

Gblocks 0.91b Results

Processed file: **pasted_alignment**

Number of sequences: **112**

Alignment assumed to be: **DNA**

New number of positions: **1258** (selected positions are underlined in blue)

	10	20	30	40	50	60
1093CAN .	=====+=====+=====+=====+=====+=====+					
1052SA .	GCCCGATAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GAT		
1116CAN .	GCCCGATAATTCTGCAGAGAATTTTCG-TGT-CAACAATTTTT	----	CATCACCCC	-GAT		
1070EIRE .	GCCCGATAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GAT		
1099CAN .	GCCCGATAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GAT		
1104CAN .	GCCCGATAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GAT		
1087CAN .	GCCCGATAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GAT		
360UK .	GCCCGATAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GAT		
2111HUN .	GCCCGATA-TTCTGCAGAGAATTTTCG-TGT-C-ACAATTTTT	----	CATCACCCC	-GAT		
217RUS .	GCCCGATAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GAT		
204UK .	GCCCGATAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GAT		
206RUS .	GCCCGATAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GAT		
261SIB .	GCCCGATAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GAT		
265SIB .	GCCCGATAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GAT		
2784THAI .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
83BEGY .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
1102CAN .	GTCCGACAATTCTGCAGAGAATTTTCG-TGT-CAACAATTTTT	----	CATCACCCC	-GCT		
588LAOS .	GTCCGACAATTCTGCAGAGAATTTTCGATGT-CGACAATTTTT	----	CATCACCCC	-GCT		
1596AT .	GTCCGACAATTCTGCAGAGAATTTTCG-TGT-CAACAATTTTT	----	CATCACCCC	-GCT		
1720CAM .	--CGACAATTCTGCAGAGAATTTTCG-TGT-CAACAATTTTT	----	CATCACCCC	-GCT		
1722CAM .	XXXXXXXXXXTCTGCAGAGAATTTTCG-TGT-CAACAATTTTT	----	CATCACCCC	-GCT		
1724CAM .	GCCCGAC-ATTCTGCAGAGA-TTTTCG-TGT-CAACAATTTTT	----	CATCACCCC	-GCT		
334USA .	GTCCGACAATTCTGCAGAGAATTTTCG-TGT-CAACAATTTTT	----	CATCACCCC	-GCT		
335USA .	GTCCGACAATTCTGCAGAGAATTTTCG-TGT-CAACAATTTTT	----	CATCACCCC	-GCT		
1081WIS .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
1069WIS .	GTCCGACAATTCTGCAGAGAATTTTCG-TGT-CAACAATTTTT	----	CATCACCCC	-GCT		
1107CAN .	GTCCGACAATTCTGCAGAGAATTTTCG-TGT-CAACAATGTTT	----	CATCACCCC	-GCT		
1108PEN .	GTCCGACAATTCTGCAGAGAATTTTCG-TGT-CAACAATGTTT	----	CATCACCCC	-GCT		
1110CAN .	GTCCGACAATTCTGCAGAGAATTTTCG-TGT-CAACAATTTTT	----	CATCACCCC	-GCT		
JBSE241 .	GCCCGACAATTCTGCAGAGAATTTTCG-TGC-CGACAATTTTT	----	CATCACCCC	-GCT		
246PHI .	GCCCGACAA-----TTTTT	----	CATCACCCC	-GCT		
51SA .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
2618ETHI .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
1068WIS .	GTCCGACAATTCTGCAGAGAATTTTCG-TGT-CAACAATTTTT	----	CATCACCCC	-GCT		
238CR .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
NR5555 .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
NR6839 .	GCCCGACAATTCTTCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CACCACCCC	-GCT		
2624ETHI .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CACCCCCCCCCT			
845EGY .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CACCCCCCCCCT			
JBPER12 .	GCCCGACGATTCTGAAGAGAATTTTCG-TGT-CGACAATTTTT	----	CGTCACCCC	-GCT		
1717VIET .	GCCCGACGATTCTGAAGAGA-TTTTCG-TGT-CGACAATTTTT	----	CGTCACCCC	-GCT		
709BRAZ .	GCCCGACGATTCTGAAGAGAATTTTCG-TGT-CGACAATTTTT	----	CGTCACCCC	-GCT		
878IRAN .	GCCCGACGATTCTGAAGAGAATTTTCG-TGT-CGACAATTTTT	----	CGTCACCCC	-GCT		
239CR .	GCCCGACGATTCTGAAGAGAATTTTCG-TGT-CGACAATTTTT	----	CGTCACCCC	-GCT		
202COM .	ACCCGACAATTCTGAAGAGAATTTTCG-TGTTTCGACAATTTTT	----	CATCACCCC	-GCT		
1064MEX .	GCCCGACGATTCTGAAGAGAATTTTCG-TGT-CGACAATTTTT	----	CGTCACCCC	-GCT		
596BRAZ .	GCCCGACGATTCTGAAGAGAATTTTCG-TGT-CGACAATTTTT	----	CGTCACCCC	-GCT		
333USA .	GCCCGACGATTCTGAAGAGAATTTTCG-TGT-CGACAATTTTT	----	CGTCACCCC	-GCT		
2610ETHI .	GCCCGACAATTCTTCAGAC--TTTTTG-GGT-CGACAATTTTT	----	CGTCACCCC	-GCT		
1044RW .	GCCCGACAATTCTTCAGAC--TTTTTG-GGT-CGACAATTTTT	----	CGTCACCCC	-GCT		
JBZN111 .	GCCCGCGGATTCTGAAGAGAATTTTCG-TGT-CGACAATTTTT	----	CGTCACCCC	-GCT		
JBZN12 .	GCCCGACAATTCTTCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
JBZN24 .	GCCCGCGGATTCTGAAGAGAATTTTCG-TGT-CGACAATTTTT	----	CGTCACCCC	-GCT		
693CHINA .	GCCCGACAATTCT--AGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
1058RW .	GCCCGACAATTCTTCAGAC--TTTTTG-GGT-CGACAATTTTT	----	CGTCACCCC	-GCT		
590AUS .	ACCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
53SA .	GCCCGACAATTCTTCAGAC--TTTTTG-GGT-CGACAATTTTT	----	CGTCACCCC	-GCT		
1075WIS .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
939GER .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
GA3804 .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
1599AT .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
1941AT .	GCCCGACA-TTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
291NE .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
2301SAR .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
2313SAR .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
271NE .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
1935GER .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
JBRS122 .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
276NE .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
272NE .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
2673ETHI .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
1084AUSW .	GCCCGACGATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
JBPER62 .	GCCCGACAATTCTGAAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
JBZN72 .	GCCCGACAATTCTTCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
1065MEX .	GCCCGACGATTCTGAAGAGAATTTTCG-TGT-CGACAATTTTT	----	CGTCACCCC	-GCT		
646HAWAI .	GCCCGACGATTCTGAAGAGAATTTTCG-TGT-CGACAATTTTT	----	CGTCACCCC	-GCT		
727INDIA .	GCCCGACGATTCTGAAGAGAATTTTCG-TGT-CGACAATTTTT	----	CGTCACCCC	-GCT		
743MALE .	GCCCGACGATTCTGAAGAGAATTTTCG-TGT-CGACAATTTTT	----	CGTCACCCC	-GCT		
1059MEX .	GCCCGACGATTCTGAAGAGAATTTTCG-TGT-CGACAATTTTT	----	CGTCACCCC	-GCT		
1061RW .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
1066MEX .	GCCCGACGATTCTGAAGAGAATTTTCG-TGT-CGACAATTTTT	----	CGTCACCCC	-GCT		
1095BALI .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
1505MAUR .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
1818ETHI .	GCCCGATAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GAT		
1934AT .	GCCCGACA-TTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
245CR .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
2710ETHI .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
274NE .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
3408PNG .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CAACAATTTTT	----	CATCACCCC	-GCT		
3409PNG .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CAACAATTTTT	----	CATCACCCC	-GCT		
410MALAY .	GCCCGACAATTCTGCAGAGGATTTTCG-TGT-CAACAATTTTT	----	CCATCACCCC	-GCT		
836EGY .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
837EGY .	GCCCGACAATCTACAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
JBRO111 .	GCCCGATAATTCTGCAGAGAATTTTCG-TGT-CGACAATTTTT	----	CATCACCCC	-GAT		
brunneoviridis4	GTCCGACAATTCTGAAGGGAATTTTCG-TGT-CGACAATTTTT	----	CATCTCCCC	-GCT		
brunneoviridis1	GTCCGACAATTCTGAAGGGAATTTTCG-TGT-CGACAATTTTT	----	CATCTCCCC	-GCT		
pleurotumCPK211	GCCCGACGATTCTGCAGAGAATTTTCG-TGT-CGACAATTTGA	----	TATCACCCC	-GCC		
PLEUROTICOLA .	XXXXXXXXGA-----TTTG-TGT-CGACA-TTTTTC	----	TCACCCC	-GCT		
epimycosCPK1981	GCTCGATCATTTCTGAAGAGAATTTTCG-TGT-CGATAATTTCT	----	CATCACCCC	-GCT		
alniCPK3124 ...	GCTCGATCATTTCTGAAGAGAATCTTCG-TGT-CGACAATTTTT	----	CACCACCCC	-GCT		
CPK5TAwa .	GCTCGATCATTTCTGAAGAGAATCTTCG-TGT-CGACAATTTTT	----	CCACCACCCC	-GCT		
2974lobau .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGCCAATTTTT	----	CATCATCCC	-GCT		
2975lobau .	GCCCGACAATTCTGCAGAGAATTTTCG-TGT-CGCCAATTTTT	----	CATCATCCC	-GCT		
aggressivumCPK3	GCTCGATCATTTCTGAAGAGAAT-----TGT-CGACAATTTTT	----	CATCACCCC	-GCT		
atrogelatinosac	GCCCGACAATTCTGAAGAGAATTTTCG-TGC-CGACAATTTTT	----	CATCACCCC	-GCT		

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atrogelatinosaC GCGGACAAATCTGAAGAGAATTTTCG-TGC-CGACAATTTTT----CATCACCC-6CT
cerinumCPK293 GCTCGACAATTCTGAATAGAATTTTCG-TGT-CAACAATTTTT----CATCACCC-6CT
cerinumCPK854 GCTCGACAATTCTGAATAGAATTTTCG-TGT-CAACAATTTTT----CATCACCC-6CT
tomentosumCPK88 GCTCGACAATTCTGAATAGAATTTTCG-TGT-CAACAATTTTT----CACCACCC-6CT
stramineaGJS028 GCGGACAAATCTGAAAAGAATTTTCG-TGT-CAACAACCTTTT----CGTCACCC-6CT
velutinumCPK312 GCGGACAAATCTGAAAAGAATTTTCG-TGT-CAATAATTTTT----CGTCACCC-6CT
catoptronGJS027 ACCCGACAATTCTGAACAGAATTTTCA-TGT-CAAATATTTTTTTTCATCACCC-6CT
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70      80      90      100     110     120
=====+=====+=====+=====+=====+=====+
1093CAN . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GGCTGTC-GTTTG
1052SA . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GGCTGTC-GTTTG
1116CAN . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GGCTGTC-GTTTG
1070EIRE . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GGCTGTC-GTTTG
1099CAN . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GGCTGTC-GTTTG
1104CAN . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GGCTGTC-GTTTG
1087CAN . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GGCTGTC-GTTTG
360UK . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GGCTGTC-GTTTG
2111HUN . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GGCTGTC-GTTTG
217RUS . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GGCTGTC-GTTTG
204UK . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GGCTGTC-GTTTG
206RUS . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GGCTGTC-GTTTG
261SIB . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GGCTGTC-GTTTG
265SIB . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GGCTGTC-GTTTG
2784THAI . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAAAAATTTTTT-----GCTGTC-GTTTG
838EGY . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAAA---TTTTTTT---GCTGTC-GTTTG
1102CAN . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAAA---TTTTTTT---GCTGTC-GTTTG
588LAOS . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAAA---TTTTTTT---GCTGTC-GTTTG
1596AT . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAAA---TTTTTTT---GCTGTC-GTTTG
1720CAN . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-GTTTG
1722CAN . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-GTTTG
1724CAN . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-GTTTG
334USA . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAAA---TTTTTTT---GCTGTC-GTTTG
335USA . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAAA---TTTTTTT---GCTGTC-GTTTG
1081WIS . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTTTTTT---GCTGTC-GTTTG
1069WIS . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAAA---TTTTTTT---GCTGTC-GTTTG
1107CAN . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAAA---TTTTTTT---GCTGTC-GTTTG
1108PEN . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAAA---TTTTTTT---GCTGTC-GTTTG
1110CAN . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAAA---TTTTTTT---GCTGTC-GTTTG
JBSE241 . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-GTTTG
246PHI . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-GTXXX
51SA . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-GTTTG
2618ETHI . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTTTT---GCTGTC-GTTTG
1068WIS . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAAA---TTTTTTT---GCTGTC-GTTTG
238CR . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTTTT---CTGTC-GTTTG
NR5555 . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTTTT---CTGTC-GTTTG
NR6839 . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTTTT---GCTGTC-GTTTG
2624ETHI . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---CCCTGTC-GTTTG
845EGY . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---CCCTGTC-GTTTG
JBPER12 . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-TTTTG
1717VIET . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTATC-TTTTG
709BRAZ . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-TTTTG
878IRAN . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-TTTTG
239CR . TTGCATTACCACTC---TG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-TTTTG
202COM . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGCTGT-TG
1064MEX . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-TTTTG
596BRAZ . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-TTTTG
333USA . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-TTTTG
2610ETHI . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTTTT---GCTGCC-GTTTG
1044RW . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTTTT---GCTGCC-GTTTG
JBNZ111 . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-TTTTG
JBNZ12 . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTTTT---GCTGCC-GTTTG
JBNZ24 . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-TTTTG
693CHINA . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTTTT---GCTGCC-GTTTG
1058RW . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTTTT---GCTGCC-GTTTG
590AUS . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTTTT---GCTGCC-GTTTG
53SA . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTTTT---GCTGCC-GTTTG
1075WIS . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-GTTTG
939GER . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-GTTTG
GA3804 . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-GTTTG
1599AT . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAAA---TTTTTTT---GCTGTC-GTTTG
1941AT . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAAA---TTTTTTT---GCTGTC-GTTTG
291NE . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTTTT---CTGTC-GTTTG
2301SAR . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAAA---TTTTTTTTT---CTGTC-GTTTG
2313SAR . TTCCGTTACCCCTCCTTTG-CAGCG-ACGCAAAA---TTTTTTTTT---GCTGTC-GTCTG
271NE . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTTTT---CTGTC-GTTTG
1935GER . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAAA---TTTTTTT---GCTGTC-GTTTG
JBRS122 . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAAA---TTTTTTT---CTGTC-GTTTG
276NE . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTTTT---GCTGCC-GTTTG
272NE . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTTTT---GCTGCC-GTTTG
2673ETHI . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTTTT---GCTGCC-GTTTG
1084AUSW . TTCCGTTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTTTTTT---GCTGTC-GTTTG
JBPER62 . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTTTT---GCTGTC-GTTTG
JBNZ72 . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTTTT---GCTGCC-GTTTG
1065MEX . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-TTTTG
646HAWAI . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-TTTTG
727INDIA . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-TTTTG
743MALE . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-TTTTG
1059MEX . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTTTT---GCTGTC-TTTTG
1061RW . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTTTT---CTGTC-GTTTG
1066MEX . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-TTTTG
1095BALI . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-GTTTG
1505MAUR . TTGCATTACCCCTCCTTTG-CA---ACGCAAA---TTTTTTT---GGCTGTC-GTTTG
1818ETHI . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GGCTGTC-GTTTG
1934AT . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAAAATTTTTT-----GCTGTC-GTTTG
245CR . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-GTTTG
2710ETHI . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-GTTTG
274NE . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GCTGTC-GTTTG
3408PNG . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAAA---TTTTTTT---GCTGTC-GTTTG
3409PNG . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAAA---TTTTTTT---GCTGTC-GTTTG
410MALAY . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTTTT---GCTGTC-TTTTG
836EGY . TTGCATTACCCCTCCTTTG-CA---ACGCAAA---TTTTTTTTT---GGCTGTC-GTTTG
837EGY . TTGCATTACCCCTCCTTTG-CA---ACGCAAA---TTTTTTT---GGCTGTC-GT-TG
JBRO111 . TTGCATTACCCCTCCTTTG-CAGCG-ACGCAAA---TTTTTTT---GGCTGTC-GTTTG
brunneoviridis4 TTCCGTTACCCCTCCTTTG-CAGC-AACGCAAAA---TTTTTTTTT---GCTGTGCTTTTG
brunneoviridis1 TTCCGTTACCCCTCCTTTG-CAGC-AACGCAAAA---TTTTTTTTT---GCTGTGCTTTTG
pleurotumCPK211 TTCCGTTACCCCTCCTTTG-GAGC-GACGCAAA---TTTTTTTTT---GGCAGCC-GTTTG
PLEUROTICOLA . TTCCGTTACCCCTCCTTTG-GAGC-GACGCAAA---TTTTTTGT---GGCAGCCTTTTG6
epimycetCPK1981 TTCCGTTACCCCTCCTTTG-CAGC-GACACAAA---TTTTTTTTT---GCTGTC-GTTTG
alniCPK3124 ... TTGGGTTACCCCTCCTTTG-CAGC-GACGCAAAA---TTTTTTTTT---GCTGTC-GTTTG
CPK5TAWA . TTCAATTACCCCTCCTTTG-CAGC-GACGCAAAA---TTTTCT---GCTGTC-GTTTG
2974lobau . TTGCATTACCCCTCCTTTG-CAGC-GACGCAAA---TTTTCTTTT---GCTGTC-GTTTG
2975lobau . TTGCATTACCCCTCCTTTG-CAGC-GACGCAAA---TTTTCTTTT---GCTGTC-GTTTG
aggressivumCPK3 TTGCATTACCCCTCCTTTG-CAGC-GACACAAGA---TTTTTTTTT---GCTGTC-GTTTG
atrogelatinosaC TTCCGTTACCCCTCCTTTG-CAGC-GACGCA-GA---TTTTTCT---GCTGTC-TTTTG

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atrogelatinosaC TTCCGTTACCCCTCCTTTG-CAGC-GACGCA-GA--TTTTTCT----GCTGTC-TTTTG
cerinumCPK293 . TTCCATTACCCCTCCTTTG-CAGC-GACGCAAA---TTTTTTTT---GCTGYCTTTTT
cerinumCPK854 . TTCCATTACCCCTCCTTTG-CAGCGGACGCAAA---TTTTTTTT---GCTGTC-TTTTG
tomentosumCPK88 TTCCATTACCCCTCCTTTG-CAGC-GACGCAAA---TTTTTTTT---GCTGTC-TTTTG
stramineaGJS028 TTCCATTACCCCTCCTTTG-CAGC-GACGCAAA---TTTTTTTT---GCTGTC-TTTTG
velutinumCPK312 TTCCATTACCCCTCCTTTG-CAGC-GACGCAAA---TTTTTTTT---GCTGTC-TTTTG
catoptronGJS027 TTCCATTACCCCTCCTTTG-CAGC-GACGCAAA---TTTTTTTT---GCAGT-ATTTTG
#####

130      140      150      160      170      180
=====+=====+=====+=====+=====+=====+
1093CAN . -GTTTT--AGTGGGGTTT-CTC--GTGCA-CCCC-ACTAGG-TCA-CT-GCTTTTTTTT--
1052SA . -GTTTT--AGTGGGGTTT-CTC--GTGCA-CCCC-ACTAGG-TCA-CT-GCTTTTTTTT--
1116CAN . -GTTTT--AGTGGGGTTT-CTC--GTGCA-CCCC-ACTAGG-TCA-CT-GCTTTTTTTT--
1070EIRE . -GTTTT--AGTGGGGTTT-CTC--GTGCA-CCCC-ACTAGG-TCA-CT-GCTTTTTTTT--
1099CAN . -GTTTT--AGTGGGGTTT-CTC--GTGCA-CCCC-ACTAGG-TCA-CT-GCTTTTTTTT--
1104CAN . -GTTTT--AGTGGGGTTT-CTC--GTGCA-CCCC-ACTAGG-TCA-CT-GCTTTTTTTT--
1087CAN . -GTTTT--AGTGGGGTTT-CTC--GTGCA-CCCC-ACTAGG-TCA-CT-GCTTTTTTTT--
360UK . -GTTTT--AGTGGGGTTT-CTC--GTGCA-CCCC-ACTAGG-TCA-CT-GCTTTTTTTT--
2111HUN . -GTTTT--AGTGGGGTTT-CTC--GTGCA-CCCC-ACTAGG-TCA-CT-GCTTTTTTTT--
217RUS . -GTTTT--AGTGGGGTTT-CTC--GTGCA-CCCC-ACTAGG-TCA-CT-GCTTTTTTTT--
204UK . -GTTTT--AGTGGGGTTT-CTC--GTGCA-CCCC-ACTAGG-TCA-CT-GCTTTTTTTT--
206RUS . -GTTTT--AGTGGGGTTT-CTC--GTGCA-CCCC-ACTAGG-TCA-CT-GCTTTTTTTT--
261SIB . -GTTTT--AGTGGGGTTT-CTC--GTGCA-CCCC-ACTAGG-TCA-CT-GCTTTTTTTT--
265SIB . -GTTTT--AGTGGGGTTT-CTC--GTGCA-CCCC-ACTAGG-TCA-CT-GCTTTTTTTT--
2784THAI . -GTTTT--AGTGGGGTTT-CTT--GTGCACCCCT-CTAGC-TCA-CT-GCTTTTTTTT--
838EGY . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCCACTAGC-TCA-CT-GCTTTTTTTT
1102CAN . -GTTTT-AAGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TC----G-TTTTTT--
588LAOS . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCCACTAGC-TCA-CT-GCTTTTTTTT
1596AT . -GTTTT-AAGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TC----G-TTTTTT--
1720CAN . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-ACTTTTTTTT--
1722CAN . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-ACTTTTTTTT--
1724CAN . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-ACTTTTTTTT--
334USA . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TC----G-TTTTTT--
335USA . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TC----G-TTTTTT--
1081WIS . -GTTTT--AGTGGGGTTT-CT--TGCA-CCCC-ACTAGC-TCA-CT-ACTTTTTTTT--
1069WIS . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TC----G-TTTTTT--
1107CAN . -GTTTT--AGTGGGGTTTT-T--TGTGCA-CCCC-ACTAGCCTC----G-TTTTTT--
1108PEN . -GTTTT--AGTGGGGTTTT-T--TGTGCA-CCCC-ACTAGCCTC----G-TTTTTT--
1110CAN . -GTTTT-AAGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TC----G-TTTTTT--
JBSER241 . -GTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCC-CT-GCTTTTTT---
246PHI . XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
51SA . -GTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCC-CT-GCTTTTTT---
2618ETHI . -GTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCC-CT-GCTTTTTT---
1068WIS . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TC----G-TTTTTT--
238CR . -GTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCC-CT-GCTTTTTT---
NR5555 . -GTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCC-CT-GCTTTTTT---
NR6839 . -GTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCC-CT-GCTTTTTT---
2624ETHI . -GTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCC-CT-GCTTTTTT---
845EGY . -GTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCC-CT-GCTTTTTT---
JBPER12 . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-GCTTTTTTTT
1717VIET . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-GCTTTTTTTT-
709BRAZ . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-GCTTTTTTTT
878IRAN . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-GCXXXXXXX
239CR . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-GCTTTTTTTT
202COM . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-G-TATTTTTT--
1064MEX . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-GCTTTTTTTT
596BRAZ . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-GCTTTTTTTT
333USA . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-GCTTTTTTTT
2610ETHI . A-TTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCA-CT-GCTTTTTT---
1044RW . A-TTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCA-CT-GCTTTTTT---
JBNZ111 . -GCTTT--AGTGGGGTTTT-T--TGTGCA-CCCC-ACTAGC-TCA-CT-GCAAT-----
JBNZ12 . A-TTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCA-CT-GCTTTTTTTT-
JBNZ24 . -GCTTT--AGTGGGGTTT-T-TTGTGCA-CCCC-ACTAGC-TCA-CT-GCAAT-----
693CHINA . AGTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCA-CT-GCTTTTTTTT---
1058RW . A-TTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCA-CT-GCTTTTTTTT---
590AUS . A-TTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCA-CT-GCTTTTTTTT---
53SA . A-TTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCA-CT-GCTTTTTTTT---
1075WIS . -GTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCA-CT-GCTTTTTT---
939GER . -GTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCA-CT-GCTTTTTT---
GA3804 . -GTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCA-CT-GCTTTTTT---
1599AT . -GTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCA-CT-GCTTTTTT---
1941AT . -GTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCA-CT-GCTTTTTT---
291NE . -GTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCA-CT-GCTTTTTT---
2301SAR . -GTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCA-CT-GCTTTTTT---
2313SAR . -GTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCA-CT-GCTTTTTT---
271NE . -GTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCA-CT-GCTTTTTT---
1935GER . -GTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCA-CT-GCTTTTTT---
JBRS122 . -GTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCA-CT-GCTTTTTT---
276NE . A-TTTTT--AGTGGGGTTT-CT-TTGTGCAACCCC-ACTAGC-TCA-CT-GCTTTTTTTT-
272NE . A-TTTTT--AGTGGGGTTT-CT-TTGTGCAACCCC-ACTAGC-TCA-CT-GCTTTTTTTT-
2673ETHI . A-TTTTT--AGTGGGGTTT-CTT-TGTGCAACCCC-ACTAGC-TCA-CT-GCTTTTTTTT-
1084AUSW . A-TTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-GCAATTTTTT-
JBPER62 . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-GCTTTTTTTT-
JBNZ72 . A-TTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCA-CT-GCTTTTTTTT-
1065MEX . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-GCTTTTTTTT
646HAWAI . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-GCTTTTTTTT
727INDIA . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-GCTTTTTTTT
743MALE . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-GCTTTTTTTT
1059MEX . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-GCTTTTTTTT
1061RW . -GTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCC-CT-GCTTTTTT---
1066MEX . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-GCTTTTTTTT
1095BALI . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-A-TTTTTTTT-
1505MAUR . A-TTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-C---TTTTTTT---
1818ETHI . -GTTTT--AGTGGGGTTT-CTC--GTGCA-CCCC-ACTAGG-TCA-CT-GCTTTTTTTT-
1934AT . -GTTTT--AGTGGGGTTT-CTC--TGTGCAACCCC-ACTAGC-TCA-CT-GCTTTTTT---
245CR . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-ACTTTTTTTT--
2710ETHI . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-ACTTTTTTTT--
274NE . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-ACTTTTTTTT--
3408PNG . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCCACTAGC-TCA--TGCGTTTTTTTT--
3409PNG . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCCACTAGC-TCA--TGCGTTTTTTTT--
410MALAY . -GTTTT--AGTGGGGTTT-GCT--GGTGA-CCCC-ACTAGC-TCA-CT-GCTTTTTTTT--
836EGY . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-C---TTTTTTT---
837EGY . -GTTTT--AGTGGGGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT---TTTTTTT---
JBRO111 . -GTTTT--AGTGGGGTTT-CTC--GTGCA-CCCC-ACTAGG-TCA-CT-GCTTTTTTTT--
brunneoviridis4 . -GTTTT--AGTGGAGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-GCTTTTTTTT---
brunneoviridis1 . -GTTTT--AGTGGAGTTT-CT--TGTGCA-CCCC-ACTAGC-TCA-CT-GCTTTTTTTT---
pleurotumCPK211 . -GCTTT--GGTGGGGTTT-T-GTGTGCA-CCCC-ACTAGC-TGC-CT-GCTTTTTTTT
PLEUROTICOLA . --CTTT--GGTGGGGTTT-C--GTGTGCA-CCCC-ACTAGC-TCA-CT-GCTTTTTTTT---
epiomycesCPK1981 . -GTTTT--AGTGGGGTTTCC--TGTGCA-CCCC-ACTAGC-TCA-CT-GCCTTTTTTTT-
alniCPK3124 ... -GTTTT--AGTGGGGT-CCCT--TGTGTA-CCCC-ACTAGC-TCA-CT-GCTTTTTTTT--
CPK5TAWA . GGTTT--AGTGGGGT-CCCT--TGTGCA-CCCC-ACTAGC-TCA-CT-GCTTTTTTTT--
2974lobau . -GTTTT--AGTGGGGTTTC-T--TGTGCA-CCCC-ACTAGC-TCA--TGCGTTTTTTTT--
2975lobau . -GTTTT--AGTGGGGTTTC-T--TGTGCA-CCCC-ACTAGC-TCA--TGCGTTTTTTTT--
aggressivumCPK3 . -GTTTT--AGTGGGGT-CCCT--TGTGCA-CCCCACTAGC-TCA-CT-GCTTTTTTTT
atrogelatinosaC . -GTTTC--AGTGGGGT-CC-C-TGCACA-CCCC-ACTGGC--CAGCT-GCTTTTTT----

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atrogelatinosaC -GTTTC--AGTGGGGTT-CC-C-TGCACA-CCCC-ACTGGC--CAGCT-GCTTTTT---
cerinumCPK293   -GTTTT--AGTGGGGTT--CTC-TGCGTA-CCCC-ACTAAC-TCA-CT-GTTTTTTT---
cerinumCPK854   -GTTTT--AGTGGGGTT--CTC-TGCGTA-CCCC-ACTAAC-TGA-CT-G-TTTTTT---
A-TTTTT--AGTGGGGTT--CTC-TGTGTA-CCCC-ACTAGC-TCA-CT-GCTTTTTT---
tomentosumCPK88 -GTTTT--AGTGGGGTTCC--TGCACA-CCCC-ACTAG--TCAACT-GCTTTTTT---
stramineaGJS028 -GTTTT--AGTGGGGTT-CC-C-TGCGCA-CCCC-ACTAGC-T-AACT-GC-TGTT---
velutinumCPK312 -GTTTT--AGTGGGGTT-CC-C-TGCGCA-CCCC-ACTAGC-T-AACT-GC-TGTT---
catoptronGJS027 A-TTTT--AGTGGGGTT-GC-C-TCTGCA-CCCC-ACTAAC-TTG-CT-ACTTGT---
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190      200      210      220      230      240
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1093CAN . -----CT-----GCTTCGCT-C-T-TACTG-CCAGCCATCATTTCAACGTGC
1052SA . -----CT-----GCTTCGCT-C-T-TACTG-CCAGCCATCATTTCAACGTGC
1116CAN . -----CT-----GCTTCGCT-C-T-TACTG-CCAGCCATCATTTCAACGTGC
1070EIRE . -----CT-----GCTTCGCT-C-T-TACTG-CCAGCCATCATTTCAACGTGC
1099CAN . -----CT-----GCTTCGCT-C-T-TACTG-CCAGCCATCATTTCAACGTGC
1104CAN . -----CT-----GCTTCGCT-C-T-TACTG-CCAGCCATCATTTCAACGTGC
1087CAN . -----CT-----GCTTCGCT-C-T-TACTG-CCAGCCATCATTTCAACGTGC
360UK . -----CT-----GCTTCGCT-C-T-TACTG-CCAGCCATCATTTCAACGTGC
2111HUN . -----CT-----GCTTCGCT-C-T-TACTG-CCAGCCATCATTTCAACGTGC
217RUS . -----CT-----GCTTCGCT-C-T-TACTG-CCAGCCATCATTTCAACGTGC
204UK . -----CT-----GCTTCGCT-C-T-TACTG-CCAGCCATCATTTCAACGTGC
206RUS . -----CT-----GCTTCGCT-C-T-TACTG-CCAGCCATCATTTCAACGTGC
261SIB . -----CT-----GCTTCGCT-C-T-TACTG-CCAGCCATCATTTCAACGTGC
265SIB . -----CT-----GCTTCGCT-C-T-TACTG-CCAGCCATCATTTCAACGTGC
2784THAI . TT-----CT-----GCTTCGCT-C-T-CAC TT-CCAGCCATCATTTCAACGTGC
838EGY . -----CT-----GCTTCGCT-C-T-CAC TT-CCAGCCATCATTTCAACGTGC
1102CAN . -----CT-----GCTTCGCT-C-T-CAC TT-CCAGCCATCATTTCAACGTAT
588LAOS . -----CT-----GCTTCGCT-C-T-CAC TT-CCAGCCATCATTTCAACGTGT
1596AT . -----CT-----GCTTCGCT-C-T-CAC TT-CCAGCCATCATTTCAACGTAT
1720CAN . -----CT-----GCTTCGCT-C-T-CAC TT-CCAGCCATCATTTCAACGTGC
1722CAN . -----CT-----GCTTCGCT-C-T-CAC TT-CCAGCCATCATTTCAACGTGC
1724CAN . -----CT-----GCTTCGCT-C-T-CAC TT-CCAGCCATCATTTCAACGTGC
334USA . -----CT-----GCTTCGCT-C-T-CAC TT-CCAGCCATCATTTCAACGTAT
335USA . -----CT-----GCTTCGCT-C-T-CAC TT-CCAGCCATCATTTCAACGTAT
1081WIS . -----CT-----ACTTTGCT-C-T-CAC TT-CCAGCCATCATTTCAACGTG
1069WIS . -----CT-----GCTTCGCT-C-T-CAC TT-CCAGCCATCATTTCAACGTAT
1107CAN . -----CT-----GCTTCGCT-C-T-CAC TT-CCAGCCATCATTTCAACGTGC
1108PEN . -----CT-----GCTTCGCT-C-T-CAC TT-CCAGCCATCATTTCAACGTGC
1110CAN . -----CT-----GCTTCGCT-C-T-CAC TT-CCAGCCATCATTTCAACGTAT
JBSER241 . -----CCT-----GCTTCACT-C-T-CAC TT-CCTCGTCATCATTTCAACGTGC
246PHI . XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
51SA . -----CCT-----GCTTCACT-C-T-CAC TT-CCTCGTCATCATTTCAACGTGC
2618ETHI . -----CCT-----GCTTCACT-C-T-CAC TT-CCTCGTCATCATTTCAACGTGC
1068WIS . -----CT-----GCTTCGCT-C-T-CAC TT-CCAGCCATCATTTCAACGTAT
238CR . -----CCT-----GCTTCACT-C-T-CAC TT-CCTCGTCATCATTTCAACGTGC
NR5555 . -----CCT-----GCTTCACT-C-T-CAC TT-CCTCGTCATCATTTCAACGTGC
NR6839 . -----CCT-----GCTTCACT-C-T-CAG TT-CTTCGTCATCATTTCAACGTGC
2624ETHI . -----CCT-----GCTTCACT-C-T-CAG TT-CTTCGTCATCATTTCAACGTGC
845EGY . -----CCT-----GCTTCACT-C-T-CAG TT-CTTCGTCATCATTTCAACGTGC
JBPER12 . TTT-----TG-----GCTTCACT-C-T-CAC TT-CCCCGCCAT---TCAACGTAC
1717VIET . -----CCT-TTTTT--GCTTCACT-C-T-CAC TT-CCAGCCAT---TCAACGTGC
709BRAZ . TTTTT-----TG-----GCTTCACT-C-T-CAC TT-CCCCGCCAT---TAAACGTAC
878IRAN . XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
239CR . TTTTTTTTTTTTTTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
202COM . -----CT-----GCTTCACT-C---ACTT-CCAGCCATCATTTCAACGTGT
1064MEX . TTTTTTTT---TG-----GCTTCACT-C-T-CAC TT-CCCCGCCAT---TCAACGTAC
596BRAZ . TTT-----TG-----GCTTCACT-C-T-CAC TT-CCCCGCCAT---TAAACGTCC
333USA . TTTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
2610ETHI . -----TG-----GCTTCA-T---T-CAC TT-CCAGTCATCATTTCAACGTGC
1044RW . -----TG-----GCTTCA-T---T-CAC TT-CCAGTCATCATTTCAACGTGC
JBNZ111 . -----TGTTTTTGTTCCT-C-T-CAC TT-CCTAGCCAT---TCAACGTGC
JBNZ12 . -----TG-----GCTTCACT---T-CAC TT-CCAGTCATCATTTCAACGTGC
JBNZ24 . -----TGTTTTTGTTCCT-C-T-CAC TT-CCTAGCCAT---TCAACGTGC
693CHINA . -----TG-----GCTTCACA-C-T-CAC TT-CCAAGTCATCATTTCAACGTGC
1058RW . -----TG-----GCTTCA-T---T-CAC TT-CCAGTCATCATTTCAACGTGC
590AUS . -----TG-----GCTTCACT---T-CAC TT-CCAGTCATCATTTCAACGTGC
53SA . -----TG-----GCTTCA-T---T-CAC TT-CCAGTCATCATTTCAACGTGC
1075WIS . -----CCT-----GCTTCACT-C-T-CAC TT-CCTCATCATCATTTCAACACGC
939GER . -----CCT-----GCTTCACT-C-T-CAC TT-CCTCATCATCATTTCAACACGC
GA3804 . -----CCT-----GCTTCACT-C-T-CAC TT-CCTCATCATCATTTCAACACGC
1599AT . -----CCT-----GCTTCACT-C-T-CAC TT-CCTAGTCATCATTTCAACACGC
1941AT . -----CCT-----GCTTCACT-C-T-CAC TT-CCTCGTCATCATTTCAACACGC
291NE . -----CCT-----GCTTCACT-C-T-CAC TT-CCTCGTCATCATTTCAACACGC
2301SAR . -----CCT-----GCTTCACT-C-T-CAC TT-CCTCGTCATCATTTCAACACGC
2313SAR . -----CCT-----GCTTCACT-C-T-CAC TT-CCTCGTCATCATTTCAACACGC
271NE . -----CCT-----GCTTCACT-C-T-CAC TT-CCTCGTCATCATTTCAACACGC
1935GER . -----CCT-----GCTTCACT-C-T-CAC TT-CCTCGTCATCATTTCAACACGC
JBRSA122 . -----CCT-----GCTTCACT-C-T-CAC TT-CCTCGTCATCATTTCAACACGC
276NE . -----TG-----GCTTCACT-C-T-CAC TT-CCAGCCATCATTTCAACGTGC
272NE . -----TG-----GCTTCACT-C-T-CAC TT-CCAGCCATCATTTCAACGTGC
2673ETHI . -----TG-----GCTTCACT-C-T-CAC TT-CCAGCCATCATTTCAACGTGC
1084AUSW . -----C-----GCTTCACT-C-T-CAC TT-CCAGCCAT---TCAACGTGC
JBPER62 . -----CCT-----GCTTCACT-C-T-CAC TT-CCAGCCATCATTTCAACGGGC
JBNZ72 . -----TG-----GCTTCACT---T-CAC TT-CCAGTCATCATTTCAACGTGC
1065MEX . -----TG-----GCTTCACT-C-T-CAC TT-CCCCGCCAT---TCAACGTAC
646HAWAI . TTT-----TG-G-----GTTTCCCT-C-T-CXXXXXXXXXXXXXXXXXXXXXXXXX
727INDIA . TTTTTTTTTTTT-TG-G-----GTTTCCXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
743MALE . TTT-----TG-G-----GTTTCCXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
1059MEX . TTTT-----TG-----GCTTCACT-C-T-CAC TT-CCCCGCCAT---TCAACGTAC
1061RW . -----CCT-----GCTTCACT-C-T-CAC TT-CCTCGTCATCATTTCAACGTGC
1066MEX . TT-----TG-----GCTTCACT-C-T-CAC TT-CCCCGCCAT---TCAACGTAC
1095BALI . -----CT-----GCTTCGCT-C-T-CAC TT-CCAGCCATCATTTCAACGTGC
1505MAUR . -----CCCT-----GCTTCACT-C-T-CAC TT-CCAGCCATCATTTCAACGTGT
1818ETHI . -----CT-----GCTTCGCT-C-T-TACTG-CCAGCCATCATTTCAACGTGC
1934AT . -----CCT-----GCTTCACT-C-T-CAC TT-CCTAGTCATCATTTCAACACGC
245CR . -----CT-----GCTTCGCT-C-T-CAC TT-CCAGCCATCATTTCAACGTGC
2710ETHI . -----CT-----GCTTCGCT-C-T-CAC TT-CCAGCCATCATTTCAACGTGC
274NE . -----CT-----GCTTCGCT-C-T-CAC TT-CCAGCCATCATTTCAACGTGC
3408PNG . -----CT-----GCTTCGCT-C-T-CAC TT-CCAAACCATCATTTCAACGTGC
3409PNG . -----CT-----GCTTCGCT-C-T-CAC TT-CCAAACCATCATTTCAACGTGC
410MALAY . -----C-----CTTCACT---TACTG-CC-AGTCATCATTTCAACGATC
836EGY . -----CCCT-----GCTTCACT-C-T-CAC TT-CCAGCCATCATTTCAACGTGT
837EGY . -----CCCT-----GCTTCACT-C-T-CAC TT-CCAGCCATCATTTCAACGTGT
JBR0111 . -----CT-----GCTTCGCT-C-T-TACTG-CCAGCCATCATTTCAACGTGC
brunneoviridis4 -----GT-----GCTTGACTCT---CACTTCGCCAGTCATCATTTCAACGTGT
brunneoviridis1 -----GT-----GCTTGACTCT---CACTTCGCCAGTCATCATTTCAACGTGT
pleurotumCPK211 -----CT-----GCTTCACTCCCCCACTGGCCAGTCATGATTTCAACGTGC
PLEUROTICOLA . -----CT-----GCTTCACTCTC-CCACTG-CCAGTCATCATTTCAACGTGC
epimycetCPK1981 -----GT-----GCTTCACTCTC---ACTG-CCAGCCGTCGTTCAACGTGC
alniCPK3124 ... -----GT-----GCTTCACTCTC---ACTG-CTAGCCATCATTTCAACGGCGC
CPK5TAW . -----GG-----GCTTCACTTTCT---ACTG-GCCGTCGTCATTTCAACGCAC
2974lobau . -----CT-----GCTTCGCTCTC---ACTT-CCAGCCATCATTTCAACGTGC
2975lobau . -----CT-----GCTTCGCTCTC---ACTT-CCAGCCATCATTTCAACGTGC
aggressivumCPK3 -----GT-----GCTTCACTATC---ACTA-CCAGCCGTCGTTCAACGTGC
atrogelatinosaC -----GT-----GCTTCACTGTC---ACTG-TTCAGTCGTCATTTCAACGTGC

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atrogelatinosaC -----GT-----GCTTCACTGTC---ACTG-TTCAGTCGTCATTCAACGTGC
cerinumCPK293 -----CT-----GTTTCGCTCTC---ACTA-CCCAAGTCGTCATTCAACGCGC
cerinumCPK854 -----CT-----GTTTCGCTCTC---ACTA-CCCAAGTCGTCATTCAACGCGC
tomentosumCPK88 -----CT-----GTTTTGCTCTC---GCTA-CCCAAGTCGTCATTCAACGCGC
stramineaGJS028 -----GT-----GCTTCACTTTC---ACTG-CCCAAGTCATCATTCAACGTGC
velutinumCPK312 -----CTGT-----GCTTCACTC---ACTG-CCTAGCCAATTTCAACGTGC
catoptronGJS027 -----ACCTTCACAATC---ACTG-CACAGTCGGCATTCAACGGTC
#####
250 260 270 280 290 300
=====+=====+=====+=====+=====+=====+
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1052SA . T--CTGCGT-CT--CATCACTTTTCAGCGATGCTAACCAC--TTTT-CCATTAATAGGAAG
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1596AT . T--CTGTGT-CT--CGTCACTTTCAGCGATGCTAACCAC--TTTT-CCATCAATAGGAAG
1720CAN . T--CGGTGT-----CATCACTTTTCAGCGATGCTAACCAC--TTTT-CCATCAATAGGAAG
1722CAN . T--CGGTGT-----CATCACTTTTCAGCGATGCTAACCAC--TTTT-CCATCAATAGGAAG
1724CAN . T--CGGTGT-----CATCACTTTTCAGCGATGCTAACCAC--TTTT-CCATCAATAGGAAG
334USA . T--CTGTGT-CT--CGTCACTTTCAGCGATGCTAACCAC--TTTT-CCATCAATAGGAAG
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1069WIS . T--CTGTGT-CT--CGTCACTTTCAGCGATGCTAACCAC--TTTT-CCATCAATAGGAAG
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239CR . XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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1064MEX . T--CTGTGT-CTTTGGTCA--TTCAGCGATGCTAACCAC--TTTT-CCATCAATAGGAAG
596BRAZ . T--CTGTGT--TTTGGTCA--TTCAGCGATGCTAACCAC--TTTT-CCATCAATAGGAAG
333USA . XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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JBRS122 . T--CTGTGT-CTTTGGTCA--TTCAGCGATGCTAACCAC--TTTT-CCATCAATAGGAAG
276NE . T--CTGTGT-CTTT-----GCGATGCTAACCAC--TTTTTCCATCAATAGGAAG
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646HAWAI . XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
727INDIA . XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
743MALE . XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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410MALAY . T--CTGCG-CCTT--ATCGCTTTTCAGTGAAGCTAACCAC--TTTTT-CATCAATAGGAAG
836EGY . T--CTGTGT-CT--CGTCACTTTCAGCAATGCTAACCAC--TTTT-CCATCAATAGGAAG
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brunneoviridis1 . T--CGGTGT-CTTTGGTCA--TTCAGCGATGCTAACCAC--TTTTT-CATCAATAGGAAG
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aggressivumCPK3 . T--CTGTCT-CT--CGTCA--TTCAGTATGCTAACCAC--TTTTTCCATCAATAGGAAG
atrogelatinosaC C--CTGTGT-CT--CGTCAGTTTCAGCGATGCTAACCAC--TTTT-CCATCAATAGGAAG

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atrogelatinosaC C--CTGTGT-CT--CGTCAGTTTCAGCGATGCTAACCAC--TTTT-CCATCAATAGGAAG
cerinumCPK293 T--TTATGT-CT--ACTCACTTCCAGCGATGCTAACCAC--TTTT-CCATCAATAGGAAG
cerinumCPK854 T--TTGTGT-CT--TGTCACCTTCCAGCGATGCTAATCAC--TTTT-CCATCAATAGGAAG
tomentosumCPK88 T--TTGTGT-CT--TGTCACCTTCCAGCGATGCTAACCAC--TTTT-TCATCAATAGGAAG
stramineaG3S028 C--CTACGT-C---GTCACCTTCCAGCGATGCTAACCAC--TTTT-CCATCAATAGGAAG
velutinumCPK312 T--CTGTAT-TC--CGTTACTTTCACCGATGCTAACCAC--TTT-TCATCAATAGGAAG
catoptronG3S027 TCCATCCAT-GCCTTTTTCATTTTCAACGATGCTAACCAC--TTTT-CCATCAATAGGAAG
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1104CAN . CCGCCGAACCTCGGCAAGGGTTCCCTT-CATCGTTTCTGGTGCG-AATTCCGGAC-GGTTT-G
1087CAN . CCGCCGAACCTCGGCAAGGGTTCCCTT-CATCGTTTCTGGTGCG-AATTCCGGAC-GGTTT-G
360UK . CCGCCGAACCTCGGTAAGGGTTCCCTT-CATCGTTTCTGGTGCG-AATTCCGGAC-GGTTT-G
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catoptronGJS027 . AAAAA---CTGACAGGCTTGACCCCGCAGGCCAGATCACCACCAAGGAGCTGGGCACC
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1116CAN	GGGTCGTTGCCACATT	CGGGCTAAATACGGAGCGGT	GTAGAATTCAACTGCCATT	ACCTCTC		
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217RUS	GGGTCGTTGCCACATT	CGGGCTAAATACGGAGCGGT	GTAGAATTCAACTGCCATT	ACCTCTC		
204UK	GGGTCGTTGCCACATT	CGGGCTAAATACGGAGCGGT	GTAGAATTCAACTGCCATT	ACCTCTC		
206RUS	GGGTCGTTGCCACATT	CGGGCTAAATACGGAGCGGT	GTAGAATTCAACTGCCATT	ACCTCTC		
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JBSER241 . GCCTACGACTATGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
246PHI . GCCTACGACTATGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
51SA . GCCTACGACTATGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
2618ETHI . GCCTACGACTATGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
1068WIS . GCCTACGACTACGCGGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTAA
238CR . GCCTACGACTATGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
NR5555 . GCCTACGACTATGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
NR6839 . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
2624ETHI . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
845EGY . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
JBPER12 . XXXXXGATCACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
1717VIET . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
709BRAZ . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
878IRAN . GCCTACGACTACGCTGGATCCTTCAGCCCCCTAACC -GGTCACGACGCCAACCTGTTTGC
239CR . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
202COM . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
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596BRAZ . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
333USA . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
2610ETHI . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGCCACGACGCCAACCTGTTTGC
1044RW . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGCCACGACGCCAACCTGTTTGC
JBNZ111 . GCCTACGACTACGCTGGATCCTTTAGCCCCCTCACC -GGCCACGACGCCAACCTGTTTGC
JBNZ12 . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGCCACGACGCCAACCTGTTTGC
JBNZ24 . GCCTACGACTACGCTGGATCCTTTAGCCCCCTCACC -GGCCACGACGCCAACCTGTTTGC
693CHINA . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACT -GGTCACGACGCCAACCTGTTTGC
1058RW . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGCCACGACGCCAACCTGTTTGC
590AUS . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
53SA . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGCCACGACGCCAACCTGTTTGC
1075WIS . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
939GER . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
GA3804 . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
1599AT . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
1941AT . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGCCACGACGCCAACCTGTTTGC
291NE . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
2301SAR . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
2313SAR . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGCCACGACGCCAACCTGTTTGC
271NE . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGCCACGACGCCAACCTGTTTGC
1935GER . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
JBRS122 . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
276NE . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
272NE . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTATTTGC
2673ETHI . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGCCACGACGCCAACCTGTTTGC
1084AUSW . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
JBPER62 . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGCCACGACGCCAACCTGTTTGC
JBNZ72 . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGCCACGACGCCAACCTGTTTGC
1065MEX . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
646HAWAI . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
727INDIA . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
743MALE . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
1059MEX . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
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1066MEX . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGCCACGACGCCAACCTATTTGC
1095BALI . GCCTACGACTATGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
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245CR . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
2710ETHI . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
274NE . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
3408PNG . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
3409PNG . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
410MALAY . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACT -GGTCACGACGCCAACCTGTTTGC
836EGY . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
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JBR0111 . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
brunneoviridis4 . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGCCACGACGCCAACCTGTTTGC
brunneoviridis1 . GCCTACGACTACGCTGGATCCTTTAGCCCCCTCACT -GGTCATGATGCCAACCTGTTTGC
pleurotumCPK211 . GCCTACRACACTACGCTGGATCCTTCAGCCCCCTCACT -GGCCACRACGCCAACCTGTTTGC
PLEUROTICOLA . GCCTACGACTACGCTGGTTCCTTCAGCCCCCTCACC -GGCCACGACGCCAACCTGTTTGC
epiomycesCPK1981 . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTGTTTGC
alniCPK3124 ... GCCTACRACACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACRACGCCAACCTGTTTGC
CPK5TAWA . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTATTTGC
2974lobau . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGTCACGACGCCAACCTATTTGC
2975lobau . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACC -GGCCACGACGCCAACCTGTTTGC
aggressivumCPK3 . GCCTACGACTACGCTGGTTCCTTCAGCCCCCTCACC -GGCCACGACGCCAACCTGTTTGC
atrogelatinosaC . GCCTACGACTACGCTGGATCCTTCAGCCCCCTCACT -GGTCACGACGCCAACCTGTTTGC

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atrogelatinosaC GCCTACGACTACGCTGGATCTTTACGCCCTCACT -GGTACGACGCCAACCTGTTTGC
cerinumCPK293 . GCCTACGACTACGCTGGATCTTTACGCCCTCACT -GGTACGACGCCAACCTGTTTGC
cerinumCPK854 . GCCTACGACTACGCTGGATCTTTACGCCCTCACT -GGTACGACGCCAACCTGTTTGC
tomentosumCPK88 GCCTACGACTACGCTGGATCTTTACGCCCTCACT -GGTACGATGCCAACCTGTTTGC
stramineaGJS028 GCCTACGACTACGCTGGATCTTTACGCCCTCACT -GGTACGACGCCAACCTGTTTGC
velutinumCPK312 GCCTACGACTACGCTGGATCTTTACGCCCTCACT -GGTACGACGCCAACCTGTTTGC
catoptronGJS027 GCTTACGACTACGCTGGATCTTTACGCCCTCACT -GGACACGACGCCAACCTGTTTGC
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	1090	1100	1110	1120	1130	1140
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1052SA .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
1116CAN .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
1070EIRE .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
1099CAN .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
1104CAN .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
1087CAN .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
360UK .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
2111HUN .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
217RUS .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
204UK .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
206RUS .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
261SIB .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
265SIB .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
2784THAI .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
838EGY .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
1102CAN .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
588LAOS .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
1596AT .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
1720CAN .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
1722CAN .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
1724CAN .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
334USA .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
335USA .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
1081WIS .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
1069WIS .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
1107CAN .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
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1110CAN .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
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246PHI .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
51SA .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
2618ETHI .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
1068WIS .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
238CR .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
NR5555 .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
NR6839 .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
2624ETHI .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
845EGY .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
JBPER12 .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
1717VIET .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
709BRAZ .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
878IRAN .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
239CR .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
202COM .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
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596BRAZ .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
333USA .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
2610ETHI .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
1044RW .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
JBZN111 .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
JBZN12 .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
JBZN24 .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
693CHINA .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
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590AUS .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
53SA .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
1075WIS .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
939GER .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
GA3804 .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
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1941AT .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
291NE .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
2301SAR .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
2313SAR .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
271NE .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
1935GER .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
JBRS122 .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
276NE .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
272NE .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
2673ETHI .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
1084AUS .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
JBPER62 .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
JBZN72 .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
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646HAWAI .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
727INDIA .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
743MALE .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
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1066MEX .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
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1818ETHI .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
1934AT .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
245CR .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
2710ETHI .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
274NE .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
3408PNG .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
3409PNG .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
410MALAY .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
836EGY .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
837EGY .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
JBRO111 .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
brunneoviridis4	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
brunneoviridis1	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
pleurotomCPK211	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
PLEUROTICOLA .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
epiomycesCPK1981	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
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CPK5TAWA .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
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2975lobau .	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
aggressivumCPK3	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT
atrogelatinosaC	CAACCCGTC	CAACCCCAAT	GCCACAC	CCCTTCAAC	CACCGATT	CTGCTGTCAAGGATTATAT

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atrogelatinosaC CAACCCGTCACACCCAATGCCACACCCCTTCAACACCGGACTGCTGTCAAGGATTATAT
cerinumCPK293 . CAACCCGTCACACCCAATGCCACACCCCTTCAACACCGGACTGCTGTCAAGGATTACAT
cerinumCPK854 . CAACCCGTCACACCCAATGCCACACCCCTTCAACACCGGACTGCTGTCAAGGATTACAT
tomentosumCPK88 CAACCCCTCCAACCCCAATGCCACACCCCTTCAACACCGGACTGCTGTCAAGGATTACAT
stramineaGJS028 CAACCCCTCCAACCCCAATGCCACACCCCTTCAACACCGGACTGCTGTCAAGGATTATAT
velutinumCPK312 CAACCCGTCACACCCAATGCCACACCCCTTCAACACCGGACTGCTGTCAAGGATTATAT
catoptronGJS027 CAACCCCTCCAACCCCAATGCCACGCCCCCTTCAACACCGGACTGCTGTCAAGGATTACAT
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1150      1160      1170      1180      1190      1200
=====+=====
1093CAN . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
1052SA . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
1116CAN . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
1070EIRE . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
1099CAN . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
1104CAN . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
1087CAN . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
360UK . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
2111HUN . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
217RUS . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
204UK . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
206RUS . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
261SIB . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
265SIB . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
278THAI . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
838EGY . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
1102CAN . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
588LAOS . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
1596AT . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
1720CAN . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
1722CAN . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
1724CAN . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
334USA . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
335USA . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
1081WIS . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
1069WIS . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
1107CAN . CAATGGAGGTGTTCCCGCCAACAAGATTGTTCTCGGCATGCCCATCTACGGACGATCATT
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204UK . CCAGAACACCGCTGGCATTGGCCAGACTTACAACCGAGTTGGAAGTGGCGGTGGTGGCTC
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1724CAN . CCAGAACACCGCTGGTATTGGCCAGACTTACAATGGTGTGGAAGTGG-----
334USA . CCAGAACACCGCTGGTATTGGCCAGACTTACAATGGTGTGGAAGTGG-----
335USA . CCAGAACACCGCTGGTATTGGCCAGACTTACAATGGTGTGGAAGTGG-----
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1069WIS . CCAGAACACCGCTGGTATTGGCCAGACTTACAATGGTGTGGAAGTGG-----
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202COM . CCAGAACACXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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333USA . CCAGAACACCGCTGGTATTGGCCAGACTTACAACCGAGTTGGAAGTGGCGGTGGTGGCTC
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837EGY . CCAGAACACCGCTGGCATTGGTCAGACTTACAACCGAGTTGGAAGTGGCGGTGGTGGCTC
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brunneoviridis4 . CCAGAACACCGCTGGTATTGGCCAGACTTACAACCGAGTTGGAAGTGG-----
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588LAOS . -----AAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
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51SA . AACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
2618ETHI . AACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
1068WIS . -----AAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
238CR . AACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
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596BRAZ . AACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
333USA . AACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
2610ETHI . AACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
1044RW . CACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
JBNZ111 . CACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
JBNZ12 . CACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGT -GCCA
JBNZ24 . CACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
693CHINA . CACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
1058RW . CACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
590AUS . AACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
53SA . AACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
1075WIS . AACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
939GER . AACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
GA3804 . AACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
1599AT . AACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
1941AT . CACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
291NE . AACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
2301SAR . AACTGGAAGCTGGGAGGCCGGTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
2313SAR . CACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
271NE . XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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JBRS122 . AACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
276NE . AACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
272NE . AACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
2673ETHI . CACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
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JBPER62 . CACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
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1065MEX . -ACTGGAAGCTGGGAGGCCGGTATTTGGGATTACAAGGCTCTTCCCAAGGCCGGT -GCCA
646HAWAI . AACTGGAAGCTGGGAGGCCGGTATTTGGGATTACAAGGCTCTTCCCAAGGCCGGT -GCCA
727INDIA . AACTGGAAGCTGGGAGGCCGGTATTTGGGATTACAAGGCTCTTCCCAAGGCCGGT -GCCA
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1934AT . AACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
245CR . AACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
2710ETHI . AACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
274NE . AACTGGAAGCTGGGAGGCCGGGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
3408PNG . CACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
3409PNG . CACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
410MALAY . AACTGGAAGCTGGGAGGCCGGCATCTGGGATTACAAGGCCCTTCCCAAGGCCGGT -GCCA
836EGY . CACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
837EGY . CACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
JBRO111 . CACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
brunneoviridis4 . -----AAGCTGGGAGGCCGGCATCTGGGATTACAAGGCCCTTCCCAAGGCCGGC -GCCA
brunneoviridis1 . -----AAGCTGGGAGGCCGGCATCTGGGATTACAAGGCCCTTCCCAAGGCCGGC -GCCA
pleurotumCPK211 . AACTGGCAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
PLEUROTICOLA . TACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
epimycetCPK1981 . AACTGGAAGCTGGGAGGCCGGTGTCTGGGATTACAAGGCTCTTCCCAAGGCCGGT -GCCA
alniCPK3124 ... -----AAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGT -GCCA
CPK5TAUW . CACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
2974lobau . CACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
2975lobau . CACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA
aggressivumCPK3 . TACTGGAAGCTGGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
atrogelatinosaC AACTGGGAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGGCCGGC -GCCA

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atrogelatinosaC AACTGGGAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGTCGGGC -GCCA
cerinumCPK293 . AACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCCCTTCCCAAGTCGGGC -GCCA
cerinumCPK854 . AACTGGAAGCTGGGAGGCCGGTATTTGGGATTACAAGGCCCTTCCCAAGTCGGGC -GCCA
tomentosumCPK88 AACTGGAAGTTGGGAGGCCGGTATCTGGGATTACAAGGCCCTTCCCAAGTCGGGC -GCCA
stramineaGJS028 CACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGTCGGGC -GCCA
velutinumCPK312 CACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCTCTTCCCAAGTCGGGC -GCCA
catoptronGJS027 AACTGGAAGCTGGGAGGCCGGTATCTGGGATTACAAGGCCCTTCCCAAGTCGGGC -GCCA
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1330      1340      1350      1360      1370      1380
=====+=====+=====+=====+=====+=====+
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1052SA . CCATCCAGTACGACTCTGTGCGAAAGGGTTACTACAGCTACAACGCCGGCACCAGGACC
1116CAN . CCATCCAGTACGACTCTGTGCGAAAGGGTTACTACAGCTACAACGCCGGCACCAGGACC
1070EIRE . CCATCCAGTACGACTCTGTGCGAAAGGGTTACTACAGCTACAACGCCGGCACCAGGACC
1099CAN . CCATCCAGTACGACTCTGTGCGAAAGGGTTACTACAGCTACAACGCCGGCACCAGGACC
1104CAN . CCATCCAGTACGACTCTGTGCGAAAGGGTTACTACAGCTACAACGCCGGCACCAGGACC
1087CAN . CCATCCAGTACGACTCTGTGCGAAAGGGTTACTACAGCTACAACGCCGGCACCAGGACC
360UK . XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
2111HUN . CCATCCAGTACGACTCTGTGCGAAAGGGTTACTACAGCTACAACGCCGGCACCAGGACC
217RUS . CCATCCAGTACGACTCTGTGCGAAAGGGTTACTACAGCTACAACGCCGGCACCAGGACC
204UK . CCATCCAGTACGACTCTGTGCGAAAGGGTTACTACAGCTACAACGCCGGCACCAGGACC
206RUS . XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
261SIB . XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
265SIB . CCATCCAGTACGACTCTGTGCGAAAGGGTTACTACAGCTACAACGCCGGCACCAGGACC
2784THAI . CGGTCCAGTACGATTCTGTGCGAAAGGGCTACTACAGCTACAAGTCCGCCACCAAGGACC
838EGY . CCGTCCAGTACGATTCTGTGCGAAAGGGCTACTACAGCTACAAGTCCGCCACCAAGGACC
1102CAN . CCGTCCAGTACGATTCTGTGCGAAAGGGCTACTACAGCTACAAGTCCGCCACCAAGGACC
588LAOS . CCGTCCAGTACGATTCTGTGCGAAAGGGCTACTACAGCTACAAGTCCGCCACCAAGGACC
1596AT . CCGTCCAGTACGATTCTGTGCGAAAGGGCTACTACAGCTACAAGTCCGCCACCAAGGACC
1720CAN . CCGTCCAGTACGATTCTGTGCGAAAGGGCTACTACAGCTACAAGTCCGCCACCAAGGACC
1722CAN . CCGTCCAGTACGATTCTGTGCGAAAGGGCTACTACAGCTACAAGTCCGCCACCAAGGACC
1724CAN . CCGTCCAGTACGATTCTGTGCGAAAGGGCTACTACAGCTACAAGTCCGCCACCAAGGACC
334USA . CCGTCCAGTACGATTCTGTGCGAAAGGGCTACTACAGCTACAAGTCCGCCACCAAGGACC
335USA . CCGTCCAGTACGACTCTGTGCGAAAGGGCTACTACAGCTACAAGTCCGCCACCAAGGACC
1081WIS . CCGTCCAGTACGATTCTGTGCGAAAGGGCTACTACAGCTACAAGTCCGCCACCAAGGACC
1069WIS . CCGTCCAGTACGATTCTGTGCGAAAGGGCTACTACAGCTACAAGTCCGCCACCAAGGACC
1107CAN . CCGTCCAGTACGATTCTGTGCGAAAGGGCTACTACAGCTACAAGTCCGCCACCAAGGACC
1108PEN . CCGTCCAGTACGATTCTGTGCGAAAGGGCTACTACAGCTACAAGTCCGCCACCAAGGACC
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246PHI . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGTACCAAGGACC
51SA . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGTACCAAGGAGC
2618ETHI . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGTACCAAGGAGC
1068WIS . CCGTCCAGTACGATTCTGTGCGAAAGGGCTACTACAGCTACAAGTCCGCCACCAAGGACC
238CR . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGTACCAAGGACC
NR5555 . XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
NR6839 . XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
2624ETHI . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGTACCAAGGAGC
845EGY . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGTACCAAGGACC
JBPER12 . CCATCCAGTACGATTCTGTGCGCAAGGGTACTACAGCTACAAGGCCGGTACCAAGGAGC
1717VIE . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGTACCAAGGAGC
709BRAZ . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGTACCAAGGACC
878IRAN . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCACCAGGAAA
239CR . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGTCCCGGTACCAAGGACC
202COM . XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
1064MEX . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGTACCAAGGACC
596BRAZ . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGTACCAAGGACC
333USA . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGTACCAAGGAGC
2610ETHI . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGTACCAAGGAGC
1044RW . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCACCAGGACC
JBNZ111 . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCACCAGGAGC
JBNZ12 . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCACCAGGAGC
JBNZ24 . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCXXXXXXXXXX
693CHINA . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCACCAGGAGC
1058RW . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCACCAGGAGC
590AUS . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGTACCAAGGACC
53SA . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGTACCAAGGACC
1075WIS . CCATCCAGTACGATTCTGTGCGAAAGGGCTACTACAGCTACAAGGCCGGCACCAGGACC
939GER . CCATCCAGTACGATTCTGTGCGAAAGGGCTACTACAGCTACAAGGCCGGCACCAGGAGC
GA3804 . CCATCCAGTACGATTCTGTGCGAAAGGGCTACTACAGCTACAAGGCCGGCACCAGGAGC
1599AT . CCATCCAGTACGATTCTGTGCGAAAGGGCTACTACAGCTACAAGGCCGGCACCAGGAGC
1941AT . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCACCAGGAGC
291NE . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGTACCAAGGXXX
2301SAR . XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
2313SAR . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCACCAGGAGC
271NE . XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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JBRSA122 . CCATCCAGTACGATTCTGTGCGAAAGGGCTACTACAGCTACAAGGCCGGCACCAGGAGC
276NE . CCATCCAGTACGATTCTGTGCGAAAGGGCTACTACAGCTACAAGGCCGGCACCAGGACC
272NE . CCATCCAGTACGATTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
2673ETHI . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGTACCAAGGAGC
1084AUSW . CCATCCAGTACGACTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGTACCAAGGAGC
JBPER62 . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGTACCAAGGAGC
JBNZ72 . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCACCAGGAGC
1065MEX . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCACCAGGAGC
646HAWAI . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCACCAGGAGC
727INDIA . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCACCAGGAGC
743MALE . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCACCAGGAGC
1059MEX . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCACCAGGAGC
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1095BALI . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGTACCAAGGACC
1505MAUR . CCATCCAGTACGACTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCACCAGGAGC
1818ETHI . CCATCCAGTACGACTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCACCAGGAGC
1934AT . CCATCCAGTACGATTCTGTGCGAAAGGGCTACTACAGCTACAAGGCCGGCACCAGGAGC
245CR . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCACCAGGACC
2710ETHI . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCACCAGGAGC
274NE . XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
3408PNG . CCATCCAGTACGACTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCACCAGGAGC
3409PNG . CCATCCAGTACGACTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCACCAGGAGC
410MALAY . CCATCCAGTATGATGATGTGGCAAAGGGTTACTACAGCTACAAGGCCGCCACCAGGAGC
836EGY . CCATCCAGTACGACTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCACCAGGACC
837EGY . CCATCCAGTACGACTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCACCAGGACC
JBR0111 . CCATCCAGTACGACTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCACCAGGAGC
brunneoviridis4 CCATCAAGTATGACGATGTGCGAAAGGGTTACTACAGCTACAAGGCCAACACCAAGGAGC
brunneoviridis1 CCATCAAGTATGACGATGTGCGAAAGGGTTACTACAGCTACAAGGCCAACACCAAGGAGC
pleurotumCPK211 CCATCAAGTACGATGATGTGCGAAAGGGTTACTACAGCTACAAGGCCAACACCAAGGAGC
PLEUROTICOLA . CCATCAAGTACGATGATGTGCGAAAGGGTTACTACAGCTACAAGGCCAACACCAAGGAGC
epimycosCPK1981 CCATCCAGTACGATGCTGTGCGAAAGGGTTACTACAGCTATAAGCCGGACACCAAGGAGC
alniCPK3124 ... CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTATAAGCCGGACACCAAGGAGC
CPK5TAWA . CGGTCCAGTACRATTCTGTGCGAAAGGGTTACTACAGCTATAAGTCCAACACCAAGGAGC
2974lobau . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCACCAGGAGC
2975lobau . CCATCCAGTACGATTCTGTGCGAAAGGGTTACTACAGCTACAAGGCCGGCACCAGGAGC
aggressivumCPK3 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
atrogelatinosaC CTATCAAGTACGATGATGTGCGAAAGGGTTACTACNGCTACAAGGCCAACACCAAGGAGC

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atrogelatinosaC  CTATCAAGTACGATGATGTCGCAAAGGGTTACTACAGCTACAACGCCAACACCAAGGAGC
cerinumCPK293 .  CCATCAAGTATGATGATGTCGCAAAGGGTTACTACAGCTACAACGCCAATACCAAGGAGC
cerinumCPK854 .  CCATCAAGTATGATGATGTCGCAAAGGGTTACTACAGCTACAACGCCAATACCAAGGAGC
tomentosumCPK88  CCATCAAGTATGATGATGTCGCAAAGGGTTACTACAGCTACAACGCCAACACCAAGGAGC
stramineaGJS028  CCATCAAGTACGATGATGTGGCAAAGGGTTACTACAGCTACAACGCCAACACCAAGGAGC
velutinumCPK312  CCATCAAGTACGATGATGTGGCAAAGGGTTACTACAGCTACAACGCCAACACCAAGGAGC
catoptronGJS027  CCATCAAGTATGATGATGTGGCAAAGGGTTACTACAGCTATAACGCCAACACCAAGGAGC
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Parameters used

Minimum Number Of Sequences For A Conserved Position: 57
 Minimum Number Of Sequences For A Flanking Position: 57
 Maximum Number Of Contiguous Nonconserved Positions: 8
 Minimum Length Of A Block: 5
 Allowed Gap Positions: With Half

Flank positions of the 33 selected block(s)

Flanks: [1 27] [33 43] [48 56] [58 79] [81 85] [87 93] [97 103] [109 114] [116 120] [122 126] [129 138] [144 149] [156 160]

New number of positions in pasted_alignment-gb: **1258** (91% of the original 1380 positions)

[Resulting alignment](#)

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