Phasia obesa

Taxonomic lineage: Brachycera > Muscomorpha > Oestroidea > Tachinidae > Phasia

Assembly: GCA 949628195.1 idPhaObes1.1 genomic

Pha_obe1 | OX451217.1:39532368-39532871 (+) | 504 nt | IncRNA:noe consensus e-value: 1.2e+00

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.91

Pha_obe2 | OX451215.1:73636358-73636782 (+) | 425 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.99

Pha_obe3 | OX451218.1:68547140-68547420 (+) | 281 nt | IncRNA:noe consensus e-value: 6.4e-11

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 8nt PSE: 0.94

Pha_obe4 | OX451218.1:68537123-68537397 (+) | 275 nt | IncRNA:noe consensus e-value: 7.6e-11

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 7nt PSE: 0.94

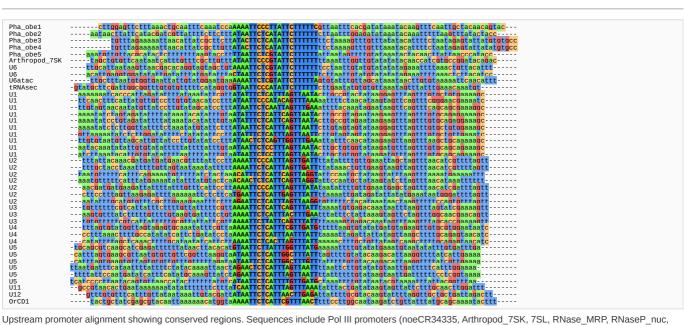
Pha_obe5 | OX451215.1:93592163-93592378 (+) | 216 nt | IncRNA:noe consensus e-value: 2.6e-07

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.96

TITI BELIANG IBLIGGEN TANATACAANGELTANGSABAT GECACANG ITAGAT EGECACTITITITI

		Pha_obe1	Pha_obe2	Pha_obe3	Pha_obe4	Pha_obe5
	Pha_obe1	-	49	40	41	33
	Pha_obe2		-	46	45	39
	Pha_obe3			-	97	51
	Pha_obe4				-	51
	Pha_obe5					-

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.