

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

**Assembly:** GCA\_035045865.1\_ASM3504586v1\_genomic

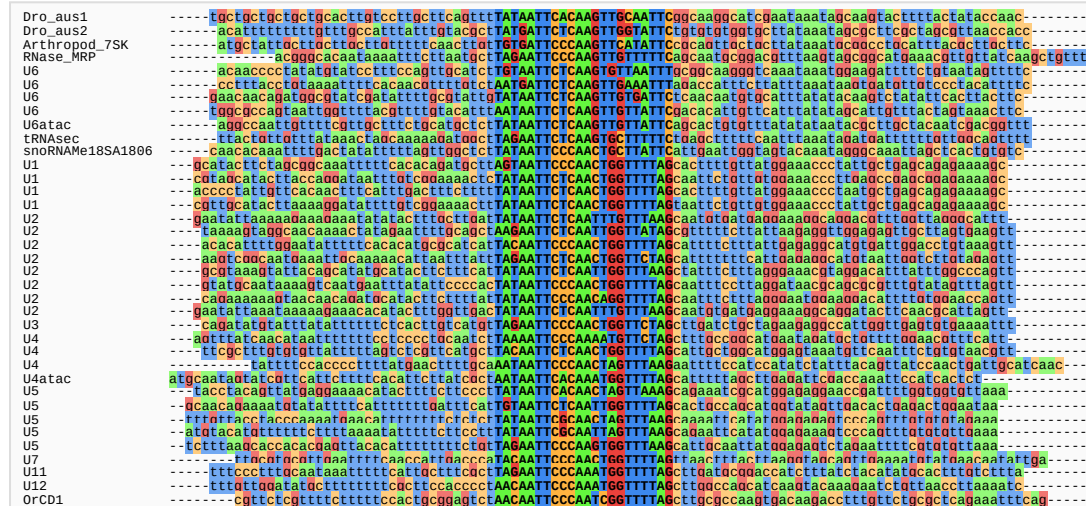
5' motif: GTGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 9nt PSE: 0.91

**Dro\_aus2 | JAWNOQ010000007.1:18100975-18101662 (+) | 688 nt | IncRNA: noe consensus e-value: 8.7e+00**

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.95

	Dro_aus1	Dro_aus2
Dro_aus1	-	32
Dro_aus2		-

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.