Cheilosia scutellata

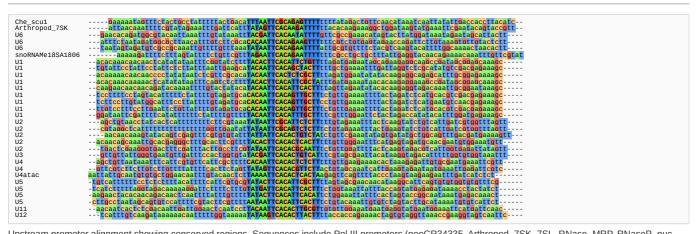
Taxonomic lineage: Brachycera > Muscomorpha > Syrphoidea > Syrphidae > Cheilosia

Assembly: GCA 955612985.1 idCheScut6.1 genomic

Che_scu1 | OY015311.1:34706897-34707182 (+) | 286 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.82

GGGCGGTTTATTATCTCACACTATGCGAGTTGGTCACATCCTTTAATTGTGGCAAAACCAAAACACAGACGGAATAGGATTGCAAATAAGCAAAAACTAAACTAAACATATTCTCATCTGCCTTATAACTAGGTGAAATCAGGT CAAAATTCTTGTACACAACTAAAATCCACTTTGCGTAAAACTCAAATTTAACTTAATTATCGCACCAAACGTTGATGTAAAGATTTGATTCCTCAAAACATTGGTGCATGGATAAAAAATGTGATCGCCTTTTTT



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.