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

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388381 GGGAAGGGGC TCTTCCTCCT CTAAACTATC ATTTCCTATG GATTCACTAA TCGGGGAATT

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431341 GTTAGCATCA CTGATATGAC TACTCTATTA ATAAAAAAGA TAGTGCAGCT AATGCAGCTT

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473401 ATCTTCGAAG GAAGATAAAG ACGTAAAAAA CATTCGGGCT AATCCCGTGT ACACCAAGAC

473461 ATCATCTGCC GTAGGTATAT ACATAAGATA ATGATTTCAA AACAAGAATA GGGCAGTTGG

473521 AGAAAGGGTT CCCTCGGGCA AAGACAGCCC CTCTAAGAGG TATCTTCTCT TATGAAACTC

473581 GAAAAAGAAC CATCCCTCTA TTCCCGACCT AACTTCTTAG AAATTCCCTT GAAAGTGGCC

473641 TTGAAACAGC TTTCTCATTC AGGAAAATAT CCTAAAACAT GGTGTAGCAA AGTCGACTTG

473701 CCCCCTTTTA TAGTCCTAAT ATAGTAAAAA AAATGAGACA GCCAAGGACA GCTTTCTTTA

473761 GATGCCAGCC TTATAGAAGA TGCGATTTAC TCGGCTCTCA TTAAGTCATT GAAAGGCAGG

473821 CTTTATCACA TGCTTTCAAA CAGGCACGAG TGTGAACCAT TCAAAGGATG CTCCGCAAGA

473881 GGAATATTAA GGATTCTTAG CTGCGGCCCC TGCTCTTAGC AAGCCCGGCG ATTGGGGGCG

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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