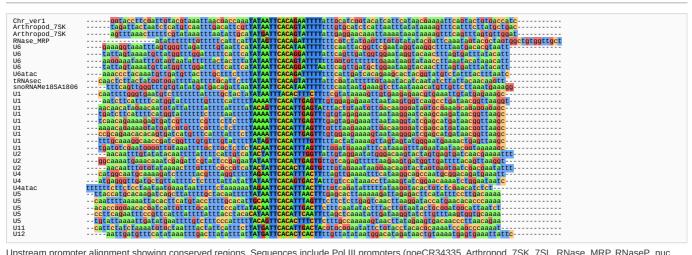
Chrysotoxum verralli

Taxonomic lineage: Brachycera > Muscomorpha > Syrphoidea > Syrphidae > Chrysotoxum

Assembly: GCA 965637335.1 idChrVerr4.hap1.1 genomic

Chr_ver1 | OZ281287.1:57120594-57120884 (+) | 291 nt | IncRNA:noe consensus e-value: 1.1e-11

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 1.00



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.