LOCUS Suaeda-glauca 474330 bp DNA circular 29-SEP-2020

DEFINITION Suaeda-glauca mitochondrion

ACCESSION Suaeda-glauca

SOURCE mitochondrion Suaeda-glauca

 ORGANISM Suaeda-glauca

 Suaeda-glauca;

REFERENCE 1 (bases 1 to 474330)

 AUTHORS Tillich,M., Lehwark,P., Pellizzer,T., Ulbricht-Jones, E.S.,

 Fischer, A., Bock, R. and Greiner,S.

 TITLE GeSeq - versatile and accurate annotation of organelle genomes

 JOURNAL Nucleic Acids Res. 45 (W1), W6-W11 (2017)

 PUBMED 28486635

COMMENT GeSeq Version 1.84

 Job GeSeqJob-20200902-174912

 Subjob Suaeda-salsa

 Creator anonymous

 Program BLAT v36x7

 blatxcutoff=25 blatncutoff=85

 blatxmaxintron=750000 blatnmaxintron=0

 annotate\_ir=false shortmatches=false

 mpimpchlororefset=false

 ncbirefs=NC\_017855.1, NC\_037304.1, NC\_020455.1,

 NC\_029317.1, NC\_035618.1, NC\_008285.1, NC\_041093.1,

 NC\_006581.1

 Program HMMER 3.3.1 disabled

 Program ARAGORN v1.2.38

 gcode=gcchloroph maxintronlen=3000

 intronoverlap=true fixintron=true

 lowscoring=false circular=true

 Program ARWEN v1.2.3 disabled

 Program MFannot v1.34 disabled

 Program Chloë v0.1.0 disabled

 Program tRNAscan-SE v1.3.1 disabled

 Program tRNAscan-SE v2.0.6 disabled

 Program RNA Editing disabled

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FEATURES Location/Qualifiers

 source 1..474330

 /organism="Suaeda-glauca"

 /organelle="mitochondrion"

 /mol\_type="genomic DNA"

 gene complement(24025..25594)

 /gene="cox1"

 /info="blatX\_hit cox1\_NC\_041093.1, position 1 - 1570, psl

 score 98.3, coverage 99.68%, match 97.97%"

 /annotator="blatX"

 CDS complement(24025..25594)

 /gene="cox1"

 /annotator="blatX"

 gene complement(26893..26966)

 /gene="trnM-CAU "

 /info="blatN\_hit trnfM-CAU\_NC\_006581.1, position 1 - 74,

 psl score 91.9, coverage 100.00%, match 91.89%; blatN\_hit

 trnfM-CAT\_NC\_020455.1, position 1 - 74, psl score 93.3,

 coverage 100.00%, match 93.24%; blatN\_hit

 trnM-CAU\_NC\_035618.1, position 1 - 74, psl score 100.0,

 coverage 100.00%, match 100.00%; blatN\_hit

 trnM\_NC\_041093.1, position 1 - 74, psl score 100.0,

 coverage 100.00%, match 100.00%; merged"

 /annotator="blatN"

 tRNA complement(26893..26966)

 /gene="trnM-CAU "

 /annotator="blatN"

 gene complement(36034..36106)

 /gene="trnK-UUU"

 /info="annotated by ARAGORN v1.2.38, score: 122.7;

 blatN\_hit trnK-TTT\_NC\_020455.1, position 1 - 73, psl

 score 100.0, coverage 100.00%, match 100.00%; blatN\_hit

 trnK-UUU\_NC\_037304.1, position 1 - 73, psl score 100.0,

 coverage 100.00%, match 100.00%; blatN\_hit

 trnK\_NC\_041093.1, position 1 - 73, psl score 100.0,

 coverage 100.00%, match 100.00%; merged"

 /annotator="ARAGORN, blatN; merged"

 tRNA complement(36034..36106)

 /gene="trnK-UUU "

 /annotator="ARAGORN, blatN; merged"

 /annotator="blatN"

 gene 47317..48683

 /gene="rrnL"

 /info="blatN\_hit rrnL\_NC\_035618.1, position 1988 - 3354,

 psl score 100.0, coverage 40.76%, match 40.76%"

 /annotator="blatN"

 rRNA 47317..48683

 /gene="rrnL"

 /annotator="blatN"

 gene 49061..49134

 /gene="trnM-CAU"

 /info="blatN\_hit trnfM-CAU\_NC\_006581.1, position 1 - 74,

 psl score 91.9, coverage 100.00%, match 91.89%; blatN\_hit

 trnfM-CAT\_NC\_020455.1, position 1 - 74, psl score 93.3,

 coverage 100.00%, match 93.24%; blatN\_hit

 trnM-CAU\_NC\_035618.1, position 1 - 74, psl score 100.0,

 coverage 100.00%, match 100.00%; blatN\_hit

 trnM\_NC\_041093.1, position 1 - 74, psl score 100.0,

 coverage 100.00%, match 100.00%; merged"

 /annotator="blatN"

 tRNA 49061..49134

 /gene="trnM-CAU"

 /annotator="blatN"

 gene 49312..54991

 /gene="nad7"

 /info="blatX\_hit nad7\_NC\_041093.1, position 1 - 1092, psl

 score 97.0, coverage 100.00%, match 100.00%"

 /annotator="blatX"

 CDS join(49312..49361,50286..50354,51282..51747,52825..53068,

 54729..54991)

 /gene="nad7"

 /annotator="blatX"

 /translation="MNGEVVERAEPHIGLLHRGTEKLIEYKTYLQALPYFDRLDYVSM

 MAQEHAHSSAVERLLNCEVPLRAQYIRVLFREITRISNHSLALTTHAMDVGALTPFLW

 AFEEREKLLEFYERVPGARMHASFIRPGGVAQDLPLGLCRDIDSSTQQFASRIDELEE

 MSTGNRIWKQRLVDIGTVTAQQAKDWGFSGVMLRGPGVCWDLRRAAPYDVYDQLDFDV

 PVGTRGDRYDRYCIRIEEMRQSVRIIVQCLNQMPSGMIKADDRKLCPPSRYRMKLSME

 SSIHHFEPYTEGFSVPAPSTYTAVEAPKGEFGVFLVSNGSNRPYRRKIRAPGSAHSQG

 LDSMSKHHMPADVVTIIGTQDIVSGEVDR"

 exon 49312..49361

 /gene="nad7"

 /annotator="blatX"

 /number=1

 intron 49362..50285

 /gene="nad7"

 /annotator="blatX"

 /number=1

 exon 50286..50354

 /gene="nad7"

 /annotator="blatX"

 /number=2

 intron 50355..51281

 /gene="nad7"

 /annotator="blatX"

 /number=2

 exon 51282..51747

 /gene="nad7"

 /annotator="blatX"

 /number=3

 intron 51748..52824

 /gene="nad7"

 /annotator="blatX"

 /number=3

 exon 52825..53068

 /gene="nad7"

 /annotator="blatX"

 /number=4

 intron 53069..54728

 /gene="nad7"

 /annotator="blatX"

 /number=4

 exon 54729..54991

 /gene="nad7"

 /annotator="blatX"

 /number=5

 gene complement(89202..89945)

 /gene="ccmC"

 /info="blatX\_hit ccmC\_NC\_035618.1, position 1 - 744, psl

 score 98.8, coverage 100.00%, match 98.79%"

 /annotator="blatX"

 CDS complement(89202..89945)

 /gene="ccmC"

 /annotator="blatX"

 /translation="MSKTRNYAQILIGSWLFLTAMAIHLSLWVAPLDFQQGGNSRILY

 VHVPVARMSILVYIVTAINTFLFLLTKHPLFLRSSGTGTEMGAFSTLFTLVTGGFRGR

 PMWGTFWVWDARLTSVFISFLIYLGALCFQKLPVEPAPISIRAGPIDIPIIKFSVNWW

 NTSHQPGSISRSGTSIHVPMLIPILSNFANFLFSTRIFFVLETRLPIPSFLESPLTEE

 IEAREGILKPSSLA\*SFCIHGRML\*ARNL"

 gene complement(90378..90974)

 /gene="atp4"

 /info="blatX\_hit atp4\_NC\_035618.1, position 1 - 597, psl

 score 97.9, coverage 100.00%, match 97.82%"

 /annotator="blatX"

 CDS complement(90378..90974)

 /gene="atp4"

 /annotator="blatX"

 /translation="MRKSSTKMQARKMLFAAILSICASSSKKISIYNEEMIVARCFIG

 FIIFSRKSLGNTFKVTLDERIQAIQEESQQFPNPNEVVPPESNEQQRLLRVSLRICGT

 VVESLPMARCAPKCEKTVQALLCRNLNVKSATLPNATSSRRTRLQDDLVTGFHFSVSE

 RFFPGSTLKASIVELVREGLAVLRMVRVGGSLKNKEDK"

 gene complement(91148..91450)

 /gene="nad4L"

 /info="blatX\_hit nad4L-1\_NC\_020455.1, position 1 - 303,

 psl score 94.8, coverage 100.00%, match 94.72%; blatX\_hit

 nad4L-2\_NC\_020455.1, position 1 - 303, psl score 94.8,

 coverage 100.00%, match 94.72%; merged"

 /annotator="blatX"

 CDS complement(91148..91450)

 /gene="nad4L"

 /annotator="blatX"

 /translation="TDSIKYFTFSMIIFISGIRGILLNRRNILIMSMSIESMLLAVNS

 NFLVFSVSSDDMMGQSFALLVPTVAAAESAIGLAIFVITFRVRGTIAVESINSIQG"

 gene complement(92951..96489)

 /gene="cox2"

 /info="blatX\_hit cox2-1\_NC\_008285.1, position 1 - 783,

 psl score 91.6, coverage 100.00%, match 94.89%"

 /annotator="blatX"

 CDS complement(join(92951..93033,94338..94655,96108..96489))

 /gene="cox2"

 /annotator="blatX"

 /translation="MIVREWLFFTIAPCDAAEPWQLGFQDAATPMMQGIIDLHHDIFF

 FLILILVFVSWILVRALWHFHYKKNPIPQRIVHGTTIEIIRTIFPSIILMFIAIPSFA

 LLYSMDEVVVDPAITIKAIGHQWYRTYEYSDYNSSDEQSLTFDSYTIPEDDPELGQSR

 LLEVDNRVVVPAKTHIRIIVTSADVLHSWAVPSSGVKCDAVPGRLNQTSILVQREGVY

 YGQCSEICGTNHAFMPIVVEAVSRKDYGSRVSNQLIP\*TGEA"

 exon complement(92951..93033)

 /gene="cox2"

 /annotator="blatX"

 /number=3

 intron complement(93034..94337)

 /gene="cox2"

 /annotator="blatX"

 /number=2

 gene complement(94338..96489)

 /gene="cox2"

 /info="blatX\_hit cox2-2\_NC\_008285.1, position 1 - 700,

 psl score 91.9, coverage 52.91%, match 50.34%"

 /annotator="blatX"

 CDS complement(join(94338..94655,96108..96489))

 /gene="cox2"

 /annotator="blatX"

 intron complement(94656..96107)

 /gene="cox2"

 /annotator="blatX"

 /number=1

 exon complement(96108..96489)

 /gene="cox2"

 /annotator="blatX"

 /number=1

 gene 104009..104080

 /gene="trnG-GCC "

 /info="blatN\_hit trnG-GCC\_NC\_035618.1, position 1 - 72,

 psl score 100.0, coverage 100.00%, match 100.00%;

 blatN\_hit trnG\_NC\_041093.1, position 1 - 72, psl score

 100.0, coverage 100.00%, match 100.00%; merged"

 /annotator="blatN"

 tRNA 104009..104082

 /gene="trnG-GCC"

 /annotator="ARAGORN"

 gene 106098..106169

 /gene="trnQ-UUG "

 /info="annotated by ARAGORN v1.2.38, score: 117.2;

 blatN\_hit trnQ-TTG\_NC\_020455.1, position 1 - 72, psl

 score 100.0, coverage 100.00%, match 100.00%; blatN\_hit

 trnQ\_NC\_041093.1, position 1 - 72, psl score 100.0,

 coverage 100.00%, match 100.00%; merged"

 /annotator="ARAGORN, blatN; merged"

 tRNA 106098..106169

 /gene="trnQ-UUG "

 /annotator="ARAGORN, blatN; merged"

 gene complement(114386..114458)

 /gene="trnM-CAU"

 /info="annotated by ARAGORN v1.2.38, score: 114.9;

 blatN\_hit trnM-CAT\_NC\_008285.1, position 1 - 73, psl

 score 98.7, coverage 100.00%, match 98.63%; blatN\_hit

 trnM-CAU\_NC\_035618.1, position 1 - 73, psl score 100.0,

 coverage 100.00%, match 100.00%; blatN\_hit

 trnM\_NC\_041093.1, position 1 - 73, psl score 100.0,

 coverage 100.00%, match 100.00%; merged"

 /annotator="ARAGORN, blatN; merged"

 tRNA complement(114386..114458)

 /gene="trnM-CAU "

 /annotator="ARAGORN, blatN; merged"

 gene complement(115364..115435)

 /gene="trnE-UUC "

 /info="annotated by ARAGORN v1.2.38, score: 112.6;

 blatN\_hit trnE-UUC\_NC\_037304.1, position 1 - 72, psl

 score 98.7, coverage 100.00%, match 98.61%; blatN\_hit

 trnE\_NC\_041093.1, position 1 - 72, psl score 100.0,

 coverage 100.00%, match 100.00%; merged"

 /annotator="ARAGORN, blatN; merged"

 tRNA complement(115364..115435)

 /gene="trnE-UUC "

 /annotator="ARAGORN, blatN; merged"

 gene 117114..117187

 /gene="trnH-GUG "

 /info="blatN\_hit trnH-GTG\_NC\_008285.1, position 1 - 74,

 psl score 97.3, coverage 100.00%, match 97.30%; blatN\_hit

 trnH-GUG\_NC\_035618.1, position 1 - 74, psl score 100.0,

 coverage 100.00%, match 100.00%; blatN\_hit

 trnH\_NC\_041093.1, position 1 - 74, psl score 100.0,

 coverage 100.00%, match 100.00%; merged"

 /annotator="blatN"

 tRNA 117114..117187

 /gene=" trnH-GUG "

 /annotator="blatN"

 gene 137889..138085

 /gene="trnV-AAC"

 /info="annotated by ARAGORN v1.2.38, score: 102.5"

 /annotator="ARAGORN"

 tRNA join(137889..137922,138028..138085)

 /gene="trnV-AAC"

 /annotator="ARAGORN"

 exon 137889..137922

 /gene="trnV-AAC"

 /annotator="ARAGORN"

 /number=1

 intron 137923..138027

 /gene="trnV-AAC"

 /annotator="ARAGORN"

 /number=1

 exon 138028..138085

 /gene="trnV-AAC"

 /annotator="ARAGORN"

 /number=2

 gene 138012..138085

 /gene="trnN-GUU"

 /info="annotated by ARAGORN v1.2.38, score: 119.0"

 /annotator="ARAGORN"

 tRNA 138012..138085

 /gene="trnN-GUU"

 /annotator="ARAGORN"

 /annotator="blatN"

 gene 138859..138941

 /gene="trnY-GUA"

 /info="blatN\_hit trnY-GTA\_NC\_020455.1, position 1 - 83,

 psl score 98.8, coverage 100.00%, match 98.80%; blatN\_hit

 trnY-GUA\_NC\_035618.1, position 1 - 83, psl score 98.8,

 coverage 100.00%, match 98.80%; blatN\_hit

 trnY\_NC\_041093.1, position 1 - 83, psl score 98.8,

 coverage 100.00%, match 98.80%; merged"

 /annotator="blatN"

 tRNA 138859..138941

 /gene="trnY-GUA "

 /annotator="blatN"

 gene 139460..143951

 /gene="nad2"

 /info="blatX\_hit nad2\_NC\_041093.1, position 1 - 915, psl

 score 96.8, coverage 100.00%, match 99.67%"

 /annotator="blatX"

 CDS join(139460..139613,141717..142289,143764..143951)

 /gene="nad2"

 /annotator="blatX"

 /translation="MIYGSTGATHFDQLAKILTGYEITGVRSSGIFMGILFIAVGSLF

 KITAVPFHMWAPDIYEGSPTPVTAFFSIAPKISISANILRVFIYGSYGATLQQIFFFC

 SIASMILGALAAMAQTKVKRLLAHSSIGHVGYIRTGFSCGTIEGIQSLLIGLFIYASM

 TIDAFAIVSALRQTRVKYIADLGALAKTNPISAITFSITMFSYAGIPPLAGFCSKFYL

 FFAALGCGAYFLAPVGVVTSVIGCFYYIRLVKRMFFDTPRTWILYEPMDRDKSLLLAM

 TSSFITSSFPYPSPLFSVTHQMALSLYL"

 exon 139460..139613

 /gene="nad2"

 /annotator="blatX"

 /number=1

 intron 139614..141716

 /gene="nad2"

 /annotator="blatX"

 /number=1

 exon 141717..142289

 /gene="nad2"

 /annotator="blatX"

 /number=2

 intron 142290..143763

 /gene="nad2"

 /annotator="blatX"

 /number=2

 exon 143764..143951

 /gene="nad2"

 /annotator="blatX"

 /number=3

 gene 144297..144875

 /gene="nad9"

 /info="blatX\_hit nad9\_NC\_041093.1, position 1 - 579, psl

 score 99.2, coverage 100.00%, match 99.14%"

 /annotator="blatX"

 CDS 144297..144875

 /gene="nad9"

 /annotator="blatX"

 /translation="MDNQFIFKYSWETLPKKWVKKIEKSEHGNRSDTNTDYPFQLLCF

 LKLHTYTRFQVLIDICGVDYPSRKRRFEVVYNLLSTRYNSRIRVQTSADEVTRISPVV

 SLFPSAGRWEREVWDMFGVSSINHPDLRRILTDYGFEGHPLRKDFPLSGYVEVRYDDP

 EKRVVSEPIEMTQEFRYFDFASPWEQRNGNEG"

 gene 145614..145687

 /gene="trnW-CCA "

 /info="annotated by ARAGORN v1.2.38, score: 118.2;

 blatN\_hit trnW\_NC\_041093.1, position 1 - 74, psl score

 98.7, coverage 100.00%, match 98.65%; blatN\_hit

 trnW-CCA\_NC\_037304.1, position 1 - 74, psl score 100.0,

 coverage 100.00%, match 100.00%; merged"

 /annotator="ARAGORN, blatN; merged"

 tRNA 145614..145687

 /gene="trnW-CCA "

 /annotator="ARAGORN, blatN; merged"

 gene 176179..177699

 /gene="atp1"

 /info="blatX\_hit atp1\_NC\_035618.1, position 1 - 1521, psl

 score 97.7, coverage 100.00%, match 97.70%"

 /annotator="blatX"

 CDS 176179..177699

 /gene="atp1"

 /annotator="blatX"

 /translation="MEFSPRAAELTTLLESRITNFYTNFQVDEIGRVVSVGDGIARVY

 GLNEIQAGEMVEFASGVKGIALNLENENVGIVVFGSDTAIKEGDLVKRTGSIVDVPAG

 KAMLGRVVDALGVPIDGRGALSDHERRRVEVKAPGIIERKSVHEPMQTGLKAVDSLVP

 IGRGQRELIIGDRQTGKTAIAIDTILNQKQLNSKATSESETLYCVYVAVGQKRSTVAQ

 LVQILSEANALEYSILVAATASDPAPLQFLAPYSGCAMGEYFRDNAMHALIIYDDLSK

 QAVAYRQMSLLLRRPPGREAFPGDVFYLHSRLLERAAKRSDQTGAGSLTALPVIETQA

 GDVSAYIPTNVISITDGQICLETELFYRGIRPAINVGLSVSRVGSAAQLKAMKQVCGS

 PKLELAQYREVAAFAQFGSDLDAATQALLNRGARLTEVLKQPQYAPLPIEKQILVIYA

 AVNGFCDRMPLDKISQYEKTIPNSVKPELLQSLKGGLTHEKKMELDAFLKECAITE"

 gene 184681..184760

 /gene="nad6"

 /info="blatX\_hit nad6\_NC\_041093.1, position 227 - 306,

 psl score 91.3, coverage 12.94%, match 11.81%"

 /annotator="blatX"

 CDS 184681..184760

 /gene="nad6"

 /annotator="blatX"

 gene complement(191903..192229)

 /gene="nad1"

 /info="blatX\_hit nad1\_NC\_041093.1, position 1 - 327, psl

 score 99.7, coverage 100.00%, match 99.69%"

 /annotator="blatX"

 CDS complement(191903..192229)

 /gene="nad1"

 /annotator="blatX"

 /translation="MAFVQRRKGPDVVGSFGLLQPLADGSKLILKEPISPSSANFSLF

 RMAPVTTFMLSLVARAVVPFDYGMVLSDPNIGLLYLFAISSLGVYGIIIAGWSSNYRG

 RPFGRL"

 gene complement(201390..201461)

 /gene="trnV-GAC "

 /info="annotated by ARAGORN v1.2.38, score: 113.4;

 blatN\_hit trnV\_NC\_029317.1, position 1 - 72, psl score

 100.0, coverage 100.00%, match 100.00%; merged"

 /annotator="ARAGORN, blatN; merged"

 tRNA complement(201390..201461)

 /gene="trnV-GAC "

 /annotator="ARAGORN, blatN; merged"

 gene 207705..208615

 /gene="trnA-UGC"

 /info="annotated by ARAGORN v1.2.38, score: 111.0"

 /annotator="ARAGORN"

 tRNA join(207705..207741,208580..208615)

 /gene="trnA-UGC"

 /annotator="ARAGORN"

 exon 207705..207741

 /gene="trnA-UGC"

 /annotator="ARAGORN"

 /number=1

 intron 207742..208579

 /gene="trnA-UGC"

 /annotator="ARAGORN"

 /number=1

 exon 208580..208615

 /gene="trnA-UGC"

 /annotator="ARAGORN"

 /number=2

 gene 212367..212441

 /gene="trnR-ACG"

 /info="annotated by ARAGORN v1.2.38, score: 115.9"

 /annotator="ARAGORN"

 tRNA 212367..212441

 /gene="trnR-ACG"

 /annotator="ARAGORN"

 gene complement(213052..213125)

 /gene="trnN-GUU"

 /info="annotated by ARAGORN v1.2.38, score: 120.5"

 /annotator="ARAGORN"

 tRNA complement(213052..213125)

 /gene="trnN-GUU"

 /annotator="ARAGORN"

 /annotator="blatN"

 gene 222793..224160

 /gene="rrn26"

 /info="blatN\_hit rrn26\_NC\_041093.1, position 1972 - 3339,

 psl score 100.0, coverage 40.97%, match 40.97%"

 /annotator="blatN"

 rRNA 222793..224160

 /gene="rrn26"

 /annotator="blatN"

 gene 224537..224610

 /gene="trnM-CAU "

 /info="blatN\_hit trnfM-CAU\_NC\_006581.1, position 1 - 74,

 psl score 91.9, coverage 100.00%, match 91.89%; blatN\_hit

 trnfM-CAT\_NC\_020455.1, position 1 - 74, psl score 93.3,

 coverage 100.00%, match 93.24%; blatN\_hit

 trnM-CAU\_NC\_035618.1, position 1 - 74, psl score 100.0,

 coverage 100.00%, match 100.00%; blatN\_hit

 trnM\_NC\_041093.1, position 1 - 74, psl score 100.0,

 coverage 100.00%, match 100.00%; merged"

 /annotator="blatN"

 tRNA 224537..224610

 /gene="trnM-CAU "

 /annotator="blatN"

 gene 224788..230467

 /gene="nad7"

 /info="blatX\_hit nad7\_NC\_041093.1, position 1 - 1092, psl

 score 97.0, coverage 100.00%, match 100.00%"

 /annotator="blatX"

 CDS join(224788..224837,225762..225830,226758..227223,

 228301..228544,230205..230467)

 /gene="nad7"

 /annotator="blatX"

 /translation="MNGEVVERAEPHIGLLHRGTEKLIEYKTYLQALPYFDRLDYVSM

 MAQEHAHSSAVERLLNCEVPLRAQYIRVLFREITRISNHSLALTTHAMDVGALTPFLW

 AFEEREKLLEFYERVPGARMHASFIRPGGVAQDLPLGLCRDIDSSTQQFASRIDELEE

 MSTGNRIWKQRLVDIGTVTAQQAKDWGFSGVMLRGPGVCWDLRRAAPYDVYDQLDFDV

 PVGTRGDRYDRYCIRIEEMRQSVRIIVQCLNQMPSGMIKADDRKLCPPSRYRMKLSME

 SSIHHFEPYTEGFSVPAPSTYTAVEAPKGEFGVFLVSNGSNRPYRRKIRAPGSAHSQG

 LDSMSKHHMPADVVTIIGTQDIVSGEVDR"

 exon 224788..224837

 /gene="nad7"

 /annotator="blatX"

 /number=1

 intron 224838..225761

 /gene="nad7"

 /annotator="blatX"

 /number=1

 exon 225762..225830

 /gene="nad7"

 /annotator="blatX"

 /number=2

 intron 225831..226757

 /gene="nad7"

 /annotator="blatX"

 /number=2

 exon 226758..227223

 /gene="nad7"

 /annotator="blatX"

 /number=3

 intron 227224..228300

 /gene="nad7"

 /annotator="blatX"

 /number=3

 exon 228301..228544

 /gene="nad7"

 /annotator="blatX"

 /number=4

 intron 228545..230204

 /gene="nad7"

 /annotator="blatX"

 /number=4

 exon 230205..230467

 /gene="nad7"

 /annotator="blatX"

 /number=5

 /annotator="blatX"

 gene 257081..257168

 /gene=" trnS-GCU"

 /info="blatN\_hit trnS-GCT\_NC\_008285.1, position 1 - 88,

 psl score 97.8, coverage 100.00%, match 97.73%; blatN\_hit

 trnS-GCU\_NC\_017855.1, position 1 - 88, psl score 100.0,

 coverage 100.00%, match 100.00%; blatN\_hit

 trnS\_NC\_041093.1, position 1 - 88, psl score 100.0,

 coverage 100.00%, match 100.00%; merged"

 /annotator="blatN"

 tRNA 257081..257168

 /gene="trnS-GCU "

 /annotator="blatN"

 gene 257544..257617

 /gene="trnF-GAA "

 /info="annotated by ARAGORN v1.2.38, score: 114.5;

 blatN\_hit trnF-GAA\_NC\_035618.1, position 1 - 74, psl

 score 98.7, coverage 100.00%, match 98.65%; blatN\_hit

 trnF\_NC\_041093.1, position 1 - 74, psl score 98.7,

 coverage 100.00%, match 98.65%; merged"

 /annotator="ARAGORN, blatN; merged"

 tRNA 257544..257617

 /gene="trnF-GAA "

 /annotator="ARAGORN, blatN; merged"

 gene 257699..257773

 /gene="trnP-UGG "

 /info="annotated by ARAGORN v1.2.38, score: 120.7;

 blatN\_hit trnF-UGG\_NC\_029317.1, position 1 - 75, psl

 score 100.0, coverage 100.00%, match 100.00%; blatN\_hit

 trnP-TGG\_NC\_020455.1, position 1 - 75, psl score 100.0,

 coverage 100.00%, match 100.00%; blatN\_hit

 trnP-UGG\_NC\_037304.1, position 1 - 75, psl score 100.0,

 coverage 100.00%, match 100.00%; blatN\_hit

 trnP\_NC\_041093.1, position 1 - 75, psl score 100.0,

 coverage 100.00%, match 100.00%; merged"

 /annotator="ARAGORN, blatN; merged"

 tRNA 257699..257773

 /gene="trnP-UGG "

 /annotator="ARAGORN, blatN; merged"

 gene complement(270665..271385)

 /gene="atp6"

 /info="blatX\_hit atp6-1\_NC\_020455.1, position 1 - 712,

 psl score 93.9, coverage 100.14%, match 94.17%; blatX\_hit

 atp6-2\_NC\_020455.1, position 1 - 712, psl score 93.9,

 coverage 100.14%, match 94.17%; merged"

 /annotator="blatX"

 CDS complement(270665..271385)

 /gene="atp6"

 /annotator="blatX"

 gene 272256..273961

 /gene="rps3"

 /info="blatX\_hit rps3\_NC\_035618.1, position 1 - 1682, psl

 score 94.7, coverage 101.37%, match 93.35%"

 /annotator="blatX"

 CDS 272256..273961

 /gene="rps3"

 /annotator="blatX"

 gene 273838..274008

 /gene="rpl16"

 /info="blatX\_hit rpl16\_NC\_037304.1, position 1 - 171, psl

 score 85.4, coverage 31.67%, match 27.04%"

 /annotator="blatX"

 CDS 273838..274008

 /gene="rpl16"

 /annotator="blatX"

 gene 282347..282703

 /gene="nad3"

 /info="blatX\_hit nad3\_NC\_035618.1, position 1 - 357, psl

 score 99.2, coverage 100.00%, match 99.16%"

 /annotator="blatX"

 CDS 282347..282703

 /gene="nad3"

 /annotator="blatX"

 /translation="MSEFAPICIYLVISLLVSLIPLGIPFPFSSNTSTYPEKLSAYEC

 GFDPFGDARSRFDIRFYLVSILFIILDPEVTFFFPWAVPLNKIDPFGFWSMMAFLLIL

 TIGFLYEWKRGASDRE"

 gene 282765..283138

 /gene="rps12"

 /info="blatX\_hit rps12\_NC\_041093.1, position 1 - 374, psl

 score 98.4, coverage 98.94%, match 97.35%"

 /annotator="blatX"

 CDS 282765..283138

 /gene="rps12"

 /annotator="blatX"

 /annotator="blatX"

 gene 294724..294800

 /gene="trnL-CAA"

 /info="blatN\_hit trnL-CAA\_NC\_035618.1, position 1 - 77,

 psl score 100.0, coverage 97.47%, match 97.47%"

 /annotator="blatN"

 tRNA 294724..294800

 /gene="trnL-CAA"

 /annotator="blatN"

 gene 302234..304522

 /gene="nad5"

 /info="blatX\_hit nad5\_NC\_041093.1, position 1 - 1452, psl

 score 98.0, coverage 100.00%, match 99.52%"

 /annotator="blatX"

 CDS join(302234..302464,303302..304522)

 /gene="nad5"

 /annotator="blatX"

 /translation="MYLLIVFLPLLGSSVAGFFGRFLGSEGTAIVTTTCVSFSSIFSL

 IAFYEVAPGASACYLRIAPWISSEMFDASWGFFFDSPTVVMLIVVTFISSLVHLYSIS

 YMSEDPHSPRFMCYLSILTFFMPMLVTGDNSLQLFLGWEGVGLASYLLIHFWFTRLQA

 DKAAIKAMLVNRVGDFGLALGISGCFTLFQTVDFSTIFACASAPRNSWIFCNMRLNAI

 TLICILLFIGAVGKSAQIGSHTWSPDAMEGPTPVSALIHAATMVTAGVFMIARCSPLF

 EYPPTALIVITFAGAMTSFLAATTGILQNDLKRVIAYSTCSQLGYMIFACGISNYSVS

 VFHLMNHAFFKALLFLSAGSVIHAMSDEQDMRKMGGLASSFPFTYAMMLMGSLSLIGF

 PFLTGFYSKDVILELAYTKYTISGNFAFWLGSVSVLFTSYYSFRLLFLTFLVPTNSFG

 RDILRCHDAPIPMAIPLILLAFGSLFVGYLAKV"

 exon 302234..302464

 /gene="nad5"

 /annotator="blatX"

 /number=1

 intron 302465..303301

 /gene="nad5"

 /annotator="blatX"

 /number=1

 exon 303302..304522

 /gene="nad5"

 /annotator="blatX"

 /number=2

 /annotator="blatN"

 gene 310034..310107

 /gene="trnF-GAA"

 /info="annotated by ARAGORN v1.2.38, score: 116.2"

 /annotator="ARAGORN"

 tRNA 310034..310107

 /gene="trnF-GAA"

 /annotator="ARAGORN"

 gene 317813..317899

 /gene="trnS-UGU"

 /info="blatN\_hit trnS-UGU\_NC\_029317.1, position 1 - 87,

 psl score 96.6, coverage 100.00%, match 96.55%; blatN\_hit

 trnS-TGA\_NC\_008285.1, position 1 - 87, psl score 97.8,

 coverage 100.00%, match 97.70%; blatN\_hit

 trnS-UGA\_NC\_035618.1, position 1 - 87, psl score 100.0,

 coverage 100.00%, match 100.00%; blatN\_hit

 trnS\_NC\_041093.1, position 1 - 87, psl score 100.0,

 coverage 100.00%, match 100.00%; merged"

 /annotator="blatN"

 tRNA 317813..317899

 /gene="trnS-UGU"

 /annotator="blatN"

 gene complement(329351..329797)

 /gene="rps7"

 /info="blatX\_hit rps7\_NC\_035618.1, position 1 - 447, psl

 score 98.5, coverage 100.00%, match 98.43%"

 /annotator="blatX"

 CDS complement(329351..329797)

 /gene="rps7"

 /annotator="blatX"

 /translation="MGGLDSEQKQLIKKLVNFRMKEGKRTKVRAIFYQTFHRPARTEG

 DVIKLMVDAVENIKPICKVEKVRVAGTIYDVPGIVARDRQQTLAIRWILEAAFKRRIS

 HRISLEKCSFDEILDAYRKRGISRKKRENLHGLASANRSFAHFRWW"

 /annotator="blatX"

 gene complement(330082..332049)

 /gene="matR "

 /info="blatX\_hit matR\_NC\_035618.1, position 1 - 1968, psl

 score 97.9, coverage 100.00%, match 97.87%; blatX\_hit

 mat-r\_NC\_041093.1, position 1 - 1968, psl score 98.1,

 coverage 100.00%, match 98.02%; merged"

 /annotator="blatX"

 CDS complement(330082..332049)

 /gene="matR "

 /annotator="blatX"

 /translation="MKEAIRMVPESIYDPEFPDTSHFRSGRGCHSALRRIKEEWGTSR

 WFLEFDIRKCFHTIDRHRLTPIFKEEIDDPKFFYSIHQVFSAGRLVGGEKGPYSVPHS

 VLLSALPGNIYLHKLDQEIGRIQQKYEIPIVQRIRSVLLKTSRIDDQENSGEEESFNA

 PQDNRAIIVDRVKSIQRKAAFHSLVSSWHTLPASTPRLGGDQKRPFVFPPSSALAAFL

 NKPSSLLFAAFLIEAAGLTPKAEFYGRECCNNNWDMRDLLKYCKRKGPLIELGEAARL

 VLRSEKGLARKLAPFKTHYLIRICYARYADDLLLGIVGAVELLIEIQKRIAHFLQSGL

 NLWAGSAGSTTIAARSTVEFLGTVIREVPPKTTPIQFLRELEKRLRVKHRIHITACHL

 RSAIHSKFRNLGNSIPIKQLTKGMSKTGSLPDAVQLAESLSTARVRSPQVSVLWETVK

 HIRQGSRGISLLHSSGQSKVPSDVQQAVSRSGMNAQKFSLYTLAGRKAAGEGGGHWSR

 SISCEFPIQIEAPIKKILRRLRDRGLISRRRPWPIHVACLTNVSDGDIVNWSAGIAIS

 PLSYYRCRDNLYQVRTIVDYQIRWSAIFTPAHKHKSSARNIIPKYSKDLNIVNQEGGK

 TLAEFPNSIELGKLGAGQDPNNKEHSTTSLV"

 gene 338995..339615

 /gene="ccmB"

 /info="blatX\_hit ccmB\_NC\_041093.1, position 1 - 621, psl

 score 99.6, coverage 100.00%, match 99.52%"

 /annotator="blatX"

 CDS 338995..339615

 /gene="ccmB"

 /annotator="blatX"

 /translation="MRRLFFKLYHKQIFFSTPITSFSPFLSYIVVTPLMLGFEKDFSC

 HFHLGPIRIPLLFPFPPAPFLRNEKEDGTLELYYLSAYCLPKILLLQLVGHRVIQISR

 VFCSFPMLQLLYQFGQSGMDRLNILLGSLVLTLLCGIHSRLALGITSSSGWNSSQNLT

 TSPTSLPSTVSRTSIETEWFHVLSSIGYFSSFVSLFPISVSISSQD"

 gene complement(344470..345651)

 /gene="cob"

 /info="blatX\_hit cob\_NC\_041093.1, position 1 - 1182, psl

 score 98.6, coverage 100.00%, match 98.56%"

 /annotator="blatX"

 CDS complement(344470..345651)

 /gene="cob"

 /annotator="blatX"

 /translation="MSIRNQRFSVLKQPIFSTLNQHLIDYPTPSNISYWWGFGSLAGI

 CLVIQIVTGVFLAMHYTPHVDLAFNSVEHIMRDVEGGWLLRYMHANGASMFLIVVHLH

 IFRGLYHASYSSPREFVWCLGVVIFLLMIVTAFIGYVLPWGQMSFWGATVITSLASAI

 PVVGDSIVTWLWGGFSVDNATLNRFFSLHHLLPFLLVGASLLHLAALHQYGSNNPLGV

 HSEMDKIAFYPYFYVKDLVGWVAFAIFFSFWIFYAPNVLGHPDNYIPANPMPTPPHIV

 PEWYFLPIYAILRSIPDKSGGVAAIAPVFICLLALPFFKSMYVRSSSFRPIYQGLFWL

 LLADCLLLGWIGCQPVEPPFVTIGQIPSFLFFLFFAITPILGRVGRRIPNSYTDETYN

 T"

 gene complement(348273..348827)

 /gene="rpl5"

 /info="blatX\_hit rpl5\_NC\_041093.1, position 1 - 555, psl

 score 99.0, coverage 100.00%, match 98.92%"

 /annotator="blatX"

 CDS complement(348273..348827)

 /gene="rpl5"

 /annotator="blatX"

 /translation="MFPLHFHYEDVSRQDPLLKPNHANVMDVPGLCEIRVVPKAAPSS

 FIIKNGKLAMEIPCGQKLIRTRRGSIGKSFRSNPFLGSNKDKGYVNDLARQSTLRGHG

 MFHFLVRISTVMSLLDSLVEIRENSIQLSMETEFCEFSPELEDHFEIFEHIRGFNVTI

 VTSANTQDETLLPWSGFLQKDEGQ"

 gene complement(385116..385477)

 /gene="sdh4"

 /info="blatX\_hit sdh4\_NC\_029317.1, position 1 - 385, psl

 score 93.3, coverage 91.41%, match 84.34%"

 /annotator="blatX"

 CDS complement(385116..385477)

 /gene="sdh4"

 /annotator="blatX"

 gene complement(385405..386202)

 /gene="cox3"

 /info="blatX\_hit cox3\_NC\_035618.1, position 1 - 798, psl

 score 98.5, coverage 100.00%, match 98.50%"

 /annotator="blatX"

 CDS complement(385405..386202)

 /gene="cox3"

 /annotator="blatX"

 /translation="MIESQRHSFHLVDPSPWPISGSLGALATTVGGVMYMHSFQGGAT

 LLSLGLLFILYTMFVWWRDVLRESTLEGHHTKVVQLGLRYGFILFIVSEVMFFFAFFW

 AFSHSSLAPAVEIGGIWPPKGIWVLDPWEIPFLNTLILLSSGAAVTWAHHAILAGKQK

 RAVYALVATVLLALVFTGFQGMEYYEAPFTISDSIYGSTFFLATGFHGFHVIIGTLFL

 IICGIRQYFGHLTKEHHVGFEAAAWYWHFVDVVWLFLFVSIYWWGGI"

 gene complement(387161..387640)

 /gene="atp8"

 /info="blatX\_hit atp8\_NC\_035618.1, position 1 - 480, psl

 score 97.5, coverage 100.00%, match 97.50%"

 /annotator="blatX"

 CDS complement(387161..387640)

 /gene="atp8"

 /annotator="blatX"

 /translation="MPQLDQFTYFTQFFWSCLFFFTFYILICNDRDGVLGISRILKLR

 NQLLSHRGNKIQSKDPKSLEDILRKGFHTGVSYMYSSLFEVSQWCEAADLFGKRKKIT

 LIPCFGEISGSRGMERNIFYLISKSSYSTSSNPGWVITCKNDIMLIHVLHGQGSFKI"

 gene complement(397370..397601)

 /gene="atp9"

 /info="blatX\_hit atp9\_NC\_041093.1, position 1 - 232, psl

 score 95.3, coverage 99.15%, match 94.44%"

 /annotator="blatX"

 CDS complement(397370..397601)

 /gene="atp9"

 /annotator="blatX"

 gene 406939..408224

 /gene="rrnS"

 /info="blatN\_hit rrnS\_NC\_035618.1, position 1 - 1277, psl

 score 98.5, coverage 67.05%, match 66.01%"

 /annotator="blatN"

 rRNA 406939..408224

 /gene="rrnS"

 /annotator="blatN"

 /annotator="blatN"

 gene 409155..409273

 /gene="rrn5"

 /info="blatN\_hit rrn5\_NC\_041093.1, position 1 - 119, psl

 score 99.2, coverage 100.00%, match 99.16%"

 /annotator="blatN"

 rRNA 409155..409273

 /gene="rrn5"

 /annotator="blatN"

 gene complement(413377..413473)

 /gene="rpl2"

 /info="blatX\_hit rpl2\_NC\_029317.1, position 922 - 1032,

 psl score 89.7, coverage 9.40%, match 8.43%"

 /annotator="blatX"

 CDS complement(413377..413473)

 /gene="rpl2"

 /annotator="blatX"

 gene complement(428814..431067)

 /gene="ccmFc"

 /info="blatX\_hit ccmFc\_NC\_041093.1, position 1 - 1338,

 psl score 97.1, coverage 100.00%, match 98.65%"

 /annotator="blatX"

 CDS complement(join(428814..429383,430300..431067))

 /gene="ccmFc"

 /annotator="blatX"

 /translation="MVQLHNFFFFITSVVVPCGTAAPVLLKWFVSRDVPTGAPFSNGT

 LIPILIPSFLLLVYLHSRKFIRSMDGVKSGVLVRASCPILLPDIIGRSSSETRARNAL

 FRFVPILHFLLLEFKGDFPYLESFCGVLRLLFFRTFFSLPRDRSAKRERARRRKGQTL

 RPNGNEQRRNEKRKCPGRPHLERRVEGVGPVAFPAPPSSGGACMGGVLPEIGLEAPAL

 PTSRQLMAVGRDYYQKVNMKMNISHGGVCIFMLGVLLSMVRLRSTNTKKIQFTQRLPL

 GSELHMGKERCCLRGLDHLHGPTFHSICGNLMIYKPSLTNDRLIFEHDESLRADLLSI

 HFWASYENGKLEHFLHRWMKNREHPNFWLSMFPEKRYFRETTSTTEVAIHTNPFTDLY

 ASIGTGSSRTGGWYTTIMKLPFLFLIRIGFLLASLGGSRSLLRQLQKDKLGWN"

 exon complement(428814..429383)

 /gene="ccmFc"

 /annotator="blatX"

 /number=2

 intron complement(429384..430299)

 /gene="ccmFc"

 /annotator="blatX"

 /number=1

 exon complement(430300..431067)

 /gene="ccmFc"

 /annotator="blatX"

 /number=1

 /annotator="blatX"

 gene complement(439401..441035)

 /gene="ccmFn"

 /info="blatX\_hit ccmFn\_NC\_041093.1, position 1 - 1740,

 psl score 97.8, coverage 93.97%, match 91.90%"

 /annotator="blatX"

 CDS complement(439401..441035)

 /gene="ccmFn"

 /annotator="blatX"

 /translation="MSIYELFHYSLVPGLFIAFTYNKKQPPAFGAAPAFWSILLSFLG

 LLFCHIPNNLSNYNVLTANAPFFYQISGTWSNHEGSILLWCRILSFYGFLLCYRGRPQ

 SHNVSKRGGHRESLLFSFVLNFVKNSILSLPRYEQKSRVLHEPQLYTLFVLRTLVDSE

 LCSREGKRTHPLLHLARDDKERASSIDEQRIDGALGIAFFFFLFLSASSDPFVRNFFV

 RTEPLAESNPVPQDPILAIHPPCIYAGDVASAMGFGLCRSKMMNGIVALHSPPMRKDA

 AEKNGTLLCSAGCGGSRITSGLFALQFKHVGAKCYPALLLRSKRSLLMLLRRRFFAFS

 SLWTRALVDTGRGRAKRFFRNGKKKTTTLPLCWTAGANTVVSDQDQEPIRIWILTCRC

 FLTVGILPGSWWAHHELGRGGWWFRDPVENASFMPRVLATACIHSVILPLLHSWTLLL

 NIVTFLCCVLGTFSIRSGLLAPVHSFATDDTRGIFLWRFFLLMTGISILLFSQMKQQA

 SVRRTYKKEMVVARSTLVHLRHLARARPRPLMLWKN"

 gene complement(452694..452766)

 /gene="trnC-GCA "

 /info="blatN\_hit trnC-GCA\_NC\_035618.1, position 1 - 73,

 psl score 100.0, coverage 100.00%, match 100.00%;

 blatN\_hit trnC\_NC\_041093.1, position 1 - 73, psl score

 100.0, coverage 100.00%, match 100.00%; merged"

 /annotator="blatN"

 tRNA complement(452694..452766)

 /gene="trnC-GCA "

 /annotator="blatN"

 gene complement(454737..454810)

 /gene="trnf-CAU "

 /info="blatN\_hit trnfM-CAU\_NC\_006581.1, position 1 - 74,

 psl score 91.9, coverage 100.00%, match 91.89%; blatN\_hit

 trnfM-CAT\_NC\_020455.1, position 1 - 74, psl score 93.3,

 coverage 100.00%, match 93.24%; blatN\_hit

 trnM-CAU\_NC\_035618.1, position 1 - 74, psl score 100.0,

 coverage 100.00%, match 100.00%; blatN\_hit

 trnM\_NC\_041093.1, position 1 - 74, psl score 100.0,

 coverage 100.00%, match 100.00%; merged"

 /annotator="blatN"

 tRNA complement(454737..454810)

 /gene="trnf-CAU "

 /annotator="blatN"

 gene complement(455188..456554)

 /gene="rrnL"

 /info="blatN\_hit rrnL\_NC\_035618.1, position 1988 - 3354,

 psl score 100.0, coverage 40.76%, match 40.76%"

 /annotator="blatN"

 rRNA complement(455188..456554)

 /gene="rrnL"

 /annotator="blatN"

 gene 466222..466295

 /gene="trnN-GUU"

 /info="annotated by ARAGORN v1.2.38, score: 120.5"

 /annotator="ARAGORN"

 tRNA 466222..466295

 /gene="trnN-GUU"

 /annotator="ARAGORN"

 gene complement(466906..466980)

 /gene="trnR-ACG"

 /info="annotated by ARAGORN v1.2.38, score: 115.9"

 /annotator="ARAGORN"

 tRNA complement(466906..466980)

 /gene="trnR-ACG"

 /annotator="ARAGORN"

 gene complement(470732..471641)

 /gene="trnA-UGC"

 /info="annotated by ARAGORN v1.2.38, score: 111.0"

 /annotator="ARAGORN"

 tRNA complement(join(470732..470767,471605..471641))

 /gene="trnA-UGC"

 /annotator="ARAGORN"

 exon complement(470732..470767)

 /gene="trnA-UGC"

 /annotator="ARAGORN"

 /number=2

 intron complement(470768..471604)

 /gene="trnA-UGC"

 /annotator="ARAGORN"

 /number=1

 exon complement(471605..471641)

 /gene="trnA-UGC"

 /annotator="ARAGORN"

 /number=1

ORIGIN

 1 TTCCTTAAGG TCTCCGGCTA AGCTGACTTC CAGCGGTAGC GAAATAGGAC TGCTTAAGCT

 61 AAAGGAACTG TTTTCTTTAT TGACTTTGTG AATCCAATAG AATAGATAAT CTAAGGTAAT

 121 CCGAGGATAA GTTTGATCTA TTGTAAGGGG CGAAGAGACA AGCATCGAGA ATTTCTGCGA

 181 AGAGGAGAAG AGACAAGTCT AGTATAGACG CCGGAAAGAA GAGCCAAGTA ACGTTGATAG

 241 ACGAAGGGGC GAAGAGCTGA TTAAATAAAG GCTAAGGAAG AAGAGTCCTA ACACCTGCTA

 301 AAAAGAATAT GGATTCCCCC TACAGGGCGC CGTCCTTGGC AACGCAGCAG ACAGTTCCTT

 361 TAGTGCATTA GACCTGGTCG ACCGGAGGTG CTTTCAGGAG TCTGAGTTCC AGGAATAATG

 421 AATAAAAGAC AAGACTGCCG ATTCCCCTTT AAGTAAGCCA CTCTAGTTTC AGTTTTCACT

 481 TTAACAGTTT GTAGTTCAAA TTCTCTAGGA CGCCTTAAAA GAAAAAGACC ACCCATGCGA

 541 GTATAATAAG ACGCCCTTCC AGGGCCTAAC CTTCTGGCTA AAGTTAAAGA ATCTGATCCA

 601 AAACTAGTCT TTTCTCTTCT TCTGAGGTGG AATAGGGAAC TCTTGACATC TTCTCTCTTT

 661 CTTCTGGGGT CTTAGGACCC ATATCAAGGC TTAGGCTTCC ACAGGAGTCT CTATAGGTTT

 721 ACAATTGCGC ATTTGGTATC GTTCAAGCAG CTAATGTAAG CCCGAGACAA ACAGTTGATG

 781 AGACACCATG TTTAGATTAG AAGAGTATAT TGGAATTGTA TAGAAGTGGA GCTTTTTCAC

 841 TTAAAGAAAG GTTTCTCTTA CTAATGTCAG CTTCCCCCGC CCGCGCAAGA GGTATAATTG

 901 ATAATATGTC GAGTCTATCC CATTATTTAT CTTCCCTTCG GCACTAGGAT CAGTGAGAAA

 961 AGCCCCAGCT TCTGTATATA AAGAATCAAT CCTGTTCTTA CCAGTCCTGT GTTTGTTTCA

 1021 AAGCAGCAAA AAAAGAATGA GTATTGCCAT TCCCTAATTG AAACCAATCC ACCCGGCGTC

 1081 TATACTAGAC GCTACTGACT CTAAAGATAC TGAGCCCTAC TTAGTTATTC AGCTCTTCGC

 1141 TTAAAAGTCT ATCAACTGGG TTCTTCAATA CCTTCGTCTA TCGACGTTAT TCAGGTCTAA

 1201 AGCCTCTGGG TCTAACGACC TTTCACTTCA GTCTTCGCAT AAAAAATCAT AAGAGAATCA

 1261 ACGTACGTAG ACTTAGCTTC ATAATGCCTA ACGGCGAAGG GAAGGTAGAC ACAAGCCGAA

 1321 GGCGCAGTAT CTACTTATGG TTGGTTCATA TTCTACTTTC TTTCATAAAA TCGAATCGAC

 1381 AAAGAATGAT TTACGAACAG AAAATCGTAA ATTAGAAATC AATTAGTGTT AGAAGAATGA

 1441 TATACTTACT CTGTTATGTT CGAAGCCTTC CAACAGTATG TTTTCCCTTT TCTTTTTGGA

 1501 AAAGAGTACA GCCTTTTGTT TCTATTTGCC TTATTTCCTG GTTGGAAAAC CCGACCGGTG

 1561 ATTTCTGACA AGTCTTTCTT CATTTCTCGA GAGAGCAGAG CAGTCAAAGA ATGAACCAAA

 1621 TGATTGTAAA ACTCAAAATC CTGTATTCCC TTTTTCAAGA CGCAGCAACA CCTATGATGC

 1681 AAGGAATAAT AGACTTACAT CATGATATCT TTTTCTTCCT CATTCTGATT TTGGTTTTCG

 1741 TATCATGGAT CTTGGTTCGC GCTTTATGGC ATTTCCACTA TAACAAAAAT ATTACTAAGT

 1801 TGGCGATTAA ATTTGCTATC CTCGTGTTCG TAGTTCTGAC TTCTCCGGTG ACTGTAGCTA

 1861 ATGCTTCTAG TTCCGAGGAG GCAGGCTTAC CTATTATGCC CTCGTCGCCG GTTCCGTCTA

 1921 TCTCAGAAAT GAGTGAAAAC TGGATTGAAA GGACGTATGG AGGCCAAGAG GAAGCATCTT

 1981 CTTCGGCTCC ACAAGCGGTC CCACAAGGGG TCAATGAAGA GCCCCCCCAA TTCGAAGTAG

 2041 AGCATTATTT ATTGAATGAT GAGATTAGAC GAGAGCAATT GTTTAATAGG CTACGCCTAC

 2101 AGTCTTTGGT GCATCCGGAT CTTGACATCG AGAATCTATT GTATTATCAA GTGGCGCTCG

 2161 AGAAAAAGAT AGAACGCTGT CTTATTCTGG ACGGCATTCC GTCTCAAAAG ATTCTAAATG

 2221 AATTAGCCTC CTTAAGGGGG ATTCTTTTTT CTCCTCGGGG TACTCCCCTA AAAGTGTCCA

 2281 CTTTGGCTCG CTATCTGCGA GAAATGGAAC AAAATGGAAT GCGTCAAGGC ATTCTTTACG

 2341 GTCGGGTTTG GAAAGCCATT CGGGAGTATG ATTTATTCAT TCATAGGTAA CTAAATCCAA

 2401 CCCCGCAAAG GATTGTTCAT GGAACTACTA TCGAGATTAT TCGGACCAGA TTTTCCAGTA

 2461 TCATCCTTAT GTTCATTGCT ATACCCGAAA CGTACAAAAT AGAGTAAATA TGGTAAAAAC

 2521 AAATGTAGTA GAGGTTGCAA AACTAGCTTA TCCGAGAATA GGGTTAGGGT TTTCTCCGCT

 2581 TCTCCCGAAA TGTGACCCTC CTGTACGACA AAACGTTGTA AGCCCGTTTC CCTTCCGGCG

 2641 TCTATACGCT ATTTGTCTCT TCGATACTGA GTCGTAAAAC GACGTTATTC AGCTCTGCCG

 2701 CTTCTGCGTC TCGTAGAGAC GCTGCGTCAT CGTGATGAGG CAACAAAGCG AATAAATAAG

 2761 TATAAAAAGA AGATAGGAAT CAGACACGAG GTTGTTTTTT CCAGCTATGA AAAATCCATG

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 473941 GAACCAGGTC ATGTATAAAT CTTCCTTTAT GAGATACCTT CTGAGTGACC TGACTCTTGT

 474001 GCATGAATTT CTCTGACAGA GGAACGTTTT AAGTAGTACT TTCTAGGTGC AAAGCATGCC

 474061 TTAACCTTCT CTCTCGAGTC TCCGAACCTC GGGTCCCCTG AAGCTGGGTT TTCCACTCTT

 474121 ATAGCTGAGC CGAATCCAGC AGTTCTTCTT GCTTTCGAAT CTTTTTCTTC TTCTTGAAAT

 474181 AGTAGCCTTA TATATATATA GAATTTCAAT TGGAATCAAT CTGATGCTTC TACTTTCACA

 474241 GAAGCTAGTT CCTTTTGGAT AAGCCTTTCA TTCTGCCCCT ACGCGGAGAC TTTCTATCCT

 474301 TAGTGAGTGA AAAGCTTCCC CTGTTAGGGT

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