## Drosophila persimilis

**Taxonomic lineage:** Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Sophophora > obscura group > pseudoobscura subgroup

Assembly: GCA\_003286085.2\_DperRS2\_genomic

## Dro\_pers1 | QMET02000324.1:47254-48469 (-) | 1216 nt | IncRNA:noe consensus e-value: 3e-179 5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 9nt PSE: 0.86

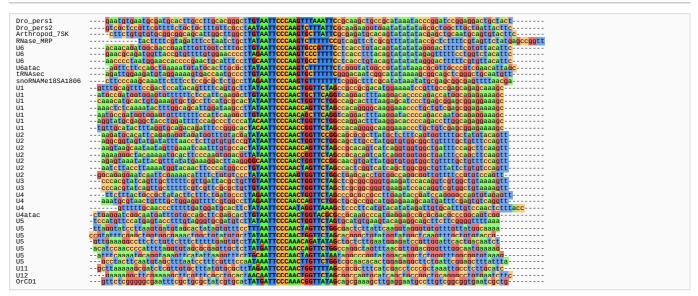
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## Dro\_pers2 | QMET02000007.1:6767284-6767821 (-) | 538 nt | IncRNA:noe consensus e-value: 5.5e-02

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

	Dro_pers1	Dro_pers2
Dro_pers1	-	28
Dro_pers2		-

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.