## Philornis downsi

Taxonomic lineage: Brachycera > Muscomorpha > Muscoidea > Muscidae > Philornis

**Assembly:** GCA 019455685.1 ASM1945568v1 genomic

## Phi\_dow1 | JAHXMU010000626.1:367607-368081 (-) | 475 nt | IncRNA:noe consensus e-value: 9.2e+00

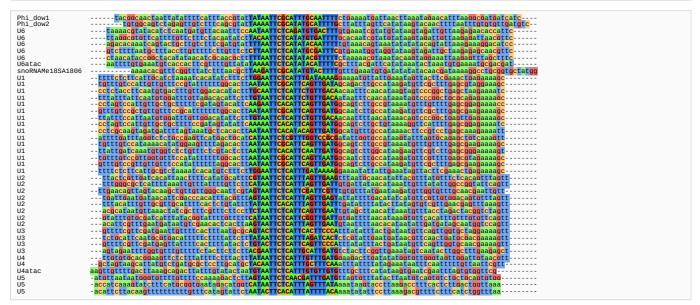
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 9nt PSE: 0.94

## Phi\_dow2 | JAHXMU010000012.1:1862811-1863052 (-) | 242 nt | IncRNA:noe consensus e-value: NA

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

	Phi_dow1	Phi_dow2
Phi_dow1	-	37
Dhi daw2		

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.