

Drosophila birchii

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

Assembly: GCA_035046345.1_ASM3504634v1_genomic

Dro_bir1 | JAWN0A010000048.1:20070447-20071660 (-) | 1214 nt | lncRNA: noe consensus e-value: 4e-193

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.84

Sequence alignment showing conserved regions for Dro_bir1. The sequence is 1214 nt long. Conserved positions are highlighted in color (red, green, blue, yellow, orange, purple, pink, brown, grey, white).

Dro_bir2 | JAWN0A010000079.1:3384717-3385110 (+) | 394 nt | lncRNA: noe consensus e-value: 7.8e-05

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

Sequence alignment showing conserved regions for Dro_bir2. The sequence is 394 nt long. Conserved positions are highlighted in color (red, green, blue, yellow, orange, purple, pink, brown, grey, white).

	Dro_bir1	Dro_bir2
Dro_bir1	-	17
Dro_bir2		-

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 showing conserved regions for Dro_bir1, Dro_bir2, and various Pol III and Pol II promoters. Conserved positions are highlighted in color (red, green, blue, yellow, orange, purple, pink, brown, grey, white).

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.