

**Assembly:** GCA\_035046425.1\_ASM3504642v1\_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.87

[illegible]

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 7nt PSE: 0.95

AGCGGGTCTGACGGCTCAGATGCTACAGGGTTTCTCCACGTCCTCCCGACTTAATCTGCGGAGCAAAAAACAGTGTATCTTCTGTGTACCAAAAAACGCGGGGAGCAACCTATGAAAAATCTGCATAAAATGCTACGCTTAATGCTAAAAATGTACAC  
 AAAAAAGCTTCTAAAAATGAAAAATCGATGAGAGAAATTTTCAAAATCAATCTCACTACTCTGCAAAAACGGGAGGAAAAATTAATTTTCCTTATGCGGGGGGGGAGGCTATGCAACCAATCTCTCTCTCTCTAGAAAAAGTAAAAAC  
 ACTACTTCTGGCTGGCTACCAAAAGCAAAATTTGCAACTCATGCCCCATTAATGTTTAAATATGGGCCTAATGTTTCAAAAACAAACAAAAAATCCAAAAAAGAAAAACAAAGAAATCCAAACAAATAAAAATGTAACCTGTAAGGCGCCATCTGATC  
 GCTACTTTTTTTTT

	Dro_ano1	Dro_ano2
Dro_ano1	-	32
Dro_ano2		-

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.