

Assembly: GCA_035042125.1_ASM3504212v1_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.88

[illegible]

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

GGGGCGGTCBAGCATCTTCTACAGCTAAAGGGTTTCTCATTCCCCCGATTTGTAACCAAAATTTGTAAGTGGGGGGGGGATCTTTTCCCCCACCCAGACACCBGACATCTCATCTTAATACAAAAATATGATTTTGTGAGAAATGTAGAA
 AAAAAACAAATATGTAAACAAATCATATCAAAAAATAAAACAAACATATTAATAAAAAAGAGAGTGTCACTATTAACAAATATCAAAATCAAAATCTTGTTTAAAAAAATTTGATTTAAAAAAATTTTATTCBAAAGAAAAATCAATATAA
 TCGAAGACACAAAAAAAATATATATACACCAACCAAGAAACCAACAAACCAACACAAACCCGTGTGTGATGTCTACAGAAATGGGGAAGGGGAGGGCCAGGGCCATGGCTCAAGCCCCCAGGGCCAAAGGGCCAG
 GGCCAAAGGCGCATCTCCCCCTCTCCCATTTGGCTGATGCTGCTCTTTT

	Dro_lon1	Dro_lon2
Dro_lon1	-	30
Dro_lon2		-

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.