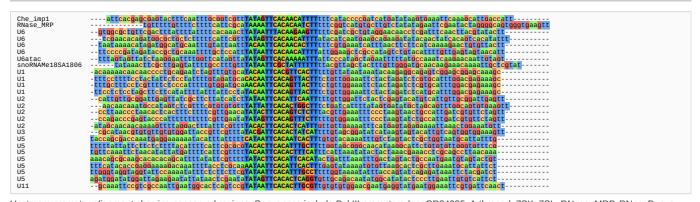
Cheilosia impressa

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

Assembly: GCA_948293265.1_idCheImpr3.1_genomic

Che_imp1 | OX411882.1:40970085-40970353 (-) | 269 nt | IncRNA:noe consensus e-value: 1.2e-10 5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.99

GGGCGGTTCGATACCTCACAGTTGTTTGCGGTTGGCTACATTCCGTTATCCAAATTGTAGCATCTAAATCGTATGCATCCATACTATAAAAAACTGCAAAAAAGTGTGTTTTGAAAAAAGTTTCACCCAAAACGAA AAACAAATCTTTCTCTATCCCTATCCCATAAGATATATAGAATATAAGCAATTCAATAAAATTGAGAAAAAACAAGTTTCAACAAAACGGTTTCTGCGAGGTAGATGCGATCGCCTTTTT



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.