

Drosophila nigricruria

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Drosophila subgenus Drosophila > replata group > mulleri subgroup

Assembly: GCA_037075265.1_ASM3707526v1_genomic

Dro_nig1 | JBAMC1010000227.1:6749324-6750251 (+) | 928 nt | lncRNA:noe consensus e-value: 2e-169

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

Sequence alignment for Dro_nig1. The sequence is 928 nt long. It shows a 5' motif of GCGGT and a 3' motif of ATCGC. The internal maximum poly-T stretch is 3 nt, and the trailing-T stretch is 7 nt. The PSE (Position-Specific Entropy) is 0.87. The sequence is color-coded to highlight conserved regions.

Dro_nig2 | JBAMC1010000107.1:16458045-16458589 (-) | 545 nt | lncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.93

Sequence alignment for Dro_nig2. The sequence is 545 nt long. It shows a 5' motif of GCGGT and a 3' motif of ATCGC. The internal maximum poly-T stretch is 3 nt, and the trailing-T stretch is 5 nt. The PSE (Position-Specific Entropy) is 0.93. The sequence is color-coded to highlight conserved regions.

	Dro_nig1	Dro_nig2
Dro_nig1	-	40
Dro_nig2		-

Pairwise sequence identity matrix (%) showing similarity between lncRNA 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.

Alignment of upstream promoter regions for Dro_nig1, Dro_nig2, and various other sequences. Conserved positions are highlighted in green and red. The alignment shows the 5' ends of the sequences, with Dro_nig1 and Dro_nig2 at the top. Other sequences include Arthropod_7SK, RNase_MRP, U6, U6atac, tRNAsec, snoRNAME18SA1806, and Pol II promoters U1 through U12 and OrCD1.

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.