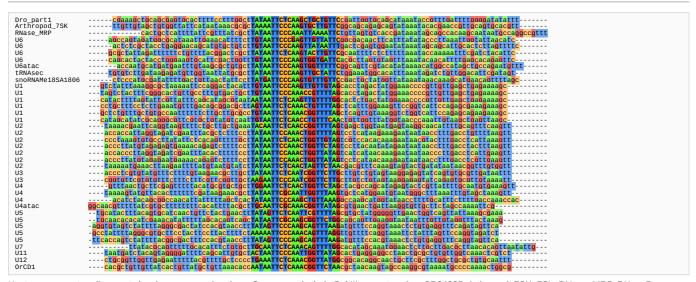
## Drosophila parthenogenetica

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

**Assembly:** GCA\_035047505.1\_ASM3504750v1\_genomic

## Dro\_part1 | JAWNPM010000247.1:1883271-1884417 (-) | 1147 nt | IncRNA:noe consensus e-value: 3e-183 5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.92 \$\$\$6\$6\$75\$\$6\$715\$\$6\$715\$\$6\$75\$\$6\$



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.