

*Drosophila paranaensis*

**Taxonomic lineage:** Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Drosophila subgenus Drosophila > repleta group > mercatorum subgroup

**Assembly:** GCA\_035047545.1\_ASM3504754v1\_genomic

**Dro\_paran1 | JAWNPL010000145.1:17911665-17912587 (-) | 923 nt | lncRNA: noe consensus e-value: 1e-170**

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.91

GGGGGGGGTCTGGATCCCGCAGTAAGACGGTTGGACACAGCCCGCTGAATCCGCACTCTGAATTTGTGTCCGCTTGGCTACGCTGGTGGGTGGTGGTAAAGAGCAACTGCTGCAAGAGAGCGCTCAAAACAGGGGCCAAGBGGCTGCGCAATTTCTGTCATCTGTATGACAGAAATATACGAGCAAGACCAACTCTATATACCTCATGTATCTGAATTAATGCAACAAAGTGATGATAGAGAAATCATGATGACGCAAGATATATGAAGAGAGAAAGCAAGAGBACCTGTATGCAACAAAGATATATCAATGCAAAACAAAAAATCAATATAAACGACATAAAAAATCAACAAAAAATGAACTAAATCAATTAATGTAGCTATAGATATTAAGATGATATCATCTGCTBTGTATGACGACACAAAAAATCTCTGACAAATATCAAAAAAATATATAAATCTGCAAAATACCAT1GG6181GTGTGTCGCGCTGTGTGTATGCGCTGACGCGCAAT1CG6GACAGCGGAGCCCAAT1GGAACCTCCCTTCTCCCTCTCTCCCTCTACCGCGGACAT1GCCA1GGGATAGACGCTCGGCCGACCTGG6CGCTGACCAAAAAATACCCATAGAGACCT1TAAAGCAAAAT1CTAAATGCAAAAGATATAAACCAAGAAATACCAAT1GGAACCT1GAAAGAAAAACAAAAAAGAAAAACCAACCAACAT1TGTATGAGAGAAACAGATATATCAAAATAGCAATATGAGCAACATACATATAAT1GGCAAAAAAGCAAAAAATGAAAAAAATCGAAAT1TGCAGAACACACCT1CGAAAAAGACCT1CGAT1TAATACACATAA1TGT1GG6TGTCTGCAAAAGGAAT1GCTATAGCT1GAT1GCCCTTTTTTTTT

**Dro\_paran2 | JAWNPL010000021.1:2245449-2246106 (+) | 658 nt | lncRNA: noe consensus e-value: NA**

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.98

GGCGGGTAAACGCTCACAACAGTAAAGGGTTGTCCACACTCCCCGACTAAATGTGATCTTCGCACCTCCGATATTCCGGTTTCGAATCGGGCTGTGCAACCCCATGCCACATGGTCATATCCGACGAAAAACAGATTACACTGAAATCATCATTTTATCAGATTAATGACGAAAAATATATATATCTTAATTAATAATAGTTTATATATGAACGCCAAAAATGATGTGTACCTTTTAAGTTGAAAGATGTTTAAATATCATCTAATGTATGAAAAATATGATATGAAAAAATATGCTTACATCTTCATCTTCATGTGAAAAATCATATGCTCAAAAAAGCTCTCTGATGGAGCAATTTACCAAGATTTACCAAGATGGGGCTCTCCGCTAAAAAAGAAAAAAAAGCAATCTGCAAAATGTGCAACAACTTTCTTCATCCCAACCAATATACTAAATATCTTATCCGACCAATTCACCAACTCTCCACACTTATGGGAATATGTCTTGGTCAAAAGCCAAACCACTAGAAATAAACCAATCTCAAAATATCTTAAACTAAAACTGCTGTGAGACACATCGAATGAAAGGAGGCCCACTACTCAACTTTCATTCCGCTCAATCCGCTTTT

	Dro_paran1	Dro_paran2
Dro_paran1	-	39
Dro_paran2		-

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.