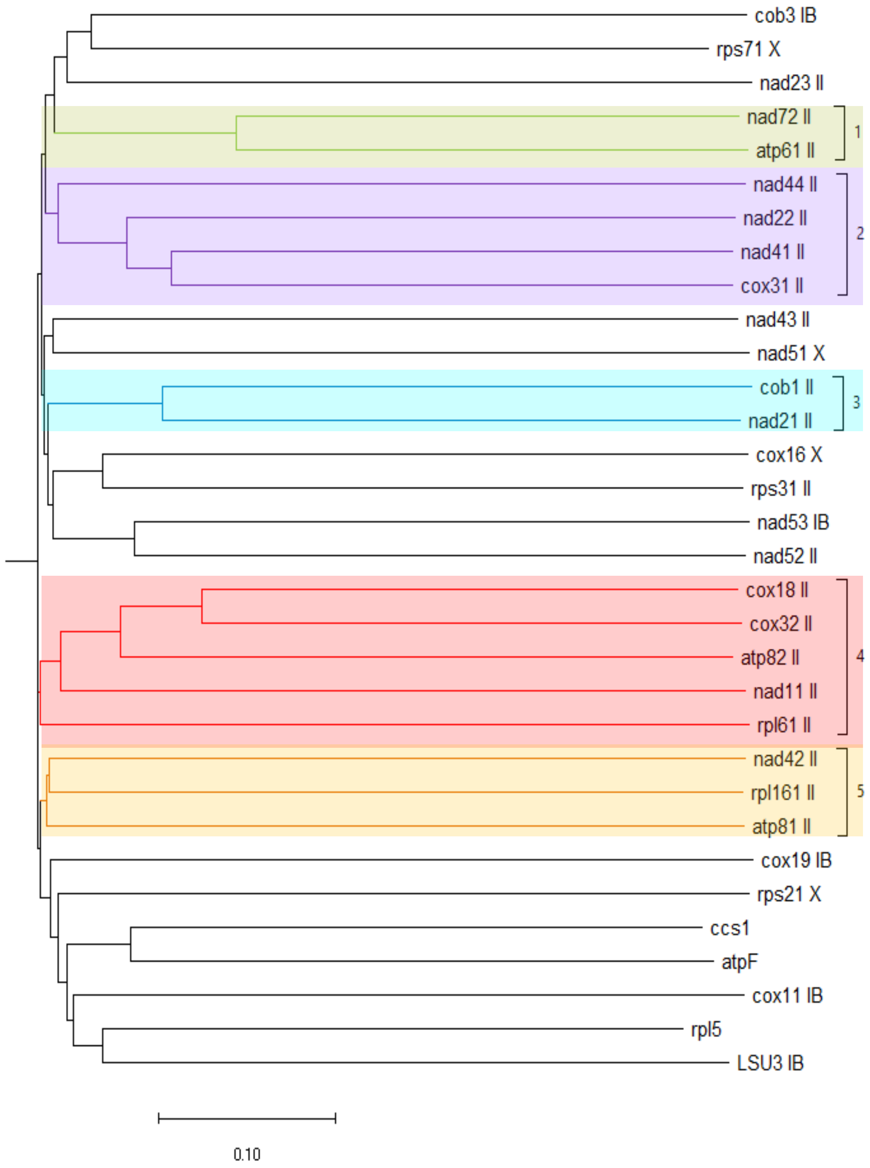
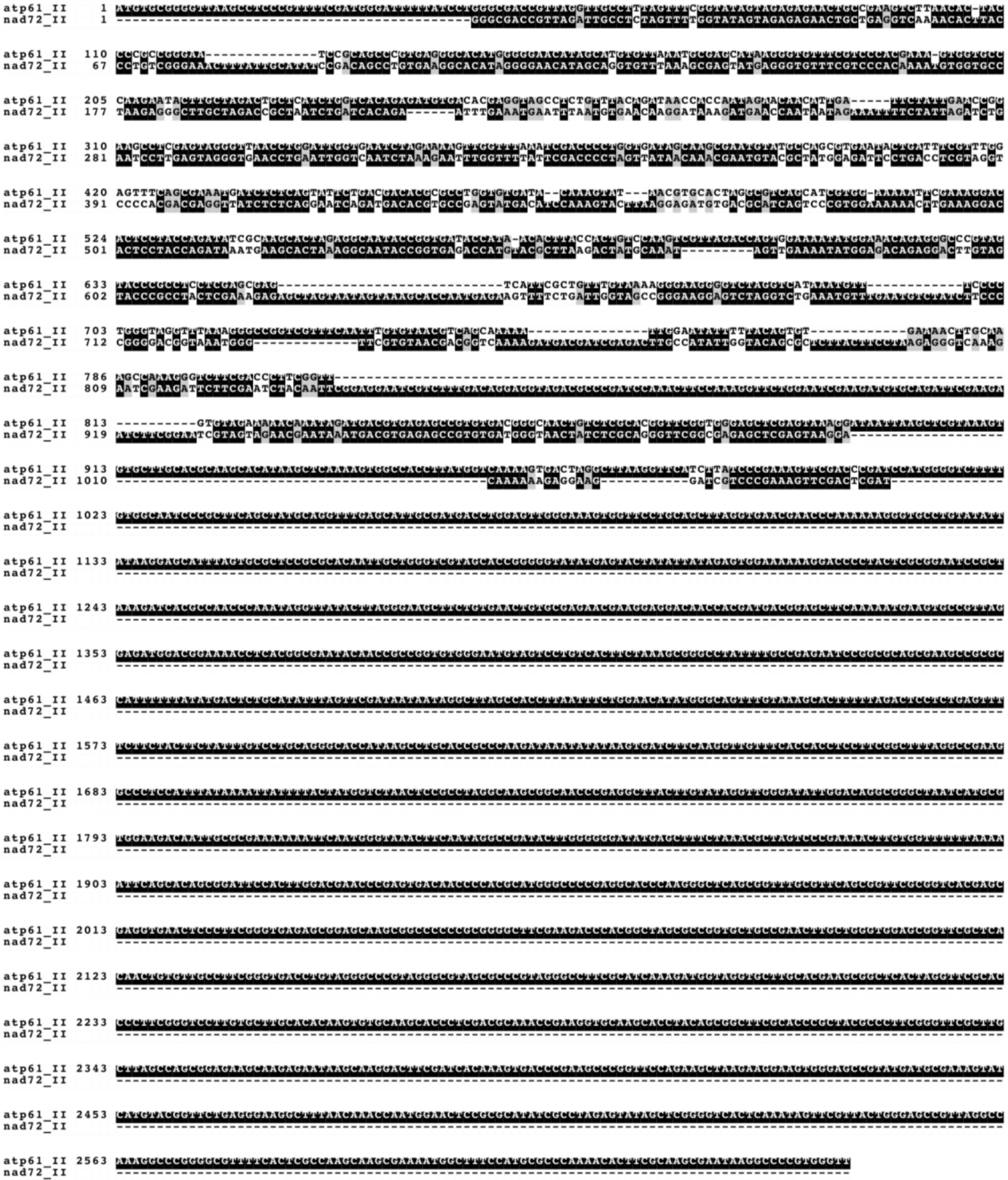


Neighbour joining tree from Clustal Omega distance matrix of ORF-lacking introns in *Ostreobium quekettii* mitochondrial and chloroplast genomes, and MAFFT alignments corresponding to clusters.

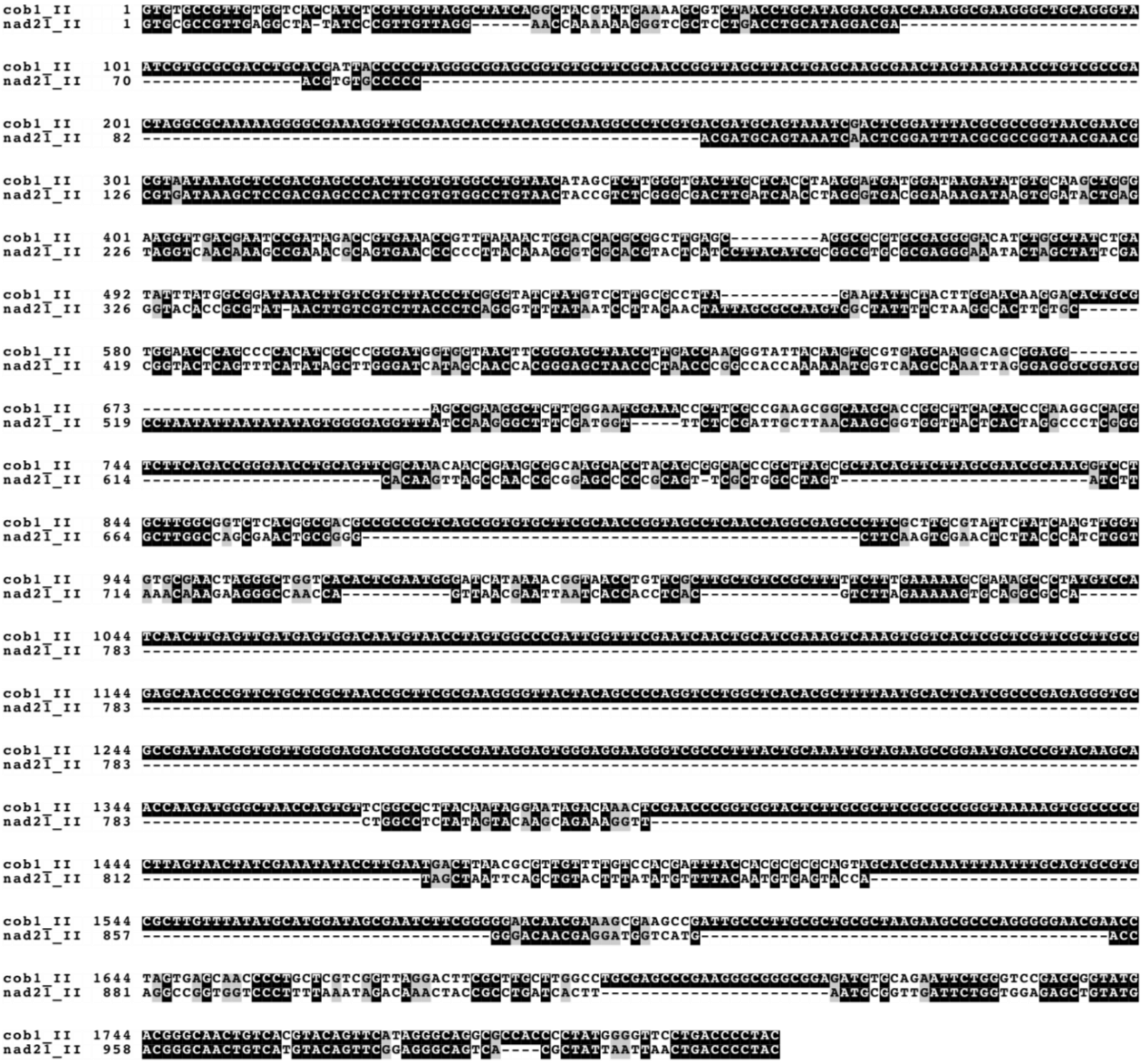
Group 1:



Group 2:


cox31_II
nad22_II
nad41_II
nad44_II

Group 3:



Group 4:

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atp82_II    1 GTGCGACCCG--------------TTCGCGAGTGAAGC------------------------------GTACGAACTCGCGCATCTATT-----------
cox18_II    1 GTGTGGTCCG--------------TTCATGGACGAAGCTCCGAACAAAATT---------------CAGAGCGAATCTGTGCACTCATT-----------
cox32_II    1 -TGCGGCCCG--------------TTCACGGTCAAAGTTTGCATGTAAACG---------------CAAAACGAACCCGTGCGCTCGCCACGGACCGACA
rpl61_II    1 GTGTGACAAGAAGTTATGCCTTGTATTGCAGTTGAAGTAT------ATACG---------------AAATATTAGCTAGGTCCTGCGATAT---TCGATA
nad11_II    1 GTGCGACCTG--------------TTTGCGTATAAGCTAT-TAGCGAAATTGCAGCCGTCGGCAACTGGAGTCTATATGCGGGTTCAACTC---CCGACA

atp82_II   46 -----------------TTATATGAACTGTATCGACCTGAAGG---TGTAAGT-----------------------------------------------
cox18_II   61 ---------------AGTTGAGTGAACTGAGCTGTCATGAGGG---TGAGAACCCGTTG--------------------------CCACAAATGTGGTAG
cox32_II   71 AACAT-------GCAAGGCGAGTGAACTGAACTGACATGAGGG---TGAGAATCCGTTG--------------------------CCACAAATGTGGCAG
rpl61_II   77 GATTTTACTAGACCAACTCGAGCACACCTAGGTGGTAACACCAGGGTGTGAAACCTCAGGGTCACTCCGAAGCGGCATACCCACATCATCAAGATCACAG
nad11_II   83 CGACCTGCGAGGCTCAGGCGAAT--ACTGAACCTTTATAGGAGATATGGCAAGTCGCTGAATTAAAGCAAAAAGGTTCAGTAATATAAGTAATGACGAAT

atp82_II   79 ------------------------------------------CCTTCCCCCCTTGAGATGGGGTGAAAGCGACGCCCACATGCTAGGG------ATGGCT
cox18_II  117 CTATCAA--------------------------------GCCCCTCCCCCCAAAGAAACGGGGTGAACGCTTTGCCCACATGCGTTGGTTCAGTAAGAAC
cox32_II  135 CAATCAA--------------------------------GTCCCTCCCCCCAAAGGAACGGGGTGAAAGCATTATCCACATGCGTCGG------GATGGC
rpl61_II  177 CGTCCAGCAGCTCATCTTTTGGCCGGGCGTTTTGCGAAGGCCTTCGCCTGCTGAGCAGCGAACCCGAAGTCCATTGTTCACACCGTGA------AGTGGC
nad11_II  181 CATTTAACGAGTGTAAGCTTGGGTGTCCGGAAGACACACGGTGTAAGCCGTAGGACCAACGGCGCTCAACATAGTATATAAACAGCGGGAACGGGAGGTT

atp82_II  131 ATG-CCGG--------------------------------------------------------------------------------------------
cox18_II  185 ACT-CGAGTCAGCGGTTGCTGACC----------------------------------------------------------------------------
cox32_II  197 ACG-CTGGTCGCTCATTACAACCT----------------------------------------------------------------------------
rpl61_II  271 GTAGCTCATAGCTTTTCACCATGTGACGCATCAAGCTTGACCTAATCAAATGTTAGCCGAGTCTGTCGGAGAAGCTATACGGCCACGCAAGTGTGGGCCT
nad11_II  281 GCT-------------------------CACTAGGTTCGCAACCGTTCGCTTCGGGCCGAA-------------------AGCGAAACAAGCACACCGCT

atp82_II  138 ----------------------------------------------GCAACTGGTT------------------------------------CCTGTGGC
cox18_II  208 ------------------------------------------CGCGGGGGATGGCT-----------------------------------CCCCAAGGT
cox32_II  220 ------------------------------------------CAAAGTGACTGGCT------------------------------------CTCGAGGT
rpl61_II  371 GCGGCTGTACGCCGCC--------------CTGCTATAGCAGCGCAGGCAATGGCTGCTTCGCGGGCGAAACCCGCAGCACCGCTACAGGGCCTCGGGGT
nad11_II  337 TCGCCCTCGTGCCGCCGCTGGCTTCGCAGGGTATCCTAGCAGTAAATGCTATAGTTGT----CGAACGTTTGTCGCGACCT----------TGGTACGAG

atp82_II  156 ATGAAGCTGGGCGTAAAAG------------------------------------------------GATGAAAGGTCTTAGGAAATGAGGCCTGATGAA
cox18_II  231 GTGAAGCTGGGCAAAACGG------------------------------------------------GAAGAAGAGCTCAAGAAGAGGAGTCTTGACGAA
cox32_II  242 GTGAAGCTGGGTAAAACGG------------------------------------------------AGTGAAGAGTCCAA----AGAATACTCGATGCA
rpl61_II  457 ACGGGGCCTGCTAGAGCATTTA-------------------------------------------AAATAGAAAAAGCCAACCAACAATGTTTC---AGA
nad11_II  423 TTAGGGATGGGGGTAGAGTGCGAATCAGCTGATGCCCTGGTTCGTAAGCATTTTGATCGAGTCATAGGTAGAACTATGTTACAAACTGCGCTGC---ATA

atp82_II  208 TCTCGAGCAAAGACGTGAT-----------------------------------------------------------------------------TAGG
cox18_II  283 TCCCAAGCAAGGGCGTGACG--------------------------------------------CCTCCGCCCGCCGGAGC-------------------
cox32_II  290 CTTCTAGCAAGGACGTGACG--------------------------------------------TCTGAGGGCAATGAGTCATACACAAACTCGAGTGGA
rpl61_II  511 GCTCAGGCGGGGTTGTAACGAACTACGTGAGTTACCGCAAGTGCTTGGCGTAAGAGTACTAGGCGCTAGTAGTAATTAGTCATTTATGACCTAAAATAGA
nad11_II  520 GTGTGGCAAAGTTCGCCGTG---------------------------------------------------------------TTACAACCCAATAAAAC

atp82_II  231 GACTTTATC-------TCTAAA----------------------------------------------------CATAG-CACCT---------------
cox18_II  320 ----------------------------------------------------------------------GCGTCATAA-CATCTCGA------------
cox32_II  346 AAGGTTATT-------GCCAAACCATGAAATTGTTTGTTTTGTTGCCTAAGCAAAGCTCGAAGAGCTTCTACGTCATAGTCGTCTCGT------------
rpl61_II  611 ACGGCTGTGAACCCCACTCGCTTCATCAGGGCGCTCTGTGCAGAGCGCAAGCAGGGCTC-AGCGGTTCCCGAACCTTGGTTGTTTGGAGGCCACGTATTT
nad11_II  557 AC-------------------------------------------------TAGGGCTC-AGCGGTCCCCGTTTTACAA---------------------

atp82_II  256 -----------------------------------------------------------AAAAGTGCTACTGATGGCT----------------------
cox18_II  337 ----------------------------------------------------------AAGAGGTGTTACCGATGGCT----------------------
cox32_II  427 ----------------------------------------------------------AAGAGGCGCTACCGATGGTT----------------------
rpl61_II  710 CGGAGTGCTGGGTAACAATGAAAAAGGGCATTGTATAGTAAGGAGTTTAGACCTAGTCCATCAACCTTGCAAAGGCTAGGCCCACGAAAGAACCTAGCCG
nad11_II  586 ----GTACTGGTGGTTATGTAAAAAGGGC----------------------------CCGAAGGCCTTACGGGGGGCCGCTACTCA--------------

atp82_II  275 --------------------------------------------------------AAGCAATTGAGTTGAACTACCTCAA-------------------
cox18_II  357 --------------------------------------------------------AA-CAATTAAGTGAACCGTGATTA--------------------
cox32_II  447 --------------------------------------------------------AA-CGATTGAGTGAACTGTGCTCG--------------------
rpl61_II  810 AACTATTCTTGCAGTTAGGTAGAGCTCCGCCCTAAAATCGTTGTATACAAGCATAAAACTTGGTAAGCCCGTCTGGTGAGGAGCTCGATGGCCAAGCGGT
nad11_II  640 ----------------------------------------------GCAACCTGCGAACCTAGTGAGCAAGCCCAGCCCAGTGGTCG-------------

atp82_II  300 ------------------TATTGAGGTTAGCGTTTG------------------------------------AAGCATCGTAATAAGGAAGCAGGGTT--
cox18_II  380 -------------------CCAAGGCTGCCCTTCGGGCAGAACCTCAACAAGAGGGATCATTTGCGATG---ACGCACCGTAATACTCAAACAGGGTTG-
cox32_II  470 -------------------CCCAAGGCGAGCACTCG-----------------------------AATG---ATGCGCCGTAACCGCGAAGCAGGGT---
rpl61_II  910 CCCCGGTCCCACTTGTTTTTTTTTCTAGTTTGCTCCCTGCTGGCGCA--------GACCCTATAGTTCGGTCCTATAAGTGATTCCGCTAACCTAGCGAC
nad11_II  681 -------------------CTCGCTTTGCTCGTTACCGGGAACCGCT--------GACCCCTTGCGCTG--CGCGCAAGTAAATCCTCTAAAAACCTCA-

atp82_II  344 -------TAATATTTCCTGGTCCCAATTT-----------------------------------------------------------------------
cox18_II  457 ------CTAATCTCTTCTTGTCTGAACTC---------------------------TATACTTTTTCGAAAGTTTATT----------------------
cox32_II  516 ----------------------------------------------------------------------------------------------------
rpl61_II 1002 CCCCCACTAAGCTCAGCCTGCGCAAAGCG--------------------------------------------------------AGCAACCCGGCCCCC
nad11_II  751 ------CTAAGTATAGCTCGCGTCTAAAGCTTATATCATATATGATTCTGGAACAGGATAACCCTTATGGAGTTCCTTCAGACCTAGCAGTTTGAGTGCA

atp82_II  366 -----------------------------------------------------------------------ATTGGGAAGACCCCTGCACTCGGAATATC
cox18_II  502 ---------------------GCGTGCTACGCACGCAAGCTAACCTTTTGAGTTCCGAAGACCTTCAATAGCTTTCAGAGACCCCTGCGTTCGGAATATC
cox32_II  516 --------------------------GCTCGCACACACAGCACTCT-----------------------------------ACTCAACGTCCATAGTATT
rpl61_II 1046 TGCTCATCGGTTAG-GCCTTGGCTGGCTGAGCAAGCGAACT-----G---------------------CGGGCCTTTGGGCCCCCCGACCTTGGGGCCTA
nad11_II  845 GCTACGCTAGCGAACGCCCTCGCTTGCTTCGCAAGCGAACC-----------------------------CGATATCGAGCCCTCTAGGTTCGCAAGAAC

atp82_II  395 GAG-------------------------------------------------------------------------------------------------
cox18_II  581 GGA-------------------------------------------------------------------------------------------------
cox32_II  555 GGA-------------------------------------------------------------------------------------------------
rpl61_II 1119 GGGGGAGCCTCCACCGAGGAGGTAACTTACTAGGTGGGTGGCCGGTAACCAGGTCGCCCCCTTTTTTTGTTTGACCTGTTAACCCCCTTCGGGGACTCGG
nad11_II  916 GCA---------------------AAGTGCT----------------------TCGCACCCTTCGTTTCCTAGAACCTTCGGCTAAGCTTTGGGACCCGA

atp82_II  398 ---------------------------------GAGGAGCCTGGAGGGGAT-----GCTATTTCATATCACCCTCAATCTCACATTGTGCTCTCGGTGTA
cox18_II  584 ---------------------------------CAAGGGCCTAGGGATATG-----TGCATATGGTAT--ATCCCGTTTCTTTGATGTGCCCTCGGTGTA
cox32_II  558 ---------------------------------CAAGGGCCTAGGTATACG------ATATATCGCGT--ATATTGTTCCTTTACTGTGCCCTCGGCGTA
rpl61_II 1219 CCGCTCGCTGTGTCTATTAATTGATCGAG---CGAAGGATCAGGTCGTGAGCTGTACCCACATGAGGTCATGGGCGCTCCTGCCTGAGCCTCGAGGTAAG
nad11_II  973 AGGCT-------TCGAATAAGTTACAGTTCGCAAAAAACCGAAGCGGCAAG-----CACCTACAGCGG--------CACCCGCTCCGCCCTCGCGGAGCT

atp82_II  460 TAGC----------------AAGAGCCTTCCGGTCTAA-----TTAGGTCGATT------------------CGGAACGGGGAAAGACCCAAAGATTCTT
cox18_II  644 AAGC----------------AGGAGCCTTCCGGCCTAA-----TTATGGCAGTT------------------CGGAACGGAAAAACCTCTAGTGTCTCTT
cox32_II  617 AAGCA--------------AAAGGGCCTTCCGGTCCCA------TATGACAGTT------------------CGGAACGGTAAAACCTCTAGTGTCTCTT
rpl61_II 1316 CACAACGCGCACGGTGC-TGCGCGGCAACCTTTAGTGA-----AATCGCTAGTTGCAAATTACACAACATAACAGGCCGGGTAGGACCTCAG--------
nad11_II 1053 AAGCTTGCGCATAGCGCAAGTTCGGCTTTCCATGCTAAAGGTCTTCGGCCGGTTGCGAAGCACAC------------------------------CGCTT

atp82_II  521 CCT-----------------------------------CATTTATGAGAAGTAGGTGCCAA---------CCA---------------------------
cox18_II  705 TGTACGTGTGGC-------------------AAAGCTACACGTCTCGAAGCAGGTCGCCAG---------CCGC--------------------------
cox32_II  679 TTCTGTAGTGACCCTCGTTATACCCAAGTAAGCGGGGGCATACTTCAAAGTAGGTAGCCAG---------CCGT--------------------------
rpl61_II 1402 -------------------------------------GTATCGACAGCTTCTAAGACAAGGCTAGTCGTGCTACGAAACGCCATCCGAGTATGAACTCCA
nad11_II 1123 CGC-----------------------------------CAAGCACGGCTCCTAGGGGTCGGCCTGCCAAGCTAT--------------------------
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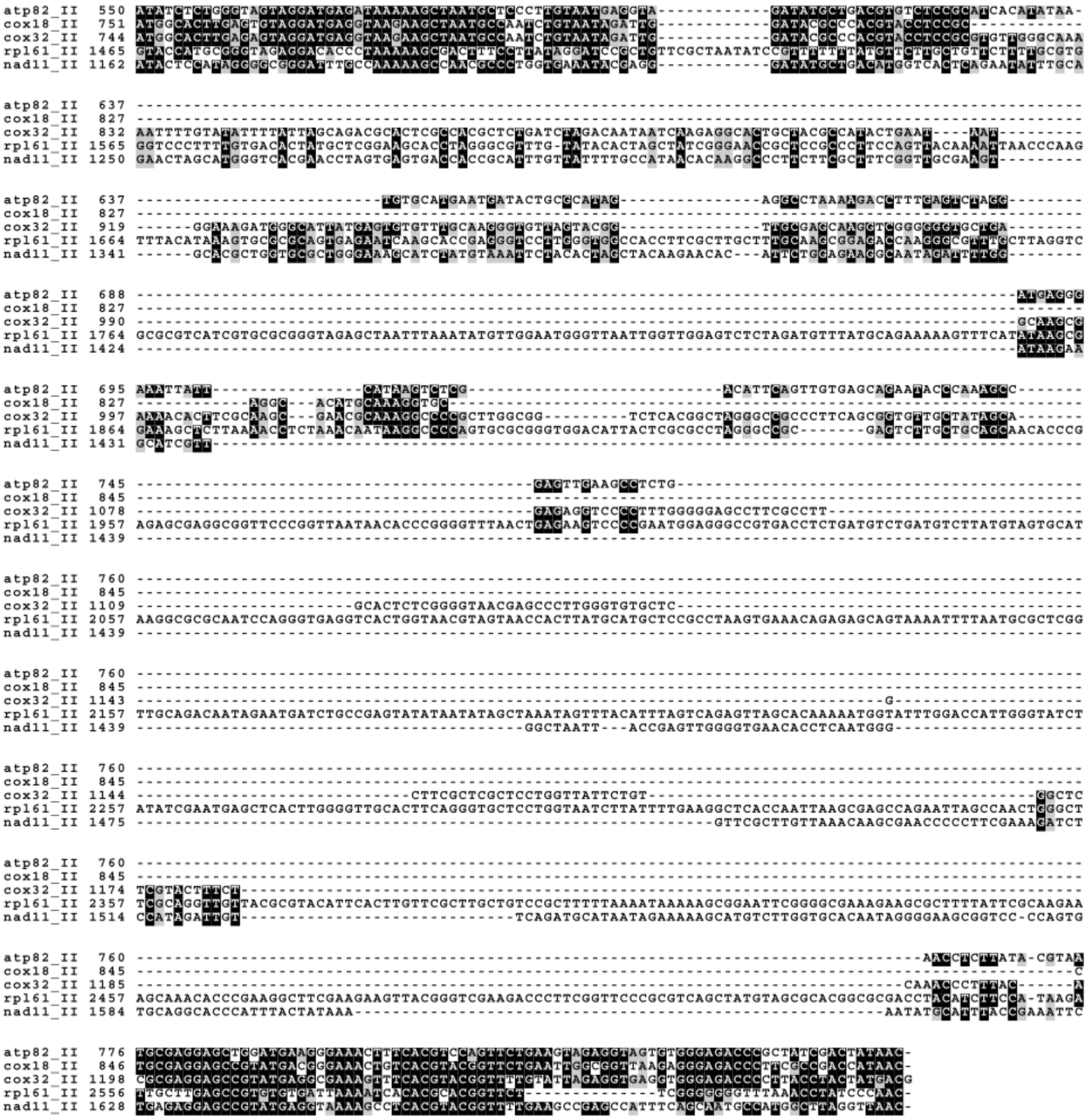

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atp82_II   550 ATATCTCTGGGTAGTAGGATGAGATAAAAAGCTAATGCTCCCTTGTAATGAGGTA------------GATATGCTGACGTGTCTCCGCATCACATATAA-
cox18_II   751 ATGGCACTTGAGTGTAGGATGAGGTAAGAAGCTAATGCCAATCTGTAATAGATTG------------GATACGCCCACGTACCTCCGC------------
cox32_II   744 ATGGCACTTGAGAGTAGGATGAGGTAAGAAGCTAATGCCAATCTGTAATAGATTG------------GATACGCCCACGTACCTCCGCGTGTTGGGCAAA
rpl61_II  1465 GTACCATGCGGGTAGAGGACACCCTAAAAAGCGACTTTCCTTATAGGATCCGCTGTTCGCTAATATCCGTTTTTTTATGTTCTTGCTGTTCTTTTGCGTG
nad11_II  1162 ATACTCCATAGGGGCGGGATTTGCCAAAAAGCCAACGCCCTGGTGAAATACGAGG------------GATATGCTGACATGGTCACTCAGAATATTTGCA

atp82_II   637 ----------------------------------------------------------------------------------------------------
cox18_II   827 ----------------------------------------------------------------------------------------------------
cox32_II   832 AATTTTGTATATTTTATTAGCAGACGCACTCGCCACGCTCTGATCTAGACAATAATCAAGAGGCACTGCTACGCCATACTGAAT----AAT---------
rpl61_II  1565 GGTCCCTTTTGTGACACTATGCTCGGAAGCACCTAGGGCGTTTG-TATACACTAGCTATCGGGAACCGCTCCGCCCTTCCAGTTACAAAATTAACCCAAG
nad11_II  1250 GAACTAGCATGGGTCACGAACCTAGTGAGTGACCACCGCATTTGTTATTTTGCCATAACACAAGGCCCTTCTTCGCTTTCGGTTGCGAAGT---------

atp82_II   637 --------------------------TGTGCATGAATGATACTGCGCATAG---------------AGGCCTAAAAGACCTTTGAGTCTAGG--------
cox18_II   827 ----------------------------------------------------------------------------------------------------
cox32_II   919 ------GGAAAGATGGGCATTATGAGTGTGTTTGCAAGGGTGTTAGTACGG---------------TTGCGAGCAAGGTCGGGGGGTGCTGA--------
rpl61_II  1664 TTTACATAAAGTGCGCGCAGTGAGAATCAAGCACCGAGGGTCCTTGGGTGGCCACCTTCGCTTGCTTTGCAAGCGGAGACCAAGGGCGTTTGCTTAGGTC
nad11_II  1341 ------GCACGCTGGTGCGCTGGGAAAGCATCTATGTAAATTCTACACTAGCTACAAGAACAC---ATTCTGGAGAAGGCAATAGATTTTGG--------

atp82_II   688 ---------------------------------------------------------------------------------------------ATGAGGG
cox18_II   827 ----------------------------------------------------------------------------------------------------
cox32_II   990 ---------------------------------------------------------------------------------------------GCAAGCG
rpl61_II  1764 GCGCGTCATCGTGCGCGGGTAGAGCTAATTTAAATATGTTGGAATGGGTTAATTGGTTGGAGTCTCTAGATGTTTATGCAGAAAAAGTTTCATATAAGCG
nad11_II  1424 ---------------------------------------------------------------------------------------------ATAAGAA

atp82_II   695 AAATTATT----------------CATAAGTCTCG---------------------------ACATTCAGTTGTGAGCAGAATACCCAAAGCC-------
cox18_II   827 ------------AGGC---ACATGCAAAGGTGC-------------------------------------------------------------------
cox32_II   997 AAAACACTTCGCAAGC---GAACGCAAAGGCCCCGCTTGGCGG---------TCTCACGGCTAGGGCCGCCCTTCAGCGGTGTTGCTATAGCA-------
rpl61_II  1864 GAAAGCTCTTAAAACCTCTAAACAATAAGGCCCCAGTGCGCGGGTGGACATTACTCGCGCCTAGGGCCGC-------GAGTCTTGCTGCAGCAACACCCG
nad11_II  1431 GCATCGTT--------------------------------------------------------------------------------------------

atp82_II   745 ------------------------------------------GAGTTGAAGCCTCTG-------------------------------------------
cox18_II   845 ----------------------------------------------------------------------------------------------------
cox32_II  1078 ------------------------------------------GAGAGGTCCCCTTTGGGGGAGCCTTCGCCTT---------------------------
rpl61_II  1957 AGAGCGAGGCGGTTCCCGGTTAATAACACCCGGGGTTTAACTGAGAAGTCCCCGAATGGAGGGCCGTGACCTCTGATGTCTGATGTCTTATGTAGTGCAT
nad11_II  1439 ----------------------------------------------------------------------------------------------------

atp82_II   760 ----------------------------------------------------------------------------------------------------
cox18_II   845 ----------------------------------------------------------------------------------------------------
cox32_II  1109 -----------------------GCACTCTCGGGGTAACGAGCCCTTGGGTGTGCTC-------------------------------------------
rpl61_II  2057 AAGGCGCGCAATCCAGGGTGAGGTCACTGGTAACGTAGTAACCACTTATGCATGCTCCGCCTAAGTGAAACAGAGAGCAGTAAAATTTTAATGCGCTCGG
nad11_II  1439 ----------------------------------------------------------------------------------------------------

atp82_II   760 ----------------------------------------------------------------------------------------------------
cox18_II   845 ----------------------------------------------------------------------------------------------------
cox32_II  1143 -------------------------------------------------------------------------------G--------------------
rpl61_II  2157 TTGCAGACAATAGAATGATCTGCCGAGTATATAATATAGCTAAATAGTTTACATTTAGTCAGAGTTAGCACAAAAATGGTATTTGGACCATTGGGTATCT
nad11_II  1439 -----------------------------------------GGCTAATT---ACCGAGTTGGGGTGAACACCTCAATGGG--------------------

atp82_II   760 ----------------------------------------------------------------------------------------------------
cox18_II   845 ----------------------------------------------------------------------------------------------------
cox32_II  1144 -----------------------------CTTCGCTCGCTCCTGGTTATTCTGT-----------------------------------------GGCTC
rpl61_II  2257 ATATCGAATGAGCTCACTTGGGGTTGCACTTCAGGGTGCTCCTGGTAATCTTATTTTGAAGGCTCACCAATTAAGCGAGCCAGAATTAGCCAACTGGGCT
nad11_II  1475 -------------------------------------------------------------GTTCGCTTGTTAAACAAGCGAACCCCCTTCGAAAGATCT

atp82_II   760 ----------------------------------------------------------------------------------------------------
cox18_II   845 ----------------------------------------------------------------------------------------------------
cox32_II  1174 TCGTACTTTCT-----------------------------------------------------------------------------------------
rpl61_II  2357 TCGCAGGTTGTTACGCGTACATTCACTTGTTCGCTTGCTGTCCGCTTTTTAAAATAAAAAGCGGAATTCGGGGCGAAAGAAGCGCTTTTATTCGCAAGAA
nad11_II  1514 CCATAGATTGT-----------------------------TCAGATGCATAATAGAAAAAGCATGTCTTGGTGCACAATAGGGGAAGCGGTCC-CCAGTG

atp82_II   760 -----------------------------------------------------------------------------------AACCTCTTATA-CGTAA
cox18_II   845 ---------------------------------------------------------------------------------------------------C
cox32_II  1185 ---------------------------------------------------------------------------------CAAACCCTTTAC------A
rpl61_II  2457 AGCAAACACCCGAAGGCTTCGAAGAAGTTACGGGTCGAAGACCCTTCGGTTCCCGCGTCAGCTATGTAGCGCACGGCGCGACCTACATCTTCCA-TAAGA
nad11_II  1584 TGCAGGCACCCATTTACTATAAA--------------------------------------------------------AATATGCATTTACCGAAATTC

atp82_II   776 TGCGAGGAGCTGGATGAAGGGAAACTTTCACGTCCAGTTCTGAAGTAGAGGTAGTGTGGGAGACCCGCTATCGACTATAAC-
cox18_II   846 TGCGAGGAGCCGTATGACGGGAAACTGTCACGTACGGTTCTGAATTGGCGGTTAAGAGGGAGACCCTTCGCCGACCATAAC-
cox32_II  1198 CGCGAGGAGCCGTATGAGGCGAAAGTTTCACGTACGGTTTTGTATTAGAGGTGAGGTGGGAGACCCCTTACCTACTATGACG
rpl61_II  2556 TTGCTTGAGCCGTGTGTGATTAAAATCACACGCACGGTTCT--------------TCGGGGGGGTTTAAACCTATCCCAAC-
nad11_II  1628 TGAGAGGAGCCGTATGAGGTAAAAGCCTCACGTACGGTTTTGAAGCCGAGCCATTTCAGCAATGCCATGGCTTAGGTTAAC-
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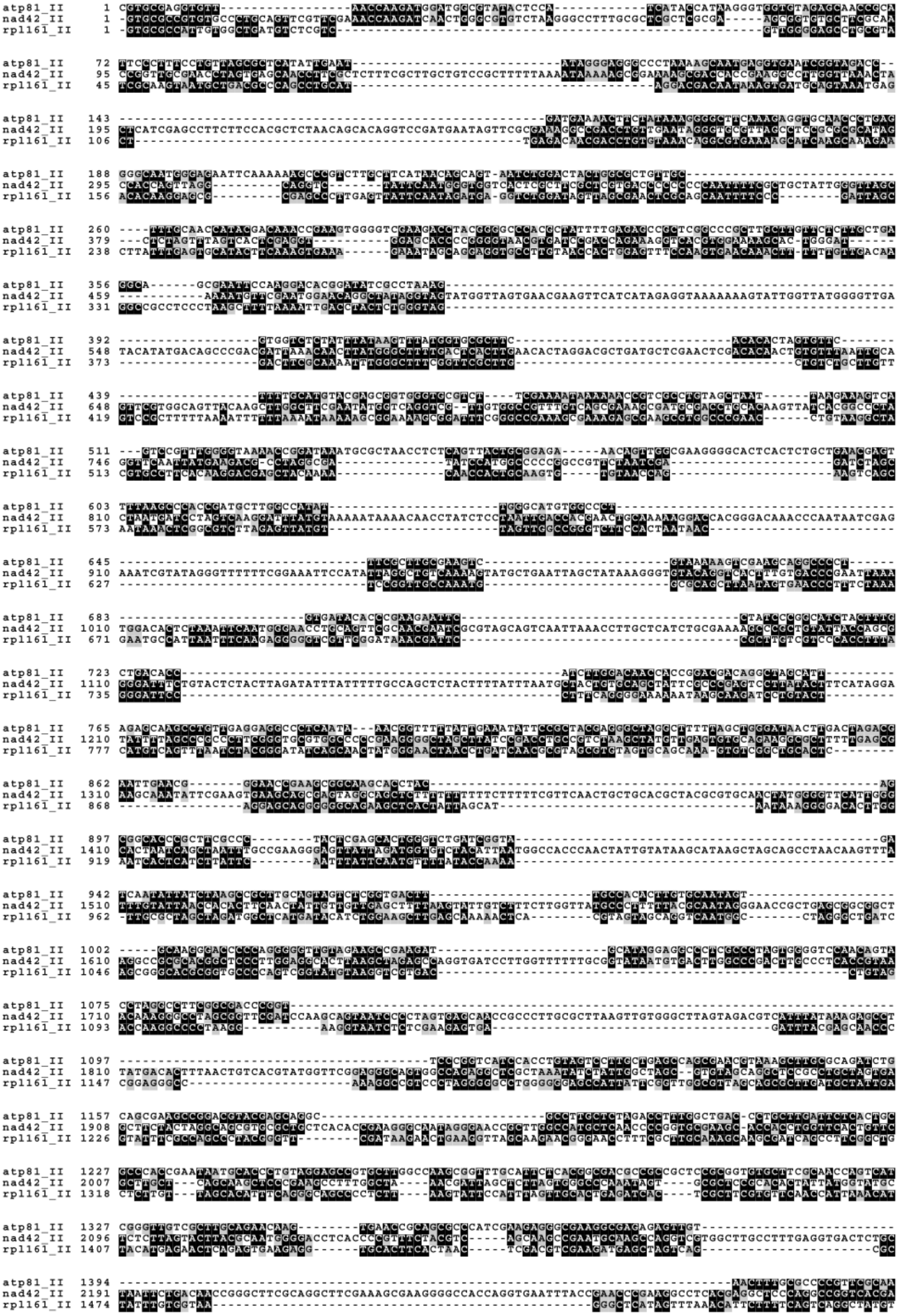
Group 5:



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atp81_II   1415 AGGTAAAACCACTTCGCAAGCGAAGAATAGCTGCAGCTTGAAGTTCGCTGCATAGGTTCTGGCCTTC---------------------------------
nad42_II   2291 ATGTAAGCACCTTTGTCGAAGCTTGCTCAGCTAGCGAAGGGGCCACCGGGCTTGGCTCCTCCCCCCCCCGAAGGGTGCATGGAAAGCCGAAGGCCAAAGG
rpl16I_II  1525 G-------------------------ACTTCTGACCAAGTAACCCATCATTTTGGGTCT---------------------------------GCTATAAC

atp81_II   1482 -------GACCTTCTCCAAAGGCCCCGCAG--------------------------------------------CGCTTATGTTTACTTGGTCAACATAA
nad42_II   2391 CCTACAGGTCTTCCTAAAAAGGGTTTCCAGTGGTGGCCAAGGAGCCGTGCTTGGCGGTCTCACGGCTAGGCCGCCGCTCAGCGGTTCCCGTTCAGAGCGA
rpl16I_II  1567 TATACAGG------CAAAGGTGATTTTTTTTAATCACCCATTGAGTGC----------------------------CTCGGGTGTTCGCTTTCAGCCTTG

atp81_II   1531 GGCTAACGCATGAGCCTTTGGTCACGCACACTCATTATTCTACACAACGTAGGGCAACTTACTGCTAAGATGAAAATGCGTGCAAGCCGTAT--------
nad42_II   2491 GGCACTCGCTATGACATGCGAAGAAGGCCGTCCACTGATGTGTATAACCTCGATAGAC------CGCGAAGGGCATTCCATGTAAGCCCGATCGCCCGGC
rpl16I_II  1633 GCCAC-----------TATAACATAGAATGTTCGGTGGCGTGACCGCCACAAAGAGAT------CGCAGGCGGAG---------AGCCGTAT--------

atp81_II   1623 ------------------------------------------GATGGGTAACTATCACGTACGGTTACGAGAAGGGGGCCCTGAGGGCGCCGCAATGGTG
nad42_II   2585 ACCTTCACTCAACCGAAGTCCACAAGACCACCCCGAAGGGCGAAGCGGTGTGCTTCGCAACCGGTTGCGAACCTGGTG-------AGCAACCTATCTGCG
rpl16I_II  1699 ------------------------------------------GAACGATAAATTTCATGTACGGTTCGGAGGGCAGTA----------------------

atp81_II   1681 ATTACCCGTT-----GTGATTAGCCGGAAGGGTTTTCTATTCTA-----------------
nad42_II   2678 GTTATCCACTACTAGGTGGCTAACCAGCCGTATAAACGGTGCCTCGGCCCCTGACCCCTAC
rpl16I_II  1735 -----------------------------------------------CCACTGACCCCCAT
```