

Odontomyia ornata

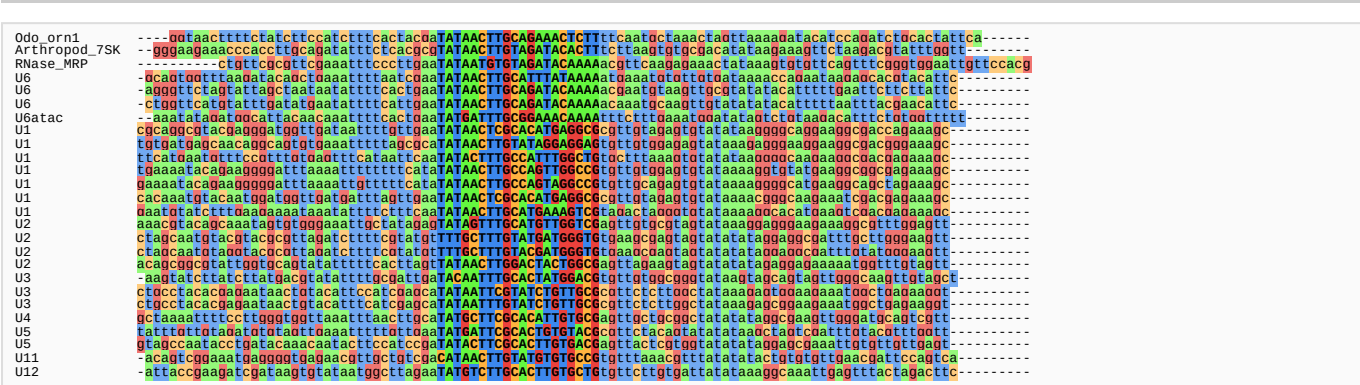
Taxonomic lineage: Brachycera > Stratiomyomorpha > Stratiomyidae > Odontomyia

Assembly: GCA_963969285.1_idOdoOrna1.1_genomic

Odo_orn1 | OZ017741.1:194910382-194910618 (-) | 237 nt | lncRNA: noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.90

GC GG T CCT C C T A T T G G T A T A A T G G G T T G A T C A T A C C C C T A A T T G T G A C G T A A T T A T A A A A A T T A A G G T C A A G A A A T C T G T T A A G T A T A A C T C T T A A T T G A G A C T T T A T A A T T A A G C A G T C T G T C T G T A G A C A A T T T C T C T A A T T T A T C A A G A A T A A G C G C G T T C A G T A A A T T A G A T T G A A T G A A T A T A A T A C A T T C T T C C A C T A A T A G G G C A A T T C G A T C G C T T T T T



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.