

**Taxonomic lineage:** Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Sophophora > obscura group > obscura subgroup

**Assembly:** GCA\_009664405.1\_UCBerk\_Dbif\_1.0\_genomic

**Dro\_bif1 | CM019043.1:44457447-44458744 (-) | 1298 nt | lncRNA: noe consensus e-value: 1e-144**

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.87

[illegible]

**Dro\_bif2 | CM019042.1:27248266-27248860 (+) | 595 nt | lncRNA: noe consensus e-value: 7.8e+00**

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

[illegible]

	Dro_bif1	Dro_bif2
Dro_bif1	-	32
Dro_bif2		-

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.