

Drosophila mettleri

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Drosophila subgenus Drosophila > replata group > mulleri subgroup

Assembly: GCA\_035047625.1\_ASM3504762v1\_genomic

Dro\_met1 | JAWNPI010000103.1:6554425-6555367 (+) | 943 nt | lncRNA: noe consensus e-value: 4e-166

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 8nt PSE: 0.88

Sequence alignment for Dro\_met1 showing conservation across multiple species. The sequence is 943 nt long. The alignment shows high conservation across the species listed, with some variations in the 3' region.

Dro\_met2 | JAWNPI010000109.1:9790784-9791323 (-) | 540 nt | lncRNA: noe consensus e-value: 1.5e-05

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 11nt PSE: 0.98

Sequence alignment for Dro\_met2 showing conservation across multiple species. The sequence is 540 nt long. The alignment shows high conservation across the species listed, with some variations in the 3' region.

	Dro_met1	Dro_met2
Dro_met1	-	37
Dro_met2		-

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

Alignment of upstream promoter regions across various species. Conserved positions are highlighted in green. The alignment shows high conservation across the species listed, with some variations in the 3' region.

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.