## Drosophila subpulchrella

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

Assembly: GCA\_014743375.2\_RU\_Dsub\_v1.1\_genomic

## Dro\_subp2 | CM025936.1:25906551-25907702 (-) | 1152 nt | IncRNA:noe consensus e-value: 1e-198

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.85

## Dro\_subp3 | CM025933.1:14809823-14810333 (-) | 511 nt | IncRNA:noe consensus e-value: 4.6e-03

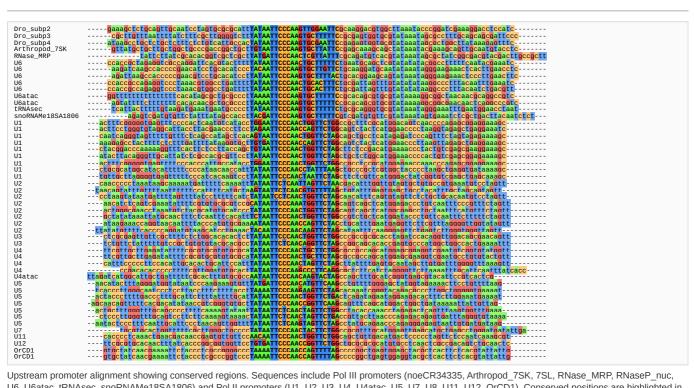
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 1.00

## Dro\_subp4 | CM025933.1:21379918-21380189 (+) | 272 nt | IncRNA:noe consensus e-value: 3.1e-04

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.91

		Dro_subp2	Dro_subp3	Dro_subp4
Dro_su	bp2	-	25	17
Dro_su	bp3		-	40
Dro_su	bp4			-

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.