

Drosophila melanocephala

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > planitibia group > cyrtoloma subgroup

Assembly: GCA_037043625.1_ASM3704362v1_genomic

Dro_mela1 | JBAMBD010000585.1:1602293-1603306 (-) | 1014 nt | lncRNA: noe consensus e-value: 3e-162

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.88

Sequence alignment showing conserved regions across Dro_mela1 and Dro_mela2. Conserved positions are highlighted in blue.

Dro_mela2 | JBAMBD010000662.1:492397-492840 (+) | 444 nt | lncRNA: noe consensus e-value: 1.9e-13

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.96

Sequence alignment showing conserved regions across Dro_mela1 and Dro_mela2. Conserved positions are highlighted in blue.

	Dro_mela1	Dro_mela2
Dro_mela1	-	27
Dro_mela2		-

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 blue.

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