Drosophila jambulina

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

Assembly: GCA_047116535.1_ASM4711653v1_genomic

Dro_jam1 | CM120411.1:22036945-22038172 (-) | 1228 nt | lncRNA:noe consensus e-value: 4e-192

5' motif: GCGGT   3' motif: ATCGC   Internal max. Poly-T: 3nt   Trailing-T: 6nt   PSE: 0.92

Dro_jam2 | CM120414.1:25287494-25287940 (-) | 447 nt | lncRNA:noe consensus e-value: 3.3e-04

5' motif: GCGGT   3' motif: ATCGC   Internal max. Poly-T: 4nt   Trailing-T: 4nt   PSE: 0.95

	Dro_jam1	Dro_jam2
Dro_jam1	-	21
Dro_jam2		-

Pairwise sequence identity matrix (%) showing similarity between lncRNA 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.