## Drosophila grimshawi

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

Assembly: GCA\_018153295.1\_ASM1815329v1\_genomic

## Dro\_gri1 | JAECXY010000044.1:10384172-10385183 (+) | 1012 nt | IncRNA:noe consensus e-value: 5e-166

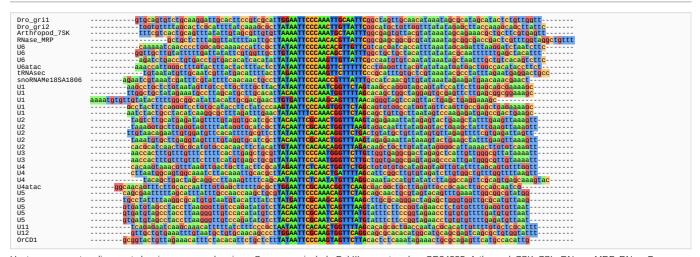
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.91

## Dro\_gri2 | JAECXY010000847.1:15002748-15003297 (-) | 550 nt | IncRNA:noe consensus e-value: 4.7e-12

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

	Dro_gri1	Dro_gri2
Dro_gri1	-	30
Dro_gri2		-

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.