Drosophila americana

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Drosophila subgenus Drosophila > virilis group **Assembly:** GCA_047116735.1_ASM4711673v1_genomic

Dro_ame1 | CM120453.1:8102481-8103597 (+) | 1117 nt | IncRNA:noe consensus e-value: 1e-189 5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.95

Dro_ame2 | CM120456.1:17986131-17986995 (+) | 865 nt | IncRNA:noe consensus e-value: 1.9e-02

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 5nt Trailing-T: 6nt PSE: 0.97

	Dro_ame1	Dro_ame2
Dro_ame1	-	42
Dro_ame2		-

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.