

Cheilosia pagana

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

Assembly: GCA_936431705.1_idChePaga1.1_genomic

Che_pag1 | OW386168.1:40004367-40004638 (-) | 272 nt | lncRNA: noe consensus e-value: 1.2e-11

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.93

GGGCGGTCGGATGCTCACAGTTGTTTGGGGTTGGCTACATTCCGTTATCCAAATTGTAGCATCTAAATCGTATGCTTTGACATCCATACATAGAAAACTGCAAAAAAGTGTGTGTTTGA AAAAGTTTACCAAAAAACGAAAGCAAAACA

AAAAACAATCTTTCTATCCTATCACATAAGATATAGAAATATAAGCAATTCAATAAAATTGAGAAAAACAAGTCAACAAAAACGATTTCTGCTGAGGTAGATGCGATCGCCTTTTT

Che_pag1	----	attctcdaagdaotacttttcaattttcdaatc	ottTATAGTTG	CAGAAATTT	tttcataccct	ootcat	atataaac	baaat	c	aaaccact	oaccatc	--
U6	---	gtccccact	tagatgccgccc	caaattttgctttatt	TATAATTC	CACAGCA	TTTT	aatag	tatttttctgtg	taagtacatt	tttattgc	atgctcacttt
U6	---	gttacaact	tagatggcgct	taaaaaatccctctttg	caTATAATTC	CACAGAA	TTTT	tttcg	ccctcagc	gcagaa	cgacat	cagcttgaagc
U6	---	tatttc	aacta	atatttcc	taagaattttcttcc	acATAATTC	CACAGAA	TTTT	cttattct	tttct	taaaac	atatac
U6atac	---	taataaa	acatagatggcg	caaatctgtattgatt	TACAATTC	CACACCA	TTTT	ttcgt	gaattttt	acaact	gaatca	gaaagaagc
snoRNAME18SA1806	-----	gtttttc	agattttt	agaattttag	tttaatt	TATAATTC	CCATAAA	TTTT	tattc	gctagg	ctttag	tattcatat
U1	---	aac	oda	odttc	oottda	atattttot	atattT	AGAAATTC	CAGTAT	TTTT	ottc	otcc
U1	---	tgtatt	tgtttt	gtgttctt	ctattttgt	atgtgc	CACAATTC	CACAGTT	TAC	TTTT	ttgtt	ggaatt
U1	---	tttct	ttttct	tattatct	tactattttt	atadac	CACAATTC	CACAGT	CAC	TTTT	ttt	ggaatt
U2	---	ttct	gggt	taggt	aaattttt	gtttt	acttgc	atca	TATAATTC	CACAT	CAAT	TTTT
U2	---	caaca	acga	aat	tacatagg	actttt	gcattc	gtt	TATAATTC	CACAT	CAAT	TTTT
U2	---	aac	ac	ga	aat	tacatagg	actttt	gcattc	gtt	TATAATTC	CACAT	CAAT
U3	---	ctc	ottt	ctc	ccccc	otott	oattacc	ottc	ottt	TATGATTC	CACACT	GTCT
U3	---	ctc	gggt	ctgt	ccccc	gtttt	gattacc	ottc	ottt	TATGATTC	CACACT	GTCT
U3	---	att	ggt	ttgt	ggga	atgac	atttct	ttttg	ctgt	TATAATTC	CACACT	GTCT
U4	---	c	o	o	a	a	t	o	a	a	t	t
U4atac	---	a	c	a	g	g	t	t	c	a	a	a
U5	---	gtttt	t	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt
U5	---	gtttt	t	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt
U5	---	gtttt	t	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt
U5	---	gtttt	t	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt
U5	---	gtttt	t	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt
U11	---	gtttt	t	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt
U12	---	gtttt	t	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt

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.