Drosophila quasianomalipes

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > anomalipes group

Assembly: GCA 035043665.1 ASM3504366v1 genomic

Dro_quas1 | JAWNMU010000485.1:990769-991808 (+) | 1040 nt | IncRNA:noe consensus e-value: 5e-165

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

Dro_quas2 | JAWNMU010000696.1:13369-13838 (-) | 470 nt | IncRNA:noe consensus e-value: 2.5e-11

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 1.00

	Dro_quas1	Dro_quas2
Dro_quas1	-	31
Dro_quas2		-

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.