

***Drosophila pandora***

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

**Assembly:** GCA\_021223865.1\_ASM2122386v1\_genomic

**Dro\_pan1 | JAJJHT010017940.1:1488667-1489718 (+) | 1052 nt | lncRNA: noe consensus e-value: 3e-184**

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.87

[illegible]

**Dro\_pan2 | JAJJHT010004648.1:1699067-1699525 (+) | 459 nt | lncRNA: noe consensus e-value: 7.6e-08**

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.95

GCGGGCTCGACGCGCTCAGAGTATCAAGGGTTTTCCACGTTCCCGACTAAATTTGGAAAGCAAAAAACACAGTTGATCTCTGATGTTGACAAAACGCCGGGGAGACAGCTAAAGAAATCGCTAAAGATTTGGTACGCTTAATGAAAAATTTGACAC  
 CAAAAAGGACTCTAAATTCAGAGGAAGAAATCATGACAGGAAGATTTATCAATCCCATCTCACTAATCTCGAAGAAACAGAGGGGAGAGAGAGCTTTCAGGAGACTCTCTCCCTCTCCACAGAAAGAAAGAAAGTAAAGTAAAT  
 TTTATTTTGGCTGGCCACCAAAAGCAAAATTTGCAACCCATGCGCTCTAATGTTAAATATGGCGGTAATGTTTCAAAACAAAGCAAAAAATCCAAAAAAGAAAGAAATCCAAACAAAGCAAAAGTAAACTGTGAGGCGCATCTGATCGC

	Dro_pan1	Dro_pan2
Dro_pan1	-	33
Dro_pan2		-

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.