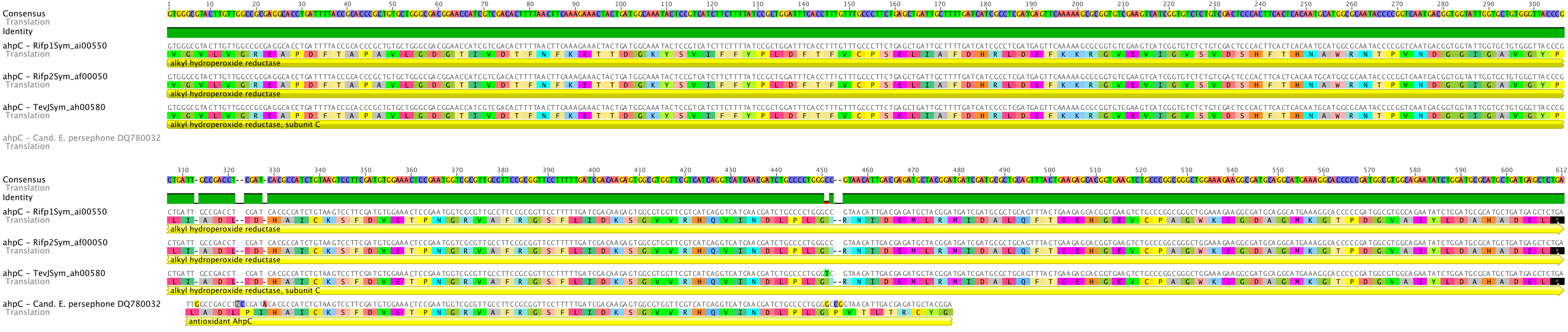


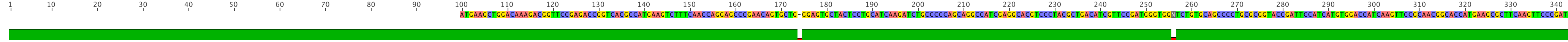
Genomic alignment visualization showing sequence identity and translation for various *aclA* genes across different species. The top part shows a consensus sequence from position 1 to 340. Below, individual gene entries are listed with their accession numbers and species names. Each entry includes the DNA sequence, the translated protein sequence (with amino acid single-letter codes), and a yellow arrow indicating the protein's length. Key proteins identified include ATP citrate lyase, alpha subunit and putative citryl-CoA synthetase large subunit. The alignment is color-coded to show conserved regions across the different sequences.

Genomic map showing gene models for aconitate hydratase/aconitase A across various species and contigs. The map includes coordinates (1-340, 350-680, 690-1020, 1030-1360, 1370-1700, 1710-1923) and sequence alignments for each gene. Species include acnA - Rfp1S1ym_bt00040, acnA - Rfp2S1ym_aa00030, acnA - TevjS1ym_az00150, and acnA - Cand. E. persephone DQ780135. The gene models are color-coded and labeled as 'aconitate hydratase/aconitase A'.



Genomic map showing the structure of the aprA gene across various strains. The map includes DNA sequence coordinates (1-330 and 340-660), protein translations, and consensus sequences. Key features include the adenylylsulfate reductase, alpha subunit and adenylylsulfate reductase, alpha subunit CDS. Strains shown include aprA - Rfp1Symb_ej00110, aprA - Rfp2Symb_bz00020, aprA - TevjSymb_ag00880, aprA - Cand. E. persephone DQ780257, and aprA - Cand. E. persephone DQ780256.

Consensus
Translation
Identity



aprB - Rifp1Sym_ej00100
Translation
ATGAAGCTGGACAAAGACGGTCCGAGACCGGTCACGCCATGAAGTCTTTCAACCAGGAGCCCGAACAGTGGCTG-GGAGTGCTACTCCTGCATCAAGATCTGCCCCAGCAGGCCATCGAGGCACGTCCCTACGCTGACATCGTCCGATGGGTGG-TCTGTGCAGCCCTGCGCGGTACCGATTCCATCATGTGGACCATCAAGTTCCGCAACGGCACCATGAAGCGCTTCAAGTTCCCGAT
V Q P L R G T D S I M W T I K F R N G T M K R F K F P I
adenylylsulfate reductase, beta subunit

aprB - Rifp2Sym_bz00040
Translation
ATGAAGCTGGACAAAGACGGTCCGAGACCGGTCACGCCATGAAGTCTTTCAACCAGGAGCCCGAACAGTGGCTG-GGAGTGCTACTCCTGCATCAAGATCTGCCCCAGCAGGCCATCGAGGCACGTCCCTACGCTGACATCGTCCGATGGGTGG-TCTGTGCAGCCCTGCGCGGTACCGATTCCATCATGTGGACCATCAAGTTCCGCAACGGCACCATGAAGCGCTTCAAGTTCCCGAT
M K L D K D G S E T G H A M K S F N Q E P E Q C W- E C Y S C I K I C P Q Q A I E A R P Y A D I V P M G G S V Q P L R G T D S I M W T I K F R N G T M K R F K F P I
adenylylsulfate reductase, beta subunit

aprB - TevJSym_ag00890
Translation
ATGAAGCTGGACAAAGACGGTCCGAGACCGGTCACGCCATGAAGTCTTTCAACCAGGAGCCCGAACAGTGGCTG-GGAGTGCTACTCCTGCATCAAGATCTGCCCCAGCAGGCCATCGAGGCACGTCCCTACGCTGACATCGTCCGATGGGTGG-TCTGTGCAGCCCTGCGCGGTACCGATTCCATCATGTGGACCATCAAGTTCCGCAACGGCACCATGAAGCGCTTCAAGTTCCCGAT
M K L D K D G S E T G H A M K S F N Q E P E Q C W- E C Y S C I K I C P Q Q A I E A R P Y A D I V P M G G S V Q P L R G T D S I M W T I K F R N G T M K R F K F P I
adenylylsulfate reductase, beta subunit

aprB - Cand. E. persephone DQ780034
Translation
GAGAAAAGCAACATGCGCAACATTTGTGCGTACTGAAAAGTGTGATGGCTGCAAGGGTCAGGACAGGACCGCTTGCATGTACACTGCCCCGATGACCTCATGAAGCTGGACAAAGACGGTCCGAGACCGGTCACGCCATGAAGTCTTTCAACCAGGAGCCCGAACAGTGGCTGGGAGTGCTACTCCTGCATCAAGATCTGCCCCAGCAGGCCATCGAGGCACGTCCCTACGC
E K C T M P T F V R T E K C D G C K G Q D R T A C M Y I C P H D L M K L D K D G S E T G H A M K S F N Q E P E Q C W G V L L L H Q D L P P A G H R G T S L R
APS reductase beta subunit

aprB - Cand. E. persephone DQ780033
Translation
AGTCTTTCAACCAGGAGCCCGAACAGTGGCTGGGAGTGCTACTCCTGCATCAAGATCTGCCCCAGCAGGCCATCGAGGCACGTCCCTACGCTGACATCGTCCGATGGGTGG-TCTGTGCAGCCCTGCGCGGTACCGATTCCATCATGTGGACCATCAAGTTCCGCAACGGCACCATGAAGCGCTTCAAGTTCCCGAT
S L S T R S P N S A G E C Y S C I K I C P Q Q A I E A R P Y A D I V P M G G S V Q P L R G T D S I M W T I K F R N G T M K R F K F P I
APS reductase beta subunit

Consensus
Translation
Identity



aprB - Rifp1Sym_ej00100
Translation
CCGCACCACCCCTGAGGGTCCCATCGACCCCTATGGTAATACGCCCGCAGCCGATATGGCCAAGATCGCTGAGCCTGGTTTCTTCAACCACAATCAGCAGAATGGCTACCGCGCTGGCGATCCCAGCGAGCTGATTTGCAAGTAA
R T T P E G S I D P Y G N T P A A D M A K I A E P G F F N H N Q Q N G Y R A G D P S E L I C K
adenylylsulfate reductase, beta subunit

aprB - Rifp2Sym_bz00040
Translation
CCGCACCACCCCTGAGGGTCCCATCGACCCCTATGGTAATACGCCCGCAGCCGATATGGCCAAGATCGCTGAGCCTGGTTTCTTCAACCACAATCAGCAGAATGGCTACCGCGCTGGCGATCCCAGCGAGCTGATTTGCAAGTAA
R T T P E G S I D P Y G N T P A A D M A K I A E P G F F N H N Q Q N G Y R A G D P S E L I C K
adenylylsulfate reductase, beta subunit

aprB - TevJSym_ag00890
Translation
CCGCACCACCCCTGAGGGTCCCATCGACCCCTATGGTAATACGCCCGCAGCCGATATGGCCAAGATCGCTGAGCCTGGTTTCTTCAACCACAATCAGCAGAATGGCTACCGCGCTGGCGATCCCAGCGAGCTGATTTGCAAGTAA
R T T P E G S I D P Y G N T P A A D M A K I A E P G F F N H N Q Q N G Y R A G D P S E L I C K
adenylylsulfate reductase, beta subunit

aprB - Cand. E. persephone DQ780034
Translation

aprB - Cand. E. persephone DQ780033
Translation
CCGCACCACCCCTGAGGGTCCCATCGACCCCTATGGTAATACGCCCGCAGCCGATATGGCCAAGATCGCTGAGCCTGGTTTCTTCAACCACAATCAGCAGAATGGCTACCGCGCTGGCGATCCCAGCGAGCTGATTTGCAAG
R T T P E G S I D P Y G N T P A A D M A K I A E P G F F N H N Q Q N G Y R A G D P S E L I C K
APS reductase beta subunit

Genomic alignment visualization showing consensus, translation, and identity for various protein variants (cbbM - Rfp1S1ym_at00130, cbbM - Rfp2S1ym_bi00210, cbbM - Tev1S1ym_aj00630, cbbM - Cand. E. persephone DQ780068, cbbM - Cand. E. persephone DQ780046) across a range of amino acid positions (1-730, 740-1,090, 1,100-1,464). The visualization includes DNA sequence, protein translation, and identity bars. Key protein names like ribulose-1,5-bisphosphate carboxylase/oxygenase and ribulose bisphosphate carboxylase are highlighted.

Genomic alignment and translation of dsrA gene variants. The image displays DNA sequences, protein translations, and protein identities for various dsrA variants. Consensus sequences are shown at the top of each section. Variants include dsrA - Rifp1Sym_am00340, dsrA - Rifp2Sym_aa00430, dsrA - TevJSym_aw00210, and dsrA - Cand. E. persephone DQ780148/DQ780147. Protein identities such as 'sulfite reductase, dissimilatory-type subunit alpha' and 'dissimilatory sulfite reductase, alpha subunit' are provided for each variant. The alignment shows high sequence conservation across the variants, with some partial sequences indicated by arrows.

Consensus
Translation
Identity

1 10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350

TTGCACCCCGTCTCAAGAAGAACTATGGCGCCTGGAGCTGGCATGATCGCCCGCGTCCCGGTGTGCTGCATCACGTTGCCAAGAGCGGTGACGAAATCTGGACCGTTCGCGCCGGTACCCAGCGTCAGATGGATCTCTTTACCATCCGCTCTGCTGATGGATATCGCCGATGAATTTGCTGAAGGCTATGTGCGCTTCACCAATTCGCTCCAACATCGAGTTTCATGGTGAGTGAGGAGTCCAAGGTTCAAGCCCTGATTGACAAGCTGACCGAGCATGGCTTCCCGATCGGTGGTACCGGCAAC

dsrB - Rifp1Sym_am00350
Translation
sulfitreductase, dissimilatory-type subunit beta

dsrB - Rifp2Sym_aa00410
Translation
sulfitreductase, dissimilatory-type subunit beta

dsrB - TevJSym_aw00190
Translation
dissimilatory sulfite reductase, beta subunit

Consensus
Translation
Identity

360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710

TCCGGTCTCCATGATCTCTCACACCCAGGGCTGGTTGCACTGTGACATCCCCGGTACTGATGCGTCCGGCGCCGTGAAGGCCCTGATGGACGAGCTGATTGAGGAATACACCAAGGAAGAGATGCCGAACCGGGTTCGCATGACCCATCTCTGCTGCCAGATCAACTGCCGGTGGTCAGGGTGATATCGCGATCAACATTCAGCACACCAAGCCACCGCGGATCGACCACGACCAAGTGCCAAACGCTCTGCGAGCGTCCACCGTGGTGGCCCGCTGTCCGGTGGCCGCTATCCGTCTCGGATGGTCAACGGTAAAGCCCTCCCTGGAGATCGACGAGAAGAAGTGCATCTGCTGCGGT

dsrB - Rifp1Sym_am00350
Translation
sulfitreductase, dissimilatory-type subunit beta

dsrB - Rifp2Sym_aa00410
Translation
sulfitreductase, dissimilatory-type subunit beta

dsrB - TevJSym_aw00190
Translation
dissimilatory sulfite reductase, beta subunit

Consensus
Translation
Identity

720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1,000 1,010 1,020 1,030 1,040 1,050 1,060 1,071

GCCTGCTTCCGCTTGTCCGCGGATGCAGATCAACGATCCTGAGCACTCAAAGTTCGGATCTGGGTGGTGGCAAGAAGTCCAACGCCCGCTCCAAGCCGACCTCCACAAGCTGGTTGCGGCAGGCATCCCCAACAAATCCGCGCGTGGCCCGAGGTCTCTGCGGTGCTCAAGCAGATCCTCAATGCCTATAAGGAAGATGCCAAGGATTGGGAACGCATCGGTGAGTGGGCTGAGCGTATCGGCTGGTCTCGCTCTTTGAGAAGACCGGTCTGCGGTTCAACAAGTATCACATCGATAACTGGCGTGGCGGTCTGTTGCAACCTGAACGCTCTGCTCACATCCGTTTCTAA

dsrB - Rifp1Sym_am00350
Translation
sulfitreductase, dissimilatory-type subunit beta

dsrB - Rifp2Sym_aa00410
Translation
sulfitreductase, dissimilatory-type subunit beta

dsrB - TevJSym_aw00190
Translation
dissimilatory sulfite reductase, beta subunit

Genomic alignment visualization showing consensus sequences and translations for the *gapA* gene across four different strains: *Rifp1Sym_dp00070*, *Rifp2Sym_ar00120*, *TeVJSym_an00400*, and *Cand. E. persephone DQ780188*. The alignment is presented in two segments, with the first segment covering positions 1 to 380 and the second segment covering positions 390 to 1139. Each segment displays the DNA consensus sequence, the corresponding amino acid translation, and a green bar representing the identity of the sequences. The protein is identified as **glyceraldehyde-3-phosphate dehydrogenase**. The alignment shows high sequence conservation across all strains, with the *Cand. E. persephone DQ780188* strain exhibiting a distinct insertion of approximately 100 amino acids between positions 810 and 910. The protein ends with a stop codon (marked with an asterisk) at position 1139.

Genomic map showing consensus, translation, and identity for isocitrate dehydrogenase (NADP) and isocitrate dehydrogenase (NADP-dependent monomeric-type) across various species and regions. The map includes coordinates (1-370, 380-740, 750-1110, 1120-1480, 1490-1860, 1870-2320) and sequence alignments for each variant.

Genomic alignment visualization showing consensus sequences, translations, and identities for various genes across different strains. The top section (residues 1-210) includes:

- Consensus Translation Identity
- korA1 - Rifp1Sym_dm00080 Translation
- korA1 - Rif2Sym_br00160 Translation
- korA1 - TevJSym_az00290 Translation

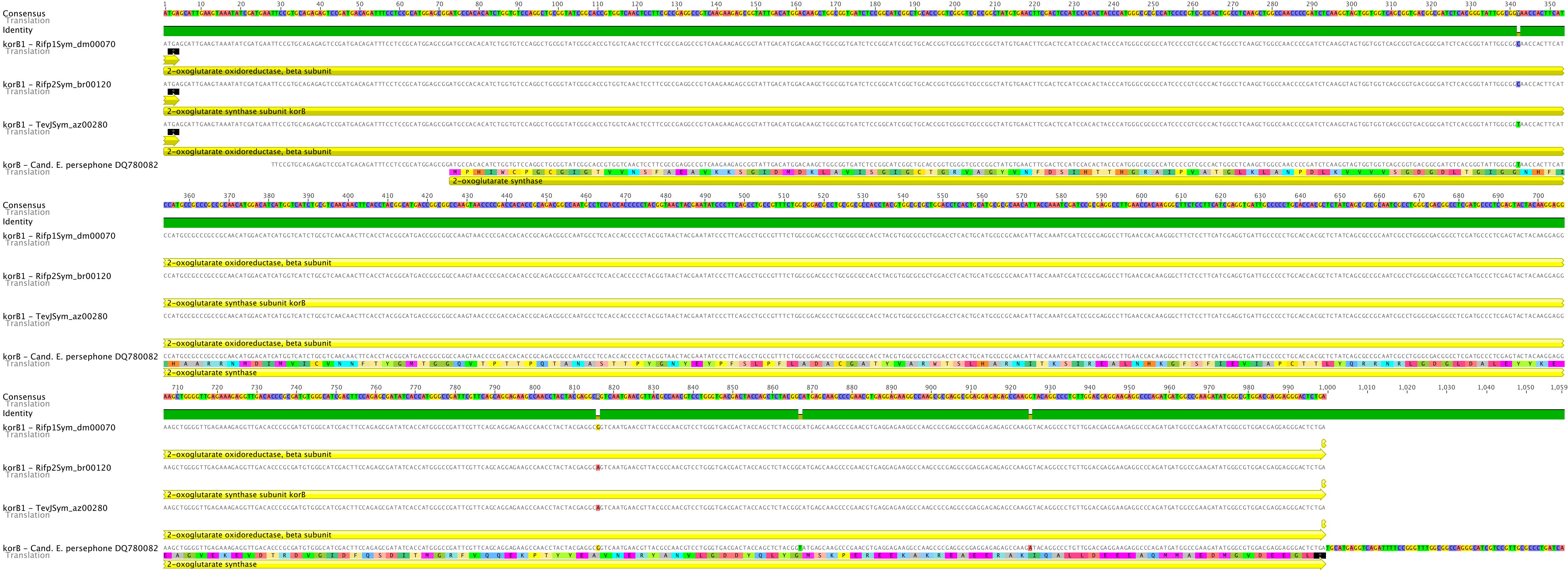
The middle section (residues 220-690) includes:

- porA - Cand. E. persephone DQ780126 Translation
- porA - Cand. E. persephone DQ780069 Translation
- korA1 - Rifp1Sym_dm00080 Translation
- korA1 - Rif2Sym_br00160 Translation
- korA1 - TevJSym_az00290 Translation
- porA - Cand. E. persephone DQ780126 Translation
- porA - Cand. E. persephone DQ780069 Translation

The bottom section (residues 700-1386) includes:

- Consensus Translation Identity
- korA1 - Rifp1Sym_dm00080 Translation
- korA1 - Rif2Sym_br00160 Translation
- korA1 - TevJSym_az00290 Translation
- porA - Cand. E. persephone DQ780126 Translation
- porA - Cand. E. persephone DQ780069 Translation
- porA - Cand. E. persephone DQ780126 Translation
- porA - Cand. E. persephone DQ780069 Translation

Annotations include gene names (e.g., 2-oxoglutarate oxidoreductase, alpha subunit; 2-oxoglutarate synthase subunit korA; pyruvate:flavodoxin/ferredoxin oxidoreductase N-terminal) and alignment markers (arrows) indicating sequence matches and gaps.



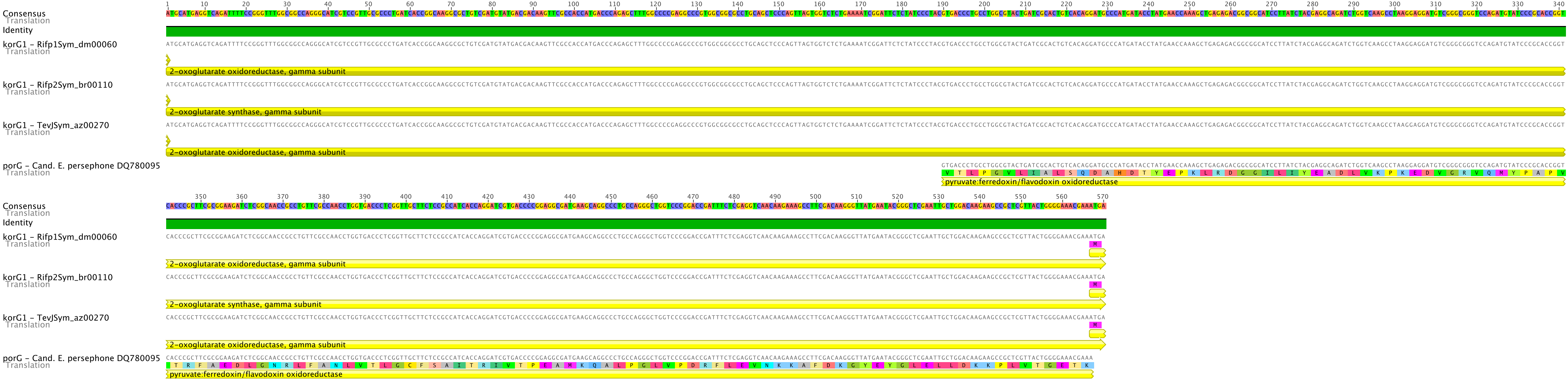
Consensus
Translation
Identity

1 10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 261
ATGGCATT CGGCAAAATCAAAGAGATCA CCGGC GTTGTCA CCA TCAA CAAGTCTTGGTGCAAGGGA TCGGGCTTCTGCGTCAATTA TTGCCCGA CCGA TGCCCTCGCCA TGTCA TCTGAA TA TAA CGCCAA GGA TA TCA TCCCCCGTT CGTCAAATCGCCGGA TGA TTGCA GGAA TTGTGA TTTCTGCCA GACGA TCTGTCCGGAA TTCGCCA TTTACGTCA CCCGCAAGGC GGAA CAAGA GGAGAA TGAGAA TCGGTAA

korD1 - Rifp1Sym_dm00090
Translation
M A F G K I K E I T G V V T I N K S W C K G C G F C V N Y C P T D A L A M S S E Y N A K G Y H P P F V K S P D D C R N C D F C Q T I C P E F A I Y V T R K A E Q E E N E N A *
2-oxoglutarate oxidoreductase, delta subunit, putative

korD1 - Rifp2Sym_br00140
Translation
M A F G K I K E I T G V V T I N K S W C K G C G F C V N Y C P T D A L A M S S E Y N A K G Y H P P F V K S P D D C R N C D F C Q T I C P E F A I Y V T R K A E Q E E N E M R
2-oxoglutarate oxidoreductase, delta subunit, putative

korD1 - TevJSym_az00300
Translation
M A F G K I K E I T G V V T I N K S W C K G C G F C V N Y C P T D A L A M S S E Y N A K G Y H P P F V K S P D D C R N C D F C Q T I C P E F A I Y V T R K A E Q E E N E M R
2-oxoglutarate oxidoreductase, delta subunit



Consensus Translation Identity
1 10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260
GTGGAA TC GA TC CC CAC CCT G CA TCC CG GT G GAA A GAA T T T T GA G GAA GA TAA GAT GAA GA TA CGT GC G CAA A T T G C CA T G G T C C T G A A C C T G G A C A A G T G C A T C G G C T G C C A C A C T G T T C G G T G A C C T G C A A A A A T A T C T G G A C C A A C C G A A A G G G T G T G G A G T A C G C C T G G T C A A T A A T G T A G A G A G T A A A C C C G G C A T T G G T T C C C T A A G A A C T G G A A G A T C A G G A A A T G G A A G G C G G C T G G G T T A A G A A A A T G G C A A

narH - Rifp1S1ym_ak00450 Translation
respiratory nitrate reductase 1 beta chain

narH - Rifp2S1ym_bt00090 Translation
respiratory nitrate reductase 1 beta chain

narH - TevjS1ym_ag00790 Translation
respiratory nitrate reductase beta chain

narH - Cand. E. persephone NZ_AASF01001412 Translation

Consensus Translation Identity
270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530
GCT GGA GCTCAA GGCCGGTGGTCGTA TCAGCAA GCTGCTGAACTCTTTGCGAA CCGTGA CATGCTGAGATCGACGACTACTACGAGCCGTTGATTA CGATTAACGCGAAATTGCA GAA CAA GCCCTCTGCTCA GAGCGGCCCACTGCA CGCCGCTCTCCAGATCA CCGCTGACGGGATGGA GAA GATCCA TTGGGGCCCTAAC TGGGAA GATGATCTGGCCGGCCGCTTGAAGATCGTTCAAAGGA CAA GAACTTCGAGGGCA

narH - Rifp1S1ym_ak00450 Translation
respiratory nitrate reductase 1 beta chain

narH - Rifp2S1ym_bt00090 Translation
respiratory nitrate reductase 1 beta chain

narH - TevjS1ym_ag00790 Translation
respiratory nitrate reductase beta chain

narH - Cand. E. persephone NZ_AASF01001412 Translation

Consensus Translation Identity
540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800
TCCAGAA GCA GATGTA CAA GGAGTTTGA AAAA CTTTCCACATGTA CCTGCGCCGCTTGCA ACCATG CCGTGAATCCGGCGTGTGTCG CCA GTTGCCTTGGCGCCATCTACA ACGGTGACGAGGA CGGCGCGGTA CTAATCGA TCAGGATCGCTGCCGAGGCTGGCGGATGCGGTCA GTGCGCTGCCATAA GAA GATCTA TTCAA CTGGGAGCTGGCAAGTCGATCCTCTGCTATCCGCGCATCGAGTCT

narH - Rifp1S1ym_ak00450 Translation
respiratory nitrate reductase 1 beta chain

narH - Rifp2S1ym_bt00090 Translation
respiratory nitrate reductase 1 beta chain

narH - TevjS1ym_ag00790 Translation
respiratory nitrate reductase beta chain

narH - Cand. E. persephone NZ_AASF01001412 Translation

Consensus Translation Identity
810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1,000 1,010 1,020 1,030 1,040 1,050 1,060 1,070
GGCATGCTTACCGCTTGGCCGATCGCTCTGTGGCCGATCCGTTATGGCCGGTGGCTTACGATGCTGACAA GATGACCGATGGCGGGGCACTGCAATGAGAA GAA CCGTATCAGTGGCAGCTGACATGTTCCCTGCA CCCCAGATCCGGCCGCTATTA GGCAGGCGCTGGAA GATGGCATTCGGCAACA TGGTTGGATGGGCTAAA GATCCCCAGTCTACAAGATGGCCATGGAGTGGAA GATGCCCTTCCGAT

narH - Rifp1S1ym_ak00450 Translation
respiratory nitrate reductase 1 beta chain

narH - Rifp2S1ym_bt00090 Translation
respiratory nitrate reductase 1 beta chain

narH - TevjS1ym_ag00790 Translation
respiratory nitrate reductase beta chain

narH - Cand. E. persephone NZ_AASF01001412 Translation

Consensus Translation Identity
1,080 1,090 1,100 1,110 1,120 1,130 1,140 1,150 1,160 1,170 1,180 1,190 1,200 1,210 1,220 1,230 1,240 1,250 1,260 1,270 1,280 1,290 1,300 1,310 1,320 1,330 1,340
CCA TCC TGAGTTCGCA CCGTCCGCA TGA TGTGGTACGTGCCGCGTGTGCGCCGTCGACAGTCA GATCGATCAGGGCAA GCTGCCACCGAA CGGATGGCGGATCCG-AA GTCGCA GCGCTGGCGTTCCCGTACCGCTAT-CTGGCCAA CCGTGTGACCGCTGGTGA TGA GGCAGCGATCCCTCA GTGCCCTCAA--CAGAATGCTGGCGATCGCGAGCAA TCAGCGCTCAA GTCGA TTGAA GGCAAGCCGAA TGTTCGGCA

narH - Rifp1S1ym_ak00450 Translation
respiratory nitrate reductase 1 beta chain

narH - Rifp2S1ym_bt00090 Translation
respiratory nitrate reductase 1 beta chain

narH - TevjS1ym_ag00790 Translation
respiratory nitrate reductase beta chain

narH - Cand. E. persephone NZ_AASF01001412 Translation

Consensus Translation Identity
1,350 1,360 1,370 1,380 1,390 1,400 1,410 1,420 1,430 1,440 1,450 1,460 1,470 1,480 1,490 1,500 1,510 1,520 1,530 1,540 1,550 1,560 1,570 1,580 1,590 1,600 1,612
CTGGAA TCTGTCGGGTTGA CTGA ACTGACGGCCGAGGAGATGTA CCA GATGCTCGGTATCGCCAACTA CGAGGA TCGCTCTGTTATCCCGACCGCCATGA GGAGA TGGTGCAGGAA GATCCCTATGCCTTCAGGGTCA GAA CCGATTTGGGCTGGCAA TACA GTTCA CCGTAGCGAGGCCGTCAGGGCTTACCCTGTTCCCGAGTCCCGGTAA ACGCA CCA TA CCCCGCA GGGCA TTAGCCCGCAA GAAGGGCTAA

narH - Rifp1S1ym_ak00450 Translation
respiratory nitrate reductase 1 beta chain

narH - Rifp2S1ym_bt00090 Translation
respiratory nitrate reductase 1 beta chain

narH - TevjS1ym_ag00790 Translation
respiratory nitrate reductase beta chain

narH - Cand. E. persephone NZ_AASF01001412 Translation

1 10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280

Consensus
Translation
Identity

narI - Rifp1Sym_ak00430
Translation
respiratory nitrate reductase 1 gamma chain

narI - Rifp2Sym_bt00110
Translation
respiratory nitrate reductase 1 gamma chain

narI - TevJSym_ag00770
Translation
respiratory nitrate reductase gamma chain

narI - Cand. E. persephone NZ_AASF01002040
Translation

misc

290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570

Consensus
Translation
Identity

narI - Rifp1Sym_ak00430
Translation
respiratory nitrate reductase 1 gamma chain

narI - Rifp2Sym_bt00110
Translation
respiratory nitrate reductase 1 gamma chain

narI - TevJSym_ag00770
Translation
respiratory nitrate reductase gamma chain

narI - Cand. E. persephone NZ_AASF01002040
Translation

misc

580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860

Consensus
Translation
Identity

narI - Rifp1Sym_ak00430
Translation
respiratory nitrate reductase 1 gamma chain

narI - Rifp2Sym_bt00110
Translation
respiratory nitrate reductase 1 gamma chain

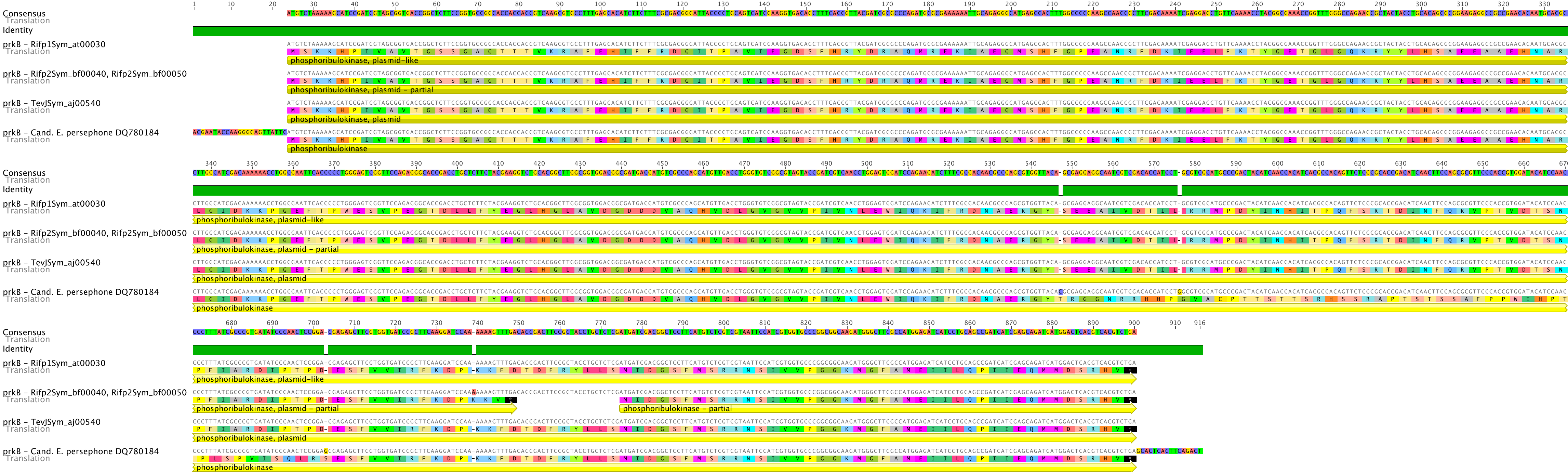
narI - TevJSym_ag00770
Translation
respiratory nitrate reductase gamma chain

narI - Cand. E. persephone NZ_AASF01002040
Translation
hypothetical protein

misc



Genomic map showing consensus sequences, translations, and identities for various genes (nosZ) across a range of positions (1 to 280). The map includes multiple entries for nosZ from different sources (e.g., nosZ - Rifp1Sym_ag00460, nosZ - Rifp2Sym_au00130, nosZ - TevjSym_ac00130) and their corresponding protein products (nitrous-oxide reductase). Consensus sequences are shown in green, and translations are shown in yellow. The map is divided into segments of 100 positions each, with positions 1, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280 marked at the top. Consensus sequences are also marked at 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, 920, 930, 940, 950, 960, 970, 980, 990, 1,000, 1,010, 1,020, 1,030, 1,040, 1,050, 1,060, 1,070, 1,080, 1,090, 1,100, 1,110, 1,120, 1,130, 1,140, 1,150, 1,160, 1,170, 1,180, 1,190, 1,200, 1,210, 1,220, 1,230, 1,240, 1,250, 1,260, 1,270, 1,280, 1,290, 1,300, 1,310, 1,320, 1,330, 1,340, 1,350, 1,360, 1,370, 1,380, 1,390, 1,400, 1,410, 1,420, 1,430, 1,440, 1,450, 1,460, 1,470, 1,480, 1,490, 1,500, 1,510, 1,520, 1,530, 1,540, 1,550, 1,560, 1,570, 1,580, 1,590, 1,600, 1,610, 1,620, 1,630, 1,640, 1,650, 1,660, 1,670, 1,680, 1,690, 1,700, 1,710, 1,720, 1,730, 1,740, 1,750, 1,760, 1,770, 1,780, 1,790, 1,800, 1,810, 1,820, 1,830, 1,840, 1,850, 1,860, 1,870, 1,880, 1,890, 1,900, 1,910, 1,920, 1,930, 1,940, 1,950, 1,960, 1,970, 1,980, 1,990, 2,000, 2,010, 2,020, 2,030, 2,040, 2,050, 2,060, 2,070, 2,080, 2,090, 2,100, 2,110, 2,120, 2,130, 2,140, 2,150, 2,160, 2,170, 2,180, 2,190, 2,200, 2,210, 2,220, 2,230, 2,240, 2,250, 2,260, 2,270, 2,280, 2,290, 2,300, 2,310. The map also includes a legend for Consensus, Translation, and Identity, and a scale bar at the bottom.



Genomic map showing consensus translation and identity for various proteins (sdhA1, sdhA) across different strains (Rifp1S1, Rifp2S1, TevJ1, Cand. E. persephone) and their putative functions (succinate dehydrogenase/fumarate reductase, putative fumarate reductase flavoprotein subunit).

