

Table 1 Suppl. The gene ontology (GO) classification of annotated unigenes from *C. forskohlii*.

Gene ontology term	Unigene number		
Biological processes	reproduction	180	
	immune system process	76	
	metabolic process	1255	
		nitrogen compound metabolic process	447
		catabolic process	278
		biosynthetic process	569
		organophosphate metabolic process	51
		secondary metabolic process	74
		methylation	47
		pigment metabolic process	53
		hormone metabolic process	19
		macromolecule metabolic process	675
		cellular metabolic process	1023
		primary metabolic process	1012
		small molecule metabolic process	377
		oxidation-reduction process	243
		organic substance metabolic process	177
		cellular process	1276
		signaling	176
		multicellular organismal process	308
		developmental process	314
		growth	67
		rhythmic process	15
		response to stimulus	689
		multi-organism process	180
		biological regulation	435
		cellular component organization or biogenesis	323
	Molecular functions	nucleic acid binding transcription factor activity	56
		catalytic activity	1075
		receptor activity	57
		structural molecule activity	34
		transporter activity	151
		binding	1089
electron carrier activity		34	
enzyme regulator activity		26	
molecular transducer activity		47	
Cellular components		extracellular region	81
	cell	1312	
	membrane	674	
	cell junction	71	
	membrane-enclosed lumen	92	
	macromolecular complex	253	
	organelle	962	
	symplast	71	

Table 2 Suppl. Mapping *C. forskohlii* unigenes to KEGG pathways.

KEGG categories represented	Number of unigenes	Number of enzyme groups
Metabolism	704	420
Carbohydrate metabolism	189	104
Energy metabolism	86	49
Lipid metabolism	62	42
Nucleotide metabolism	38	23
Amino acid metabolism	107	68
Metabolism of other amino acids	38	31
Glycan biosynthesis and metabolism	22	13
Metabolism of cofactors and vitamins	39	32
Metabolism of terpenoids and polyketides	33	26
Biosynthesis of other secondary metabolites	31	18
Xenobiotics biodegradation and metabolism	54	14
Genetic Information Processing	205	36
Transcription	32	4
Translation	79	18
Folding, sorting, and degradation	83	10
Replication and repair	11	4
Environmental Information Processing	177	31
Membrane transport	4	0
Signal transduction	172	31
Signaling molecules and interaction	1	0
Cellular Processes	128	34
Transport and catabolism	58	16
Cell motility	6	4
Cell growth and death	40	9
Cell communication	24	5
Organismal Systems	260	46
Immune system	62	7
Endocrine system	61	13
Circulatory system	13	4
Digestive system	11	5
Excretory system	13	3
Nervous system	59	8
Sensory system	3	1
Development	12	2
Environmental adaptation	26	3
Human Diseases	329	48
Cancers	85	15
Immune diseases	4	1
Neurodegenerative diseases	68	11
Substance dependence	11	4
Cardiovascular diseases	3	0
Endocrine and metabolic diseases	17	8
Infectious diseases	141	9

Table 3 Suppl. The list of identified unigenes possibly involved in the biosynthesis of secondary metabolites according to KEGG mapping.

No.	Unigene name	Enzyme name
1	qsqaca0_0027_B11.ab1	1-deoxy-D-xylulose-5-phosphate synthase
2	qsqaca0_0033_E01.ab1	1-deoxy-D-xylulose-5-phosphate reductoisomerase
3	qsqaca.CleanEST.seq.Contig395	(E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase
4	qsqaca0_0030_A09.ab1	(E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase
5	qsqaca0_0045_A10.ab1	acetyl-CoA C-acetyltransferase
6	qsqaca0_0005_F09.ab1	hydroxymethylglutaryl-CoA reductase
7	qsqaca0_0011_B09.ab1	hydroxymethylglutaryl-CoA reductase
8	qsqaca0_0017_H08.ab1	mevalonate kinase
9	qsqaca0_0011_F07.ab1	isopentenyl-diphosphate delta-isomerase
10	qsqaca0_0031_C07.ab1	geranylgeranyl diphosphate synthase, type II
11	qsqaca0_0034_H09.ab1	protein-S-isoprenylcysteine O-methyltransferase
12	qsqaca.CleanEST.seq.Contig447	myrcene/ocimene synthase
13	qsqaca0_0047_A01.ab1	(+)-neomenthol dehydrogenase
14	qsqaca0_0031_B03.ab1	beta-amyrin synthase
15	qsqaca0_0013_B02.ab1	ent-copalyl diphosphate synthase
16	qsqaca0_0042_C10.ab1	ent-kaurenoic acid hydroxylase
17	qsqaca0_0008_A10.ab1	cytochrome P450, family 82, subfamily G, polypeptide 1
18	qsqaca0_0018_E08.ab1	phytoene synthase
19	qsqaca.CleanEST.seq.Contig212	15-cis-phytoene desaturase
20	qsqaca0_0027_D11.ab1	zeta-carotene desaturase
21	qsqaca0_0014_A07.ab1	lycopene beta-cyclase
22	qsqaca.CleanEST.seq.Contig158	zeaxanthin epoxidase
23	qsqaca.CleanEST.seq.Contig182	(+)-abscisic acid 8'-hydroxylase
24	qsqaca0_0016_C12.ab1	aldehyde dehydrogenase (NAD <sup>+</sup> )
25	qsqaca0_0029_F05.ab1	aldehyde dehydrogenase (NAD <sup>+</sup> )
26	qsqaca0_0005_F07.ab1	[EC:1.14.-.-]
27	qsqaca0_0009_B01.ab1	[EC:1.14.-.-]
28	qsqaca0_0009_H06.ab1	[EC:1.14.-.-]
29	qsqaca0_0041_A05.ab1	[EC:1.14.-.-]
30	qsqaca0_0043_H05.ab1	[EC:1.14.-.-]
31	qsqaca0_0005_H11.ab1	transketolase
32	qsqaca0_0013_D02.ab1	acetyl-CoA carboxylase carboxyl transferase subunit alpha
33	qsqaca.CleanEST.seq.Contig206	acetyl-CoA carboxylase carboxyl transferase subunit beta
34	qsqaca0_0010_G05.ab1	phenylalanine ammonia-lyase
35	qsqaca.CleanEST.seq.Contig246	beta-glucosidase
36	qsqaca0_0005_C09.ab1	beta-glucosidase
37	qsqaca0_0014_A11.ab1	beta-glucosidase
38	qsqaca0_0023_D11.ab1	beta-glucosidase
39	qsqaca.CleanEST.seq.Contig260	4-coumarate--CoA ligase
40	qsqaca0_0021_F11.ab1	4-coumarate--CoA ligase
41	qsqaca0_0033_E11.ab1	4-coumarate--CoA ligase
42	qsqaca0_0039_H06.ab1	coniferyl-aldehyde dehydrogenase
43	qsqaca.CleanEST.seq.Contig371	cinnamyl-alcohol dehydrogenase
44	qsqaca.CleanEST.seq.Contig398	cinnamyl-alcohol dehydrogenase
45	qsqaca0_0013_G11.ab1	cinnamyl-alcohol dehydrogenase
46	qsqaca0_0013_C01.ab1	peroxidase
47	qsqaca0_0019_B09.ab1	peroxidase
48	qsqaca0_0012_D07.ab1	shikimate O-hydroxycinnamoyltransferase
49	qsqaca0_0016_E06.ab1	coumaroylquininate(coumaroylshikimate) 3'-monooxygenase
50	qsqaca0_0012_D07.ab1	shikimate O-hydroxycinnamoyltransferase
51	qsqaca0_0016_E06.ab1	coumaroylquininate(coumaroylshikimate) 3'-monooxygenase
52	qsqaca0_0015_C05.ab1	flavonoid 3'-monooxygenase
53	qsqaca0_0012_D07.ab1	shikimate O-hydroxycinnamoyltransferase
54	qsqaca0_0016_E06.ab1	coumaroylquininate(coumaroylshikimate) 3'-monooxygenase
55	qsqaca0_0015_C05.ab1	flavonoid 3'-monooxygenase
56	qsqaca.CleanEST.seq.Contig243	aspartate aminotransferase
57	qsqaca.CleanEST.seq.Contig99	tyrosine decarboxylase
58	qsqaca.CleanEST.seq.Contig243	aspartate aminotransferase

59	qsqaca_0034_F01.ab1	xanthine dehydrogenase/oxidase
60	qsqaca_0015_A02.ab1	urate oxidase
61	qsqaca_0007_E11.ab1	4,5-DOPA dioxygenase extradiol
62	qsqaca_0041_B01.ab1	cytochrome P450, family 83, subfamily B, polypeptide 1
63	qsqaca.CleanEST.seq.Contig268	hexokinase
64	qsqaca.CleanEST.seq.Contig268	hexokinase

---