Scaptodrosophila lebanonensis

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Scaptodrosophila > victoria group

Assembly: GCA 003285725.2 SlebRS2 genomic

Sca_leb1 | QMEN02000214.1:5254279-5255300 (-) | 1022 nt | IncRNA:noe consensus e-value: 1e-192

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

Sca_leb2 | QMEN02000053.1:833116-833845 (-) | 730 nt | IncRNA:noe consensus e-value: 8.3e-03

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.93

	Sca_leb1	Sca_leb2
Sca_leb1	-	41
Sca_leb2		-

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.