Hypselothyrea guttata

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

Assembly: GCA 035045125.1 ASM3504512v1 genomic

Hyp_gut1 | JAWNNJ010000415.1:1073250-1074254 (-) | 1005 nt | IncRNA:noe consensus e-value: 3e-176

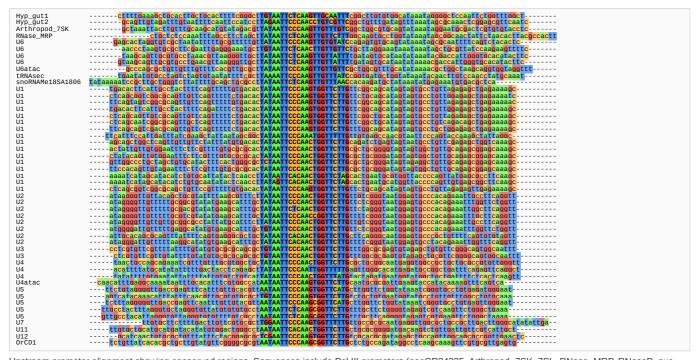
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.88

Hyp_gut2 | JAWNNJ010001046.1:214853-215119 (+) | 267 nt | IncRNA:noe consensus e-value: 7.7e-09

5' motif: GTGGT 3' motif: ATCAC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.84

	Hyp_gut1	Hyp_gut2
Hyp_gut1	-	18
Hyp_gut2		-

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.