## Drosophila willistoni

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

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

# Dro\_wil1 | JAFEWB010000700.1:1681565-1683266 (-) | 1702 nt | IncRNA:noe consensus e-value: 1.7e-81

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

### Dro\_wil2 | JAFEWB010000737.1:88588-88846 (-) | 259 nt | IncRNA:noe consensus e-value: 3.5e-03

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

#### Dro\_wil4 | JAFEWB010000737.1:77981-78237 (-) | 257 nt | IncRNA:noe consensus e-value: 1.7e-02

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

### Dro\_wil5 | JAFEWB010000737.1:124153-124408 (+) | 256 nt | IncRNA:noe consensus e-value: NA

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

	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 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