

**Assembly:** GCA\_035042345.1\_ASM3504234v1\_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.85

GGGGCGGCGTCTGTCATTCACAGCAGTAAAAAGCGGTGGAGACATCCCGTTCCTATTACACGCAAACTCAGAAATTGTGTCCACTTTGGGTATACACAGCAGAAATTTATGATGTAAAAAGGCATATACCAATTTCGTATCTTCACAAAG  
 CAAAAATCCAAAGCAAAATTTATGCAAAATATAAACACCATATATAAAAAATGAACACACAAAGAACTCAAAACAAAGAAATACGAAATCGCAAAAGATATAATTCAGACCAAAAAAGTATATCCAAATGCAAAACAAACCACTAAAAAG  
 AAGCATCAACATCAAAAAAAATTCACCACTAAATGTGAACAGAGTTGATGAACATTGTTGTATTTATCGAAAAAATAAAAATCTCTGAAAAAATCTATAAAAATCACTTAAATCGCATGTGGTGTGTGTGTCTCC  
 GTTCGTGAAATCTGCTGACGBCGCCATCGGCCCAATCCAAAGGGGCTGATTCGACGGGAGAGAGAGGAGTGGTCCAGAAACGGGGGGGGATTTCTCTGAGGAGAGAGATCTACACAGGAGCAAAAGACACACACATCGCTCTAG  
 GAGAGAGAGAGACACCAATAGACATGGTGGTACGATTTGGGGCTGACCATCTCTCTGTCTCTCTGCTGATTTGACGATTTGAGTGAATGAGCATCGGTCGCTCAAGTCGGGCCAGAGAGCTTTGGGAAAAAGGCTCGCTGGGGCGGCTCGAG  
 AATCATCAACCATAGACGATTTTAAAGCAAAATCTAAATGAACACAAGATGATAACCAAAAAACAAACACAAACAAACAAAGAAAGTGCACCAACATATTTACTTAATTAATGGCAAAAAGGAAAAAAATGCAAAATACGACACACACCTTTCGA  
 AAAACGACCTTCGAAAAATACACACATATGCTGGGTGCTGGGAATCTGATGTTGCTCGCCCTTTT

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 4nt PSE: 0.98

GGGCGGTCGAGATATCTGACAGCGTAAAGGGTTTTCACATCCCCGAGAGTATGTAATGGCCAAATTTGTAATGCGGGGGGGGATTTCTTCTCCACCCGAAAGAAACCCATCATCTCATCTCTTAAATGGGCGGCGCTATTATTTGTAACAAACAGG  
ACCGACCAACCCCGGTGTAATCAAAAAATATGATTTTGAAGAAATGAGAAATATACAAAGATGTAAACAAACACATATGAAAGATGAAACAAACAAACAAAGAGTGCTGAAAAAAACAAATCAACAAACAAACAAATCTGTGTAAAAAA  
AATGGTTTATAAAAAATATCGAAGAAACAAACAAACAAATAAATAAAAAAG  
CCAAAGCCAGAGGCCAATCCCCCTCCCTCTTTGGGATAGATAGATCGCTCTTTT

	Dro_fung1	Dro_fung2
Dro_fung1	-	33
Dro_fung2		-

Pairwise sequence identity matrix (%) showing similarity between lncRNA sequences.

[illegible]

Upstream promoter alignment showing conserved regions. Sequences include Pol III promoters (noeCR34335, Arthropod\_7SK, 7SL, RNase\_MRP, RNaseP\_nuc, U6, U6atac, tRNAsec, snoRNAme18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in the alignment.