## Drosophila merina

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

Assembly: GCA\_035047645.1\_ASM3504764v1\_genomic

## Dro\_merin1 | JAWNPH010000059.1:17103736-17104767 (-) | 1032 nt | IncRNA:noe consensus e-value: 2e-184

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.80

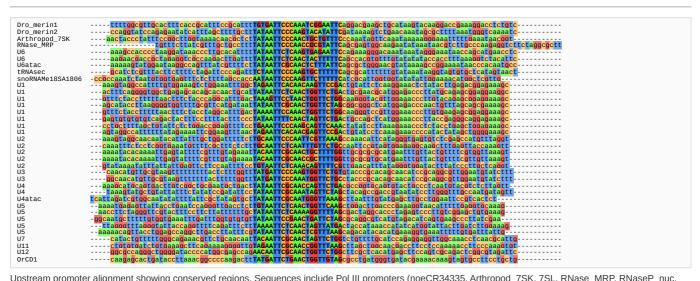
## Dro\_merin2 | JAWNPH010000054.1:8600509-8600733 (+) | 225 nt | IncRNA:noe consensus e-value: 8.9e-05

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

GGCGGTCGAGCGCCTCACAGTTATCAAGGGTTGGCCACACTCCCGACTAATTGTGGTAACCCCTGGCGGAGCTCTGCTGGAATACCAACGTTACGTTAGATTCCTGTAACCTTCTGCGCGATATCCGCTTAACGATTTCGATTCTGCTCA

	Dro_merin1	Dro_merin2
Dro_merin1	-	12
Dro_merin2		-

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.