Collessia kirishimana

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

Assembly: GCA 035078785.1 ASM3507878v1 genomic

Col_kir1 | JAWNPV010004117.1:2643-3861 (-) | 1219 nt | IncRNA:noe consensus e-value: 1e-125

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.87

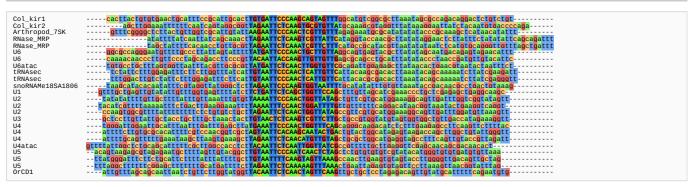
Col_kir2 | JAWNPV010000614.1:11781-12030 (-) | 250 nt | IncRNA:noe consensus e-value: 1.7e+00

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 14nt PSE: 0.97

	Col_kir1	Col_kir2
Col_kir1	-	12

Col_kir2

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.