

Phania funesta

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

Assembly: GCA_963932375.1_idPhaFune2.1_genomic

Pha_fun1 | OZ010652.1:50018690-50019077 (-) | 388 nt | lncRNA: noe consensus e-value: 1.8e-03

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.98

5'GCGGTTTCATACCTCTGCATTGAAAGGGTGTTCACATTCCTTAACCAATTGTGAATTCCTTTAAAGAAAGCCCTCTTAATGACGGGGGGATTTCTGAATTCACAAATATATACACAAATCTCTCTCTACCAAAAAAGCAATTTCCTCTGATTTGTTAAGCTTBTATATGATTTATCTCAAAATAAAAAGTAAAAATATACAACTCAAGAGGGTTCATCAAAATCAATCTCAATTTCGAAAAAACCAACAAATATTGACACTAATTCCTCAATCTCTCTCTCAATGA

[illegible]

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.