Coelopa pilipes

Taxonomic lineage: Brachycera > Muscomorpha > Sciomyzoidea > Coelopidae > Coelopa

Assembly: GCA 947389925.1 idCoePili4.1 genomic

Coe_pil1 | OX376696.1:61796596-61797280 (-) | 685 nt | IncRNA:noe consensus e-value: 2.5e+00

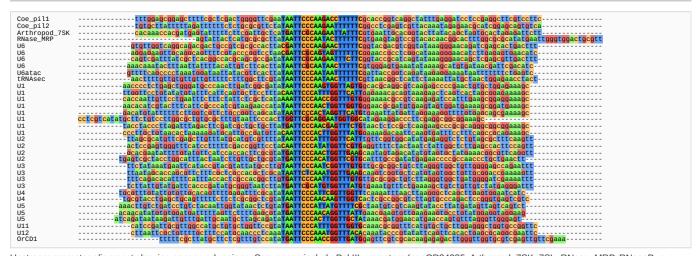
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 7nt PSE: 0.98

Coe_pil2 | OX376700.1:26671956-26672235 (-) | 280 nt | IncRNA:noe consensus e-value: 1.8e-10

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

	Coe_pil1	Coe_pil2
Coe_pil1	-	26
Coe_pil2		-

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.