Drosophila multiciliata

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > haleakalae group > anthrax subgroup

Assembly: GCA 037043605.1 ASM3704360v1 genomic

Dro_mult1 | JBAMBF010000301.1:6182294-6183272 (-) | 979 nt | IncRNA:noe consensus e-value: 5e-157

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

Dro_mult2 | JBAMBF010000157.1:1516490-1516995 (-) | 506 nt | IncRNA:noe consensus e-value: 2.5e-11

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 4nt PSE: 1.00

	Dro_mult1	Dro_mult2
Dro_mult1	-	30
Dro_mult2		-

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