Phortica okadai

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Phortica > Phortica subgenus Phortica

Assembly: GCA 034638295.1 ASM3463829v1 genomic

Pho_oka1 | CM067852.1:24755706-24756736 (+) | 1031 nt | IncRNA:noe consensus e-value: 1.6e-18

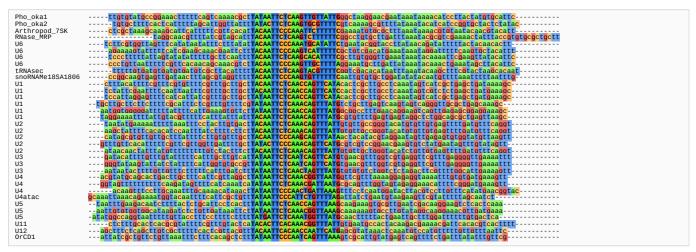
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.88

Pho_oka2 | CM067848.1:49828309-49828709 (+) | 401 nt | IncRNA:noe consensus e-value: 3.4e-03

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.89

	Pho_oka1	Pho_oka2
Pho_oka1	-	28
Pho_oka2		-

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.