Supplementary Material

Table

Table S1 Statistical analysis of transcriptome sequencing data

Samples	Clean reads	Q30[1]	Mapped Reads
CK-1	23,190,564	92.95%	91.51%
CK-2	23,398,129	92.97%	92.37%
CK-3	28,549,311	92.42%	90.86%
MJ-1	25,432,291	93.56%	92.57%
MJ-2	25,783,350	92.95%	92.15%
MJ-3	25,268,504	93.70%	92.06%

[1]Q30 represents reads with a sequence accuracy greater than 99.99%; Mapped Reads represents reads annotated on the reference genome.

Table S2 Primers used in qRT-PCR and vectors construction

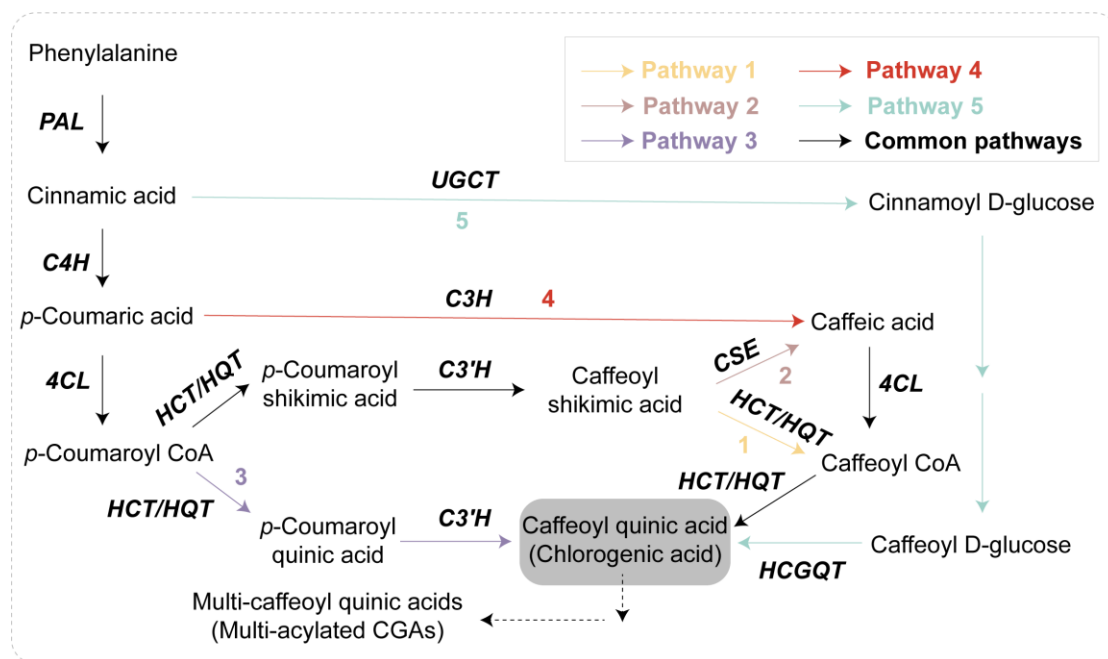| Primers	Primers' application	Primers sequences (5'→3')
DAD1-F		GACATCTCGAGGATCTGGCG
DAD1-R		TGAGCAAACTCGCCGTACTT
LOX2S-F		CGCCTACTCTCCGGTCATTC
LOX2S-R		CGGTTGGTTGGACGGTGATA
JAZ-F		GGAAACGCATCTTGGCAGTG
JAZ-R		TGTCCTCACGTTCGCAATGA
MYC2-F		GGAGTTCAACGAACAACGGC
MYC2-R		CGTCGAGATCTGAGTGGTCG
aroDE-F		TCATTGAGTAACGTGCCGCT
aroDE-R		GCACTGCCCCGTTTTCAAAT
GOT1-F		CCAAACGCCCCCTAAGTGAT
GOT1-R		ACGCCTACACGCCCATAAAA
C4H-F		AAAGGGCAGGACATGGTGTT
C4H-R	qRT-PCR	TGTTCGTGAAAAACGGCACC
4CL-F		ACCAACCCGGTGAGATATGC
4CL-R		CAGTGTGAAGCCAACCTTGC
HCT-F		GTTGACCCGAGAGCAACTCA
HCT-R		TGTACAGCTTGCTGTCCTGG
CSE-F		GCACATTCCACGTCAACCAC
CSE-R		CGTGATCGAGTTGCTCCTGA
CCoAOMT-F		GAAAACCGATCACATGGCGG
CCoAOMT-R		TAGCTCTTTCATGGGTGCCG
COMT-F		TGCAAATGCGTTGTCGATCC
COMT-R		ACCCTGTTGTGTGCAAGTGA
ubiquitin C-F		CAGCAACACCCCCTTTACTCT
ubiquitin C-R		AGGATGGAAATCGGGGTGGA
35S:: CtHCT-eGFP-F		ACGCGTCCCGGGGCGGTACCATGAAGATCGCCGTGACAGA
35S:: CtHCT-eGFP-R	Vector construction	AGCTCTGCAGGTCGACTTAGATATCGTACAAGAACTTGCT
pET28a (+)-CtHCT-F		AATGGGTCGCGGATCCATGAAGATCGCCGTGACAGA
pET28a (+)-CtHCT-R		TGCTCGAGTGCGGCCGCTTAGATATCGTACAAGAACTTGCT

Figures

Figure S1

Figure S1 Biosynthetic pathways of chlorogenic acid in plants.
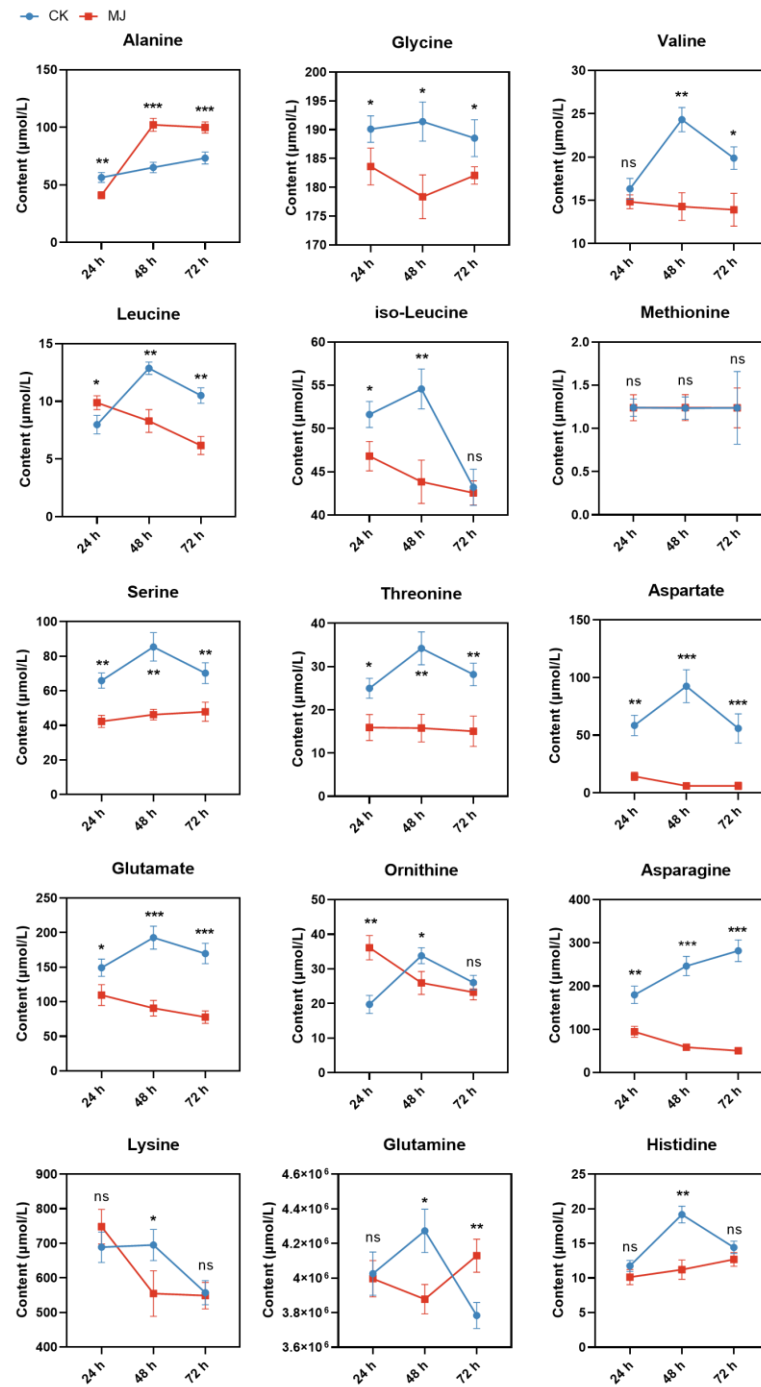
Figure S2

Figure S2 Temporal changes of amino acid in MJ-treated *C. tinctorius* cells.
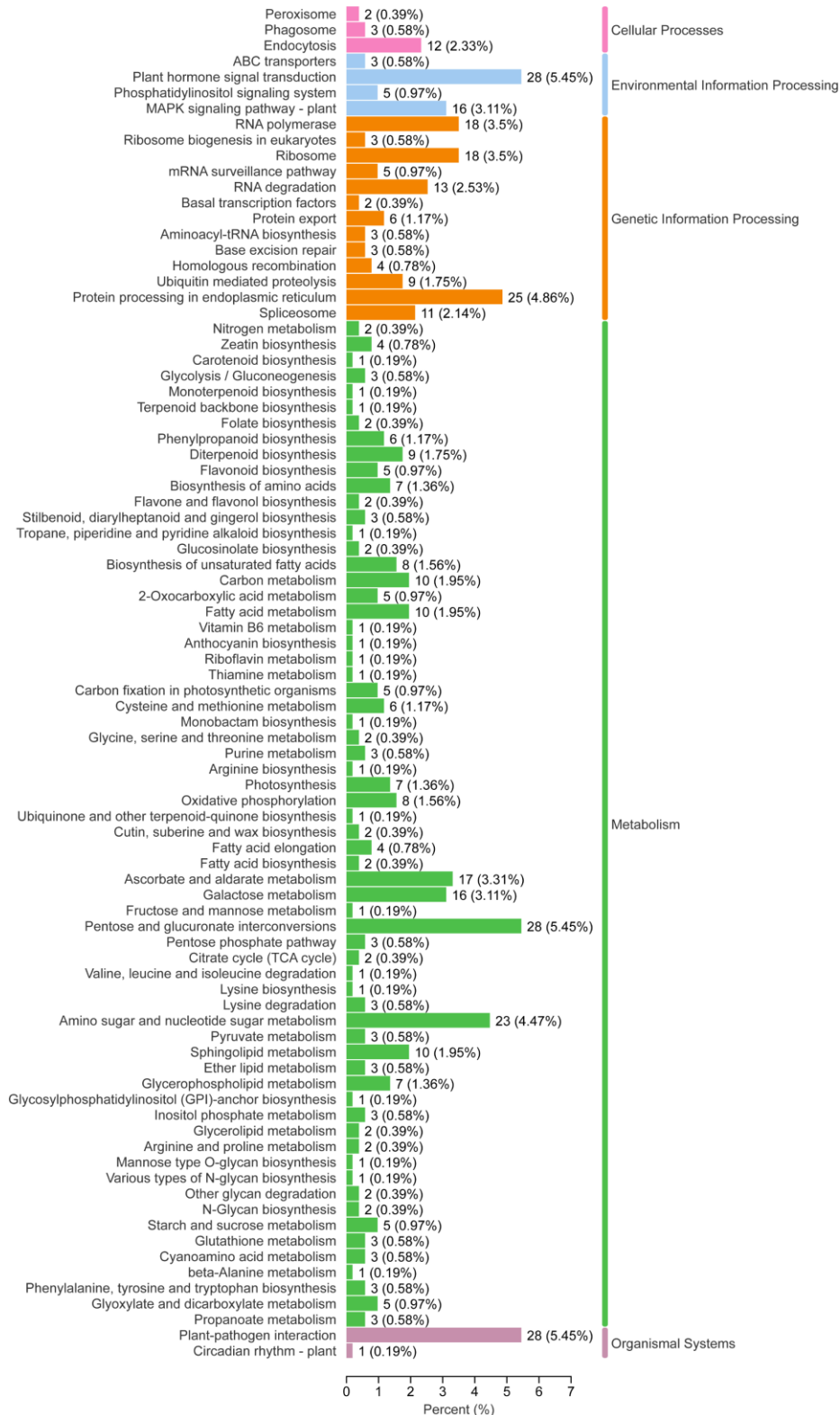
Figure S3

Figure S3 KEGG pathway annotation of new genes from *C. tinctorius* cells.
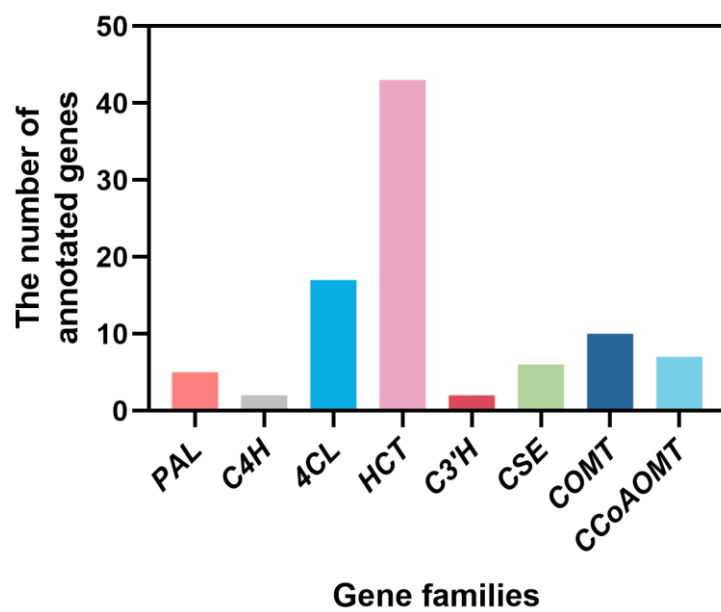
Figure S4

Figure S4 The annotation results of gene families involved in CGAs biosynthesis pathway in *C. tinctorius* cells.
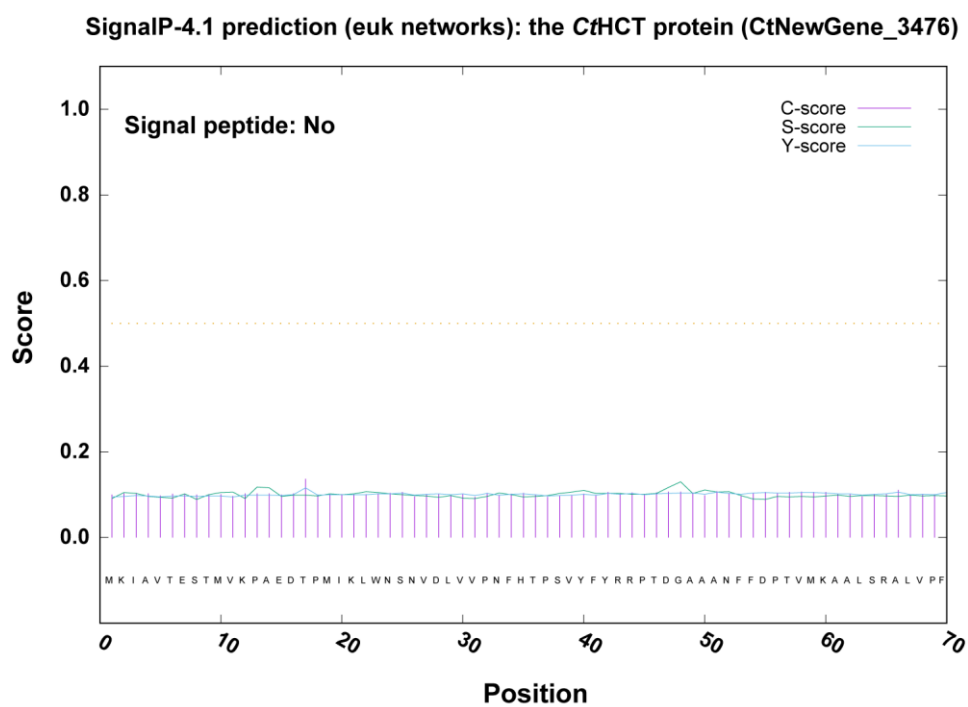
Figure S5

Figure S5 Signal peptide prediction (https://services.healthtech.dtu.dk/services/SignalP-4.1/) of the *Ct*HCT protein (CtNewGene 3476)
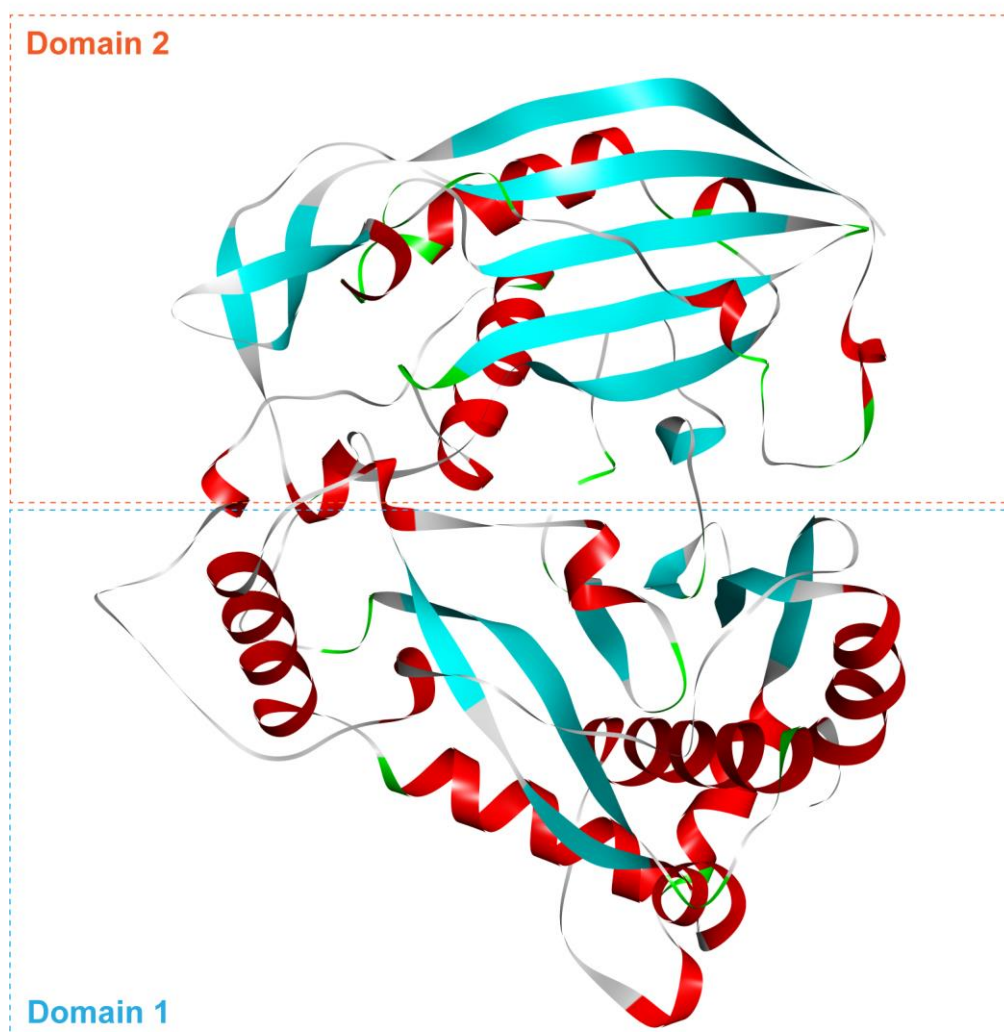
Figure S6

Figure S6 Protein structure prediction of the *Ct*HCT protein (CtNewGene 3476) through homologous modeling.