## Drosophila setosimentum

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

Assembly: GCA 035043505.1 ASM3504350v1 genomic

## Dro\_set1 | JAWNMY010000006.1:6124978-6126009 (+) | 1032 nt | IncRNA:noe consensus e-value: 4e-161

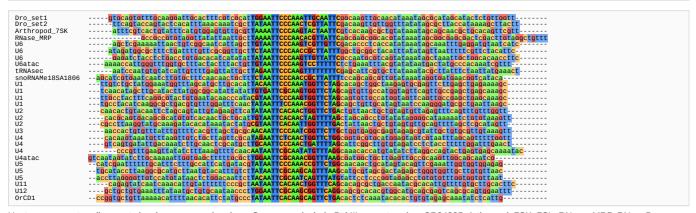
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.88

## Dro\_set2 | JAWNMY010000090.1:15016344-15016976 (+) | 633 nt | IncRNA:noe consensus e-value: 4.0e-07

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

	Dro_set1	Dro_set2
Dro_set1	-	32
Dro_set2		-

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.