTTGTATGATTATGGGCGTTGGTTAG TAGTAGTTACTGGTTGGACATTGTTTGTTGGTGTATATATTGTAATTGAGATTGCTCGGGGGAATTAGG AGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAAC ACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACA GTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATA

		CAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTG TTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACC ACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTG CTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCC AGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAG CTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGG ACTGCCA
51	opt_COX10*-opt_ND6-3'UTR	ATGGCCGCCAGCCCCCACACCCTGAGCAGCCGCCTGCTGACCGGCTGCGTGGGCGGCAGCGTGTG GTACCTGGAGCGCCGCACCATGATGTACGCCCTGTTCCTGCTGAGCGTGGGCCTGGTGATGGGCTTC GTGGGCTTCAGCAGCAAGCCCAGCCCCATCTACGGCGGCCTGGTGCTGATCGTGAGCGGCGTGGTG GGCTGCGTGATCATCCTGAACTTCGGCGGCGGCTACATGGGCCTGATGGTGTTCCTGATCTACCTGG GCGGCATGATGGTGGTGTTCGGCTACACCACCGCCATGGCCATCGAGGAGTACCCCGAGGCCTGGG GCAGCGGCGTGGAGGTGCTGGTGAGCGTGCTGGTGGGCCTGGCCATGGAGGTGGGCCTGGTGCTG TGGGTGAAGGAGTACGACGGCGTGGTGGTGGTGGTGAACTTCAACAGCGTGGGCAGCTGGATGATC TACGAGGGCGAGGGCAGCGGCCTGATCCGCGAGGACCCCATCGGCGCCGGCGCCCTGTACGACTA CGGCCGCTGGCTGGTGGTGGTGACCGGCTGGACCCTGTTCGTGGGCGTGTACATCGTGATCGAGAT CGCCCGCGGCAACTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATG TTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTG CTCAGTGATCACTTGACAGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCAT CAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCA ACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTC CATCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAG TGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCC CTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCC TTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCT TGGGAGTCTCAAGCTGGACTGCCAGCCCCTGTCCTCCCTTCACCCCCATTGCGTATGAGCATTTCAGA ACTCCAAGGAGTCACAGGCATCTTTATAGTTCACGTTAACATATAGACACTGTTGGAAGCAGTTCCTTC TAAAAGGGTAGCCCTGGACTTAATACCAGCCGGATACCTCTGGCCCCCACCCCATTACTGTACCTCTG GAGTCACTACTGTGGGTCGCCACTCCTCTGCTACACAGCACGGCTTTTTCAAGGCTGTATTGAGAAGG GAAGTTAGGAAGAAGGGTGTGCTGGGCTAACCAGCCCACAGAGCTCACATTCCTGTCCCTTGGGTGA AAAATACATGTCCATCCTGATATCTCCTGAATTCAGAAATTAGCCTCCACATGTGCAATGGCTTTAAGA GCCAGAAGCAGGGTTCTGGGAATTTTGCAAGTTACCTGTGGCCAGGTGTGGTCTCGGTTACCAAATAC GGTTACCTGCAGCTTTTTAGTCCTTTGTGCTCCCACGGGTCTACAGAGTCCCATCTGCCCAAAGGTCT TGAAGCTTGACAGGATGTTTTCGATTACTCAGTCTCCCAGGGCACTACTGGTCCGTAGGATTCGATTG GTCGGGGTAGGAGAGTTAAACAACATTTAAACAGAGTTCTCTCAAAAATGTCTAAAGGGATTGTAGGTA GATAACATCCAATCACTGTTTGCACTTATCTGAAATCTTCCCTCTTGGCTGCCCCCAGGTATTTACTGT GGAGAACATTGCATAGGAATGTCTGGAAAAAGCTTCTACAACTTGTTACAGCCTTCACATTTGTAGAAG CTTT
52	opt_COX10*-opt_ND6-3'UTR*	ATGGCCGCCAGCCCCCACACCCTGAGCAGCCGCCTGCTGACCGGCTGCGTGGGCGGCAGCGTGTG GTACCTGGAGCGCCGCACCATGATGTACGCCCTGTTCCTGCTGAGCGTGGGCCTGGTGATGGGCTTC GTGGGCTTCAGCAGCAAGCCCAGCCCCATCTACGGCGGCCTGGTGCTGATCGTGAGCGGCGTGGTG GGCTGCGTGATCATCCTGAACTTCGGCGGCGGCTACATGGGCCTGATGGTGTTCCTGATCTACCTGG GCGGCATGATGGTGGTGTTCGGCTACACCACCGCCATGGCCATCGAGGAGTACCCCGAGGCCTGGG GCAGCGGCGTGGAGGTGCTGGTGAGCGTGCTGGTGGGCCTGGCCATGGAGGTGGGCCTGGTGCTG TGGGTGAAGGAGTACGACGGCGTGGTGGTGGTGGTGAACTTCAACAGCGTGGGCAGCTGGATGATC TACGAGGGCGAGGGCAGCGGCCTGATCCGCGAGGACCCCATCGGCGCCGGCGCCCTGTACGACTA CGGCCGCTGGCTGGTGGTGGTGACCGGCTGGACCCTGTTCGTGGGCGTGTACATCGTGATCGAGAT CGCCCGCGGCAACTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATG TTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTG CTCAGTGATCACTTGACAGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCAT CAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCA ACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTC CATCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAG TGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCC CTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCC TTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCT TGGGAGTCTCAAGCTGGACTGCCA

53	opt_COX10*-ND1-3'UTR	ATGGCCGCCAGCCCCCACACCCTGAGCAGCCGCCTGCTGACCGGCTGCGTGGGCGGCAGCGTGTG GTACCTGGAGCGCCGCACCATGGCCAACCTCCTACTCCTCATTGTACCCATTCTAATCGCAATGGCAT TCCTAATGCTTACCGAACGAAAAATTCTAGGCTATATGCAACTACGCAAAGGCCCCAACGTTGTAGGC CCCTACGGGCTACTACAACCCTTCGCTGACGCCATAAAACTCTTCACCAAAGAGCCCCTAAAACCCGC CACATCTACCATCACCCTCTACATCACCGCCCCGACCTTAGCTCTCACCATCGCTCTTCTACTATGGAC CCCCCTCCCCATGCCCAACCCCCTGGTCAACCTCAACCTAGGCCTCCTATTTATTCTAGCCACCTCTA GCCTAGCCGTTTACTCAATCCTCTGGTCAGGGTGGGCATCAAACTCAAACTACGCCCTGATCGGCGCA CTGCGAGCAGTAGCCCAAACAATCTCATATGAAGTCACCCTAGCCATCATTCTACTATCAACATTACTA ATGAGTGGCTCCTTTAACCTCTCCACCCTTATCACAACACAAGAACACCTCTGGTTACTCCTGCCATCA TGGCCCTTGGCCATGATGTGGTTTATCTCCACACTAGCAGAGACCAACCGAACCCCCTTCGACCTTGC CGAAGGGGAGTCCGAACTAGTCTCAGGCTTCAACATCGAATACGCCGCAGGCCCCTTCGCCCTATTC TTCATGGCCGAATACACAAACATTATTATGATGAACACCCTCACCACTACAATCTTCCTAGGAACAACA TATGACGCACTCTCCCCTGAACTCTACACAACATATTTTGTCACCAAGACCCTACTTCTAACCTCCCTG TTCTTATGGATTCGAACAGCATACCCCCGATTCCGCTACGACCAACTCATGCACCTCCTATGGAAAAAC TTCCTACCACTCACCCTAGCATTACTTATGTGGTATGTCTCCATGCCCATTACAATCTCCAGCATTCCC CCTCAAACCTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTG GTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAG TGATCACTTGACAGTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCT CAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCC ACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCC TTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGA GCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCC TTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTA ACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGG AGTCTCAAGCTGGACTGCCAGCCCCTGTCCTCCCTTCACCCCCATTGCGTATGAGCATTTCAGAACTC CAAGGAGTCACAGGCATCTTTATAGTTCACGTTAACATATAGACACTGTTGGAAGCAGTTCCTTCTAAA AGGGTAGCCCTGGACTTAATACCAGCCGGATACCTCTGGCCCCCACCCCATTACTGTACCTCTGGAGT CACTACTGTGGGTCGCCACTCCTCTGCTACACAGCACGGCTTTTTCAAGGCTGTATTGAGAAGGGAAG TTAGGAAGAAGGGTGTGCTGGGCTAACCAGCCCACAGAGCTCACATTCCTGTCCCTTGGGTGAAAAAT ACATGTCCATCCTGATATCTCCTGAATTCAGAAATTAGCCTCCACATGTGCAATGGCTTTAAGAGCCAG AAGCAGGGTTCTGGGAATTTTGCAAGTTACCTGTGGCCAGGTGTGGTCTCGGTTACCAAATACGGTTA CCTGCAGCTTTTTAGTCCTTTGTGCTCCCACGGGTCTACAGAGTCCCATCTGCCCAAAGGTCTTGAAG CTTGACAGGATGTTTTCGATTACTCAGTCTCCCAGGGCACTACTGGTCCGTAGGATTCGATTGGTCGG GGTAGGAGAGTTAAACAACATTTAAACAGAGTTCTCTCAAAAATGTCTAAAGGGATTGTAGGTAGATAA CATCCAATCACTGTTTGCACTTATCTGAAATCTTCCCTCTTGGCTGCCCCCAGGTATTTACTGTGGAGA ACATTGCATAGGAATGTCTGGAAAAAGCTTCTACAACTTGTTACAGCCTTCACATTTGTAGAAGCTTT
54	opt_COX10*-ND1-3'UTR*	ATGGCCGCCAGCCCCCACACCCTGAGCAGCCGCCTGCTGACCGGCTGCGTGGGCGGCAGCGTGTG GTACCTGGAGCGCCGCACCATGGCCAACCTCCTACTCCTCATTGTACCCATTCTAATCGCAATGGCAT TCCTAATGCTTACCGAACGAAAAATTCTAGGCTATATGCAACTACGCAAAGGCCCCAACGTTGTAGGC CCCTACGGGCTACTACAACCCTTCGCTGACGCCATAAAACTCTTCACCAAAGAGCCCCTAAAACCCGC CACATCTACCATCACCCTCTACATCACCGCCCCGACCTTAGCTCTCACCATCGCTCTTCTACTATGGAC CCCCCTCCCCATGCCCAACCCCCTGGTCAACCTCAACCTAGGCCTCCTATTTATTCTAGCCACCTCTA GCCTAGCCGTTTACTCAATCCTCTGGTCAGGGTGGGCATCAAACTCAAACTACGCCCTGATCGGCGCA CTGCGAGCAGTAGCCCAAACAATCTCATATGAAGTCACCCTAGCCATCATTCTACTATCAACATTACTA ATGAGTGGCTCCTTTAACCTCTCCACCCTTATCACAACACAAGAACACCTCTGGTTACTCCTGCCATCA TGGCCCTTGGCCATGATGTGGTTTATCTCCACACTAGCAGAGACCAACCGAACCCCCTTCGACCTTGC CGAAGGGGAGTCCGAACTAGTCTCAGGCTTCAACATCGAATACGCCGCAGGCCCCTTCGCCCTATTC TTCATGGCCGAATACACAAACATTATTATGATGAACACCCTCACCACTACAATCTTCCTAGGAACAACA TATGACGCACTCTCCCCTGAACTCTACACAACATATTTTGTCACCAAGACCCTACTTCTAACCTCCCTG TTCTTATGGATTCGAACAGCATACCCCCGATTCCGCTACGACCAACTCATGCACCTCCTATGGAAAAAC TTCCTACCACTCACCCTAGCATTACTTATGTGGTATGTCTCCATGCCCATTACAATCTCCAGCATTCCC CCTCAAACCTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTG GTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAG TGATCACTTGACAGTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCT CAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCC ACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCC TTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGA GCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCC TTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTA ACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGG AGTCTCAAGCTGGACTGCCA

55	opt_COX10*-opt_ND1-3'UTR	ATGGCCGCCAGCCCCCACACCCTGAGCAGCCGCCTGCTGACCGGCTGCGTGGGCGGCAGCGTGTG GTACCTGGAGCGCCGCACCATGGCCAACCTGCTGCTGCTGATCGTGCCCATCCTGATCGCCATGGCC TTCCTGATGCTGACCGAGCGCAAGATCCTGGGCTACATGCAGCTGCGCAAGGGCCCCAACGTGGTG GGCCCCTACGGCCTGCTGCAGCCCTTCGCCGACGCCATCAAGCTGTTCACCAAGGAGCCCCTGAAG CCCGCCACCAGCACCATCACCCTGTACATCACCGCCCCCACCCTGGCCCTGACCATCGCCCTGCTGC TGTGGACCCCCCTGCCCATGCCCAACCCCCTGGTGAACCTGAACCTGGGCCTGCTGTTCATCCTGGC CACCAGCAGCCTGGCCGTGTACAGCATCCTGTGGAGCGGCTGGGCCAGCAACAGCAACTACGCCCT GATCGGCGCCCTGCGCGCCGTGGCCCAGACCATCAGCTACGAGGTGACCCTGGCCATCATCCTGCT GAGCACCCTGCTGATGAGCGGCAGCTTCAACCTGAGCACCCTGATCACCACCCAGGAGCACCTGTGG CTGCTGCTGCCCAGCTGGCCCCTGGCCATGATGTGGTTCATCAGCACCCTGGCCGAGACCAACCGCA CCCCCTTCGACCTGGCCGAGGGCGAGAGCGAGCTGGTGAGCGGCTTCAACATCGAGTACGCCGCCG GCCCCTTCGCCCTGTTCTTCATGGCCGAGTACACCAACATCATCATGATGAACACCCTGACCACCACC ATCTTCCTGGGCACCACCTACGACGCCCTGAGCCCCGAGCTGTACACCACCTACTTCGTGACCAAGA CCCTGCTGCTGACCAGCCTGTTCCTGTGGATCCGCACCGCCTACCCCCGCTTCCGCTACGACCAGCT GATGCACCTGCTGTGGAAGAACTTCCTGCCCCTGACCCTGGCCCTGCTGATGTGGTACGTGAGCATG CCCATCACCATCAGCAGCATCCCCCCCCAGACCTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCT CCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAA GATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTAAATATTACCCAAAATGC TCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGT CTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATAC ACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTG GCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTC AAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCA CACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTG GGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCAGCCCCTGTCCTCCCTTCACCCCCA TTGCGTATGAGCATTTCAGAACTCCAAGGAGTCACAGGCATCTTTATAGTTCACGTTAACATATAGACA CTGTTGGAAGCAGTTCCTTCTAAAAGGGTAGCCCTGGACTTAATACCAGCCGGATACCTCTGGCCCCC ACCCCATTACTGTACCTCTGGAGTCACTACTGTGGGTCGCCACTCCTCTGCTACACAGCACGGCTTTT TCAAGGCTGTATTGAGAAGGGAAGTTAGGAAGAAGGGTGTGCTGGGCTAACCAGCCCACAGAGCTCA CATTCCTGTCCCTTGGGTGAAAAATACATGTCCATCCTGATATCTCCTGAATTCAGAAATTAGCCTCCA CATGTGCAATGGCTTTAAGAGCCAGAAGCAGGGTTCTGGGAATTTTGCAAGTTACCTGTGGCCAGGTG TGGTCTCGGTTACCAAATACGGTTACCTGCAGCTTTTTAGTCCTTTGTGCTCCCACGGGTCTACAGAGT CCCATCTGCCCAAAGGTCTTGAAGCTTGACAGGATGTTTTCGATTACTCAGTCTCCCAGGGCACTACT GGTCCGTAGGATTCGATTGGTCGGGGTAGGAGAGTTAAACAACATTTAAACAGAGTTCTCTCAAAAAT GTCTAAAGGGATTGTAGGTAGATAACATCCAATCACTGTTTGCACTTATCTGAAATCTTCCCTCTTGGC TGCCCCCAGGTATTTACTGTGGAGAACATTGCATAGGAATGTCTGGAAAAAGCTTCTACAACTTGTTAC AGCCTTCACATTTGTAGAAGCTTT
56	opt_COX10*-opt_ND1-3'UTR*	ATGGCCGCCAGCCCCCACACCCTGAGCAGCCGCCTGCTGACCGGCTGCGTGGGCGGCAGCGTGTG GTACCTGGAGCGCCGCACCATGGCCAACCTGCTGCTGCTGATCGTGCCCATCCTGATCGCCATGGCC TTCCTGATGCTGACCGAGCGCAAGATCCTGGGCTACATGCAGCTGCGCAAGGGCCCCAACGTGGTG GGCCCCTACGGCCTGCTGCAGCCCTTCGCCGACGCCATCAAGCTGTTCACCAAGGAGCCCCTGAAG CCCGCCACCAGCACCATCACCCTGTACATCACCGCCCCCACCCTGGCCCTGACCATCGCCCTGCTGC TGTGGACCCCCCTGCCCATGCCCAACCCCCTGGTGAACCTGAACCTGGGCCTGCTGTTCATCCTGGC CACCAGCAGCCTGGCCGTGTACAGCATCCTGTGGAGCGGCTGGGCCAGCAACAGCAACTACGCCCT GATCGGCGCCCTGCGCGCCGTGGCCCAGACCATCAGCTACGAGGTGACCCTGGCCATCATCCTGCT GAGCACCCTGCTGATGAGCGGCAGCTTCAACCTGAGCACCCTGATCACCACCCAGGAGCACCTGTGG CTGCTGCTGCCCAGCTGGCCCCTGGCCATGATGTGGTTCATCAGCACCCTGGCCGAGACCAACCGCA CCCCCTTCGACCTGGCCGAGGGCGAGAGCGAGCTGGTGAGCGGCTTCAACATCGAGTACGCCGCCG GCCCCTTCGCCCTGTTCTTCATGGCCGAGTACACCAACATCATCATGATGAACACCCTGACCACCACC ATCTTCCTGGGCACCACCTACGACGCCCTGAGCCCCGAGCTGTACACCACCTACTTCGTGACCAAGA CCCTGCTGCTGACCAGCCTGTTCCTGTGGATCCGCACCGCCTACCCCCGCTTCCGCTACGACCAGCT GATGCACCTGCTGTGGAAGAACTTCCTGCCCCTGACCCTGGCCCTGCTGATGTGGTACGTGAGCATG CCCATCACCATCAGCAGCATCCCCCCCCAGACCTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCT CCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAA GATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTAAATATTACCCAAAATGC TCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGT CTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATAC ACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTG GCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTC AAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCA CACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTG GGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCA

57	COX8-ND4-3'UTR	ATGTCCGTCCTGACGCGCCTGCTGCTGCGGGGCTTGACACGGCTCGGCTCGGCGGCTCCAGTGCGG CGCGCCAGAATCCATTCGTTGATGCTAAAACTAATCGTCCCAACAATTATGTTACTACCACTGACATGG CTTTCCAAAAAACACATGATTTGGATCAACACAACCACCCACAGCCTAATTATTAGCATCATCCCTCTA CTATTTTTTAACCAAATCAACAACAACCTATTTAGCTGTTCCCCAACCTTTTCCTCCGACCCCCTAACAA CCCCCCTCCTAATGCTAACTACCTGGCTCCTACCCCTCACAATCATGGCAAGCCAACGCCACTTATCC AGTGAACCACTATCACGAAAAAAACTCTACCTCTCTATGCTAATCTCCCTACAAATCTCCTTAATTATGA CATTCACAGCCACAGAACTAATCATGTTTTATATCTTCTTCGAAACCACACTTATCCCCACCTTGGCTAT CATCACCCGATGGGGCAACCAGCCAGAACGCCTGAACGCAGGCACATACTTCCTATTCTACACCCTA GTAGGCTCCCTTCCCCTACTCATCGCACTAATTTACACTCACAACACCCTAGGCTCACTAAACATTCTA CTACTCACTCTCACTGCCCAAGAACTATCAAACTCCTGGGCCAACAACTTAATGTGGCTAGCTTACACA ATGGCTTTTATGGTAAAGATGCCTCTTTACGGACTCCACTTATGGCTCCCTAAAGCCCATGTCGAAGCC CCCATCGCTGGGTCAATGGTACTTGCCGCAGTACTCTTAAAACTAGGCGGCTATGGTATGATGCGCCT CACACTCATTCTCAACCCCCTGACAAAACACATGGCCTACCCCTTCCTTGTACTATCCCTATGGGGCAT GATTATGACAAGCTCCATCTGCCTACGACAAACAGACCTAAAATCGCTCATTGCATACTCTTCAATCAG CCACATGGCCCTCGTAGTAACAGCCATTCTCATCCAAACCCCCTGGAGCTTCACCGGCGCAGTCATTC TCATGATCGCCCACGGGCTTACATCCTCATTACTATTCTGCCTAGCAAACTCAAACTACGAACGCACTC ACAGTCGCATCATGATCCTCTCTCAAGGACTTCAAACTCTACTCCCACTAATGGCTTTTTGGTGGCTTC TAGCAAGCCTCGCTAACCTCGCCTTACCCCCCACTATTAACCTACTGGGAGAACTCTCTGTGCTAGTA ACCACGTTCTCCTGGTCAAATATCACTCTCCTACTTACAGGACTCAACATGCTAGTCACAGCCCTATAC TCCCTCTACATGTTTACCACAACACAATGGGGCTCACTCACCCACCACATTAACAACATGAAACCCTCA TTCACACGAGAAAACACCCTCATGTTCATGCACCTATCCCCCATTCTCCTCCTATCCCTCAACCCCGAC ATCATTACCGGGTTTTCCTCTTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGC GAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAA TTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAG AAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCT CTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCT TTTGGTTCCATCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGC CAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGA GCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAAC CATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACAT GTTTGCCTTGGGAGTCTCAAGCTGGACTGCCAGCCCCTGTCCTCCCTTCACCCCCATTGCGTATGAGC ATTTCAGAACTCCAAGGAGTCACAGGCATCTTTATAGTTCACGTTAACATATAGACACTGTTGGAAGCA GTTCCTTCTAAAAGGGTAGCCCTGGACTTAATACCAGCCGGATACCTCTGGCCCCCACCCCCATTACTG TACCTCTGGAGTCACTACTGTGGGTCGCCACTCCTCTGCTACACAGCACGGCTTTTTCAAGGCTGTAT TGAGAAGGGAAGTTAGGAAGAAGGGTGTGCTGGGCTAACCAGCCCACAGAGCTCACATTCCTGTCCC TTGGGTGAAAAATACATGTCCATCCTGATATCTCCTGAATTCAGAAATTAGCCTCCACATGTGCAATGG CTTTAAGAGCCAGAAGCAGGGTTCTGGGAATTTTGCAAGTTACCTGTGGCCAGGTGTGGTCTCGGTTA CCAAATACGGTTACCTGCAGCTTTTTAGTCCTTTGTGCTCCCACGGGTCTACAGAGTCCCATCTGCCC AAAGGTCTTGAAGCTTGACAGGATGTTTTCGATTACTCAGTCTCCCAGGGCACTACTGGTCCGTAGGA TTCGATTGGTCGGGGTAGGAGAGTTAAACAACATTTAAACAGAGTTCTCTCAAAAATGTCTAAAGGGAT TGTAGGTAGATAACATCCAATCACTGTTTGCACTTATCTGAAATCTTCCCTCTTGGCTGCCCCCAGGTA TTTACTGTGGAGAACATTGCATAGGAATGTCTGGAAAAAGCTTCTACAACTTGTTACAGCCTTCACATT TGTAGAAGCTTT
58	COX8-ND4-3'UTR*	ATGTCCGTCCTGACGCGCCTGCTGCTGCGGGGCTTGACACGGCTCGGCTCGGCGGCTCCAGTGCGG CGCGCCAGAATCCATTCGTTGATGCTAAAACTAATCGTCCCAACAATTATGTTACTACCACTGACATGG CTTTCCAAAAAACACATGATTTGGATCAACACAACCACCCACAGCCTAATTATTAGCATCATCCCTCTA CTATTTTTTAACCAAATCAACAACAACCTATTTAGCTGTTCCCCAACCTTTTCCTCCGACCCCCTAACAA CCCCCCTCCTAATGCTAACTACCTGGCTCCTACCCCTCACAATCATGGCAAGCCAACGCCACTTATCC AGTGAACCACTATCACGAAAAAAACTCTACCTCTCTATGCTAATCTCCCTACAAATCTCCTTAATTATGA CATTCACAGCCACAGAACTAATCATGTTTTATATCTTCTTCGAAACCACACTTATCCCCACCTTGGCTAT CATCACCCGATGGGGCAACCAGCCAGAACGCCTGAACGCAGGCACATACTTCCTATTCTACACCCTA GTAGGCTCCCTTCCCCTACTCATCGCACTAATTTACACTCACAACACCCTAGGCTCACTAAACATTCTA CTACTCACTCTCACTGCCCAAGAACTATCAAACTCCTGGGCCAACAACTTAATGTGGCTAGCTTACACA ATGGCTTTTATGGTAAAGATGCCTCTTTACGGACTCCACTTATGGCTCCCTAAAGCCCATGTCGAAGCC CCCATCGCTGGGTCAATGGTACTTGCCGCAGTACTCTTAAAACTAGGCGGCTATGGTATGATGCGCCT CACACTCATTCTCAACCCCCTGACAAAACACATGGCCTACCCCTTCCTTGTACTATCCCTATGGGGCAT GATTATGACAAGCTCCATCTGCCTACGACAAACAGACCTAAAATCGCTCATTGCATACTCTTCAATCAG CCACATGGCCCTCGTAGTAACAGCCATTCTCATCCAAACCCCCTGGAGCTTCACCGGCGCAGTCATTC TCATGATCGCCCACGGGCTTACATCCTCATTACTATTCTGCCTAGCAAACTCAAACTACGAACGCACTC ACAGTCGCATCATGATCCTCTCTCAAGGACTTCAAACTCTACTCCCACTAATGGCTTTTTGGTGGCTTC TAGCAAGCCTCGCTAACCTCGCCTTACCCCCCACTATTAACCTACTGGGAGAACTCTCTGTGCTAGTA ACCACGTTCTCCTGGTCAAATATCACTCTCCTACTTACAGGACTCAACATGCTAGTCACAGCCCTATAC TCCCTCTACATGTTTACCACAACACAATGGGGCTCACTCACCCACCACATTAACAACATGAAACCCTCA TTCACACGAGAAAACACCCTCATGTTCATGCACCTATCCCCCATTCTCCTCCTATCCCTCAACCCCGAC ATCATTACCGGGTTTTCCTCTTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGC GAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAA TTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAG AAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCT CTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCT TTTGGTTCCATCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGC CAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGA GCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAAC CATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACAT GTTTGCCTTGGGAGTCTCAAGCTGGACTGCCA

59	COX8-opt_ND4-3'UTR	ATGTCCGTCCTGACGCGCCTGCTGCTGCGGGGCTTGACACGGCTCGGCTCGGCGGCTCCAGTGCGG CGCGCCAGAATCCATTCGTTGATGCTGAAGCTGATCGTGCCCACCATCATGCTGCTGCCTCTGACCTG GCTGAGCAAGAAACACATGATCTGGATCAACACCACCACGCACAGCCTGATCATCAGCATCATCCCTC TGCTGTTCTTCAACCAGATCAACAACAACCTGTTCAGCTGCAGCCCCACCTTCAGCAGCGACCCTCTG ACAACACCTCTGCTGATGCTGACCACCTGGCTGCTGCCCCTCACAATCATGGCCTCTCAGAGACACCT GAGCAGCGAGCCCCTGAGCCGGAAGAAACTGTACCTGAGCATGCTGATCTCCCTGCAGATCTCTCTG ATCATGACCTTCACCGCCACCGAGCTGATCATGTTCTACATCTTTTTCGAGACAACGCTGATCCCCACA CTGGCCATCATCACCAGATGGGGCAACCAGCCTGAGAGACTGAACGCCGGCACCTACTTTCTGTTCT ACACCCTCGTGGGCAGCCTGCCACTGCTGATTGCCCTGATCTACACCCACAACACCCTGGGCTCCCT GAACATCCTGCTGCTGACACTGACAGCCCAAGAGCTGAGCAACAGCTGGGCCAACAATCTGATGTGG CTGGCCTACACAATGGCCTTCATGGTCAAGATGCCCCTGTACGGCCTGCACCTGTGGCTGCCTAAAG CTCATGTGGAAGCCCCTATCGCCGGCTCTATGGTGCTGGCTGCAGTGCTGCTGAAACTCGGCGGCTA CGGCATGATGCGGCTGACCCTGATTCTGAATCCCCTGACCAAGCACATGGCCTATCCATTTCTGGTGC TGAGCCTGTGGGGCATGATTATGACCAGCAGCATCTGCCTGCGGCAGACCGATCTGAAGTCCCTGAT CGCCTACAGCTCCATCAGCCACATGGCCCTGGTGGTCACCGCCATCCTGATTCAGACCCCTTGGAGC TTTACAGGCGCCGTGATCCTGATGATTGCCCACGGCCTGACAAGCAGCCTGCTGTTTTGTCTGGCCAA CAGCAACTACGAGCGGACCCACAGCAGAATCATGATCCTGTCTCAGGGCCTGCAGACCCTCCTGCCT CTTATGGCTTTTTGGTGGCTGCTGGCCTCTCTGGCCAATCTGGCACTGCCTCCTACCATCAATCTGCT GGGCGAGCTGAGCGTGCTGGTCACCACATTCAGCTGGTCCAATATCACCCTGCTGCTCACCGGCCTG AACATGCTGGTTACAGCCCTGTACTCCCTGTACATGTTCACCACCACACAGTGGGGAAGCCTGACACA CCACATCAACAATATGAAGCCCAGCTTCACCCGCGAGAACACCCTGATGTTCATGCATCTGAGCCCCA TTCTGCTGCTGTCCCTGAATCCTGATATCATCACCGGCTTCTCCAGCTGAGAGCACTGGGACGCCCAC CGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCT GGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTAAAT ATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTT TCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATG GGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACTCCACAT GCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTG AGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTG GTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCT GTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCAGCCCCTGTC CTCCCTTCACCCCCATTGCGTATGAGCATTTCAGAACTCCAAGGAGTCACAGGCATCTTTATAGTTCAC GTTAACATATAGACACTGTTGGAAGCAGTTCCTTCTAAAAGGGTAGCCCTGGACTTAATACCAGCCGG ATACCTCTGGCCCCCACCCCATTACTGTACCTCTGGAGTCACTACTGTGGGTCGCCACTCCTCTGCTA CACAGCACGGCTTTTTCAAGGCTGTATTGAGAAGGGAAGTTAGGAAGAAGGGTGTGCTGGGCTAACC AGCCCACAGAGCTCACATTCCTGTCCCTTGGGTGAAAAATACATGTCCATCCTGATATCTCCTGAATTC AGAAATTAGCCTCCACATGTGCAATGGCTTTAAGAGCCAGAAGCAGGGTTCTGGGAATTTTGCAAGTT ACCTGTGGCCAGGTGTGGTCTCGGTTACCAAATACGGTTACCTGCAGCTTTTTAGTCCTTTGTGCTCC CACGGGTCTACAGAGTCCCATCTGCCCAAAGGTCTTGAAGCTTGACAGGATGTTTTCGATTACTCAGT CTCCCAGGGCACTACTGGTCCGTAGGATTCGATTGGTCGGGGTAGGAGAGTTAAACAACATTTAAACA GAGTTCTCTCAAAAATGTCTAAAGGGATTGTAGGTAGATAACATCCAATCACTGTTTGCACTTATCTGA AATCTTCCCTCTTGGCTGCCCCCAGGTATTTACTGTGGAGAACATTGCATAGGAATGTCTGGAAAAAG CTTCTACAACTTGTTACAGCCTTCACATTTGTAGAAGCTTT
60	COX8-opt_ND4-3'UTR*	ATGTCCGTCCTGACGCGCCTGCTGCTGCGGGGCTTGACACGGCTCGGCTCGGCGGCTCCAGTGCGG CGCGCCAGAATCCATTCGTTGATGCTGAAGCTGATCGTGCCCACCATCATGCTGCTGCCTCTGACCTG GCTGAGCAAGAAACACATGATCTGGATCAACACCACCACGCACAGCCTGATCATCAGCATCATCCCTC TGCTGTTCTTCAACCAGATCAACAACAACCTGTTCAGCTGCAGCCCCACCTTCAGCAGCGACCCTCTG ACAACACCTCTGCTGATGCTGACCACCTGGCTGCTGCCCCTCACAATCATGGCCTCTCAGAGACACCT GAGCAGCGAGCCCCTGAGCCGGAAGAAACTGTACCTGAGCATGCTGATCTCCCTGCAGATCTCTCTG ATCATGACCTTCACCGCCACCGAGCTGATCATGTTCTACATCTTTTTCGAGACAACGCTGATCCCCACA CTGGCCATCATCACCAGATGGGGCAACCAGCCTGAGAGACTGAACGCCGGCACCTACTTTCTGTTCT ACACCCTCGTGGGCAGCCTGCCACTGCTGATTGCCCTGATCTACACCCACAACACCCTGGGCTCCCT GAACATCCTGCTGCTGACACTGACAGCCCAAGAGCTGAGCAACAGCTGGGCCAACAATCTGATGTGG CTGGCCTACACAATGGCCTTCATGGTCAAGATGCCCCTGTACGGCCTGCACCTGTGGCTGCCTAAAG CTCATGTGGAAGCCCCTATCGCCGGCTCTATGGTGCTGGCTGCAGTGCTGCTGAAACTCGGCGGCTA CGGCATGATGCGGCTGACCCTGATTCTGAATCCCCTGACCAAGCACATGGCCTATCCATTTCTGGTGC TGAGCCTGTGGGGCATGATTATGACCAGCAGCATCTGCCTGCGGCAGACCGATCTGAAGTCCCTGAT CGCCTACAGCTCCATCAGCCACATGGCCCTGGTGGTCACCGCCATCCTGATTCAGACCCCTTGGAGC TTTACAGGCGCCGTGATCCTGATGATTGCCCACGGCCTGACAAGCAGCCTGCTGTTTTGTCTGGCCAA CAGCAACTACGAGCGGACCCACAGCAGAATCATGATCCTGTCTCAGGGCCTGCAGACCCTCCTGCCT CTTATGGCTTTTTGGTGGCTGCTGGCCTCTCTGGCCAATCTGGCACTGCCTCCTACCATCAATCTGCT GGGCGAGCTGAGCGTGCTGGTCACCACATTCAGCTGGTCCAATATCACCCTGCTGCTCACCGGCCTG AACATGCTGGTTACAGCCCTGTACTCCCTGTACATGTTCACCACCACACAGTGGGGAAGCCTGACACA CCACATCAACAATATGAAGCCCAGCTTCACCCGCGAGAACACCCTGATGTTCATGCATCTGAGCCCCA TTCTGCTGCTGTCCCTGAATCCTGATATCATCACCGGCTTCTCCAGCTGAGAGCACTGGGACGCCCAC CGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCT GGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTAAAT ATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTT TCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATG GGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACTCCACAT GCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTG AGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTG GTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCT GTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCA

61	COX8-opt_ND4*-3'UTR	ATGTCCGTCCTGACGCGCCTGCTGCTGCGGGGCTTGACACGGCTCGGCTCGGCGGCTCCAGTGCGG CGCGCCAGAATCCATTCGTTGATGCTGAAGCTGATCGTGCCCACCATCATGCTGCTGCCCCTGACCT GGCTGAGCAAGAAGCACATGATCTGGATCAACACCACCACCCACAGCCTGATCATCAGCATCATCCCC CTGCTGTTCTTCAACCAGATCAACAACAACCTGTTCAGCTGCAGCCCCACCTTCAGCAGCGACCCCCT GACCACCCCCCTGCTGATGCTGACCACCTGGCTGCTGCCCCTGACCATCATGGCCAGCCAGCGCCAC CTGAGCAGCGAGCCCCTGAGCCGCAAGAAGCTGTACCTGAGCATGCTGATCAGCCTGCAGATCAGCC TGATCATGACCTTCACCGCCACCGAGCTGATCATGTTCTACATCTTCTTCGAGACCACCCTGATCCCC ACCCTGGCCATCATCACCCGCTGGGGCAACCAGCCCGAGCGCCTGAACGCCGGCACCTACTTCCTGT TCTACACCCTGGTGGGCAGCCTGCCCCTGCTGATCGCCCTGATCTACACCCACAACACCCTGGGCAG CCTGAACATCCTGCTGCTGACCCTGACCGCCCAGGAGCTGAGCAACAGCTGGGCCAACAACCTGATG TGGCTGGCCTACACCATGGCCTTCATGGTGAAGATGCCCCTGTACGGCCTGCACCTGTGGCTGCCCA AGGCCCACGTGGAGGCCCCCATCGCCGGCAGCATGGTGCTGGCCGCCGTGCTGCTGAAGCTGGGC GGCTACGGCATGATGCGCCTGACCCTGATCCTGAACCCCCTGACCAAGCACATGGCCTACCCCTTCC TGGTGCTGAGCCTGTGGGGCATGATCATGACCAGCAGCATCTGCCTGCGCCAGACCGACCTGAAGAG CCTGATCGCCTACAGCAGCATCAGCCACATGGCCCTGGTGGTGACCGCCATCCTGATCCAGACCCCC TGGAGCTTCACCGGCGCCGTGATCCTGATGATCGCCCACGGCCTGACCAGCAGCCTGCTGTTCTGCC TGGCCAACAGCAACTACGAGCGCACCCACAGCCGCATCATGATCCTGAGCCAGGGCCTGCAGACCCT GCTGCCCCTGATGGCCTTCTGGTGGCTGCTGGCCAGCCTGGCCAACCTGGCCCTGCCCCCCACCAT CAACCTGCTGGGCGAGCTGAGCGTGCTGGTGACCACCTTCAGCTGGAGCAACATCACCCTGCTGCTG ACCGGCCTGAACATGCTGGTGACCGCCCTGTACAGCCTGTACATGTTCACCACCACCCAGTGGGGCA GCCTGACCCACCACATCAACAACATGAAGCCCAGCTTCACCCGCGAGAACACCCTGATGTTCATGCAC CTGAGCCCCATCCTGCTGCTGAGCCTGAACCCCGACATCATCACCGGCTTCAGCAGCTAAGAGCACT GGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGA AGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTT TTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAA AAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCT TCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACG CACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTC TGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGG CCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAG GACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTG CCAGCCCCTGTCCTCCCTTCACCCCCATTGCGTATGAGCATTTCAGAACTCCAAGGAGTCACAGGCAT CTTTATAGTTCACGTTAACATATAGACACTGTTGGAAGCAGTTCCTTCTAAAAGGGTAGCCCTGGACTT AATACCAGCCGGATACCTCTGGCCCCCACCCCATTACTGTACCTCTGGAGTCACTACTGTGGGTCGCC ACTCCTCTGCTACACAGCACGGCTTTTTCAAGGCTGTATTGAGAAGGGAAGTTAGGAAGAAGGGTGTG CTGGGCTAACCAGCCCACAGAGCTCACATTCCTGTCCCTTGGGTGAAAAATACATGTCCATCCTGATA TCTCCTGAATTCAGAAATTAGCCTCCACATGTGCAATGGCTTTAAGAGCCAGAAGCAGGGTTCTGGGA ATTTTGCAAGTTACCTGTGGCCAGGTGTGGTCTCGGTTACCAAATACGGTTACCTGCAGCTTTTTAGTC CTTTGTGCTCCCACGGGTCTACAGAGTCCCATCTGCCCAAAGGTCTTGAAGCTTGACAGGATGTTTTC GATTACTCAGTCTCCCAGGGCACTACTGGTCCGTAGGATTCGATTGGTCGGGGTAGGAGAGTTAAACA ACATTTAAACAGAGTTCTCTCAAAAATGTCTAAAGGGATTGTAGGTAGATAACATCCAATCACTGTTTGC ACTTATCTGAAATCTTCCCTCTTGGCTGCCCCCAGGTATTTACTGTGGAGAACATTGCATAGGAATGTC TGGAAAAAGCTTCTACAACTTGTTACAGCCTTCACATTTGTAGAAGCTTT
62	COX8-opt_ND4*-3'UTR*	ATGTCCGTCCTGACGCGCCTGCTGCTGCGGGGCTTGACACGGCTCGGCTCGGCGGCTCCAGTGCGG CGCGCCAGAATCCATTCGTTGATGCTGAAGCTGATCGTGCCCACCATCATGCTGCTGCCCCTGACCT GGCTGAGCAAGAAGCACATGATCTGGATCAACACCACCACCCACAGCCTGATCATCAGCATCATCCCC CTGCTGTTCTTCAACCAGATCAACAACAACCTGTTCAGCTGCAGCCCCACCTTCAGCAGCGACCCCCT GACCACCCCCCTGCTGATGCTGACCACCTGGCTGCTGCCCCTGACCATCATGGCCAGCCAGCGCCAC CTGAGCAGCGAGCCCCTGAGCCGCAAGAAGCTGTACCTGAGCATGCTGATCAGCCTGCAGATCAGCC TGATCATGACCTTCACCGCCACCGAGCTGATCATGTTCTACATCTTCTTCGAGACCACCCTGATCCCC ACCCTGGCCATCATCACCCGCTGGGGCAACCAGCCCGAGCGCCTGAACGCCGGCACCTACTTCCTGT TCTACACCCTGGTGGGCAGCCTGCCCCTGCTGATCGCCCTGATCTACACCCACAACACCCTGGGCAG CCTGAACATCCTGCTGCTGACCCTGACCGCCCAGGAGCTGAGCAACAGCTGGGCCAACAACCTGATG TGGCTGGCCTACACCATGGCCTTCATGGTGAAGATGCCCCTGTACGGCCTGCACCTGTGGCTGCCCA AGGCCCACGTGGAGGCCCCCATCGCCGGCAGCATGGTGCTGGCCGCCGTGCTGCTGAAGCTGGGC GGCTACGGCATGATGCGCCTGACCCTGATCCTGAACCCCCTGACCAAGCACATGGCCTACCCCTTCC TGGTGCTGAGCCTGTGGGGCATGATCATGACCAGCAGCATCTGCCTGCGCCAGACCGACCTGAAGAG CCTGATCGCCTACAGCAGCATCAGCCACATGGCCCTGGTGGTGACCGCCATCCTGATCCAGACCCCC TGGAGCTTCACCGGCGCCGTGATCCTGATGATCGCCCACGGCCTGACCAGCAGCCTGCTGTTCTGCC TGGCCAACAGCAACTACGAGCGCACCCACAGCCGCATCATGATCCTGAGCCAGGGCCTGCAGACCCT GCTGCCCCTGATGGCCTTCTGGTGGCTGCTGGCCAGCCTGGCCAACCTGGCCCTGCCCCCCACCAT CAACCTGCTGGGCGAGCTGAGCGTGCTGGTGACCACCTTCAGCTGGAGCAACATCACCCTGCTGCTG ACCGGCCTGAACATGCTGGTGACCGCCCTGTACAGCCTGTACATGTTCACCACCACCCAGTGGGGCA GCCTGACCCACCACATCAACAACATGAAGCCCAGCTTCACCCGCGAGAACACCCTGATGTTCATGCAC CTGAGCCCCATCCTGCTGCTGAGCCTGAACCCCGACATCATCACCGGCTTCAGCAGCTAAGAGCACT GGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGA AGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTT TTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAA AAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCT TCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACG CACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTC TGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGG CCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAG

		GACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTG CCA
63	COX8-ND6- 3'UTR	ATGTCCGTCCTGACGCGCCTGCTGCTGCGGGGCTTGACACGGCTCGGCTCGGCGGCTCCAGTGCGG CGCGCCAGAATCCATTCGTTGATGATGTATGCTTTGTTTCTGTTGAGTGTGGGTTTAGTAATGGGGTTT GTGGGGTTTTCTTCTAAGCCTTCTCCTATTTATGGGGGTTTAGTATTGATTGTTAGCGGTGTGGTCGGG TGTGTTATTATTCTGAATTTTGGGGGAGGTTATATGGGTTTAATGGTTTTTTTAATTTATTTAGGGGGAA TGATGGTTGTCTTTGGATATACTACAGCGATGGCTATTGAGGAGTATCCTGAGGCATGGGGGTCAGGG GTTGAGGTCTTGGTGAGTGTTTTAGTGGGGTTAGCGATGGAGGTAGGATTGGTGCTGTGGGTGAAAG AGTATGATGGGGTGGTGGTTGTGGTAAACTTTAATAGTGTAGGAAGCTGGATGATTTATGAAGGAGAG GGGTCAGGGTTGATTCGGGAGGATCCTATTGGTGCGGGGGCTTTGTATGATTATGGGCGTTGGTTAG TAGTAGTTACTGGTTGGACATTGTTTGTTGGTGTATATATTGTAATTGAGATTGCTCGGGGGAATTAGG AGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAAC ACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACA GTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATA CAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTG TTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACC ACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTG CTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCC AGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAG CTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGG ACTGCCAGCCCCTGTCCTCCCTTCACCCCCATTGCGTATGAGCATTTCAGAACTCCAAGGAGTCACAG GCATCTTTATAGTTCACGTTAACATATAGACACTGTTGGAAGCAGTTCCTTCTAAAAGGGTAGCCCTGG ACTTAATACCAGCCGGATACCTCTGGCCCCCACCCCATTACTGTACCTCTGGAGTCACTACTGTGGGT CGCCACTCCTCTGCTACACAGCACGGCTTTTTCAAGGCTGTATTGAGAAGGGAAGTTAGGAAGAAGG GTGTGCTGGGCTAACCAGCCCACAGAGCTCACATTCCTGTCCCTTGGGTGAAAAATACATGTCCATCC TGATATCTCCTGAATTCAGAAATTAGCCTCCACATGTGCAATGGCTTTAAGAGCCAGAAGCAGGGTTCT GGGAATTTTGCAAGTTACCTGTGGCCAGGTGTGGTCTCGGTTACCAAATACGGTTACCTGCAGCTTTT TAGTCCTTTGTGCTCCCACGGGTCTACAGAGTCCCATCTGCCCAAAGGTCTTGAAGCTTGACAGGATG TTTTCGATTACTCAGTCTCCCAGGGCACTACTGGTCCGTAGGATTCGATTGGTCGGGGTAGGAGAGTT AAACAACATTTAAACAGAGTTCTCTCAAAAATGTCTAAAGGGATTGTAGGTAGATAACATCCAATCACT GTTTGCACTTATCTGAAATCTTCCCTCTTGGCTGCCCCCAGGTATTTACTGTGGAGAACATTGCATAGG AATGTCTGGAAAAAGCTTCTACAACTTGTTACAGCCTTCACATTTGTAGAAGCTTT
64	COX8-ND6- 3'UTR*	ATGTCCGTCCTGACGCGCCTGCTGCTGCGGGGCTTGACACGGCTCGGCTCGGCGGCTCCAGTGCGG CGCGCCAGAATCCATTCGTTGATGATGTATGCTTTGTTTCTGTTGAGTGTGGGTTTAGTAATGGGGTTT GTGGGGTTTTCTTCTAAGCCTTCTCCTATTTATGGGGGTTTAGTATTGATTGTTAGCGGTGTGGTCGGG TGTGTTATTATTCTGAATTTTGGGGGAGGTTATATGGGTTTAATGGTTTTTTTAATTTATTTAGGGGGAA TGATGGTTGTCTTTGGATATACTACAGCGATGGCTATTGAGGAGTATCCTGAGGCATGGGGGTCAGGG GTTGAGGTCTTGGTGAGTGTTTTAGTGGGGTTAGCGATGGAGGTAGGATTGGTGCTGTGGGTGAAAG AGTATGATGGGGTGGTGGTTGTGGTAAACTTTAATAGTGTAGGAAGCTGGATGATTTATGAAGGAGAG GGGTCAGGGTTGATTCGGGAGGATCCTATTGGTGCGGGGGCTTTGTATGATTATGGGCGTTGGTTAG TAGTAGTTACTGGTTGGACATTGTTTGTTGGTGTATATATTGTAATTGAGATTGCTCGGGGGAATTAGG AGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAAC ACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACA GTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATA CAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTG TTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACC ACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTG CTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCC AGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAG CTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGG ACTGCCA

65	COX8-opt_ND6-3'UTR	ATGTCCGTCCTGACGCGCCTGCTGCTGCGGGGCTTGACACGGCTCGGCTCGGCGGCTCCAGTGCGG CGCGCCAGAATCCATTCGTTGATGATGTACGCCCTGTTCCTGCTGAGCGTGGGCCTGGTGATGGGCT TCGTGGGCTTCAGCAGCAAGCCCAGCCCCATCTACGGCGGCCTGGTGCTGATCGTGAGCGGCGTGG TGGGCTGCGTGATCATCCTGAACTTCGGCGGCGGCTACATGGGCCTGATGGTGTTCCTGATCTACCT GGGCGGCATGATGGTGGTGTTCGGCTACACCACCGCCATGGCCATCGAGGAGTACCCCGAGGCCTG GGGCAGCGGCGTGGAGGTGCTGGTGAGCGTGCTGGTGGGCCTGGCCATGGAGGTGGGCCTGGTGC TGTGGGTGAAGGAGTACGACGGCGTGGTGGTGGTGGTGAACTTCAACAGCGTGGGCAGCTGGATGA TCTACGAGGGCGAGGGCAGCGGCCTGATCCGCGAGGACCCCATCGGCGCCGGCGCCCTGTACGAC TACGGCCGCTGGCTGGTGGTGGTGACCGGCTGGACCCTGTTCGTGGGCGTGTACATCGTGATCGAG ATCGCCCGCGGCAACTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCA TGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGG TGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGC ATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTC CAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGT TCCATCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAA AGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACC CCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGT CCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGC CTTGGGAGTCTCAAGCTGGACTGCCAGCCCCTGTCCTCCCTTCACCCCCATTGCGTATGAGCATTTCA GAACTCCAAGGAGTCACAGGCATCTTTATAGTTCACGTTAACATATAGACACTGTTGGAAGCAGTTCCT TCTAAAAGGGTAGCCCTGGACTTAATACCAGCCGGATACCTCTGGCCCCCACCCCATTACTGTACCTC TGGAGTCACTACTGTGGGTCGCCACTCCTCTGCTACACAGCACGGCTTTTTCAAGGCTGTATTGAGAA GGGAAGTTAGGAAGAAGGGTGTGCTGGGCTAACCAGCCCACAGAGCTCACATTCCTGTCCCTTGGGT GAAAAATACATGTCCATCCTGATATCTCCTGAATTCAGAAATTAGCCTCCACATGTGCAATGGCTTTAA GAGCCAGAAGCAGGGTTCTGGGAATTTTGCAAGTTACCTGTGGCCAGGTGTGGTCTCGGTTACCAAAT ACGGTTACCTGCAGCTTTTTAGTCCTTTGTGCTCCCACGGGTCTACAGAGTCCCATCTGCCCAAAGGT CTTGAAGCTTGACAGGATGTTTTCGATTACTCAGTCTCCCAGGGCACTACTGGTCCGTAGGATTCGAT TGGTCGGGGTAGGAGAGTTAAACAACATTTAAACAGAGTTCTCTCAAAAATGTCTAAAGGGATTGTAG GTAGATAACATCCAATCACTGTTTGCACTTATCTGAAATCTTCCCTCTTGGCTGCCCCCAGGTATTTAC TGTGGAGAACATTGCATAGGAATGTCTGGAAAAAGCTTCTACAACTTGTTACAGCCTTCACATTTGTAG AAGCTTT
66	COX8-opt_ND6-3'UTR*	ATGTCCGTCCTGACGCGCCTGCTGCTGCGGGGCTTGACACGGCTCGGCTCGGCGGCTCCAGTGCGG CGCGCCAGAATCCATTCGTTGATGATGTACGCCCTGTTCCTGCTGAGCGTGGGCCTGGTGATGGGCT TCGTGGGCTTCAGCAGCAAGCCCAGCCCCATCTACGGCGGCCTGGTGCTGATCGTGAGCGGCGTGG TGGGCTGCGTGATCATCCTGAACTTCGGCGGCGGCTACATGGGCCTGATGGTGTTCCTGATCTACCT GGGCGGCATGATGGTGGTGTTCGGCTACACCACCGCCATGGCCATCGAGGAGTACCCCGAGGCCTG GGGCAGCGGCGTGGAGGTGCTGGTGAGCGTGCTGGTGGGCCTGGCCATGGAGGTGGGCCTGGTGC TGTGGGTGAAGGAGTACGACGGCGTGGTGGTGGTGGTGAACTTCAACAGCGTGGGCAGCTGGATGA TCTACGAGGGCGAGGGCAGCGGCCTGATCCGCGAGGACCCCATCGGCGCCGGCGCCCTGTACGAC TACGGCCGCTGGCTGGTGGTGGTGACCGGCTGGACCCTGTTCGTGGGCGTGTACATCGTGATCGAG ATCGCCCGCGGCAACTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCA TGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGG TGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGC ATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTC CAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGT TCCATCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAA AGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACC CCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGT CCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGC CTTGGGAGTCTCAAGCTGGACTGCCA
67	COX8-ND1-3'UTR	ATGTCCGTCCTGACGCGCCTGCTGCTGCGGGGCTTGACACGGCTCGGCTCGGCGGCTCCAGTGCGG CGCGCCAGAATCCATTCGTTGATGGCCAACCTCCTACTCCTCATTGTACCCATTCTAATCGCAATGGC ATTCCTAATGCTTACCGAACGAAAAATTCTAGGCTATATGCAACTACGCAAAGGCCCCAACGTTGTAGG CCCCTACGGGCTACTACAACCCTTCGCTGACGCCATAAAACTCTTCACCAAAGAGCCCCTAAAACCCG CCACATCTACCATCACCCTCTACATCACCGCCCCGACCTTAGCTCTCACCATCGCTCTTCTACTATGGA CCCCCCTCCCCATGCCCAACCCCCTGGTCAACCTCAACCTAGGCCTCCTATTTATTCTAGCCACCTCT AGCCTAGCCGTTTACTCAATCCTCTGGTCAGGGTGGGCATCAAACTCAAACTACGCCCTGATCGGCGC ACTGCGAGCAGTAGCCCAAACAATCTCATATGAAGTCACCCTAGCCATCATTCTACTATCAACATTACT AATGAGTGGCTCCTTTAACCTCTCCACCCTTATCACAACACAAGAACACCTCTGGTTACTCCTGCCATC ATGGCCCTTGGCCATGATGTGGTTTATCTCCACACTAGCAGAGACCAACCGAACCCCCTTCGACCTTG CCGAAGGGGAGTCCGAACTAGTCTCAGGCTTCAACATCGAATACGCCGCAGGCCCCTTCGCCCTATT CTTCATGGCCGAATACACAAACATTATTATGATGAACACCCTCACCACTACAATCTTCCTAGGAACAAC ATATGACGCACTCTCCCCTGAACTCTACACAACATATTTTGTCACCAAGACCCTACTTCTAACCTCCCT GTTCTTATGGATTCGAACAGCATACCCCCGATTCCGCTACGACCAACTCATGCACCTCCTATGGAAAA ACTTCCTACCACTCACCCTAGCATTACTTATGTGGTATGTCTCCATGCCCATTACAATCTCCAGCATTC CCCCTCAAACCTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTG TGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTC AGTGATCACTTGACAGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAG CTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACC CCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCAT CCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGT GAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTT CCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTC TAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGG

		GAGTCTCAAGCTGGACTGCCAGCCCCTGTCCTCCCTTCACCCCCATTGCGTATGAGCATTTCAGAACT CCAAGGAGTCACAGGCATCTTTATAGTTCACGTTAACATATAGACACTGTTGGAAGCAGTTCCTTCTAA AAGGGTAGCCCTGGACTTAATACCAGCCGGATACCTCTGGCCCCCACCCCATTACTGTACCTCTGGA GTCACTACTGTGGGTCGCCACTCCTCTGCTACACAGCACGGCTTTTTCAAGGCTGTATTGAGAAGGGA AGTTAGGAAGAAGGGTGTGCTGGGCTAACCAGCCCACAGAGCTCACATTCCTGTCCCTTGGGTGAAA AATACATGTCCATCCTGATATCTCCTGAATTCAGAAATTAGCCTCCACATGTGCAATGGCTTTAAGAGC CAGAAGCAGGGTTCTGGGAATTTTGCAAGTTACCTGTGGCCAGGTGTGGTCTCGGTTACCAAATACGG TTACCTGCAGCTTTTTAGTCCTTTGTGCTCCCACGGGTCTACAGAGTCCCATCTGCCCAAAGGTCTTGA AGCTTGACAGGATGTTTTCGATTACTCAGTCTCCCAGGGCACTACTGGTCCGTAGGATTCGATTGGTC GGGGTAGGAGAGTTAAACAACATTTAAACAGAGTTCTCTCAAAAATGTCTAAAGGGATTGTAGGTAGAT AACATCCAATCACTGTTTGCACTTATCTGAAATCTTCCCTCTTGGCTGCCCCCAGGTATTTACTGTGGA GAACATTGCATAGGAATGTCTGGAAAAAGCTTCTACAACTTGTTACAGCCTTCACATTTGTAGAAGCTT T
68	COX8-ND1-3'UTR*	ATGTCCGTCCTGACGCGCCTGCTGCTGCGGGGCTTGACACGGCTCGGCTCGGCGGCTCCAGTGCGG CGCGCCAGAATCCATTCGTTGATGGCCAACCTCCTACTCCTCATTGTACCCATTCTAATCGCAATGGC ATTCCTAATGCTTACCGAACGAAAAATTCTAGGCTATATGCAACTACGCAAAGGCCCCAACGTTGTAGG CCCCTACGGGCTACTACAACCCTTCGCTGACGCCATAAAACTCTTCACCAAAGAGCCCCTAAAACCCG CCACATCTACCATCACCCTCTACATCACCGCCCCGACCTTAGCTCTCACCATCGCTCTTCTACTATGGA CCCCCCTCCCCATGCCCAACCCCCTGGTCAACCTCAACCTAGGCCTCCTATTTATTCTAGCCACCTCT AGCCTAGCCGTTTACTCAATCCTCTGGTCAGGGTGGGCATCAAACTCAAACTACGCCCTGATCGGCGC ACTGCGAGCAGTAGCCCAAACAATCTCATATGAAGTCACCCTAGCCATCATTCTACTATCAACATTACT AATGAGTGGCTCCTTTAACCTCTCCACCCTTATCACAACACAAGAACACCTCTGGTTACTCCTGCCATC ATGGCCCTTGGCCATGATGTGGTTTATCTCCACACTAGCAGAGACCAACCGAACCCCCTTCGACCTTG CCGAAGGGGAGTCCGAACTAGTCTCAGGCTTCAACATCGAATACGCCGCAGGCCCCTTCGCCCTATT CTTCATGGCCGAATACACAAACATTATTATGATGAACACCCTCACCACTACAATCTTCCTAGGAACAAC ATATGACGCACTCTCCCCTGAACTCTACACAACATATTTTGTCACCAAGACCCTACTTCTAACCTCCCT GTTCTTATGGATTCGAACAGCATACCCCCGATTCCGCTACGACCAACTCATGCACCTCCTATGGAAAA ACTTCCTACCACTCACCCTAGCATTACTTATGTGGTATGTCTCCATGCCCATTACAATCTCCAGCATTC CCCCTCAAACCTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTG TGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTC AGTGATCACTTGACAGTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAG CTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACC CCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCAT CCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGT GAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTT CCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTC TAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGG GAGTCTCAAGCTGGACTGCCA
69	COX8-opt_ND1-3'UTR	ATGTCCGTCCTGACGCGCCTGCTGCTGCGGGGCTTGACACGGCTCGGCTCGGCGGCTCCAGTGCGG CGCGCCAGAATCCATTCGTTGATGGCCAACCTGCTGCTGCTGATCGTGCCCATCCTGATCGCCATGG CCTTCCTGATGCTGACCGAGCGCAAGATCCTGGGCTACATGCAGCTGCGCAAGGGCCCCAACGTGGT GGGCCCCTACGGCCTGCTGCAGCCCTTCGCCGACGCCATCAAGCTGTTCACCAAGGAGCCCCTGAA GCCCGCCACCAGCACCATCACCCTGTACATCACCGCCCCCACCCTGGCCCTGACCATCGCCCTGCTG CTGTGGACCCCCCTGCCCATGCCCAACCCCCTGGTGAACCTGAACCTGGGCCTGCTGTTCATCCTGG CCACCAGCAGCCTGGCCGTGTACAGCATCCTGTGGAGCGGCTGGGCCAGCAACAGCAACTACGCCC TGATCGGCGCCCTGCGCGCCGTGGCCCAGACCATCAGCTACGAGGTGACCCTGGCCATCATCCTGC TGAGCACCCTGCTGATGAGCGGCAGCTTCAACCTGAGCACCCTGATCACCACCCAGGAGCACCTGTG GCTGCTGCTGCCCAGCTGGCCCCTGGCCATGATGTGGTTCATCAGCACCCTGGCCGAGACCAACCG CACCCCCTTCGACCTGGCCGAGGGCGAGAGCGAGCTGGTGAGCGGCTTCAACATCGAGTACGCCGC CGGCCCCTTCGCCCTGTTCTTCATGGCCGAGTACACCAACATCATCATGATGAACACCCTGACCACCA CCATCTTCCTGGGCACCACCTACGACGCCCTGAGCCCCGAGCTGTACACCACCTACTTCGTGACCAA GACCCTGCTGCTGACCAGCCTGTTCCTGTGGATCCGCACCGCCTACCCCCGCTTCCGCTACGACCAG CTGATGCACCTGCTGTGGAAGAACTTCCTGCCCCTGACCCTGGCCCTGCTGATGTGGTACGTGAGCA TGCCCATCACCATCAGCAGCATCCCCCCCCAGACCTAAGAGCACTGGGACGCCCACCGCCCCTTTCC CTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAAC AAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTAAATATTACCCAAAAT GCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGG GTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACAT ACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAG TGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCC TCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCC CACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGAC TGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCAGCCCCTGTCCTCCCTTCACCCC CATTGCGTATGAGCATTTCAGAACTCCAAGGAGTCACAGGCATCTTTATAGTTCACGTTAACATATAGA CACTGTTGGAAGCAGTTCCTTCTAAAAGGGTAGCCCTGGACTTAATACCAGCCGGATACCTCTGGCCC CCACCCCATTACTGTACCTCTGGAGTCACTACTGTGGGTCGCCACTCCTCTGCTACACAGCACGGCTT TTTCAAGGCTGTATTGAGAAGGGAAGTTAGGAAGAAGGGTGTGCTGGGCTAACCAGCCCACAGAGCT CACATTCCTGTCCCTTGGGTGAAAAATACATGTCCATCCTGATATCTCCTGAATTCAGAAATTAGCCTC

		CACATGTGCAATGGCTTTAAGAGCCAGAAGCAGGGTTCTGGGAATTTTGCAAGTTACCTGTGGCCAGG TGTGGTCTCGGTTACCAAATACGGTTACCTGCAGCTTTTTAGTCCTTTGTGCTCCCACGGGTCTACAGA GTCCCATCTGCCCAAAGGTCTTGAAGCTTGACAGGATGTTTTCGATTACTCAGTCTCCCAGGGCACTA CTGGTCCGTAGGATTCGATTGGTCGGGGTAGGAGAGTTAAACAACATTTAAACAGAGTTCTCTCAAAA ATGTCTAAAGGGATTGTAGGTAGATAACATCCAATCACTGTTTGCACTTATCTGAAATCTTCCCTCTTG GCTGCCCCCAGGTATTTACTGTGGAGAACATTGCATAGGAATGTCTGGAAAAAGCTTCTACAACTTGTT ACAGCCTTCACATTTGTAGAAGCTTT
70	COX8-opt_ND1-3'UTR*	ATGTCCGTCCTGACGCGCCTGCTGCTGCGGGGCTTGACACGGCTCGGCTCGGCGGCTCCAGTGCGG CGCGCCAGAATCCATTCGTTGATGGCCAACCTGCTGCTGCTGATCGTGCCCATCCTGATCGCCATGG CCTTCCTGATGCTGACCGAGCGCAAGATCCTGGGCTACATGCAGCTGCGCAAGGGCCCCAACGTGGT GGGCCCCTACGGCCTGCTGCAGCCCTTCGCCGACGCCATCAAGCTGTTCACCAAGGAGCCCCTGAA GCCCGCCACCAGCACCATCACCCTGTACATCACCGCCCCCACCCTGGCCCTGACCATCGCCCTGCTG CTGTGGACCCCCCTGCCCATGCCCAACCCCCTGGTGAACCTGAACCTGGGCCTGCTGTTCATCCTGG CCACCAGCAGCCTGGCCGTGTACAGCATCCTGTGGAGCGGCTGGGCCAGCAACAGCAACTACGCCC TGATCGGCGCCCTGCGCGCCGTGGCCCAGACCATCAGCTACGAGGTGACCCTGGCCATCATCCTGC TGAGCACCCTGCTGATGAGCGGCAGCTTCAACCTGAGCACCCTGATCACCACCCAGGAGCACCTGTG GCTGCTGCTGCCCAGCTGGCCCCTGGCCATGATGTGGTTCATCAGCACCCTGGCCGAGACCAACCG CACCCCCTTCGACCTGGCCGAGGGCGAGAGCGAGCTGGTGAGCGGCTTCAACATCGAGTACGCCGC CGGCCCCTTCGCCCTGTTCTTCATGGCCGAGTACACCAACATCATCATGATGAACACCCTGACCACCA CCATCTTCCTGGGCACCACCTACGACGCCCTGAGCCCCGAGCTGTACACCACCTACTTCGTGACCAA GACCCTGCTGCTGACCAGCCTGTTCCTGTGGATCCGCACCGCCTACCCCCGCTTCCGCTACGACCAG CTGATGCACCTGCTGTGGAAGAACTTCCTGCCCCTGACCCTGGCCCTGCTGATGTGGTACGTGAGCA TGCCCATCACCATCAGCAGCATCCCCCCCCAGACCTAAGAGCACTGGGACGCCCACCGCCCCTTTCC CTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAAC AAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTTAAATATTACCCAAAAT GCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGG GTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACAT ACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAG TGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCC TCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCC CACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGAC TGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCA
71	OPA1-ND4-3'UTR	GTGCTGCCCGCCTAGAAAGGGTGAAGTGGTTGTTTCCGTGACGGACTGAGTACGGGTGCCTGTCAGG CTCTTGCGGAAGTCCATGCGCCATTGGGAGGGCCTCGGCCGCGGCTCTGTGCCCTTGCTGCTGAGG GCCACTTCCTGGGTCATTCCTGGACCGGGAGCCGGGCTGGGGCTCACACGGGGGCTCCCGCGTGG CCGTCTCGGCGCCTGCGTGACCTCCCCGCCGGCGGGATGTGGCGACTACGTCGGGCCGCTGTGGC CTGATGCTAAAACTAATCGTCCCAACAATTATGTTACTACCACTGACATGGCTTTCCAAAAAACACATG ATTTGGATCAACACAACCACCCACAGCCTAATTATTAGCATCATCCCTCTACTATTTTTTAACCAAATCA ACAACAACCTATTTAGCTGTTCCCCAACCTTTTCCTCCGACCCCCTAACAACCCCCCTCCTAATGCTAA CTACCTGGCTCCTACCCCTCACAATCATGGCAAGCCAACGCCACTTATCCAGTGAACCACTATCACGA AAAAAACTCTACCTCTCTATGCTAATCTCCCTACAAATCTCCTTAATTATGACATTCACAGCCACAGAAC TAATCATGTTTTATATCTTCTTCGAAACCACACTTATCCCCACCTTGGCTATCATCACCCGATGGGGCA ACCAGCCAGAACGCCTGAACGCAGGCACATACTTCCTATTCTACACCCTAGTAGGCTCCCTTCCCCTA CTCATCGCACTAATTTACACTCACAACACCCTAGGCTCACTAAACATTCTACTACTCACTCTCACTGCC CAAGAACTATCAAACTCCTGGGCCAACAACTTAATGTGGCTAGCTTACACAATGGCTTTTATGGTAAAG ATGCCTCTTTACGGACTCCACTTATGGCTCCCTAAAGCCCATGTCGAAGCCCCCATCGCTGGGTCAAT GGTACTTGCCGCAGTACTCTTAAAACTAGGCGGCTATGGTATGATGCGCCTCACACTCATTCTCAACC CCCTGACAAAACACATGGCCTACCCCTTCCTTGTACTATCCCTATGGGGCATGATTATGACAAGCTCC ATCTGCCTACGACAAACAGACCTAAAATCGCTCATTGCATACTCTTCAATCAGCCACATGGCCCTCGTA GTAACAGCCATTCTCATCCAAACCCCCTGGAGCTTCACCGGCGCAGTCATTCTCATGATCGCCCACGG GCTTACATCCTCATTACTATTCTGCCTAGCAAACTCAAACTACGAACGCACTCACAGTCGCATCATGAT CCTCTCTCAAGGACTTCAAACTCTACTCCCACTAATGGCTTTTTGGTGGCTTCTAGCAAGCCTCGCTAA CCTCGCCTTACCCCCCACTATTAACCTACTGGGAGAACTCTCTGTGCTAGTAACCACGTTCTCCTGGT CAAATATCACTCTCCTACTTACAGGACTCAACATGCTAGTCACAGCCCTATACTCCCTCTACATGTTTA CCACAACACAATGGGGCTCACTCACCCACCACATTAACAACATGAAACCCTCATTCACACGAGAAAAC ACCCTCATGTTCATGCACCTATCCCCCATTCTCCTCCTATCCCTCAACCCCGACATCATTACCGGGTTT TCCTCTTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTA ATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGA TCACTTGACAGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAG TCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACC CTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTAC CACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCT

		CATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGT GACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAA TACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTC TCAAGCTGGACTGCCAGCCCCTGTCCTCCCTTCACCCCCATTGCGTATGAGCATTTCAGAACTCCAAG GAGTCACAGGCATCTTTATAGTTCACGTTAACATATAGACACTGTTGGAAGCAGTTCCTTCTAAAAGGG TAGCCCTGGACTTAATACCAGCCGGATACCTCTGGCCCCCACCCCATTACTGTACCTCTGGAGTCACT ACTGTGGGTCGCCACTCCTCTGCTACACAGCACGGCTTTTTCAAGGCTGTATTGAGAAGGGAAGTTAG GAAGAAGGGTGTGCTGGGCTAACCAGCCCACAGAGCTCACATTCCTGTCCCTTGGGTGAAAAATACAT GTCCATCCTGATATCTCCTGAATTCAGAAATTAGCCTCCACATGTGCAATGGCTTTAAGAGCCAGAAGC AGGGTTCTGGGAATTTTGCAAGTTACCTGTGGCCAGGTGTGGTCTCGGTTACCAAATACGGTTACCTG CAGCTTTTTAGTCCTTTGTGCTCCCACGGGTCTACAGAGTCCCATCTGCCCAAAGGTCTTGAAGCTTG ACAGGATGTTTTCGATTACTCAGTCTCCCAGGGCACTACTGGTCCGTAGGATTCGATTGGTCGGGGTA GGAGAGTTAAACAACATTTAAACAGAGTTCTCTCAAAAATGTCTAAAGGGATTGTAGGTAGATAACATC CAATCACTGTTTGCACTTATCTGAAATCTTCCCTCTTGGCTGCCCCCAGGTATTTACTGTGGAGAACAT TGCATAGGAATGTCTGGAAAAAGCTTCTACAACTTGTTACAGCCTTCACATTTGTAGAAGCTTT
72	OPA1-ND4-3'UTR*	GTGCTGCCCGCCTAGAAAGGGTGAAGTGGTTGTTTCCGTGACGGACTGAGTACGGGTGCCTGTCAGG CTCTTGCGGAAGTCCATGCGCCATTGGGAGGGCCTCGGCCGCGGCTCTGTGCCCTTGCTGCTGAGG GCCACTTCCTGGGTCATTCCTGGACCGGGAGCCGGGCTGGGGCTCACACGGGGGCTCCCGCGTGG CCGTCTCGGCGCCTGCGTGACCTCCCCGCCGGCGGGATGTGGCGACTACGTCGGGCCGCTGTGGC CTGATGCTAAAACTAATCGTCCCAACAATTATGTTACTACCACTGACATGGCTTTCCAAAAAACACATG ATTTGGATCAACACAACCACCCACAGCCTAATTATTAGCATCATCCCTCTACTATTTTTTAACCAAATCA ACAACAACCTATTTAGCTGTTCCCCAACCTTTTCCTCCGACCCCCTAACAACCCCCCTCCTAATGCTAA CTACCTGGCTCCTACCCCTCACAATCATGGCAAGCCAACGCCACTTATCCAGTGAACCACTATCACGA AAAAAACTCTACCTCTCTATGCTAATCTCCCTACAAATCTCCTTAATTATGACATTCACAGCCACAGAAC TAATCATGTTTTATATCTTCTTCGAAACCACACTTATCCCCACCTTGGCTATCATCACCCGATGGGGCA ACCAGCCAGAACGCCTGAACGCAGGCACATACTTCCTATTCTACACCCTAGTAGGCTCCCTTCCCCTA CTCATCGCACTAATTTACACTCACAACACCCTAGGCTCACTAAACATTCTACTACTCACTCTCACTGCC CAAGAACTATCAAACTCCTGGGCCAACAACTTAATGTGGCTAGCTTACACAATGGCTTTTATGGTAAAG ATGCCTCTTTACGGACTCCACTTATGGCTCCCTAAAGCCCATGTCGAAGCCCCCATCGCTGGGTCAAT GGTACTTGCCGCAGTACTCTTAAAACTAGGCGGCTATGGTATGATGCGCCTCACACTCATTCTCAACC CCCTGACAAAACACATGGCCTACCCCTTCCTTGTACTATCCCTATGGGGCATGATTATGACAAGCTCC ATCTGCCTACGACAAACAGACCTAAAATCGCTCATTGCATACTCTTCAATCAGCCACATGGCCCTCGTA GTAACAGCCATTCTCATCCAAACCCCCTGGAGCTTCACCGGCGCAGTCATTCTCATGATCGCCCACGG GCTTACATCCTCATTACTATTCTGCCTAGCAAACTCAAACTACGAACGCACTCACAGTCGCATCATGAT CCTCTCTCAAGGACTTCAAACTCTACTCCCACTAATGGCTTTTTGGTGGCTTCTAGCAAGCCTCGCTAA CCTCGCCTTACCCCCCACTATTAACCTACTGGGAGAACTCTCTGTGCTAGTAACCACGTTCTCCTGGT CAAATATCACTCTCCTACTTACAGGACTCAACATGCTAGTCACAGCCCTATACTCCCTCTACATGTTTA CCACAACACAATGGGGCTCACTCACCCACCACATTAACAACATGAAACCCTCATTCACACGAGAAAAC ACCCTCATGTTCATGCACCTATCCCCCATTCTCCTCCTATCCCTCAACCCCGACATCATTACCGGGTTT TCCTCTTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTA ATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGA TCACTTGACAGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAG TCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACC CTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTAC CACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCT CATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGT GACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAA TACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTC TCAAGCTGGACTGCCA

73	OPA1-opt_ND4-3'UTR	GTGCTGCCCGCCTAGAAAGGGTGAAGTGGTTGTTTCCGTGACGGACTGAGTACGGGTGCCTGTCAGG CTCTTGCGGAAGTCCATGCGCCATTGGGAGGGCCTCGGCCGCGGCTCTGTGCCCTTGCTGCTGAGG GCCACTTCCTGGGTCATTCCTGGACCGGGAGCCGGGCTGGGGCTCACACGGGGGCTCCCGCGTGG CCGTCTCGGCGCCTGCGTGACCTCCCCGCCGGCGGGATGTGGCGACTACGTCGGGCCGCTGTGGC CTGATGCTGAAGCTGATCGTGCCCACCATCATGCTGCTGCCTCTGACCTGGCTGAGCAAGAAACACAT GATCTGGATCAACACCACCACGCACAGCCTGATCATCAGCATCATCCCTCTGCTGTTCTTCAACCAGA TCAACAACAACCTGTTCAGCTGCAGCCCCACCTTCAGCAGCGACCCTCTGACAACACCTCTGCTGATG CTGACCACCTGGCTGCTGCCCCTCACAATCATGGCCTCTCAGAGACACCTGAGCAGCGAGCCCCTGA GCCGGAAGAAACTGTACCTGAGCATGCTGATCTCCCTGCAGATCTCTCTGATCATGACCTTCACCGCC ACCGAGCTGATCATGTTCTACATCTTTTTCGAGACAACGCTGATCCCCACACTGGCCATCATCACCAG ATGGGGCAACCAGCCTGAGAGACTGAACGCCGGCACCTACTTTCTGTTCTACACCCTCGTGGGCAGC CTGCCACTGCTGATTGCCCTGATCTACACCCACAACACCCTGGGCTCCCTGAACATCCTGCTGCTGAC ACTGACAGCCCAAGAGCTGAGCAACAGCTGGGCCAACAATCTGATGTGGCTGGCCTACACAATGGCC TTCATGGTCAAGATGCCCCTGTACGGCCTGCACCTGTGGCTGCCTAAAGCTCATGTGGAAGCCCCTAT CGCCGGCTCTATGGTGCTGGCTGCAGTGCTGCTGAAACTCGGCGGCTACGGCATGATGCGGCTGAC CCTGATTCTGAATCCCCTGACCAAGCACATGGCCTATCCATTTCTGGTGCTGAGCCTGTGGGGCATGA TTATGACCAGCAGCATCTGCCTGCGGCAGACCGATCTGAAGTCCCTGATCGCCTACAGCTCCATCAG CCACATGGCCCTGGTGGTCACCGCCATCCTGATTCAGACCCCTTGGAGCTTTACAGGCGCCGTGATC CTGATGATTGCCCACGGCCTGACAAGCAGCCTGCTGTTTTGTCTGGCCAACAGCAACTACGAGCGGA CCCACAGCAGAATCATGATCCTGTCTCAGGGCCTGCAGACCCTCCTGCCTCTTATGGCTTTTTGGTGG CTGCTGGCCTCTCTGGCCAATCTGGCACTGCCTCCTACCATCAATCTGCTGGGCGAGCTGAGCGTGC TGGTCACCACATTCAGCTGGTCCAATATCACCCTGCTGCTCACCGGCCTGAACATGCTGGTTACAGCC CTGTACTCCCTGTACATGTTCACCACCACACAGTGGGGAAGCCTGACACACCACATCAACAATATGAA GCCCAGCTTCACCCGCGAGAACACCCTGATGTTCATGCATCTGAGCCCCATTCTGCTGCTGTCCCTGA ATCCTGATATCATCACCGGCTTCTCCAGCTGAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGC TGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATT ATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCC CCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTT TATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACA GCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCA CTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAA GGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACA CATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGG GATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCAGCCCCTGTCCTCCCTTCACCCCCATT GCGTATGAGCATTTCAGAACTCCAAGGAGTCACAGGCATCTTTATAGTTCACGTTAACATATAGACACT GTTGGAAGCAGTTCCTTCTAAAAGGGTAGCCCTGGACTTAATACCAGCCGGATACCTCTGGCCCCCAC CCCATTACTGTACCTCTGGAGTCACTACTGTGGGTCGCCACTCCTCTGCTACACAGCACGGCTTTTTC AAGGCTGTATTGAGAAGGGAAGTTAGGAAGAAGGGTGTGCTGGGCTAACCAGCCCACAGAGCTCACA TTCCTGTCCCTTGGGTGAAAAATACATGTCCATCCTGATATCTCCTGAATTCAGAAATTAGCCTCCACA TGTGCAATGGCTTTAAGAGCCAGAAGCAGGGTTCTGGGAATTTTGCAAGTTACCTGTGGCCAGGTGTG GTCTCGGTTACCAAATACGGTTACCTGCAGCTTTTTAGTCCTTTGTGCTCCCACGGGTCTACAGAGTC CCATCTGCCCAAAGGTCTTGAAGCTTGACAGGATGTTTTCGATTACTCAGTCTCCCAGGGCACTACTG GTCCGTAGGATTCGATTGGTCGGGGTAGGAGAGTTAAACAACATTTAAACAGAGTTCTCTCAAAAATGT CTAAAGGGATTGTAGGTAGATAACATCCAATCACTGTTTGCACTTATCTGAAATCTTCCCTCTTGGCTG CCCCCAGGTATTTACTGTGGAGAACATTGCATAGGAATGTCTGGAAAAAGCTTCTACAACTTGTTACAG CCTTCACATTTGTAGAAGCTTT
74	OPA1-opt_ND4-3'UTR*	GTGCTGCCCGCCTAGAAAGGGTGAAGTGGTTGTTTCCGTGACGGACTGAGTACGGGTGCCTGTCAGG CTCTTGCGGAAGTCCATGCGCCATTGGGAGGGCCTCGGCCGCGGCTCTGTGCCCTTGCTGCTGAGG GCCACTTCCTGGGTCATTCCTGGACCGGGAGCCGGGCTGGGGCTCACACGGGGGCTCCCGCGTGG CCGTCTCGGCGCCTGCGTGACCTCCCCGCCGGCGGGATGTGGCGACTACGTCGGGCCGCTGTGGC CTGATGCTGAAGCTGATCGTGCCCACCATCATGCTGCTGCCTCTGACCTGGCTGAGCAAGAAACACAT GATCTGGATCAACACCACCACGCACAGCCTGATCATCAGCATCATCCCTCTGCTGTTCTTCAACCAGA TCAACAACAACCTGTTCAGCTGCAGCCCCACCTTCAGCAGCGACCCTCTGACAACACCTCTGCTGATG CTGACCACCTGGCTGCTGCCCCTCACAATCATGGCCTCTCAGAGACACCTGAGCAGCGAGCCCCTGA GCCGGAAGAAACTGTACCTGAGCATGCTGATCTCCCTGCAGATCTCTCTGATCATGACCTTCACCGCC ACCGAGCTGATCATGTTCTACATCTTTTTCGAGACAACGCTGATCCCCACACTGGCCATCATCACCAG ATGGGGCAACCAGCCTGAGAGACTGAACGCCGGCACCTACTTTCTGTTCTACACCCTCGTGGGCAGC CTGCCACTGCTGATTGCCCTGATCTACACCCACAACACCCTGGGCTCCCTGAACATCCTGCTGCTGAC ACTGACAGCCCAAGAGCTGAGCAACAGCTGGGCCAACAATCTGATGTGGCTGGCCTACACAATGGCC TTCATGGTCAAGATGCCCCTGTACGGCCTGCACCTGTGGCTGCCTAAAGCTCATGTGGAAGCCCCTAT CGCCGGCTCTATGGTGCTGGCTGCAGTGCTGCTGAAACTCGGCGGCTACGGCATGATGCGGCTGAC CCTGATTCTGAATCCCCTGACCAAGCACATGGCCTATCCATTTCTGGTGCTGAGCCTGTGGGGCATGA TTATGACCAGCAGCATCTGCCTGCGGCAGACCGATCTGAAGTCCCTGATCGCCTACAGCTCCATCAG CCACATGGCCCTGGTGGTCACCGCCATCCTGATTCAGACCCCTTGGAGCTTTACAGGCGCCGTGATC CTGATGATTGCCCACGGCCTGACAAGCAGCCTGCTGTTTTGTCTGGCCAACAGCAACTACGAGCGGA CCCACAGCAGAATCATGATCCTGTCTCAGGGCCTGCAGACCCTCCTGCCTCTTATGGCTTTTTGGTGG CTGCTGGCCTCTCTGGCCAATCTGGCACTGCCTCCTACCATCAATCTGCTGGGCGAGCTGAGCGTGC TGGTCACCACATTCAGCTGGTCCAATATCACCCTGCTGCTCACCGGCCTGAACATGCTGGTTACAGCC CTGTACTCCCTGTACATGTTCACCACCACACAGTGGGGAAGCCTGACACACCACATCAACAATATGAA GCCCAGCTTCACCCGCGAGAACACCCTGATGTTCATGCATCTGAGCCCCATTCTGCTGCTGTCCCTGA ATCCTGATATCATCACCGGCTTCTCCAGCTGAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGC TGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATT ATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCC CCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTT

		TATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACA GCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCA CTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAA GGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACA CATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGG GATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCA
75	OPA1-opt_ND4*-3'UTR	GTGCTGCCCGCCTAGAAAGGGTGAAGTGGTTGTTTCCGTGACGGACTGAGTACGGGTGCCTGTCAGG CTCTTGCGGAAGTCCATGCGCCATTGGGAGGGCCTCGGCCGCGGCTCTGTGCCCTTGCTGCTGAGG GCCACTTCCTGGGTCATTCCTGGACCGGGAGCCGGGCTGGGGCTCACACGGGGGCTCCCGCGTGG CCGTCTCGGCGCCTGCGTGACCTCCCCGCCGGCGGGATGTGGCGACTACGTCGGGCCGCTGTGGC CTGATGCTGAAGCTGATCGTGCCCACCATCATGCTGCTGCCCCTGACCTGGCTGAGCAAGAAGCACA TGATCTGGATCAACACCACCACCCACAGCCTGATCATCAGCATCATCCCCCTGCTGTTCTTCAACCAG ATCAACAACAACCTGTTCAGCTGCAGCCCCACCTTCAGCAGCGACCCCCTGACCACCCCCCTGCTGA TGCTGACCACCTGGCTGCTGCCCCTGACCATCATGGCCAGCCAGCGCCACCTGAGCAGCGAGCCCC TGAGCCGCAAGAAGCTGTACCTGAGCATGCTGATCAGCCTGCAGATCAGCCTGATCATGACCTTCACC GCCACCGAGCTGATCATGTTCTACATCTTCTTCGAGACCACCCTGATCCCCACCCTGGCCATCATCAC CCGCTGGGGCAACCAGCCCGAGCGCCTGAACGCCGGCACCTACTTCCTGTTCTACACCCTGGTGGG CAGCCTGCCCCTGCTGATCGCCCTGATCTACACCCACAACACCCTGGGCAGCCTGAACATCCTGCTG CTGACCCTGACCGCCCAGGAGCTGAGCAACAGCTGGGCCAACAACCTGATGTGGCTGGCCTACACCA TGGCCTTCATGGTGAAGATGCCCCTGTACGGCCTGCACCTGTGGCTGCCCAAGGCCCACGTGGAGG CCCCCATCGCCGGCAGCATGGTGCTGGCCGCCGTGCTGCTGAAGCTGGGCGGCTACGGCATGATGC GCCTGACCCTGATCCTGAACCCCCTGACCAAGCACATGGCCTACCCCTTCCTGGTGCTGAGCCTGTG GGGCATGATCATGACCAGCAGCATCTGCCTGCGCCAGACCGACCTGAAGAGCCTGATCGCCTACAGC AGCATCAGCCACATGGCCCTGGTGGTGACCGCCATCCTGATCCAGACCCCCTGGAGCTTCACCGGCG CCGTGATCCTGATGATCGCCCACGGCCTGACCAGCAGCCTGCTGTTCTGCCTGGCCAACAGCAACTA CGAGCGCACCCACAGCCGCATCATGATCCTGAGCCAGGGCCTGCAGACCCTGCTGCCCCTGATGGC CTTCTGGTGGCTGCTGGCCAGCCTGGCCAACCTGGCCCTGCCCCCCACCATCAACCTGCTGGGCGA GCTGAGCGTGCTGGTGACCACCTTCAGCTGGAGCAACATCACCCTGCTGCTGACCGGCCTGAACATG CTGGTGACCGCCCTGTACAGCCTGTACATGTTCACCACCACCCAGTGGGGCAGCCTGACCCACCACA TCAACAACATGAAGCCCAGCTTCACCCGCGAGAACACCCTGATGTTCATGCACCTGAGCCCCATCCTG CTGCTGAGCCTGAACCCCGACATCATCACCGGCTTCAGCAGCTAAGAGCACTGGGACGCCCACCGCC CCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGT TTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTAAATATTAC CCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCC TTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGG GTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACTCCACATGCCC AGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTC AGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTC CCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCA CTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCAGCCCCTGTCCTCCC TTCACCCCCATTGCGTATGAGCATTTCAGAACTCCAAGGAGTCACAGGCATCTTTATAGTTCACGTTAA CATATAGACACTGTTGGAAGCAGTTCCTTCTAAAAGGGTAGCCCTGGACTTAATACCAGCCGGATACC TCTGGCCCCCACCCCATTACTGTACCTCTGGAGTCACTACTGTGGGTCGCCACTCCTCTGCTACACAG CACGGCTTTTTCAAGGCTGTATTGAGAAGGGAAGTTAGGAAGAAGGGTGTGCTGGGCTAACCAGCCC ACAGAGCTCACATTCCTGTCCCTTGGGTGAAAAATACATGTCCATCCTGATATCTCCTGAATTCAGAAA TTAGCCTCCACATGTGCAATGGCTTTAAGAGCCAGAAGCAGGGTTCTGGGAATTTTGCAAGTTACCTG TGGCCAGGTGTGGTCTCGGTTACCAAATACGGTTACCTGCAGCTTTTTAGTCCTTTGTGCTCCCACGG GTCTACAGAGTCCCATCTGCCCAAAGGTCTTGAAGCTTGACAGGATGTTTTCGATTACTCAGTCTCCCA GGGCACTACTGGTCCGTAGGATTCGATTGGTCGGGGTAGGAGAGTTAAACAACATTTAAACAGAGTTC TCTCAAAAATGTCTAAAGGGATTGTAGGTAGATAACATCCAATCACTGTTTGCACTTATCTGAAATCTTC CCTCTTGGCTGCCCCCAGGTATTTACTGTGGAGAACATTGCATAGGAATGTCTGGAAAAAGCTTCTAC AACTTGTTACAGCCTTCACATTTGTAGAAGCTTT

76	OPA1-opt_ND4*-3'UTR*	GTGCTGCCCGCCTAGAAAGGGTGAAGTGGTTGTTTCCGTGACGGACTGAGTACGGGTGCCTGTCAGG CTCTTGCGGAAGTCCATGCGCCATTGGGAGGGCCTCGGCCGCGGCTCTGTGCCCTTGCTGCTGAGG GCCACTTCCTGGGTCATTCCTGGACCGGGAGCCGGGCTGGGGCTCACACGGGGGCTCCCGCGTGG CCGTCTCGGCGCCTGCGTGACCTCCCCGCCGGCGGGATGTGGCGACTACGTCGGGCCGCTGTGGC CTGATGCTGAAGCTGATCGTGCCCACCATCATGCTGCTGCCCCTGACCTGGCTGAGCAAGAAGCACA TGATCTGGATCAACACCACCACCCACAGCCTGATCATCAGCATCATCCCCCTGCTGTTCTTCAACCAG ATCAACAACAACCTGTTCAGCTGCAGCCCCACCTTCAGCAGCGACCCCCTGACCACCCCCCTGCTGA TGCTGACCACCTGGCTGCTGCCCCTGACCATCATGGCCAGCCAGCGCCACCTGAGCAGCGAGCCCC TGAGCCGCAAGAAGCTGTACCTGAGCATGCTGATCAGCCTGCAGATCAGCCTGATCATGACCTTCACC GCCACCGAGCTGATCATGTTCTACATCTTCTTCGAGACCACCCTGATCCCCACCCTGGCCATCATCAC CCGCTGGGGCAACCAGCCCGAGCGCCTGAACGCCGGCACCTACTTCCTGTTCTACACCCTGGTGGG CAGCCTGCCCCTGCTGATCGCCCTGATCTACACCCACAACACCCTGGGCAGCCTGAACATCCTGCTG CTGACCCTGACCGCCCAGGAGCTGAGCAACAGCTGGGCCAACAACCTGATGTGGCTGGCCTACACCA TGGCCTTCATGGTGAAGATGCCCCTGTACGGCCTGCACCTGTGGCTGCCCAAGGCCCACGTGGAGG CCCCCATCGCCGGCAGCATGGTGCTGGCCGCCGTGCTGCTGAAGCTGGGCGGCTACGGCATGATGC GCCTGACCCTGATCCTGAACCCCCTGACCAAGCACATGGCCTACCCCTTCCTGGTGCTGAGCCTGTG GGGCATGATCATGACCAGCAGCATCTGCCTGCGCCAGACCGACCTGAAGAGCCTGATCGCCTACAGC AGCATCAGCCACATGGCCCTGGTGGTGACCGCCATCCTGATCCAGACCCCCTGGAGCTTCACCGGCG CCGTGATCCTGATGATCGCCCACGGCCTGACCAGCAGCCTGCTGTTCTGCCTGGCCAACAGCAACTA CGAGCGCACCCACAGCCGCATCATGATCCTGAGCCAGGGCCTGCAGACCCTGCTGCCCCTGATGGC CTTCTGGTGGCTGCTGGCCAGCCTGGCCAACCTGGCCCTGCCCCCCACCATCAACCTGCTGGGCGA GCTGAGCGTGCTGGTGACCACCTTCAGCTGGAGCAACATCACCCTGCTGCTGACCGGCCTGAACATG CTGGTGACCGCCCTGTACAGCCTGTACATGTTCACCACCACCCAGTGGGGCAGCCTGACCCACCACA TCAACAACATGAAGCCCAGCTTCACCCGCGAGAACACCCTGATGTTCATGCACCTGAGCCCCATCCTG CTGCTGAGCCTGAACCCCGACATCATCACCGGCTTCAGCAGCTAAGAGCACTGGGACGCCCACCGCC CCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGT TTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTTAAATATTAC CCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCC TTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGG GTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACTCCACATGCCC AGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTC AGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTC CCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCA CTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCA
77	OPA1-ND6-3'UTR	GTGCTGCCCGCCTAGAAAGGGTGAAGTGGTTGTTTCCGTGACGGACTGAGTACGGGTGCCTGTCAGG CTCTTGCGGAAGTCCATGCGCCATTGGGAGGGCCTCGGCCGCGGCTCTGTGCCCTTGCTGCTGAGG GCCACTTCCTGGGTCATTCCTGGACCGGGAGCCGGGCTGGGGCTCACACGGGGGCTCCCGCGTGG CCGTCTCGGCGCCTGCGTGACCTCCCCGCCGGCGGGATGTGGCGACTACGTCGGGCCGCTGTGGC CTGATGATGTATGCTTTGTTTCTGTTGAGTGTGGGTTTAGTAATGGGGTTTGTGGGGTTTTCTTCTAAG CCTTCTCCTATTTATGGGGGTTTAGTATTGATTGTTAGCGGTGTGGTCGGGTGTGTTATTATTCTGAAT TTTGGGGGAGGTTATATGGGTTTAATGGTTTTTTTAATTTATTTAGGGGGAATGATGGTTGTCTTTGGAT ATACTACAGCGATGGCTATTGAGGAGTATCCTGAGGCATGGGGGTCAGGGGTTGAGGTCTTGGTGAG TGTTTTAGTGGGGTTAGCGATGGAGGTAGGATTGGTGCTGTGGGTGAAAGAGTATGATGGGGTGGTG GTTGTGGTAAACTTTAATAGTGTAGGAAGCTGGATGATTTATGAAGGAGAGGGGTCAGGGTTGATTCG GGAGGATCCTATTGGTGCGGGGGCTTTGTATGATTATGGGCGTTGGTTAGTAGTAGTTACTGGTTGGA CATTGTTTGTTGGTGTATATATTGTAATTGAGATTGCTCGGGGGAATTAGGAGCACTGGGACGCCCAC CGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCT GGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTTAAAT ATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTT TCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATG GGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACTCCACAT GCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTG AGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTG GTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCT GTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCAGCCCCTGTC CTCCCTTCACCCCCATTGCGTATGAGCATTTCAGAACTCCAAGGAGTCACAGGCATCTTTATAGTTCAC GTTAACATATAGACACTGTTGGAAGCAGTTCCTTCTAAAAGGGTAGCCCTGGACTTAATACCAGCCGG ATACCTCTGGCCCCCACCCCATTACTGTACCTCTGGAGTCACTACTGTGGGTCGCCACTCCTCTGCTA CACAGCACGGCTTTTTCAAGGCTGTATTGAGAAGGGAAGTTAGGAAGAAGGGTGTGCTGGGCTAACC AGCCCACAGAGCTCACATTCCTGTCCCTTGGGTGAAAAATACATGTCCATCCTGATATCTCCTGAATTC AGAAATTAGCCTCCACATGTGCAATGGCTTTAAGAGCCAGAAGCAGGGTTCTGGGAATTTTGCAAGTT ACCTGTGGCCAGGTGTGGTCTCGGTTACCAAATACGGTTACCTGCAGCTTTTTAGTCCTTTGTGCTCC CACGGGTCTACAGAGTCCCATCTGCCCAAAGGTCTTGAAGCTTGACAGGATGTTTTCGATTACTCAGT CTCCCAGGGCACTACTGGTCCGTAGGATTCGATTGGTCGGGGTAGGAGAGTTAAACAACATTTAAACA GAGTTCTCTCAAAAATGTCTAAAGGGATTGTAGGTAGATAACATCCAATCACTGTTTGCACTTATCTGA AATCTTCCCTCTTGGCTGCCCCCAGGTATTTACTGTGGAGAACATTGCATAGGAATGTCTGGAAAAAG CTTCTACAACTTGTTACAGCCTTCACATTTGTAGAAGCTTT

78	OPA1-ND6-3'UTR*	GTGCTGCCCGCCTAGAAAGGGTGAAGTGGTTGTTTCCGTGACGGACTGAGTACGGGTGCCTGTCAGG CTCTTGCGGAAGTCCATGCGCCATTGGGAGGGCCTCGGCCGCGGCTCTGTGCCCTTGCTGCTGAGG GCCACTTCCTGGGTCATTCCTGGACCGGGAGCCGGGCTGGGGCTCACACGGGGGCTCCCGCGTGG CCGTCTCGGCGCCTGCGTGACCTCCCCGCCGGCGGGATGTGGCGACTACGTCGGGCCGCTGTGGC CTGATGATGTATGCTTTGTTTCTGTTGAGTGTGGGTTTAGTAATGGGGTTTGTGGGGTTTTCTTCTAAG CCTTCTCCTATTTATGGGGGTTTAGTATTGATTGTTAGCGGTGTGGTCGGGTGTGTTATTATTCTGAAT TTTGGGGGAGGTTATATGGGTTTAATGGTTTTTTTAATTTATTTAGGGGGAATGATGGTTGTCTTTGGAT ATACTACAGCGATGGCTATTGAGGAGTATCCTGAGGCATGGGGGTCAGGGGTTGAGGTCTTGGTGAG TGTTTTAGTGGGGTTAGCGATGGAGGTAGGATTGGTGCTGTGGGTGAAAGAGTATGATGGGGTGGTG GTTGTGGTAAACTTTAATAGTGTAGGAAGCTGGATGATTTATGAAGGAGAGGGGTCAGGGTTGATTCG GGAGGATCCTATTGGTGCGGGGGCTTTGTATGATTATGGGCGTTGGTTAGTAGTAGTTACTGGTTGGA CATTGTTTGTTGGTGTATATATTGTAATTGAGATTGCTCGGGGGAATTAGGAGCACTGGGACGCCCAC CGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCT GGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTAAAT ATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTT TCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATG GGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCACACGCACACTCCACAT GCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTG AGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTG GTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGCTAGGACCCGGCTGCT GTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGACTGCCA
79	OPA1-opt_ND6-3'UTR	GTGCTGCCCGCCTAGAAAGGGTGAAGTGGTTGTTTCCGTGACGGACTGAGTACGGGTGCCTGTCAGG CTCTTGCGGAAGTCCATGCGCCATTGGGAGGGCCTCGGCCGCGGCTCTGTGCCCTTGCTGCTGAGG GCCACTTCCTGGGTCATTCCTGGACCGGGAGCCGGGCTGGGGCTCACACGGGGGCTCCCGCGTGG CCGTCTCGGCGCCTGCGTGACCTCCCCGCCGGCGGGATGTGGCGACTACGTCGGGCCGCTGTGGC CTGATGATGTACGCCCTGTTCCTGCTGAGCGTGGGCCTGGTGATGGGCTTCGTGGGCTTCAGCAGCA AGCCCAGCCCCATCTACGGCGGCCTGGTGCTGATCGTGAGCGGCGTGGTGGGCTGCGTGATCATCC TGAACTTCGGCGGCGGCTACATGGGCCTGATGGTGTTCCTGATCTACCTGGGCGGCATGATGGTGGT GTTCGGCTACACCACCGCCATGGCCATCGAGGAGTACCCCGAGGCCTGGGGCAGCGGCGTGGAGGT GCTGGTGAGCGTGCTGGTGGGCCTGGCCATGGAGGTGGGCCTGGTGCTGTGGGTGAAGGAGTACGA CGGCGTGGTGGTGGTGGTGAACTTCAACAGCGTGGGCAGCTGGATGATCTACGAGGGCGAGGGCAG CGGCCTGATCCGCGAGGACCCCATCGGCGCCGGCGCCCTGTACGACTACGGCCGCTGGCTGGTGGT GGTGACCGGCTGGACCCTGTTCGTGGGCGTGTACATCGTGATCGAGATCGCCCGCGGCAACTAAGA GCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACA CAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAG TTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATAC AAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGT TTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCA CACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGC TGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCA GGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGC TAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGA CTGCCAGCCCCTGTCCTCCCTTCACCCCCATTGCGTATGAGCATTTCAGAACTCCAAGGAGTCACAGG CATCTTTATAGTTCACGTTAACATATAGACACTGTTGGAAGCAGTTCCTTCTAAAAGGGTAGCCCTGGA CTTAATACCAGCCGGATACCTCTGGCCCCCACCCCATTACTGTACCTCTGGAGTCACTACTGTGGGTC GCCACTCCTCTGCTACACAGCACGGCTTTTTCAAGGCTGTATTGAGAAGGGAAGTTAGGAAGAAGGGT GTGCTGGGCTAACCAGCCCACAGAGCTCACATTCCTGTCCCTTGGGTGAAAAATACATGTCCATCCTG ATATCTCCTGAATTCAGAAATTAGCCTCCACATGTGCAATGGCTTTAAGAGCCAGAAGCAGGGTTCTG GGAATTTTGCAAGTTACCTGTGGCCAGGTGTGGTCTCGGTTACCAAATACGGTTACCTGCAGCTTTTTA GTCCTTTGTGCTCCCACGGGTCTACAGAGTCCCATCTGCCCAAAGGTCTTGAAGCTTGACAGGATGTT TTCGATTACTCAGTCTCCCAGGGCACTACTGGTCCGTAGGATTCGATTGGTCGGGGTAGGAGAGTTAA ACAACATTTAAACAGAGTTCTCTCAAAAATGTCTAAAGGGATTGTAGGTAGATAACATCCAATCACTGTT TGCACTTATCTGAAATCTTCCCTCTTGGCTGCCCCCAGGTATTTACTGTGGAGAACATTGCATAGGAAT GTCTGGAAAAAGCTTCTACAACTTGTTACAGCCTTCACATTTGTAGAAGCTTT
80	OPA1-opt_ND6-3'UTR*	GTGCTGCCCGCCTAGAAAGGGTGAAGTGGTTGTTTCCGTGACGGACTGAGTACGGGTGCCTGTCAGG CTCTTGCGGAAGTCCATGCGCCATTGGGAGGGCCTCGGCCGCGGCTCTGTGCCCTTGCTGCTGAGG GCCACTTCCTGGGTCATTCCTGGACCGGGAGCCGGGCTGGGGCTCACACGGGGGCTCCCGCGTGG CCGTCTCGGCGCCTGCGTGACCTCCCCGCCGGCGGGATGTGGCGACTACGTCGGGCCGCTGTGGC CTGATGATGTACGCCCTGTTCCTGCTGAGCGTGGGCCTGGTGATGGGCTTCGTGGGCTTCAGCAGCA AGCCCAGCCCCATCTACGGCGGCCTGGTGCTGATCGTGAGCGGCGTGGTGGGCTGCGTGATCATCC TGAACTTCGGCGGCGGCTACATGGGCCTGATGGTGTTCCTGATCTACCTGGGCGGCATGATGGTGGT GTTCGGCTACACCACCGCCATGGCCATCGAGGAGTACCCCGAGGCCTGGGGCAGCGGCGTGGAGGT GCTGGTGAGCGTGCTGGTGGGCCTGGCCATGGAGGTGGGCCTGGTGCTGTGGGTGAAGGAGTACGA CGGCGTGGTGGTGGTGGTGAACTTCAACAGCGTGGGCAGCTGGATGATCTACGAGGGCGAGGGCAG CGGCCTGATCCGCGAGGACCCCATCGGCGCCGGCGCCCTGTACGACTACGGCCGCTGGCTGGTGGT GGTGACCGGCTGGACCCTGTTCGTGGGCGTGTACATCGTGATCGAGATCGCCCGCGGCAACTAAGA GCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACA CAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAG TTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATAC AAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGT TTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCA CACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGC TGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCA GGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGC

		TAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGA CTGCCA
81	OPA1-ND1-3'UTR	GTGCTGCCCGCCTAGAAAGGGTGAAGTGGTTGTTTCCGTGACGGACTGAGTACGGGTGCCTGTCAGG CTCTTGCGGAAGTCCATGCGCCATTGGGAGGGCCTCGGCCGCGGCTCTGTGCCCTTGCTGCTGAGG GCCACTTCCTGGGTCATTCCTGGACCGGGAGCCGGGCTGGGGCTCACACGGGGGCTCCCGCGTGG CCGTCTCGGCGCCTGCGTGACCTCCCCGCCGGCGGGATGTGGCGACTACGTCGGGCCGCTGTGGC CTGATGGCCAACCTCCTACTCCTCATTGTACCCATTCTAATCGCAATGGCATTCCTAATGCTTACCGAA CGAAAAATTCTAGGCTATATGCAACTACGCAAAGGCCCCAACGTTGTAGGCCCCTACGGGCTACTACA ACCCTTCGCTGACGCCATAAAACTCTTCACCAAAGAGCCCCTAAAACCCGCCACATCTACCATCACCC TCTACATCACCGCCCCGACCTTAGCTCTCACCATCGCTCTTCTACTATGGACCCCCCTCCCCATGCCC AACCCCCTGGTCAACCTCAACCTAGGCCTCCTATTTATTCTAGCCACCTCTAGCCTAGCCGTTTACTCA ATCCTCTGGTCAGGGTGGGCATCAAACTCAAACTACGCCCTGATCGGCGCACTGCGAGCAGTAGCCC AAACAATCTCATATGAAGTCACCCTAGCCATCATTCTACTATCAACATTACTAATGAGTGGCTCCTTTAA CCTCTCCACCCTTATCACAACACAAGAACACCTCTGGTTACTCCTGCCATCATGGCCCTTGGCCATGA TGTGGTTTATCTCCACACTAGCAGAGACCAACCGAACCCCCTTCGACCTTGCCGAAGGGGAGTCCGA ACTAGTCTCAGGCTTCAACATCGAATACGCCGCAGGCCCCTTCGCCCTATTCTTCATGGCCGAATACA CAAACATTATTATGATGAACACCCTCACCACTACAATCTTCCTAGGAACAACATATGACGCACTCTCCC CTGAACTCTACACAACATATTTTGTCACCAAGACCCTACTTCTAACCTCCCTGTTCTTATGGATTCGAAC AGCATACCCCCGATTCCGCTACGACCAACTCATGCACCTCCTATGGAAAAACTTCCTACCACTCACCC TAGCATTACTTATGTGGTATGTCTCCATGCCCATTACAATCTCCAGCATTCCCCCTCAAACCTAAGAGC ACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACA AGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTT TTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACA AAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTT TCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCAC ACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCT GTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCA GGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGC TAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGA CTGCCAGCCCCTGTCCTCCCTTCACCCCCATTGCGTATGAGCATTTCAGAACTCCAAGGAGTCACAGG CATCTTTATAGTTCACGTTAACATATAGACACTGTTGGAAGCAGTTCCTTCTAAAAGGGTAGCCCTGGA CTTAATACCAGCCGGATACCTCTGGCCCCCACCCCATTACTGTACCTCTGGAGTCACTACTGTGGGTC GCCACTCCTCTGCTACACAGCACGGCTTTTTCAAGGCTGTATTGAGAAGGGAAGTTAGGAAGAAGGGT GTGCTGGGCTAACCAGCCCACAGAGCTCACATTCCTGTCCCTTGGGTGAAAAATACATGTCCATCCTG ATATCTCCTGAATTCAGAAATTAGCCTCCACATGTGCAATGGCTTTAAGAGCCAGAAGCAGGGTTCTG GGAATTTTGCAAGTTACCTGTGGCCAGGTGTGGTCTCGGTTACCAAATACGGTTACCTGCAGCTTTTTA GTCCTTTGTGCTCCCACGGGTCTACAGAGTCCCATCTGCCCAAAGGTCTTGAAGCTTGACAGGATGTT TTCGATTACTCAGTCTCCCAGGGCACTACTGGTCCGTAGGATTCGATTGGTCGGGGTAGGAGAGTTAA ACAACATTTAAACAGAGTTCTCTCAAAAATGTCTAAAGGGATTGTAGGTAGATAACATCCAATCACTGTT TGCACTTATCTGAAATCTTCCCTCTTGGCTGCCCCCAGGTATTTACTGTGGAGAACATTGCATAGGAAT GTCTGGAAAAAGCTTCTACAACTTGTTACAGCCTTCACATTTGTAGAAGCTTT
82	OPA1-ND1-3'UTR*	GTGCTGCCCGCCTAGAAAGGGTGAAGTGGTTGTTTCCGTGACGGACTGAGTACGGGTGCCTGTCAGG CTCTTGCGGAAGTCCATGCGCCATTGGGAGGGCCTCGGCCGCGGCTCTGTGCCCTTGCTGCTGAGG GCCACTTCCTGGGTCATTCCTGGACCGGGAGCCGGGCTGGGGCTCACACGGGGGCTCCCGCGTGG CCGTCTCGGCGCCTGCGTGACCTCCCCGCCGGCGGGATGTGGCGACTACGTCGGGCCGCTGTGGC CTGATGGCCAACCTCCTACTCCTCATTGTACCCATTCTAATCGCAATGGCATTCCTAATGCTTACCGAA CGAAAAATTCTAGGCTATATGCAACTACGCAAAGGCCCCAACGTTGTAGGCCCCTACGGGCTACTACA ACCCTTCGCTGACGCCATAAAACTCTTCACCAAAGAGCCCCTAAAACCCGCCACATCTACCATCACCC TCTACATCACCGCCCCGACCTTAGCTCTCACCATCGCTCTTCTACTATGGACCCCCCTCCCCATGCCC AACCCCCTGGTCAACCTCAACCTAGGCCTCCTATTTATTCTAGCCACCTCTAGCCTAGCCGTTTACTCA ATCCTCTGGTCAGGGTGGGCATCAAACTCAAACTACGCCCTGATCGGCGCACTGCGAGCAGTAGCCC AAACAATCTCATATGAAGTCACCCTAGCCATCATTCTACTATCAACATTACTAATGAGTGGCTCCTTTAA CCTCTCCACCCTTATCACAACACAAGAACACCTCTGGTTACTCCTGCCATCATGGCCCTTGGCCATGA TGTGGTTTATCTCCACACTAGCAGAGACCAACCGAACCCCCTTCGACCTTGCCGAAGGGGAGTCCGA ACTAGTCTCAGGCTTCAACATCGAATACGCCGCAGGCCCCTTCGCCCTATTCTTCATGGCCGAATACA CAAACATTATTATGATGAACACCCTCACCACTACAATCTTCCTAGGAACAACATATGACGCACTCTCCC CTGAACTCTACACAACATATTTTGTCACCAAGACCCTACTTCTAACCTCCCTGTTCTTATGGATTCGAAC AGCATACCCCCGATTCCGCTACGACCAACTCATGCACCTCCTATGGAAAAACTTCCTACCACTCACCC TAGCATTACTTATGTGGTATGTCTCCATGCCCATTACAATCTCCAGCATTCCCCCTCAAACCTAAGAGC ACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAACACA AGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGACAGTT TTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAATACA AAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTGTT TCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACCAC ACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTGCT

		GTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTTGTGACTGAGCCA GGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATAGC TAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTGGA CTGCCA
83	OPA1-opt_ND1-3'UTR	GTGCTGCCCGCCTAGAAAGGGTGAAGTGGTTGTTTCCGTGACGGACTGAGTACGGGTGCCTGTCAGG CTCTTGCGGAAGTCCATGCGCCATTGGGAGGGCCTCGGCCGCGGCTCTGTGCCCTTGCTGCTGAGG GCCACTTCCTGGGTCATTCCTGGACCGGGAGCCGGGCTGGGGCTCACACGGGGGCTCCCGCGTGG CCGTCTCGGCGCCTGCGTGACCTCCCCGCCGGCGGGATGTGGCGACTACGTCGGGCCGCTGTGGC CTGATGGCCAACCTGCTGCTGCTGATCGTGCCCATCCTGATCGCCATGGCCTTCCTGATGCTGACCG AGCGCAAGATCCTGGGCTACATGCAGCTGCGCAAGGGCCCCAACGTGGTGGGCCCCTACGGCCTGC TGCAGCCCTTCGCCGACGCCATCAAGCTGTTCACCAAGGAGCCCCTGAAGCCCGCCACCAGCACCAT CACCCTGTACATCACCGCCCCCACCCTGGCCCTGACCATCGCCCTGCTGCTGTGGACCCCCCTGCCC ATGCCCAACCCCCTGGTGAACCTGAACCTGGGCCTGCTGTTCATCCTGGCCACCAGCAGCCTGGCCG TGTACAGCATCCTGTGGAGCGGCTGGGCCAGCAACAGCAACTACGCCCTGATCGGCGCCCTGCGCG CCGTGGCCCAGACCATCAGCTACGAGGTGACCCTGGCCATCATCCTGCTGAGCACCCTGCTGATGAG CGGCAGCTTCAACCTGAGCACCCTGATCACCACCCAGGAGCACCTGTGGCTGCTGCTGCCCAGCTGG CCCCTGGCCATGATGTGGTTCATCAGCACCCTGGCCGAGACCAACCGCACCCCCTTCGACCTGGCCG AGGGCGAGAGCGAGCTGGTGAGCGGCTTCAACATCGAGTACGCCGCCGGCCCCTTCGCCCTGTTCT TCATGGCCGAGTACACCAACATCATCATGATGAACACCCTGACCACCACCATCTTCCTGGGCACCACC TACGACGCCCTGAGCCCCGAGCTGTACACCACCTACTTCGTGACCAAGACCCTGCTGCTGACCAGCC TGTTCCTGTGGATCCGCACCGCCTACCCCCGCTTCCGCTACGACCAGCTGATGCACCTGCTGTGGAA GAACTTCCTGCCCCTGACCCTGGCCCTGCTGATGTGGTACGTGAGCATGCCCATCACCATCAGCAGC ATCCCCCCCCAGACCTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCAT GTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGT GCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGC ATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTC CAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGT TCCATCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAA AGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACC CCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGT CCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGC CTTGGGAGTCTCAAGCTGGACTGCCAGCCCCTGTCCTCCCTTCACCCCCATTGCGTATGAGCATTTCA GAACTCCAAGGAGTCACAGGCATCTTTATAGTTCACGTTAACATATAGACACTGTTGGAAGCAGTTCCT TCTAAAAGGGTAGCCCTGGACTTAATACCAGCCGGATACCTCTGGCCCCCACCCCATTACTGTACCTC TGGAGTCACTACTGTGGGTCGCCACTCCTCTGCTACACAGCACGGCTTTTTCAAGGCTGTATTGAGAA GGGAAGTTAGGAAGAAGGGTGTGCTGGGCTAACCAGCCCACAGAGCTCACATTCCTGTCCCTTGGGT GAAAAATACATGTCCATCCTGATATCTCCTGAATTCAGAAATTAGCCTCCACATGTGCAATGGCTTTAA GAGCCAGAAGCAGGGTTCTGGGAATTTTGCAAGTTACCTGTGGCCAGGTGTGGTCTCGGTTACCAAAT ACGGTTACCTGCAGCTTTTTAGTCCTTTGTGCTCCCACGGGTCTACAGAGTCCCATCTGCCCAAAGGT CTTGAAGCTTGACAGGATGTTTTCGATTACTCAGTCTCCCAGGGCACTACTGGTCCGTAGGATTCGAT TGGTCGGGGTAGGAGAGTTAAACAACATTTAAACAGAGTTCTCTCAAAAATGTCTAAAGGGATTGTAG GTAGATAACATCCAATCACTGTTTGCACTTATCTGAAATCTTCCCTCTTGGCTGCCCCCAGGTATTTAC TGTGGAGAACATTGCATAGGAATGTCTGGAAAAAGCTTCTACAACTTGTTACAGCCTTCACATTTGTAG AAGCTTT
84	OPA1-opt_ND1-3'UTR*	GTGCTGCCCGCCTAGAAAGGGTGAAGTGGTTGTTTCCGTGACGGACTGAGTACGGGTGCCTGTCAGG CTCTTGCGGAAGTCCATGCGCCATTGGGAGGGCCTCGGCCGCGGCTCTGTGCCCTTGCTGCTGAGG GCCACTTCCTGGGTCATTCCTGGACCGGGAGCCGGGCTGGGGCTCACACGGGGGCTCCCGCGTGG CCGTCTCGGCGCCTGCGTGACCTCCCCGCCGGCGGGATGTGGCGACTACGTCGGGCCGCTGTGGC CTGATGGCCAACCTGCTGCTGCTGATCGTGCCCATCCTGATCGCCATGGCCTTCCTGATGCTGACCG AGCGCAAGATCCTGGGCTACATGCAGCTGCGCAAGGGCCCCAACGTGGTGGGCCCCTACGGCCTGC TGCAGCCCTTCGCCGACGCCATCAAGCTGTTCACCAAGGAGCCCCTGAAGCCCGCCACCAGCACCAT CACCCTGTACATCACCGCCCCCACCCTGGCCCTGACCATCGCCCTGCTGCTGTGGACCCCCCTGCCC ATGCCCAACCCCCTGGTGAACCTGAACCTGGGCCTGCTGTTCATCCTGGCCACCAGCAGCCTGGCCG TGTACAGCATCCTGTGGAGCGGCTGGGCCAGCAACAGCAACTACGCCCTGATCGGCGCCCTGCGCG CCGTGGCCCAGACCATCAGCTACGAGGTGACCCTGGCCATCATCCTGCTGAGCACCCTGCTGATGAG CGGCAGCTTCAACCTGAGCACCCTGATCACCACCCAGGAGCACCTGTGGCTGCTGCTGCCCAGCTGG CCCCTGGCCATGATGTGGTTCATCAGCACCCTGGCCGAGACCAACCGCACCCCCTTCGACCTGGCCG AGGGCGAGAGCGAGCTGGTGAGCGGCTTCAACATCGAGTACGCCGCCGGCCCCTTCGCCCTGTTCT TCATGGCCGAGTACACCAACATCATCATGATGAACACCCTGACCACCACCATCTTCCTGGGCACCACC TACGACGCCCTGAGCCCCGAGCTGTACACCACCTACTTCGTGACCAAGACCCTGCTGCTGACCAGCC TGTTCCTGTGGATCCGCACCGCCTACCCCCGCTTCCGCTACGACCAGCTGATGCACCTGCTGTGGAA GAACTTCCTGCCCCTGACCCTGGCCCTGCTGATGTGGTACGTGAGCATGCCCATCACCATCAGCAGC ATCCCCCCCCAGACCTAAGAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCAT GTTGTGGTAATTCTGGAACACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGT

		GCTCAGTGATCACTTGACAGTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGC ATCAGCTCAGTCAGTGAATACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTTATACATCTCTCCTC CAACCCCACCCTCTATTCTGTTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGT TCCATCCTTACCACCACACCACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAA AGTGTGAGCCTCATGATCTGCTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACC CCCTTCCTTGTGACTGAGCCAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGT CCTTCTAACAATACCAATAGCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGC CTTGGGAGTCTCAAGCTGGACTGCCA
85	β-actin-S primer	CGAGATCGTGCGGGACAT
86	β-actin-A primer	CAGGAAGGAGGGCTGGAAC
87	ND4-S primer	CTGCCTACGACAAACAGAC
88	ND4-A primer	AGTGCGTTCGTAGTTTGAG
89	ND6-F primer	ATGATGTATGCTTTGTTTCTG
90	ND6-R primer	CTAATTCCCCCGAGCAATCTC
91	ND6-S primer	AGTGTGGGTTTAGTAATG
92	ND6-A primer	TGCCTCAGGATACTCCTC
93	β-actin-F primer	CTCCATCCTGGCCTCGCTGT
94	β-actin-R primer	GCTGTCACCTTCACCGTTCC
95	ND6-F primer	GGGTTTTCTTCTAAGCCTTCTCC
96	ND6-R primer	CCATCATACTCTTTCACCCACAG
97	opt_ND6-F primer	CGCCTGCTGACCGGCTGCGT
98	opt_ND6-R	CCAGGCCTCGGGGTACTCCT
99	ND1-F primer	ATGGCCGCATCTCCGCACACT
100	ND1-R primer	TTAGGTTTGAGGGGGAATGCT
101	ND1-F primer	AACCTCAACCTAGGCCTCCTA
102	ND1-R primer	TGGCAGGAGTAACCAGAGGTG
103	ND1-F primer	AGGAGGCTCTGTCTGGTATCTTG
104	ND1-R primer	TTTTAGGGGCTCTTTGGTGAA
105	opt-ND1-F primer	GCCGCCTGCTGACCGGCTGCGT
106	opt-ND1-R primer	TGATGTACAGGGTGATGGTGCTGG
107	ND4-S primer	GCCAACAGCAACTACGAGC
108	ND4-A primer	TGATGTTGCTCCAGCTGAAG
109	opt-ND4-S primer	GCCTGACCCTGATCCTGAAC
110	opt-ND4-A primer	GTGCGCTCGTAGTTGCTGTT
111	hsACO2	GGGCAGTGCCTCCCCGCCCCGCCGCTGGCGTCAAGTTCAGCTCCACGTGTGCCATCAGTGGATCCG ATCCGTCCAGCCATGGCTTCCTATTCCAAGATGGTGTGACCAGACATGCTTCCTGCTCCCCGCTTAGC CCACGGAGTGACTGTGGTTGTGGTGGGGGGGTTCTTAAAATAACTTTTTAGCCCCCGTCTTCCTATTTT GAGTTTGGTTCAGATCTTAAGCAGCTCCATGCAACTGTATTTATTTTTGATGACAAGACTCCCATCTAAA GTTTTTCTCCTGCCTGATCATTTCATTGGTGGCTGAAGGATTCTAGAGAACCTTTTGTTCTTGCAAGGA AAACAAGAATCCAAAACCAGTGACTGTTCTGTGA
112	hsATP5B	GGGGTCTTTGTCCTCTGTACTGTCTCTCTCCTTGCCCCTAACCCAAAAAGCTTCATTTTTCTGTGTAGG CTGCACAAGAGCCTTGATTGAAGATATATTCTTTCTGAACAGTATTTAAGGTTTCCAATAAAATGTACAC CCCTCAG

113	hsAK2	TGTTGGGTCCAAGAAGGAATTTCTTTCCATCCCTGTGAGGCAATGGGTGGGAATGATAGGACAGGCAA AGAGAAGCTTCCTCAGGCTAGCAAAAATATCATTTGATGTATTGATTAAAAAAGCACTTGCTTGATGTAT CTTTGGCGTGTGTGCTACTCTCATCTGTGTGTATGTGTGTTGTGTGTGTGTGTGTGCATGCACATAT GTGTTCACTCTGCTACTTTGTAAGTTTTAGGCTAGGTTGCTTTACCAGCTGTTTACTTCTTTTTTGTTGTT GTTTTGAGACAAGGTTTCGCTCTGCCACCCTGGCTGGAGTGCAGTGGCGTGATCTTGGCTCACGGCA ACCTCTGCCTCCTGGGGCTCAAGCAATTATCCCACCTCAGCCTCCTGAGCAGCTGGGACTACAGGTG CATGCCACAACACCTGGCTGATATTTGTATTTTTTGTAGAGACAGGATTTTGCCAAGTTGCCCAGGCTG GTCTTGAACTCCTAGGCTTAAGCAATCCACCCACCTTGGCCTCCTGAAGTGCCAGGATCACAGACGTG AGCCACTACACCCAGCCCAGCTGTTTACTTCTTTAACCATACTTTTGATTTTATTTTTTGACCAAAATGA ACTAACCCAGGTAATCTTCCAGGGACCGCAATTCCAGAACCTCATAGTATTTCTTCCATTTCCAGCAGC TGATTAGAAGTCCAGGATCATGTGAAGTCAGGCAGGGTCACAGTTCCTGATGGCACATTATGGACAGA GAATTCCATTTTGTTTTCTAACCCATGATGAAAACCCACGTGAGTCAGTGTGTGAACAGGGATCATTAA TTTTTTCCCCCTAGGTGGAAGGAAAAAGGCACTTACTTTGCAGGTTACAGAAATTACTGGGAGAGGAT ATCGTCATAAAAAGAGCCAGGCCAAATTGGAATATTTTTGTGATCTGCATCATGATGCTGAAAATAGCA ATTATTTGGGAATTGGGTTTGAAAACTGAATTGTTGCCAGAGAATTAAACCAGGTGAAAGGTCCTTTTG AATTCAGATTGTCTTCTGAACATCCAGGCTGATCATCTGAGAGCAGTCAAATCTACTTCCCCAAAAAGA GACCAGGGTAGGTTTATTTGCTTTTATTTTTAATGTTTGCCTGTGTTTCCAAGTGTGAACAAAACAGTGT GTGATCTATTCTTGGATTCATTTTGATCAGTATTTATTCAAACCCAGTCTCTCTCCAGGACATAAAACTG AAATCAGATATGTTCTTTTTAAGCCCAAACCCTCTCCTTTCTAGATCCAACCCTTCACCCCTAATTTTAT GATGGCTATAGCCATGGACTTCCCCAAGAAAAGATCACCCAGAAATAAGACCACCTGTGACAGTTACC AGCTTTTATTCATAACCTTAGCTTCCCAACTATTGAGCATTTTCTAAGGTCCCTGCTGTCTTTTGGTCTC TGGTTTGATTTGTGGCAAACAGATGAAGTAACAGACTGCTATGAAGGACCACAAAAACGGCAGCCTCT GGAAAAACCATTAGAAAGTCAGTGGCAGATCCAGTAAATAATATCGCCAGCCTCAGCATAATCTGCTG CTGACTCGATTCAGTGGACTCTAAAGTGCCCAGCCTCCTGACCTGAGCTCTCCTGCCATCTGTGAGAC TACCAGAGGTCTTATCTGCTGTCCACATGGCAACTGGGCATGAGTACCTGGCCACCTTGCTTCCCTCT TTGCCTGGTCCAAGTGAGTGTCTGCTGCCTCTGTCCTGCCTTGTTTTCCTGGCTCTAAACCAACTCCA CCCACTCTTAATGGAAACTCAGTCTGGCTTTGTGTGTTTCTGGGAAGCACATGACTTCTGGGAATGGG CAAGGAAGAGGAGTGAAACAAAAACTGTCAGCTATGTGTGCCTGGTCTGGGATCCTTCTCTGGGTGAC AGTGGCATCATGAATCTTAGAATCAGCTCCCC
114	hsALDH2	GAATCATGCAAGCTTCCTCCCTCAGCCATTGATGGAAAGTTCAGCAAGATCAGCAACAAAACCAAGAA AAATGATCCTTGCGTGCTGAATATCTGAAAAGAGAAATTTTTCCTACAAAATCTCTTGGGTCAAGAAAG TTCTAGAATTTGAATTGATAAACATGGTGGGTTGGCTGAGGGTAAGAGTATATGAGGAACCTTTTAAAC GACAACAATACTGCTAGCTTTCAGGATGATTTTTAAAAAATAGATTCAAATGTGTTATCCTCTCTCTGAA ACGCTTCCTATAACTCGAGTTTATAGGGGAAGAAAAAGCTATTGTTTACAATTATATCACCATTAAGGCA ACTGCTACACCCTGCTTTGTATTCTGGGCTAAGATTCATTAAAAACTAGCTGCTCTTAACTTACA
115	hsCOX10	GAGCACTGGGACGCCCACCGCCCCTTTCCCTCCGCTGCCAGGCGAGCATGTTGTGGTAATTCTGGAA CACAAGAAGAGAAATTGCTGGGTTTAGAACAAGATTATAAACGAATTCGGTGCTCAGTGATCACTTGAC AGTTTTTTTTTTTTTTAAATATTACCCAAAATGCTCCCCAAATAAGAAATGCATCAGCTCAGTCAGTGAAT ACAAAAAAGGAATTATTTTTCCCTTTGAGGGTCTTTATACATCTCTCCTCCAACCCCACCCTCTATTCTG TTTCTTCCTCCTCACATGGGGGTACACATACACAGCTTCCTCTTTTGGTTCCATCCTTACCACCACACC ACACGCACACTCCACATGCCCAGCAGAGTGGCACTTGGTGGCCAGAAAGTGTGAGCCTCATGATCTG CTGTCTGTAGTTCTGTGAGCTCAGGTCCCTCAAAGGCCTCGGAGCACCCCCTTCCTGGTGACTGAGC CAGGGCCTGCATTTTTGGTTTTCCCCACCCCACACATTCTCAACCATAGTCCTTCTAACAATACCAATA GCTAGGACCCGGCTGCTGTGCACTGGGACTGGGGATTCCACATGTTTGCCTTGGGAGTCTCAAGCTG GACTGCCAGCCCCTGTCCTCCCTTCACCCCCATTGCGTATGAGCATTTCAGAACTCCAAGGAGTCACA GGCATCTTTATAGTTCACGTTAACATATAGACACTGTTGGAAGCAGTTCCTTCTAAAAGGGTAGCCCTG GACTTAATACCAGCCGGATACCTCTGGCCCCCACCCCATTACTGTACCTCTGGAGTCACTACTGTGGG TCGCCACTCCTCTGCTACACAGCACGGCTTTTTCAAGGCTGTATTGAGAAGGGAAGTTAGGAAGAAGG GTGTGCTGGGCTAACCAGCCCACAGAGCTCACATTCCTGTCCCTTGGGTGAAAAATACATGTCCATCC TGATATCTCCTGAATTCAGAAATTAGCCTCCACATGTGCAATGGCTTTAAGAGCCAGAAGCAGGGTTCT GGGAATTTTGCAAGTTATCCTGTGGCCAGGTGTGGTCTCGGTTACCAAATACGGTTACCTGCAGCTTT TTAGTCCTTTGTGCTCCCACGGGTCTGCAGAGTCCCATCTGCCCAAAGGTCTTGAAGCTTGACAGGAT GTTTTCATTACTCAGTCTCCCAGGGCACTGCTGGTCCGTAGGGATTCATTGGTCGGGGTGGGAGAGTT AAACAACATTTAAACAGAGTTCTCTCAAAAATGTCTAAAGGGATTGTAGGTAGATAACATCCAATCACT GTTTGCACTTATCTGAAATCTTCCCTCTTGGCTGCCCCCAGGTATTTACTGTGGAGAACATTGCATAGG AATGTCTGGAAAAAGCCTCTACAACTTGTTACAGCCTTCACATTTGTACAATTCATTGATTCTCTTTTCC TTCCACAATAAAATGGTATACAAGAAC
116	hsUQCRFS1	GAGACTTGGACTCAAGTCATAGGCTTCTTTCAGTCTTTATGTCACCTCAGGAGACTTATTTGAGAGGAA GCCTTCTGTACTTGAAGTTGATTTGAAATATGTAAGAATTGATGATGTATTTGCAAACATTAATGTGAAA TAAATTGAATTTAATGTTGAATACTTTCAGGCATTCACTTAATAAAGACACTGTTAAGCACTGTTATGCT CAGTCATACACGCGAAAGGTACAATGTCTTTTAGCTAATTCTAATTAAAAATTACAGACTGGTGTACAA GATACTTGTG
117	hsNDUFV1	CCCACCACCCTGGCCTGCTGTCCTGCGTCTATCCATGTGGAATGCTGGACAATAAAGCGAGTGCTGC CCACCCTCCAGCTGCC
118	hsNDUFV2	TTTATATTGAACTGTAAATATGTCACTAGAGAAATAAAATATGGACTTCCAATCTACGTAAACTTA
119	hsSOD2	ACCACGATCGTTATGCTGAGTATGTTAAGCTCTTTATGACTGTTTTTGTAGTGGTATAGAGTACTGCAG AATACAGTAAGCTGCTCTATTGTAGCATTTCTTGATGTTGCTTAGTCACTTATTTCATAAACAACTTAAT GTTCTGAATAATTTCTTACTAAACATTTTGTTATTGGGCAAGTGATTGAAAATAGTAAATGCTTTGTGTG ATTGA
120	hsCOX6c	TCTTGGAATATAAAGAATTTCTTCAGGTTGAATTACCTAGAAGTTTGTCACTGACTTGTGTTCCTGAACT ATGACACATGAATATGTGGGCTAAGAAATAGTTCCTCTTGATAAATAAACAATTAACAAATACTTTGGAC AGTAAGTCTTTCTCAGTTCTTAATGATAATGCAGGGCACTTACTAGCATAAGAATTGGTTTGGGATTTAA

		CTGTTTATGAAGCTAACTTGATTTCCGTGTTTTGTTAAAATTTCATTGTTCTAGCACATCTTTAACTGTGATAGTT
121	hsIRP1	GAGACGTGCACTTGGTCGTGCGCCCAGGGAGGAAGCCGCACCACCAGCCAGCGCAGGCCCTGGTGGAGAGGCCTCCCTGGCTGCCTCTGGGAGGGGTGCTGCCTTGTAGATGGAGCAAGTGAGCACTGAGGGTCTGGTGCCAATCCTGTAGGCACAAAACCAGAAGTTTCTACATTCTCTATTTTTGTTAATCATCTTCTCTTTTTCCAGAATTTGGAAGCTAGAATGGTGGGAATGTCAGTAGTGCCAGAAAGAGAGAACCAAGCTTGTCTTTAAAGTTACTGATCACAGGACGTTGCTTTTTCACTGTTTCCTATTAATCTTCAGCTGAACACAAGCAAACCTTCTCAGGAGGTGTCTCCTACCCTCTTATTGTTCCTCTTACGCTCTGCTCAATGAAACCTTCCTCTTGAGGGTCATTTTCCTTTCTGTATTAATTATACCAGTGTTAAGTGACATAGATAAGAACTTTGCACACTTCAAATCAGAGCAGTGATTCTCTCTTCTCTCCCCTTTTCCTTCAGAGTGAATCATCCAGACTCCTCATGGATAGGTCGGGTGTTAAAGTTGTTTTGATTATGTACCTTTTGATAGATCCACATAAAAAGAAATGTGAAGTTTTCTTTTACTATCTTTTCATTTATCAAGCAGAGACCTTTGTTGGGAGGCGGTTTGGGAGAACACATTTCTAATTTGAATGAAATGAAATCTATTTTCAGTG
122	hsMRPS12	CAGAAGAAGTGACGGCTGGGGGCACAGTGGGCTGGGCGCCCCTGCAGAACATGAACCTTCCGCTCCTGGCTGCCACAGGGTCCTCCGATGCTGGCCTTTGCGCCTCTAGAGGCAGCCACTCATGGATTCAAGTCCTGGCTCCGCCTCTTCCATCAGGACCACT
123	hsATP5J2	AGAGGACACACTCTGCACCCCCCCACCCCACGACCTTGGCCCGAGCCCCTCCGTGAGGAA
124	mSOD2	AGCCCTTCCGCCAGGCTGTGTGTCAGGCCCGTGGTGGGTGTTTTGTAGTAGTGTAGAGCATTGCA
125	hsOXA1L	CTTATGTTCTGTGCGCATTCTGGCAGGAATTCTGTCTCTTCAGAGACTCATCCTCAAAACAAGACTTGACACTGTGTCCTTGCCCCAGTCCTAGGAACTGTGGCACACAGAGATGTTCATTTTAAAAACGGATTTCATGAAACACTCTTGTACTTATGTTTATAAGAGAGCACTGGGTAGCCAAGTGATCTTCCCATTCACAGAGTTAGTAAACCTCTGTACTACATGCTG
126	MTS-COX10	MAASPHTLSSRLLTGCVGGSVWYLERRT
127	MTS-COX8	MSVLTRLLLRGLTRLGSAAPVRRARIHSL
128	MTS-OPA1	MWRLRRAAVA
129	hsCOX10	MAASPHTLSSRLLTGCVGGSVWYLERRT
130	scRPM2	MAFKSFIYSKGYHRSAAQKKTATSFFDSSYQYLRQNQGLVNSDPVLHASHLHPHPVVVANVNYNNVDDILHPHDLDSSINNTNNPLTHEELLYNQNVSLRSLKQQQSTNYVNNNNNNQHRYY
131	lcSirt5	MRKRSLRCHLWSANASLSPRKDEVTSRKESENLVKGKKNKKSHLHLLLFTASKIGTDSVFDVQKSKECCKELGLLFTSLIHSIGSFPFDEEPKAAAVFLPGSLPQLTVLVLAPGSGSCPTGKSTPHLAASGRNAELLRPQNSMIVRQFTCRGTISSHLCAHLRKPHDSRNMARP
132	tbNDUS7	MLRRTSFNFTGRAMISRGSPEWSHRLDLKKGKKTTMMHKLGTSKPNNALQYAQMTL
133	ncQCR2	MISRSALSRGSQLALRRPAAAKTAQRGFAAAAASPAASYEPTTIAG
134	hsATP5G2	MPELILYVAITLSVAERLVGPGHACAEPSFRSSRCSAPLCLLCSGSSSPATAPHPLKMFACSKFVSTPSLVKSTSQLLSRPLSAVVLKRPEILTDESLSSLAVSCPLTSLVSSRSFQTSAISRDIDTA
135	hsLACTB	MYRLMSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGLGLGLGLALGVKLAGGLRGAAPAQSPAAPDPEASPLAEPPQEQSLAPWSPQTPAPPCSRCFARAIESSRDLL
136	spilv1	MTVLAPLRRLHTRAAFSSYGREIALQKRFLNLNSCSAVRRYGTGFSNNLRIKKLKNAFGVVRANSTKSTSTVTTASPIKYDSSFVGKTGGEIFHDMMLKHNVKHVFGYPGGAILPVFDAIYRSPHFEFILPRHEQAAGHA
137	gmCOX2	MILCPLEAFIVQHILTISVMGLLSCFRSTVLRKCSKGSSGMSRFLYTNNFQRNLISSGGNESYYGYFNRRSYTSLYMGTGTVGGITSARIRVPNVGCEGFMCSSHLSITQRNSRLIHSTSKIVPN
138	crATP6	MALQQAAPRVFGLLGRAPVALGQSGILTGSSGFKNQGFNGSLQSVENHVYAQAFSTSSQEEQAAPSIQGASGMKLPGMAGSMLLGKSRSGLRTGSMVPFAAQQAMNM
139	hsOPA1	MWRLRRAAVACEVCQSLVKHSSGIKGSLPLQKLHLVSRSIYHSHHPTLKLQRPQLRTSFQQFSSLTNLPLRKLKFSPIKYGYQPRRN
140	hsSDHD	MAVLWRLSAVCGALGGRALLLRTPVVRPAHISAFLQDRPIPEWCGVQHIHLSPSHH
141	hsADCK3	MAAILGDTIMVAKGLVKLTQAAVETHLQHLGIGGELIMAARALQSTAVEQIGMFLGKVQGQDKHEEYFAENFGGPEGEFHFSVPHAAGASTDFSSASAPDQSAPPSLGHAHSEGPAPAYVASGPFREAGFPGQASSPLGRANGRLFANPRDSFSAMGFQRRF
142	osP0644B06.24-2	MALLLRHSPKLRRAHAILGCERGTVVRHFSSSTCSSLVKEDTVSSSNLHPEYAKKIGGSDFSHDRQSGKELQNFKVSPQEASRASNFMRASKYGMPITANGVHSLFSCGQVVPSRCF
143	Neurospora crassa ATP9 (ncATP9)	MASTRVLASRLASQMAASAKVARPAVRVAQVSKRTIQTGSPLQTLKRTQMTSIVNATTRQAFQKRA
144	hsGHITM	MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSRE
145	hsNDUFAB1	MASRVLSAYVSRLPAAFAPLPRVRMLAVARPLSTALCSAGTQTRLGTLQPALVLAQVPGRVTQLCRQY
146	hsATP5G3	MFACAKLACTPSLIRAGSRVAYRPISASVLSRPEASRTGEGSTVFNGAQNGVSQLIQREFQTSAISR
147	crATP6_hsADCK3	MALQQAAPRVFGLLGRAPVALGQSGILTGSSGFKNQGFNGSLQSVENHVYAQAFSTSSQEEQAAPSIQGASGMKLPGMAGSMLLGKSRSGLRTGSMVPFAAQQAMNMGGMAAILGDTIMVAKGLVKLTQAAVETHLQHLGIGGELIMAARALQSTAVEQIGMFLGKVQGQDKHEEYFAENFGGPEGEFHFSVPHAAGASTDFSSASAPDQSAPPSLGHAHSEGPAPAYVASGPFREAGFPGQASSPLGRANGRLFANPRDSFSAMGFQRRFGG
148	ncATP9_ncATP9	MASTRVLASRLASQMAASAKVARPAVRVAQVSKRTIQTGSPLQTLKRTQMTSIVNATTRQAFQKRAMASTRVLASRLASQMAASAKVARPAVRVAQVSKRTIQTGSPLQTLKRTQMTSIVNATTRQAFQKRA

149	zmLOC100282174	MALLRAAVSELRRRGRGALTPLPALSSLLSSLSPRSPASTRPEPNNPHADRRHVIALRRCPPLPASAVLAPELLHARGLLPRHWSHASPLSTSSSSSRPADKAQLTWVDKWIPEAARPY
150	ncATP9_zmLOC100282174_spilv1_ncATP9	MASTRVLASRLASQMAASAKVARPAVRVAQVSKRTIQTGSPLQTLKRTQMTSIVNATTRQAFQKRAMALLRAAVSELRRRGRGALTPLPALSSLLSSLSPRSPASTRPEPNNPHADRRHVIALRRCPPLPASAVLAPELLHARGLLPRHWSHASPLSTSSSSSRPADKAQLTWVDKWIPEAARPYMTVLAPLRRLHTRAAFSSYGREIALQKRFLNLNSCSAVRRYGTGFSNNLRIKKLKNAFGVVRANSTKSTSTVTTASPIKYDSSFVGKTGGEIFHDMMLKHNVKHVFGYPGGAILPVFDAIYRSPHFEFILPRHEQAAGHAMASTRVLASRLASQMAASAKVARPAVRVAQVSKRTIQTGSPLQTLKRTQMTSIVNATTRQAFQKRA
151	zmLOC100282174_hsADCK3_crATP6_hsATP5G3	MALLRAAVSELRRRGRGALTPLPALSSLLSSLSPRSPASTRPEPNNPHADRRHVIALRRCPPLPASAVLAPELLHARGLLPRHWSHASPLSTSSSSSRPADKAQLTWVDKWIPEAARPYMAAILGDTIMVAKGLVKLTQAAVETHLQHLGIGGELIMAARALQSTAVEQIGMFLGKVQGQDKHEEYFAENFGGPEGEFHFSVPHAAGASTDFSSASAPDQSAPPSLGHAHSEGPAPAYVASGPFREAGFPGQASSPLGRANGRLFANPRDSFSAMGFQRRFMALQQAAPRVFGLLGRAPVALGQSGILTGSSGFKNQGFNGSLQSVENHVYAQAFSTSSQEEQAAPSIQGASGMKLPGMAGSMLLGKSRSGLRTGSMVPFAAQQAMNMMFACAKLACTPSLIRAGSRVAYRPISASVLSRPEASRTGEGSTVFNGAQNGVSQLIQREFQTSAISR
152	zmLOC100282174_hsADCK3_hsATP5G3	MALLRAAVSELRRRGRGALTPLPALSSLLSSLSPRSPASTRPEPNNPHADRRHVIALRRCPPLPASAVLAPELLHARGLLPRHWSHASPLSTSSSSSRPADKAQLTWVDKWIPEAARPYMAAILGDTIMVAKGLVKLTQAAVETHLQHLGIGGELIMAARALQSTAVEQIGMFLGKVQGQDKHEEYFAENFGGPEGEFHFSVPHAAGASTDFSSASAPDQSAPPSLGHAHSEGPAPAYVASGPFREAGFPGQASSPLGRANGRLFANPRDSFSAMGFQRRFMFACAKLACTPSLIRAGSRVAYRPISASVLSRPEASRTGEGSTVFNGAQNGVSQLIQREFQTSAISR
153	ncATP9_zmLOC100282174	MASTRVLASRLASQMAASAKVARPAVRVAQVSKRTIQTGSPLQTLKRTQMTSIVNATTRQAFQKRAMALLRAAVSELRRRGRGALTPLPALSSLLSSLSPRSPASTRPEPNNPHADRRHVIALRRCPPLPASAVLAPELLHARGLLPRHWSHASPLSTSSSSSRPADKAQLTWVDKWIPEAARPY
154	hsADCK3_zmLOC100282174_crATP6_hsATP5G3	MAAILGDTIMVAKGLVKLTQAAVETHLQHLGIGGELIMAARALQSTAVEQIGMFLGKVQGQDKHEEYFAENFGGPEGEFHFSVPHAAGASTDFSSASAPDQSAPPSLGHAHSEGPAPAYVASGPFREAGFPGQASSPLGRANGRLFANPRDSFSAMGFQRRFMALLRAAVSELRRRGRGALTPLPALSSLLSSLSPRSPASTRPEPNNPHADRRHVIALRRCPPLPASAVLAPELLHARGLLPRHWSHASPLSTSSSSSRPADKAQLTWVDKWIPEAARPYMALQQAAPRVFGLLGRAPVALGQSGILTGSSGFKNQGFNGSLQSVENHVYAQAFSTSSQEEQAAPSIQGASGMKLPGMAGSMLLGKSRSGLRTGSMVPFAAQQAMNMMFACAKLACTPSLIRAGSRVAYRPISASVLSRPEASRTGEGSTVFNGAQNGVSQLIQREFQTSAISR
155	crATP6_hsADCK3_zmLOC100282174_hsATP5G3	MALQQAAPRVFGLLGRAPVALGQSGILTGSSGFKNQGFNGSLQSVENHVYAQAFSTSSQEEQAAPSIQGASGMKLPGMAGSMLLGKSRSGLRTGSMVPFAAQQAMNMMAAILGDTIMVAKGLVKLTQAAVETHLQHLGIGGELIMAARALQSTAVEQIGMFLGKVQGQDKHEEYFAENFGGPEGEFHFSVPHAAGASTDFSSASAPDQSAPPSLGHAHSEGPAPAYVASGPFREAGFPGQASSPLGRANGRLFANPRDSFSAMGFQRRFMALLRAAVSELRRRGRGALTPLPALSSLLSSLSPRSPASTRPEPNNPHADRRHVIALRRCPPLPASAVLAPELLHARGLLPRHWSHASPLSTSSSSSRPADKAQLTWVDKWIPEAARPYMFACAKLACTPSLIRAGSRVAYRPISASVLSRPEASRTGEGSTVFNGAQNGVSQLIQREFQTSAISR
156	hsADCK3_zmLOC100282174	MAAILGDTIMVAKGLVKLTQAAVETHLQHLGIGGELIMAARALQSTAVEQIGMFLGKVQGQDKHEEYFAENFGGPEGEFHFSVPHAAGASTDFSSASAPDQSAPPSLGHAHSEGPAPAYVASGPFREAGFPGQASSPLGRANGRLFANPRDSFSAMGFQRRFGGMALLRAAVSELRRRGRGALTPLPALSSLLSSLSPRSPASTRPEPNNPHADRRHVIALRRCPPLPASAVLAPELLHARGLLPRHWSHASPLSTSSSSSRPADKAQLTWVDKWIPEAARPYGG
157	hsADCK3_zmLOC100282174_crATP6	MAAILGDTIMVAKGLVKLTQAAVETHLQHLGIGGELIMAARALQSTAVEQIGMFLGKVQGQDKHEEYFAENFGGPEGEFHFSVPHAAGASTDFSSASAPDQSAPPSLGHAHSEGPAPAYVASGPFREAGFPGQASSPLGRANGRLFANPRDSFSAMGFQRRFGGMALLRAAVSELRRRGRGALTPLPALSSLLSSLSPRSPASTRPEPNNPHADRRHVIALRRCPPLPASAVLAPELLHARGLLPRHWSHASPLSTSSSSSRPADKAQLTWVDKWIPEAARPYGGMALQQAAPRVFGLLGRAPVALGQSGILTGSSGFKNQGFNGSLQSVENHVYAQAFSTSSQEEQAAPSIQGASGMKLPGMAGSMLLGKSRSGLRTGSMVPFAAQQAMNMGG
158	ncATP9_zmLOC100282174_spilv1_GNFP_ncATP9	MASTRVLASRLASQMAASAKVARPAVRVAQVSKRTIQTGSPLQTLKRTQMTSIVNATTRQAFQKRAMALLRAAVSELRRRGRGALTPLPALSSLLSSLSPRSPASTRPEPNNPHADRRHVIALRRCPPLPASAVLAPELLHARGLLPRHWSHASPLSTSSSSSRPADKAQLTWVDKWIPEAARPYMTVLAPLRRLHTRAAFSSYGREIALQKRFLNLNSCSAVRRYGTGFSNNLRIKKLKNAFGVVRANSTKSTSTVTTASPIKYDSSFVGKTGGEIFHDMMLKHNVKHVFGYPGGAILPVFDAIYRSPHFEFILPRHEQAAGHAVSGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEMASTRVLASRLASQMAASAKVARPAVRVAQVSKRTIQTGSPLQTLKRTQMTSIVNATTRQAFQKRA
159	ncATP9_zmLOC100282174_spilv1_lcSirt5_osP0644B06.24-2_hsATP5G2_ncATP9	MASTRVLASRLASQMAASAKVARPAVRVAQVSKRTIQTGSPLQTLKRTQMTSIVNATTRQAFQKRAMALLRAAVSELRRRGRGALTPLPALSSLLSSLSPRSPASTRPEPNNPHADRRHVIALRRCPPLPASAVLAPELLHARGLLPRHWSHASPLSTSSSSSRPADKAQLTWVDKWIPEAARPYMTVLAPLRRLHTRAAFSSYGREIALQKRFLNLNSCSAVRRYGTGFSNNLRIKKLKNAFGVVRANSTKSTSTVTTASPIKYDSSFVGKTGGEIFHDMMLKHNVKHVFGYPGGAILPVFDAIYRSPHFEFILPRHEQAAGHAMRKRSLRCHLWSANASLSPRKDEVTSRKESENLVKGKKNKKSHLHLLLFTASKIGTDSVFDVQKSKECCKELGLLFTSLIHSIGSFPFDEEPKAAAVFLPGSLPQLTVLVLAPGSGSCPTGKSTPHLAASGRNAELLRPQNSMIVRQFTCRGTISSHLCAHLRKPHDSRNMARPMALLLRHSPKLRRAHAILGCERGTVVRHFSSSTCSSLVKEDTVSSSNLHPEYAKKIGGSDFSHDRQSGKELQNFKVSPQEASRASNFMRASKYGMPITANGVHSLFSCGQVVPSRCFMPELILYVAITLSVAERLVGPGHACAEPSFRSSRCSAPLCLLCSGSSSPATAPHPLKMFACSKFVSTPSLVKSTSQLLSRPLSAVVLKRPEILTDESLSSLAVSCPLTSLVSSRSFQTSAISRDIDTAMASTRVLASRLASQMAASAKVARPAVRVAQVSKRTIQTGSPLQTLKRTQMTSIVNATTRQAFQKRA
160	ND4	MLKLIVPTIMLLPLTWLSKKHMIWINTTTHSLIISIPLLFFNQINNNLFSCSPTFSSDPLTTPLLMLTTWLLPLTIMASQRHLSSEPLSRKKLYLSMLISLQISLIMTFTATELIMFYIFFETTLIPTLAIITRWGNQPERLNAGTYFLFYTLVGSLPLLIALIYTHNTLGSLNILLLTLTAQELSNSWANNLMWLAYTMAFMVKMPLYGLHLWLPKAHVEAPIAGSMVLAAVLLKLGGYGMMRLTLILNPLTKHMAYPFLVLSLWGMIMTSSICLRQTDLKSLIAYSSISHMALVVT

		AILIQTPWSFTGAVILMIAHGLTSSLLFCLANSNYERTHSRIMILSQGLQTLLPLMAFWWLLASLANLALPPTINLLGELSVLVTTFSWSNITLLLTGLNMLVTALYSLYMFTTTQWGSLTHHINNMKPSFTRENTLMFMHLSPILLLSLNPDIITGFSS
161	ND6	MMYALFLLSVGLVMGFVGFSSKPSPIYGGLVLIVSGVVGCVIILNFGGGYMGLMVFLIYLGGMMVVFGYTTAMAIEEYPEAWGSGVEVLVSVLVGLAMEVGLVLWVKEYDGVVVVVNFNSVGSWMIYEGEGSGLIREDPIGAGALYDYGRWLVVVTGWTLFVGVYIVIEIARGN
162	ND1	MANLLLLIVPILIAMAFLMLTERKILGYMQLRKGPNVVGPYGLLQPFADAIKLFTKEPLKPATSTITLYITAPTLALTIALLLWTPLPMPNPLVNLNLGLLFILATSSLAVYSILWSGWASNSNYALIGALRAVAQTISYEVTLAIILLSTLLMSGSFNLSTLITTQEHLWLLLPSWPLAMMWFISTLAETNRTPFDLAEGESELVSGFNIEYAAGPFALFFMAEYTNIIMMNTLTTTIFLGTTYDALSPELYTTYFVTKTLLLTSLFLWIRTAYPRFRYDQLMHLLWKNFLPLTLALLMWYVSMPITISSIPPQT

Adeno-associated virus (AAV)

[0067] Adeno-associated virus (AAV) is a small virus that infects humans and some other primate species. The compositions disclosed herein comprises firstly an adeno-associated virus (AAV) genome or a derivative thereof.

[0068] An AAV genome is a polynucleotide sequence which encodes functions needed for production of an AAV viral particle. These functions include those operating in the replication and packaging cycle for AAV in a host cell, including encapsidation of the AAV genome into an AAV viral particle. Naturally occurring AAV viruses are replication-deficient and rely on the provision of helper functions in trans for completion of a replication and packaging cycle. Accordingly, the AAV genome of the vector of the invention is typically replication-deficient.

[0069] The AAV genome can be in single-stranded form, either positive or negative-sense, or alternatively in double-stranded form. The use of a double-stranded form allows bypass of the DNA replication step in the target cell and so can accelerate transgene expression.

[0070] The AAV genome may be from any naturally derived serotype or isolate or Glade of AAV. Thus, the AAV genome may be the full genome of a naturally occurring AAV virus. As is known to the skilled person, AAV viruses occurring in nature may be classified according to various biological systems.

[0071] Commonly, AAV viruses are referred to in terms of their serotype. A serotype corresponds to a variant subspecies of AAV which owing to its profile of expression of capsid surface antigens has a distinctive reactivity which can be used to distinguish it from other variant subspecies. Typically, a virus having a particular AAV serotype does not efficiently cross-react with neutralising antibodies specific for any other AAV serotype. AAV serotypes include AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, AAV13, AAV14, AAV15, and AAV16, also recombinant serotypes, such as Rec2 and Rec3, recently identified from primate brain.

[0072] A preferred serotype of AAV for use in the invention is AAV2. Other serotypes of particular interest for use in the invention include AAV4, AAV5 and AAV8 which efficiently transduce tissue in the eye, such as the retinal pigmented epithelium. The serotype of AAV which is used can be an

AAV serotype which is not AAV4. Reviews of AAV serotypes may be found in Choi et al (Curr Gene Ther. 2005; 5(3); 299-310) and Wu et al (Molecular Therapy. 2006; 14(3), 316-327). The sequences of AAV genomes or of elements of AAV genomes including ITR sequences, rep or cap genes for use in the invention may be derived from the following accession numbers for AAV whole genome sequences: Adeno-associated virus 1 NC_002077, AF063497; Adeno-associated virus 2 NC_001401; Adeno-associated virus 3 NC_001729; Adeno-associated virus 3B NC_001863; Adeno-associated virus 4 NC_001829; Adeno-associated virus 5 Y18065, AF085716; Adeno-associated virus 6 NC_001862; Avian AAV ATCC VR-865 AY186198, AY629583, NC_004828; Avian AAV strain DA-1 NC_006263, AY629583; Bovine AAV NC_005889, AY388617.

[0073] AAV viruses may also be referred to in terms of clades or clones. This refers to the phylogenetic relationship of naturally derived AAV viruses, and typically to a phylogenetic group of AAV viruses which can be traced back to a common ancestor, and includes all descendants thereof. Additionally, AAV viruses may be referred to in terms of a specific isolate, i.e. a genetic isolate of a specific AAV virus found in nature. The term genetic isolate describes a population of AAV viruses which has undergone limited genetic mixing with other naturally occurring AAV viruses, thereby defining a recognisably distinct population at a genetic level.

[0074] Examples of clades and isolates of AAV that may be used in the invention include: Clade A: AAV1 NC_002077, AF063497, AAV6 NC_001862, Hu. 48 AY530611, Hu 43 AY530606, Hu 44 AY530607, Hu 46 AY530609; Clade B: Hu. 19 AY530584, Hu. 20 AY530586, Hu 23 AY530589, Hu22 AY530588, Hu24 AY530590, Hu21 AY530587, Hu27 AY530592, Hu28 AY530593, Hu 29 AY530594, Hu63 AY530624, Hu64 AY530625, Hu13 AY530578, Hu56 AY530618, Hu57 AY530619, Hu49 AY530612, Hu58 AY530620, Hu34 AY530598, Hu35 AY530599, AAV2 NC_001401, Hu45 AY530608, Hu47 AY530610, Hu51 AY530613, Hu52 AY530614, Hu T41 AY695378, Hu S17 AY695376, Hu T88 AY695375, Hu T71 AY695374, Hu T70 AY695373, Hu T40 AY695372, Hu T32 AY695371, Hu T17 AY695370, Hu LG15 AY695377; Clade C: Hu9 AY530629, Hu10 AY530576, Hu11 AY530577, Hu53 AY530615, Hu55 AY530617, Hu54 AY530616, Hu7 AY530628, Hu18 AY530583, Hu15 AY530580, Hu16 AY530581, Hu25 AY530591, Hu60 AY530622, Ch5 AY243021, Hu3 AY530595, Hu1 AY530575, Hu4 AY530602 Hu2, AY530585, Hu61 AY530623; Clade D: Rh62 AY530573, Rh48 AY530561, Rh54 AY530567, Rh55 AY530568, Cy2 AY243020, AAV7 AF513851, Rh35 AY243000, Rh37 AY242998, Rh36 AY242999, Cy6 AY243016, Cy4 AY243018, Cy3 AY243019, Cy5 AY243017, Rh13 AY243013; Clade E: Rh38 AY530558, Hu66 AY530626, Hu42 AY530605, Hu67 AY530627, Hu40 AY530603, Hu41 AY530604, Hu37 AY530600, Rh40 AY530559, Rh2 AY243007, Bb1 AY243023, Bb2

AY243022, Rh10 AY243015, Hu17 AY530582, Hu6 AY530621, Rh25 AY530557, Pi2 AY530554, Pi1 AY530553, Pi3 AY530555, Rh57 AY530569, Rh50 AY530563, Rh49 AY530562, Hu39 AY530601, Rh58 AY530570, Rh61 AY530572, Rh52 AY530565, Rh53 AY530566, Rh51 AY530564, Rh64 AY530574, Rh43 AY530560, AAV8 AF513852, Rh8 AY242997, Rh1 AY530556; Clade F: Hu14 (AAV9) AY530579, Hu31 AY530596, Hu32 AY530597, Clonal Isolate AAV5 Y18065, AF085716, AAV 3 NC_001729, AAV 3B NC_001863, AAV4 NC_001829, Rh34 AY243001, Rh33 AY243002, Rh32 AY243003.

[0075] The skilled person can select an appropriate serotype, Glade, clone or isolate of AAV for use in the present invention on the basis of their common general knowledge. For instance, the AAV5 capsid has been shown to transduce primate cone photoreceptors efficiently as evidenced by the successful correction of an inherited color vision defect (Mancuso et al., Nature 2009, 461:784-7).

[0076] It should be understood however that the invention also encompasses use of an AAV genome of other serotypes that may not yet have been identified or characterised. The AAV serotype determines the tissue specificity of infection (or tropism) of an AAV virus. Accordingly, preferred AAV serotypes for use in AAV viruses administered to patients in accordance with the invention are those which have natural tropism for or a high efficiency of infection of target cells within eye in LHON. Thus, AAV serotypes for use in AAV viruses administered to patients can be ones which infect cells of the neurosensory retina and retinal pigment epithelium.

[0077] Typically, the AAV genome of a naturally derived serotype or isolate or Glade of AAV comprises at least one inverted terminal repeat sequence (ITR). An ITR sequence acts in cis to provide a functional origin of replication, and allows for integration and excision of the vector from the genome of a cell. In preferred embodiments, one or more ITR sequences flank the polynucleotide sequence encoding ND4, ND6, or ND1 or a variant thereof. Preferred ITR sequences are those of AAV2, and variants thereof. The AAV genome typically also comprises packaging genes, such as rep and/or cap genes which encode packaging functions for an AAV viral particle. The rep gene encodes one or more of the proteins Rep78, Rep68, Rep52 and Rep40 or variants thereof. The cap gene encodes one or more capsid proteins such as VP1, VP2 and VP3 or variants thereof. These proteins make up the capsid of an AAV viral particle. Capsid variants are discussed below.

[0078] A promoter will be operably linked to each of the packaging genes. Specific examples of such promoters include the p5, p19 and p40 promoters (Laughlin et al., 1979, PNAS, 76:5567-5571). For example, the p5 and p19 promoters are generally used to express the rep gene, while the p40 promoter is generally used to express the cap gene.

[0079] As discussed above, the AAV genome used in the vector of the invention may therefore be the full genome of a naturally occurring AAV virus. For example, a vector comprising a full AAV genome may be used to prepare AAV virus in vitro. However, while such a vector may in principle be administered to patients, this will be done rarely in practice. Preferably the AAV genome will be derivatised for the purpose of administration to patients. Such derivatisation is standard in the art and the present invention encompasses the use of any known derivative of an AAV genome, and derivatives which could be generated by applying techniques known in the art. Derivatisation of the AAV genome and of the AAV capsid are reviewed in Coura and Nardi (Virology Journal, 2007, 4:99), and in Choi et al and Wu et al, referenced above.

[0080] Derivatives of an AAV genome include any truncated or modified forms of an AAV genome which allow for expression of a ND4, ND6, or ND1 transgene from a vector of the invention in vivo. Typically, it is possible to truncate the AAV genome significantly to include minimal viral sequence yet retain the above function. This is preferred for safety reasons to reduce the risk of recombination of the vector with wild-type virus, and also to avoid triggering a cellular immune response by the presence of viral gene proteins in the target cell.

[0081] Typically, a derivative will include at least one inverted terminal repeat sequence (ITR), preferably more than one ITR, such as two ITRs or more. One or more of the ITRs may be derived from AAV genomes having different serotypes, or may be a chimeric or mutant ITR. A preferred mutant ITR is one having a deletion of a trs (terminal resolution site). This deletion allows for continued replication of the genome to generate a single-stranded genome which contains both coding and complementary sequences i.e. a self-complementary AAV genome. This allows for bypass of DNA replication in the target cell, and so enables accelerated transgene expression.

[0082] The one or more ITRs will preferably flank the polynucleotide sequence encoding ND4, ND6, ND1, or a variant thereof at either end. The inclusion of one or more ITRs is preferred to aid concatamer formation of the vector of the invention in the nucleus of a host cell, for example following the conversion of single-stranded vector DNA into double-stranded DNA by the action of host cell DNA polymerases. The formation of such episomal concatamers protects the vector construct during the life of the host cell, thereby allowing for prolonged expression of the transgene in vivo.

[0083] In preferred embodiments, ITR elements will be the only sequences retained from the native AAV genome in the derivative. Thus, a derivative will preferably not include the rep and/or cap genes of the native genome and any other sequences of the native genome. This is preferred for the reasons described above, and also to reduce the possibility of integration of the vector into the host cell genome. Additionally, reducing the size of the AAV genome allows for increased flexibility in incorporating other sequence elements (such as regulatory elements) within the vector in addition to the transgene.

[0084] With reference to the AAV2 genome, the following portions could therefore be removed in a derivative of the invention: One inverted terminal repeat (ITR) sequence, the replication (rep) and capsid (cap) genes (NB: the rep gene in the wildtype AAV genome should not to be confused with ND4, ND6, or ND1, the human gene affected in LHON). However, in some embodiments, including in vitro embodiments, derivatives may additionally include one or more rep and/or cap genes or other viral sequences of an AAV genome. Naturally occurring AAV virus integrates with a high frequency at a specific site on human chromosome 19, and shows a negligible frequency of random integration, such that retention of an integrative capacity in the vector may be tolerated in a therapeutic setting.

[0085] Where a derivative genome comprises genes encoding capsid proteins i.e. VP1, VP2 and/or VP3, the derivative may be a chimeric, shuffled or capsid-modified derivative of one or more naturally occurring AAV viruses. In particular, the invention encompasses the provision of capsid protein sequences from different serotypes, clades, clones, or isolates of AAV within the same vector i.e. pseudotyping.

[0086] Chimeric, shuffled or capsid-modified derivatives will be typically selected to provide one or more desired functionalities for the viral vector. Thus, these derivatives may display increased efficiency of gene delivery, decreased immunogenicity (humoral or cellular), an altered tropism range and/or improved targeting of a particular cell type compared to an AAV viral vector comprising a naturally occurring AAV genome, such as that of AAV2. Increased efficiency of gene delivery may be effected by improved receptor or co-receptor binding at the cell surface, improved internalisation, improved trafficking within the cell and into the nucleus, improved uncoating of the viral particle and improved conversion of a single-stranded genome to double-stranded form. Increased efficiency may also relate to an altered tropism range or targeting of a specific cell population, such that the vector dose is not diluted by administration to tissues where it is not needed.

[0087] Chimeric capsid proteins include those generated by recombination between two or more capsid coding sequences of naturally occurring AAV serotypes. This may be performed for example by a marker rescue approach in which non-infectious capsid sequences of one serotype are cotransfected with capsid sequences of a different serotype, and directed selection is used to select for capsid sequences having desired properties. The capsid sequences of the different serotypes can be altered by homologous recombination within the cell to produce novel chimeric capsid proteins.

[0088] Chimeric capsid proteins also include those generated by engineering of capsid protein sequences to transfer specific capsid protein domains, surface loops or specific amino acid residues between two or more capsid proteins, for example between two or more capsid proteins of different serotypes.

[0089] Shuffled or chimeric capsid proteins may also be generated by DNA shuffling or by error-prone PCR. Hybrid AAV capsid genes can be created by randomly fragmenting the sequences of related AAV genes e.g. those encoding capsid proteins of multiple different serotypes and then subsequently reassembling the fragments in a self-priming polymerase reaction, which may also cause crossovers in regions of sequence homology. A library of hybrid AAV genes created in this way by shuffling the capsid genes of several serotypes can be screened to identify viral clones having a desired functionality. Similarly, error prone PCR may be used to randomly mutate AAV capsid genes to create a diverse library of variants which may then be selected for a desired property.

[0090] The sequences of the capsid genes may also be genetically modified to introduce specific deletions, substitutions or insertions with respect to the native wild-type sequence. In particular, capsid genes may be modified by the insertion of a sequence of an unrelated protein or peptide within an open reading frame of a capsid coding sequence, or at the N- and/or C-terminus of a capsid coding sequence.

[0091] The unrelated protein or peptide may advantageously be one which acts as a ligand for a particular cell type, thereby conferring improved binding to a target cell or improving the specificity of targeting of the vector to a particular cell population. An example might include the use of RGD peptide to block uptake in the retinal pigment epithelium and thereby enhance transduction of surrounding retinal tissues (Cronin et al., 2008 ARVO Abstract: D1048). The unrelated protein may also be one which assists purification of the viral particle as part of the production process i.e. an epitope or affinity tag. The site of insertion will typically be selected so as not to interfere with other functions of the viral particle e.g. internalisation, trafficking of the viral particle. The skilled person can identify suitable sites for insertion based on their common general knowledge. Particular sites are disclosed in Choi et al, referenced above.

[0092] The invention additionally encompasses the provision of sequences of an AAV genome in a different order and configuration to that of a native AAV genome. The invention also encompasses the replacement of one or more AAV sequences or genes with sequences from another virus or with chimeric genes composed of sequences from more than one virus. Such chimeric genes may be composed of sequences from two or more related viral proteins of different viral species.

[0093] The vector of the invention takes the form of a polynucleotide sequence comprising an AAV genome or derivative thereof and a sequence encoding ND4, ND6, ND1 or a variant thereof.

[0094] For the avoidance of doubt, the invention also provides an AAV viral particle comprising a vector of the invention. The AAV particles of the invention include transcapsidated forms wherein an AAV genome or derivative having an ITR of one serotype is packaged in the capsid of a different serotype. The AAV particles of the invention also include mosaic forms wherein a mixture of unmodified capsid proteins from two or more different serotypes makes up the viral envelope. The AAV particle also includes chemically modified forms bearing ligands adsorbed to the capsid surface. For example, such ligands may include antibodies for targeting a particular cell surface receptor.

[0095] The invention additionally provides a host cell comprising a vector or AAV viral particle of the invention.

Recombinant nucleic acid sequences

[0096] Also disclosed herein are recombinant nucleic acid sequences comprising a polynucleotide sequence encoding a NADH dehydrogenase subunit-4 (ND4), NADH dehydrogenase subunit-1 (ND1) and NADH dehydrogenase subunit-6 (ND6) polypeptide or a variant thereof.

[0097] The polynucleotide sequence for ND4 is shown in **SEQ ID NO: 6** and encodes the protein shown in **SEQ ID NO: 160**. Further nucleic acid sequences for ND4 are **SEQ ID NO: 7 and 8.** The polynucleotide sequence for ND6 is shown in **SEQ ID NO: 9** and encodes the protein shown in **SEQ ID NO: 161**. A further nucleic acid sequence for ND6 is **SEQ ID NO: 10.** The polynucleotide sequence for ND1 is shown in **SEQ ID NO: 11** and encodes the protein shown in **SEQ ID NO: 162**. A further nucleic acid sequence for ND1 is **SEQ ID NO: 12.**

[0098] A variant of any one of **SEQ ID NO: 160, 161, or 162** may comprise truncations, mutants or homologues thereof, and any transcript variants thereof which encode a functional ND4, ND6, or ND1 polypeptide. Any homologues mentioned herein are typically at least 70% homologous to a relevant region of ND4, ND6, or ND1, and can functionally compensate for the polypeptide deficiency.

[0099] Homology can be measured using known methods. For example the UWGCG Package provides the BESTFIT program which can be used to calculate homology (for example used on its default settings) (Devereux et at (1984) Nucleic Acids Research 12, 387-395). The PILEUP and BLAST algorithms can be used to calculate homology or line up sequences (typically on their default settings), for example as described in Altschul S. F. (1993) J Mol Evol 36:290-300; Altschul, S, F et at (1990) J Mol Biol 215:403-10. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/).

[00100] In preferred embodiments, a recombinant nucleic acid sequence may encode a polypeptide which is at least 55%, 65%, 70%, 75%, 80%, 85%, 90% and more preferably at least 95%, 97%, 99%, 99.5%, or 100% homologous to a relevant region of ND4, ND6, or ND1 (**SEQ ID NO: 160, 161, or 162**) over at least 20, preferably at least 30, for instance at least 40, 60, 100, 200, 300, 400 or more contiguous amino acids, or even over the entire sequence of the recombinant nucleic acid. The relevant region will be one which provides for functional activity of ND4, ND6, or ND1.

[00101] Alternatively, and preferably the recombinant nucleic acid sequence may encode a polypeptide having at least 70%, 75%, 80%, 85%, 90% and more preferably at least 95%, 97%, 99%, 99.5%, or 100% homologous to full-length ND4, ND6, or ND1 (**SEQ ID NO: 160, 161, or 162**) over its entire sequence. Typically the recombinant nucleic acid sequence differs from the relevant region of ND4, ND6, or ND1 (**SEQ ID NO: 160, 161, or 162**) by at least, or less than, 2, 5, 10, 20, 40, 50 or 60 mutations (each of which can be substitutions, insertions or deletions).

[00102] A recombinant nucleic acid ND4, ND6, or ND1 polypeptide may have a percentage identity with a particular region of **SEQ ID NO: 160, 161, or 162** which is the same as any of the specific percentage homology values (i.e. it may have at least 70%, 80% or 90% and more preferably at least 95%, 97%, 99% identity) across any of the lengths of sequence mentioned above.

[00103] Variants of ND4, ND6, or ND1 (**SEQ ID NO: 160, 161, or 162**) also include truncations. Any truncation may be used so long as the variant is still functional. Truncations will typically be made to remove sequences that are non-essential for the protein activity and/or do not affect conformation of the folded protein, in particular folding of the active site. Appropriate truncations can routinely be identified by systematic truncation of sequences of varying length from the N- or C-terminus. Preferred truncations are N-terminal and may remove all other sequences except for the catalytic domain.

[00104] Variants of ND4, ND6, or ND1 (**SEQ ID NO: 160, 161, or 162**) further include mutants which have one or more, for example, 2, 3, 4, 5 to 10, 10 to 20, 20 to 40 or more, amino acid insertions, substitutions or deletions with respect to a particular region of ND4, ND6, or ND1 (**SEQ ID NO: 160, 161, or 162**). Deletions and insertions are made preferably outside of the catalytic domain as described below. Substitutions are also typically made in regions that are non-essential for protease activity and/or do not affect conformation of the folded protein.

[00105] Substitutions preferably introduce one or more conservative changes, which replace amino acids with other amino acids of similar chemical structure, similar chemical properties or similar side-chain volume. The amino acids introduced may have similar polarity, hydrophilicity, hydrophobicity, basicity, acidity, neutrality or charge to the amino acids they replace. Alternatively, the conservative change may introduce another amino acid that is aromatic or aliphatic in the place of a pre-existing aromatic or aliphatic amino acid. Conservative amino acid changes are well known in the art and may be selected in accordance with the properties of the amino acids.

[00106] Similarly, preferred variants of the polynucleotide sequence of ND4, ND6, or ND1 (**SEQ ID NO: 6, 9, or 11**) include polynucleotides having at least 70%, 75%, 80%, 85%, 90% and more preferably at least 95%, 96%, 97%, 98%, 99%, or 99.5% homologous to a relevant region of ND4, ND6, or ND1 (**SEQ ID NO: 6, 9, or 11**). Preferably the variant displays these levels of homology to full-length ND4, ND6, or ND1 (**SEQ ID NO: 6, 9, or 11**) over its entire sequence.

[00107] Mitochondrial targeting sequences (MTSs) and three prime untranslated regions (3'UTRs) can be used to target proteins or mRNA to the mitochondria. The charge, length, and structure of the MTS can be important for protein import into the mitochondria. Particular 3'UTRs may drive mRNA localization to the mitochondrial surface and thus facilitate cotranslational protein import into the mitochondria.

[00108] The polynucleotide sequence for a mitochondrial targeting sequence can encode a polypeptide selected from hsCOX10, hsCOX8, scRPM2, lcSirt5, tbNDUS7, ncQCR2, hsATP5G2, hsLACTB, spilv1, gmCOX2, crATP6, hsOPA1, hsSDHD, hsADCK3, osP0644B06.24-2, Neurospora crassa ATP9 (ncATP9), hsGHITM, hsNDUFAB1, hsATP5G3, crATP6 _hsADCK3, ncATP9_ncATP9, zmLOC100282174, ncATP9_zmLOC100282174_spilv1_ncATP9, zmLOC100282174_hsADCK3_crATP6 _hsATP5G3, zmLOC100282174_hsADCK3_hsATP5G3, ncATP9_zmLOC100282174, hsADCK3_zmLOC100282174_crATP6 _hsATP5G3, crATP6_hsADCK3_zmLOC100282174_hsATP5G3, hsADCK3_zmLOC100282174, hsADCK3_zmLOC100282174_crATP6, ncATP9_zmLOC100282174_spilv1_GNFP_ncATP9, and ncATP9_zmLOC100282174_spilv1_lcSirt5_osP0644B06.24-2_hsATP5G2_ncATP9 (see Table 1 for SEQ ID NO). In one example, the polynucleotide sequences, COX10 (**SEQ ID NO: 1, 2, or 3**) can encode the mitochondrial targeting sequence, MTS-COX10 (**SEQ ID NO: 126**). In another example, the polynucleotide sequences, COX8 (**SEQ ID NO: 4**) can encode the mitochondrial targeting sequence, MTS-COX8 (**SEQ ID NO: 127**). In another example, the polynucleotide sequences, OPA1 (**SEQ ID NO: 5**) can encode the mitochondrial targeting sequence, MTS-OPA1 (**SEQ ID NO: 128**).

[00109] The 3'UTR nucleic acid sequence can be selected from hsACO2 (**SEQ ID NO: 111**), hsATP5B (**SEQ ID NO: 112**), hsAK2 (**SEQ ID NO: 113**), hsALDH2 (**SEQ ID NO: 114**), hsCOX10 (**SEQ ID NO: 115**), hsUQCRFS1 (**SEQ ID NO: 116**), hsNDUFV1 (**SEQ ID NO: 117**), hsNDUFV2 (**SEQ ID NO: 118**), hsSOD2 (**SEQ ID NO: 119**), hsCOX6c (**SEQ ID NO: 120**), hsIRP1 (**SEQ ID NO: 121**), hsMRPS12 (**SEQ ID NO: 122**), hsATP5J2 (**SEQ ID NO: 123**), rnSOD2 (**SEQ ID NO: 124**), and hsOXA1L (**SEQ ID NO: 125**). The 3'UTR nucleic acid sequence can also be a variant having at least 70%, 75%, 80%, 85%, 90% and more preferably at least 95%, 96%, 97%, 98%, 99%, 99.5%, or 100% homologous to any 3'UTR nucleic acid sequence listed here. For example, the 3'UTR nucleic acid sequence can be **SEQ ID NO: 13 or 14.**

[00110] Also disclosed herein are recombinant nucleic acid sequences comprising a mitochondrial targeting sequence, a mitochondrial protein coding sequence, and a 3'UTR nucleic acid sequence. For example, the recombinant nucleic acid sequence can be selected from **SEQ ID NO: 15-84.** The recombinant nucleic acid sequence can also be a variant having at least 70%, 75%, 80%, 85%, 90% and more preferably at least 95%, 96%, 97%, 98%, 99%, 99.5%, or 100% homologous to any recombinant nucleic acid sequence listed here.

Promoters and regulatory sequences

[00111] The vector of the invention also includes elements allowing for the expression of the disclosed transgene in vitro or in vivo. Thus, the vector typically comprises a promoter sequence operably linked to the polynucleotide sequence encoding the ND4, ND6, or ND1 transgene or a variant thereof.

[00112] Any suitable promoter may be used. The promoter sequence may be constitutively active i.e. operational in any host cell background, or alternatively may be active only in a specific host cell environment, thus allowing for targeted expression of the transgene in a particular cell type. The promoter may show inducible expression in response to presence of another factor, for example a factor present in a host cell. In any event, where the vector is administered for therapy, the promoter must be functional in a retinal cell background.

[00113] In some embodiments, it is preferred that the promoter shows retinal-cell specific expression in order to allow for the transgene to only be expressed in retinal cell populations. Thus, expression from the promoter may be retinal-cell specific, for example confined only to cells of the neurosensory retina and retinal pigment epithelium.

[00114] Preferred promoters for the ND4, ND6, or ND1 transgene include the chicken beta-actin (CBA) promoter, optionally in combination with a cytomegalovirus (CME) enhancer element. In some cases, the preferred promoters for the ND4, ND6, or ND1 transgene comprises the CAG promoter. A particularly preferred promoter is a hybrid CBA/CAG promoter, for example the promoter used in the rAVE expression cassette. Examples of promoters based on human sequences that would induce retina specific gene expression include rhodospin kinase for rods and cones (Allocca et al., 2007, J Viol 81:11372-80), PR2.1 for cones only (Mancuso et al. 2009, Nature) and/or RPE65 for the retinal pigment epithelium (Bainbridge et al., 2008, N Eng J Med).

[00115] The vector of the invention may also comprise one or more additional regulatory sequences with may act pre- or post-transcriptionally. The regulatory sequence may be part of the native ND4, ND6, or ND1 gene locus or may be a heterologous regulatory sequence. The vector of the invention may comprise portions of the 5'UTR or 3'UTR from the native ND4, ND6, or ND1 transcript.

[00116] Regulatory sequences are any sequences which facilitate expression of the transgene i.e. act to increase expression of a transcript, improve nuclear export of mRNA or enhance its stability. Such regulatory sequences include for example enhancer elements, postregulatory elements and polyadenylation sites. A preferred polyadenylation site is the Bovine Growth Hormone poly-A signal. In the context of the vector of the invention such regulatory sequences will be cis-acting. However, the invention also encompasses the use of trans-acting regulatory sequences located on additional genetic constructs.

[00117] A preferred postregulatory element for use in a vector of the invention is the woodchuck hepatitis postregulatory element (WPRE) or a variant thereof. Another regulatory sequence which may be used in a vector of the present invention is a scaffold-attachment region (SAR). Additional regulatory sequences may be selected by the skilled person on the basis of their common general knowledge.

Preparation of vector

[00118] The vector of the invention may be prepared by standard means known in the art for provision of vectors for gene therapy. Thus, well established public domain transfection, packaging and purification methods can be used to prepare a suitable vector preparation.

[00119] As discussed above, a vector of the invention may comprise the full genome of a naturally occurring AAV virus in addition to a polynucleotide sequence encoding ND4, ND6, or ND1 or a variant thereof. However, commonly a derivatised genome will be used, for instance a

derivative which has at least one inverted terminal repeat sequence (ITR), but which may lack any AAV genes such as rep or cap.

[00120] In such embodiments, in order to provide for assembly of the derivatised genome into an AAV viral particle, additional genetic constructs providing AAV and/or helper virus functions will be provided in a host cell in combination with the derivatised genome. These additional constructs will typically contain genes encoding structural AAV capsid proteins i.e. cap, VP1, VP2, VP3, and genes encoding other functions required for the AAV life cycle, such as rep. The selection of structural capsid proteins provided on the additional construct will determine the serotype of the packaged viral vector.

[00121] A particularly preferred packaged viral vector for use in the invention comprises a derivatised genome of AAV2 in combination with AAV5 or AAV8 capsid proteins. This packaged viral vector typically comprises one or more AAV2 ITRs.

[00122] As mentioned above, AAV viruses are replication incompetent and so helper virus functions, preferably adenovirus helper functions will typically also be provided on one or more additional constructs to allow for AAV replication.

[00123] All of the above additional constructs may be provided as plasmids or other episomal elements in the host cell, or alternatively one or more constructs may be integrated into the genome of the host cell.

[00124] In these aspects, the invention provides a method for production of a vector of the invention. The method comprises providing a vector which comprises an adeno-associated virus (AAV) genome or a derivative thereof and a polynucleotide sequence encoding ND4, ND6, or ND1 or a variant thereof in a host cell, and providing means for replication and assembly of the vector into an AAV viral particle. Preferably, the method comprises providing a vector comprising a derivative of an AAV genome and a polynucleotide sequence encoding ND4, ND6, or ND1 or a variant thereof, together with one or more additional genetic constructs encoding AAV and/or helper virus functions. Typically, the derivative of an AAV genome comprises at least one ITR. Optionally, the method further comprises a step of purifying the assembled viral particles. Additionally, the method may comprise a step of formulating the viral particles for therapeutic use.

Methods of therapy and medical uses

[00125] As discussed above, the present inventors have surprisingly demonstrated that a vector of the invention may be used to address the cellular dysfunction underlying LHON. In particular, they have shown that use of the vector can correct the defect associated with LHON. This provides a means whereby the degenerative process of the disease can be treated, arrested, palliated or prevented.

[00126] The invention therefore provides a method of treating or preventing LHON in a patient in need thereof, comprising administering a therapeutically effective amount of a vector of the invention to the patient by direct retinal, subretinal or intravitreal injection. Accordingly, LHON is thereby treated or prevented in the patient.

[00127] In a related aspect, the invention provides for use of a vector of the invention in a method of treating or preventing LHON by administering said vector to a patient by direct retinal, subretinal or intravitreal injection. Additionally, the invention provides the use of a vector of the invention in the manufacture of a medicament for treating or preventing LHON by direct retinal, subretinal or intravitreal injection.

[00128] In all these embodiments, the vector of the invention may be administered in order to prevent the onset of one or more symptoms of LHON. The patient may be asymptomatic. The subject may have a predisposition to the disease. The method or use may comprise a step of identifying whether or not a subject is at risk of developing, or has, LHON. A prophylactically effective amount of the vector is administered to such a subject. A prophylactically effective amount is an amount which prevents the onset of one or more symptoms of the disease.

[00129] Alternatively, the vector may be administered once the symptoms of the disease have appeared in a subject i.e. to cure existing symptoms of the disease. A therapeutically effective amount of the antagonist is administered to such a subject. A therapeutically effective amount is an amount which is effective to ameliorate one or more symptoms of the disease. Such an amount may also arrest, slow or reverse some loss of peripheral vision associated with LHON. Such an amount may also arrest, slow or reverse onset of LHON.

[00130] A typical single dose is between 10^{10} and 10^{12} genome particles, depending on the amount of remaining retinal tissue that requires transduction. A genome particle is defined herein as an AAV capsid that contains a single stranded DNA molecule that can be quantified with a sequence specific method (such as real-time PCR). That dose may be provided as a single dose, but may be repeated for the fellow eye or in cases where vector may not have targeted the correct region of retina for whatever reason (such as surgical complication). The treatment is preferably a single permanent treatment for each eye, but repeat injections, for example in future years and/or with different AAV serotypes may be considered.

[00131] The invention also provides a method of monitoring treatment or prevention of LHON in a patient comprising measuring activity ex vivo in retinal cells obtained from said patient

following administration of the AAV vector of the invention by direct retinal, subretinal or intravitreal injection. This method can allow for determination of the efficacy of treatment.

Pharmaceutical Compositions

[00132] The vector of the invention can be formulated into pharmaceutical compositions. These compositions may comprise, in addition to the vector, a pharmaceutically acceptable excipient, carrier, buffer, stabiliser or other materials well known to those skilled in the art. Such materials should be non-toxic and should not interfere with the efficacy of the active ingredient. The precise nature of the carrier or other material may be determined by the skilled person according to the route of administration, i.e. here direct retinal, subretinal or intravitreal injection.

[00133] The pharmaceutical composition is typically in liquid form. Liquid pharmaceutical compositions generally include a liquid carrier such as water, petroleum, animal or vegetable oils, mineral oil or synthetic oil. Physiological saline solution, magnesium chloride, dextrose or other saccharide solution or glycols such as ethylene glycol, propylene glycol or polyethylene glycol may be included. In some cases, a surfactant, such as pluronic acid (PF68) 0.001% may be used.

[00134] For injection at the site of affliction, the active ingredient will be in the form of an aqueous solution which is pyrogen-free and has suitable pH, isotonicity and stability. Those of relevant skill in the art are well able to prepare suitable solutions using, for example, isotonic vehicles such as Sodium Chloride Injection, Ringer's Injection, Lactated Ringer's Injection. Preservatives, stabilisers, buffers, antioxidants and/or other additives may be included, as required.

[00135] For delayed release, the vector may be included in a pharmaceutical composition which is formulated for slow release, such as in microcapsules formed from biocompatible polymers or in liposomal carrier systems according to methods known in the art.

Samples

[00136] Samples that are suitable for use in the methods described herein can be nucleic acid samples from a subject. A "nucleic acid sample" as used herein can include RNA or DNA, or a combination thereof. In another embodiment, a "polypeptide sample" (e.g., peptides or proteins, or fragments therefrom) can be used to ascertain information that an amino acid change has occurred, which is the result of a genetic variant. Nucleic acids and polypeptides can be extracted from one or more samples including but not limited to, blood, saliva, urine, mucosal scrapings of the lining of the mouth, expectorant, serum, tears, skin, tissue, or hair. A nucleic acid sample can be assayed for nucleic acid information. "Nucleic acid information," as used herein, includes a nucleic acid sequence itself, the presence/absence of genetic variation in the nucleic acid sequence, a physical property which varies depending on the nucleic acid sequence (e.g., Tm), and the amount of the nucleic acid (e.g., number of mRNA copies). A "nucleic acid" means any one of DNA, RNA, DNA including artificial nucleotides, or RNA including artificial nucleotides. As used herein, a "purified nucleic acid" includes cDNAs, fragments of genomic nucleic acids, nucleic acids produced using the polymerase chain reaction (PCR), nucleic acids formed by restriction enzyme treatment of genomic nucleic acids, recombinant nucleic acids, and chemically synthesized nucleic acid molecules. A "recombinant" nucleic acid molecule includes a nucleic acid molecule made by an artificial combination of two otherwise separated segments of sequence, e.g., by chemical synthesis or by the manipulation of isolated segments of nucleic acids by genetic engineering techniques. As used herein, a "polypeptide" includes proteins, fragments of proteins, and peptides, whether isolated from natural sources, produced by recombinant techniques, or chemically synthesized. A polypeptide may have one or more modifications, such as a post-translational modification (e.g., glycosylation, phosphorylation, etc.) or any other modification (e.g., pegylation, etc.). The polypeptide may contain one or more non-naturally-occurring amino acids (e.g., such as an amino acid with a side chain modification).

[00137] In some embodiments, the nucleic acid sample can comprise cells or tissue, for example, cell lines. Exemplary cell types from which nucleic acids can be obtained using the methods described herein include, but are not limited to, the following: a blood cell such as a B lymphocyte, T lymphocyte, leukocyte, erythrocyte, macrophage, or neutrophil; a muscle cell such as a skeletal cell, smooth muscle cell or cardiac muscle cell; a germ cell, such as a sperm or egg; an epithelial cell; a connective tissue cell, such as an adipocyte, chondrocyte; fibroblast or osteoblast; a neuron; an astrocyte; a stromal cell; an organ specific cell, such as a kidney cell, pancreatic cell, liver cell, or a keratinocyte; a stem cell; or any cell that develops therefrom. A cell from which nucleic acids can be obtained can be a blood cell or a particular type of blood cell including, for example, a hematopoietic stem cell or a cell that arises from a hematopoietic stem cell such as a red blood cell, B lymphocyte, T lymphocyte, natural killer cell, neutrophil, basophil, eosinophil, monocyte, macrophage, or platelet. Generally, any type of stem cell can be used including, without limitation, an embryonic stem cell, adult stem cell, or pluripotent stem cell.

[00138] In some embodiments, a nucleic acid sample can be processed for RNA or DNA isolation, for example, RNA or DNA in a cell or tissue sample can be separated from other components of the nucleic acid sample. Cells can be harvested from a nucleic acid sample using standard techniques, for example, by centrifuging a cell sample and resuspending the pelleted cells, for example, in a buffered solution, for example, phosphate-buffered saline (PBS). In some embodiments, after centrifuging the cell suspension to obtain a cell pellet, the cells can be lysed to extract DNA. In some embodiments, the nucleic acid sample can be concentrated and/or purified to isolate DNA. All nucleic acid samples obtained from a subject, including those subjected to any sort of further processing, are considered to be obtained from the subject. In some embodiments, standard techniques and kits known in the art can be used to extract RNA or DNA from a nucleic acid sample, including, for example, phenol extraction, a QIAAMP® Tissue Kit (Qiagen, Chatsworth, Calif.), a WIZARD® Genomic DNA purification kit (Promega), or a Qiagen Autopure method using Puregene chemistry, which can enable purification of highly stable DNA well-suited for archiving.

[00139] In some embodiments, determining the identity of an allele or determining copy number can, but need not, include obtaining a nucleic acid sample comprising RNA and/or DNA from a subject, and/or assessing the identity, copy number, presence or absence of one or more genetic variations and their chromosomal locations within the genomic DNA (i.e. subject's genome) derived from the nucleic acid sample.

[00140] The individual or organization that performs the determination need not actually carry out the physical analysis of a nucleic acid sample from a subject. In some embodiments, the methods can include using information obtained by analysis of the nucleic acid sample by a third party. In some embodiments, the methods can include steps that occur at more than one site. For example, a nucleic acid sample can be obtained from a subject at a first site, such as at a health care provider or at the subject's home in the case of a self-testing kit. The nucleic acid sample can be analyzed at the same or a second site, for example, at a laboratory or other testing facility.

Nucleic Acids

[00141] The nucleic acids and polypeptides described herein can be used in methods and kits of the present disclosure. In some embodiments, aptamers that specifically bind the nucleic acids and polypeptides described herein can be used in methods and kits of the present disclosure. As used herein, a nucleic acid can comprise a deoxyribonucleotide (DNA) or ribonucleotide (RNA), whether singular or in polymers, naturally occurring or non-naturally occurring, double-stranded or single-stranded, coding, for example a translated gene, or non-coding, for example a regulatory region, or any fragments, derivatives, mimetics or complements thereof. In some embodiments, nucleic acids can comprise oligonucleotides, nucleotides, polynucleotides, nucleic acid sequences, genomic sequences, complementary DNA (cDNA), antisense nucleic acids, DNA regions, probes, primers, genes, regulatory regions, introns, exons, open-reading frames, binding sites, target nucleic acids and allele-specific nucleic acids.

[00142] A "probe," as used herein, includes a nucleic acid fragment for examining a nucleic acid in a specimen using the hybridization reaction based on the complementarity of nucleic acid.

[00143] A "hybrid" as used herein, includes a double strand formed between any one of the abovementioned nucleic acid, within the same type, or across different types, including DNA-DNA, DNA-RNA, RNA-RNA or the like.

[00144] "Isolated" nucleic acids, as used herein, are separated from nucleic acids that normally flank the gene or nucleotide sequence (as in genomic sequences) and/or has been completely or partially purified from other transcribed sequences (e.g., as in an RNA library). For example, isolated nucleic acids of the disclosure can be substantially isolated with respect to the complex cellular milieu in which it naturally occurs, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized. In some instances, the isolated material can form part of a composition, for example, a crude extract containing other substances, buffer system or reagent mix. In some embodiments, the material can be purified to essential homogeneity using methods known in the art, for example, by polyacrylamide gel electrophoresis (PAGE) or column chromatography (e.g., HPLC). With regard to genomic DNA (gDNA), the term "isolated" also can refer to nucleic acids that are separated from the chromosome with which the genomic DNA is naturally associated. For example, the isolated nucleic acid molecule can contain less than about 250 kb, 200 kb, 150 kb, 100 kb, 75 kb, 50 kb, 25 kb, 10 kb, 5 kb, 4 kb, 3 kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of the nucleotides that flank the nucleic acid molecule in the gDNA of the cell from which the nucleic acid molecule is derived.

[00145] Nucleic acids can be fused to other coding or regulatory sequences can be considered isolated. For example, recombinant DNA contained in a vector is included in the definition of "isolated" as used herein. In some embodiments, isolated nucleic acids can include recombinant DNA molecules in heterologous host cells or heterologous organisms, as well as partially or substantially purified DNA molecules in solution. Isolated nucleic acids also encompass in vivo and in vitro RNA transcripts of the DNA molecules of the present disclosure. An isolated nucleic acid molecule or nucleotide sequence can be synthesized chemically or by recombinant means. Such isolated nucleotide sequences can be useful, for example, in the manufacture of the encoded polypeptide, as probes for isolating homologous sequences (e.g., from other mammalian species), for gene mapping (e.g., by in situ hybridization with chromosomes), or for detecting expression of the gene, in tissue (e.g., human tissue), such as by Northern blot analysis or other hybridization techniques disclosed herein. The disclosure also pertains to nucleic acid sequences that hybridize under high stringency hybridization conditions, such as for selective hybridization, to a nucleotide

sequence described herein Such nucleic acid sequences can be detected and/or isolated by allele- or sequence-specific hybridization (e.g., under high stringency conditions). Stringency conditions and methods for nucleic acid hybridizations are well known to the skilled person (see, e.g., Current Protocols in Molecular Biology, Ausubel, F. et al., John Wiley & Sons, (1998), and Kraus, M. and Aaronson, S., Methods Enzymol., 200:546-556 (1991), the entire teachings of which are incorporated by reference herein.

[00146] Calculations of "identity" or "percent identity" between two or more nucleotide or amino acid sequences can be determined by aligning the sequences for optimal comparison purposes (e.g., gaps can be introduced in the sequence of a first sequence). The nucleotides at corresponding positions are then compared, and the percent identity between the two sequences is a function of the number of identical positions shared by the sequences (i.e. % identity = # of identical positions/total # of positions x 100). For example, a position in the first sequence is occupied by the same nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences, taking into account the number of gaps, and the length of each gap, which need to be introduced for optimal alignment of the two sequences.

[00147] In some embodiments, the length of a sequence aligned for comparison purposes is at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, or at least 95%, of the length of the reference sequence. The actual comparison of the two sequences can be accomplished by well-known methods, for example, using a mathematical algorithm. A non-limiting example of such a mathematical algorithm is described in Karlin, S. and Altschul, S., Proc. Natl. Acad. Sci. USA, 90- 5873-5877 (1993). Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0), as described in Altschul, S. et al., Nucleic Acids Res., 25:3389-3402 (1997). When utilizing BLAST and Gapped BLAST programs, any relevant parameters of the respective programs (e.g., NBLAST) can be used. For example, parameters for sequence comparison can be set at score= 100, word length= 12, or can be varied (e.g., W=5 or W=20). Other examples include the algorithm of Myers and Miller, CABIOS (1989), ADVANCE, ADAM, BLAT, and FASTA. In some embodiments, the percent identity between two amino acid sequences can be accomplished using, for example, the GAP program in the GCG software package (Accelrys, Cambridge, UK).

[00148] "Probes" or "primers" can be oligonucleotides that hybridize in a base-specific manner to a complementary strand of a nucleic acid molecule. Probes can include primers, which can be a single-stranded oligonucleotide probe that can act as a point of initiation of templatedirected DNA synthesis using methods including but not limited to, polymerase chain reaction (PCR) and ligase chain reaction (LCR) for amplification of a target sequence. Oligonucleotides, as described herein, can include segments or fragments of nucleic acid sequences, or their complements. In some embodiments, DNA segments can be between 5 and 10,000 contiguous bases, and can range from 5, 10, 12, 15, 20, or 25 nucleotides to 10, 15, 20, 25, 30, 40, 50, 100, 200, 500, 1000 or 10,000 nucleotides. In addition to DNA and RNA, probes and primers can include polypeptide nucleic acids (PNA), as described in Nielsen, P. et al., Science 254: 1497-1500 (1991). A probe or primer can comprise a region of nucleotide sequence that hybridizes to at least about 15, typically about 20-25, and in certain embodiments about 40, 50, 60 or 75, consecutive nucleotides of a nucleic acid molecule.

[00149] The present disclosure also provides isolated nucleic acids, for example, probes or primers, that contain a fragment or portion that can selectively hybridize to a nucleic acid that comprises, or consists of, a nucleotide sequence, wherein the nucleotide sequence can comprise at least one polymorphism or polymorphic allele contained in the genetic variations described herein or the wild-type nucleotide that is located at the same position, or the complements thereof. In some embodiments, the probe or primer can be at least 70% identical, at least 80% identical, at least 85% identical, at least 90% identical, or at least 95% identical, to the contiguous nucleotide sequence or to the complement of the contiguous nucleotide sequence.

[00150] In some embodiments, a nucleic acid probe can be an oligonucleotide capable of hybridizing with a complementary region of a gene associated with a condition (e.g., LHON) containing a genetic variation described herein. The nucleic acid fragments of the disclosure can be used as probes or primers in assays such as those described herein.

[00151] The nucleic acids of the disclosure, such as those described above, can be identified and isolated using standard molecular biology techniques well known to the skilled person. In some embodiments, DNA can be amplified and/or can be labeled (e.g., radiolabeled, fluorescently labeled) and used as a probe for screening, for example, a cDNA library derived from an organism. cDNA can be derived from mRNA and can be contained in a suitable vector. For example, corresponding clones can be isolated, DNA obtained fallowing in vivo excision, and the cloned insert can be sequenced in either or both orientations by art-recognized methods to identify the correct reading frame encoding a polypeptide of the appropriate molecular weight. Using these or similar methods, the polypeptide and the DNA encoding the polypeptide can be isolated, sequenced and further characterized.

[00152] In some embodiments, nucleic acid can comprise one or more polymorphisms, variations, or mutations, for example, single nucleotide polymorphisms (SNPs), single nucleotide variations (SNVs), copy number variations (CNVs), for example, insertions, deletions, inversions, and translocations. In some embodiments, nucleic acids can comprise analogs, for example, phosphorothioates, phosphoramidates, methyl phosphonate, chiralmethyl phosphonates, 2-0-methyl ribonucleotides, or modified nucleic acids, for example, modified backbone residues or linkages, or nucleic acids combined with carbohydrates, lipids, polypeptide or other materials, or peptide nucleic acids (PNAs), for example, chromatin, ribosomes, and transcriptosomes. In some embodiments nucleic acids can comprise nucleic acids in various structures, for example, A DNA, B DNA, Z-form DNA, siRNA, tRNA, and ribozymes. In some embodiments, the nucleic acid may be naturally or non-naturally polymorphic, for example, having one or more sequence differences, for example, additions, deletions and/or substitutions, as compared to a reference sequence. In some embodiments, a reference sequence can be based on publicly available information, for example, the U.C. Santa Cruz Human Genome Browser Gateway (genome.ucsc.edu/cgi-bin/hgGateway) or the NCBI website (www.ncbi.nlm.nih.gov). In some embodiments, a reference sequence can be determined by a practitioner of the present disclosure using methods well known in the art, for example, by sequencing a reference nucleic acid.

[00153] In some embodiments, a probe can hybridize to an allele, SNP, SNV, or CNV as described herein. In some embodiments, the probe can bind to another marker sequence associated with LHON as described herein.

[00154] One of skill in the art would know how to design a probe so that sequence specific hybridization can occur only if a particular allele is present in a genomic sequence from a test nucleic acid sample. The disclosure can also be reduced to practice using any convenient genotyping method, including commercially available technologies and methods for genotyping particular genetic variations

[00155] Control probes can also be used, for example, a probe that binds a less variable sequence, for example, a repetitive DNA associated with a centromere of a chromosome, can be used as a control. In some embodiments, probes can be obtained from commercial sources. In some embodiments, probes can be synthesized, for example, chemically or in vitro, or made from chromosomal or genomic DNA through standard techniques. In some embodiments sources of DNA that can be used include genomic DNA, cloned DNA sequences, somatic cell hybrids that contain one, or a part of one, human chromosome along with the normal chromosome complement of the

host, and chromosomes purified by flow cytometry or microdissection. The region of interest can be isolated through cloning, or by site-specific amplification using PCR.

[00156] One or more nucleic acids for example, a probe or primer, can also be labeled, for example, by direct labeling, to comprise a detectable label. A detectable label can comprise any label capable of detection by a physical, chemical, or a biological process for example, a radioactive label, such as 32P or 3H, a fluorescent label, such as FITC, a chromophore label, an affinity-ligand label, an enzyme label, such as alkaline phosphatase, horseradish peroxidase, or I2 galactosidase, an enzyme cofactor label, a hapten conjugate label, such as digoxigenin or dinitrophenyl, a Raman signal generating label, a magnetic label, a spin label, an epitope label, such as the FLAG or HA epitope, a luminescent label, a heavy atom label, a nanoparticle label, an electrochemical label, a light scattering label, a spherical shell label, semiconductor nanocrystal label, such as quantum dots (described in U.S. Pat. No. 6,207,392), and probes labeled with any other signal generating label known to those of skill in the art, wherein a label can allow the probe to be visualized with or without a secondary detection molecule. A nucleotide can be directly incorporated into a probe with standard techniques, for example, nick translation, random priming, and PCR labeling. A "signal," as used herein, include a signal suitably detectable and measurable by appropriate means, including fluorescence, radioactivity, chemiluminescence, and the like.

[00157] Non-limiting examples of label moieties useful for detection include, without limitation, suitable enzymes such as horseradish peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; members of a binding pair that are capable of forming complexes such as streptavidin/biotin, avidin/biotin or an antigen/antibody complex including, for example, rabbit IgG and anti-rabbit IgG; fluorophores such as umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, tetramethyl rhodamine, eosin, green fluorescent protein, erythrosin, coumarin, methyl coumarin, pyrene, malachite green, stilbene, lucifer yellow, Cascade Blue, Texas Red, dichlorotriazinylamine fluorescein, dansyl chloride, phycoerythrin, fluorescent lanthanide complexes such as those including Europium and Terbium, cyanine dye family members, such as Cy3 and Cy5, molecular beacons and fluorescent derivatives thereof, as well as others known in the art as described, for example, in Principles of Fluorescence Spectroscopy, Joseph R. Lakowicz (Editor), Plenum Pub Corp, 2nd edition (July 1999) and the 6th Edition of the Molecular Probes Handbook by Richard P. Hoagland; a luminescent material such as luminol; light scattering or plasmon resonant materials such as gold or silver particles or quantum dots; or radioactive material include 14C, 123I, 124I, 125I, Tc99m, 32P, 33P, 35S or 3H.

[00158] Other labels can also be used in the methods of the present disclosure, for example, backbone labels. Backbone labels comprise nucleic acid stains that bind nucleic acids in a sequence independent manner. Non-limiting examples include intercalating dyes such as phenanthridines and acridines (e.g., ethidium bromide, propidium iodide, hexidium iodide, dihydroethidium, ethidium homodimer-1 and -2, ethidium monoazide, and ACMA); some minor grove binders such as indoles and imidazoles (e.g., Hoechst 33258, Hoechst 33342, Hoechst 34580 and DAPI); and miscellaneous nucleic acid stains such as acridine orange (also capable of intercalating), 7-AAD, actinomycin D, LDS751, and hydroxystilbamidine. All of the aforementioned nucleic acid stains are commercially available from suppliers such as Molecular Probes, Inc. Still other examples of nucleic acid stains include the following dyes from Molecular Probes: cyanine dyes such as SYTOX Blue, SYTOX Green, SYTOX Orange, POPO-1, POPO-3, YOYO-1, YOYO-3, TOTO-1, TOTO-3, JOJO-1, LOLO-1, BOBO-1, BOBO-3, PO-PRO-1, PO-PRO-3, BO-PRO-1, BO-PRO-3, TO-PRO-1, TO-PRO-3, TO-PRO-5, JO-PRO-1, LO-PRO-1, YO-PRO-1, YO-PRO-3, PicoGreen, OliGreen, RiboGreen, SYBR Gold, SYBR Green I, SYBR Green II, SYBR DX, SYTO-40, -41, -42, -43, -44, -45 (blue), SYTO-13, -16, -24, -21, -23, -12, -11, -20, -22, -15, -14, -25 (green), SYTO-81, -80, -82, -83, -84, -85 (orange), SYTO-64, -17, -59, -61, -62, -60, -63 (red).

[00159] In some embodiments, fluorophores of different colors can be chosen, for example, 7-amino-4-methylcoumarin-3-acetic acid (AMCA), 5-(and-6)-carboxy-X-rhodamine, lissamine rhodamine B, 5-(and-6)-carboxyfluorescein, fluorescein-5-isothiocyanate (FITC), 7-diethylaminocoumarin-3-carboxylic acid, tetramethylrhodamine-5-(and-6)-isothiocyanate, 5-(and-6)-carboxytetramethylrhodamine, 7-hydroxycoumarin-3-carboxylic acid, 6-[fluorescein 5-(and-6)-carboxamido]hexanoic acid, N-(4,4-difluoro-5,7-dimethyl-4-bora-3a,4a diaza-3-indacenepropionic acid, eosin-5-isothiocyanate, erythrosin-5- isothiocyanate, TRITC, rhodamine, tetramethylrhodamine, R-phycoerythrin, Cy-3, Cy-5, Cy-7, Texas Red, Phar-Red, allophycocyanin (APC),and CASCADETM blue acetylazide, such that each probe in or not in a set can be distinctly visualized. In some embodiments, fluorescently labeled probes can be viewed with a fluorescence microscope and an appropriate filter for each fluorophore, or by using dual or triple band-pass filter sets to observe multiple fluorophores. In some embodiments, techniques such as flow cytometry can be used to examine the hybridization pattern of the probes.

[00160] In other embodiments, the probes can be indirectly labeled, for example, with biotin or digoxygenin, or labeled with radioactive isotopes such as 32P and/or 3H. As a non-limiting example, a probe indirectly labeled with biotin can be detected by avidin conjugated to a detectable marker. For example, avidin can be conjugated to an enzymatic marker such as alkaline phosphatase

or horseradish peroxidase. In some embodiments, enzymatic markers can be detected using colorimetric reactions using a substrate and/or a catalyst for the enzyme. In some embodiments, catalysts for alkaline phosphatase can be used, for example, 5-bromo-4-chloro-3-indolylphosphate and nitro blue tetrazolium. In some embodiments, a catalyst can be used for horseradish peroxidase, for example, diaminobenzoate.

Formulations, routes of administration, and effective doses

[00161] Yet another aspect of the present disclosure relates to formulations, routes of administration and effective doses for pharmaceutical compositions comprising an agent or combination of agents of the instant disclosure. Such pharmaceutical compositions can be used to treat a condition (e.g., LHON) as described above.

[00162] Compounds of the disclosure can be administered as pharmaceutical formulations including those suitable for oral (including buccal and sub-lingual), rectal, nasal, topical, transdermal patch, pulmonary, vaginal, suppository, or parenteral (including intraocular, intravitreal, intramuscular, intraarterial, intrathecal, intradermal, intraperitoneal, subcutaneous and intravenous) administration or in a form suitable for administration by aerosolization, inhalation or insufflation. General information on drug delivery systems can be found in Ansel et al., Pharmaceutical Dosage Forms and Drug Delivery Systems (Lippencott Williams & Wilkins, Baltimore Md. (1999).

[00163] In various embodiments, the pharmaceutical composition includes carriers and excipients (including but not limited to buffers, carbohydrates, mannitol, polypeptides, amino acids, antioxidants, bacteriostats, chelating agents, suspending agents, thickening agents and/or preservatives), water, oils including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like, saline solutions, aqueous dextrose and glycerol solutions, flavoring agents, coloring agents, detackifiers and other acceptable additives, adjuvants, or binders, other pharmaceutically acceptable auxiliary substances to approximate physiological conditions, such as pH buffering agents, tonicity adjusting agents, emulsifying agents, wetting agents and the like. Examples of excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. In some embodiments, the pharmaceutical preparation is substantially free of preservatives. In other embodiments, the pharmaceutical preparation can contain at least one preservative. General methodology on pharmaceutical dosage forms is found in Ansel et al., Pharmaceutical Dosage Forms and Drug Delivery Systems (Lippencott, Williams, & Wilkins, Baltimore Md. (1999)). It can be recognized that, while any suitable carrier known to those of ordinary skill in the art can be employed to administer the compositions of this disclosure, the type of carrier can vary depending on the mode of administration.

[00164] Compounds can also be encapsulated within liposomes using well-known technology. Biodegradable microspheres can also be employed as carriers for the pharmaceutical compositions of this disclosure. Suitable biodegradable microspheres are disclosed, for example, in U.S. Pat. Nos. 4,897,268, 5,075,109, 5,928,647, 5,811,128, 5,820,883, 5,853,763, 5,814,344 and 5,942,252.

[00165] The compound can be administered in liposomes or microspheres (or microparticles). Methods for preparing liposomes and microspheres for administration to a subject are well known to those of skill in the art. U.S. Pat. No. 4,789,734, the contents of which are hereby incorporated by reference, describes methods for encapsulating biological materials in liposomes. Essentially, the material is dissolved in an aqueous solution, the appropriate phospholipids and lipids added, and along with surfactants if required, and the material dialyzed or sonicated, as necessary. A review of known methods is provided by G. Gregoriadis, Chapter 14, "Liposomes," Drug Carriers in Biology and Medicine, pp. 2.sup.87-341 (Academic Press, 1979).

[00166] Microspheres formed of polymers or polypeptides are well known to those skilled in the art, and can be tailored for passage through the gastrointestinal tract directly into the blood stream. Alternatively, the compound can be incorporated and the microspheres, or composite of microspheres, implanted for slow release over a period of time ranging from days to months. See, for example, U.S. Pat. Nos. 4,906,474, 4,925,673 and 3,625,214, and Jein, TIPS 19:155-157 (1998), the contents of which are hereby incorporated by reference.

[00167] The concentration of drug can be adjusted, the pH of the solution buffered and the isotonicity adjusted to be compatible with intraocular or intravitreal injection.

[00168] The compounds of the disclosure can be formulated as a sterile solution or suspension, in suitable vehicles. The pharmaceutical compositions can be sterilized by conventional, well-known sterilization techniques, or can be sterile filtered. The resulting aqueous solutions can be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration. Suitable formulations and additional carriers are described in Remington "The Science and Practice of Pharmacy" (20th Ed., Lippincott Williams & Wilkins, Baltimore MD), the teachings of which are incorporated by reference in their entirety herein.

[00169] The agents or their pharmaceutically acceptable salts can be provided alone or in combination with one or more other agents or with one or more other forms. For example, a formulation can comprise one or more agents in particular proportions, depending on the relative potencies of each agent and the intended indication. For example, in compositions for targeting two

different host targets, and where potencies are similar, about a 1:1 ratio of agents can be used. The two forms can be formulated together, in the same dosage unit e.g., in one cream, suppository, tablet, capsule, aerosol spray, or packet of powder to be dissolved in a beverage; or each form can be formulated in a separate unit, e.g., two creams, two suppositories, two tablets, two capsules, a tablet and a liquid for dissolving the tablet, two aerosol sprays, or a packet of powder and a liquid for dissolving the powder, etc.

[00170] The term "pharmaceutically acceptable salt" means those salts which retain the biological effectiveness and properties of the agents used in the present disclosure, and which are not biologically or otherwise undesirable.

[00171] Typical salts are those of the inorganic ions, such as, for example, sodium, potassium, calcium, magnesium ions, and the like. Such salts include salts with inorganic or organic acids, such as hydrochloric acid, hydrobromic acid, phosphoric acid, nitric acid, sulfuric acid, methanesulfonic acid, p toluenesulfonic acid, acetic acid, fumaric acid, succinic acid, lactic acid, mandelic acid, malic acid, citric acid, tartaric acid or maleic acid. In addition, if the agent(s) contain a carboxyl group or other acidic group, it can be converted into a pharmaceutically acceptable addition salt with inorganic or organic bases. Examples of suitable bases include sodium hydroxide, potassium hydroxide, ammonia, cyclohexylamine, dicyclohexyl-amine, ethanolamine, diethanolamine, triethanolamine, and the like.

[00172] A pharmaceutically acceptable ester or amide refers to those which retain biological effectiveness and properties of the agents used in the present disclosure, and which are not biologically or otherwise undesirable. Typical esters include ethyl, methyl, isobutyl, ethylene glycol, and the like. Typical amides include unsubstituted amides, alkyl amides, dialkyl amides, and the like.

[00173] In some embodiments, an agent can be administered in combination with one or more other compounds, forms, and/or agents, e.g., as described above. Pharmaceutical compositions with one or more other active agents can be formulated to comprise certain molar ratios. For example, molar ratios of about 99:1 to about 1:99 of a first active agent to the other active agent can be used. In some subset of the embodiments, the range of molar ratios of a first active agent: other active agents are selected from about 80:20 to about 20:80; about 75:25 to about 25:75, about 70:30 to about 30:70, about 66:33 to about 33:66, about 60:40 to about 40:60; about 50:50; and about 90:10 to about 10:90. The molar ratio of a first active: other active agents can be about 1:9, and in some embodiments can be about 1:1. The two agents, forms and/or compounds can be formulated together, in the same dosage unit e.g., in one cream, suppository, tablet, capsule, or packet of powder

to be dissolved in a beverage; or each agent, form, and/or compound can be formulated in separate units, e.g., two creams, suppositories, tablets, two capsules, a tablet and a liquid for dissolving the tablet, an aerosol spray a packet of powder and a liquid for dissolving the powder, etc.

[00174] If necessary or desirable, the agents and/or combinations of agents can be administered with still other agents. The choice of agents that can be co-administered with the agents and/or combinations of agents of the instant disclosure can depend, at least in part, on the condition being treated.

[00175] The agent(s) (or pharmaceutically acceptable salts, esters or amides thereof) can be administered per se or in the form of a pharmaceutical composition wherein the active agent(s) is in an admixture or mixture with one or more pharmaceutically acceptable carriers. A pharmaceutical composition, as used herein, can be any composition prepared for administration to a subject. Pharmaceutical compositions for use in accordance with the present disclosure can be formulated in conventional manner using one or more physiologically acceptable carriers, comprising excipients, diluents, and/or auxiliaries, e.g., which facilitate processing of the active agents into preparations that can be administered. Proper formulation can depend at least in part upon the route of administration chosen. The agent(s) useful in the present disclosure, or pharmaceutically acceptable salts, esters, or amides thereof, can be delivered to a subject using a number of routes or modes of administration, including oral, buccal, topical, rectal, transdermal, transmucosal, subcutaneous, intravenous, intraocular, intravitreal, and intramuscular applications, as well as by inhalation.

[00176] In some embodiments, oils or non-aqueous solvents can be used to bring the agents into solution, due to, for example, the presence of large lipophilic moieties. Alternatively, emulsions, suspensions, or other preparations, for example, liposomal preparations, can be used. With respect to liposomal preparations, any known methods for preparing liposomes for treatment of a condition can be used. See, for example, Bangham et al., J. Mol. Biol. 23: 238-252 (1965) and Szoka et al., Proc. Natl Acad. Sci. USA 75: 4194-4198 (1978), incorporated herein by reference. Ligands can also be attached to the liposomes to direct these compositions to particular sites of action. Agents of this disclosure can also be integrated into foodstuffs, e.g., cream cheese, butter, salad dressing, or ice cream to facilitate solubilization, administration, and/or compliance in certain subject populations.

[00177] The compounds of the disclosure can be formulated for parenteral administration (e.g., by injection, for example, intraocular or intravitreal injection) and can be presented in unit dose form in ampoules, pre-filled syringes, small volume infusion or in multi-dose containers with an added preservative. The compositions can take such forms as suspensions, solutions, or emulsions in oily or aqueous vehicles, for example, solutions in aqueous polyethylene glycol.

[00178] For injectable formulations, the vehicle can be chosen from those known in art to be suitable, including aqueous solutions or oil suspensions, or emulsions, with sesame oil, corn oil, cottonseed oil, or peanut oil, as well as elixirs, mannitol, dextrose, or a sterile aqueous solution, and similar pharmaceutical vehicles. The formulation can also comprise polymer compositions which are biocompatible, biodegradable, such as poly(lactic-co-glycolic)acid. These materials can be made into micro or nanospheres, loaded with drug and further coated or derivatized to provide superior sustained release performance. Vehicles suitable for periocular or intraocular injection include, for example, suspensions of therapeutic agent in injection grade water, liposomes and vehicles suitable for lipophilic substances. Other vehicles for periocular or intraocular injection are well known in the art.

[00179] In some embodiments, the composition is formulated in accordance with routine procedures as a pharmaceutical composition adapted for intravenous administration to human beings. Typically, compositions for intravenous administration are solutions in sterile isotonic aqueous buffer. Where necessary, the composition can also include a solubilizing agent and a local anesthetic such as lidocaine to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients can be mixed prior to administration.

[00180] When administration is by injection, the active compound can be formulated in aqueous solutions, specifically in physiologically compatible buffers such as Hanks solution, Ringer's solution, or physiological saline buffer. The solution can contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Alternatively, the active compound can be in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use. In some embodiments, the pharmaceutical composition does not comprise an adjuvant or any other substance added to enhance the immune response stimulated by the peptide. In some embodiments, the pharmaceutical composition comprises a substance that inhibits an immune response to the peptide. Methods of formulation are known in the art, for example, as disclosed in Remington's Pharmaceutical Sciences, latest edition, Mack Publishing Co., Easton P.

[00181] In some embodiments, eye disorders can be effectively treated with ophthalmic solutions, suspensions, ointments or inserts comprising an agent or combination of agents of the

present disclosure. Eye drops can be prepared by dissolving the active ingredient in a sterile aqueous solution such as physiological saline, buffering solution, etc., or by combining powder compositions to be dissolved before use. Other vehicles can be chosen, as is known in the art, including but not limited to: balance salt solution, saline solution, water soluble polyethers such as polyethyene glycol, polyvinyls, such as polyvinyl alcohol and povidone, cellulose derivatives such as methylcellulose and hydroxypropyl methylcellulose, petroleum derivatives such as mineral oil and white petrolatum, animal fats such as lanolin, polymers of acrylic acid such as carboxypolymethylene gel, vegetable fats such as peanut oil and polysaccharides such as dextrans, and glycosaminoglycans such as sodium hyaluronate. If desired, additives ordinarily used in the eye drops can be added. Such additives include isotonizing agents (e.g., sodium chloride, etc.), buffer agent (e.g., boric acid, sodium monohydrogen phosphate, sodium dihydrogen phosphate, etc.), preservatives (e.g., benzalkonium chloride, benzethonium chloride, chlorobutanol, etc.), thickeners (e.g., saccharide such as lactose, mannitol, maltose, etc.; e.g., hyaluronic acid or its salt such as sodium hyaluronate, potassium hyaluronate, etc.; e.g., mucopolysaccharide such as chondroitin sulfate, etc.; e.g., sodium polyacrylate, carboxyvinyl polymer, crosslinked polyacrylate, polyvinyl alcohol, polyvinyl pyrrolidone, methyl cellulose, hydroxy propyl methylcellulose, hydroxyethyl cellulose, carboxymethyl cellulose, hydroxy propyl cellulose or other agents known to those skilled in the art).

[00182] The solubility of the components of the present compositions can be enhanced by a surfactant or other appropriate co-solvent in the composition. Such cosolvents include polysorbate 20, 60, and 80, Pluronic F68, F-84 and P-103, cyclodextrin, or other agents known to those skilled in the art. Such co-solvents can be employed at a level of from about 0.01% to 2% by weight.

[00183] The compositions of the disclosure can be packaged in multidose form. Preservatives can be preferred to prevent microbial contamination during use. Suitable preservatives include: benzalkonium chloride, thimerosal, chlorobutanol, methyl paraben, propyl paraben, phenylethyl alcohol, edetate disodium, sorbic acid, Onamer M, or other agents known to those skilled in the art. In the prior art ophthalmic products, such preservatives can be employed at a level of from 0.004% to 0.02%. In the compositions of the present application the preservative, preferably benzalkonium chloride, can be employed at a level of from 0.001% to less than 0.01%, e.g., from 0.001% to 0.008%, preferably about 0.005% by weight. It has been found that a concentration of benzalkonium chloride of 0.005% can be sufficient to preserve the compositions of the present disclosure from microbial attack.

[00184] In some embodiments, the agents of the present disclosure are delivered in soluble rather than suspension form, which allows for more rapid and quantitative absorption to the sites of

action. In general, formulations such as jellies, creams, lotions, suppositories and ointments can provide an area with more extended exposure to the agents of the present disclosure, while formulations in solution, e.g., sprays, provide more immediate, short-term exposure.

[00185] It is envisioned additionally, that the compounds of the disclosure can be attached releasably to biocompatible polymers for use in sustained release formulations on, in or attached to inserts for topical, intraocular, periocular, or systemic administration. The controlled release from a biocompatible polymer can be utilized with a water soluble polymer to form an instillable formulation, as well. The controlled release from a biocompatible polymer, such as for example, PLGA microspheres or nanospheres, can be utilized in a formulation suitable for intra ocular implantation or injection for sustained release administration, as well any suitable biodegradable and biocompatible polymer can be used.

EXAMPLES

[00186] The following exemplary embodiments further describe the present invention. It should be understood that these examples are only intended to illustrate the invention, but not to limit the scope of the present invention. Unless otherwise indicated, the methods and conditions disclosed in e.g., sambrook et al, molecular cloning: a laboratory manual (New York: cold spring harbor laboratory press, 1989) or the conditions recommended by the manufacturer can be used in the examples below.

Example 1 – ND4 plasmid and virus preparation

[00187] *1.1 plasmid preparation*

[00188] The nucleotide sequence for human ND4 (**SEQ ID NO: 6**) was obtained based on US National Center for Biotechnology Information reference sequence yp_003024035.1. The sequences for the non-optimized mitochondrial targeting sequence COX10 is **SEQ ID NO: 1**. The optimized sequences for the mitochondrial targeting sequence COX10 (opt_COX10, **SEQ ID NO: 2**) and the coding sequence of human ND4 (opt_ND4, **SEQ ID NO: 7**) were designed to improve the transcription efficiency and the translation efficiency. The optimized COX10-ND4 sequence, which is about 75.89% homology to the non-optimized COX10-ND4, was followed by a three prime untranslated region (*i.e.*, 3'UTR, **SEQ ID NO: 13**) to a recombinant nucleic acid, opt_COX10-opt_ND4-3'UTR (as shown in **SEQ ID NO: 31**).

[00189] The synthesized recombinant nucleic acid, opt_COX10-opt_ND4-3'UTR, was incorporated into an adeno-associated virus (AAV) vector by PCR amplification (**FIG. 1**). The opt_COX10-opt_ND4-3'UTR was cut by the EcoRI/SalI restriction enzymes to form cohesive ends, and then embedded into an AAV vector with EcoRI/SalI restriction sites, such as the pSNaV vector, to generate the pSNaV/rAAV2/2-ND4 plasmid (i.e., the pAAV2-optimized ND4 plasmid). The pAAV2-opt_ND4 plasmid was compared to the non-optimized pAAV2-ND4 plasmid.

[00190] The recon screening and identifying steps were similar to the CN102634527B: the plasmid was cultured at 37 °C in a LB plate. Blue colonies and white colonies were appeared, where white colonies were recombinant clones. The white colonies were picked, added to 100 mg/L ampicillin-containing LB culture medium, cultured at 37 °C, 200 rpm for 8 hours and then the plasmid were extracted from the cultured bacterial medium based on the Biomiga plasmid extraction protocol. The identification of the plasmid was confirmed using the EcoRI/SalI restriction enzymes.

[00191] *1.2 cell transfection*

[00192] One day before transfection, HEK293 cells were inoculated to 225 cm^2 cell culture bottle: at the inoculation density of 3.0×10^7 cells/ml, the culture medium was the Dulbecco's Modified Eagle Medium (DMEM) with 10% bovine serum, at 37 °C in a 5% CO_2 incubator overnight. The culture medium were replaced with fresh DMEM with 10% bovine serum on the day of transfection.

[00193] After the cells grow to 80-90%, discard the culture medium and transfect the cells with the pAAV2-ND4 and pAAV2-opt_ND4 plasmid, using the PlasmidTrans (VGTC) transfection kit. The detailed transfection protocol was described in CN102634527B example 1. The cells were collected 48 h after the transfection.

[00194] *1.3 Collection, concentration and purification of the recombinant adeno-associated virus*

[00195] Virus collection: 1) dry ice ethanol bath (or liquid nitrogen) and a 37 °C water bath were prepared; 2) the transfected cells along with media were collected in a 15 ml centrifuge tube; 3) the cells were centrifuged for 3 minutes at 1000 rpm/min; the cells and supernatant were separated; the supernatant were stored separately; and the cells were re-suspended in 1 ml of PBS; 4) the cell suspension were transferred between the dry ice-ethanol bath and 37 °C water bath repeatedly, freeze thawing for four times for 10 minutes each, slightly shaking after each thawing.

[00196] Virus concentration : 1) cell debris were removed with 10,000 g centrifugation; the centrifugal supernatant was transferred to a new centrifuge tube; 2) impurities were removed by filtering with a 0.45 μm filter; 3) each 1/2 volume of 1M NaCl and 10% PEG 8000 solution were added in the sample, uniformly mixed, and stored at 4 °C overnight; 4) supernatant was discarded after 12,000 rpm centrifugation for 2 h; after the virus precipitate was completely dissolving in an appropriate amount of PBS solution, sterilizing the sample with a 0.22 μm filter; 5) adding

benzonase nuclease was added to remove residual plasmid DNA (final concentration at 50 U/ml). The tube was inverted several times to mix thoroughly and then incubated at 37 °C for 30 minutes; 6) the sample was filtered with a 0.45 μm filtration head; the filtrate is the concentrated rAAV2 virus.

[00197] Virus purification : 1) CsCl was added to the concentrated virus solution until a density of 1.41 g/ml (refraction index at 1.372); 2) the sample was added to in the ultracentrifuge tube and filled the tube with pre-prepared 1.41 g/ml CsCl solution; 3) centrifuged at 175,000 g for 24 hours to form a density gradient. Sequential collection of different densities of the sample was performed. The enriched rAAV2 particles were collected; 4) repeating the process one more time. The virus was loaded to a 100 kDa dialysis bag and dialyzed/desalted at 4 °C overnight. The concentrated and purified recombinant adeno-associated virus were rAAV2-ND4 and rAAV2-optimized ND4.

[00198] Similarly, other mitochondrial targeting sequences (MTS), such as OPA1 (**SEQ ID NO: 5**) can be used to replace COX10 in the above example and create AAV with recombinant plasmids.

Example 2 – intravitreal injection of rAAV2 in rabbit eyes

[00199] Twelve rabbits were divided into 2 group: rAAV2-ND4 and rAAV2-optimized ND4. Virus solution (1×10^{10} vg/0.05 mL) was punctured into the vitreous cavity from 3 mm outside the corneal limbus at the pars plana. After the intravitreal injection, the eyes were examined using slit lamp exam and fundus photography inspection. Injection for 30 days. RT-PCR detection and immunoblotting were carried out in each group respectively.

Example 3 – real-time PCR for the expression of ND4

[00200] The RNAs from the transfected rAAV2-ND4 and rAAV2-optimized ND4 rabbit optic nerve cells were extracted using the TRIZOL total RNA extraction kit. cDNA templates were synthesized by reverse transcription of the extracted RNA.

[00201] The NCBI conserved structural domain analysis software were used to analyze the conservative structure of ND4, ensuring that the designed primers amplified fragments were located at non-conserved region; then primers were designed according to the fluorescent quantitative PCR primer design principle:

β-actin-S： CGAGATCGTGCGGGACAT (**SEQ ID NO: 85**);

β-actin-A： CAGGAAGGAGGGCTGGAAC (**SEQ ID NO: 86**);

ND4-S： CTGCCTACGACAAACAGAC (**SEQ ID NO: 87**);

ND4-A： AGTGCGTTCGTAGTTTGAG (**SEQ ID NO: 88**);

[00202] The fluorescent quantitative PCR reaction and protocol: fluorescence quantitative PCR were measured in a real-time PCR detection system. In a 0.2 ml PCR reaction tube, SYBR green mix 12.5 μl, ddH_2O 8 μl, 1 μl of each primer, and the cDNA sample 2.5 μl, were added to an overall volume of 25 μl. Each sample was used for amplification of the target gene and amplifying the reference gene β-actin, and each amplification were repeated three times. The common reagents were added together and then divided separately to minimize handling variation. The fluorescent quantitative PCR were carried out: pre-denaturation at 95 °C for 1 s, denaturation at 94 °C for 15 s, annealing at 55 °C for 15 sec, extension at 72 °C for 45 s. A total of 40 cycles of amplification reaction were performed and fluorescence signal acquisition was done at the extension phase of each cycle. After the reaction, a 94 °C to 55 °C melting curve analysis was done. By adopting a relative quantitative method research of gene expression level difference to beta-actin was used as an internal reference gene.

[00203] As shown in **FIG. 2**, the relative expression level (mRNA level) of the rAAV2-ND4 and rAAV2-optimized ND4 were 0.42 ± 0.23 and 0.57 ± 0.62, respectively ($p < 0.05$, **FIG. 2**). The results unexpectedly show that the optimized ND4 (opt_ND4, **SEQ ID NO: 7**) coding nucleic acid sequence and the corresponding recombinant nucleic acid (opt_COX10-opt_ND4-3'UTR, **SEQ ID NO: 31**) surprisingly increased the transcription efficiency, increasing the expression of the rAAV2-optimized ND4 by about 36%. The results showed that the transcription efficiency of the rAAV2-optimized ND4 is significantly higher.

Example 4 - immunoblotting detection of ND4 expression

[00204] The ND4 protein was purified from the rabbit nerve cells transfected by rAAV2-optimized ND4 and rAAV2-ND4, respectively. After a 10% polyacrylamide gel electrophoresis, and transferred to a polyvinylidene difluoride membrane (Bio-Rad, HER-hercules, CA, USA) for immune detection. β-actin was used as an internal reference gene. The film strip was observed on an automatic image analysis instrument (Li-Cor; Lincoln, NE, USA) and analyzed using the integrated optical density of the protein band with integral normalization method, so as to obtain the same sample corresponding optical density value. The statistical analysis software SPSS 19.0 was used for the data analysis.

[00205] The results was shown in **FIG. 3**. The average relative protein expression level of ND4 for rAAV2-optimized ND4 (left black column) and rAAV2-ND4 was 0.32 ± 0.11 and 0.68 ± 0.20, respectively ($p < 0.01$, **FIG. 3**). The results unexpectedly show that the optimized ND4 coding nucleic acid sequence (opt_ND4, **SEQ ID NO: 7**) and the corresponding recombinant nucleic acid (opt_COX10-opt_ND4-3'UTR, **SEQ ID NO: 31**) surprisingly increased the translation efficiency, increasing the expression of the rAAV2-optimized ND4 by about 112%. The results showed that the translation efficiency of the rAAV2-optimized ND4 is also significantly higher.

Example 5 - rabbits intraocular pressure and eye-ground photography

[00206] Slit lamp examination and intraocular pressure measurement was performed on both groups of rabbits at 1, 3, 7, and 30 days after the surgery. No obviously abnormality, conjunctival congestion, secretions, or endophthalmitis were observed and the intraocular pressure were not elevated in all the rabbits.

[00207] The fundus photographic results were shown in **FIG. 4**. No obvious damage or complication to the optic nerve and retinal vascular of the rabbits, indicating the standard intravitreal injection is safe without noticeable inflammation reaction or other complications.

Example 6 – human clinical trial

[00208] Two groups of patients were tested: 1) between 2011 and 2012, 9 patients received intravitreal injection of 1×10^{10} vg/0.05 mL rAAV2-ND4 in a single eye, as a control group; and 2) between 2017 and January 2018, 20 patients received intravitreal injection of 1×10^{10} vg/0.05 mL rAAV2-optimized ND4 in a single eye, as an experimental group. The results of the clinical trial were analyzed using the statistical analysis SPSS 19.0.

[00209] The comparison of the two groups is shown in Table 2. The fastest eyesight improving time was 1 month in the experimental group, which was significantly faster than the control group at 3 months ($p < 0.01$); the optimal recovery of vision for the experimental group was 1.0, which was obviously higher than the control group at 0.8 ($p < 0.01$); the average recovery of vision in the experimental group was 0.582 ± 0.086, which was obviously higher than the control group at 0.344 ± 0.062 ($p < 0.01$). The fundus photographic results were shown in **FIG. 5**. No obvious damage or complication to the optic nerve and retinal vascular of the patients in the experimental and control groups, indicating the safety of the intravitreal injection of rAAV2-optimized ND4 and rAAV2-ND4.

Table 2: The comparison of rAAV2-optimized ND4 and rAAV2-ND4 in LHON gene therapy

group	Patient number	Fastest eyesight improving time (month)	Number of patients with improved vision	optimal recovery of vision	average recovery of vision
control	9	3	6 (67%)	0.8	0.344±0.062
experimental	20	1	15 (75%)	1.0	0.582±0.086

P value		＜0.01	＜0.01	＜0.01	＜0.01

Example 7 – OPA1 as the mitochondrial targeting sequences

[00210] The COX10 and 3'UTR sequences in the recombinant nucleic acid (opt_COX10-opt_ND4-3'UTR, **SEQ ID NO: 31**) in examples 1-6 were replaced with another mitochondrial targeted sequence, OPA1 (**SEQ ID NO: 5**) and another 3'UTR sequence, 3'UTR* (**SEQ ID NO: 14**) respectively, to generate a new recombinant nucleic acid, OPA1-opt_ND4-3'UTR* (**SEQ ID NO: 74**).

[00211] Experimental methods were the same as examples 1-6, where the recombinant nucleic acid opt_COX10-opt_ND4-3'UTR (**SEQ ID NO: 31**) was replaced by OPA1-opt_ND4-3'UTR* (**SEQ ID NO: 74**). It was found that, the optimized ND4 sequence has significantly improved transcription and translation efficiencies, expression levels, as well as higher efficacy and safety in treating LHON when compared to non-optimized ND4 (COX10-ND4-3'UTR, **SEQ ID NO: 15**).

Example 8 – optimized ND4 sequence opt_ND4*

[00212] Similar experimental methods in examples 1-6 were followed using the nucleic acid, opt_COX10*-opt_ND4*-3'UTR (**SEQ ID NO: 47**). Follow the similar procedures as in example 1, virus tagged with a fluorescent protein, EGFP, was prepared as rAAV2-ND4-EGFP and rAAV2-opt_ND4*-EGFP.

[00213] The frozen 293T cell was resuscitated and allowed to grow in a T75 flask to about 90%. The cells were precipitated and resuspended in DMEM complete medium to a cell density of 5×10^4 cells/mL. The cells were resuspended. About 100 μl of the cell suspension (about 5000 cells) were added in each well of a 96 well plate. The cells were cultured and grown to 50% under 37 °C and 5% CO_2. About 0.02 μl PBS was mixed with 2×10^{10} vg/0.02 μl of the virus rAAV2-ND4-EGFP and rAAV2-opt_ND4*-EGFP, respectively. After 48 hours, fluorescence microscopy and RT-PCR detection and immunoblotting experiments were performed. As shown in **FIG. 6**, EGFP was successfully expressed, indicating that rAAV carrying the EGFP gene was successfully transfected in the 293T cells and rAAV2-ND4-EGFP and rAAV2-opt_ND4*-EGFP were successfully expressed.

[00214] Real-time PCR tests similar to example 3 was following using the following primers:

β-actin-S： CGAGATCGTGCGGGACAT (**SEQ ID NO: 85**);

β-actin-A： CAGGAAGGAGGGCTGGAAC (**SEQ ID NO: 86**);

ND4-S: GCCAACAGCAACTACGAGC (**SEQ ID NO: 107**);

ND4-A: TGATGTTGCTCCAGCTGAAG (**SEQ ID NO: 108**);

[00215] The results unexpectedly show that the optimized ND4* (opt_ND4, **SEQ ID NO: 8**) coding nucleic acid sequence and the corresponding recombinant nucleic acid (opt_COX10*-opt_ND4*-3'UTR, **SEQ ID NO: 47**) surprisingly increased the transcription efficiency, increasing the expression of the rAAV2-opt_ND4 by about 20%. The results showed that the transcription efficiency of the rAAV2-opt_ND4 is significantly higher.

[00216] **FIG. 7** shows the ND4 expression in 293T cells. The average expression of ND4 protein for rAAV2-ND4 is 0.36, while the average expression of ND4 protein for rAAV2-opt_ND4* is 1.65, which is about 4.6 times higher than the rAAV2-ND4 group ($p < 0.01$) (see **FIG. 8**).

[00217] **FIG. 9** shows the ND4 expression in rabbit optic nerve cells. The average expression of ND4 protein for rAAV2-ND4 is 0.16, while the average expression of ND4 protein for rAAV2-opt_ND4* is 0.48, which is about 3 times higher than the rAAV2-ND4 group ($p < 0.01$) (see **FIG. 10**).

[00218] Similar to example 5, slit lamp examination and intraocular pressure measurement was performed on both groups of rabbits at 1, 3, 7, and 30 days after the surgery. No obviously abnormality, conjunctival congestion, secretions, or endophthalmitis were observed and the intraocular pressure were not elevated in all the rabbits.

[00219] The fundus photographic results for rAAV2-ND4 and rAAV2-opt_ND4* were shown in **FIG. 11**. No obvious damage or complication to the optic nerve and retinal vascular of the rabbits, indicating the standard intravitreal injection is safe without noticeable inflammation reaction or other complications.

[00220] Eye balls from both rabbit groups were removed after the slit lamp examination and intraocular pressure measurement. Eye balls were fixed, and dehydrated using paraffin. Tissues were pathologically sectioned along the direction of optic nerves. After further dehydration, the tissue sample was dyed using hematoxylin and eosin. The microscope inspection result is referred to **FIG. 12**. As shown in the HE staining results, the rabbit retinal ganglion fiber layer was not damaged and the number of ganglion cells was not reduced, indicating the intravitreal injection did not produce retinal toxicity or nerve damage, and can be used safely.

[00221] Experimental methods were the same as example 8, where the recombinant nucleic acid opt_COX10*-opt_ND4*-3'UTR (**SEQ ID NO: 47**) was replaced by OPA1-opt_ND4*-3'UTR* (**SEQ ID NO: 76**). It was found that, the optimized ND4 sequence has significantly improved transcription and translation efficiencies, expression levels, as well as higher efficacy and safety in treating LHON when compared to non-optimized ND4 (COX10-ND4-3'UTR, **SEQ ID NO: 15**).

Example 9 – ND6 sequence

[00222] Similar experimental methods in examples 1-6 were followed using the nucleic acid, COX10-ND6-3'UTR (**SEQ ID NO: 21**), which is the combination (5' to 3') of COX10 (**SEQ ID NO: 1**), ND6 (**SEQ ID NO: 9**), and 3'UTR (**SEQ ID NO: 13**).

[00223] The plasmid screening for COX10-ND6-3'UTR (**SEQ ID NO: 21**) used the following primers:

ND6-F: ATGATGTATGCTTTGTTTCTG (**SEQ ID NO: 89**),

ND6-R: CTAATTCCCCCGAGCAATCTC (**SEQ ID NO: 90**),

[00224] The transfected and screened virus rAAV2-ND6 had a viral titer of 2.0×10^{11} vg/mL. Similar to example 5, slit lamp examination and intraocular pressure measurement was performed on three groups of rabbits (A: rAAV2-ND6; B: rAAV-GFP; C: PBS) at 1, 7, and 30 days after the surgery (**FIG. 13**). No obviously abnormality, conjunctival congestion, secretions, or endophthalmitis were observed and the intraocular pressure were not elevated in all the rabbits.

[00225] Real-time PCR tests similar to example 3 was following using the following primers:

β-actin-S：CGAGATCGTGCGGGACAT (**SEQ ID NO: 85**);

β-actin-A：CAGGAAGGAGGGCTGGAAC (**SEQ ID NO: 86**);

ND6-S: AGTGTGGGTTTAGTAATG (**SEQ ID NO: 91**);

ND4-A: TGCCTCAGGATACTCCTC (**SEQ ID NO: 92**);

[00226] The results show that the expression of ND6 for rAAV2-ND6 and control (PBS) was 0.59 ± 0.06 and 0.41 ± 0.03, respectively. The results showed that the transcription efficiency of the rAAV2-ND6 is higher than the control group ($p<0.01$).

Example 10 – optimized opt_ND6 sequence

[00227] Similar experimental methods in examples 1-6 were followed using the nucleic acid, opt_COX10*-opt_ND6-3'UTR (**SEQ ID NO: 51**), which is the combination (5' to 3') of opt_COX10* (**SEQ ID NO: 3**), opt_ND6 (**SEQ ID NO: 10**), and 3'UTR (**SEQ ID NO: 13**).

[00228] Three groups of rabbits were injected: A: 10^{10} vg/50 μl of rAAV2-opt_ND6, B: 10^{10} vg/50 μl of rAAV2-ND6 (example 9), and C: 10^{10} vg/50 μl of rAAV2-EGFP. **FIG. 14** shows the fundus photographic results for rabbits injected with rAAV2-opt_ND6 (A), rAAV2-ND6 (B), rAAV-EGFP (C), respectively. No obviously abnormality, conjunctival congestion, secretions, or endophthalmitis were observed and the intraocular pressure were not elevated in all the rabbits.

[00229] Real-time PCR tests similar to example 3 was following using the following primers:

β-actin-F：CTCCATCCTGGCCTCGCTGT (**SEQ ID NO: 93**);

β-actin-R: GCTGTCACCTTCACCGTTCC (**SEQ ID NO: 94**);

ND6-F: GGGTTTTCTTCTAAGCCTTCTCC (**SEQ ID NO: 95**);

ND6-R: CCATCATACTCTTTCACCCACAG (**SEQ ID NO: 96**);

opt_ND6-F: CGCCTGCTGACCGGCTGCGT (**SEQ ID NO: 97**);

opt_ND6-R: CCAGGCCTCGGGGTACTCCT (**SEQ ID NO: 98**);

[00230] As shown in **FIG. 15**, rAAV2-opt_ND6 (A) and rAAV2-ND6 (B) both had higher ($p<0.05$) relative ND6 expression levels than the control group (C). rAAV2-opt_ND6 (A) had a little higher relative ND6 expression levels than rAAV2-ND6 (B). As shown in the western blot in **FIG. 16**, rAAV2-opt_ND6 (A) had more than 3 times higher relative ND6 expression levels than rAAV2-ND6 (B).

[00231] Experimental methods were the same as example 8, where the recombinant nucleic acids, COX10-ND6-3'UTR (**SEQ ID NO: 21**) and opt_COX10*-opt_ND6-3'UTR (**SEQ ID NO: 51**), were replaced by OPA1-ND6-3'UTR (**SEQ ID NO:** 77) and OPA1-opt_ND6-3'UTR (**SEQ ID NO: 79**). It was found that, the optimized ND6 sequence has significantly improved transcription and translation efficiencies, expression levels, as well as higher efficacy and safety in treating LHON.

Example 11 – ND1 and opt_ND1 sequences

[00232] Similar experimental methods in examples 1-6 were followed using rAAV2-ND1, COX10-ND1-3'UTR (**SEQ ID NO: 25**), which is the combination (5' to 3') of COX10 (**SEQ ID NO: 1**), ND1 (**SEQ ID NO: 11**), and 3'UTR (**SEQ ID NO: 13**); and rAAV2-opt_ND1, opt_COX10*-opt_ND1-3'UTR (**SEQ ID NO: 55**), which is the combination (5' to 3') of opt_COX10* (**SEQ ID NO: 3**), opt_ND1 (**SEQ ID NO: 12**), and 3'UTR (**SEQ ID NO: 13**).

[00233] The plasmid screening for COX10-ND1-3'UTR (**SEQ ID NO: 25**) used the following primers:

ND1-F: ATGGCCGCATCTCCGCACACT (**SEQ ID NO: 99**),

ND1-R: TTAGGTTTGAGGGGGAATGCT (**SEQ ID NO: 100**),

[00234] The plasmid screening for opt_COX10*-opt_ND1-3'UTR (**SEQ ID NO: 55**) used the following primers:

ND1-F: AACCTCAACCTAGGCCTCCTA (**SEQ ID NO: 101**),

ND1-R: TGGCAGGAGTAACCAGAGGTG (**SEQ ID NO: 102**),

[00235] Three groups of rabbits were injected: A: 10^{10} vg/50 μl of rAAV2-opt_ND1, B: 10^{10} vg/50 μl of rAAV2-ND1 (example 9), and C: 10^{10} vg/50 μl of rAAV2-EGFP. No obviously abnormality, conjunctival congestion, secretions, or endophthalmitis were observed and the intraocular pressure were not elevated in all the rabbits.

[00236] Real-time PCR tests similar to example 3 was following using the following primers:

ND1-F: AGGAGGCTCTGTCTGGTATCTTG (**SEQ ID NO: 103**);

ND1-R: TTTTAGGGGCTCTTTGGTGAA (**SEQ ID NO: 104**);

opt_ND1-F: GCCGCCTGCTGACCGGCTGCGT (**SEQ ID NO: 105**);

opt_ND1-R: TGATGTACAGGGTGATGGTGCTGG (**SEQ ID NO: 106**);

[00237] As shown in **FIG. 17**, rAAV2-opt_ND1 (A) and rAAV2-ND1 (B) both had higher ($p<0.05$) relative ND1 expression levels than the control group (C). As shown in the western blot in **FIG. 18**, rAAV2-opt_ND1 (A) had more than 2 times higher relative ND6 expression levels than rAAV2-ND1 (B).

[00238] Experimental methods were the same as example 8, where the recombinant nucleic acids, COX10-ND1-3'UTR (**SEQ ID NO: 25**) and opt_COX10*-opt_ND1-3'UTR (**SEQ ID NO: 55**), were replaced by OPA1-ND1-3'UTR (**SEQ ID NO: 81**) and OPA1-opt_ND1-3'UTR (**SEQ ID NO: 83**). It was found that, the optimized ND1 sequence has significantly improved transcription and translation efficiencies, expression levels, as well as higher efficacy and safety in treating LHON.

Example 12 – other fusion proteins

[00239] Similar experimental methods in examples 1-6 can be followed using other fusion proteins as set forth in SEQ ID NO: 15-84. And similar results are expected to be achieved.

Example 13 – formulation development

[00240] AAV2 virus samples were used to screen different AAV formulations. The stability of the different AAV formulations were evaluated using the StepOnePlus real-time PCR system. The viral titer of each formulation under a freeze/thaw cycle condition was measured.

[00241] First, three different formulations were tested under 1, 2, 3, 4, and 5 freeze/thaw cycles and the viral titers were measured and summarized in Table 3. The three formulations tested were: A: phosphate-buffered saline (PBS); B: 1% α,α-trehalose dehydrate, 1% L-histidine monohydrochloride monohydrate, and 1% polysorbate 20; and C: 180 mM NaCl, 10 mM NaH_2PO_4/Na_2HPO_4, and 0.001% poloxamer 188, pH 7.3. As shown in Table 3, formulation C has the lowest relative standard deviation (RSD) after 5 freeze/thaw cycles, indicating superior stability as an AAV formulation.

Table 3 – the viral titers of formulations A, B, and C

viral titers	0 cycle	1 cycle	2 cycles	3 cycles	4 cycles	5 cycles	RSD

A	1.15E+11	9.48E+10	6.16E+10	2.90E+10	1.56E+10	5.26E+09	83.18
B	4.25E+11	5.12E+11	6.66E+11	4.30E+11	4.77E+11	4.20E+11	19.30
C	4.96E+11	6.91E+11	7.69E+11	6.82E+11	6.83E+11	7.27E+11	13.90

[00242] As shown in Table 3, formulation C has the lowest relative standard deviation (RSD) after 5 freeze/thaw cycles, indicating superior stability as an AAV formulation.

[00243] Second, another group of three different formulations were tested under 1, 2, 3, 4, and 5 freeze/thaw cycles and the viral titers were measured and summarized in Table 4. The three formulations tested were: D: phosphate-buffered saline (PBS), pH 7.2-7.4; E: PBS and 0.001% poloxamer 188, pH 7.2-7.4; and F: 80 mM NaCl, 5 mM NaH_2PO_4, 40 mM Na_2HPO_4, 5 mM KH_2PO_4 and 0.001% poloxamer 188, 7.2-7.4.

Table 4 – the viral titers of formulations D, E, and F

viral titers	0 cycle	1 cycle	2 cycles	3 cycles	4 cycles	5 cycles	RSD
D	1.13E+10	4.62E+09	2.25E+09	1.25E+09	1.01E+09	9.48E+08	113.25
E	4.72E+10	5.48E+10	5.33E+10	5.33E+10	4.94E+10	4.08E+10	10.53
F	6.61E+10	6.08E+10	6.47E+10	6.84E+10	6.52E+10	6.05E+10	4.81

[00244] As shown in Table 4, formulation F has the lowest relative standard deviation (RSD) after 5 freeze/thaw cycles, indicating superior stability as an AAV formulation. Overall, formulation F also has the lowest RSD among all tested formulations and can be used as the AAV formulation for future development.

[00245] While preferred embodiments of the present invention have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the invention. It should be understood that various alternatives to the embodiments of the invention described herein may be employed in practicing the invention. It is intended that the following claims define the scope of the invention and that methods and structures within the scope of these claims and their equivalents be covered thereby.

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CLAIMS

WHAT IS CLAIMED IS:

1. A recombinant nucleic acid, comprising:

a mitochondrial targeting sequence;

a mitochondrial protein coding sequence comprising a sequence that is at least 90% identical to a sequence selected from the group consisting of SEQ ID NO: 7, 10, and 12; and

a 3'UTR nucleic acid sequence.

2. The recombinant nucleic acid of claim 1, wherein said mitochondrial targeting sequence encodes a polypeptide comprising a peptide sequence that is at least 90% identical to a sequence selected from the group consisting of SEQ ID NO: 129-159.

3. The recombinant nucleic acid of claim 1, wherein said mitochondrial targeting sequence comprises a sequence that is at least 90% identical to a sequence selected from the group consisting of SEQ ID NO: 2-5.

4. The recombinant nucleic acid of claim 1, wherein said mitochondrial targeting sequence comprises a sequence that encodes a polypeptide selected from the group consisting of hsCOX10, hsCOX8, scRPM2, lcSirt5, tbNDUS7, ncQCR2, hsATP5G2, hsLACTB, spilv1, gmCOX2, crATP6, hsOPA1, hsSDHD, hsADCK3, osP0644B06.24-2, Neurospora crassa ATP9 (ncATP9), hsGHITM, hsNDUFAB1, hsATP5G3, crATP6_hsADCK3, ncATP9_ncATP9, zmLOC100282174, ncATP9_zmLOC100282174_spilv1_ncATP9, zmLOC100282174_hsADCK3_crATP6_hsATP5G3, zmLOC100282174_hsADCK3_hsATP5G3, ncATP9_zmLOC100282174, hsADCK3_zmLOC100282174_crATP6_hsATP5G3, crATP6_hsADCK3_zmLOC100282174_hsATP5G3, hsADCK3_zmLOC100282174, hsADCK3_zmLOC100282174_crATP6, ncATP9_zmLOC100282174_spilv1_GNFP_ncATP9, and ncATP9_zmLOC100282174_spilv1_lcSirt5_osP0644B06.24-2_hsATP5G2_ncATP9.

5. The recombinant nucleic acid of claim 1, wherein said mitochondrial protein is selected from a group consisting of NADH dehydrogenase 4 (ND4), NADH dehydrogenase 6 (ND6), NADH dehydrogenase 1 (ND1), and a variant thereof.

6. The recombinant nucleic acid of claim 5, wherein said mitochondrial protein comprises NADH dehydrogenase 4 (ND4), or a variant thereof.

7. The recombinant nucleic acid of claim 6, wherein said mitochondrial protein coding sequence comprises a sequence that is at least 99% identical to a sequence as set forth in SEQ ID NO: 7.

8. The recombinant nucleic acid of claim 5, wherein said mitochondrial protein comprises NADH dehydrogenase 6 (ND6), or a variant thereof.

9. The recombinant nucleic acid of claim 8, wherein said mitochondrial protein coding sequence comprises a sequence that is at least 90% identical to a sequence as set forth in SEQ ID NO: 10.

10. The recombinant nucleic acid of claim 5, wherein said mitochondrial protein comprises NADH dehydrogenase 1 (ND1), or a variant thereof.

11. The recombinant nucleic acid of claim 10, wherein said mitochondrial protein coding sequence comprises a sequence that is at least 90% identical to a sequence as set forth in SEQ ID NO: 12.

12. The recombinant nucleic acid of claim 1, wherein said 3'UTR nucleic acid sequence comprises a sequence selected from the group consisting of hsACO2, hsATP5B, hsAK2, hsALDH2, hsCOX10, hsUQCRFS1, hsNDUFV1, hsNDUFV2, hsSOD2, hsCOX6c, hsIRP1, hsMRPS12, hsATP5J2, rnSOD2, and hsOXA1L.

13. The recombinant nucleic acid of claim 1, wherein said 3'UTR nucleic acid sequence comprises a sequence that is at least 90% identical to a sequence selected from the group consisting of SEQ ID NO: 111-125.

14. An adeno-associated viral (AAV) vector comprising a recombinant nucleic acid, comprising: a mitochondrial targeting sequence; a mitochondrial protein coding sequence comprising a sequence that is at least 90% identical to a sequence selected from the group consisting of SEQ ID NO: 7, 10, and 12; and a 3'UTR nucleic acid sequence.

15. The AAV vector of claim 14, wherein said AAV vector is a recombinant AAV (rAAV) vector.

16. The AAV vector of claim 15, wherein said rAAV vector is rAAV2 vector.

17. A pharmaceutical composition, comprising an adeno-associated virus (AAV) comprising a recombinant nucleic acid and a pharmaceutically acceptable excipient thereof, wherein said recombinant nucleic acid comprises: a mitochondrial targeting sequence; a

mitochondrial protein coding sequence comprising a sequence that is at least 90% identical to a sequence selected from the group consisting of SEQ ID NO: 7, 10, and 12; and a 3'UTR nucleic acid sequence.

18. The pharmaceutical composition of claim 17, wherein said pharmaceutically acceptable excipient comprises phosphate-buffered saline (PBS), α,α-trehalose dehydrate, L-histidine monohydrochloride monohydrate, polysorbate 20, NaCl, NaH_2PO_4, Na_2HPO_4, KH_2PO_4, K_2HPO_4, poloxamer 188, or any combination thereof.

19. The pharmaceutical composition of claim 18, wherein said pharmaceutically acceptable excipient comprises poloxamer 188.

20. The pharmaceutical composition of claim 19, wherein said pharmaceutically acceptable excipient comprises 0.0001%-0.01% poloxamer 188.

21. The pharmaceutical composition of claim 17, wherein said pharmaceutical composition has a viral titer of at least 5.0×10^{10} vg/mL.

22. The pharmaceutical composition of claim 17, when said pharmaceutical composition is subject to five freeze/thaw cycles, said pharmaceutical composition retains at least 60%, 70%, 80%, or 90% of a viral titer as compared to the viral titer prior to the five freeze/thaw cycles.

23. A method of treating Leber's hereditary optic neuropathy (LHON), comprising administering a pharmaceutical composition to a patient in need thereof, wherein said pharmaceutical composition comprises an adeno-associated virus (AAV) comprising the recombinant nucleic acid of claim 1.

24. The method of claim 23, wherein said pharmaceutical composition is administered via intravitreal injection.

25. The method of claim 24, further comprising administering methylprednisolone to said patient.

26. The method of claim 25, wherein said methylprednisolone is administered daily for at least 2 days prior to said intravitreal injection of said pharmaceutical composition.

27. The method of claim 26, wherein said methylprednisolone is administered intravenously at a daily dose of about 80 mg/60 kg.

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28. The method of claim 23, further comprising administering creatine phosphate sodium to said patient.

29. The method of claim 23, wherein said administering said pharmaceutical composition generates a higher average recovery of vision than a comparable pharmaceutical composition without said recombinant nucleic acid.

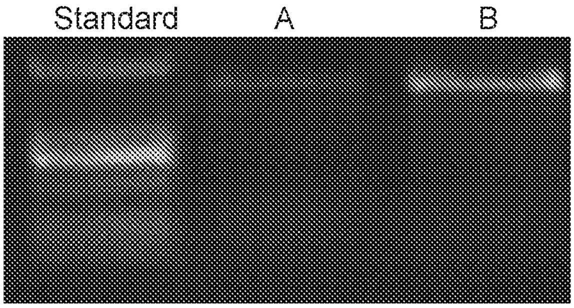


FIG. 1

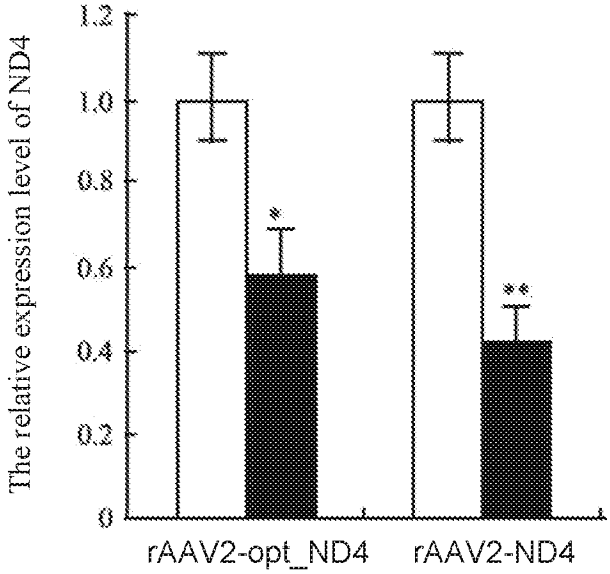
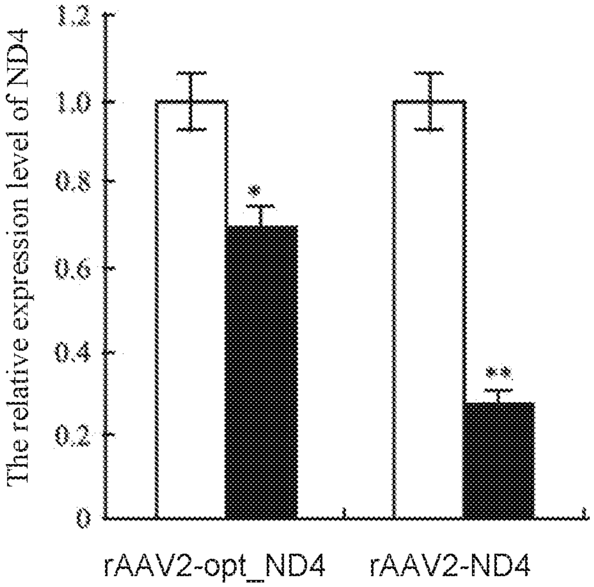

1.2
1.0
0.8
0.6
0.4
0.2
0
The relative expression level of ND4
*
**
rAAV2-opt_ND4
rAAV2-ND4

FIG. 2


1.2
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0.2
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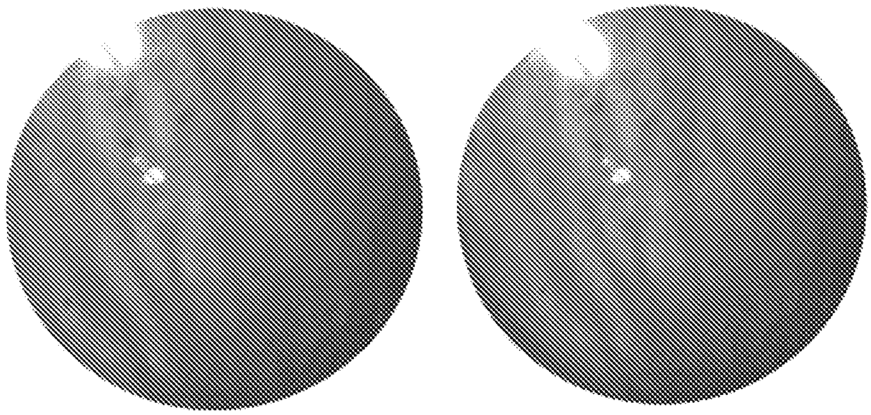
rAAV2-opt_ND4
rAAV2-ND4

FIG. 3



rAAV2-ND4 rAAV2-opt_ND4

FIG. 4

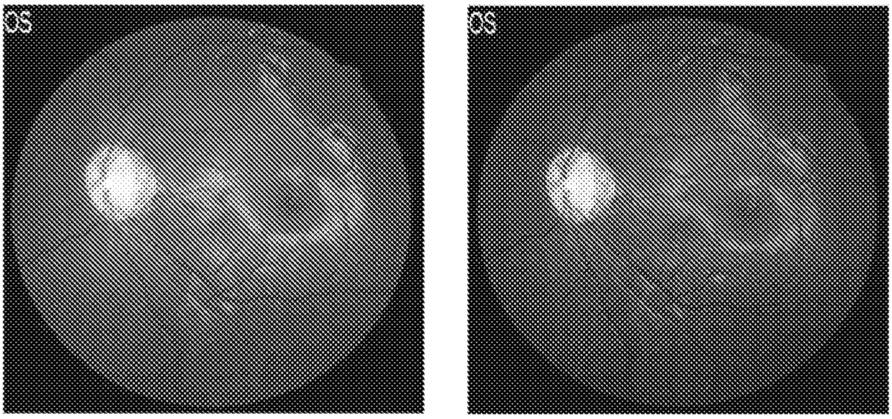


FIG. 5

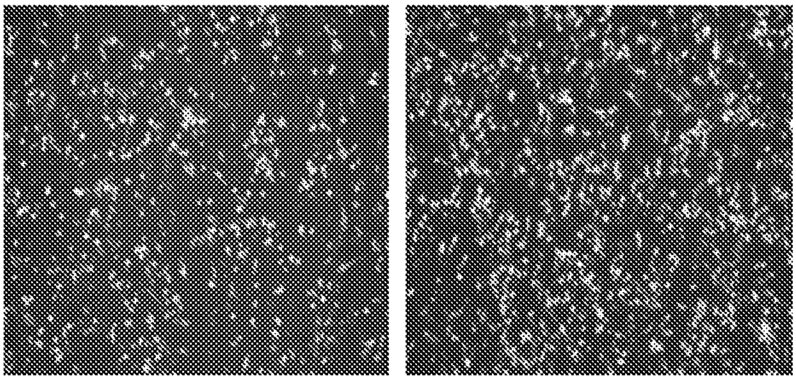


FIG. 6

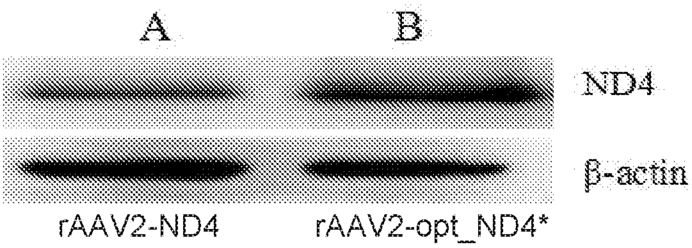
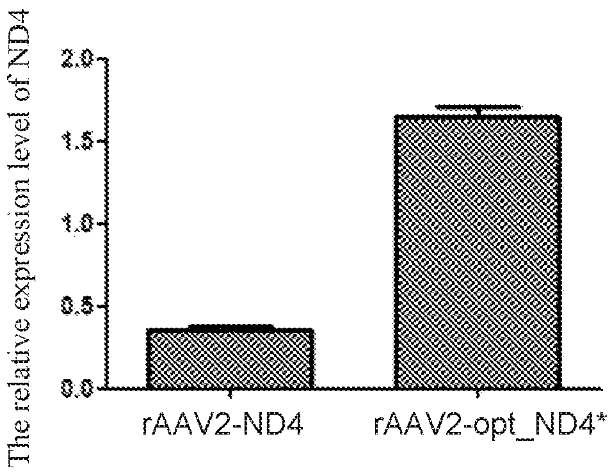


FIG. 7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0.0
rAAV2-ND4
rAAV2-opt_ND4*

FIG. 8

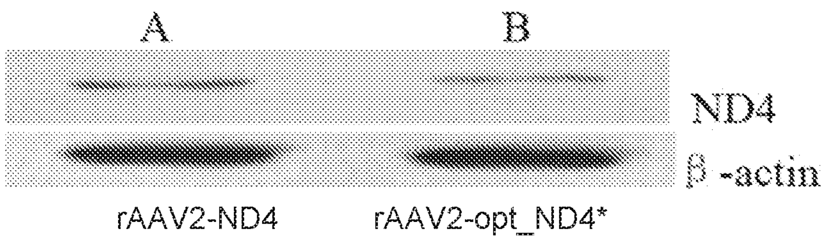
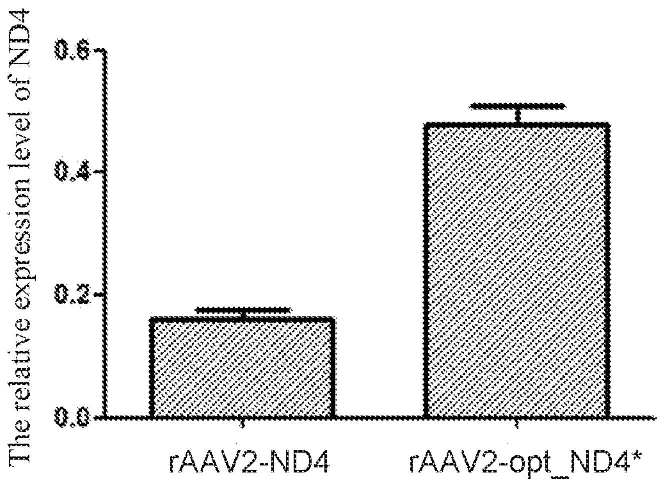


FIG. 9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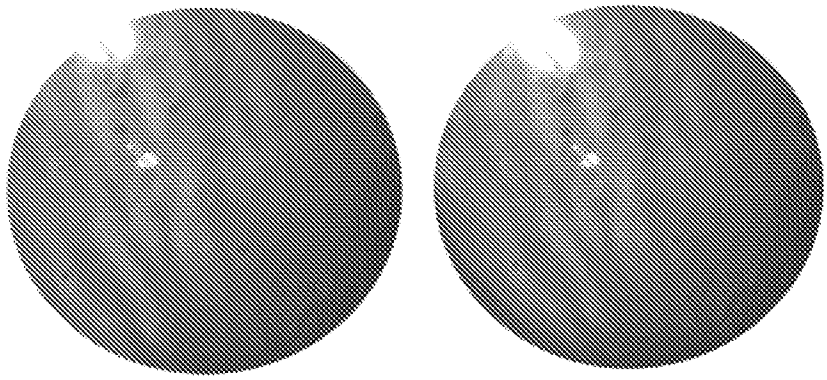
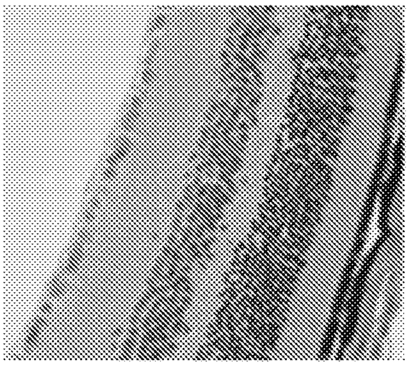
0.0
rAAV2-ND4
rAAV2-opt_ND4*

FIG. 10

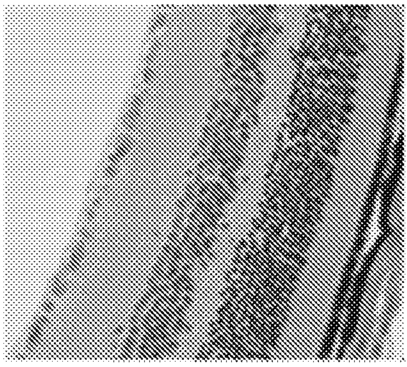


rAAV2-ND4 rAAV2-opt_ND4*

FIG. 11



rAAV2-ND4



rAAV2-opt_ND4*

FIG. 12

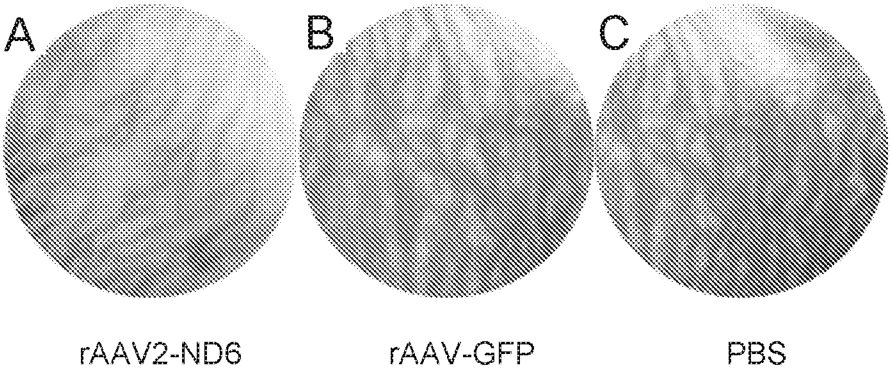
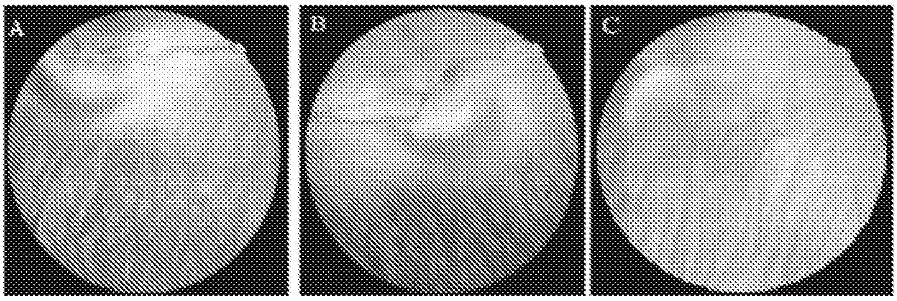


FIG. 13



A B C

FIG. 14

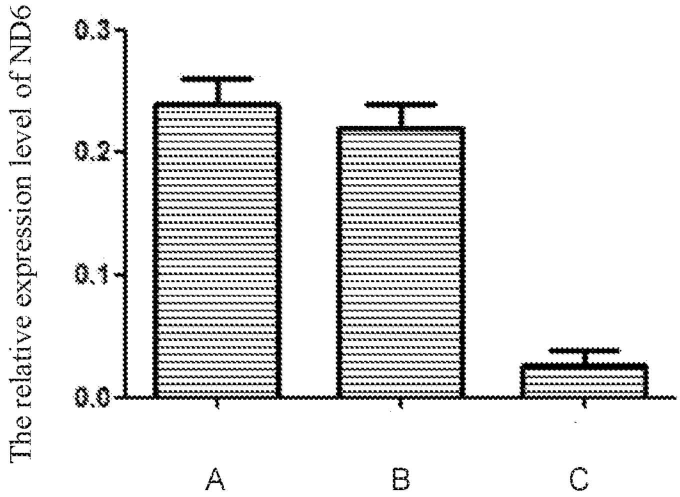


FIG. 15

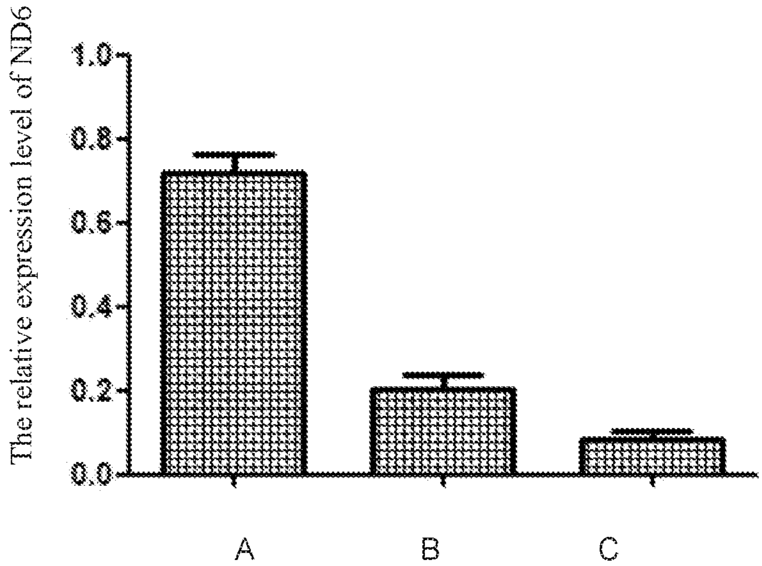


FIG. 16

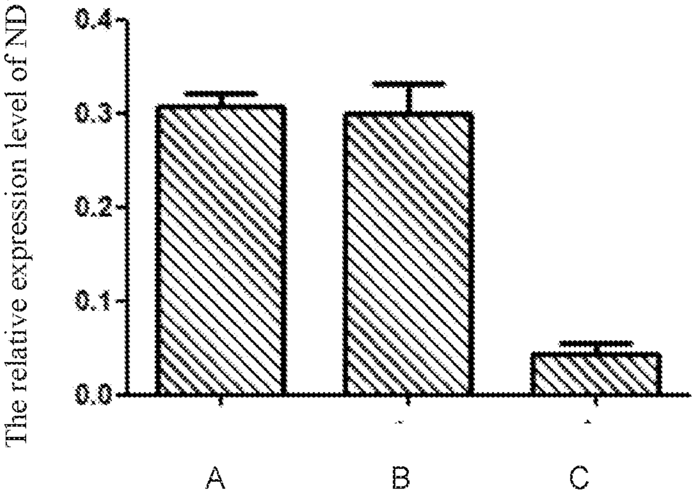


FIG. 17

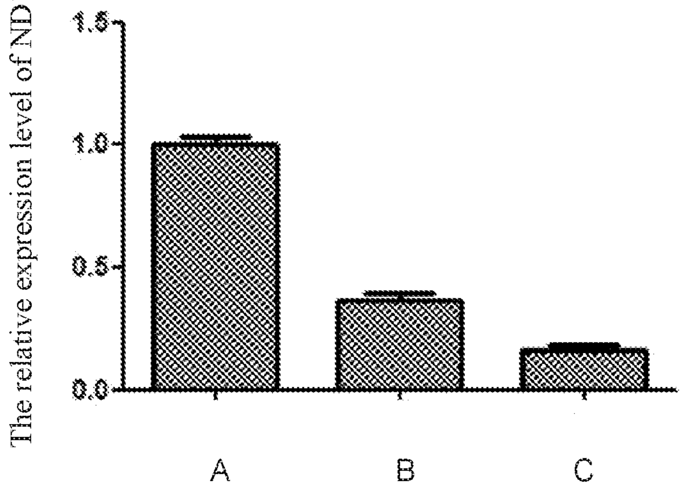


FIG. 18

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<120> COMPOSITIONS AND METHODS FOR TREATING LEBER'S HEREDITARY
       OPTIC NEUROPATHY

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<150> PCT/CN2019/070461
<151> 2019-01-04

<150> PCT/CN2018/113799
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attctcaacc atagtccttc taacaatacc aatagctagg acccggctgc tgtgcactgg 2040

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<223> ND4-S primer

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<400> 88
agtgcgttcg tagtttgag 19

<210> 89
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<223> ND6-F primer

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<210> 90
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<223> ND6-R primer

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<210> 91
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agtgtgggtt tagtaatg 18

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

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agtgactgtt ctgtga   376

<210> 112
<211> 146
<212> DNA
<213> Homo sapiens

<400> 112
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ctgtgtaggc tgcacaagag ccttgattga agatatattc tttctgaaca gtatttaagg   120

tttccaataa aatgtacacc cctcag   146

<210> 113
<211> 1956
<212> DNA
<213> Homo sapiens

<400> 113
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<400> 114
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accaagaaaa atgatccttg cgtgctgaat atctgaaaag agaaattttt cctacaaaat 120

ctcttgggtc aagaaagttc tagaatttga attgataaac atggtgggtt ggctgagggt 180

aagagtatat gaggaacctt ttaaacgaca acaatactgc tagctttcag gatgattttt 240

aaaaaataga ttcaaatgtg ttatcctctc tctgaaacgc ttcctataac tcgagtttat 300

aggggaagaa aaagctattg tttacaatta tatcaccatt aaggcaactg ctacaccctg 360

ctttgtattc tgggctaaga ttcattaaaa actagctgct cttaacttac a 411

<210> 115
<211> 1465
<212> DNA
<213> Homo sapiens

<400> 115
gagcactggg acgcccaccg cccctttccc tccgctgcca ggcgagcatg ttgtggtaat 60

tctggaacac aagaagagaa attgctgggt ttagaacaag attataaacg aattcggtgc 120

tcagtgatca cttgacagtt tttttttttt ttaaatatta cccaaaatgc tccccaaata 180

agaaatgcat cagctcagtc agtgaataca aaaaaggaat tatttttccc tttgagggtc 240

tttatacatc tctcctccaa ccccaccctc tattctgttt cttcctcctc acatgggggt 300

acacatacac agcttcctct tttggttcca tccttaccac cacaccacac gcacactcca 360

catgcccagc agagtggcac ttggtggcca gaaagtgtga gcctcatgat ctgctgtctg 420

tagttctgtg agctcaggtc cctcaaaggc ctcggagcac ccccttcctg gtgactgagc 480 cagggcctgc atttttggtt ttccccaccc cacacattct caaccatagt ccttctaaca 540

ataccaatag ctaggacccg gctgctgtgc actgggactg gggattccac atgtttgcct 600

tgggagtctc aagctggact gccagcccct gtcctccctt cacccccatt gcgtatgagc 660

atttcagaac tccaaggagt cacaggcatc tttatagttc acgttaacat atagacactg 720

ttggaagcag ttccttctaa aagggtagcc ctggacttaa taccagccgg atacctctgg 780

cccccacccc attactgtac ctctggagtc actactgtgg gtcgccactc ctctgctaca 840

cagcacggct ttttcaaggc tgtattgaga agggaagtta ggaagaaggg tgtgctgggc 900

taaccagccc acagagctca cattcctgtc ccttgggtga aaaatacatg tccatcctga 960

tatctcctga attcagaaat tagcctccac atgtgcaatg gctttaagag ccagaagcag 1020

ggttctggga attttgcaag ttatcctgtg gccaggtgtg gtctcggtta ccaaatacgg 1080

ttacctgcag ctttttagtc ctttgtgctc ccacgggtct gcagagtccc atctgcccaa 1140

aggtcttgaa gcttgacagg atgttttcat tactcagtct cccagggcac tgctggtccg 1200

tagggattca ttggtcgggg tgggagagtt aaacaacatt taaacagagt tctctcaaaa 1260

atgtctaaag ggattgtagg tagataacat ccaatcactg tttgcactta tctgaaatct 1320

tccctcttgg ctgcccccag gtatttactg tggagaacat tgcataggaa tgtctggaaa 1380

aagcctctac aacttgttac agccttcaca tttgtacaat tcattgattc tcttttcctt 1440

ccacaataaa atggtataca agaac 1465

<210> 116
<211> 288
<212> DNA
<213> Homo sapiens

<400> 116
gagacttgga ctcaagtcat aggcttcttt cagtctttat gtcacctcag gagacttatt 60

tgagaggaag ccttctgtac ttgaagttga tttgaaatat gtaagaattg atgatgtatt 120

tgcaaacatt aatgtgaaat aaattgaatt taatgttgaa tactttcagg cattcactta 180

ataaagacac tgttaagcac tgttatgctc agtcatacac gcgaaaggta caatgtcttt 240

tagctaattc taattaaaaa ttacagactg gtgtacaaga tacttgtg 288

<210> 117
<211> 83

<212> DNA
<213> Homo sapiens

<400> 117
cccaccaccc tggcctgctg tcctgcgtct atccatgtgg aatgctggac aataaagcga   60

gtgctgccca ccctccagct gcc   83

<210> 118
<211> 66
<212> DNA
<213> Homo sapiens

<400> 118
tttatattga actgtaaata tgtcactaga gaaataaaat atggacttcc aatctacgta   60

aactta   66

<210> 119
<211> 214
<212> DNA
<213> Homo sapiens

<400> 119
accacgatcg ttatgctgag tatgttaagc tctttatgac tgtttttgta gtggtataga   60

gtactgcaga atacagtaag ctgctctatt gtagcatttc ttgatgttgc ttagtcactt   120

atttcataaa caacttaatg ttctgaataa tttcttacta aacattttgt tattgggcaa   180

gtgattgaaa atagtaaatg ctttgtgtga ttga   214

<210> 120
<211> 286
<212> DNA
<213> Homo sapiens

<400> 120
tcttggaata taaagaattt cttcaggttg aattacctag aagtttgtca ctgacttgtg   60

ttcctgaact atgacacatg aatatgtggg ctaagaaata gttcctcttg ataaataaac   120

aattaacaaa tactttggac agtaagtctt tctcagttct taatgataat gcagggcact   180

tactagcata agaattggtt tgggatttaa ctgtttatga agctaacttg atttccgtgt   240

tttgttaaaa tttcattgtt ctagcacatc tttaactgtg atagtt   286

<210> 121
<211> 721

<212> DNA
<213> Homo sapiens

<400> 121
gagacgtgca cttggtcgtg cgcccaggga ggaagccgca ccaccagcca gcgcaggccc   60

tggtggagag gcctccctgg ctgcctctgg gaggggtgct gccttgtaga tggagcaagt   120

gagcactgag ggtctggtgc caatcctgta ggcacaaaac cagaagtttc tacattctct   180

atttttgtta atcatcttct ctttttccag aatttggaag ctagaatggt gggaatgtca   240

gtagtgccag aaagagagaa ccaagcttgt ctttaaagtt actgatcaca ggacgttgct   300

ttttcactgt ttcctattaa tcttcagctg aacacaagca aaccttctca ggaggtgtct   360

cctaccctct tattgttcct cttacgctct gctcaatgaa accttcctct tgagggtcat   420

tttcctttct gtattaatta taccagtgtt aagtgacata gataagaact ttgcacactt   480

caaatcagag cagtgattct ctcttctctc ccctttcct tcagagtgaa tcatccagac   540

tcctcatgga taggtcgggt gttaaagttg ttttgattat gtacctttg atagatccac   600

ataaaaagaa atgtgaagtt ttcttttact atcttttcat ttatcaagca gagacctttg   660

ttgggaggcg gtttgggaga acacatttct aatttgaatg aaatgaaatc tattttcagt   720

g   721

<210> 122
<211> 163
<212> DNA
<213> Homo sapiens

<400> 122
cagaagaagt gacggctggg ggcacagtgg gctgggcgcc cctgcagaac atgaaccttc   60

cgctcctggc tgccacaggg tcctccgatg ctggcctttg cgcctctaga ggcagccact   120

catggattca agtcctggct ccgcctcttc catcaggacc act   163

<210> 123
<211> 60
<212> DNA
<213> Homo sapiens

<400> 123
agaggacaca ctctgcaccc ccccacccca cgaccttggc ccgagcccct ccgtgaggaa   60

<210> 124

<211> 65
<212> DNA
<213> Rattus norvegicus

<400> 124
agcccttccg ccaggctgtg tgtcaggccc gtggtgggtg ttttgtagta gtgtagagca   60

ttgca   65

<210> 125
<211> 231
<212> DNA
<213> Homo sapiens

<400> 125
cttatgttct gtgcgcattc tggcaggaat tctgtctctt cagagactca tcctcaaaac   60

aagacttgac actgtgtcct tgccccagtc ctaggaactg tggcacacag agatgttcat   120

tttaaaaacg gatttcatga aacactcttg tacttatgtt tataagagag cactgggtag   180

ccaagtgatc ttcccattca cagagttagt aaacctctgt actacatgct g   231

<210> 126
<211> 28
<212> PRT
<213> Homo sapiens

<400> 126

Met Ala Ala Ser Pro His Thr Leu Ser Ser Arg Leu Leu Thr Gly Cys
1   5   10   15

Val Gly Gly Ser Val Trp Tyr Leu Glu Arg Arg Thr
            20   25

<210> 127
<211> 29
<212> PRT
<213> Homo sapiens

<400> 127

Met Ser Val Leu Thr Arg Leu Leu Leu Arg Gly Leu Thr Arg Leu Gly
1   5   10   15

Ser Ala Ala Pro Val Arg Arg Ala Arg Ile His Ser Leu
            20   25

<210> 128
<211> 10
<212> PRT
<213> Homo sapiens

<400> 128

Met Trp Arg Leu Arg Arg Ala Ala Val Ala
1   5   10

<210> 129
<211> 28
<212> PRT
<213> Homo sapiens

<400> 129

Met Ala Ala Ser Pro His Thr Leu Ser Ser Arg Leu Leu Thr Gly Cys
1   5   10   15

Val Gly Gly Ser Val Trp Tyr Leu Glu Arg Arg Thr
            20   25

<210> 130
<211> 122
<212> PRT
<213> Saccharomyces cerevisiae

<400> 130

Met Ala Phe Lys Ser Phe Ile Tyr Ser Lys Gly Tyr His Arg Ser Ala
1   5   10   15

Ala Gln Lys Lys Thr Ala Thr Ser Phe Phe Asp Ser Ser Tyr Gln Tyr
            20   25   30

Leu Arg Gln Asn Gln Gly Leu Val Asn Ser Asp Pro Val Leu His Ala
        35   40   45

Ser His Leu His Pro His Pro Val Val Val Ala Asn Val Asn Tyr Asn
    50   55   60

Asn Val Asp Asp Ile Leu His Pro His Asp Leu Asp Ser Ser Ile Asn
65   70   75   80

Asn Thr Asn Asn Pro Leu Thr His Glu Glu Leu Leu Tyr Asn Gln Asn
                85   90   95

Val Ser Leu Arg Ser Leu Lys Gln Gln Gln Ser Thr Asn Tyr Val Asn
            100   105   110

Asn Asn Asn Asn Asn Gln His Arg Tyr Tyr
        115   120

<210> 131
<211> 174
<212> PRT
<213> Larimichthys crocea

<400> 131

Met Arg Lys Arg Ser Leu Arg Cys His Leu Trp Ser Ala Asn Ala Ser
1   5   10   15

Leu Ser Pro Arg Lys Asp Glu Val Thr Ser Arg Lys Glu Ser Glu Asn
            20   25   30

Leu Val Lys Gly Lys Lys Asn Lys Lys Ser His Leu His Leu Leu Leu
        35   40   45

Phe Thr Ala Ser Lys Ile Gly Thr Asp Ser Val Phe Asp Val Gln Lys
    50   55   60

Ser Lys Glu Cys Cys Lys Glu Leu Gly Leu Leu Phe Thr Ser Leu Ile
65   70   75   80

His Ser Ile Gly Ser Phe Pro Phe Asp Glu Glu Pro Lys Ala Ala Ala
                85   90   95

Val Phe Leu Pro Gly Ser Leu Pro Gln Leu Thr Val Leu Val Leu Ala
            100   105   110

Pro Gly Ser Gly Ser Cys Pro Thr Gly Lys Ser Thr Pro His Leu Ala
        115   120   125

Ala Ser Gly Arg Asn Ala Glu Leu Leu Arg Pro Gln Asn Ser Met Ile
    130   135   140

Val Arg Gln Phe Thr Cys Arg Gly Thr Ile Ser Ser His Leu Cys Ala
145   150   155   160

His Leu Arg Lys Pro His Asp Ser Arg Asn Met Ala Arg Pro
                165   170

<210> 132
<211> 56
<212> PRT
<213> Trypanosoma brucei

<400> 132

Met Leu Arg Arg Thr Ser Phe Asn Phe Thr Gly Arg Ala Met Ile Ser
1   5   10   15

Arg Gly Ser Pro Glu Trp Ser His Arg Leu Asp Leu Lys Lys Gly Lys
            20   25   30

Lys Thr Thr Met Met His Lys Leu Gly Thr Ser Lys Pro Asn Asn Ala
        35   40   45

Leu Gln Tyr Ala Gln Met Thr Leu
    50   55

<210> 133
<211> 46
<212> PRT
<213> Neurospora crassa

<400> 133

Met Ile Ser Arg Ser Ala Leu Ser Arg Gly Ser Gln Leu Ala Leu Arg
1   5   10   15

Arg Pro Ala Ala Ala Lys Thr Ala Gln Arg Gly Phe Ala Ala Ala Ala
            20   25   30

Ala Ser Pro Ala Ala Ser Tyr Glu Pro Thr Thr Ile Ala Gly
        35   40   45

<210> 134
<211> 128
<212> PRT

<213> Homo sapiens

<400> 134

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Met Pro Glu Leu Ile Leu Tyr Val Ala Ile Thr Leu Ser Val Ala Glu
1               5                   10                  15

Arg Leu Val Gly Pro Gly His Ala Cys Ala Glu Pro Ser Phe Arg Ser
            20                  25                  30

Ser Arg Cys Ser Ala Pro Leu Cys Leu Leu Cys Ser Gly Ser Ser Ser
        35                  40                  45

Pro Ala Thr Ala Pro His Pro Leu Lys Met Phe Ala Cys Ser Lys Phe
    50                  55                  60

Val Ser Thr Pro Ser Leu Val Lys Ser Thr Ser Gln Leu Leu Ser Arg
65                  70                  75                  80

Pro Leu Ser Ala Val Val Leu Lys Arg Pro Glu Ile Leu Thr Asp Glu
                85                  90                  95

Ser Leu Ser Ser Leu Ala Val Ser Cys Pro Leu Thr Ser Leu Val Ser
            100                 105                 110

Ser Arg Ser Phe Gln Thr Ser Ala Ile Ser Arg Asp Ile Asp Thr Ala
        115                 120                 125
```

<210> 135
<211> 115
<212> PRT
<213> Homo sapiens

<400> 135

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Met Tyr Arg Leu Met Ser Ala Val Thr Ala Arg Ala Ala Ala Pro Gly
1               5                   10                  15

Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg Ala Gly
            20                  25                  30

Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly Leu Gly Leu
        35                  40                  45
```

Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu Arg Gly Ala Ala
    50   55   60

Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu Ala Ser Pro Leu Ala
65   70   75   80

Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro Trp Ser Pro Gln Thr Pro
                85   90   95

Ala Pro Pro Cys Ser Arg Cys Phe Ala Arg Ala Ile Glu Ser Ser Arg
            100   105   110

Asp Leu Leu
        115

<210> 136
<211> 140
<212> PRT
<213> Schizosaccharomyces pombe

<400> 136

Met Thr Val Leu Ala Pro Leu Arg Arg Leu His Thr Arg Ala Ala Phe
1   5   10   15

Ser Ser Tyr Gly Arg Glu Ile Ala Leu Gln Lys Arg Phe Leu Asn Leu
            20   25   30

Asn Ser Cys Ser Ala Val Arg Arg Tyr Gly Thr Gly Phe Ser Asn Asn
        35   40   45

Leu Arg Ile Lys Lys Leu Lys Asn Ala Phe Gly Val Val Arg Ala Asn
    50   55   60

Ser Thr Lys Ser Thr Ser Thr Val Thr Thr Ala Ser Pro Ile Lys Tyr
65   70   75   80

Asp Ser Ser Phe Val Gly Lys Thr Gly Gly Glu Ile Phe His Asp Met
                85   90   95

Met Leu Lys His Asn Val Lys His Val Phe Gly Tyr Pro Gly Gly Ala
            100   105   110

Ile Leu Pro Val Phe Asp Ala Ile Tyr Arg Ser Pro His Phe Glu Phe
        115   120   125

Ile Leu Pro Arg His Glu Gln Ala Ala Gly His Ala
    130   135   140

<210> 137
<211> 125
<212> PRT
<213> Glycine max

<400> 137

Met Ile Leu Cys Pro Leu Glu Ala Phe Ile Val Gln His Ile Leu Thr
1   5   10   15

Ile Ser Val Met Gly Leu Leu Ser Cys Phe Arg Ser Thr Val Leu Arg
            20   25   30

Lys Cys Ser Lys Gly Ser Ser Gly Met Ser Arg Phe Leu Tyr Thr Asn
        35   40   45

Asn Phe Gln Arg Asn Leu Ile Ser Ser Gly Gly Asn Glu Ser Tyr Tyr
    50   55   60

Gly Tyr Phe Asn Arg Arg Ser Tyr Thr Ser Leu Tyr Met Gly Thr Gly
65   70   75   80

Thr Val Gly Gly Ile Thr Ser Ala Arg Ile Arg Val Pro Asn Val Gly
                85   90   95

Cys Glu Gly Phe Met Cys Ser Ser His Leu Ser Ile Thr Gln Arg Asn
            100   105   110

Ser Arg Leu Ile His Ser Thr Ser Lys Ile Val Pro Asn
        115   120   125

<210> 138
<211> 107
<212> PRT
<213> Chlamydomonas reinhardtii

<400> 138

Met Ala Leu Gln Gln Ala Ala Pro Arg Val Phe Gly Leu Leu Gly Arg
1   5   10   15

Ala Pro Val Ala Leu Gly Gln Ser Gly Ile Leu Thr Gly Ser Ser Gly
            20   25   30

Phe Lys Asn Gln Gly Phe Asn Gly Ser Leu Gln Ser Val Glu Asn His
        35   40   45

Val Tyr Ala Gln Ala Phe Ser Thr Ser Ser Gln Glu Glu Gln Ala Ala
    50   55   60

Pro Ser Ile Gln Gly Ala Ser Gly Met Lys Leu Pro Gly Met Ala Gly
65   70   75   80

Ser Met Leu Leu Gly Lys Ser Arg Ser Gly Leu Arg Thr Gly Ser Met
                85   90   95

Val Pro Phe Ala Ala Gln Gln Ala Met Asn Met
            100   105

<210> 139
<211> 87
<212> PRT
<213> Homo sapiens

<400> 139

Met Trp Arg Leu Arg Arg Ala Ala Val Ala Cys Glu Val Cys Gln Ser
1   5   10   15

Leu Val Lys His Ser Ser Gly Ile Lys Gly Ser Leu Pro Leu Gln Lys
            20   25   30

Leu His Leu Val Ser Arg Ser Ile Tyr His Ser His His Pro Thr Leu
        35   40   45

Lys Leu Gln Arg Pro Gln Leu Arg Thr Ser Phe Gln Gln Phe Ser Ser
    50   55   60

Leu Thr Asn Leu Pro Leu Arg Lys Leu Lys Phe Ser Pro Ile Lys Tyr

65   70   75   80

Gly Tyr Gln Pro Arg Arg Asn
                85

<210> 140
<211> 56
<212> PRT
<213> Homo sapiens

<400> 140

Met Ala Val Leu Trp Arg Leu Ser Ala Val Cys Gly Ala Leu Gly Gly
1   5   10   15

Arg Ala Leu Leu Leu Arg Thr Pro Val Val Arg Pro Ala His Ile Ser
            20   25   30

Ala Phe Leu Gln Asp Arg Pro Ile Pro Glu Trp Cys Gly Val Gln His
        35   40   45

Ile His Leu Ser Pro Ser His His
    50   55

<210> 141
<211> 162
<212> PRT
<213> Homo sapiens

<400> 141

Met Ala Ala Ile Leu Gly Asp Thr Ile Met Val Ala Lys Gly Leu Val
1   5   10   15

Lys Leu Thr Gln Ala Ala Val Glu Thr His Leu Gln His Leu Gly Ile
            20   25   30

Gly Gly Glu Leu Ile Met Ala Ala Arg Ala Leu Gln Ser Thr Ala Val
        35   40   45

Glu Gln Ile Gly Met Phe Leu Gly Lys Val Gln Gly Gln Asp Lys His
    50   55   60

Glu Glu Tyr Phe Ala Glu Asn Phe Gly Gly Pro Glu Gly Glu Phe His

65   70   75   80

Phe Ser Val Pro His Ala Ala Gly Ala Ser Thr Asp Phe Ser Ser Ala
                85   90   95

Ser Ala Pro Asp Gln Ser Ala Pro Pro Ser Leu Gly His Ala His Ser
            100   105   110

Glu Gly Pro Ala Pro Ala Tyr Val Ala Ser Gly Pro Phe Arg Glu Ala
        115   120   125

Gly Phe Pro Gly Gln Ala Ser Ser Pro Leu Gly Arg Ala Asn Gly Arg
    130   135   140

Leu Phe Ala Asn Pro Arg Asp Ser Phe Ser Ala Met Gly Phe Gln Arg
145   150   155   160

Arg Phe

<210> 142
<211> 117
<212> PRT
<213> Oryza sativa

<400> 142

Met Ala Leu Leu Leu Arg His Ser Pro Lys Leu Arg Arg Ala His Ala
1   5   10   15

Ile Leu Gly Cys Glu Arg Gly Thr Val Val Arg His Phe Ser Ser Ser
            20   25   30

Thr Cys Ser Ser Leu Val Lys Glu Asp Thr Val Ser Ser Ser Asn Leu
        35   40   45

His Pro Glu Tyr Ala Lys Lys Ile Gly Gly Ser Asp Phe Ser His Asp
    50   55   60

Arg Gln Ser Gly Lys Glu Leu Gln Asn Phe Lys Val Ser Pro Gln Glu
65   70   75   80

Ala Ser Arg Ala Ser Asn Phe Met Arg Ala Ser Lys Tyr Gly Met Pro
                85   90   95

Ile Thr Ala Asn Gly Val His Ser Leu Phe Ser Cys Gly Gln Val Val
            100   105   110

Pro Ser Arg Cys Phe
        115

<210> 143
<211> 66
<212> PRT
<213> Neurospora crassa

<400> 143

Met Ala Ser Thr Arg Val Leu Ala Ser Arg Leu Ala Ser Gln Met Ala
1   5   10   15

Ala Ser Ala Lys Val Ala Arg Pro Ala Val Arg Val Ala Gln Val Ser
            20   25   30

Lys Arg Thr Ile Gln Thr Gly Ser Pro Leu Gln Thr Leu Lys Arg Thr
        35   40   45

Gln Met Thr Ser Ile Val Asn Ala Thr Thr Arg Gln Ala Phe Gln Lys
    50   55   60

Arg Ala
65

<210> 144
<211> 44
<212> PRT
<213> Homo sapiens

<400> 144

Met Leu Ala Ala Arg Leu Val Cys Leu Arg Thr Leu Pro Ser Arg Val
1   5   10   15

Phe His Pro Ala Phe Thr Lys Ala Ser Pro Val Val Lys Asn Ser Ile
            20   25   30

Thr Lys Asn Gln Trp Leu Leu Thr Pro Ser Arg Glu
        35   40

<210> 145
<211> 68
<212> PRT
<213> Homo sapiens

<400> 145

Met Ala Ser Arg Val Leu Ser Ala Tyr Val Ser Arg Leu Pro Ala Ala
1   5   10   15

Phe Ala Pro Leu Pro Arg Val Arg Met Leu Ala Val Ala Arg Pro Leu
            20   25   30

Ser Thr Ala Leu Cys Ser Ala Gly Thr Gln Thr Arg Leu Gly Thr Leu
        35   40   45

Gln Pro Ala Leu Val Leu Ala Gln Val Pro Gly Arg Val Thr Gln Leu
    50   55   60

Cys Arg Gln Tyr
65

<210> 146
<211> 67
<212> PRT
<213> Homo sapiens

<400> 146

Met Phe Ala Cys Ala Lys Leu Ala Cys Thr Pro Ser Leu Ile Arg Ala
1   5   10   15

Gly Ser Arg Val Ala Tyr Arg Pro Ile Ser Ala Ser Val Leu Ser Arg
            20   25   30

Pro Glu Ala Ser Arg Thr Gly Glu Gly Ser Thr Val Phe Asn Gly Ala
        35   40   45

Gln Asn Gly Val Ser Gln Leu Ile Gln Arg Glu Phe Gln Thr Ser Ala
    50   55   60

Ile Ser Arg
65

<210> 147
<211> 273
<212> PRT
<213> Artificial Sequence

<220>
<223> crATP6_hsADCK3

<400> 147

Met Ala Leu Gln Gln Ala Ala Pro Arg Val Phe Gly Leu Leu Gly Arg
1   5   10   15

Ala Pro Val Ala Leu Gly Gln Ser Gly Ile Leu Thr Gly Ser Ser Gly
            20   25   30

Phe Lys Asn Gln Gly Phe Asn Gly Ser Leu Gln Ser Val Glu Asn His
        35   40   45

Val Tyr Ala Gln Ala Phe Ser Thr Ser Ser Gln Glu Glu Gln Ala Ala
    50   55   60

Pro Ser Ile Gln Gly Ala Ser Gly Met Lys Leu Pro Gly Met Ala Gly
65   70   75   80

Ser Met Leu Leu Gly Lys Ser Arg Ser Gly Leu Arg Thr Gly Ser Met
                85   90   95

Val Pro Phe Ala Ala Gln Gln Ala Met Asn Met Gly Gly Met Ala Ala
            100   105   110

Ile Leu Gly Asp Thr Ile Met Val Ala Lys Gly Leu Val Lys Leu Thr
        115   120   125

Gln Ala Ala Val Glu Thr His Leu Gln His Leu Gly Ile Gly Gly Glu
    130   135   140

Leu Ile Met Ala Ala Arg Ala Leu Gln Ser Thr Ala Val Glu Gln Ile
145   150   155   160

Gly Met Phe Leu Gly Lys Val Gln Gly Gln Asp Lys His Glu Glu Tyr
                165   170   175

Phe Ala Glu Asn Phe Gly Gly Pro Glu Gly Glu Phe His Phe Ser Val
            180   185   190

Pro His Ala Ala Gly Ala Ser Thr Asp Phe Ser Ser Ala Ser Ala Pro
        195   200   205

Asp Gln Ser Ala Pro Pro Ser Leu Gly His Ala His Ser Glu Gly Pro
    210   215   220

Ala Pro Ala Tyr Val Ala Ser Gly Pro Phe Arg Glu Ala Gly Phe Pro
225   230   235   240

Gly Gln Ala Ser Ser Pro Leu Gly Arg Ala Asn Gly Arg Leu Phe Ala
                245   250   255

Asn Pro Arg Asp Ser Phe Ser Ala Met Gly Phe Gln Arg Arg Phe Gly
            260   265   270

Gly

<210> 148
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> ncATP9_ncATP9

<400> 148

Met Ala Ser Thr Arg Val Leu Ala Ser Arg Leu Ala Ser Gln Met Ala
1   5   10   15

Ala Ser Ala Lys Val Ala Arg Pro Ala Val Arg Val Ala Gln Val Ser
            20   25   30

Lys Arg Thr Ile Gln Thr Gly Ser Pro Leu Gln Thr Leu Lys Arg Thr
        35   40   45

```
Gln Met Thr Ser Ile Val Asn Ala Thr Thr Arg Gln Ala Phe Gln Lys
    50                  55                  60

Arg Ala Met Ala Ser Thr Arg Val Leu Ala Ser Arg Leu Ala Ser Gln
65                  70                  75                  80

Met Ala Ala Ser Ala Lys Val Ala Arg Pro Ala Val Arg Val Ala Gln
                85                  90                  95

Val Ser Lys Arg Thr Ile Gln Thr Gly Ser Pro Leu Gln Thr Leu Lys
            100                 105                 110

Arg Thr Gln Met Thr Ser Ile Val Asn Ala Thr Thr Arg Gln Ala Phe
        115                 120                 125

Gln Lys Arg Ala
    130
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<210> 149
<211> 119
<212> PRT
<213> Zea mays

<400> 149

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Met Ala Leu Leu Arg Ala Ala Val Ser Glu Leu Arg Arg Arg Gly Arg
1               5                   10                  15

Gly Ala Leu Thr Pro Leu Pro Ala Leu Ser Ser Leu Leu Ser Ser Leu
            20                  25                  30

Ser Pro Arg Ser Pro Ala Ser Thr Arg Pro Glu Pro Asn Asn Pro His
        35                  40                  45

Ala Asp Arg Arg His Val Ile Ala Leu Arg Arg Cys Pro Pro Leu Pro
    50                  55                  60

Ala Ser Ala Val Leu Ala Pro Glu Leu Leu His Ala Arg Gly Leu Leu
65                  70                  75                  80

Pro Arg His Trp Ser His Ala Ser Pro Leu Ser Thr Ser Ser Ser Ser
                85                  90                  95
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Ser Arg Pro Ala Asp Lys Ala Gln Leu Thr Trp Val Asp Lys Trp Ile
            100   105   110

Pro Glu Ala Ala Arg Pro Tyr
        115

<210> 150
<211> 391
<212> PRT
<213> Artificial Sequence

<220>
<223> ncATP9_zmLOC100282174_spilv1_ncATP9

<400> 150

Met Ala Ser Thr Arg Val Leu Ala Ser Arg Leu Ala Ser Gln Met Ala
1   5   10   15

Ala Ser Ala Lys Val Ala Arg Pro Ala Val Arg Val Ala Gln Val Ser
            20   25   30

Lys Arg Thr Ile Gln Thr Gly Ser Pro Leu Gln Thr Leu Lys Arg Thr
        35   40   45

Gln Met Thr Ser Ile Val Asn Ala Thr Thr Arg Gln Ala Phe Gln Lys
    50   55   60

Arg Ala Met Ala Leu Leu Arg Ala Ala Val Ser Glu Leu Arg Arg Arg
65   70   75   80

Gly Arg Gly Ala Leu Thr Pro Leu Pro Ala Leu Ser Ser Leu Leu Ser
                85   90   95

Ser Leu Ser Pro Arg Ser Pro Ala Ser Thr Arg Pro Glu Pro Asn Asn
            100   105   110

Pro His Ala Asp Arg Arg His Val Ile Ala Leu Arg Arg Cys Pro Pro
        115   120   125

Leu Pro Ala Ser Ala Val Leu Ala Pro Glu Leu Leu His Ala Arg Gly
    130   135   140

Leu Leu Pro Arg His Trp Ser His Ala Ser Pro Leu Ser Thr Ser Ser
145   150   155   160

Ser Ser Ser Arg Pro Ala Asp Lys Ala Gln Leu Thr Trp Val Asp Lys
                165   170   175

Trp Ile Pro Glu Ala Ala Arg Pro Tyr Met Thr Val Leu Ala Pro Leu
            180   185   190

Arg Arg Leu His Thr Arg Ala Ala Phe Ser Ser Tyr Gly Arg Glu Ile
        195   200   205

Ala Leu Gln Lys Arg Phe Leu Asn Leu Asn Ser Cys Ser Ala Val Arg
    210   215   220

Arg Tyr Gly Thr Gly Phe Ser Asn Asn Leu Arg Ile Lys Lys Leu Lys
225   230   235   240

Asn Ala Phe Gly Val Val Arg Ala Asn Ser Thr Lys Ser Thr Ser Thr
                245   250   255

Val Thr Thr Ala Ser Pro Ile Lys Tyr Asp Ser Ser Phe Val Gly Lys
            260   265   270

Thr Gly Gly Glu Ile Phe His Asp Met Met Leu Lys His Asn Val Lys
        275   280   285

His Val Phe Gly Tyr Pro Gly Gly Ala Ile Leu Pro Val Phe Asp Ala
    290   295   300

Ile Tyr Arg Ser Pro His Phe Glu Phe Ile Leu Pro Arg His Glu Gln
305   310   315   320

Ala Ala Gly His Ala Met Ala Ser Thr Arg Val Leu Ala Ser Arg Leu
                325   330   335

Ala Ser Gln Met Ala Ala Ser Ala Lys Val Ala Arg Pro Ala Val Arg
            340   345   350

Val Ala Gln Val Ser Lys Arg Thr Ile Gln Thr Gly Ser Pro Leu Gln

355 360 365

Thr Leu Lys Arg Thr Gln Met Thr Ser Ile Val Asn Ala Thr Thr Arg
370 375 380

Gln Ala Phe Gln Lys Arg Ala
385 390

<210> 151
<211> 455
<212> PRT
<213> Artificial Sequence

<220>
<223> zmLOC100282174_hsADCK3_crATP6 _hsATP5G3

<400> 151

Met Ala Leu Leu Arg Ala Ala Val Ser Glu Leu Arg Arg Arg Gly Arg
1 5 10 15

Gly Ala Leu Thr Pro Leu Pro Ala Leu Ser Ser Leu Leu Ser Ser Leu
20 25 30

Ser Pro Arg Ser Pro Ala Ser Thr Arg Pro Glu Pro Asn Asn Pro His
35 40 45

Ala Asp Arg Arg His Val Ile Ala Leu Arg Arg Cys Pro Pro Leu Pro
50 55 60

Ala Ser Ala Val Leu Ala Pro Glu Leu Leu His Ala Arg Gly Leu Leu
65 70 75 80

Pro Arg His Trp Ser His Ala Ser Pro Leu Ser Thr Ser Ser Ser Ser
85 90 95

Ser Arg Pro Ala Asp Lys Ala Gln Leu Thr Trp Val Asp Lys Trp Ile
100 105 110

Pro Glu Ala Ala Arg Pro Tyr Met Ala Ala Ile Leu Gly Asp Thr Ile
115 120 125

Met Val Ala Lys Gly Leu Val Lys Leu Thr Gln Ala Ala Val Glu Thr

130 135 140

His Leu Gln His Leu Gly Ile Gly Gly Glu Leu Ile Met Ala Ala Arg
145 150 155 160

Ala Leu Gln Ser Thr Ala Val Glu Gln Ile Gly Met Phe Leu Gly Lys
165 170 175

Val Gln Gly Gln Asp Lys His Glu Glu Tyr Phe Ala Glu Asn Phe Gly
180 185 190

Gly Pro Glu Gly Glu Phe His Phe Ser Val Pro His Ala Ala Gly Ala
195 200 205

Ser Thr Asp Phe Ser Ser Ala Ser Ala Pro Asp Gln Ser Ala Pro Pro
210 215 220

Ser Leu Gly His Ala His Ser Glu Gly Pro Ala Pro Ala Tyr Val Ala
225 230 235 240

Ser Gly Pro Phe Arg Glu Ala Gly Phe Pro Gly Gln Ala Ser Ser Pro
245 250 255

Leu Gly Arg Ala Asn Gly Arg Leu Phe Ala Asn Pro Arg Asp Ser Phe
260 265 270

Ser Ala Met Gly Phe Gln Arg Arg Phe Met Ala Leu Gln Gln Ala Ala
275 280 285

Pro Arg Val Phe Gly Leu Leu Gly Arg Ala Pro Val Ala Leu Gly Gln
290 295 300

Ser Gly Ile Leu Thr Gly Ser Ser Gly Phe Lys Asn Gln Gly Phe Asn
305 310 315 320

Gly Ser Leu Gln Ser Val Glu Asn His Val Tyr Ala Gln Ala Phe Ser
325 330 335

Thr Ser Ser Gln Glu Glu Gln Ala Ala Pro Ser Ile Gln Gly Ala Ser
340 345 350

Gly Met Lys Leu Pro Gly Met Ala Gly Ser Met Leu Leu Gly Lys Ser
        355   360   365

Arg Ser Gly Leu Arg Thr Gly Ser Met Val Pro Phe Ala Ala Gln Gln
    370   375   380

Ala Met Asn Met Met Phe Ala Cys Ala Lys Leu Ala Cys Thr Pro Ser
385   390   395   400

Leu Ile Arg Ala Gly Ser Arg Val Ala Tyr Arg Pro Ile Ser Ala Ser
                405   410   415

Val Leu Ser Arg Pro Glu Ala Ser Arg Thr Gly Glu Gly Ser Thr Val
            420   425   430

Phe Asn Gly Ala Gln Asn Gly Val Ser Gln Leu Ile Gln Arg Glu Phe
        435   440   445

Gln Thr Ser Ala Ile Ser Arg
    450   455

<210> 152
<211> 348
<212> PRT
<213> Artificial Sequence

<220>
<223> zmLOC100282174_hsADCK3_hsATP5G3

<400> 152

Met Ala Leu Leu Arg Ala Ala Val Ser Glu Leu Arg Arg Arg Gly Arg
1   5   10   15

Gly Ala Leu Thr Pro Leu Pro Ala Leu Ser Ser Leu Leu Ser Ser Leu
            20   25   30

Ser Pro Arg Ser Pro Ala Ser Thr Arg Pro Glu Pro Asn Asn Pro His
        35   40   45

Ala Asp Arg Arg His Val Ile Ala Leu Arg Arg Cys Pro Pro Leu Pro
    50   55   60

Ala Ser Ala Val Leu Ala Pro Glu Leu Leu His Ala Arg Gly Leu Leu
65   70   75   80

Pro Arg His Trp Ser His Ala Ser Pro Leu Ser Thr Ser Ser Ser Ser
                85   90   95

Ser Arg Pro Ala Asp Lys Ala Gln Leu Thr Trp Val Asp Lys Trp Ile
            100   105   110

Pro Glu Ala Ala Arg Pro Tyr Met Ala Ala Ile Leu Gly Asp Thr Ile
        115   120   125

Met Val Ala Lys Gly Leu Val Lys Leu Thr Gln Ala Ala Val Glu Thr
    130   135   140

His Leu Gln His Leu Gly Ile Gly Gly Glu Leu Ile Met Ala Ala Arg
145   150   155   160

Ala Leu Gln Ser Thr Ala Val Glu Gln Ile Gly Met Phe Leu Gly Lys
                165   170   175

Val Gln Gly Gln Asp Lys His Glu Glu Tyr Phe Ala Glu Asn Phe Gly
            180   185   190

Gly Pro Glu Gly Glu Phe His Phe Ser Val Pro His Ala Ala Gly Ala
        195   200   205

Ser Thr Asp Phe Ser Ser Ala Ser Ala Pro Asp Gln Ser Ala Pro Pro
    210   215   220

Ser Leu Gly His Ala His Ser Glu Gly Pro Ala Pro Ala Tyr Val Ala
225   230   235   240

Ser Gly Pro Phe Arg Glu Ala Gly Phe Pro Gly Gln Ala Ser Ser Pro
                245   250   255

Leu Gly Arg Ala Asn Gly Arg Leu Phe Ala Asn Pro Arg Asp Ser Phe
            260   265   270

Ser Ala Met Gly Phe Gln Arg Arg Phe Met Phe Ala Cys Ala Lys Leu

275 280 285

Ala Cys Thr Pro Ser Leu Ile Arg Ala Gly Ser Arg Val Ala Tyr Arg
290 295 300

Pro Ile Ser Ala Ser Val Leu Ser Arg Pro Glu Ala Ser Arg Thr Gly
305 310 315 320

Glu Gly Ser Thr Val Phe Asn Gly Ala Gln Asn Gly Val Ser Gln Leu
325 330 335

Ile Gln Arg Glu Phe Gln Thr Ser Ala Ile Ser Arg
340 345

<210> 153
<211> 185
<212> PRT
<213> Artificial Sequence

<220>
<223> ncATP9_zmLOC100282174

<400> 153

Met Ala Ser Thr Arg Val Leu Ala Ser Arg Leu Ala Ser Gln Met Ala
1 5 10 15

Ala Ser Ala Lys Val Ala Arg Pro Ala Val Arg Val Ala Gln Val Ser
20 25 30

Lys Arg Thr Ile Gln Thr Gly Ser Pro Leu Gln Thr Leu Lys Arg Thr
35 40 45

Gln Met Thr Ser Ile Val Asn Ala Thr Thr Arg Gln Ala Phe Gln Lys
50 55 60

Arg Ala Met Ala Leu Leu Arg Ala Ala Val Ser Glu Leu Arg Arg Arg
65 70 75 80

Gly Arg Gly Ala Leu Thr Pro Leu Pro Ala Leu Ser Ser Leu Leu Ser
85 90 95

Ser Leu Ser Pro Arg Ser Pro Ala Ser Thr Arg Pro Glu Pro Asn Asn

            100   105   110

Pro His Ala Asp Arg Arg His Val Ile Ala Leu Arg Arg Cys Pro Pro
        115   120   125

Leu Pro Ala Ser Ala Val Leu Ala Pro Glu Leu Leu His Ala Arg Gly
    130   135   140

Leu Leu Pro Arg His Trp Ser His Ala Ser Pro Leu Ser Thr Ser Ser
145   150   155   160

Ser Ser Ser Arg Pro Ala Asp Lys Ala Gln Leu Thr Trp Val Asp Lys
                165   170   175

Trp Ile Pro Glu Ala Ala Arg Pro Tyr
            180   185

<210> 154
<211> 455
<212> PRT
<213> Artificial Sequence

<220>
<223> hsADCK3_zmLOC100282174_crATP6 _hsATP5G3

<400> 154

Met Ala Ala Ile Leu Gly Asp Thr Ile Met Val Ala Lys Gly Leu Val
1   5   10   15

Lys Leu Thr Gln Ala Ala Val Glu Thr His Leu Gln His Leu Gly Ile
            20   25   30

Gly Gly Glu Leu Ile Met Ala Ala Arg Ala Leu Gln Ser Thr Ala Val
        35   40   45

Glu Gln Ile Gly Met Phe Leu Gly Lys Val Gln Gly Gln Asp Lys His
    50   55   60

Glu Glu Tyr Phe Ala Glu Asn Phe Gly Gly Pro Glu Gly Glu Phe His
65   70   75   80

Phe Ser Val Pro His Ala Ala Gly Ala Ser Thr Asp Phe Ser Ser Ala

85 90 95

Ser Ala Pro Asp Gln Ser Ala Pro Pro Ser Leu Gly His Ala His Ser
100 105 110

Glu Gly Pro Ala Pro Ala Tyr Val Ala Ser Gly Pro Phe Arg Glu Ala
115 120 125

Gly Phe Pro Gly Gln Ala Ser Ser Pro Leu Gly Arg Ala Asn Gly Arg
130 135 140

Leu Phe Ala Asn Pro Arg Asp Ser Phe Ser Ala Met Gly Phe Gln Arg
145 150 155 160

Arg Phe Met Ala Leu Leu Arg Ala Ala Val Ser Glu Leu Arg Arg Arg
165 170 175

Gly Arg Gly Ala Leu Thr Pro Leu Pro Ala Leu Ser Ser Leu Leu Ser
180 185 190

Ser Leu Ser Pro Arg Ser Pro Ala Ser Thr Arg Pro Glu Pro Asn Asn
195 200 205

Pro His Ala Asp Arg Arg His Val Ile Ala Leu Arg Arg Cys Pro Pro
210 215 220

Leu Pro Ala Ser Ala Val Leu Ala Pro Glu Leu Leu His Ala Arg Gly
225 230 235 240

Leu Leu Pro Arg His Trp Ser His Ala Ser Pro Leu Ser Thr Ser Ser
245 250 255

Ser Ser Ser Arg Pro Ala Asp Lys Ala Gln Leu Thr Trp Val Asp Lys
260 265 270

Trp Ile Pro Glu Ala Ala Arg Pro Tyr Met Ala Leu Gln Gln Ala Ala
275 280 285

Pro Arg Val Phe Gly Leu Leu Gly Arg Ala Pro Val Ala Leu Gly Gln
290 295 300

Ser Gly Ile Leu Thr Gly Ser Ser Gly Phe Lys Asn Gln Gly Phe Asn
305   310   315   320

Gly Ser Leu Gln Ser Val Glu Asn His Val Tyr Ala Gln Ala Phe Ser
                325   330   335

Thr Ser Ser Gln Glu Glu Gln Ala Ala Pro Ser Ile Gln Gly Ala Ser
            340   345   350

Gly Met Lys Leu Pro Gly Met Ala Gly Ser Met Leu Leu Gly Lys Ser
        355   360   365

Arg Ser Gly Leu Arg Thr Gly Ser Met Val Pro Phe Ala Ala Gln Gln
    370   375   380

Ala Met Asn Met Met Phe Ala Cys Ala Lys Leu Ala Cys Thr Pro Ser
385   390   395   400

Leu Ile Arg Ala Gly Ser Arg Val Ala Tyr Arg Pro Ile Ser Ala Ser
                405   410   415

Val Leu Ser Arg Pro Glu Ala Ser Arg Thr Gly Glu Gly Ser Thr Val
            420   425   430

Phe Asn Gly Ala Gln Asn Gly Val Ser Gln Leu Ile Gln Arg Glu Phe
        435   440   445

Gln Thr Ser Ala Ile Ser Arg
    450   455

<210> 155
<211> 455
<212> PRT
<213> Artificial Sequence

<220>
<223> crATP6 _hsADCK3_zmLOC100282174_hsATP5G3

<400> 155

Met Ala Leu Gln Gln Ala Ala Pro Arg Val Phe Gly Leu Leu Gly Arg
1   5   10   15

Ala Pro Val Ala Leu Gly Gln Ser Gly Ile Leu Thr Gly Ser Ser Gly
            20   25   30

Phe Lys Asn Gln Gly Phe Asn Gly Ser Leu Gln Ser Val Glu Asn His
        35   40   45

Val Tyr Ala Gln Ala Phe Ser Thr Ser Ser Gln Glu Glu Gln Ala Ala
    50   55   60

Pro Ser Ile Gln Gly Ala Ser Gly Met Lys Leu Pro Gly Met Ala Gly
65   70   75   80

Ser Met Leu Leu Gly Lys Ser Arg Ser Gly Leu Arg Thr Gly Ser Met
                85   90   95

Val Pro Phe Ala Ala Gln Gln Ala Met Asn Met Met Ala Ala Ile Leu
            100   105   110

Gly Asp Thr Ile Met Val Ala Lys Gly Leu Val Lys Leu Thr Gln Ala
        115   120   125

Ala Val Glu Thr His Leu Gln His Leu Gly Ile Gly Gly Glu Leu Ile
    130   135   140

Met Ala Ala Arg Ala Leu Gln Ser Thr Ala Val Glu Gln Ile Gly Met
145   150   155   160

Phe Leu Gly Lys Val Gln Gly Gln Asp Lys His Glu Glu Tyr Phe Ala
                165   170   175

Glu Asn Phe Gly Gly Pro Glu Gly Glu Phe His Phe Ser Val Pro His
            180   185   190

Ala Ala Gly Ala Ser Thr Asp Phe Ser Ser Ala Ser Ala Pro Asp Gln
        195   200   205

Ser Ala Pro Pro Ser Leu Gly His Ala His Ser Glu Gly Pro Ala Pro
    210   215   220

Ala Tyr Val Ala Ser Gly Pro Phe Arg Glu Ala Gly Phe Pro Gly Gln

225 230 235 240

Ala Ser Ser Pro Leu Gly Arg Ala Asn Gly Arg Leu Phe Ala Asn Pro
245 250 255

Arg Asp Ser Phe Ser Ala Met Gly Phe Gln Arg Arg Phe Met Ala Leu
260 265 270

Leu Arg Ala Ala Val Ser Glu Leu Arg Arg Arg Gly Arg Gly Ala Leu
275 280 285

Thr Pro Leu Pro Ala Leu Ser Ser Leu Leu Ser Ser Leu Ser Pro Arg
290 295 300

Ser Pro Ala Ser Thr Arg Pro Glu Pro Asn Asn Pro His Ala Asp Arg
305 310 315 320

Arg His Val Ile Ala Leu Arg Arg Cys Pro Pro Leu Pro Ala Ser Ala
325 330 335

Val Leu Ala Pro Glu Leu Leu His Ala Arg Gly Leu Leu Pro Arg His
340 345 350

Trp Ser His Ala Ser Pro Leu Ser Thr Ser Ser Ser Ser Ser Arg Pro
355 360 365

Ala Asp Lys Ala Gln Leu Thr Trp Val Asp Lys Trp Ile Pro Glu Ala
370 375 380

Ala Arg Pro Tyr Met Phe Ala Cys Ala Lys Leu Ala Cys Thr Pro Ser
385 390 395 400

Leu Ile Arg Ala Gly Ser Arg Val Ala Tyr Arg Pro Ile Ser Ala Ser
405 410 415

Val Leu Ser Arg Pro Glu Ala Ser Arg Thr Gly Glu Gly Ser Thr Val
420 425 430

Phe Asn Gly Ala Gln Asn Gly Val Ser Gln Leu Ile Gln Arg Glu Phe
435 440 445

Gln Thr Ser Ala Ile Ser Arg
    450   455

<210> 156
<211> 285
<212> PRT
<213> Artificial Sequence

<220>
<223> hsADCK3_zmLOC100282174

<400> 156

Met Ala Ala Ile Leu Gly Asp Thr Ile Met Val Ala Lys Gly Leu Val
1   5   10   15

Lys Leu Thr Gln Ala Ala Val Glu Thr His Leu Gln His Leu Gly Ile
            20   25   30

Gly Gly Glu Leu Ile Met Ala Ala Arg Ala Leu Gln Ser Thr Ala Val
        35   40   45

Glu Gln Ile Gly Met Phe Leu Gly Lys Val Gln Gly Gln Asp Lys His
    50   55   60

Glu Glu Tyr Phe Ala Glu Asn Phe Gly Gly Pro Glu Gly Glu Phe His
65   70   75   80

Phe Ser Val Pro His Ala Ala Gly Ala Ser Thr Asp Phe Ser Ser Ala
                85   90   95

Ser Ala Pro Asp Gln Ser Ala Pro Pro Ser Leu Gly His Ala His Ser
            100   105   110

Glu Gly Pro Ala Pro Ala Tyr Val Ala Ser Gly Pro Phe Arg Glu Ala
        115   120   125

Gly Phe Pro Gly Gln Ala Ser Ser Pro Leu Gly Arg Ala Asn Gly Arg
    130   135   140

Leu Phe Ala Asn Pro Arg Asp Ser Phe Ser Ala Met Gly Phe Gln Arg
145   150   155   160

Arg Phe Gly Gly Met Ala Leu Leu Arg Ala Ala Val Ser Glu Leu Arg
                165   170   175

Arg Arg Gly Arg Gly Ala Leu Thr Pro Leu Pro Ala Leu Ser Ser Leu
            180   185   190

Leu Ser Ser Leu Ser Pro Arg Ser Pro Ala Ser Thr Arg Pro Glu Pro
        195   200   205

Asn Asn Pro His Ala Asp Arg Arg His Val Ile Ala Leu Arg Arg Cys
    210   215   220

Pro Pro Leu Pro Ala Ser Ala Val Leu Ala Pro Glu Leu Leu His Ala
225   230   235   240

Arg Gly Leu Leu Pro Arg His Trp Ser His Ala Ser Pro Leu Ser Thr
                245   250   255

Ser Ser Ser Ser Ser Arg Pro Ala Asp Lys Ala Gln Leu Thr Trp Val
            260   265   270

Asp Lys Trp Ile Pro Glu Ala Ala Arg Pro Tyr Gly Gly
        275   280   285

<210> 157
<211> 394
<212> PRT
<213> Artificial Sequence

<220>
<223> hsADCK3_zmLOC100282174_crATP6

<400> 157

Met Ala Ala Ile Leu Gly Asp Thr Ile Met Val Ala Lys Gly Leu Val
1   5   10   15

Lys Leu Thr Gln Ala Ala Val Glu Thr His Leu Gln His Leu Gly Ile
            20   25   30

Gly Gly Glu Leu Ile Met Ala Ala Arg Ala Leu Gln Ser Thr Ala Val
        35   40   45

Glu Gln Ile Gly Met Phe Leu Gly Lys Val Gln Gly Gln Asp Lys His
    50   55   60

Glu Glu Tyr Phe Ala Glu Asn Phe Gly Gly Pro Glu Gly Glu Phe His
65   70   75   80

Phe Ser Val Pro His Ala Ala Gly Ala Ser Thr Asp Phe Ser Ser Ala
                85   90   95

Ser Ala Pro Asp Gln Ser Ala Pro Pro Ser Leu Gly His Ala His Ser
            100   105   110

Glu Gly Pro Ala Pro Ala Tyr Val Ala Ser Gly Pro Phe Arg Glu Ala
        115   120   125

Gly Phe Pro Gly Gln Ala Ser Ser Pro Leu Gly Arg Ala Asn Gly Arg
    130   135   140

Leu Phe Ala Asn Pro Arg Asp Ser Phe Ser Ala Met Gly Phe Gln Arg
145   150   155   160

Arg Phe Gly Gly Met Ala Leu Leu Arg Ala Ala Val Ser Glu Leu Arg
                165   170   175

Arg Arg Gly Arg Gly Ala Leu Thr Pro Leu Pro Ala Leu Ser Ser Leu
            180   185   190

Leu Ser Ser Leu Ser Pro Arg Ser Pro Ala Ser Thr Arg Pro Glu Pro
        195   200   205

Asn Asn Pro His Ala Asp Arg Arg His Val Ile Ala Leu Arg Arg Cys
    210   215   220

Pro Pro Leu Pro Ala Ser Ala Val Leu Ala Pro Glu Leu Leu His Ala
225   230   235   240

Arg Gly Leu Leu Pro Arg His Trp Ser His Ala Ser Pro Leu Ser Thr
                245   250   255

Ser Ser Ser Ser Ser Arg Pro Ala Asp Lys Ala Gln Leu Thr Trp Val

260 265 270

Asp Lys Trp Ile Pro Glu Ala Ala Arg Pro Tyr Gly Gly Met Ala Leu
275 280 285

Gln Gln Ala Ala Pro Arg Val Phe Gly Leu Leu Gly Arg Ala Pro Val
290 295 300

Ala Leu Gly Gln Ser Gly Ile Leu Thr Gly Ser Ser Gly Phe Lys Asn
305 310 315 320

Gln Gly Phe Asn Gly Ser Leu Gln Ser Val Glu Asn His Val Tyr Ala
325 330 335

Gln Ala Phe Ser Thr Ser Ser Gln Glu Glu Gln Ala Ala Pro Ser Ile
340 345 350

Gln Gly Ala Ser Gly Met Lys Leu Pro Gly Met Ala Gly Ser Met Leu
355 360 365

Leu Gly Lys Ser Arg Ser Gly Leu Arg Thr Gly Ser Met Val Pro Phe
370 375 380

Ala Ala Gln Gln Ala Met Asn Met Gly Gly
385 390

<210> 158
<211> 574
<212> PRT
<213> Artificial Sequence

<220>
<223> ncATP9_zmLOC100282174_spilv1_GNFP_ncATP9

<400> 158

Met Ala Ser Thr Arg Val Leu Ala Ser Arg Leu Ala Ser Gln Met Ala
1 5 10 15

Ala Ser Ala Lys Val Ala Arg Pro Ala Val Arg Val Ala Gln Val Ser
20 25 30

Lys Arg Thr Ile Gln Thr Gly Ser Pro Leu Gln Thr Leu Lys Arg Thr

35 40 45

Gln Met Thr Ser Ile Val Asn Ala Thr Thr Arg Gln Ala Phe Gln Lys
50 55 60

Arg Ala Met Ala Leu Leu Arg Ala Ala Val Ser Glu Leu Arg Arg Arg
65 70 75 80

Gly Arg Gly Ala Leu Thr Pro Leu Pro Ala Leu Ser Ser Leu Leu Ser
85 90 95

Ser Leu Ser Pro Arg Ser Pro Ala Ser Thr Arg Pro Glu Pro Asn Asn
100 105 110

Pro His Ala Asp Arg Arg His Val Ile Ala Leu Arg Arg Cys Pro Pro
115 120 125

Leu Pro Ala Ser Ala Val Leu Ala Pro Glu Leu Leu His Ala Arg Gly
130 135 140

Leu Leu Pro Arg His Trp Ser His Ala Ser Pro Leu Ser Thr Ser Ser
145 150 155 160

Ser Ser Ser Arg Pro Ala Asp Lys Ala Gln Leu Thr Trp Val Asp Lys
165 170 175

Trp Ile Pro Glu Ala Ala Arg Pro Tyr Met Thr Val Leu Ala Pro Leu
180 185 190

Arg Arg Leu His Thr Arg Ala Ala Phe Ser Ser Tyr Gly Arg Glu Ile
195 200 205

Ala Leu Gln Lys Arg Phe Leu Asn Leu Asn Ser Cys Ser Ala Val Arg
210 215 220

Arg Tyr Gly Thr Gly Phe Ser Asn Asn Leu Arg Ile Lys Lys Leu Lys
225 230 235 240

Asn Ala Phe Gly Val Val Arg Ala Asn Ser Thr Lys Ser Thr Ser Thr
245 250 255

Val Thr Thr Ala Ser Pro Ile Lys Tyr Asp Ser Ser Phe Val Gly Lys
            260   265   270

Thr Gly Gly Glu Ile Phe His Asp Met Met Leu Lys His Asn Val Lys
        275   280   285

His Val Phe Gly Tyr Pro Gly Gly Ala Ile Leu Pro Val Phe Asp Ala
    290   295   300

Ile Tyr Arg Ser Pro His Phe Glu Phe Ile Leu Pro Arg His Glu Gln
305   310   315   320

Ala Ala Gly His Ala Val Ser Gly Glu Gly Asp Ala Thr Tyr Gly Lys
                325   330   335

Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp
            340   345   350

Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg
        355   360   365

Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro
    370   375   380

Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn
385   390   395   400

Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn
                405   410   415

Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu
            420   425   430

Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met
        435   440   445

Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His
    450   455   460

Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn

465 470 475 480

Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
485 490 495

Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Met Ala Ser Thr
500 505 510

Arg Val Leu Ala Ser Arg Leu Ala Ser Gln Met Ala Ala Ser Ala Lys
515 520 525

Val Ala Arg Pro Ala Val Arg Val Ala Gln Val Ser Lys Arg Thr Ile
530 535 540

Gln Thr Gly Ser Pro Leu Gln Thr Leu Lys Arg Thr Gln Met Thr Ser
545 550 555 560

Ile Val Asn Ala Thr Thr Arg Gln Ala Phe Gln Lys Arg Ala
565 570

<210> 159
<211> 810
<212> PRT
<213> Artificial Sequence

<220>
<223> ncATP9_zmLOC100282174_spilv1_lcSirt5_osP0644B06.24-2_hsATP5G2_ncATP9

<400> 159

Met Ala Ser Thr Arg Val Leu Ala Ser Arg Leu Ala Ser Gln Met Ala
1 5 10 15

Ala Ser Ala Lys Val Ala Arg Pro Ala Val Arg Val Ala Gln Val Ser
20 25 30

Lys Arg Thr Ile Gln Thr Gly Ser Pro Leu Gln Thr Leu Lys Arg Thr
35 40 45

Gln Met Thr Ser Ile Val Asn Ala Thr Thr Arg Gln Ala Phe Gln Lys
50 55 60

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Arg Ala Met Ala Leu Leu Arg Ala Ala Val Ser Glu Leu Arg Arg Arg
65                  70                  75                  80

Gly Arg Gly Ala Leu Thr Pro Leu Pro Ala Leu Ser Ser Leu Leu Ser
                85                  90                  95

Ser Leu Ser Pro Arg Ser Pro Ala Ser Thr Arg Pro Glu Pro Asn Asn
            100                 105                 110

Pro His Ala Asp Arg Arg His Val Ile Ala Leu Arg Arg Cys Pro Pro
        115                 120                 125

Leu Pro Ala Ser Ala Val Leu Ala Pro Glu Leu Leu His Ala Arg Gly
    130                 135                 140

Leu Leu Pro Arg His Trp Ser His Ala Ser Pro Leu Ser Thr Ser Ser
145                 150                 155                 160

Ser Ser Ser Arg Pro Ala Asp Lys Ala Gln Leu Thr Trp Val Asp Lys
                165                 170                 175

Trp Ile Pro Glu Ala Ala Arg Pro Tyr Met Thr Val Leu Ala Pro Leu
            180                 185                 190

Arg Arg Leu His Thr Arg Ala Ala Phe Ser Ser Tyr Gly Arg Glu Ile
        195                 200                 205

Ala Leu Gln Lys Arg Phe Leu Asn Leu Asn Ser Cys Ser Ala Val Arg
    210                 215                 220

Arg Tyr Gly Thr Gly Phe Ser Asn Asn Leu Arg Ile Lys Lys Leu Lys
225                 230                 235                 240

Asn Ala Phe Gly Val Val Arg Ala Asn Ser Thr Lys Ser Thr Ser Thr
                245                 250                 255

Val Thr Thr Ala Ser Pro Ile Lys Tyr Asp Ser Ser Phe Val Gly Lys
            260                 265                 270

Thr Gly Gly Glu Ile Phe His Asp Met Met Leu Lys His Asn Val Lys
        275                 280                 285
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His Val Phe Gly Tyr Pro Gly Gly Ala Ile Leu Pro Val Phe Asp Ala
    290                 295                 300

Ile Tyr Arg Ser Pro His Phe Glu Phe Ile Leu Pro Arg His Glu Gln
305                 310                 315                 320

Ala Ala Gly His Ala Met Arg Lys Arg Ser Leu Arg Cys His Leu Trp
                325                 330                 335

Ser Ala Asn Ala Ser Leu Ser Pro Arg Lys Asp Glu Val Thr Ser Arg
            340                 345                 350

Lys Glu Ser Glu Asn Leu Val Lys Gly Lys Lys Asn Lys Lys Ser His
        355                 360                 365

Leu His Leu Leu Leu Phe Thr Ala Ser Lys Ile Gly Thr Asp Ser Val
    370                 375                 380

Phe Asp Val Gln Lys Ser Lys Glu Cys Cys Lys Glu Leu Gly Leu Leu
385                 390                 395                 400

Phe Thr Ser Leu Ile His Ser Ile Gly Ser Phe Pro Phe Asp Glu Glu
                405                 410                 415

Pro Lys Ala Ala Ala Val Phe Leu Pro Gly Ser Leu Pro Gln Leu Thr
            420                 425                 430

Val Leu Val Leu Ala Pro Gly Ser Gly Ser Cys Pro Thr Gly Lys Ser
        435                 440                 445

Thr Pro His Leu Ala Ala Ser Gly Arg Asn Ala Glu Leu Leu Arg Pro
    450                 455                 460

Gln Asn Ser Met Ile Val Arg Gln Phe Thr Cys Arg Gly Thr Ile Ser
465                 470                 475                 480

Ser His Leu Cys Ala His Leu Arg Lys Pro His Asp Ser Arg Asn Met
                485                 490                 495
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Ala Arg Pro Met Ala Leu Leu Leu Arg His Ser Pro Lys Leu Arg Arg
            500   505   510

Ala His Ala Ile Leu Gly Cys Glu Arg Gly Thr Val Val Arg His Phe
        515   520   525

Ser Ser Ser Thr Cys Ser Ser Leu Val Lys Glu Asp Thr Val Ser Ser
    530   535   540

Ser Asn Leu His Pro Glu Tyr Ala Lys Lys Ile Gly Gly Ser Asp Phe
545   550   555   560

Ser His Asp Arg Gln Ser Gly Lys Glu Leu Gln Asn Phe Lys Val Ser
                565   570   575

Pro Gln Glu Ala Ser Arg Ala Ser Asn Phe Met Arg Ala Ser Lys Tyr
            580   585   590

Gly Met Pro Ile Thr Ala Asn Gly Val His Ser Leu Phe Ser Cys Gly
        595   600   605

Gln Val Val Pro Ser Arg Cys Phe Met Pro Glu Leu Ile Leu Tyr Val
    610   615   620

Ala Ile Thr Leu Ser Val Ala Glu Arg Leu Val Gly Pro Gly His Ala
625   630   635   640

Cys Ala Glu Pro Ser Phe Arg Ser Ser Arg Cys Ser Ala Pro Leu Cys
                645   650   655

Leu Leu Cys Ser Gly Ser Ser Ser Pro Ala Thr Ala Pro His Pro Leu
            660   665   670

Lys Met Phe Ala Cys Ser Lys Phe Val Ser Thr Pro Ser Leu Val Lys
        675   680   685

Ser Thr Ser Gln Leu Leu Ser Arg Pro Leu Ser Ala Val Val Leu Lys
    690   695   700

Arg Pro Glu Ile Leu Thr Asp Glu Ser Leu Ser Ser Leu Ala Val Ser
705   710   715   720

Cys Pro Leu Thr Ser Leu Val Ser Ser Arg Ser Phe Gln Thr Ser Ala
                725   730   735

Ile Ser Arg Asp Ile Asp Thr Ala Met Ala Ser Thr Arg Val Leu Ala
            740   745   750

Ser Arg Leu Ala Ser Gln Met Ala Ala Ser Ala Lys Val Ala Arg Pro
        755   760   765

Ala Val Arg Val Ala Gln Val Ser Lys Arg Thr Ile Gln Thr Gly Ser
    770   775   780

Pro Leu Gln Thr Leu Lys Arg Thr Gln Met Thr Ser Ile Val Asn Ala
785   790   795   800

Thr Thr Arg Gln Ala Phe Gln Lys Arg Ala
                805   810

<210> 160
<211> 459
<212> PRT
<213> Homo sapiens

<400> 160

Met Leu Lys Leu Ile Val Pro Thr Ile Met Leu Leu Pro Leu Thr Trp
1   5   10   15

Leu Ser Lys Lys His Met Ile Trp Ile Asn Thr Thr Thr His Ser Leu
            20   25   30

Ile Ile Ser Ile Ile Pro Leu Leu Phe Phe Asn Gln Ile Asn Asn Asn
        35   40   45

Leu Phe Ser Cys Ser Pro Thr Phe Ser Ser Asp Pro Leu Thr Thr Pro
    50   55   60

Leu Leu Met Leu Thr Thr Trp Leu Leu Pro Leu Thr Ile Met Ala Ser
65   70   75   80

Gln Arg His Leu Ser Ser Glu Pro Leu Ser Arg Lys Lys Leu Tyr Leu

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                85                  90                  95

Ser Met Leu Ile Ser Leu Gln Ile Ser Leu Ile Met Thr Phe Thr Ala
            100                 105                 110

Thr Glu Leu Ile Met Phe Tyr Ile Phe Phe Glu Thr Thr Leu Ile Pro
        115                 120                 125

Thr Leu Ala Ile Ile Thr Arg Trp Gly Asn Gln Pro Glu Arg Leu Asn
    130                 135                 140

Ala Gly Thr Tyr Phe Leu Phe Tyr Thr Leu Val Gly Ser Leu Pro Leu
145                 150                 155                 160

Leu Ile Ala Leu Ile Tyr Thr His Asn Thr Leu Gly Ser Leu Asn Ile
                165                 170                 175

Leu Leu Leu Thr Leu Thr Ala Gln Glu Leu Ser Asn Ser Trp Ala Asn
            180                 185                 190

Asn Leu Met Trp Leu Ala Tyr Thr Met Ala Phe Met Val Lys Met Pro
        195                 200                 205

Leu Tyr Gly Leu His Leu Trp Leu Pro Lys Ala His Val Glu Ala Pro
    210                 215                 220

Ile Ala Gly Ser Met Val Leu Ala Ala Val Leu Leu Lys Leu Gly Gly
225                 230                 235                 240

Tyr Gly Met Met Arg Leu Thr Leu Ile Leu Asn Pro Leu Thr Lys His
                245                 250                 255

Met Ala Tyr Pro Phe Leu Val Leu Ser Leu Trp Gly Met Ile Met Thr
            260                 265                 270

Ser Ser Ile Cys Leu Arg Gln Thr Asp Leu Lys Ser Leu Ile Ala Tyr
        275                 280                 285

Ser Ser Ile Ser His Met Ala Leu Val Val Thr Ala Ile Leu Ile Gln
    290                 295                 300
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Thr Pro Trp Ser Phe Thr Gly Ala Val Ile Leu Met Ile Ala His Gly
305 310 315 320

Leu Thr Ser Ser Leu Leu Phe Cys Leu Ala Asn Ser Asn Tyr Glu Arg
325 330 335

Thr His Ser Arg Ile Met Ile Leu Ser Gln Gly Leu Gln Thr Leu Leu
340 345 350

Pro Leu Met Ala Phe Trp Trp Leu Leu Ala Ser Leu Ala Asn Leu Ala
355 360 365

Leu Pro Pro Thr Ile Asn Leu Leu Gly Glu Leu Ser Val Leu Val Thr
370 375 380

Thr Phe Ser Trp Ser Asn Ile Thr Leu Leu Leu Thr Gly Leu Asn Met
385 390 395 400

Leu Val Thr Ala Leu Tyr Ser Leu Tyr Met Phe Thr Thr Thr Gln Trp
405 410 415

Gly Ser Leu Thr His His Ile Asn Asn Met Lys Pro Ser Phe Thr Arg
420 425 430

Glu Asn Thr Leu Met Phe Met His Leu Ser Pro Ile Leu Leu Leu Ser
435 440 445

Leu Asn Pro Asp Ile Ile Thr Gly Phe Ser Ser
450 455

<210> 161
<211> 174
<212> PRT
<213> Homo sapiens

<400> 161

Met Met Tyr Ala Leu Phe Leu Leu Ser Val Gly Leu Val Met Gly Phe
1 5 10 15

Val Gly Phe Ser Ser Lys Pro Ser Pro Ile Tyr Gly Gly Leu Val Leu
20 25 30

Ile Val Ser Gly Val Val Gly Cys Val Ile Ile Leu Asn Phe Gly Gly
        35   40   45

Gly Tyr Met Gly Leu Met Val Phe Leu Ile Tyr Leu Gly Gly Met Met
    50   55   60

Val Val Phe Gly Tyr Thr Thr Ala Met Ala Ile Glu Glu Tyr Pro Glu
65   70   75   80

Ala Trp Gly Ser Gly Val Glu Val Leu Val Ser Val Leu Val Gly Leu
                85   90   95

Ala Met Glu Val Gly Leu Val Leu Trp Val Lys Glu Tyr Asp Gly Val
            100   105   110

Val Val Val Val Asn Phe Asn Ser Val Gly Ser Trp Met Ile Tyr Glu
        115   120   125

Gly Glu Gly Ser Gly Leu Ile Arg Glu Asp Pro Ile Gly Ala Gly Ala
    130   135   140

Leu Tyr Asp Tyr Gly Arg Trp Leu Val Val Val Thr Gly Trp Thr Leu
145   150   155   160

Phe Val Gly Val Tyr Ile Val Ile Glu Ile Ala Arg Gly Asn
                165   170

<210> 162
<211> 316
<212> PRT
<213> Homo sapiens

<400> 162

Met Ala Asn Leu Leu Leu Leu Ile Val Pro Ile Leu Ile Ala Met Ala
1   5   10   15

Phe Leu Met Leu Thr Glu Arg Lys Ile Leu Gly Tyr Met Gln Leu Arg
            20   25   30

Lys Gly Pro Asn Val Val Gly Pro Tyr Gly Leu Leu Gln Pro Phe Ala

```
        35                  40                  45

Asp Ala Ile Lys Leu Phe Thr Lys Glu Pro Leu Lys Pro Ala Thr Ser
    50                  55                  60

Thr Ile Thr Leu Tyr Ile Thr Ala Pro Thr Leu Ala Leu Thr Ile Ala
65                  70                  75                  80

Leu Leu Leu Trp Thr Pro Leu Pro Met Pro Asn Pro Leu Val Asn Leu
                85                  90                  95

Asn Leu Gly Leu Leu Phe Ile Leu Ala Thr Ser Ser Leu Ala Val Tyr
            100                 105                 110

Ser Ile Leu Trp Ser Gly Trp Ala Ser Asn Ser Asn Tyr Ala Leu Ile
        115                 120                 125

Gly Ala Leu Arg Ala Val Ala Gln Thr Ile Ser Tyr Glu Val Thr Leu
    130                 135                 140

Ala Ile Ile Leu Leu Ser Thr Leu Leu Met Ser Gly Ser Phe Asn Leu
145                 150                 155                 160

Ser Thr Leu Ile Thr Thr Gln Glu His Leu Trp Leu Leu Leu Pro Ser
                165                 170                 175

Trp Pro Leu Ala Met Met Trp Phe Ile Ser Thr Leu Ala Glu Thr Asn
            180                 185                 190

Arg Thr Pro Phe Asp Leu Ala Glu Gly Glu Ser Glu Leu Val Ser Gly
        195                 200                 205

Phe Asn Ile Glu Tyr Ala Ala Gly Pro Phe Ala Leu Phe Phe Met Ala
    210                 215                 220

Glu Tyr Thr Asn Ile Ile Met Met Asn Thr Leu Thr Thr Thr Ile Phe
225                 230                 235                 240

Leu Gly Thr Thr Tyr Asp Ala Leu Ser Pro Glu Leu Tyr Thr Thr Tyr
                245                 250                 255
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Phe Val Thr Lys Thr Leu Leu Leu Thr Ser Leu Phe Leu Trp Ile Arg
            260                 265                 270

Thr Ala Tyr Pro Arg Phe Arg Tyr Asp Gln Leu Met His Leu Leu Trp
        275                 280                 285

Lys Asn Phe Leu Pro Leu Thr Leu Ala Leu Leu Met Trp Tyr Val Ser
    290                 295                 300

Met Pro Ile Thr Ile Ser Ser Ile Pro Pro Gln Thr
305                 310                 315
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