Ferdinandea cuprea

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

Assembly: GCA 963576555.1 idFerCupr2.1 genomic

Fer_cup1 | OY754958.1:123872657-123872924 (-) | 268 nt | IncRNA:noe consensus e-value: 4.5e-14

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.98

Fer_cup2 | OY754960.1:43035522-43035694 (-) | 173 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 1.00

	Fer_cup1	Fer_cup2
Fer_cup1	-	43
Fer_cup2		-

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.