Liodrosophila aerea

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Liodrosophila

Assembly: GCA 035045005.1 ASM3504500v1 genomic

Lio_aer1 | JAWNNL010000964.1:1160120-1161098 (+) | 979 nt | IncRNA:noe consensus e-value: 5e-183

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.82

Lio_aer2 | JAWNNL010000728.1:39901-40403 (+) | 503 nt | IncRNA:noe consensus e-value: 9.6e-05

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.86

	Lio_aer1	Lio_aer2
Lio_aer1	-	30
Lio_aer2		-

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.