

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

**Assembly:** GCA\_037044515.1\_ASM3704451v1\_genomic

Pho\_mag1 | JBAMP010002727.1:32956-34017 (+) | 1062 nt | lncRNA: noe consensus e-value: 2.3e-09

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.93

[illegible]

Pho\_mag2 | JBAMBP010002929.1:54590-54979 (-) | 390 nt | lncRNA:oe consensus e-value: 1.2e-04

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.88

[illegible]

	Pho_mag1	Pho_mag2
Pho_mag1	-	26
Pho_mag2		-

Pairwise sequence identity matrix (%) showing similarity between lncRNA sequences.

[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.