Drosophila suzukii

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Sophophora > melanogaster group > suzukii subgroup

Assembly: GCA_043229965.1_CBGP_Dsuzu_IsoJpt1.0_genomic

Dro_suz1 | CM091709.1:8229665-8230813 (-) | 1149 nt | IncRNA:noe consensus e-value: 1e-198

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.84

Dro_suz2 | CM091711.1:16017768-16018302 (-) | 535 nt | IncRNA:noe consensus e-value: 2.3e-02

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 1.00

Dro_suz3 | CM091711.1:8229209-8229458 (+) | 250 nt | IncRNA:noe consensus e-value: 1.3e-03

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.90

AACTIGAAACAAG ICCAGCAATGGAAAAATAATAAGC IGTGTGGTTAGCACTIGGTTGGTTGTGGTTAATCCCCTCCGCCTTCCAAGTGATCGCTATT

	Dro_suz1	Dro_suz2	Dro_suz3
Dro_suz1	-	33	13
Dro_suz2		-	35
Dro_suz3			-

Pairwise sequence identity matrix (%) showing similarity between IncRNA sequences.

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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.