Leucozona laternaria

Taxonomic lineage: Brachycera > Muscomorpha > Syrphoidea > Syrphidae > Leucozona

Assembly: GCA 932273885.2 idLeuLate1.2 genomic

Leu_lat1 | OW026367.1:8627689-8627974 (-) | 286 nt | IncRNA:noe consensus e-value: 1.4e-11

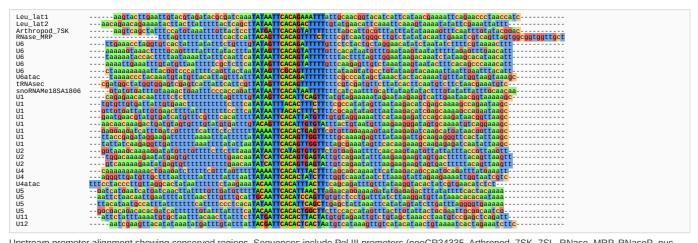
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.93

Leu_lat2 | OW026367.1:111213052-111213331 (-) | 280 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ACCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.95

	Leu_lat1	Leu_lat2
Leu_lat1	-	44
Leu_lat2		-

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.