

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

**Assembly:** GCA\_018902025.2\_UCI\_dwil\_1.1\_genomic

5' motif: GTGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.97

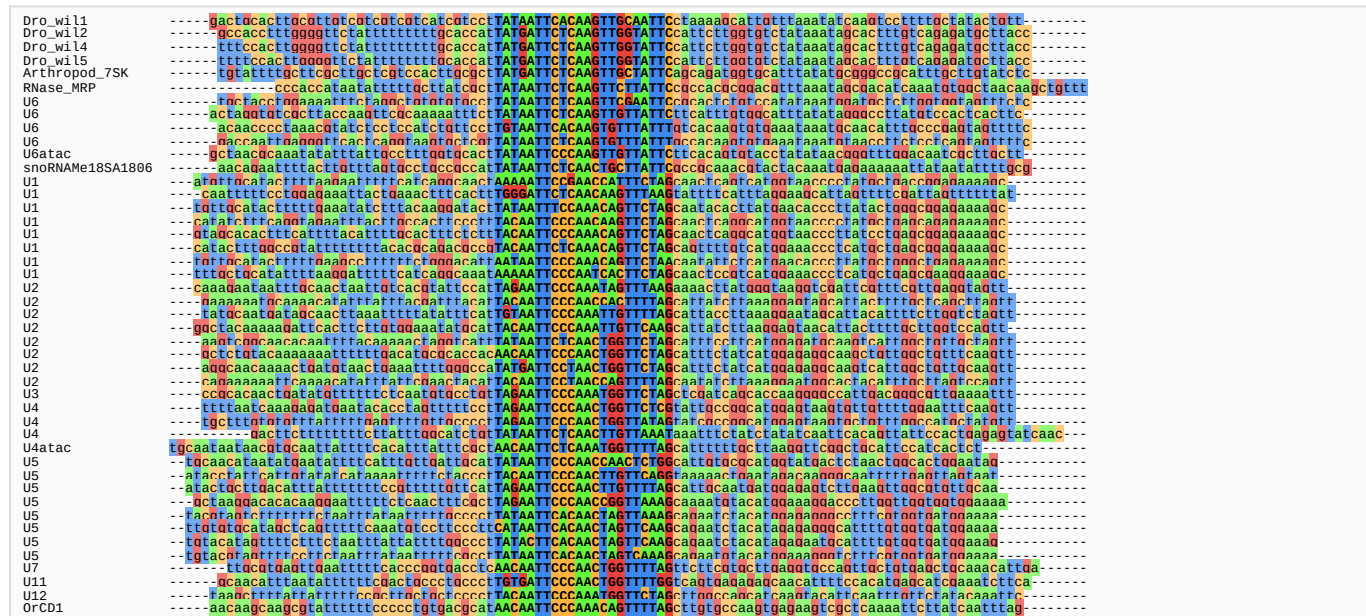
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.98

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	Dro_wil1	Dro_wil2	Dro_wil4	Dro_wil5
Dro_wil1	-	9	9	9
Dro_wil2		-	99	99
Dro_wil4			-	99
Dro_wil5				-

Pairwise sequence identity matrix (%) showing similarity between lncRNA 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.