

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

Assembly: GCA_051940825.1 ASM5194082v1 genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.94

[illegible]

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

[illegible]

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.91

59CGGTGCGAGCCCTCACAGTCTCTCAAGGGTGGCCACTTTCCCGCACTAATTGTGGTAGCAATTCGCTCGCCACCTCATAAACATGAAATAAGTTAAGAAAAACCAAACTGTTCGAAGGAAATTAATGCAAGTATAGTGCCAAAGCA
TGCACCAACCAAAAAATAAGTAGTTCAGTAAGAGTATGGAATATGATTTAAATAAAATGAGATCTAAAAATCTGTATATGATTATAGAAACCGCTAAAAACGAAAAAACAAAAAAACAATTTAAAGATAAGGAGGGGATA

	Dro_aur1	Dro_aur2	Dro_aur3
Dro_aur1	-	22	19
Dro_aur2		-	53
Dro_aur3			-

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

[illegible]

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.