Drosophila sturtevanti

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Sophophora > saltans group > sturtevanti subgroup

Assembly: GCA_018150375.1_ASM1815037v1_genomic

Dro_stu1 | JAECWJ010000594.1:6375170-6376520 (+) | 1351 nt | IncRNA:noe consensus e-value: 2e-125

5' motif: GTGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 8nt PSE: 0.94

Dro_stu2 | JAECWJ010000378.1:1849769-1850417 (-) | 649 nt | IncRNA:noe consensus e-value: 1.1e-01

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.95

	Dro_stu1	Dro_stu2
Dro_stu1	-	33
Dro_stu2		-

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.