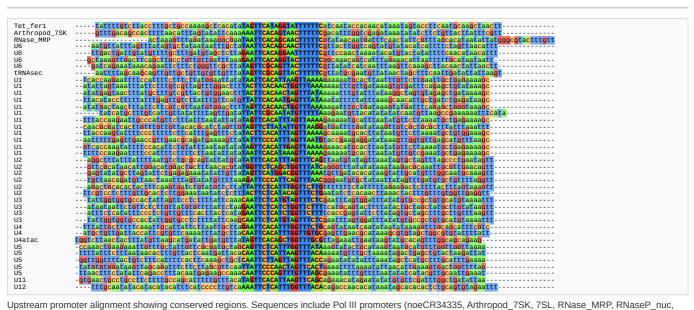
Tetanocera ferruginea

Taxonomic lineage: Brachycera > Muscomorpha > Sciomyzoidea > Sciomyzidae > Tetanocera

Assembly: GCA 958299015.1 idTetFerr1.1 genomic

Tet_fer1 | OY282641.1:128678173-128678611 (-) | 439 nt | IncRNA:noe consensus e-value: 6.1e-02

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.92



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.