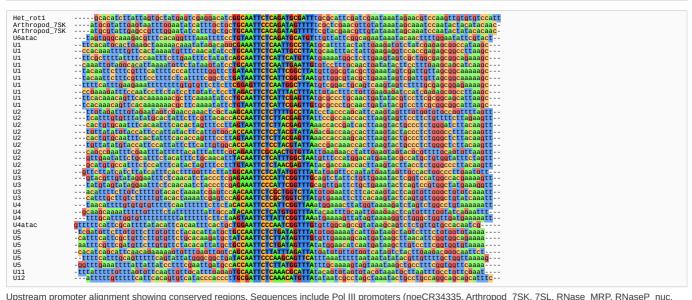
## Heteromyza rotundicornis

Taxonomic lineage: Brachycera > Muscomorpha > Sphaeroceroidea > Heleomyzidae > Heteromyza

Assembly: GCA\_951394025.1\_idHetRotu1.1\_genomic

## Het\_rot1 | OX596010.1:86506485-86507055 (-) | 571 nt | IncRNA:noe consensus e-value: 2.4e-14

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.84



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.