

Drosophila montana

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Drosophila subgenus Drosophila > virilis group

Assembly: GCA_035044405.1_ASM3504440v1_genomic

Dro_mont1 | JAWNMB010002089.1:328592-329735 (-) | 1144 nt | lncRNA: noe consensus e-value: 5e-182

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.94

[illegible]

Dro_mont2 | JAWNMB010001354.1:2440344-2441166 (+) | 823 nt | lncRNA: noe consensus e-value: 1.5e-02

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 5nt Trailing-T: 5nt PSE: 0.97

[illegible]

	Dro_mont1	Dro_mont2
Dro_mont1	-	40
Dro_mont2		-

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.