

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

Assembly: GCA_035047465.1_ASM3504746v1_genomic

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

[illegible]

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

GGGCGGCGCGGGCGGTTTCACACAGCTCAGGGTTGATCATCACAGGTTCCCGCACATATGTTGTAATCCAGTAAAAATATGATGCAAAATGTACGCAAAATGTACGCAAAACACCAACACCAACACCAACACGAGGGCAACAAACACACAGAGATGTGAAAAAATATGATGTTGTAATAAAAAAGAGATAGGTTGTGCAAAATTTGTATGAAAGATGATGAAATAAAAAAGAAATACGGATGAAACCAATACGATGCAAAACACCCATCTTCTTATATATTTGTATGAAAGAGATGATGAAATATATATATGATGATGAAAGAGAGAAATATGTTGTAATATCCCTCCCGCCGAATCCCAATCAACACCTGCAAAAGTTGTTGTTTAAATGTTATGATGATGAGAAATGAGAGAGAGAAATAGGAAATAGCAAAATATACCCATTTCAACTTATATAGATACATAGGATCTGACTTGAAAGAAAGAGAAACCAACACCTGTAAGAAACCAATATATAAATGAAATAAAAAAGAGAGAGATGCGGGATCTGTCCATCGGACGACGATATCGGGACGACATACGCAAAATCTAGCGTGTGTTGGTGGTATCTACCTCCGACABCCACATAAATTAACCCGTCGTGGGACBCTGAGGAGAGAGGGGGGATGTCGCGACACAGATCTCTCCGCCCCCTTCTCAATATGATGCGCTTTTTTTT

	Dro_sord1	Dro_sord2
Dro_sord1	-	34
Dro_sord2		-

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, J6, 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.