

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

Assembly: GCA_900245975.1_DGUA_6_genomic

Dro_gua1 | OUUW01000012.1:2046268-2047707 (-) | 1440 nt | IncRNA: noe consensus e-value: 8e-124

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.83

[illegible]

Dro_gua2 | OUUW01000006.1:4027876-4028432 (+) | 557 nt | lncRNA: noe consensus e-value: 9.6e-01

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.97

[illegible]

	Dro_gua1	Dro_gua2
Dro_gua1	-	22
Dro_gua2		-

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.