

Drosophila yakuba

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

Assembly: GCA_016746365.2_Prin_Dyak_Tai18E2_2.1_genomic

Dro_yak1 | CM028601.2:16782999-16784079 (+) | 1081 nt | lncRNA: noe consensus e-value: 4e-200

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.79

[illegible]

Dro_yak2 | CM028598.2:5053198-5053857 (+) | 660 nt | lncRNA: no consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 8nt PSE: 0.96

[illegible]

	Dro_yak1	Dro_yak2
Dro_yak1	-	34
Dro_yak2		-

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.