

Drosophila picticornis

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > planitibia group > picticornis subgroup

Assembly: GCA_035043845.1_ASM3504384v1_genomic

Dro_pic1 | JAWNMR010000122.1:13167637-13168672 (-) | 1036 nt | lncRNA: noe consensus e-value: 3e-160
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.92

Dro_pic2 | JAWNMR010000492.1:13858549-13859055 (-) | 507 nt | lncRNA: noe consensus e-value: 7.7e-15
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 1.00

	Dro_pic1	Dro_pic2
Dro_pic1	-	29
Dro_pic2		-

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

Dro_pic1

Dro_pic2

Arthropod_7SK

RNase_MRP

U6

U6

U6atac

tRNAsec

snoRNAme18SA1806

U1

U1

U1

U1

U2

U2

U3

U4

U4

U4atac

U5

U5

U5

U5

U11

U12

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.