Cordilura impudica

Taxonomic lineage: Brachycera > Muscomorpha > Muscoidea > Scathophagidae > Cordilura > Cordilura subgenus Cordilura

Assembly: GCA 963682025.1 idCorImpu1.1 genomic

Cor_imp1 | OY821517.1:75522939-75523219 (-) | 281 nt | IncRNA:noe consensus e-value: 1.4e-02

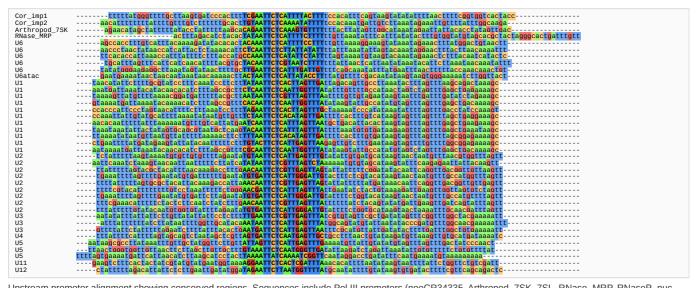
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.99

Cor_imp2 | OY821520.1:106422322-106422580 (+) | 259 nt | IncRNA:noe consensus e-value: 1.2e-05

5' motif: GCGAT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 9nt PSE: 0.93

	Cor_imp1	Cor_imp2
Cor_imp1	-	55
Cor_imp2		-

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.