Drosophila malerkotliana malerkotliana

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Sophophora > melanogaster group >

ananassae subgroup

Assembly: GCA_018153235.1_ASM1815323v1_genomic

Dro_mal1 | JAECXV010000067.1:18491963-18493024 (-) | 1062 nt | IncRNA:noe consensus e-value: 6e-183

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.83

Dro_mal2 | JAECXV010000058.1:10616875-10617404 (-) | 530 nt | IncRNA:noe consensus e-value: 3.4e-06

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

S TITULIS OF THE CONTROL OF THE CONT

	Dro_mal1	Dro_mal2
Dro_mal1	-	32
Dro_mal2		-

Pairwise sequence identity matrix (%) showing similarity between IncRNA 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.