

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

Assembly: GCA_005876895.1_DaztRS1_genomic

Dro_azt1 | VCKU01000016.1:3096280-3097538 (+) | 1259 nt | lncRNA: noe consensus e-value: 1e-180

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.83

[illegible]

Dro_azt2 | VCKU01000091.1:4428411-4428953 (+) | 543 nt | lncRNA: no consensus e-value: 5.2e-03

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

[illegible]

	Dro_azt1	Dro_azt2
Dro_azt1	-	30
Dro_azt2		-

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.