

**Assembly:** GCA\_035042365.1\_ASM3504236v1\_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.87

GGGGCGGGTCTGTCATTCCAGCAGTAAAAAGCGGTGGACACATCCCGTCTCTATACACGCATCTCAGAAATTTGTGTCACATTGGGTACAAACGCCAGAAATTTATGATTAAGAAAAAGCAATATCCAAATTTCTCATTTCTCAGAGCG  
AAAAATCCAGAGCAAAATCAAGCAGAAATATGCAAAAATATAAAACACCAATATATAAAAGTGAACACACAAAAGTCTAAACAGAGAAATCGACAAATCGCAAAATATAATATCGACCCAAAAGATATATCCATGCCAAACCAAAATGGT  
AAAAATCAAGACATAAAACACTAAAAAAATGCAACTTAATGTAACTAGGTATAAAATCTATGTTGTTTATCTCAGBAGAAAAAATAATATCTTGAAAAATCTAAAAAAAATATATAAACTCAAAACTTGCATTTGGTGTG  
TGTGTCCCGTTCTGTAATTCGTGACGCGTCAAGCTCGGCCCAATCCAAAAGGGCTGACTCAGTGGGAAGAGGAAGTGGTCCCAACCGGGGGGGGTTACCTCTCCAGAACCAATCTAGAGCAACGGGACAGCAACACACAA  
CATCGCTCTACAGAAGAGGACACCACTAGACAAATGGGTGATGATGGGGTTTGTGCTCTCTCTCTGCTCCCTCTCTGATGATCTCTCAGTATGTGTACAGCAATCACTGGTCAAGTGGCCCAAGTCTGCGAAAAAGCGTGGCTCA  
GGGCGCTCCCAAAAAATCAACATAGACGCTTAAGGCAAAATCTAAATGAACAAAAATATAAGAGCAATCAACAAAAAGAAAACCAAAATATTCAGAAAAATGTCACAAACATTTCTAATAATGGCAAAAAGGAAAAATCTGCAAA  
ATTACCAACACACCCCTTCGAAAAACCGCTCAGTAAGATACACATCACTCTGGGAGCTCGTGGAAATGTTGATCGCCCTTTT

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 4nt PSE: 0.99

[illegible]

	Dro_div1	Dro_div2
Dro_div1	-	31
Dro_div2		-

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.