



Neighbour joining tree from Clustal Omega distance matrix of ORF-lacking introns in *Ostreobium quekettii* mitochondrial and chloroplast genomes, and MAFFT alignments corresponding to clusters.

cox31_II 778 --- TAA --- ----- GATTTGTTTCGAAGC
nad22_II 850 GCTTCC --- ----- TTTCCTTTGAGGAA
nad41_II 649 --- TTTTCC --- ----- CTTCCCTTCCAGCAA
nad44_II 2585 TTTTCCGAGGTTAGCGGAGCTAGCGTGGTTATCGTGCATAGCGCACGATAACGTGATAGTTGGCCCTAGGGCGTTAGCCTTGACGGTATCGCTGCGAAGCGG

cox31_II 799 GTC -----
nad22_II 876 GCG -----
nad41_II 688 GCG -----
nad44_II 2695 AACCTTCGGCTTCCATTAGCAACACGCAAGTCTAGCAACCTTCGGTGGCTGGCGAAGTATGTTATACAATACAATTCAATGGTTAGGTAGCGGGGGTTCTTCCT

cox31_II 802 -----
nad22_II 879 -----
nad41_II 691 -----
nad44_II 2805 CGATGCTCATGCAGGTACCGCGAAGCTTAGGTTAACAAAAATGCTGTTAGGGCTAAGTGGCGAAGACCCGTAATACTCTTTGTAGAGGAAAGGGTCCAAGTCCCC

cox31_II 802 -----
nad22_II 879 -----
nad41_II 691 -----
nad44_II 2915 GTATCTCTTACGGACATATATAATTCACCGTCTTAGGTCATATTTTTAGTGTGATTAGGCTGGGGCTCTAGGAGCCGAAGGCTTTGGGAATGGAAGCCTTCG

cox31_II 802 -----
nad22_II 879 -----
nad41_II 691 -----
nad44_II 3025 CGGATCGGCTTACGACAGGTGCTTACACCGAAGCGAAGTTACAGGTTGAGAACCGGGAACCGAAGGCTACCGGGGCTCCGCTAGGCTTGGCGCTTC

cox31_II 815 -----
nad22_II 945 -----
nad41_II 691 -----
nad44_II 3135 GGTTCGGCTCTTACGACAGGTGCTTACACCGAAGCGAAGTTACAGGTTGAGAACCGGGAACCGAAGGCTACCGGGGCTCCGCTAGGCTTGGCGCTTC

cox31_II 815 -----
nad22_II 1025 -----
nad41_II 768 -----
nad44_II 3245 AACCTTCGGCTTACGACAGGTGCTTACACCGAAGCGAAGTTACAGGTTGAGAACCGGGAACCGAAGGCTACCGGGGCTCCGCTAGGCTTGGCGCTTC

cox31_II 815 -----
nad22_II 1135 -----
nad41_II 825 -----
nad44_II 3320 GGTTCGGCTCTTACGACAGGTGCTTACACCGAAGCGAAGTTACAGGTTGAGAACCGGGAACCGAAGGCTACCGGGGCTCCGCTAGGCTTGGCGCTTC

cox31_II 846 -----
nad22_II 1215 -----
nad41_II 875 -----
nad44_II 3430 CGACGCCCGCTCAGCGGTTGCGGTTTCCCGGTTTACCTTGTACTCGGTTGGCGTCCCGCTGTAGCAGGCTCCACAAGGATAGTTTAAAGGACGCTCCACCTATTGT

cox31_II 846 -----
nad22_II 1215 -----
nad41_II 875 -----
nad44_II 3540 TAAAGCAAAGTTACGCGCGTCAAGCATCGAACATTTTCAGCTGGCTTCGCAAGCGAAGCCACTCATAGGTTGTAAGCTTTAGAAAATCGCGAGCATGACTTGT

cox31_II 846 -----
nad22_II 1215 -----
nad41_II 875 -----
nad44_II 3650 CCGCCAGATTGTCATGCTGTTTCTCGGCATCTCTTCTTACGCAATGACTGATAACCGGAGCGGGGAGCGGGTAAGTCGACGGTTGACGTACCGCGGTAGCAAAA

cox31_II 872 -----
nad22_II 1247 -----
nad41_II 904 -----
nad44_II 3760 GACGGGTACGAATGACGTGAGTTACCTACTCTGATCTATGCAATAGATCGATAACCGGAGCGGGGAGCGGGTAAGTCGACGGTTGACGTACCGCGGTAGCAAAA

cox31_II 872 -----
nad22_II 1247 -----
nad41_II 904 -----
nad44_II 3870 CTGCCCGCTGGGCAATCGATCTCAAGCGCCTTCTTCGTTGCTTGGAAATGGGGACCCGCTTGGTGTATTGATTGTAACCGGAGCGCTCCGAAAGGTTGATGG

cox31_II 872 -----
nad22_II 1247 -----
nad41_II 904 -----
nad44_II 3980 TGTGGTCCCAATGGGGGACCCAAAGCCCGAGGCTGAGGCTCCGATGCTCAAAAAGCTTCGTTTATATCTATTAACGAGCCACAGATCTGCAAGGCT

cox31_II 896 GAGAG -----
nad22_II 1286 GAGAG -----
nad41_II 937 GAGAG -----
nad44_II 4090 GAGAGGGAAGCCCTGGGGGCTTGGTCAAGACTTCCTCGTACCCGGAAGCCCTTGCTTGAATTTCTTGCATCTCAATACGACGTTACTCTGCTCGACGCCGA

cox31_II 901 -----
nad22_II 1291 -----
nad41_II 942 -----
nad44_II 4200 AGTATAAATCTGTATTCTTGGCGAAGCTCGGGCTTGTATTATGATCTCTATGAGTGGGGTTAATTATAATCTTGAAGAGCCGCTGATAGCCACTATCTTGC

cox31_II 940 AAGTTCGGCGAGGCTGAGTATGAGC -----
nad22_II 1330 AAGTTCGGCGAGGCTGAGTATGAGC -----
nad41_II 981 AAGTTCGGCGAGGCTGAGTATGAGC -----
nad44_II 4310 AAGTTCGGCGAGGCTGAGTATGAGC -----

cox31_II 967 -----
nad22_II 1357 -----
nad41_II 1009 -----
nad44_II 4420 CCTTTGACGCTTTGACGACCAAGCGCCTTAGGCTTTATAGCGGGCAGCCTTACAGGCTGTCCACGGGCCTGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCT

cox31_II 1007 GCGAACTTCCACTCG -----
nad22_II 1401 GCGAACTTCCACTCG -----
nad41_II 1042 GCGAACTTCCACTCG -----
nad44_II 4528 CTAAATTTGACGCAAA -----

Group 3:

cob1_II 1 GTGTGCCGTTGGTCAACCATCCGTTGTAGGCTATCAGGCTACGTATGAAAAGGCTCTAACCTGCATAGGACGACCAAAGGCGAAGGGCTGCAGGGTA
nad2I_II 1 GTGCGCCGTTGAGGCTA-TATCCGTTGTAGG-----AACCAAAAAGGCTCGCTCTAACCTGCATAGGACGA-----

cob1_II 101 ATCGTGGCGACCTGCACGATTTACCCCTAGGGCGGAGCGGTGTGCTTCGCAACCGGTTAGCTTACTGAGCAAGCGAAC TAGTAAATACCTGTGCGCGA
nad2I_II 70 -----ACGTTG@CCCC-----

cob1_II 201 CTAGGCGCAAAAAGGGGCGAAAGGTTGCGAAGCACCTACAGCCGAAGGCCCTCGTGCAGATGCAATGAAATGCACTCGGATTTACGCGCCGGTAAACGAACG
nad2I_II 82 -----ACGATGCAGTAAATCAACTCGGATTTACGCGCCGGTAAACGAACG

cob1_II 301 CGTATAAAGCTCCGACGAGCCCACTTCGTGTGGCCTGTAAACATAGCTCTTGGGTGACTTGTCTACCTAAGGATGATGGATAAGATATGTCCAAGCTGGG
nad2I_II 126 CCGTATAAAGCTCCGACGAGCCCACTTCGTGTGGCCTGTAACTACCGTCTCGGGGCACTGTATCAACCTAGGCTGACGGAAAAGATAAGTGGATACTGAG

cob1_II 401 AAGGTTGACGAATCCGATAGACCGTGAACCGGTTAAACTGGACACCGCGCTGAGG-----AGGCGCGTCCGAGGGGACATCTGGCTATCTGA
nad2I_II 226 TAGGTCRACRAAGCCGAAACGCAAGTGAACCCCTTACAAAAGGTCGACCGTACCATCTTACATCGCGCGTGGCGGAGGGAATACTAGCTATCTGA

cob1_II 492 TATTTATGCGCGATAAACTTGTCTTACCCTCGGGTATCTATGTCTTGGCCTTA-----GAATATCACTTGGAAACAGGACACTGGC
nad2I_II 326 TAGGTCRACRAAGCCGAAACGCAAGTGAACCCCTTACAAAAGGTCGACCGTACCATCTTACATCGCGCGTGGCGGAGGGAATACTAGCTATCTGA

cob1_II 580 TGGATCCAGCCCACTATCGCCCGGAAAGGTCCTAACTTGGGAGTAAAGCTTCAACCAAGGGTATTCAAGTCCGTTGAGGAAAGGACAGCGAGG-----
nad2I_II 419 CCGTACTCAGTTTCAATATAGCTTGGGATCAATGCAACCAAGGAGTAAACCAACCGCCGACCAAAATAAGTGTCAAGCAAAATTAGGGAGGCGGAGG

cob1_II 673 -----AGCCGAGGCTCTTGGAAAGGAAACCTTCGCGGAAGCGGCAAGCACCGGCTTCAACCCGAAGGCCAGG
nad2I_II 519 CCTAATATATATATATAGTGGGAGGTTTATCCAAAGGGCTTCCGATGG-----TTCCGCGATTGCTTAAACAGCGGTGGTACTACATAGCCCTCGG

cob1_II 744 FCTTCAGACCGGGAACCTGCAGTTCCAAACCAACCGAAGCGGCAGGACCTACAGCGGCAACCGGTTAGCGCTACAGTCTTACGGAACCGAAAGGTCCT
nad2I_II 614 -----CAAAAGTTAGCAACCGCGGAGCCCGCAGT-TGGCTGGCCTAGT-----ATCTT

cob1_II 844 GCTTGGCGGTCTACGCGGACGCGCGCTCAGCGGTGTGCTTCGCAACCGGTAGCCCTCAACAGGCGAGCCCTTGCCTGCGTATCTCATCAGTGGT
nad2I_II 664 GCTTGGCGGCGAAGTGGCGG-----CTTCAGGGAACCTTACCCATCTGGT

cob1_II 944 GTGCGAATAGGGTGGTCACTCGAATGGGAACCTAACAACGGTAACCTGTTCGCTTGGTGTCCGCTTTCTCTTGA AAAAGCCAAAGGCCCTATGTCGA
nad2I_II 714 AAAACAAGAAGGGCCAAACA-----GTAAAGGAATTAACAACCAACCAAG-----GTCTAAGAAAAGTGCAGCGCCCA-----

cob1_II 1044 TCAACTTGAGTTGATGAGTGGCAAAATGTAACCTAGTGGCCCGATGGTTTCGAAATCAACTGCATCGAAAGTCAAAAGTGGTCACTCGCTCGTTCGTTGGC
nad2I_II 783 -----

cob1_II 1144 GAGCAACCCGTTCTGCTCGCTAACCGCTTCGCGAAGGGTTACTACAGCCCAAGGCTTGGCTCACAGCTTTTAAATGCACATCGCCCGAGAGGGTGC
nad2I_II 783 -----

cob1_II 1244 GCCGATAACGGTGGTTGGGGAGGACGGAGGCCGATAGGAGTGGGAGGAAGGGTCGCCCTTACTGCAAAATGTAGAAGCCGGAATGACCCGTACAAGCA
nad2I_II 783 -----

cob1_II 1344 ACCAAGATGGGCTAACCAAGTTCGGCCCTTACATAGGATAGACCAACCTGAACCCGGTGGTACTCTTGGCTTCGCGCCGGGTAAAAAGTGGCCCCG
nad2I_II 783 -----CTGGCCCTTATAGTACAAAGCAAAAGGTT-----

cob1_II 1444 CTAGTAACTATCGAATATACCTTGAATGACTTACGCTTGGTTTGGCCCAAGATTTACCAAGCGGCTAGTACAGCAAAATTTAAATTTGAGTGGGTC
nad2I_II 812 -----TAGCTAATTCAGCTCTACTTATATGTTTACAAATCTGAGTACCA-----

cob1_II 1544 CGCTTGTTTATATGATGGATAGCGAATCTTCGGGGGAAACAACGAAGGCBAAGCCGATTGCCCTTGGCTGCGCTAAGAAGCGCCAGGGGGAACGAACC
nad2I_II 857 -----GGGACAACGAGGATGCTATG-----ACC

cob1_II 1644 TAGTGAACAACCCCTGCTCGGTTAGGACTTCCCTTGGCTTGGCCGCGAGCCGAAAGGGCGGGGAGATGTCAGAAATCTGGGTCCGAGCGGTATG
nad2I_II 881 AGGCCGTTGGTCCCTTTAAATAAGCAAACTACCGCCGATCACTT-----AATCGGTTGATCTGGTGGAGAGCGTATG

cob1_II 1744 ACGGGCAACTGTCACTACAGTTCATAGGGCAGGCGCCACCCCTATGGGGTCTCTGACCCCTAC
nad2I_II 958 ACGGGCAACTGTCACTACAGTTCAGGGCAGTCA-----CGCTATTAATTAACCTGACCCCTAC

Group 4:

atp82_II 1 GTGGACCCG-----TTCCGGAGTGAAGC-----GTACGAAGTCGGCACTAT-----
cox18_II 1 GTGGAGTCCG-----TTCAATGCAAGACTCCGGACAAATTT-----CAGACCGAATCTGCACTATCT-----
cox32_II 1 TTGGGTCGCG-----TTGAGGCTGCAAGTTCCTATGTAACG-----CABAAGGAAACCGTGGCTCCGACGGACGGAC
rp161_II 1 GTGGACACAAAGTATGCCITGTATTTGCGCTTGAAGT-----ATAACG-----AAATATTAAGTAGCTGGGCAAT--TCGANA
nad11_II 1 GTGGACCCG-----TTCCGGATTAAGCAT--TNGCGAAATTTGACAGCGTGGCAACTGGATCTATATCGGGTCAACTC--CGGACA

atp82_II 46 -----TTATATGAAGCTGTATGCACTGAAGG-----TGTATGT-----
cox18_II 61 -----TGTATGTAAGTCTGCTTGTGAGGG-----TGTATGCGGTTG-----CGCAANNAGTGGTGG
rp161_II 71 AACT-----CCAGGGGAGTGAAGTGAAGTCAATGAGGG-----TGTGAATTCGGTTG-----CCCAATATGTCGACG
nad11_II 83 CGACTGCGGAGGCTCAGGCGAAT--ACTGAACCTTTATAGGAGATATGGCAAGTCGCTGAATTAAGCAAAAAGGTTTCAGTATATAGTAAATGACAAAT

atp82_II 79 -----CCATCCCGCTTGTAGAGGGGGTGAAGGACCCGACATATGAGGG-----ATGGCT
cox18_II 117 ATATACAA-----GCGCTCCCGCAAGAGGGGGTGAAGGCTTTCCGCAAGGCTTGGCTTCACTAGAAAG
cox32_II 135 AAACAA-----GCGCTCCCGCAAGAGGGGGTGAAGGCTTTCCGCAAGGCTTGGCTTCACTAGAAAG
rp161_II 177 GGTCCAGCAGCTCATCTTTTGGCCGGGCTTTTGGCAAGGCGTTCCCGCTGAGCAGCGAACCCGAGTCCATGTTCCACACCGTGA--ATGGCC
nad11_II 181 CATTTACAGGTGTAAAGCTTGGGTGTCGGGAAGACACAGGTTGTAAGCGGTAGGACCAACGGCGCTCAACATATATTAACAGGCGGAACGGGAGGTT

atp82_II 131 TTG-CCGG-----
cox18_II 185 AGT-CGAGCCAGCGCGGTGCTGACC-----
cox32_II 197 ACG-CTGGCCGCTCAATAAACC-----
rp161_II 271 GTAGCTCAAGCTTTTCAAGCATGTGACGCATCAAGCTTGACCTAATCAAATGTTAGCCGAGTCTGTCCGGAAGGCTATACGGCCACGCAAGTGTGGGCCCT
nad11_II 281 GGT-----CACTAGGTTTGCACCCGTTCCGTTCCGGCCGAA-----AGCGAAACAGCACCCGCT

atp82_II 138 -----CCACCGGTT-----CTGTGGC
cox18_II 208 -----CCCGGGGAGTGGG-----CCGAGGT
cox32_II 220 -----CAAGTCCGCGCT-----CTCGAGGT
rp161_II 371 GCGGCTGTACCGGCC-----CTGCTATAGCAGCCAGGCGAATGGCGCTTCCGGGGCAAAACCCGAGCACCCTACAGGGC--CCGGGT
nad11_II 337 TCGCCCTCGTCCCGCGCTGGCTTCCGAGGGTATCCTAGCAGTAAATGCTATGCTGT-----CGAACGTTTGTCCGGACCT-----TGTATCAGG

atp82_II 156 ATGAAAGCTGGCGTAAAG-----GATGAAAGCTCTTGGAAAATGAGGCTCGATGAA
cox18_II 231 GTGAAGCTGGCGTAAAG-----GATGAAAGCTCTTGGAAAATGAGGCTCGATGAA
cox32_II 242 GTGAAGCTGGCGTAAAG-----GATGAAAGCTCTTGGAAAATGAGGCTCGATGAA
rp161_II 457 ACGGGCCCGGCTTGAAGCATTTA-----AAATAGAAAATGCAACCCACAACTGTTTC--AGA
nad11_II 423 TTAGGGTGGGGTAGAGTGGGAATCAGCTGATGCCCTGGTTTGTAAAGCATTGATCGAGTATAGTAGAACTATGTTCAAACTCCGCTGC--ATA

atp82_II 208 TCTCCAGCAAAGCGGTGAT-----
cox18_II 283 TCCCAAGCAAAGGCGTGAAG-----CTCCGCCCCCGGGAGG-----TAGG
cox32_II 290 CTTCTAGCAAAGGCGTGAAG-----CTCGAGGGCAATGAGTATACACAACTCGAGGAGG
rp161_II 511 GCTCAGGCGGGGTTGTHACGCACTACTGAGTACCGCAAGTGTGGCGTAAAGTACTAGGCGCTAGTAGTAAATTAGTATTGACCTAAATAGGA
nad11_II 520 GTTGGCCAAAGTTCGGCGTG-----TTCAACCCCAATAAACC

atp82_II 231 GACTTTAAC-----TCTAAA-----CATAG-CACCT
cox18_II 320 -----CCGCATAA-CACCTCGA-----
cox32_II 346 MAGGTAAAT-----GCCAAACCATGAAATGTTTGTGTTGCTAAGCAAGCTTGGAGAGCTTACCGCATAGTGGCTCGT
rp161_II 611 ACGCGTGGGAACCCCATCGCTTCTCAGGGCGCTCTGTGAGAGGCGAAGCGGCTC-AGCGGTTCCGAAACCTGGTGTGGTGGAGGCCAGTATT
nad11_II 557 AC-----TAGGGCTC-AGCGTCCGCTTTHCA

atp82_II 256 -----AAAAGTCTACGATGGCT
cox18_II 337 -----AAGAGGCTTACCGATGGCT
cox32_II 427 -----AAGAGGCTTACCGATGGCT
rp161_II 710 CCGAGTCTGGGTAAACAATGAAAAAGGCGATTGTATAGTAAAGGATTTAGACCTAGTCCATCAACCTGCAAAAGCTAGGGCCACGAAAGAACCTAGCCG
nad11_II 586 -----GTACTGTTGTTATGTAAAAAGGGC-----CCGAAAGCCCTACGGGGCCGCTACTCA-

atp82_II 275 -----AAGCAATTGAGTGAAGTACCTCAA
cox18_II 357 -----AA-CRATTHAGTGAAGCTGATTA
cox32_II 447 -----AA-CGATTGAGTGAAGTGTCTCG
rp161_II 810 AACTATTCTTGCAGTTAGGTAGAGCTCCGCCCTAAAATCGTTGTATACAAGCATAAACTTGGTAAAGCCGCTTGGTGAAGAGCTCGATGGCCAAAGCGGT
nad11_II 640 -----GCAACCTGCCAACTTGTGAGCAACCCGACCGAGTGGTCG

atp82_II 300 -----TATGAGGCTTAGCGTATG-----NAGCANCGTAAATAGGAAAGCAGGGTT--
cox18_II 380 -----CCAAGGCGGCCCTTCCGGGAGAAGCTTAAACAAGAGGATGATTGCGAGT--ACGCCACCGTAATATCAAAACGGGTTG-
cox32_II 470 -----CCCAAAGCGAGCACCG-----AATG-----ATGGCCGTAAGCCGCAAGCAGGTT-
rp161_II 910 CCCCAGTCCCACTTGTGTTTTTTCTAGTTTCCCGCTGTGGGGA-----GACGCTAAGTTCGGTCTAAGTGAATTCGGCAACCTAGCAGC
nad11_II 681 -----GACGCTTGGCTGTTACCGGAAAGGCT-----GACGCTTGGCTG--CGGCAAGTAACTCCGTAANNAACCTCA-

atp82_II 344 -----TAATATTTCCGGTCCCAATTT-----TATACTTTTTCGAAAGTTTATT-----
cox18_II 457 -----CTAACTCTTCTGCTGAACTC-----
cox32_II 516 -----CCCCAATAGCTCAGCTTCGCAATGCG-----AGCAACCCGCGCCCC
rp161_II 1002 -----CTAAGTATAGCGCCGCTTAAGCCTTATATCATATATGATTCTGGAACAGGATAACCCCTTATGGAGTTCCTTCAGACCTAGCAGTTTGAAGTGA
nad11_II 751 -----

atp82_II 366 -----ATGGGAAGACCCCGCAACCGGAATATC
cox18_II 502 -----CGCTCCACCGCAACCGCAACCTTAACTTTGAGTTCGAAGACCTTCAATAGTTCAGAGACCCCGCTCCGGAATATC
cox32_II 516 -----GCTCCCAACAACAGCACTC-----ACCAACCGTCAATAGTATT
rp161_II 1046 TGCTCATCGGTTAG-GCCTTGGCTGGGACAGCGAAGCT-----G-----CGGGCTTGGGGCCGACCGGCGCA
nad11_II 845 GCTACGCTAGCGAAGCCCTCGTTCCTGCTCCGAGCGAACC-----CGAATCGAGCCCTGAGGTAAGGCAAG

atp82_II 395 GAG-----
cox18_II 581 GGA-----
cox32_II 555 GGA-----
rp161_II 1119 GGGGAGCCCTCCACCGAGAGGTAACCTACTAGTGGTGGCCGGTAACAGAGTTCGCCCCCTTTTTTGTGTTGACCTGTAAACCCCTTCGGGGACTCGG
nad11_II 916 GCA-----AAGTGCT-----TCGCACCTTCGTTTCTAGAACCTTCGGCTAAGCTTTGGGACCCGA

atp82_II 398 -----GAGGAGCCTGCGAGGGAT-----GCTATTTTCATAACCCCTCAAGTCTCATATGTTGCTCTCGGTGTA
cox18_II 584 -----CAAGGCTTAGCGATATG-----TGATATGCTAT--ATCCGTTTCTTGAAGTCCCTCGGTGTA
cox32_II 558 -----CAAGGCTTAGCGATATG-----ATATACCGG--ATATTTCTGTTACGTTGCTCGGCGTA
rp161_II 1219 CCGCTCGCTGTCTTAAATGATCGAG--CGAAGCTTAGCTTGTGCTGCTGATCAAGAGGACATGGGGCCCGCCGCTGAGGCGAGGAG
nad11_II 973 AGGCT-----TCGAAATAGTTACAGTTCCGAAACCGAAGCGGAGC-----CAAGAGAGG-----CACCGCTCCGCCCCCGGAGCT

atp82_II 460 TAGG-----AAGAGCTTCCGGTCTAA-----ATAGGTCGATT-----CGGAACGGGAAAGACCAAAAGATCTT
cox18_II 644 AAGAGCTTCCGGTCTAA-----ATAGGTCGATT-----CGGAACGGGAAAGACCAAAAGATCTT
cox32_II 617 AAGGA-----AAGAGCTTCCGGTCTAA-----ATAGGTCGATT-----CGGAACGGGAAAGACCAAAAGATCTT
rp161_II 1316 GCAACCGCGCAGGCTG-CGCGCGCAAGCTTGAAGNA-----AATCGTAGTTCGAAATTAACAACAATAA--CGGGCCGGTAGGAGCTCAG--
nad11_II 1053 AAGTTTGGCATAGCGCAAGTTCGGCTTCCATGCTAAAGGTTCTGCGCGGTTGCGAAGCAC-----GCGCT

atp82_II 521 CCT-----CCA-----
cox18_II 705 TGTAAGTGGG-----CAAGCTCGAAGAGGTCGCAAGGTCGCAAG-----CCG-----
cox32_II 679 TTCTGTAGTACCCCTCGTTATACCAAGTAAAGCGGGGCAACTTCAAGTGAAGTGGCAG-----ATGT-----
rp161_II 1402 -----GAAAGCGAGCTTCAAGCAAGCTAGTCTGTG--CGAAACGCCATCCGAGTATGAACCTCA
nad11_II 1123 GCG-----AARGACCGGCTTAGGGTGGGCTGCAAGCTAT-----

atp82_II 550 ATATCTCTGGGTAGTAGGATGAGATAAAAAGCTAATGCTCCTTGTAAATGAGGTA-----GATATGCTGACGTGTCTCCGGATCACATATAA-
cox18_II 751 ATGGCACTTGAAGTGTAGGATGAGGTAAGAAGCTAATGCCAATCTGTAATAGATGT-----GATAGCCACGTAACCTCCGG-----
cox32_II 744 ATGGCACTTGAAGTGTAGGATGAGGTAAGAAGCTAATGCCAATCTGTAATAGATGT-----GATAGCCACGTAACCTCCGGGTGGGCAAAA
rp161_II 1465 GTACCAATGGGGTAGAGGACACCTTAAAAGCGACTTTCCTAATAGGATCCGGCTTTCGCTAATATCCGTTTATTAAAGTTCTTGCTGTCTTATAGCTG
nad11_II 1162 ATACTCTAATGGGGCGGGAATTCGCAAAAAGCCAAAGCCCTGGTCAAAATACAGG-----GATATGCTGACATGGTCACTGAGAAATATGCA

atp82_II 637 -----
cox18_II 827 -----
cox32_II 832 AATTTTGTATATTTTATTAGCAGACGCMCTCGCCNCGCTCGATCAGACAATAATCAAGAGGCCACTGCCACGCCAFACTGAAT-----AAH-----
rp161_II 1565 GGTCCCTTTTGTGACACTATGCTCGGAAGCACCTAGGGCGTTTG-PATACACTAGCTATCGGGAACCGCCCGCCCTCCAGTACAAAATTAACCCAA
nad11_II 1250 GAACTAGCATGGGTCACGAACCTAGTGTAGTGACCAACCGCAATTTGTATTTCGCTAATACACAAAGCCCTCTTCGCTTCCGTTGCGAAGT-----

atp82_II 637 -----TCGTGCAAGAATGATACTGCCCAFAAG-----AGGGCTAAAMGACCTTTGAGTCAAG-----
cox18_II 827 -----
cox32_II 919 -----GHAAGAGTCCGATTTATGAGTGTTCACAAAGGCTTAACTACGG-----TGGCGACCAAGCTGGGGGGGCGCGA-----
rp161_II 1664 TTTACATAAATGGCCCGCATGAGAAATCAAGCCGAGGTCCTTGGGGCCACCTTCGCTTGTTCGCAACCGGAGACAGAGGGCGATTCCTAGTGT
nad11_II 1341 -----GCCCTGCTCGGCGGGGAAACATCTATGTAATCTCACACAGCTACAAGAACAC-----ATTCGGAGAACGAATAGATTAGG-----

atp82_II 688 -----ATCAGCC
cox18_II 827 -----
cox32_II 990 -----GCAAGCC
rp161_II 1764 CGCGCTCATCGTGC CGGGTAGAGCTAATTTAAATATGTTGGAATGGTTAATTGGTTGGAGTCTCTAGATGTTTATGCAGAAAAAGTTTCATATAAGCC
nad11_II 1424 -----ATAAGAA

atp82_II 695 AATTTAAT-----CATTAAGTCTGG-----ACATTAGTTGTGAGCAGAAACCCAAAGCC-----
cox18_II 827 -----AGGC-----ACATGCAAGGCGG-----
cox32_II 997 AATACACTTCGGAGGC-----GAAAGCCAAAGGCCCGGCTTGGCGG-----TCTCACGGCTAGGGCCGCCCTTCAGCGGTTCCTATAGCA
rp161_II 1864 GAAAGCTCTTAAACCTTAAACAATAAGCCCCAGATGCGCGGGTGACATTACTCGCCCTAGGGCCG-----GAGCTTTGCTGAGCCACACCCGG
nad11_II 1431 GCATCGTT-----

atp82_II 745 -----GACTTCAAGCCCTCTG-----
cox18_II 845 -----
cox32_II 1078 -----GACAGTCTCCCTTTGGGGGAGCCTTCGCCTT-----
rp161_II 1957 AGAGCGAGGGGTTCCCGGTTAATAACACCCGGGGTTTAACTGAGAAATCCCGGAATGGAGGGCCGTAACCTCTGATGCTGATGCTTATGTAGTGCAT
nad11_II 1439 -----

atp82_II 760 -----
cox18_II 845 -----
cox32_II 1109 -----GCACTCTCGGGGTAAACGAGCCCTTGGGTGTGCTC-----
rp161_II 2057 AAGGCGCGCAATCCAGGGTGAAGTCACTGGTAAACGTAAGCAACCTTATGATGCTCCGCCTAAGTGAACAGAGAGCAGTAAAATTTAATGCGCTCGG
nad11_II 1439 -----

atp82_II 760 -----
cox18_II 845 -----
cox32_II 1143 -----G-----
rp161_II 2157 TTGCAGACAATAAGATGATCTGCCAGTATATAATATAGCTAAATAGTTTACATTAGTCAGAGTATGACACAAAATGGTATTGGACCATTGGGTATCT
nad11_II 1439 -----GGCTAATT--ACCGAGTTGGGGTGAACACCTCAATGGG-----

atp82_II 760 -----
cox18_II 845 -----
cox32_II 1144 -----CITCGCTCGCTCCTGGTTATTCTGT-----GGCTC
rp161_II 2257 ATATCGAATGAGTCACTTGGGGTTGCACCTCAGGGTGCTCCTGGTAATCTTATTTTGAAGGCTCACCAATTAAGCGAGCCAGAATTAGCCAACCTGGGCT
nad11_II 1475 -----GTTGCTTGTAAACAAGCGAACCCCTTCGAAAATCT

atp82_II 760 -----
cox18_II 845 -----
cox32_II 1174 TCGTACTTTCN-----
rp161_II 2357 TCGCAGGTTGTTACGCGTACATTCACTTGTTCGTTGCTGCTCGCTTTTTAAAATAAAAAGCGGAATTCGGGGCGAAAGAAGCGCTTTTATTCGCAAGAA
nad11_II 1514 CCATAGATTGT-----TCAGATGCATAATAAGAAAAGCATGTCTTGGTGCAATAAGGGGAAGCGGTCC-CCAGTG

atp82_II 760 -----ANCCCTTATA-CGTAA
cox18_II 845 -----C-----
cox32_II 1185 AGCAAAACCCGAAAGGCTTCGAAGAAGTTACGGGTGCAAGACCCCTTCGGTCCCGCTCAGCTATGTAGCGCACGGCGGACCTACAGCTTCA-TAAGC
rp161_II 2457 TGCAGGCACCCATTACTATAAA-----AATATGCAATACGAAATTC

atp82_II 776 TCGGAGGAGCTGCAATGAAGGGAACCTTCACGTCAGTCTGAACAGAGGTAGTGGGGAGACCCGCTATCGNCAATAAC-
cox18_II 846 TCGGAGGAGCCGTATGACGGGAAACCTTCACGTCAGTCTGAATGGCGGTTAAGAGGGAGACCCCTTCGCCGACATAAC-
cox32_II 1198 CGCGAGGAGCCGTATGAGGGGAAACCTTCACGTCAGTCTGAATGGCGGTTAAGAGGGAGACCCCTTCGCCGACATAAC-
rp161_II 2556 TTGCTTAGACCCGTGAGGATAAAATTCACAGTACGGTCT-----TCGGGGGGGTTAAACCTATCCCAAC-
nad11_II 1628 TGAAGGAGCCGTATGAGGTAAAAGCCTTCACGTACGGTTTGAAGCCGAGCCATTTCAAGGATGCAAGGCTTAGGTTAAC-

Group 5:

atp81_II 1 CCGCGAGGTTT-----AACCAAGATGGATCGCTAFACTCCA-----TCATACATAAGGGTGGTGTAGACCAACCGCA
nad42_II 1 -GTGGCCCGTGTCCCTGCAGTTCGTTGGAACCAAGATCAACTGGCCGGTCTAAGGGCCCTTTCGGCTCGCTGGCA-----AGGGGGAGCTTGGCAA
rpl161_II 1 -GTGGCCCGTGTGGCTGATGCTCGTC-----GTGGGGAGCTTGGCAA-----GTGGGGAGCTTGGCAA

atp81_II 72 TCCGCTTCCGCTAGCCCTCATATGAA-----ATAGGGAGGCCCTAAAAGCAATGGGTGATTCGGTAGAC--
nad42_II 75 CCGGTTGGGACATAGGACCAACCTTGGCTCTTTCGCTGCTGTCGGCTTTTAAAAATAAAGCCGAMAGGGACCAACCGAGCCCTGGTAAACTA
rpl161_II 45 TCCGCTTCCGCTAGCCCTCATATGAA-----AGGACGCAAAAGAGTGTCTGATTAATGAG

atp81_II 143 -----GATGMAACTTCTATAAGGGGCTTCHAAAGGGGCAAGCTGTAG
nad42_II 195 CTTATCGAGCCTTCTCCACGCTCTAACACGACAGGTCCGATGAATAGTTCGGANAGGCGACCTTGAATAGGGTGGGTAGCTGCGGCGCATAG
rpl161_II 106 CT-----TGAGACACAGCCTGTCTAAAAGGGCGGAAAGCATCANGCAAAAG

atp81_II 188 GGGCAATGGGAAATTCAAAAAGCCGCTTCTCATACCGCACTAACTGGACTAATGGCGCTGTTGC-----
nad42_II 295 CAGCGAGTTAGC-----CAGGTC-----GGAGCACCCTGGGNAACGAGACCGACAGAAAGGTCACCGGGAAGACAC--GGGAT--
rpl161_II 156 ACACAGAGAGC-----GGGACCTTGAATATTCAAAGAGGCA--GGGACGATGATGACGAAAGCCAGCAATTTTC-----GATTAGC

atp81_II 260 ---TTTCAACATACGACAAACCGAAAGGGGGTCCAGACCTACGGGGCCACCCATTTTGNAGCCGCTCGGCCGCTCTCTGTTCTCCTCTGCTGA
nad42_II 379 ---CTCAGTATAGTACACCGAGG-----GGAGCACCCTGGGNAACGAGACCGACAGAAAGGTCACCGGGAAGACAC--GGGAT--
rpl161_II 238 CTTATTCAGTATAGTACACCGAGG-----GGAGCACCCTGGGNAACGAGACCGACAGAAAGGTCACCGGGAAGACAC--GGGAT--

atp81_II 356 GGC-----GCCAATCCAGGGACACGGATATCGCCCTAAAG--
nad42_II 459 ---AAAAATCGAATGGACAGGCTATAGGACTATGGTATAGTGAACGAAATTCATCATAGAGTAAAAAAGTATTGGTTATGGGGTTGA
rpl161_II 331 GGGCGCTCCTTAACTTTAAAATTGACTACTCTGGGTAG-----

atp81_II 392 -----GTGGCTCTATATATAAGTTATGGTCCGCTTC-----ACACACTAGGTTTC
nad42_II 548 TACATATGACAGCCGACCATTAACAACCTTATGGCTTTGACCACTGAACACTAGGACGCTGATGCTCGAACTCGACACACTGTCTTAAATTCGA
rpl161_II 373 -----GACTCCCAAATTTGGGCTTTCGGTCCGCTTC-----GCTCTCCTTGT

atp81_II 648 -----TTTTCAAGTACCGAGCTGGTGGCTCCGC-----TGGAAATAAAAACCGTCCGCGTAGTAAAT-----TAAAGAAAGTGA
nad42_II 439 GTTCTGGCAGTTTCAAGCTTCCGATATGCTAGCTG-----TGGTGGCCGTTTTCAGGAAAGCGATGGGACCGCAAGTATACCGGCCCA
rpl161_II 419 GTCCCTTTTAAAATTTTAAAATAAAGCGCAAAAGCGGATTCGGGGCCAAAGCAAAAGCGGAAAGCGGCGGCGGCGCAAC-----CTGTAAAGCTA

atp81_II 511 ---GTCCGTTGGGTAAGCCGGAATTAATGCGCTAACCTCTCAGTACGGGGAGA-----AACGTTGGCGAAGGGGCACTCACTCTGCTGAAGGACT
nad42_II 746 GGTTCATATGAGAGGCTTCCGATGCGCA-----TGGTGGCCGTTTTCAGGAAAGCGATGGGACCGCAAGTATACCGGCCCA
rpl161_II 513 CGGCTTCCAGAGGACCACTAAGAA-----CAACCACTGCAAGT-----GTAAGCGG-----AGGTCAGC

atp81_II 603 TTTAAGCCCAACCGATGCTTGGCCATAT-----GGGCATGTGGCCCT--
nad42_II 810 CTAATGACCTAGTCAAGGATTTATGAAAAATAAACCAACCTATCTCCAAATGACCAACCAAGCGAAAAAGGACCCGGGACAAACCAATAATCGAG
rpl161_II 573 AAATAACCTGGCTCTTAAAGTATG-----TACTTGGCCGGCTTTCACCTATATAC

atp81_II 645 -----TTCGCTTCCGACCTC-----GTAAAGGCHCAAGCAGGCCCT--
nad42_II 910 AAATCGTATAGGGTTTTTCGGAATTCATATGCTCTCAAAATATGCTGAATTAGCTATAAAGGTTACACAGGCTACCTTGTGACCCGAAATAAAA
rpl161_II 627 -----TCGGTTCGCAAAAT-----CCGACGCTAATAGTGAACCTTCTCAAA

atp81_II 683 -----TGGATCACCCGAAAGAAATC-----CTATCCCGGCAATCACTTTC
nad42_II 1010 TGGACACTCAAAATCAATGGCACTTCCAGTTCGCAACCAAGCGCTAGCAGTCAATTAACCTTGTCTATGCGAAAGCCCGCTGATTAACAGGG
rpl161_II 671 GAATGCCATTAATTCAGAGGGGCTCTGGGATAAACGATTC-----CCGAGCTAATAGTGAACCTTCTCAAA

atp81_II 723 CTGACAC-----ACCTGGGCAAAACCCGACGCGAGGCTAGCTTT--
nad42_II 1110 GGGATTTGCTACTCTACTTAGATATTTATTTTTCGACGCTCTACTTTTATTAATGCAAGGTCAGCTATTCGCGGACCTTCAATTTATCATAGGA
rpl161_II 735 GGGATTCC-----CTTCAAGGGAAAAAATAAGCAAGATCTCTATC

atp81_II 765 AGACCAAGCCGCTGGAGAGCCCGAATAT-----ATCGCTTTTAAAGGAAATTCGGGTAGCAAGCGCTAGCCCTTTTAGCGGAAACTGACAGAGCC
nad42_II 1210 TTTTTCAGCCGCTGGTGGGCTCGGTC-----TGGTGGCCGTTTTCAGGAAAGCGATGGGACCGCAAGTATACCGGCCCA
rpl161_II 777 CAGGCACTTAAATTCAGAGGGGCTCTGGGATAAACGATTC-----CCGAGCTAATAGTGAACCTTCTCAAA

atp81_II 862 AATTGACG-----GGACCGAAGCGGCAAGCACCTAG--AG
nad42_II 1310 AAGCAATATTTCGAAGTGAAGCAGCGATAGCGAGCTTATTTTTCCTTTTCGTTCAAGTGTGCACGCTACCGCTGCAACTATGGGTTCAATGGG
rpl161_II 868 -----AGGACAGGGGCAAGGCTCAATTAAGCAT-----ATAAAGGGGACACTGG

atp81_II 897 GGGACCGGCTCCGCC-----TTCGAGCAGCTGGGCTGATGGGTA
nad42_II 1410 CACTAATCAGCTAATTTGCCGAAGGGATTAATGATGGGCTCACTAATTAAGGCCCACTAATTTGATAAAGCATAAGCTAGCAGCTAACAAAGTTA
rpl161_II 919 AATCACTATCTATTTC-----AATATTCAATGTTTATACAAAA

atp81_II 942 TCAATATTATTAAGCCGCTTGCAGTACCTCCGGTACT-----TGGCAACCTTGCATAGT
nad42_II 1510 TTTGATTAACCACTTCAACTATGTTGTTGGCTTTAAGTATTGCTTCTTGGTATGCCCCTTTACGCAATAGGAAACCGCTGAGCGGCGCT
rpl161_II 962 TTTGGGTAAGTCAAGGCTCATGATCATCTGGAAGCTGAGCAAAAACTCA-----GATAGAGCAAGGCAATGGC-----CTAGGCTGATC

atp81_II 1002 -----GCAGGCAACCCGAGGCTTGGAGAGCGANGIT-----GCAAGGAGCCGCTCCGCTTGGGCTCAAGTAA
nad42_II 1610 AAGCCGCGCAGGCTCCCTTGGAGGCACTAAGCAAGAGGAGGTGATCCTTGGTTTTTGGCTATAATGTGACTGGCCGCACTTGGCCTCAAGTAA
rpl161_II 1046 AAGCCGCGCAGGCTCCCTGAGTGGTAAAGGCTGAGC-----CTGATG

atp81_II 1075 CTTGGCTTTGGGCAACCGG-----CAAAGCAATTAATCTAGTGAAGCAAGCCCTTGGCTTAAAGTGTGGGCTTAGTAGCTCAATTAAGAGGCT
nad42_II 1710 ACAAAGGCTTGGGCTTCCAG-----AAGTAAATCTCGAAGAGTGA-----GATTACAGCAGACCC
rpl161_II 1093 ACAAGGCTTAAAG-----AAGTAAATCTCGAAGAGTGA-----GATTACAGCAGACCC

atp81_II 1097 -----TCCCGTCAACCACTTAGTCTTTCGCGGCGCAGCGAACCTAAAGTTCGGCAGATCTG
nad42_II 1810 TATGACATTTAACTGTACGATAGTTTCGGAGGCAAGGCGCAGAGCTCGCTAAATATGATTGCTAGC-----GTTAGCAGCTCCGCTTCTAGTGA
rpl161_II 1147 CCGAGGGC-----AAGGCGCTCCCTGGGGCCCTGAGCCATTAATCGGTTGGCTAGCGGCTTCTAGCTATTGA

atp81_II 1157 CAGCGAAGCCGGACCTACGAGCAGC-----GCTTGGCTTAGACTTGGCTGAG--CGGCTTATTCTCAGCAGC
nad42_II 1908 GCTTCACTAGGAGGCTGGCTGCTCACACCGAAGGCAAGGAAACCGCTTGGCCATGCTCAACCCCGGTGGGAAAG--ACCCTGTTCTCAGCTGTC
rpl161_II 1226 GTATTTCGCCGCGCAGCGGTT-----CGATAAGACAGGAGGTTAGCAAGAGCGGAACTTTTGGCTGCAAGCAAGCCACTGCGGCTG

atp81_II 1227 GGCACCGAATATGACCTTGGAGGCGCTCCATGGCCAGCGGTTGCAATCCACGCGGACCGCCGCTCCGGGTGTGCTTCGCANCCGCTCAT
nad42_II 2007 GCTTGGCT-----CAGCAAGCTCCGAGGCTTGGCA-----AACGATAGCCTTATGGGCGCAAAAGT-----GCCTCCGCACTATTAAGGTTGCT
rpl161_II 1318 CTATTGT-----AAGCACTTCAAGGCGAGCCCTCTT-----AAGTATCCATTAAGTTCAGAGAGATCAG-----TCGCTTCTGCTTCAACCATTAACAT

atp81_II 1327 GGGTTCGCTTTCAGAGAACAG-----TGAACCGAGGCTCATCGAAGAGCGGAAAGGAGAGGTTT
nad42_II 2096 TCTTATGCTACTACGCAAGGGGACCTCACCGGTTTCAAGCTC-----AGCAAGCGAAGGCAAGCAGCTGTTGGCTTGCCTTGGAGTCACTGCTC
rpl161_II 1407 TACATGCAACTCAGAGGAGAGG-----TGCATCTCACTAG-----TGAAGCGAAGGAGGAGTACAG-----CGC

atp81_II 1394 -----AAATTTGGCCGCTTGGCA
nad42_II 2191 TATTTGCTCAACCGGCTTCGAGGCTTCGAAAGCAAGGGGCAAGGTTTACCTAAAGCGAGGCTTCTGAGGCTCCAGGCGCTCAGG
rpl161_II 1474 TATTTGCTCAACCGGCTTCGAGGCTTCGAAAGCAAGGGGCAAGGTTTACCTAAAGCGAGGCTTCTGAGGCTCCAGGCGCTCAGG


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atp81_II 1415 AGGTAAAACCACTTCGCAAGCGAAGAAATAGCTGCAAGCTTGAAGTTCCGCTGCATAGGTTCTGGCCCTC-----
nad42_II 2291 ATGTAAAGCACCTTGTCTGAAAGCTTCTCAGCTAGCGAAGGGCCACCGGGCTTGGCTCCTCCGCCCCCGAAGGGTGCATGAAAGCCGAAGGCCAANGG
rp1161_II 1525 G-----ACCTTCTGACCAAGTAAACCATGATTTTGGGTCT-----GCATTAAC

atp81_II 1482 -----GACCTTCTCCAAAGGCCCCCGCAG-----EGCTTATGTTTAACTTGGTCAACATAA
nad42_II 2391 CCTACAGGCTCTTCCCTAAAAGGCTTCCAGTGGTGGCCANGGAGCCGTGCTTGGCGGTCTCACGGCTAGGCCGCCCTCAAGCTTCCGGTTCAGAGCGA
rp1161_II 1567 TATACAGG-----CAAAGGTGATTTTITTTAAACACCCTTGAGTGC-----CTCGGGTGTTCGGTTCAGCCCTE

atp81_II 1531 GGCTAACGGATGAGCCTTGGTCACGCACACCATTTATCTACACAAGGTAGGGCAACTTACTGCTAAGATGAAAAAGCGTGCAGCCGTAT-----
nad42_II 2491 GGCACTCGGTATGACATGGGAAGAAGGCGTCCACTGATGTCTANAACCTGATAGAC-----CGGAAAGGCATTCATGTAAGCCCGATCGCCCGGC
rp1161_II 1633 GCCAC-----TATTAACATAGAAATTCGGTGGGTGACCGGCACAAAGAGAT-----CGCAGGCGGAG-----AGCCGTAT-----

atp81_II 1623 -----GATGGGTAAACATACAGTACGGTTACGAGAGGGGGCCCTGAGGGCCCGCAATGCTE
nad42_II 2585 ACCTTCACTCAACCGAAGTCCACAAGACCACCCGAAGGGCGAACGGTGTGCTCGCAACCGGTTCCGAACCTGGTC-----AGCAACTATCTGCC
rp1161_II 1699 -----GAAACGATAAATTCATGTACGGTTCGGAGGGCAGTA-----

atp81_II 1681 ATTACCCGTH-----GTGATAGCCGGAAGGGTTTCTAATCTA-----
nad42_II 2678 GTTATCCACTACTAGGTGGCTAACCAAGCCGTAAAAAGGGGCTCGGCCCTGACCCCTAC
rp1161_II 1735 -----CCACTGACCCCAT

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