

## *Drosophila anceps*

**Taxonomic lineage:** Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Drosophila subgenus Drosophila > repleta group > mulleri subgroup

**Assembly:** GCA\_035045945.1\_ASM3504594v1\_genomic

**Dro\_anc1 | JAWNON010000186.1:2947947-2948865 (-) | 919 nt | lncRNA: noe consensus e-value: 6e-169**

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.88

[illegible]

**Dro\_anc2 | JAWNON010000004.1:1219053-1219759 (-) | 707 nt | lncRNA: no consensus e-value: 1.1e+00**

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.94

[illegible]

	Dro_anc1	Dro_anc2
Dro_anc1	-	47
Dro_anc2		-

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

[illegible]

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.