SUPPLEMENTAL INFORMATION

RNAPolII_LSU sequence alignment (accession no. KX347439) 1,181/1,184 base pairs (99%) similarity.

KM820664 GCGCTGGACGACGTGCACGCTTCGTACGACGGCACGGTGCGGAACGCGAATCAGGAGCTC 1 GCGCTGGAAGACGTGCACGCTTCGTACGACGGCACGGTGCGGAACGCGAATCAGGAGCTC 60
KM820664 ATCCAGCTGGCGTATGGCGAAGACGGCCTGGACGGCGCACGCATCGAGGGCAACCAGGCC 61 ATCCAGCTGGCGTATGGCGAAGACGGCCTGGACGGCGCACGCATCGAGGGCAACCAGGCC 120
KM820664 TTCCCGATTCCGCACATGACGAACTCGGAGATGGTGGACAGGTACCGCTACGAATACAGG 121 TTCCCGATTCCGCACATGACGAACTCGGAGATGGTGGACAGGTACCGCTACGAATACAGG 180
KM820664 GACGAGGGCGGCTTCTCGGACAACATGGGCGGCCAATACATGGATCCGTTCGTGCGCGAC 181 GACGAGGGCGGCTTCTCGGACAACATGGGCGGCCAATACATGGATCCGTTCGTGCGCGAC 240
KM820664 TCGCTGCTGCGCGATCCGCAGAGCGTGCTGAGGCTGCAAGAGGAGTTCGACCAGCTCATG 241 TCGCTGCTGCGCGATCCGCAGAGCGTGCTGAGGCTGCAAGAGGAGTTCGACCAGCTCATG 300
KM820664 AAGGACCGCGCGATGTCGCGCCTCATCATCGACATGGAGGACAAGAACAAGCTCAAGATG 301 AAGGACCGCGCGATGTCGCGCCTCATCATCGACATGGAGGACAAGAACAAGCTCAAGATG 360
KM820664 AACCTGCCTGTGAACGTCGCGCGTCTCATCCAGAACGCGCGCACGACGATGGGTAAGCGC 361 AACCTGCCTGTGAACGTCGCGCGTCTCATCCAGAACGCGCGCACGACGATGGGTAAGCGC 420
KM820664 AGTCAGGTGTCGAACTTAAACCCGATCACTGTGATCAACCGCGTGCGGGAGCTGCAGGAG 421 AGTCAGGTGTCGAACTTAAACCCGATCACTGTGATCAACCGCGTGCGGGAGCTGCAGGAG 480
KM820664 GACCTCGTGCAGCTGTTTCCCTCACACCACAAGGACTACCACGGCCGCTTCGTGAACGCG 481 GACCTCGTGCAGCTGTTTCCCTCACACCACAAGGACTACCACGGCCGCTTCGTGAACGCG 540
KM820664 CTCAGCCGGGAGCGTGTGGAGCGGGCACTGACGCTCTTCGGCATCCATCTGCGCCAGATT 541 CTCAGCCGGGAGCGTGTGGAGCGGGCACTGACGCTCTTCGGCATCCATCTGCGCCAGATT 600
KM820664 CTCGGCTCCAAGCGGGTGCTGAAGGAGTACAAGCTGAACGACAAGGCGTTCGAGTACTTG 601 CTCGGCTCCAAGCGGGTGCTGAAGGAGTACAAGCTGAACGACAAGGCGTTCGAGTACTTG 660
KM820664 CTGAAGGAGATCCGCACCAAATACCAGCAGTCCCTCATCACCCCTGGTGAGATCATCGGC 661 CTGAAGGAAATCCGCACCAAATACCAGCAGTCCCTCATCACCCCTGGTGAGATCATCGGC 720
KM820664 GCCATCGCCGCGCAGTCGTGCGGCGAGCCAGCGACGCAGATGACGCTGAATACCTTYCAC 721 GCCATCGCCGCGCAGTCGTGCGGCGAGCCAGCGACGCAGATGACGCTGAATACCTTTCAC 780
KM820664 AACGCCGGCATCTCGTCCAAGAACGTGACCCTCGGCGTGCCGCGGCTACTGGAGCTGCTG 781 AACGCCGGCATCTCGTCCAAGAACGTGACCCTCGGCGTGCCGCGGCTACTGGAGCTGCTG 840
KM820664 AATGTAAGCAAGAACCAGCGCAATGCCAGCGTGGCCGTCTGCCTCATCCACGAGTACCAG 841 AATGTAAGCAAGAACCAGCGCAATGCCAGCGTGGCCGTCTGCCTCATCCACGAGTACCAG 900
KM820664 AAGCGCAACAAGGCACAGGAGGCACAGCAGTTCATCGAGTACTGCACGCTGGCGAACATC 901 AAGCGCAACAAGGCACAGGAGGCACAGCAGTTCATCGAGTACTGCACGCTGGCGAACATC 960
KM820664 ACAACGACGGTGCAGATCATCTACGACCCCAACCCGCGAAACACCGTCGTTGCCGAAGAC 961 ACAACGACGGTGCAGATCATCTACGACCCCAACCCGCGAAACACCGTCGTTGCCGAAGAC 1020
KM820664 GAGGAGATGATTCGCTGGGAGCAGGCGGTGATGAACGAGGAGGAGGAGGAGCAGGACGCG 1021 GAGGAGATGATTCGCTGGGAGCAGGCGGTGATGAACGAGGAGGAGGAGGAGCAGGACGCG 1080
KM820664 GACCAGCCACCGTCGCCCTTTATCGCGCGTCTTATCCTCGACAACGACCTCTTCAACGAC 1081 GACCAGCCACCGTCGCCCTTTATCGCGCGTCTTATCCTCGACAACGACCTCTTCAACGAC 1140
KM820664 AAGCGGCTTAACATGAAAGATGTGAAGAGCGCGATCCGGCAGGT 1141 AAGCGGCTTAACATGAAAGATGTGAAGAGCGCGATCCGGCAGGT 1184

ITS-1 Sequence alignment (accession no. KX347438) 282/295 base pairs (96%) similarity

JX195640 CTGGATCATTTTCCGATGATTACACCAAAAAAAACATACAATCAAAACACGGGGAGGTGT 1 CTGGATCATTTTCCGATGATTACACCAAAAAAAACATACAATGAAAACACGGGGAGGTGT 60
JX195640 CTCTCTCTTTTTGTCAGATAGCGCCTTTCCCACATACACACACACACAACAATATATATG 61 ATCTCTCTTTTTGTCAGATAACGCCTTTCCCACAT- - ACACACACACAACAATATATATG 118
JX195640 TATATATGTAGTGTTATACTCAATTATACAGTAAACAGAAAAACAAAGGCCGGTCGACAT 119 TATATATGTATTGTTATACTCAATTATACAGTAAACAGAAAAACAAAGGCCGGTCGACAT 178
JX195640 ATAAACACCGCGCG- -TATATATATATACAACGAAAATGTCCTTTCTTACGGGGGCTTTT 179 ATAAACACCGCACGTATATATATATATACAACGAAAATGTCCCTTCTTACGGGGGCTTTT 238
JX195640 CTGGCGGTGTGTTGTGGATAAC- GCTCACATAACGTGTCGCG- TGGATGACTTGG 328 239 CTGGCGGTGTGTTGTGGATAACGGCTCACATAACGTGTCGCGATGGATGACTTGG 293