

# Drosophila vallismaia

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

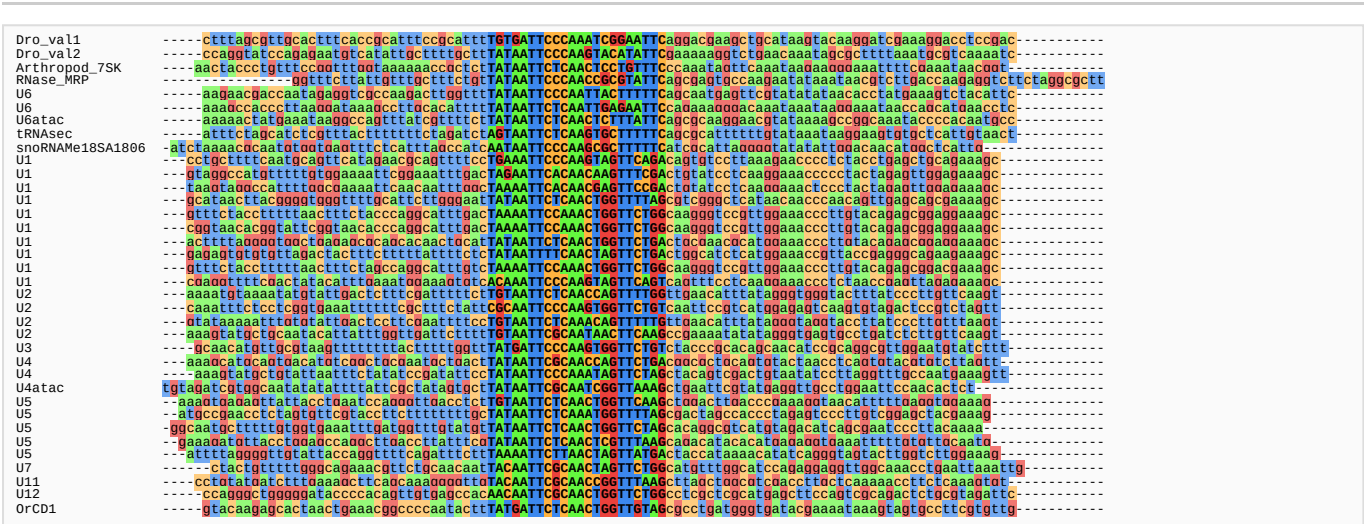
**Assembly:** GCA\_035047325.1\_ASM3504732v1\_genomic

**Dro\_val1 | JAWNPU010000055.1:17373857-17374896 (-) | 1040 nt | lncRNA: noe consensus e-value: 1e-182**  
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.84

**Dro\_val2 | JAWNPU010000001.1:8784346-8784512 (+) | 167 nt | lncRNA: noe consensus e-value: 7.6e-06**  
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 2nt Trailing-T: 5nt PSE: 0.95

	Dro_val1	Dro_val2
Dro_val1	-	10
Dro_val2		-

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, snoRNA18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in the alignment.