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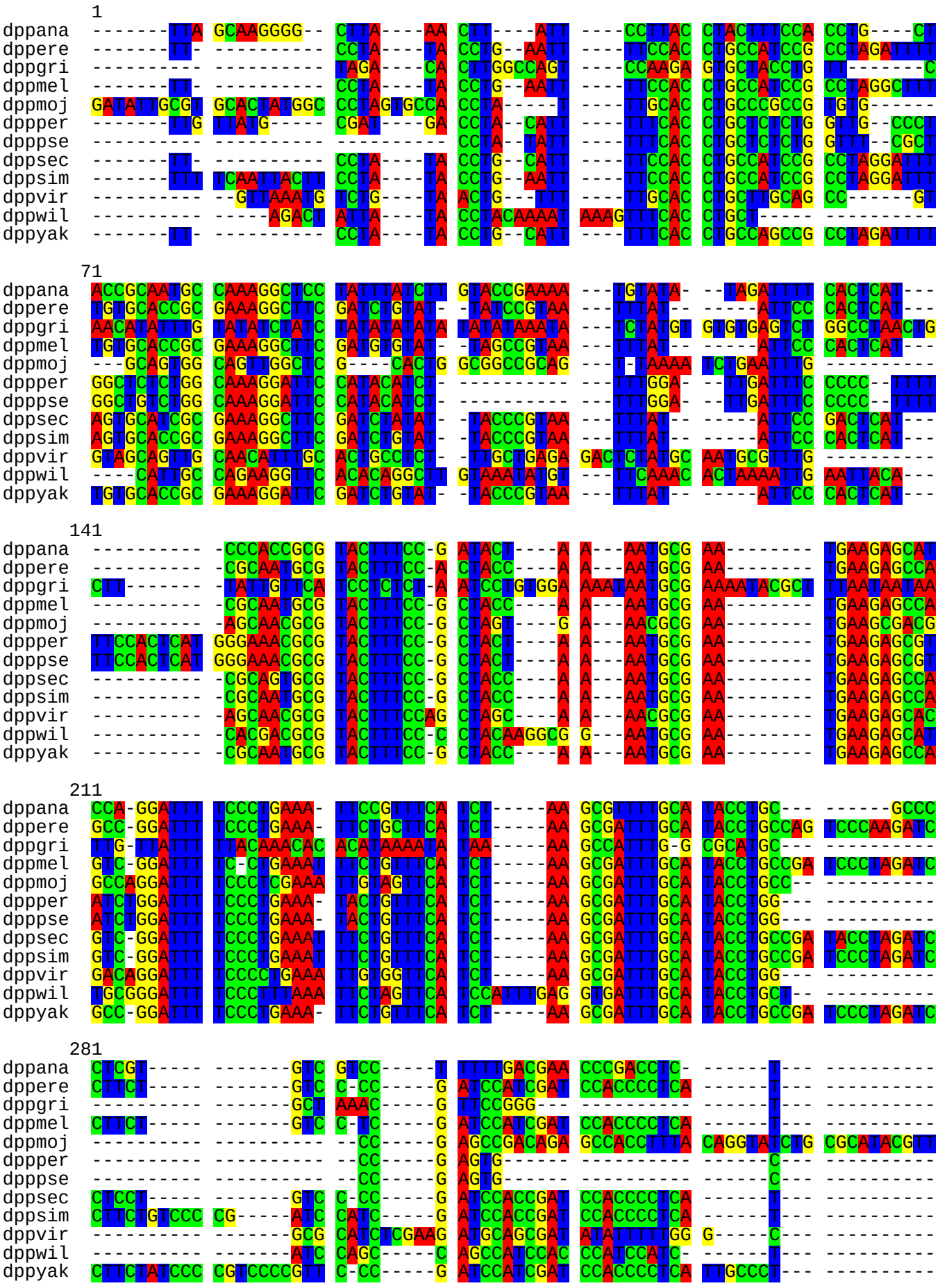

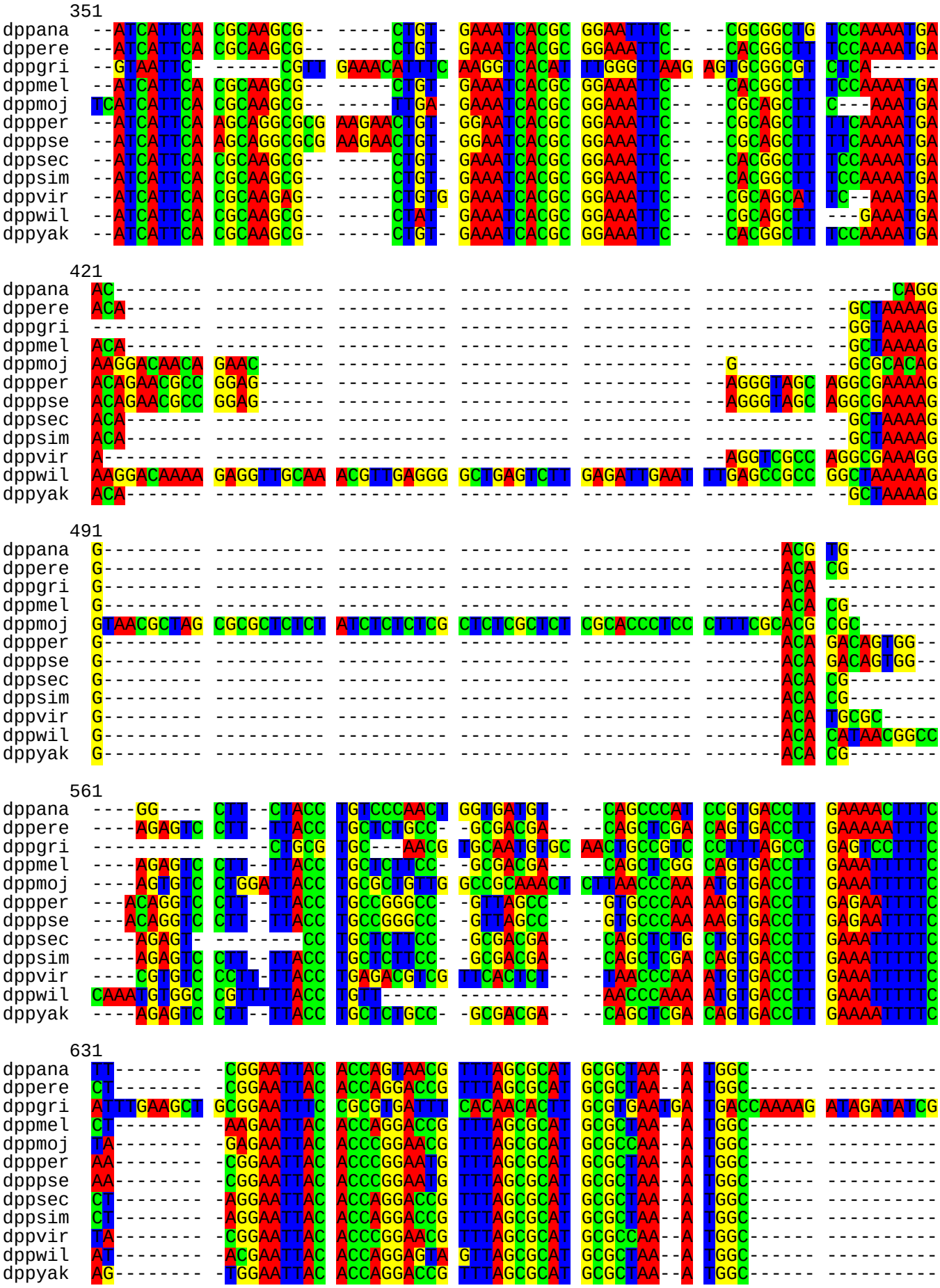
351
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dppere --ATCATTCA CGCAAGCG-- -----CTGT- GAAATCACGC GGAAATTC-- --CACGGCTT TCCAAAATGA
dppgri --GTAATTC- ------CGTT GAAACATTTC AAGGTCACAT TTGGGTTAAG AGTGCGGCGT CTCA------
dppmel --ATCATTCA CGCAAGCG-- -----CTGT- GAAATCACGC GGAAATTC-- --CACGGCTT TCCAAAATGA
dppmoj TCATCATTCA CGCAAGCG-- -----TTGA- GAAATCACGC GGAAATTC-- --CGCAGCTT C----AAATGA
dppper --ATCATTCA AGCAGGCGCG AAGAACTGT- GGAATCACGC GGAAATTC-- --CGCAGCTT TTCAAAATGA
dpppse --ATCATTCA AGCAGGCGCG AAGAACTGT- GGAATCACGC GGAAATTC-- --CGCAGCTT TTCAAAATGA
dppsec --ATCATTCA CGCAAGCG-- -----CTGT- GAAATCACGC GGAAATTC-- --CACGGCTT TCCAAAATGA
dppsim --ATCATTCA CGCAAGCG-- -----CTGT- GAAATCACGC GGAAATTC-- --CACGGCTT TCCAAAATGA
dppvir --ATCATTCA CGCAAGAG-- -----CTGTG GAAATCACGC GGAAATTC-- --CGCAGCAT TC--AAATGA
dppwil --ATCATTCA CGCAAGCG-- -----CTAT- GAAATCACGC GGAAATTC-- --CGCAGCTT ---GAAATGA
dppyak --ATCATTCA CGCAAGCG-- -----CTGT- GAAATCACGC GGAAATTC-- --CACGGCTT TCCAAAATGA
421
dppana AC-------- ---------- ---------- ---------- ---------- ---------- ------CAGG
dppere ACA------- ---------- ---------- ---------- ---------- ---------- --GCTAAAAG
dppgri ---------- ---------- ---------- ---------- ---------- ---------- --GGTAAAAG
dppmel ACA------- ---------- ---------- ---------- ---------- ---------- --GCTAAAAG
dppmoj AAGGACAACA GAAC------ ---------- ---------- ---------- --G------- --GCGCACAG
dppper ACAGAACGCC GGAG------ ---------- ---------- ---------- --AGGGTAGC AGGCGAAAAG
dpppse ACAGAACGCC GGAG------ ---------- ---------- ---------- --AGGGTAGC AGGCGAAAAG
dppsec ACA------- ---------- ---------- ---------- ---------- ---------- --GCTAAAAG
dppsim ACA------- ---------- ---------- ---------- ---------- ---------- --GCTAAAAG
dppvir A--------- ---------- ---------- ---------- ---------- --AGGTCGCC AGGCGAAAGG
dppwil AAGGACAAAA GAGGTTGCAA ACGTTGAGGG GCTGAGTCTT GAGATTGAAT TTGAGCCGCC GGCTAAAAAG
dppyak ACA------- ---------- ---------- ---------- ---------- ---------- --GCTAAAAG
491
dppana G--------- ---------- ---------- ---------- ---------- -------ACG TG--------
dppere G--------- ---------- ---------- ---------- ---------- -------ACA CG--------
dppgri G--------- ---------- ---------- ---------- ---------- -------ACA ----------
dppmel G--------- ---------- ---------- ---------- ---------- -------ACA CG--------
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dppper G--------- ---------- ---------- ---------- ---------- -------ACA GACAGTGG--
dpppse G--------- ---------- ---------- ---------- ---------- -------ACA GACAGTGG--
dppsec G--------- ---------- ---------- ---------- ---------- -------ACA CG--------
dppsim G--------- ---------- ---------- ---------- ---------- -------ACA CG--------
dppvir G--------- ---------- ---------- ---------- ---------- -------ACA TGCGC-----
dppwil G--------- ---------- ---------- ---------- ---------- -------ACA CATAACGGCC
dppyak G--------- ---------- ---------- ---------- ---------- -------ACA CG--------
561
dppana ----GG---- CTT--CTACC TGTCCCAACT GGTGATGT-- --CAGCCCAT CCGTGACCTT GAAAACTTTC
dppere ----AGAGTC CTT--TTACC TGCTCTGCC- -GCGACGA-- --CAGCTCGA CAGTGACCTT GAAAAATTTC
dppgri ---------- -----CTGCG TGC---AACG TGCAATGTGC AACTGCGGTC CCTTTAGCCT GAGTCCTTTC
dppmel ----AGAGTC CTT--TTACC TGCTCTTCC- -GCGACGA-- --CAGCTCGG CAGTGACCTT GAAATTTTTC
dppmoj ----AGTGTC CTGGATTACC TGCGCTGTTG GCCGCAAACT CTTAACCCAA ATGTGACCTT GAAATTTTTC
dppper ---ACAGGTC CTT--TTACC TGCCGGGCC- -GTTAGCC-- --GTGCCCAA AAGTGACCTT GAGAATTTTC
dpppse ---ACAGGTC CTT--TTACC TGCCGGGCC- -GTTAGCC-- --GTGCCCAA AAGTGACCTT GAGAATTTTC
dppsec ----AGAGTC --------CC TGCTCTTCC- -GCGACGA-- --CAGCTCTG CTGTGACCTT GAAATTTTTC
dppsim ----AGAGTC CTT--TTACC TGCTCTTCC- -GCGACGA-- --CAGCTCGA CAGTGACCTT GAAATTTTTC
dppvir ----CGTGTC CCTT-TTACC TGAGACGTCG TTCACTCT-- --TAACCCAA ATGTGACCTT GAAATTTTTC
dppwil CAAAAGTGGC CGTTTTTACC TGTT------ ---------- --AACCCAAA ATGTGACCTT GAAATTTTTC
dppyak ----AGAGTC CTT--TTACC TGCTCTGCC- -GCGACGA-- --CAGCTCGA CAGTGACCTT GAAAATTTTC
631
dppana TT-------- -CGGAATTAC ACCAGTAACG TTTAGCGCAT GCGCTAA--A TGGC------ ----------
dppere CT-------- -CGGAATTAC ACCAGGACCG TTTAGCGCAT GCGCTAA--A TGGC------ ----------
dppgri ATTTGAAGCT GCGGAATTTC CGCGTGATTT CACAACACTT GCGTGAATGA TGACCAAAAG ATAGATATCG
dppmel CT-------- -AAGAATTAC ACCAGGACCG TTTAGCGCAT GCGCTAA--A TGGC------ ----------
dppmoj TA-------- -GAGAATTAC ACCCGGAACG TTTAGCGCAT GCGCCAA--A TGGC------ ----------
dppper AA-------- -CGGAATTAC ACCCGGAATG TTTAGCGCAT GCGCTAA--A TGGC------ ----------
dpppse AA-------- -CGGAATTAC ACCCGGAATG TTTAGCGCAT GCGCTAA--A TGGC------ ----------
dppsec CT-------- -AGGAATTAC ACCAGGACCG TTTAGCGCAT GCGCTAA--A TGGC------ ----------
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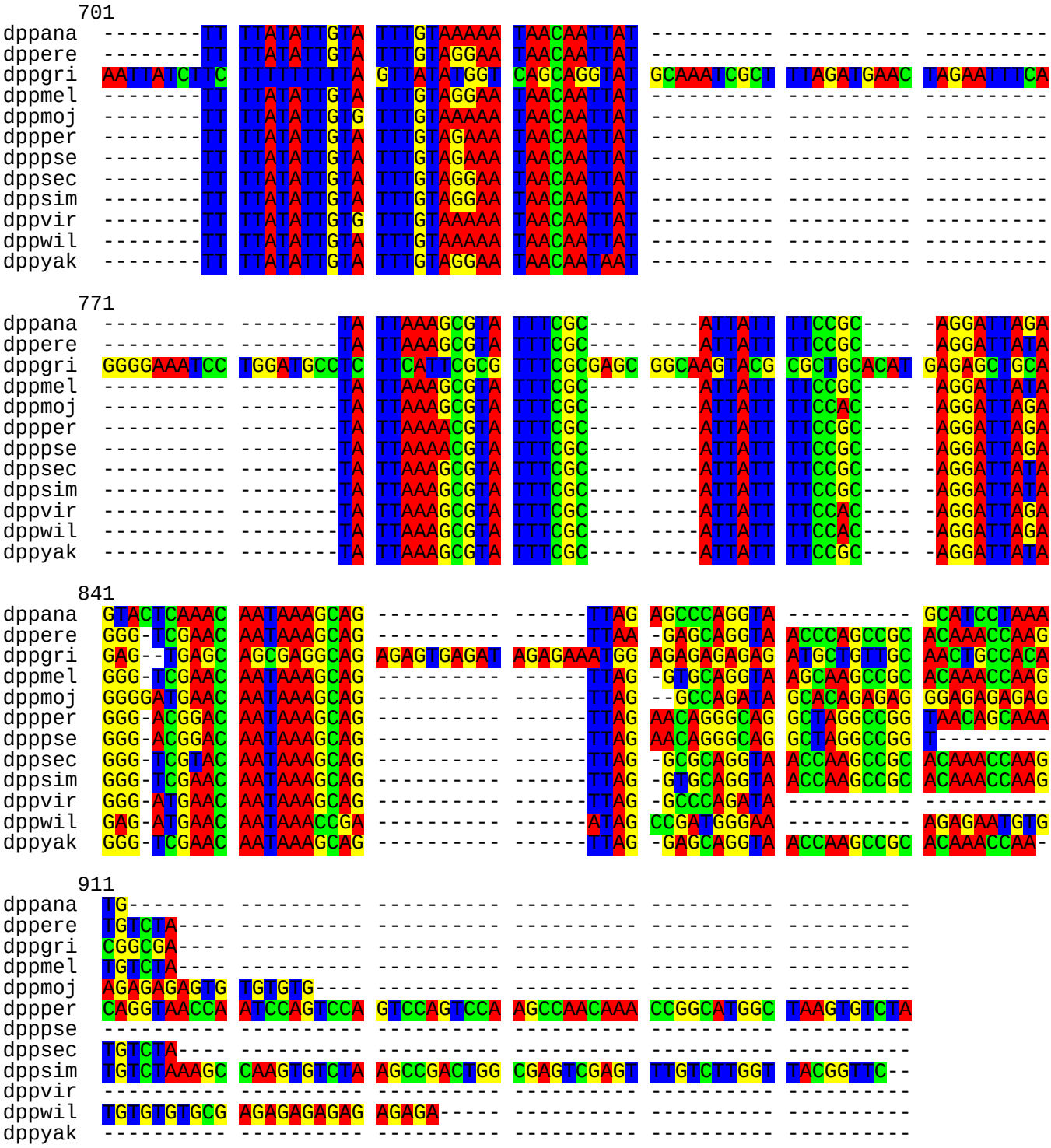
dppvir TA-------- -CGGAATTAC ACCCGGAACG TTTAGCGCAT GCGCCAA--A TGGC------ ----------
dppwil AT-------- -ACGAATTAC ACCAGGAGTA GTTAGCGCAT GCGCTAA--A TGGC------ ----------
dppyak AG-------- -TGGAATTAC ACCAGGACCG TTTAGCGCAT GCGCTAA--A TGGC------ ----------


701
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dppmel --------TT TTATATTGTA TTTGTAGGAA TAACAATTAT ---------- ---------- ----------
dppmoj --------TT TTATATTGTG TTTGTAAAAA TAACAATTAT ---------- ---------- ----------
dpppper --------TT TTATATTGTA TTTGTAGAAA TAACAATTAT ---------- ---------- ----------
dppppse --------TT TTATATTGTA TTTGTAGAAA TAACAATTAT ---------- ---------- ----------
dppsec --------TT TTATATTGTA TTTGTAGGAA TAACAATTAT ---------- ---------- ----------
dppsim --------TT TTATATTGTA TTTGTAGGAA TAACAATTAT ---------- ---------- ----------
dppvir --------TT TTATATTGTG TTTGTAAAAA TAACAATTAT ---------- ---------- ----------
dppwil --------TT TTATATTGTA TTTGTAAAAA TAACAATTAT ---------- ---------- ----------
dppyak --------TT TTATATTGTA TTTGTAGGAA TAACAATAAT ---------- ---------- ----------
771
dppana ---------- --------TA TTAAAGCGTA TTTCGC---- ----ATTATT TTCCGC---- -AGGATTAGA
dppere ---------- --------TA TTAAAGCGTA TTTCGC---- ----ATTATT TTCCGC---- -AGGATTATA
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dppmel ---------- --------TA TTAAAGCGTA TTTCGC---- ----ATTATT TTCCGC---- -AGGATTATA
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dppsim ---------- --------TA TTAAAGCGTA TTTCGC---- ----ATTATT TTCCGC---- -AGGATTATA
dppvir ---------- --------TA TTAAAGCGTA TTTCGC---- ----ATTATT TTCCAC---- -AGGATTAGA
dppwil ---------- --------TA TTAAAGCGTA TTTCGC---- ----ATTATT TTCCAC---- -AGGATTAGA
dppyak ---------- --------TA TTAAAGCGTA TTTCGC---- ----ATTATT TTCCGC---- -AGGATTATA
841
dppana GTACTCAAAC AATAAAGCAG ---------- ------TTAG AGCCCAGGTA ---------- GCATCCTAAA
dppere GGG-TCGAAC AATAAAGCAG ---------- ------TTAA -GAGCAGGTA ACCCAGCCGC ACAAACCAAG
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dppmel GGG-TCGAAC AATAAAGCAG ---------- ------TTAG -GTGCAGGTA AGCAAGCCGC ACAAACCAAG
dppmoj GGGGATGAAC AATAAAGCAG ---------- ------TTAG --GCCAGATA GCACAGAGAG GGAGAGAGAG
dpppper GGG-ACGGAC AATAAAGCAG ---------- ------TTAG AACAGGGCAG GCTAGGCCGG TAACAGCAAA
dppppse GGG-ACGGAC AATAAAGCAG ---------- ------TTAG AACAGGGCAG GCTAGGCCGG T---------
dppsec GGG-TCGTAC AATAAAGCAG ---------- ------TTAG -GCGCAGGTA ACCAAGCCGC ACAAACCAAG
dppsim GGG-TCGAAC AATAAAGCAG ---------- ------TTAG -GTGCAGGTA ACCAAGCCGC ACAAACCAAG
dppvir GGG-ATGAAC AATAAAGCAG ---------- ------TTAG -GCCCAGATA ---------- ----------
dppwil GAG-ATGAAC AATAAACCGA ---------- ------ATAG CCGATGGGAA ---------- AGAGAATGTG
dppyak GGG-TCGAAC AATAAAGCAG ---------- ------TTAG -GAGCAGGTA ACCAAGCCGC ACAAACCAA-
911
dppana TG-------- ---------- ---------- ---------- ---------- ----------
dppere TGTCTA---- ---------- ---------- ---------- ---------- ----------
dppgri CGGCGA---- ---------- ---------- ---------- ---------- ----------
dppmel TGTCTA---- ---------- ---------- ---------- ---------- ----------
dppmoj AGAGAGAGTG TGTGTG---- ---------- ---------- ---------- ----------
dpppper CAGGTAACCA ATCCAGTCCA GTCCAGTCCA AGCCAACAAA CCGGCATGGC TAAGTGTCTA
dppppse ---------- ---------- ---------- ---------- ---------- ----------
dppsec TGTCTA---- ---------- ---------- ---------- ---------- ----------
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dppvir ---------- ---------- ---------- ---------- ---------- ----------
dppwil TGTGTGTGCG AGAGAGAGAG AGAGA----- ---------- ---------- ----------
dppyak ---------- ---------- ---------- ---------- ---------- ----------