Drosophila lacertosa

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Drosophila subgenus Drosophila > robusta group > lacertosa subgroup

Assembly: GCA_004143845.1_ASM414384v1_genomic

Dro_lac1 | SCDZ01000261.1:173586-174932 (+) | 1347 nt | IncRNA:noe consensus e-value: 2e-157

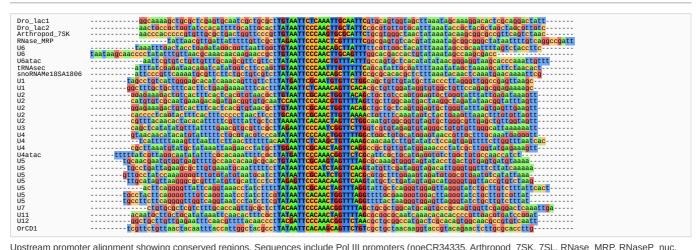
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.89

Dro_lac2 | SCDZ01000243.1:8906-9483 (+) | 578 nt | IncRNA:noe consensus e-value: 8.4e+00

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.99

	Dro_lac1	Dro_lac2
Dro_lac1	-	28
Dro_lac2		-

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.