

Drosophila quadrilineata

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Drosophila subgenus Drosophila > immigrans group > quadrilineata subgroup

Assembly: GCA_018150725.1_ASM1815072v1_genomic

Dro_quad1 | JAECWN010000219.1:763570-764684 (-) | 1115 nt | lncRNA: noe consensus e-value: 3e-182

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.97

Sequence alignment for Dro_quad1. The sequence is 1115 nt long. The 5' motif is GCGGT and the 3' motif is ATCGC. The internal maximum poly-T stretch is 3 nt, and the trailing T stretch is 6 nt. The PSE value is 0.97. The sequence is shown in a single line with color coding for conservation.

Dro_quad2 | JAECWN010000432.1:6648492-6648899 (+) | 408 nt | lncRNA: noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.86

Sequence alignment for Dro_quad2. The sequence is 408 nt long. The 5' motif is GCGGT and the 3' motif is ATCGC. The internal maximum poly-T stretch is 3 nt, and the trailing T stretch is 6 nt. The PSE value is 0.86. The sequence is shown in a single line with color coding for conservation.

	Dro_quad1	Dro_quad2
Dro_quad1	-	25
Dro_quad2		-

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.

Sequence alignment showing conserved regions across various promoters. The alignment includes sequences for 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.

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.