

Collessia kirishimana

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

Assembly: GCA\_035078785.1\_ASM3507878v1\_genomic

Col\_kir1 | JAWNVP010004117.1:2643-3861 (-) | 1219 nt | lncRNA: noe consensus e-value: 1e-125

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

Sequence of Col\_kir1 (1219 nt) with highlighted conserved regions.

Col\_kir2 | JAWNVP01000614.1:11781-12030 (-) | 250 nt | lncRNA: noe consensus e-value: 1.7e+00

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

Sequence of Col\_kir2 (250 nt) with highlighted conserved regions.

	Col_kir1	Col_kir2
Col_kir1	-	12
Col_kir2		-

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.

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