

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

**Assembly:** GCA\_024703675.1\_RU\_Dneb\_q3p\_genomic

**Dro\_neb1 | JANFPS010000003.1:7050864-7052632 (+) | 1769 nt | lncRNA: noe consensus e-value: 1.8e-72**

5' motif: GTGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.90

[illegible]

**Dro\_neb2 | JANFPS010000003.1:15784351-15785017 (-) | 667 nt | lncRNA: noe consensus e-value: 2.4e-01**

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.90

5'GCGGTCGTAAGGCTCAGCAGTGCAAGGGTCGGTCGATTTCCCAACTAATTGCGTCAAACTCTTGACCACAAAAAAATGAGTCAAAACCAAAACCTTTGACGACACCAAGTCAAGCAAAAACCTTTGTCAACACAGTGCACGACGCCCCATTCATTAATTTCTGCGTGGTGGGGGGTTGTGGGGCGTTAAAGTGGAGAACTAAAAACCATCTTGAAGCCAGCAAGCAACCAAGATTCAGCAAAAAACGTAAGAGAGAAATTTCAAACCTTCAGAAAAACGCGAGATCAAAAAAGAGAGAGATGCTGAAATTTCTGATTATGTAATTTGGGCTTGGGGGGGGGAAAAATTTGGGATATAAAGAAAAAAATTAAGATGTTCTAATCAACCCCATCTTCTCGCCCCCAGCGATGAAGCAAAAAACCCCAATGATTAACCAACACACTATTCAGAAAGGAACACCACTCAAGCTATAAAAAGACGCGCCGCCACGCAATGAAAAACTAAAAAGCCCCCATGATTTGATAAGCAAGAGAAACCAAAAAAACAAGAGAAAAAATTTATCAAAATAATTAATTAATAATCAACAAATGAAATAAAAAATGCTGTTGAGGCTCAAGGAGAAAAATTAACAAATTTCCAAATTTGATGCCCTTTTT

	Dro_neb1	Dro_neb2
Dro_neb1	-	22
Dro_neb2		-

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.