## Drosophila engyochracea

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > grimshawi group > orphnopeza subgroup

Assembly: GCA\_035042385.1\_ASM3504238v1\_genomic

## Dro\_eng1 | JAWNLK010000099.1:9395642-9396674 (+) | 1033 nt | IncRNA:noe consensus e-value: 2e-165

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.92

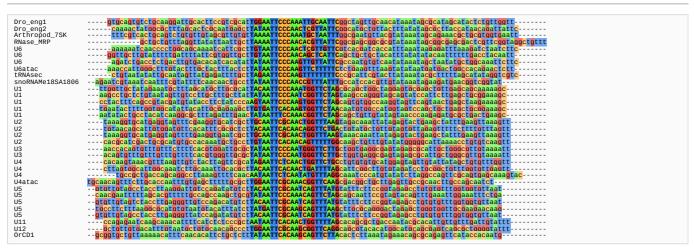
## Dro\_eng2 | JAWNLK010000167.1:14966322-14966844 (-) | 523 nt | IncRNA:noe consensus e-value: 5.3e-14

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 1.00

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	Dro_eng1	Dro_eng2
Dro_eng1	-	32
Dro_eng2		-

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.