

# Cheilosia impressa

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

Assembly: GCA\_948293265.1\_idChelImpr3.1\_genomic

Che\_imp1 | OX411882.1:40970085-40970353 (-) | 269 nt | lncRNA: noe consensus e-value: 1.2e-10

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.99

666CGGTTGATACCTCACAGTGTGTTGCGGTTGGCTACATTCCGTTATCCAAATGTAGCATCTAAATCGTATGCTTTGACATCCATACATATAAAAACTGCAAAAAGTGTGTTTGAAAAAGTTTACCCTAAACGAAAGCAAAACAAATGAAACAAATCTTTCTCTATCCTATCACATAAGATATATAGAATATAAGCAATCAATAAAAATTGAGAAAAACAAGTTTCAACAAAAACGGTTTCTGCGAGGTAGATGCGATCGCCTTTTT

Che_imp1	----	attcagagcdaotactttcaatttcodotcottiTATAAGTTCAACAACATTTTTtcatccccaatcatdatataaotdaaattcaaadcattdaccatt-----
RNAse_MRP	----	tgttttttgttttccttttcatttcgcaTAAAAATTCACACAATCTTTttcggtcatgtccttgcctatatagaattcgaatactagggcagtggtggaatt-----
U6	----	gtggcctgttcgactttattttttcacaaactTATAATTACAAAGAGTTtttcgacgcctgtaggaaacaacctcgatttcaactttacgtatactt-----
U6	----	tcaaacacagaatccctcctctttttcattcctTATAAGTTCAACAACATTTTatacatcaatdaaacaadaataatacaactattcaaatcacatattt-----
U6	----	taataaaacatagatggcatgcaatttgatttaattTACAATTACACAACACTTTTTtctgaaatcatttaactcttctcatcaaaagaactgtgttactt-----
U6	----	ttcccgatagataccgctgcaaattttgcctcattTATAATTCAACAACATTTTattggaagctcgccatagctctgtacattttgtgaatgaatacatt-----
U6atac	----	tttaoatattatcaadaaatttttccataaattTATAAGTTCAAAAAATTTattcccaaacadaaattttatcccaatcaaaacaattttao-----
snoRNAme18SA1806	----	tataaacctccttgagttattttgcctttgtttTATAATTGCTATTTTTTtacgtttagctactttgttggatgcaacaagaacaataattcctcgtat-----
U1	----	acaaaaacaacacccctgcagaatctagtttgcaTACAATTACAGTTACACTTTttgtataataaatacaagagcgagagtcgaagcgaagcaaaagc-----
U1	----	tttccttttccactactttctcatttttgatgacacACAATTTCACAGTACTTTcttcttgaatttccactaatctcgatcatttccacagaagaac-----
U1	----	tttgcctttcctcgtttttcccaatttttggaatgcaACAATTTCACAGTACTTTctgttggaaattctactagatctcgtgcatttggacgagaagc-----
U1	----	ttcctctctagctttctcatattttatttctcctTACAATTACAGTTACTTTctgttggaaattctactagatctcattgatttggacgagaagc-----
U2	----	cattgttgcggttgagttatcgttcttattcattTATAATTACAGTTCAATTttgttggattctactcgagatcattgctattgttcggaattgagtt-----
U2	----	aaacaacaaatcccatadctctcctttctototottTATTATTCACACTGGCTTTctaatcattttataatataatcctaacaatttcccaattotgaatt-----
U2	----	ccttaacccctaacactcactttcttttctgtgaacataTACTTTCACAGTCTCTttacgttgaatttccctaaagtaactgccattgactgtttctagtt-----
U2	----	ccagaccgagatcccattttttttctgttgaataTATAAGTTTCACAGTTCTTTttgtggaatttccctaaagtaactgcgattgactgtttctagtt-----
U3	----	atadcaacaacaaaaatttgaactttatttctttTACACTTCACACTCATTTtttcttgaatttcaataaataaadaaaataaacctgaatttgaatt-----
U3	----	cgcataacgtgtgtgttggaattaccgttctgtttTACAGTTCACACTATCATTTgttagcggatattcaatagatgacattgtcagtggtggaagtt-----
U5	----	taccagcgaccaaatgaggaaaaaatacatttattttTATAATTCAACAATCACTTTgtgtacaaaaattgtctagtagctcgttggaatgcattatttg-----
U5	----	tttttatttcttctcttttacaattttcattcccccTACACTTCACATTGCTTTtctaatcccccacaataaodattctotototctgaatttttcc-----
U5	----	ttttcaaatctcaacataattatgattttcattcgtttttTACAATTTCACACTTTCATttcattaaataatactactaaacgaacccctgcagccttaacaaa-----
U5	----	aaacagcgcaagcacacacagcattttataattcgtttttTATACTTCACATTTCACATactgatttaaatttgactgactgccaatggaatgaatgactgt-----
U5	----	tttcatcacaccgaadaaaacaaattttaccctccaaAAATAATTACATTTCACATTtgaatataaaattctttaaodactcacttgaattcattattct-----
U5	----	ttgggtaggtaggtattcccaaaatatttctcttctcgtTATAAGTTTCACACTTCAGGTtttgcagacaataatggcataatacccttgaattctgcattct-----
U5	----	agatggatagattagaagaattataaactcgaataTATAAGTTTCACACTTCAGGTtttgcagacaataatggcataatacccttgaattctgcattct-----
U11	----	gcaaatccgtcgccaattgaaatggcacctcagtcctTATAATTTCACACTTCGCTTgtgtgtggaacgaattgaggtatgaatgggaattcgtgattcaact-----

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.