## Drosophila watanabei

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

Assembly: GCA\_008042575.1\_UCB\_Dwat\_1.0\_genomic

## Dro\_wat1 | VNJS01006105.1:2303-3529 (-) | 1227 nt | IncRNA:noe consensus e-value: 6e-189

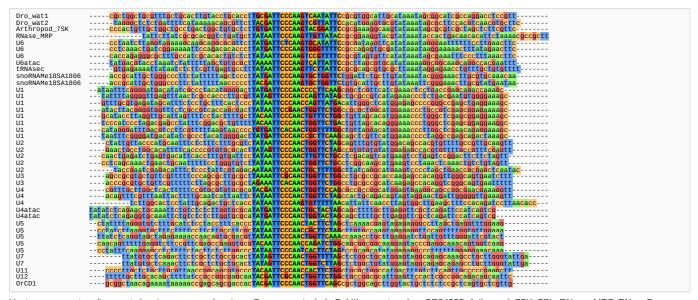
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.96

## Dro\_wat2 | VNJS01001491.1:180862-181321 (+) | 460 nt | IncRNA:noe consensus e-value: 6.6e-03

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.98

	Dro_wat1	Dro_wat2
Dro_wat1	-	27
Dro_wat2		-

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.