

Assembly: GCA_017639315.2_ASM1763931v2_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.84

Dro_ana2 | CM029946.2:13430590-13431060 (+) | 471 nt | lncRNA: noe consensus e-value: 2.5e-05

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 5nt Trailing-T: 6nt PSE: 0.95

	Dro_ana1	Dro_ana2
Dro_ana1	-	33
Dro_ana2		-

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

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.

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