

Drosophila teissieri

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

Assembly: GCA_016746235.2_Prin_Dtei_1.1_genomic

Dro_tei1 | CM028596.2:16788747-16789828 (+) | 1082 nt | lncRNA: noe consensus e-value: 3e-198

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.86

[illegible]

Dro_tei2 | CM028593.2:5076857-5077335 (+) | 479 nt | lncRNA: noe consensus e-value: 1.8e-04

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 10nt PSE: 1.00

TCCGCTCAGCCGCTCAGAGTGATCAAGGCTGCCCCGTTCTCCACTAATGTGGCAAAAAAGATGTTCCCATCTTATGGGTAAGATTTCCCGCTTTGACGGGATGAGTCCGCTCTTACGGGATAAATGTGTGATCATGTGAG
 TGGAGTTGATGTGTGCGGGCTGTGAAATGAAAGCTGCTCCGCAATCGAAGAAGTCTAGCTAGTGTAGCTAGTAAAGTGTAGCGCGCTTTGTTCGGCTGGGTAAAAATGTATGAGAAAACTCCGGTATAACAGTCAAGGAGAAAGA
 GTATTTGGTCGTATCTCTCTCAGCAATGGTGTATATAAGAAATTAACCTTGAGAAAGTCAAAACCAAAACAGCAAAAGATCCAAAAAAATTAAGAACAAATCAAAATTAACATAAACAAACCAACCTGTGTGGTGCCTGCGCGGGGAATCGA
 TCCCTCCGCTGTGATCGCTTTTTTTTT

	Dro_tei1	Dro_tei2
Dro_tei1	-	23
Dro_tei2		-

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.