Drosophila glabriapex

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > glabriapex group > glabriapex subgroup

Assembly: GCA 035042305.1 ASM3504230v1 genomic

Dro_gla1 | JAWNLN010000067.1:10506714-10507741 (+) | 1028 nt | IncRNA:noe consensus e-value: 5e-164

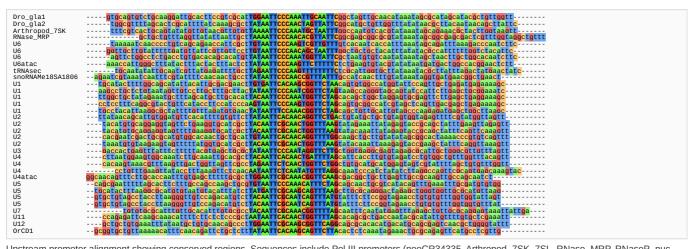
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.93

Dro_gla2 | JAWNLN010000066.1:9929792-9930136 (-) | 345 nt | IncRNA:noe consensus e-value: 7.7e-11

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

	Dro_gla1	Dro_gla2
Dro_gla1	-	21
Dro_gla2		-

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.