Drosophila pseudotakahashii

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

Assembly: GCA_035046095.1_ASM3504609v1_genomic

Dro_pseud1 | JAWNOE010000218.1:1513807-1514939 (+) | 1133 nt | lncRNA:noe consensus e-value: 8e-196

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

Dro_pseud2 | JAWNOE010000105.1:3035943-3036475 (+) | 533 nt | lncRNA:noe consensus e-value: 7.7e-03

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

Dro_pseud3 | JAWNOE010000105.1:15702694-15702942 (-) | 249 nt | lncRNA:noe consensus e-value: 8.2e-06

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

Dro_pseud4 | JAWNOE010000105.1:15707483-15707693 (-) | 211 nt | lncRNA:noe consensus e-value: 9.8e-07

5' motif: GCGGT   3' motif: ATCGC   Internal max. Poly-T: 3nt   Trailing-T: 4nt   PSE: 0.93

	Dro_pseud1	Dro_pseud2	Dro_pseud3	Dro_pseud4
Dro_pseud1	-	33	15	10
Dro_pseud2		-	36	32
Dro_pseud3			-	63
Dro_pseud4				-

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 the alignment.