

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Drosophila subgenus Drosophila > robusta group > robusta subgroup

Assembly: GCA_035043565.1_ASM3504356v1_genomic

Dro_rob1 | JAWNMW010000570.1:9154243-9155417 (+) | 1175 nt | lncRNA: noe consensus e-value: 1e-183

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.91

[illegible]

Dro_rob2 | JAWNMW010000257.1:6813141-6813889 (-) | 749 nt | lncRNA: no consensus e-value: 2.2e-02

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 7nt PSE: 0.92

[illegible]

	Dro_rob1	Dro_rob2
Dro_rob1	-	36
Dro_rob2		-

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.