## Drosophila bipectinata

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

Assembly: GCA\_030179905.2\_DbipHiC1v2\_genomic

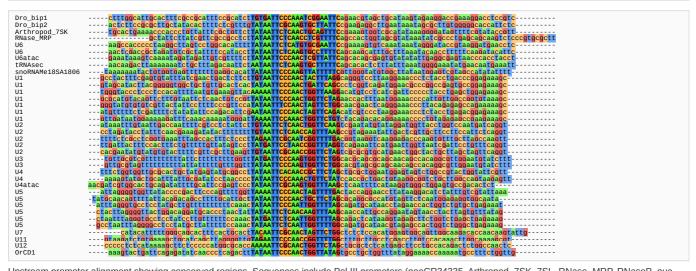
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## Dro\_bip2 | CM058211.1:16205768-16206290 (+) | 523 nt | IncRNA:noe consensus e-value: 8.4e-07

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

	Dro_bip1	Dro_bip2
Dro_bip1	-	32
Dro_bip2		-

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.