

## Supplementary Information

### Biosynthetic Insights into *p*-Hydroxybenzoic Acid-Derived Benzopyrans

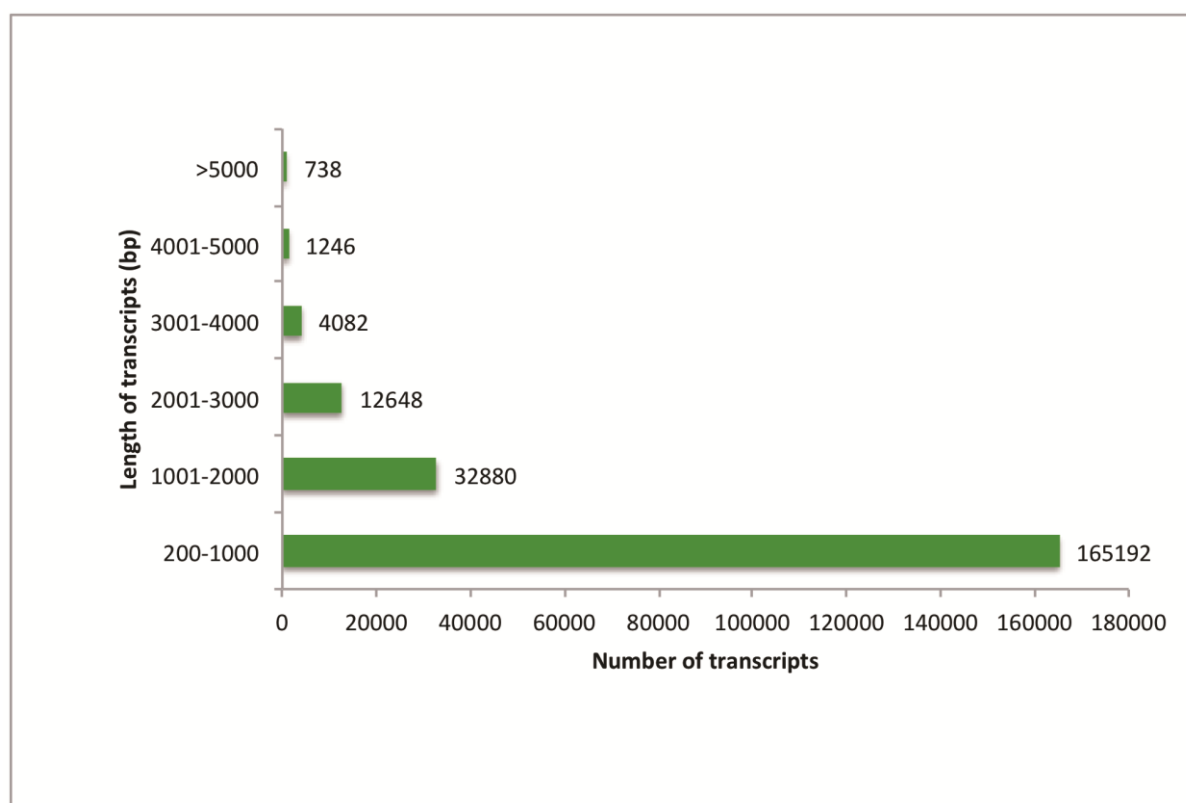
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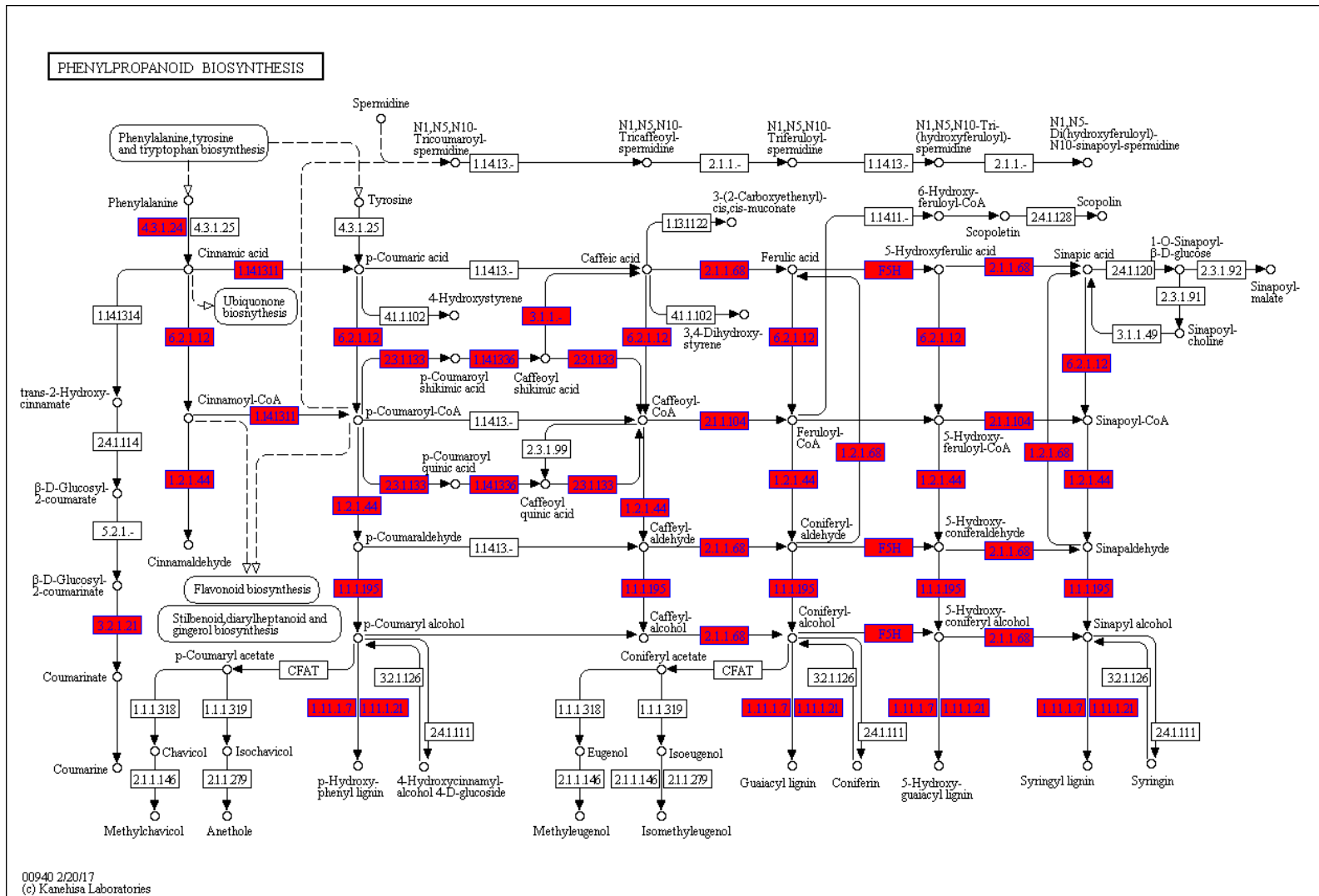
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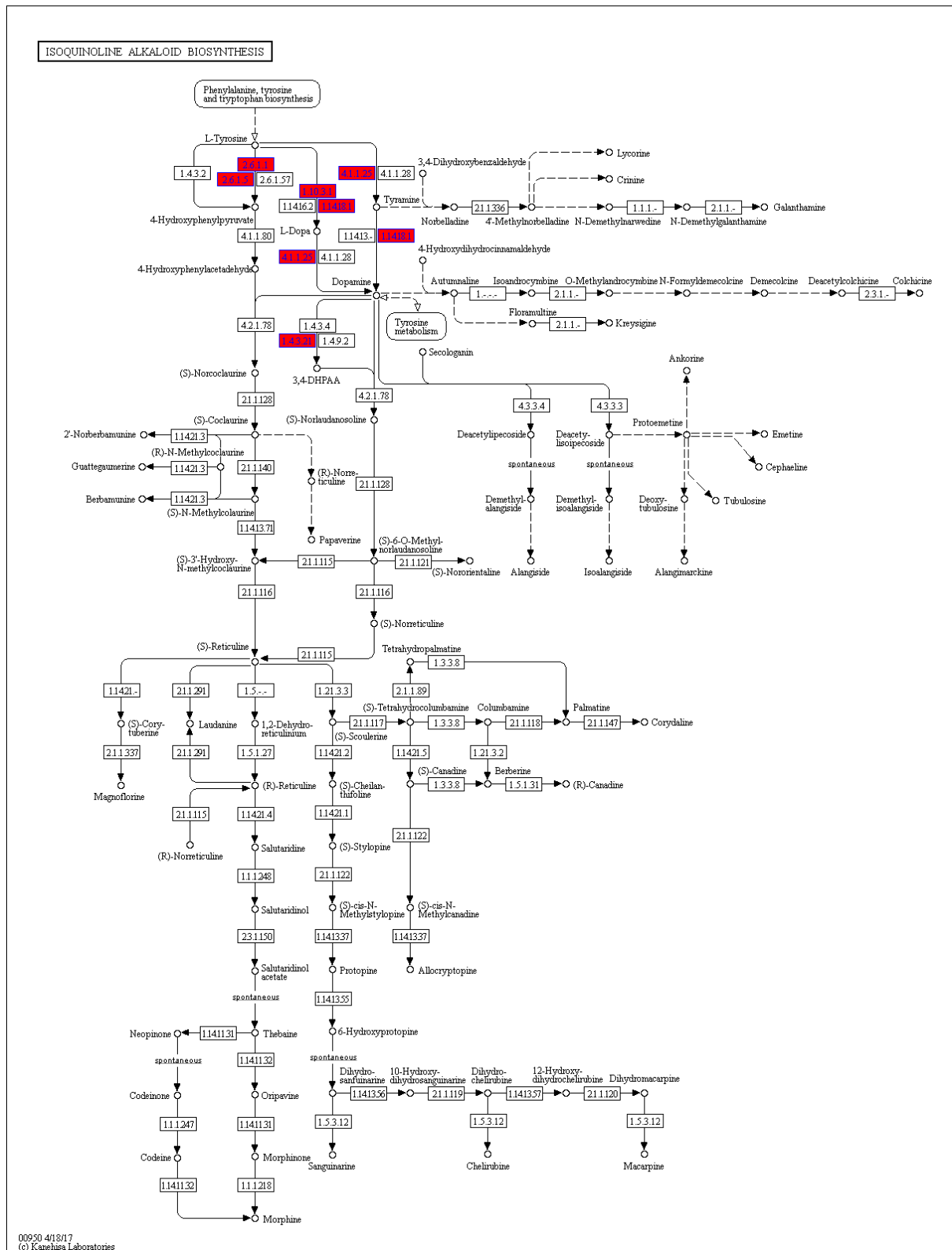


**Figure S1.** Length distribution of the assembled transcripts.

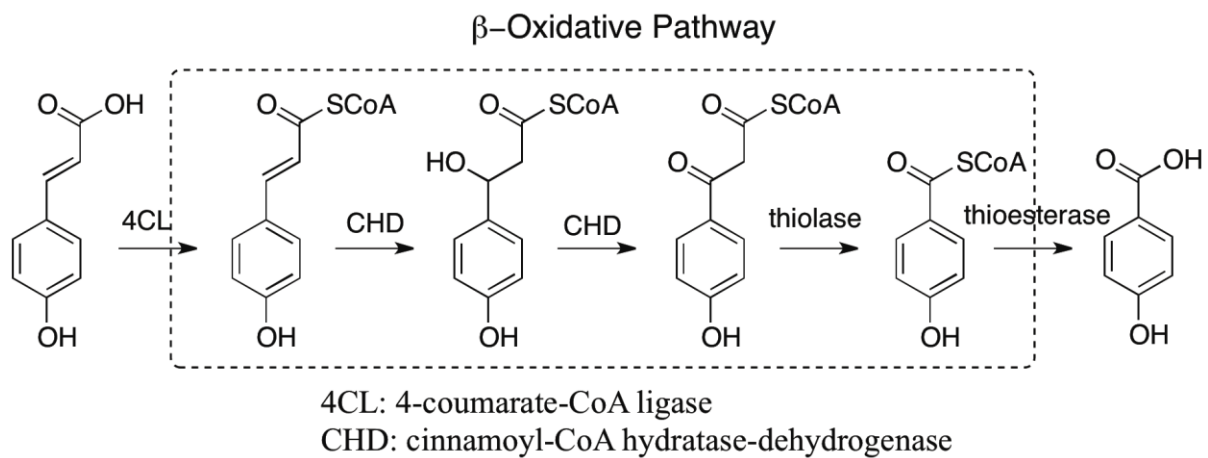
\*e-mail: andrluca@yahoo.com.br; maysaf@iq.unesp.br



**Figure S2.** KEGG view on a metabolic pathway (map00940, Phenylpropanoid biosynthesis). Genes encoding the proteins in the red boxes were identified in the transcriptome of leaves of *Piper gaudichaudianum*.



**Figure S3.** KEGG view on a metabolic pathway (map00950, Isoquinoline alkaloid biosynthesis). Genes encoding the proteins in the red boxes were identified in the transcriptome of leaves of *Piper gaudichaudianum*.



**Figure S4.** Proposed  $\beta$ -oxidative pathway for the biosynthesis of *p*-hydroxybenzoic acid.

Score	Expect	Identities	Gaps	Strand
880 bits(476)	0.0	642/725(89%)	0/725(0%)	Plus/Plus
Query 1	ACCCAAAACCATTTTCTTGGAAAGCCCCACCCAGTTC	TTTTC	CGAATAAGAGGGAGCA	60
Sbjct 784	ACCCAAAACCATTTTCTTGGAAAGCCTCCACCCAGTTC	TTTTC	CGAATAAGATGGAGCA	843
Query 61	TTTTTGAATTCGAAATACTCCCCGTCCATTCTATCCAACCTGAGGAAAGTCCACCTGCC			120
Sbjct 844	TTTTTGAATTCAAAATACTCTCCATCCATTCAATCCAACCTGAGGATAGTCCACCTGCC			903
Query 121	ATACATATTTGCCAATGAGGTTGGAATACAGGAAAAGCAGCAAGCCAACCAGCAGTAGCT			180
Sbjct 904	ATACATATTTGCCAGTGTGGTTCAAATACAGGAAAAGCAGCAGGCCAGCCAGCAGTAGAT			963
Query 181	TTTTGTTTATCCGTCAAGTTGCCCATCCATAGACAGGTTGAGTACTGTATGCCACCTA			240
Sbjct 964	TTTTGCTTATCCCTCACGTTGCCCATCCATAGACAGGTTGGGTACTGTATGCCACCTA			1023
Query 241	GCTGTTTTAACAGTTGGCACATACGTTGATCTTCCATCATCTGTATGAATCCCTGATGC			300
Sbjct 1024	GCTGTTTTAACAGTCGGCACATACGTAGATCTCCATCATCTCGTATGAAACCTGATGC			1083
Query 301	CACAGTGGAGTCACTTGAAACCCCTCTGATACACGACGATCAAACCTCTGAGGAGGAACC			360
Sbjct 1084	CACACTGGGGTCACTTGAAATCCTTCTGATACACGGCGGTTGAACTCTGAGGAGGAACC			1143
Query 361	TCTCCTTGTGGAGGCGATGCTCCTTCCGAGTAACAAAGTACTCCCCAACATCAACTCA			420
Sbjct 1144	TCTCTTTGTGGAGGGGATGCTCCGTTCCGAGCTACAAAGTACTCCCCAACATCAACTCA			1203
Query 421	TCCCTACTTCCCCAGAAATCTTCGATCTTCAGAAAACGACAGATATAATTATCATCC			480
Sbjct 1204	TCCCTACTTCCCCAGAAGTCTTCGATCTTCCGAGTACTGACATATATACTTGTCTATCC			1263
Query 481	GCACCAAGAATCTGCGCCCCAACACCAGTAAACCTTTTCCCATATATCGCCTCATCCAAC			540
Sbjct 1264	GCGCCAAGTATCTGCGCCCCAACGCCAGTAAACCGGCGCCATAAATCGCCTCATCCAGC			1323
Query 541	GCCCCAACCTACCAGAAAACGCAGGATTCTCCACCGAATACATAAAACAGAACTCTGC			600
Sbjct 1324	GGCCCTAACCTACCGGTAAACGCAGGATTCTCCACCGAATACATAAAGCAGAACTCTGC			1383
Query 601	TTCTTCTCCGGGATCGCCACCTTGAAGTACCACCCCTCAAAAAACCTCCGCGGCTCCCA			660
Sbjct 1384	CTCTTTTCAGGAATACAAACCTTGAATACCACCCCTCAAAGAACCTCCGCGCTGTTCCA			1443
Query 661	TCAAAATGATACCCGCTGTGTGGTGTTCGGAGGTGGCGGTTGGGGGAGTGGGGGTAG			720
Sbjct 1444	TCAAAATGGTACCCACTATGAGGAGTACGAAGATGCCGGTTGGGAGGTGTGGGAGTATAC			1503
Query 721	ACGGG	725		
Sbjct 1504	ACGGG	1508		

**Figure S5.** Nucleotide alignment of the transcripts from *Piper gaudichaudianum* (Subject) and *Peperomia obtusifolia* (Query) encoding tocopherol cyclase.

**Table S1.** Enzymes involved in the secondary metabolism of *Piper gaudichaudianum* based on the transcriptome data

K number	EC number	Name	FPKM (max) <sup>a</sup>
K00001	EC:1.1.1.1	alcohol dehydrogenase	62.87
K00006	EC:1.1.1.8	glycerol-3-phosphate dehydrogenase (NAD <sup>+</sup> )	11.85
K00013	EC:1.1.1.23	histidinol dehydrogenase	23.52
K00016	EC:1.1.1.27	L-lactate dehydrogenase	5.83
K00021	EC:1.1.1.34	hydroxymethylglutaryl-CoA reductase (NADPH)	52.01
K00025	EC:1.1.1.37	malate dehydrogenase	111.36
K00026	EC:1.1.1.37	malate dehydrogenase	190.85
K00030	EC:1.1.1.41	isocitrate dehydrogenase (NAD <sup>+</sup> )	46.73
K00031	EC:1.1.1.42	isocitrate dehydrogenase	320.41
K00033	EC:1.1.1.44 1.1.1.343	6-phosphogluconate dehydrogenase	111.56
K00036	EC:1.1.1.49 1.1.1.363	glucose-6-phosphate 1-dehydrogenase	72.78
K00052	EC:1.1.1.85	3-isopropylmalate dehydrogenase	7.07
K00053	EC:1.1.1.86	ketol-acid reductoisomerase	133.50
K00083	EC:1.1.1.195	cinnamyl-alcohol dehydrogenase	474.04
K00088	EC:1.1.1.205	IMP dehydrogenase	6.90
K00099	EC:1.1.1.267	1-deoxy-D-xylulose-5-phosphate reductoisomerase	72.73
K00106	EC:1.17.1.4 1.17.3.2	xanthine dehydrogenase/oxidase	8.77
K00111	EC:1.1.5.3	glycerol-3-phosphate dehydrogenase	11.72
K00121	EC:1.1.1.284 1.1.1.1	S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase	79.16
K00128	EC:1.2.1.3	aldehyde dehydrogenase (NAD <sup>+</sup> )	486.86
K00133	EC:1.2.1.11	aspartate-semialdehyde dehydrogenase	16.49
K00134	EC:1.2.1.12	glyceraldehyde 3-phosphate dehydrogenase	966.46

**Table S1.** Enzymes involved in the secondary metabolism of *Piper gaudichaudianum* based on the transcriptome data (cont.)

K number	EC number	Name	FPKM (max) <sup>a</sup>
K00145	EC:1.2.1.38	<i>N</i> -acetyl-gamma-glutamyl-phosphate reductase	32.23
K00161	EC:1.2.4.1	pyruvate dehydrogenase E1 component alpha subunit	31.56
K00162	EC:1.2.4.1	pyruvate dehydrogenase E1 component beta subunit	102.22
K00164	EC:1.2.4.2	2-oxoglutarate dehydrogenase E1 component	49.58
K00166	EC:1.2.4.4	2-oxoisovalerate dehydrogenase E1 component alpha subunit	142.45
K00167	EC:1.2.4.4	2-oxoisovalerate dehydrogenase E1 component beta subunit	12.95
K00213	EC:1.3.1.21	7-dehydrocholesterol reductase	41.12
K00215	EC:1.17.1.8	4-hydroxy-tetrahydrodipicolinate reductase	13.66
K00218	EC:1.3.1.33	protochlorophyllide reductase	104.45
K00225	EC:1.3.2.3	L-galactono-1,4-lactone dehydrogenase	8.76
K00227	EC:1.14.19.20	delta7-sterol 5-desaturase	24.18
K00228	EC:1.3.3.3	coproporphyrinogen III oxidase	18.26
K00231	EC:1.3.3.4 1.3.3.15	protoporphyrinogen/coproporphyrinogen III oxidase	30.53
K00232	EC:1.3.3.6	acyl-CoA oxidase	58.68
K00234	EC:1.3.5.1	succinate dehydrogenase (ubiquinone) flavoprotein subunit	36.71
K00235	EC:1.3.5.1	succinate dehydrogenase (ubiquinone) iron-sulfur subunit	26.08
K00236		succinate dehydrogenase (ubiquinone) cytochrome b560 subunit	1.46
K00237		succinate dehydrogenase (ubiquinone) membrane anchor subunit	1.21
K00249	EC:1.3.8.7	acyl-CoA dehydrogenase	25.47
K00264	EC:1.4.1.13 1.4.1.14	glutamate synthase (NADPH/NADH)	255.17
K00276	EC:1.4.3.21	primary-amine oxidase	58.52
K00281	EC:1.4.4.2	glycine dehydrogenase	77.81

**Table S1.** Enzymes involved in the secondary metabolism of *Piper gaudichaudianum* based on the transcriptome data (cont.)

K number	EC number	Name	FPKM (max) <sup>a</sup>
K00286	EC:1.5.1.2	pyrroline-5-carboxylate reductase	5.83
K00318	EC:1.5.-.-	proline dehydrogenase	4.39
K00382	EC:1.8.1.4	dihydrolipoamide dehydrogenase	48.50
K00422	EC:1.10.3.1	polyphenol oxidase	103.10
K00430	EC:1.11.1.7	peroxidase	1018.33
K00454	EC:1.13.11.12	lipoxygenase	129.54
K00457	EC:1.13.11.27	4-hydroxyphenylpyruvate dioxygenase	43.00
K00475	EC:1.14.11.9	naringenin 3-dioxygenase	12.34
K00487	EC:1.14.13.11	trans-cinnamate 4-monooxygenase	42.09
K00510	EC:1.14.14.18	heme oxygenase 1	158.20
K00511	EC:1.14.14.17	squalene monooxygenase	7.57
K00514	EC:1.3.5.6	zeta-carotene desaturase	16.91
K00517	E1.14.-.-	indol-3-yl-methylglucosinolate hydroxylase	2.40
K00547	EC:2.1.1.10	homocysteine <i>S</i> -methyltransferase	17.01
K00548	EC:2.1.1.13	5-methyltetrahydrofolate-homocysteine methyltransferase	1.87
K00549	EC:2.1.1.14	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase	130.78
K00550	EC:2.1.1.16	methylene-fatty-acyl-phospholipid synthase	1.75
K00559	EC:2.1.1.41	sterol 24- <i>C</i> -methyltransferase	9.55
K00588	EC:2.1.1.104	caffeoyl-CoA <i>O</i> -methyltransferase	26.80
K00591	EC:2.1.1.114 2.1.1.64	polyprenyldihydroxybenzoate methyltransferase / 3-demethylubiquinol 3- <i>O</i> -methyltransferase	4.98
K00600	EC:2.1.2.1	glycine hydroxymethyltransferase	118.55
K00601	EC:2.1.2.2	phosphoribosylglycinamide formyltransferase	3.06



**Table S1.** Enzymes involved in the secondary metabolism of *Piper gaudichaudianum* based on the transcriptome data (cont.)

K number	EC number	Name	FPKM (max) <sup>a</sup>
K00602	EC:2.1.2.3 3.5.4.10	phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP cyclohydrolase	21.82
K00605	EC:2.1.2.10	aminomethyltransferase	111.49
K00606	EC:2.1.2.11	3-methyl-2-oxobutanoate hydroxymethyltransferase	13.84
K00611	EC:2.1.3.3	ornithine carbamoyltransferase	7.13
K00615	EC:2.2.1.1	transketolase	94.81
K00616	EC:2.2.1.2	transaldolase	86.52
K00620	EC:2.3.1.35 2.3.1.1	glutamate <i>N</i> -acetyltransferase / amino-acid <i>N</i> -acetyltransferase	21.33
K00622	EC:2.3.1.5	arylamine <i>N</i> -acetyltransferase	1.05
K00626	EC:2.3.1.9	acetyl-CoA <i>C</i> -acetyltransferase	54.85
K00627	EC:2.3.1.12	pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase)	27.28
K00630	EC:2.3.1.15	glycerol-3-phosphate <i>O</i> -acyltransferase	31.53
K00640	EC:2.3.1.30	serine <i>O</i> -acetyltransferase	88.36
K00655	EC:2.3.1.51	1-acyl-sn-glycerol-3-phosphate acyltransferase	6.43
K00658	EC:2.3.1.61	2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase)	66.31
K00660	EC:2.3.1.74	chalcone synthase	2.20
K00688	EC:2.4.1.1	glycogen phosphorylase	82.30
K00700	EC:2.4.1.18	1,4- $\alpha$ -glucan branching enzyme	25.40
K00703	EC:2.4.1.21	starch synthase	17.56
K00760	EC:2.4.2.8	hypoxanthine phosphoribosyltransferase	17.59
K00764	EC:2.4.2.14	amidophosphoribosyltransferase	26.80
K00765	EC:2.4.2.17	ATP phosphoribosyltransferase	13.96
K00766	EC:2.4.2.18	anthranilate phosphoribosyltransferase	17.03

**Table S1.** Enzymes involved in the secondary metabolism of *Piper gaudichaudianum* based on the transcriptome data (cont.)

K number	EC number	Name	FPKM (max) <sup>a</sup>
K00787	EC:2.5.1.1 2.5.1.10	farnesyl diphosphate synthase	24.05
K00789	EC:2.5.1.6	S-adenosylmethionine synthetase	1267.37
K00791	EC:2.5.1.75	tRNA dimethylallyltransferase	36.30
K00793	EC:2.5.1.9	riboflavin synthase	11.04
K00794	EC:2.5.1.78	6,7-dimethyl-8-ribityllumazine synthase	22.08
K00800	EC:2.5.1.19	3-phosphoshikimate 1-carboxyvinyltransferase	74.50
K00801	EC:2.5.1.21	farnesyl-diphosphate farnesyltransferase	21.64
K00811	EC:2.6.1.1	aspartate aminotransferase, chloroplastic	35.63
K00815	EC:2.6.1.5	tyrosine aminotransferase	3.94
K00817	EC:2.6.1.9	histidinol-phosphate aminotransferase	28.63
K00818	EC:2.6.1.11	acetylmethionine aminotransferase	2.54
K00819	EC:2.6.1.13	ornithine-oxo-acid transaminase	11.22
K00826	EC:2.6.1.42	branched-chain amino acid aminotransferase	119.34
K00827	EC:2.6.1.44 2.6.1.40	alanine-glyoxylate transaminase / (R)-3-amino-2-methylpropionate-pyruvate transaminase	15.82
K00830	EC:2.6.1.44 2.6.1.45 2.6.1.51	alanine-glyoxylate transaminase / serine-glyoxylate transaminase / serine-pyruvate transaminase	353.23
K00844	EC:2.7.1.1	hexokinase	42.74
K00850	EC:2.7.1.11	6-phosphofructokinase 1	52.40
K00851	EC:2.7.1.12	gluconokinase	20.64
K00861	EC:2.7.1.26	riboflavin kinase	17.56
K00869	EC:2.7.1.36	mevalonate kinase	12.39
K00872	EC:2.7.1.39	homoserine kinase	6.75
K00873	EC:2.7.1.40	pyruvate kinase	90.08

**Table S1.** Enzymes involved in the secondary metabolism of *Piper gaudichaudianum* based on the transcriptome data (cont.)

K number	EC number	Name	FPKM (max) <sup>a</sup>
K00891	EC:2.7.1.71	shikimate kinase	20.07
K00895	EC:2.7.1.90	diphosphate-dependent phosphofructokinase	44.51
K00901	EC:2.7.1.107	diacylglycerol kinase (ATP)	53.94
K00919	EC:2.7.1.148	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	21.67
K00927	EC:2.7.2.3	phosphoglycerate kinase	179.56
K00928	EC:2.7.2.4	aspartate kinase	10.50
K00930	EC:2.7.2.8	acetylglutamate kinase	12.20
K00938	EC:2.7.4.2	phosphomevalonate kinase	12.31
K00939	EC:2.7.4.3	adenylate kinase	49.87
K00940	EC:2.7.4.6	nucleoside-diphosphate kinase	169.75
K00948	EC:2.7.6.1	ribose-phosphate pyrophosphokinase	42.13
K00966	EC:2.7.7.13	mannose-1-phosphate guanylyltransferase	31.07
K00975	EC:2.7.7.27	glucose-1-phosphate adenyltransferase	173.73
K00981	EC:2.7.7.41	phosphatidate cytidyltransferase	10.89
K00991	EC:2.7.7.60	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase	14.21
K00993	EC:2.7.8.1	ethanolaminephosphotransferase	51.61
K01047	EC:3.1.1.4	secretory phospholipase A2	15.48
K01057	EC:3.1.1.31	6-phosphogluconolactonase	24.66
K01061	EC:3.1.1.45	carboxymethylenebutenolidase	121.63
K01068	EC:3.1.2.2	acyl-coenzyme A thioesterase 1/2/4	11.95
K01081	EC:3.1.3.5	5'-nucleotidase	5.64
K01114	EC:3.1.4.3	phospholipase C	45.13

**Table S1.** Enzymes involved in the secondary metabolism of *Piper gaudichaudianum* based on the transcriptome data (cont.)

K number	EC number	Name	FPKM (max) <sup>a</sup>
K01115	EC:3.1.4.4	phospholipase D1/2	76.95
K01188	EC:3.2.1.21	beta-glucosidase	68.38
K01214	EC:3.2.1.68	isoamylase	3.73
K01438	EC:3.5.1.16	acetylornithine deacetylase	7.98
K01476	EC:3.5.3.1	arginase	25.78
K01490	EC:3.5.4.6	AMP deaminase	8.75
K01568	EC:4.1.1.1	pyruvate decarboxylase	23.04
K01580	EC:4.1.1.15	glutamate decarboxylase	172.72
K01581	EC:4.1.1.17	ornithine decarboxylase	3.45
K01586	EC:4.1.1.20	diaminopimelate decarboxylase	13.22
K01590	EC:4.1.1.22	histidine decarboxylase	79.68
K01592	EC:4.1.1.25	tyrosine decarboxylase	18.17
K01597	EC:4.1.1.33	diphosphomevalonate decarboxylase	33.56
K01599	EC:4.1.1.37	uroporphyrinogen decarboxylase	25.42
K01609	EC:4.1.1.48	indole-3-glycerol phosphate synthase	75.55
K01610	EC:4.1.1.49	phosphoenolpyruvate carboxykinase (ATP)	23.48
K01613	EC:4.1.1.65	phosphatidylserine decarboxylase	43.75
K01620	EC:4.1.2.48	threonine aldolase	7.80
K01623	EC:4.1.2.13	fructose-bisphosphate aldolase, class I	709.80
K01624	EC:4.1.2.13	fructose-bisphosphate aldolase, class II	2.33
K01626	EC:2.5.1.54	3-deoxy-7-phosphoheptulonate synthase	160.00
K01637	EC:4.1.3.1	isocitrate lyase	2.39

**Table S1.** Enzymes involved in the secondary metabolism of *Piper gaudichaudianum* based on the transcriptome data (cont.)

K number	EC number	Name	FPKM (max) <sup>a</sup>
K01638	EC:2.3.3.9	malate synthase	2.51
K01641	EC:2.3.3.10	hydroxymethylglutaryl-CoA synthase	13.62
K01647	EC:2.3.3.1	citrate synthase	48.58
K01648	EC:2.3.3.8	ATP citrate (pro- <i>S</i> )-lyase	38.17
K01649	EC:2.3.3.13	2-isopropylmalate synthase	12.42
K01652	EC:2.2.1.6	acetolactate synthase I/II/III large subunit	43.61
K01653	EC:2.2.1.6	acetolactate synthase I/III small subunit	41.14
K01657	EC:4.1.3.27	anthranilate synthase component I	32.53
K01658	EC:4.1.3.27	anthranilate synthase component II	37.50
K01661	EC:4.1.3.36	naphthoate synthase	10.89
K01662	EC:2.2.1.7	1-deoxy-D-xylulose-5-phosphate synthase	55.47
K01663	EC:2.4.2.- 4.1.3.-	glutamine amidotransferase / cyclase	9.98
K01676	EC:4.2.1.2	fumarate hydratase, class I	1.41
K01679	EC:4.2.1.2	fumarate hydratase, class II	9.28
K01681	EC:4.2.1.3	aconitate hydratase	61.42
K01687	EC:4.2.1.9	dihydroxy-acid dehydratase	7.94
K01689	EC:4.2.1.11	enolase	214.27
K01693	EC:4.2.1.19	imidazoleglycerol-phosphate dehydratase	16.16
K01695	EC:4.2.1.20	tryptophan synthase alpha chain	22.16
K01696	EC:4.2.1.20	tryptophan synthase beta chain	34.67
K01698	EC:4.2.1.24	porphobilinogen synthase	8.21
K01703	EC:4.2.1.33 4.2.1.35	3-isopropylmalate/( <i>R</i> )-2-methylmalate dehydratase large subunit	75.24

**Table S1.** Enzymes involved in the secondary metabolism of *Piper gaudichaudianum* based on the transcriptome data (cont.)

K number	EC number	Name	FPKM (max) <sup>a</sup>
K01704	EC:4.2.1.33 4.2.1.35	3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit	19.81
K01714	EC:4.3.3.7	4-hydroxy-tetrahydrodipicolinate synthase	20.52
K01719	EC:4.2.1.75	uroporphyrinogen-III synthase	59.09
K01723	EC:4.2.1.92	hydroperoxide dehydratase	137.07
K01733	EC:4.2.3.1	threonine synthase	24.60
K01735	EC:4.2.3.4	3-dehydroquinate synthase	60.18
K01736	EC:4.2.3.5	chorismate synthase	109.42
K01738	EC:2.5.1.47	cysteine synthase A	349.08
K01739	EC:2.5.1.48	cystathionine gamma-synthase	80.68
K01749	EC:2.5.1.61	hydroxymethylbilane synthase	35.62
K01754	EC:4.3.1.19	threonine dehydratase	7.03
K01755	EC:4.3.2.1	argininosuccinate lyase	11.71
K01756	EC:4.3.2.2	adenylosuccinate lyase	17.28
K01760	EC:4.4.1.8	cystathionine beta-lyase	12.36
K01762	EC:4.4.1.14	1-aminocyclopropane-1-carboxylate synthase	5.58
K01770	EC:4.6.1.12	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	11.66
K01772	EC:4.99.1.1 4.99.1.9	protoporphyrin/coproporphyrin ferrochelatase	29.23
K01778	EC:5.1.1.7	diaminopimelate epimerase	49.96
K01783	EC:5.1.3.1	ribulose-phosphate 3-epimerase	44.22
K01785	EC:5.1.3.3	aldose 1-epimerase	38.77
K01792	EC:5.1.3.15	glucose-6-phosphate 1-epimerase	174.01
K01803	EC:5.3.1.1	triosephosphate isomerase (TIM)	322.78

**Table S1.** Enzymes involved in the secondary metabolism of *Piper gaudichaudianum* based on the transcriptome data (cont.)

K number	EC number	Name	FPKM (max) <sup>a</sup>
K01807	EC:5.3.1.6	ribose 5-phosphate isomerase A	50.91
K01808	EC:5.3.1.6	ribose 5-phosphate isomerase B	1.50
K01809	EC:5.3.1.8	mannose-6-phosphate isomerase	23.52
K01810	EC:5.3.1.9	glucose-6-phosphate isomerase	67.99
K01814	EC:5.3.1.16	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase	10.97
K01817	EC:5.3.1.24	phosphoribosylanthranilate isomerase	24.43
K01823	EC:5.3.3.2	isopentenyl-diphosphate delta-isomerase	26.82
K01824	EC:5.3.3.5	cholestenol delta-isomerase	26.55
K01834	EC:5.4.2.11	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	2.84
K01835	EC:5.4.2.2	phosphoglucomutase	37.85
K01845	EC:5.4.3.8	glutamate-1-semialdehyde 2,1-aminomutase	26.77
K01850	EC:5.4.99.5	chorismate mutase	23.94
K01853	EC:5.4.99.8	cycloartenol synthase	3.85
K01859	EC:5.5.1.6	chalcone isomerase	12.50
K01885	EC:6.1.1.17	glutamyl-tRNA synthetase	46.21
K01895	EC:6.2.1.1	acetyl-CoA synthetase	19.98
K01899	EC:6.2.1.4 6.2.1.5	succinyl-CoA synthetase alpha subunit	63.05
K01900	EC:6.2.1.4 6.2.1.5	succinyl-CoA synthetase beta subunit	38.46
K01904	EC:6.2.1.12	4-coumarate-CoA ligase	22.08
K01918	EC:6.3.2.1	pantoate-beta-alanine ligase	22.83
K01923	EC:6.3.2.6	phosphoribosylaminoimidazole-succinocarboxamide synthase	6.24
K01933	EC:6.3.3.1	phosphoribosylformylglycinamide cyclo-ligase	14.04

**Table S1.** Enzymes involved in the secondary metabolism of *Piper gaudichaudianum* based on the transcriptome data (cont.)

K number	EC number	Name	FPKM (max) <sup>a</sup>
K01940	EC:6.3.4.5	argininosuccinate synthase	25.85
K01945	EC:6.3.4.13	phosphoribosylamine-glycine ligase	8.14
K01952	EC:6.3.5.3	phosphoribosylformylglycinamide synthase	9.39
K01953	EC:6.3.5.4	asparagine synthase (glutamine-hydrolysing)	4566.76
K01961	EC:6.4.1.2 6.3.4.14	acetyl-CoA carboxylase, biotin carboxylase subunit	32.19
K01962	EC:6.4.1.2	acetyl-CoA carboxylase carboxyl transferase subunit alpha	23.78
K01963	EC:6.4.1.2	acetyl-CoA carboxylase carboxyl transferase subunit beta	2.31
K02160		acetyl-CoA carboxylase biotin carboxyl carrier protein	8.18
K02257	EC:2.5.1.-	protoheme IX farnesyltransferase	12.99
K02259		cytochrome c oxidase assembly protein subunit 15	16.64
K02291	EC:2.5.1.32 2.5.1.99	15- <i>cis</i> -phytoene/all- <i>trans</i> -phytoene synthase	117.19
K02293	EC:1.3.5.5	15- <i>cis</i> -phytoene desaturase	44.38
K02437		glycine cleavage system H protein	147.03
K02492	EC:1.2.1.70	glutamyl-tRNA reductase	33.44
K02495	EC:1.3.98.3	oxygen-independent coproporphyrinogen III oxidase	6.27
K02548	EC:2.5.1.74 2.5.1.-	1,4-dihydroxy-2-naphthoate octaprenyltransferase	32.19
K02552	EC:5.4.4.2	menaquinone-specific isochorismate synthase	38.78
K03183	EC:2.1.1.163 2.1.1.201	demethylmenaquinone methyltransferase / 2-methoxy-6-polyprenyl-1,4-benzoquinol methylase	37.49
K03403	EC:6.6.1.1	magnesium chelatase subunit H	94.07
K03404	EC:6.6.1.1	magnesium chelatase subunit D	21.41
K03405	EC:6.6.1.1	magnesium chelatase subunit I	67.19
K03428	EC:2.1.1.11	magnesium-protoporphyrin <i>O</i> -methyltransferase	42.35



**Table S1.** Enzymes involved in the secondary metabolism of *Piper gaudichaudianum* based on the transcriptome data (cont.)

K number	EC number	Name	FPKM (max) <sup>a</sup>
K03526	EC:1.17.7.1 1.17.7.3	( <i>E</i> )-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase	84.76
K03527	EC:1.17.7.4	4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase	624.57
K03781	EC:1.11.1.6	catalase	8280.56
K03782	EC:1.11.1.21	catalase-peroxidase	1.23
K03787	EC:3.1.3.5	5'-nucleotidase	11.68
K03809	EC:1.6.5.2	NAD(P)H dehydrogenase (quinone)	50.70
K03841	EC:3.1.3.11	fructose-1,6-bisphosphatase I	76.12
K04035	EC:1.14.13.81	magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase	294.25
K04040	EC:2.5.1.62 2.5.1.133	chlorophyll/bacteriochlorophyll a synthase	30.41
K04120	EC:5.5.1.13	<i>ent</i> -copalyl diphosphate synthase	1.07
K04121	EC:4.2.3.19	<i>ent</i> -kaurene synthase	2.34
K04122	EC:1.14.13.78	<i>ent</i> -kaurene oxidase	5.42
K04123	EC:1.14.13.79	<i>ent</i> -kaurenoic acid hydroxylase	2.07
K04124	EC:1.14.11.15	gibberellin 3-beta-dioxygenase	1.52
K04125	EC:1.14.11.13	gibberellin 2-oxidase	7.07
K05278	EC:1.14.11.23	flavonol synthase	1.23
K05280	EC:1.14.13.21	flavonoid 3'-monooxygenase	25.96
K05282	EC:1.14.11.12	gibberellin 20-oxidase	18.34
K05349	EC:3.2.1.21	beta-glucosidase	11.88
K05350	EC:3.2.1.21	beta-glucosidase	29.39
K05356	EC:2.5.1.84 2.5.1.85	all- <i>trans</i> -nonaprenyl-diphosphate synthase	79.93
K05359	EC:4.2.1.91 4.2.1.51	arogenate/prephenate dehydratase	17.59

**Table S1.** Enzymes involved in the secondary metabolism of *Piper gaudichaudianum* based on the transcriptome data (cont.)

K number	EC number	Name	FPKM (max) <sup>a</sup>
K05894	EC:1.3.1.42	12-oxophytodienoic acid reductase	32.29
K05917	EC:1.14.13.70	sterol 14-demethylase	23.15
K05928	EC:2.1.1.95	tocopherol <i>O</i> -methyltransferase	19.94
K05933	EC:1.14.17.4	aminocyclopropanecarboxylate oxidase	1863.77
K06001	EC:4.2.1.20	tryptophan synthase beta chain	12.13
K06013	EC:3.4.24.84	STE24 endopeptidase	31.63
K06125	EC:2.5.1.39	4-hydroxybenzoate polyprenyltransferase	7.29
K06126	EC:1.14.13.-	ubiquinone biosynthesis monooxygenase Coq6	18.66
K06127	EC:2.1.1.201	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase	6.38
K06443	EC:5.5.1.19	lycopene beta-cyclase	22.47
K06444	EC:5.5.1.18	lycopene epsilon-cyclase	10.16
K07508	EC:2.3.1.16	acetyl-CoA acyltransferase 2	1.22
K07509	EC:2.3.1.16	acetyl-CoA acyltransferase	3.02
K07511	EC:4.2.1.17	enoyl-CoA hydratase	1.20
K07513	EC:2.3.1.16	acetyl-CoA acyltransferase 1	90.80
K08081	EC:1.1.1.206	tropinone reductase I	28.36
K08099	EC:3.1.1.14	chlorophyllase	72.63
K08101	EC:1.3.7.4	phytochromobilin:ferredoxin oxidoreductase	17.35
K08241	EC:2.1.1.141	jasmonate <i>O</i> -methyltransferase	18.94
K08242	EC:2.1.1.143	24-methylenesterol <i>C</i> -methyltransferase	26.23
K08246	EC:5.5.1.9	cycloeucalenol cycloisomerase	15.92
K08683	EC:1.1.1.35 1.1.1.178	3-hydroxyacyl-CoA dehydrogenase / 3-hydroxy-2-methylbutyryl-CoA dehydrogenase	1.30

**Table S1.** Enzymes involved in the secondary metabolism of *Piper gaudichaudianum* based on the transcriptome data (cont.)

K number	EC number	Name	FPKM (max) <sup>a</sup>
K08730	EC:2.7.8.29	phosphatidylserine synthase 2	1.53
K09587	EC:1.14.13.-	steroid 22-alpha-hydroxylase	7.18
K09588	EC:1.14.-.-	cytochrome P450 family 90 subfamily A polypeptide 1	112.53
K09699	EC:2.3.1.168	2-oxoisovalerate dehydrogenase E2 component (dihydrolipoyl transacylase)	12.28
K09753	EC:1.2.1.44	cinnamoyl-CoA reductase	8.13
K09754	EC:1.14.13.36	coumaroylquininate(coumaroylshikimate) 3'-monooxygenase	9.69
K09755	EC:1.14.-.-	ferulate-5-hydroxylase	38.70
K09828	EC:1.3.1.72 1.3.1.-	delta24-sterol reductase	4.06
K09832	EC:1.14.19.41	sterol 22-desaturase	2.07
K09833	EC:2.5.1.115 2.5.1.116	homogentisate phytyltransferase / homogentisate geranylgeranyltransferase	49.18
K09834	EC:5.5.1.24	tocopherol cyclase	20.53
K09835	EC:5.2.1.13	prolycopene isomerase	9.50
K09837	EC:1.14.99.45	carotene epsilon-monooxygenase	3.45
K09838	EC:1.14.15.21	zeaxanthin epoxidase	55.85
K09839	EC:1.23.5.1	violaxanthin de-epoxidase	10.06
K09840	EC:1.13.11.51	9-cis-epoxycarotenoid dioxygenase	41.35
K09841	EC:1.1.1.288	xanthoxin dehydrogenase	229.54
K09842	EC:1.2.3.14	abscisic-aldehyde oxidase	13.54
K10046	EC:5.1.3.18 5.1.3.-	GDP-D-mannose 3', 5'-epimerase	156.44
K10047	EC:3.1.3.25 3.1.3.93	inositol-phosphate phosphatase / L-galactose 1-phosphate phosphatase	7.42
K10203	EC:2.3.1.199	elongation of very long chain fatty acids protein 6	1.73
K10206	EC:2.6.1.83	LL-diaminopimelate aminotransferase	22.69

**Table S1.** Enzymes involved in the secondary metabolism of *Piper gaudichaudianum* based on the transcriptome data (cont.)

K number	EC number	Name	FPKM (max) <sup>a</sup>
K10251	EC:1.1.1.62 1.1.1.330	17beta-estradiol 17-dehydrogenase / very-long-chain 3-oxoacyl-CoA reductase	45.74
K10258	EC:1.3.1.93	very-long-chain enoyl-CoA reductase	44.35
K10525	EC:5.3.99.6	allene oxide cyclase	33.35
K10526	EC:6.2.1.-	OPC-8:0 CoA ligase 1	27.41
K10527	EC:4.2.1.17 1.1.1.35 1.1.1.211	enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase	96.99
K10528	EC:4.1.2.-	hydroperoxide lyase	20.66
K10703	EC:4.2.1.134	very-long-chain (3 <i>R</i> )-3-hydroxyacyl-CoA dehydratase	20.87
K10775	EC:4.3.1.24	phenylalanine ammonia-lyase	26.83
K10960	EC:1.3.1.83 1.3.1.111	geranylgeranyl diphosphate/geranylgeranyl-bacteriochlorophyllide <i>a</i> reductase	92.85
K11262	EC:6.4.1.2 6.3.4.14	acetyl-CoA carboxylase / biotin carboxylase 1	12.52
K11517	EC:1.1.3.15	( <i>S</i> )-2-hydroxy-acid oxidase	338.43
K11752	EC:3.5.4.26 1.1.1.193	diaminohydroxyphosphoribosylaminopyrimidine deaminase / 5-amino-6-(5-phosphoribosylamino)uracil reductase	19.80
K11755	EC:3.6.1.31 3.5.4.19	phosphoribosyl-ATP pyrophosphohydrolase / phosphoribosyl-AMP cyclohydrolase	7.49
K11778	EC:2.5.1.87	ditrans, polycis-polyprenyl diphosphate synthase	21.81
K11808	EC:4.1.1.21	phosphoribosylaminoimidazole carboxylase	9.03
K11820	EC:2.4.1.195	<i>N</i> -hydroxythioamide <i>S</i> -beta-glucosyltransferase	3.27
K12153	EC:1.14.14.40	phenylalanine <i>N</i> -monooxygenase	4.53
K12355	EC:1.2.1.68	coniferyl-aldehyde dehydrogenase	11.11
K12502	EC:2.1.1.295	MPBQ/MSBQ methyltransferase	87.78
K12524	EC:2.7.2.4 1.1.1.3	bifunctional aspartokinase / homoserine dehydrogenase 1	15.94
K12638	EC:1.14.13.112	3-epi-6-deoxocathasterone 23-monooxygenase	47.25

**Table S1.** Enzymes involved in the secondary metabolism of *Piper gaudichaudianum* based on the transcriptome data (cont.)

K number	EC number	Name	FPKM (max) <sup>a</sup>
K12639	EC:1.14.13.-	cytochrome P450 family 724 subfamily B polypeptide 1	3.91
K12640	EC:1.14.-.-	brassinosteroid-6-oxidase 2	17.21
K12657	EC:2.7.2.11 1.2.1.41	delta-1-pyrroline-5-carboxylate synthetase	33.11
K13035	EC:3.5.5.4 4.2.1.65	beta-cyano-L-alanine hydratase/nitrilase	32.54
K13065	EC:2.3.1.133	shikimate <i>O</i> -hydroxycinnamoyltransferase	13.29
K13066	EC:2.1.1.68	caffeic acid 3- <i>O</i> -methyltransferase	21.39
K13071	EC:1.14.15.17	pheophorbide <i>a</i> oxygenase	53.23
K13427	EC:1.14.13.39	nitric-oxide synthase, plant	11.37
K13496	EC:2.4.1.-	UDP-glucosyl transferase 73C	50.70
K13506	EC:2.3.1.15	glycerol-3-phosphate <i>O</i> -acyltransferase 3/4	28.50
K13508	EC:2.3.1.15 2.3.1.198	glycerol-3-phosphate acyltransferase	17.25
K13513	EC:2.3.1.- 2.3.1.51	lysocardiolipin and lysophospholipid acyltransferase	4.71
K13519	EC:2.3.1.51 2.3.1.23 2.3.1.-	lysophospholipid acyltransferase	37.00
K13523	EC:2.3.1.51 2.3.1.-	lysophosphatidic acid acyltransferase / lysophosphatidylinositol acyltransferase	17.14
K13600	EC:1.14.13.122	chlorophyllide <i>a</i> oxygenase	92.13
K13606	EC:1.1.1.294	chlorophyll(ide) <i>b</i> reductase	21.46
K13679	EC:2.4.1.242	granule-bound starch synthase	281.65
K13789	EC:2.5.1.1 2.5.1.10 2.5.1.29	geranylgeranyl diphosphate synthase, type II	43.05
K13832	EC:4.2.1.10 1.1.1.25	3-dehydroquinate dehydratase / shikimate dehydrogenase	7.26
K13953	EC:1.1.1.1	alcohol dehydrogenase, propanol-preferring	39.09
K14066	EC:2.5.1.1	geranyl diphosphate synthase	21.93
K14085	EC:1.2.1.31 1.2.1.8 1.2.1.3	aldehyde dehydrogenase family 7 member A1	174.02

**Table S1.** Enzymes involved in the secondary metabolism of *Piper gaudichaudianum* based on the transcriptome data (cont.)

K number	EC number	Name	FPKM (max) <sup>a</sup>
K14157	EC:1.5.1.8 1.5.1.9	alpha-aminoadipic semialdehyde synthase	5.49
K14163	EC:6.1.1.17 6.1.1.15	bifunctional glutamyl/prolyl-tRNA synthetase	1.57
K14190	EC:2.7.7.69	GDP-L-galactose phosphorylase	486.43
K14272	EC:2.6.1.4 2.6.1.2 2.6.1.44	glutamate--glyoxylate aminotransferase	298.51
K14423	EC:1.14.13.72	4,4-dimethyl-9beta,19-cyclopropylsterol-4alpha-methyl oxidase	8.58
K14424	EC:1.14.13.72	4-alpha-methyl-delta7-sterol-4alpha-methyl oxidase	37.49
K14454	EC:2.6.1.1	aspartate aminotransferase, cytoplasmic	64.80
K14455	EC:2.6.1.1	aspartate aminotransferase, mitochondrial	23.38
K14652	EC:4.1.99.12 3.5.4.25	3,4-dihydroxy 2-butanone 4-phosphate synthase / GTP cyclohydrolase II	27.61
K14674	EC:3.1.1.3 3.1.1.13 3.1.1.4 2.3.1.51	TAG lipase / steryl ester hydrolase / phospholipase A2 / LPA acyltransferase	3.42
K14677	EC:3.5.1.14	aminoacylase	17.34
K14682	EC:2.3.1.1	amino-acid <i>N</i> -acetyltransferase	7.82
K14759	EC:5.4.4.2 2.2.1.9 4.2.99.20 4.2.1.113	isochorismate synthase / 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase / 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase / <i>O</i> -succinylbenzoate synthase	1.22
K14760	EC:6.2.1.26	acyl-activating enzyme 14	8.24
K15086	EC:4.2.3.25	(3 <i>S</i> )-linalool synthase	1.21
K15095	EC:1.1.1.208	(+)-neomenthol dehydrogenase	5.29
K15227	EC:1.3.1.78	arogenate dehydrogenase (NADP+), plant	12.20
K15397	EC:2.3.1.199	3-ketoacyl-CoA synthase	79.05
K15404	EC:4.1.99.5	aldehyde decarbonylase	6.45
K15633	EC:5.4.2.12	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	116.99

**Table S1.** Enzymes involved in the secondary metabolism of *Piper gaudichaudianum* based on the transcriptome data (cont.)

K number	EC number	Name	FPKM (max) <sup>a</sup>
K15634	EC:5.4.2.12	probable phosphoglycerate mutase	144.15
K15728	EC:3.1.3.4	phosphatidate phosphatase LPIN	19.20
K15744	EC:5.2.1.12	zeta-carotene isomerase	11.71
K15746	EC:1.14.13.129	beta-carotene 3-hydroxylase	57.46
K15747	EC:1.14.-.-	beta-ring hydroxylase	2.78
K15849	EC:2.6.1.1 2.6.1.78 2.6.1.79	bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase	56.69
K15893		hydroxypyruvate reductase 1	252.87
K15918	EC:2.7.1.31	D-glycerate 3-kinase	103.56
K15919		hydroxypyruvate reductase 2	18.60
K16860	EC:3.1.4.4	phospholipase D3/4	13.24
K16911	EC:3.6.4.13	ATP-dependent RNA helicase DDX21	47.85
K17069	EC:2.5.1.49 2.5.1.47	<i>O</i> -acetylhomoserine/ <i>O</i> -acetylserine sulfhydrylase	2.00
K17497	EC:5.4.2.8	phosphomannomutase	46.79
K17744	EC:1.1.1.316	L-galactose dehydrogenase	184.43
K18010	EC:1.17.7.2	7-hydroxymethyl chlorophyll a reductase	49.96
K18368	EC:3.1.1.-	caffeoylshikimate esterase	6.89
K18447	EC:3.6.1.21	ADP-sugar diphosphatase	6.49
K18532	EC:2.7.4.3	adenylate kinase	95.37
K18649	EC:3.1.3.25 3.1.3.93 3.1.3.15	inositol-phosphate phosphatase / L-galactose 1-phosphate phosphatase / histidinol-phosphatase	5.92
K18857	EC:1.1.1.1	alcohol dehydrogenase class-P	9.64
K19073	EC:1.3.1.75	divinyl chlorophyllide a 8-vinyl-reductase	11.54
K19269	EC:3.1.3.18 3.1.3.48	phosphoglycolate phosphatase	57.95

<sup>a</sup>Maximum FPKM value obtained out of all the transcripts associated with the respective KO. FPKM: fragments *per* kilobase of transcript per million fragments mapped.

**Table S2.** Enzymes possible involved in *p*-hydroxybenzoic acid biosynthesis based on the transcriptome data of *Piper gaudichaudianum*

SeqName	UniProt	RefSeq	Protein	Organism	E value	Similarity / %
c32138_g1_i1	A0A088RXV2	XP_010701546.1	3-ketoacyl-CoA thiolase	<i>Leishmania panamensis</i>	0	95
c32138_g1_i2	A0A088RXV2	XP_010701546.1	3-ketoacyl-CoA thiolase	<i>Leishmania panamensis</i>	0	94
c87909_g13_i3	A0A1U7YX07	XP_010243983.1	3-ketoacyl-CoA thiolase 2, peroxisomal	<i>Nelumbo nucifera</i>	0	91
c87909_g13_i2	A0A1S3C4N7	XP_008457258.1	3-ketoacyl-CoA thiolase 2, peroxisomal	<i>Cucumis melo</i>	0	89
c87909_g13_i7	A0A1S3C4N7	XP_008457258.1	3-ketoacyl-CoA thiolase 2, peroxisomal	<i>Cucumis melo</i>	0	89
c87909_g14_i2	A0A1U7YX07	XP_010243983.1	3-ketoacyl-CoA thiolase 2, peroxisomal	<i>Nelumbo nucifera</i>	0	88
c87909_g14_i3	A0A1U7YX07	XP_010243983.1	3-ketoacyl-CoA thiolase 2, peroxisomal	<i>Nelumbo nucifera</i>	0	88
c85495_g1_i7	J9YIZ4	–	cinnamoyl-CoA hydratase-dehydrogenase	<i>Petunia hybrida</i>	0	86
c81656_g2_i2	A0A172W624	–	cinnamoyl-CoA hydratase-dehydrogenase	<i>Populus davidiana</i>	0	86
c85495_g1_i3	J9YIZ4	–	cinnamoyl-CoA hydratase-dehydrogenase	<i>Petunia hybrida</i>	0	85
c81656_g2_i1	J9YIZ4	–	cinnamoyl-CoA hydratase-dehydrogenase	<i>Petunia hybrida</i>	3.9e <sup>-180</sup>	86
c81656_g1_i1	A0A172W624	–	cinnamoyl-CoA hydratase-dehydrogenase	<i>Populus davidiana</i>	3.2e <sup>-164</sup>	88
c87909_g14_i1	A0A1U7YX07	XP_010243983.1	3-ketoacyl-CoA thiolase 2, peroxisomal	<i>Nelumbo nucifera</i>	6.1e <sup>-161</sup>	85
c71889_g2_i1	Q9U0V9	XP_001683404.1	3-ketoacyl-CoA thiolase	<i>Leishmania major</i>	3.2e <sup>-156</sup>	100
c87909_g13_i5	–	XP_010935683.1	3-ketoacyl-CoA thiolase 2, peroxisomal	<i>Elaeis guineensis</i>	4.6e <sup>-149</sup>	88
c87909_g14_i4	–	XP_008800565.1	3-ketoacyl-CoA thiolase 2, peroxisomal	<i>Phoenix dactylifera</i>	8.0e <sup>-140</sup>	84
c72648_g1_i4	M2SCB5	WP_008601709.1	3-ketoacyl-CoA thiolase	<i>Pacificimonas flava</i>	2.3e <sup>-120</sup>	82
c72648_g1_i2	M2SCB5	WP_008601709.1	3-ketoacyl-CoA thiolase	<i>Pacificimonas flava</i>	5.4e <sup>-120</sup>	82
c72648_g1_i3	M2SCB5	WP_008601709.1	3-ketoacyl-CoA thiolase	<i>Pacificimonas flava</i>	1.7e <sup>-117</sup>	82
c87909_g13_i6	A0A1U7YX07	XP_010243983.1	3-ketoacyl-CoA thiolase 2, peroxisomal	<i>Nelumbo nucifera</i>	2.8e <sup>-117</sup>	92
c87909_g13_i1	–	XP_010935683.1	3-ketoacyl-CoA thiolase 2, peroxisomal	<i>Elaeis guineensis</i>	6.7e <sup>-117</sup>	89
c72648_g1_i1	M2SCB5	WP_008601709.1	3-ketoacyl-CoA thiolase	<i>Pacificimonas flava</i>	3.9e <sup>-115</sup>	82
c81656_g1_i2	A0A172W624	–	cinnamoyl-CoA hydratase-dehydrogenase	<i>Populus davidiana</i>	2.8e <sup>-109</sup>	85
c69458_g1_i2	N1MWN6	WP_006966934.1	3-ketoacyl-CoA thiolase	<i>Sphingobium japonicum</i>	1.1e <sup>-89</sup>	86



**Table S2.** Enzymes possible involved in *p*-hydroxybenzoic acid biosynthesis based on the transcriptome data of *Piper gaudichaudianum* (cont.)

SeqName	UniProt	RefSeq	Protein	Organism	E value	Similarity / %
c65952_g1_i1	M2TJY8	WP_008603601.1	3-ketoacyl-CoA thiolase	<i>Pacificimonas flava</i>	1.4e <sup>-88</sup>	85
c32552_g1_i1	R9NXM7	XP_012187065.1	3-ketoacyl-CoA thiolase	<i>Pseudozyma hubeiensis</i>	9.8e <sup>-80</sup>	99
c67722_g1_i3	M4VI71	WP_015467294.1	3-ketoacyl-CoA thiolase	<i>Micavibrio aeruginosavorus</i>	3.3e <sup>-77</sup>	87
c65952_g1_i2	M2TJY8	WP_008603601.1	3-ketoacyl-CoA thiolase	<i>Pacificimonas flava</i>	1.1e <sup>-75</sup>	86
c64595_g2_i1	–	WP_033965298.1	4-hydroxybenzoyl-CoA thioesterase	<i>Sphingomonas</i> sp.	1.2e <sup>-68</sup>	100
c85495_g1_i6	A0A172W624	–	cinnamoyl-CoA hydratase-dehydrogenase	<i>Populus davidiana</i>	5.1e <sup>-67</sup>	83
c145599_g1_i1	R9NXM7	XP_012187065.1	3-ketoacyl-CoA thiolase	<i>Pseudozyma hubeiensis</i>	5.5e <sup>-60</sup>	95
c24409_g1_i1	H0EAN8	–	3-ketoacyl-CoA thiolase	<i>Patulibacter medicamentivorans</i>	1.1e <sup>-52</sup>	83
c59016_g1_i1	M2TJY8	WP_008603601.1	3-ketoacyl-CoA thiolase	<i>Pacificimonas flava</i>	9.5e <sup>-52</sup>	81
c83814_g4_i2	Q9SX65	NP_175266.1	1,4-dihydroxy-2-naphthoyl- thioesterase 1	<i>Arabidopsis thaliana</i>	1.2e <sup>-50</sup>	83

**Table S3.** Transcripts with significant homology with 4-hydroxybenzoate geranyltransferase 2 genes

SeqName	RefSeq	Protein	Organism	E value
c77903_g1_i1	XP_015945685.1	4-hydroxybenzoate polyprenyltransferase	<i>Arachis duranensis</i>	2e <sup>-128</sup>
	XP_011071842.2	4-hydroxybenzoate geranyltransferase 2	<i>Sesamum indicum</i>	6e <sup>-122</sup>
c88362_g2_i2	XP_009401152.1	4-hydroxybenzoate polyprenyltransferase	<i>Musa acuminata</i> subsp. <i>Malaccensis</i>	5e <sup>-77</sup>
	XP_009794833.1	4-hydroxybenzoate geranyltransferase 2	<i>Nicotiana sylvestris</i>	2e <sup>-73</sup>
c88362_g2_i4	XP_015961403.1	4-hydroxybenzoate polyprenyltransferase	<i>Arachis duranensis</i>	4e <sup>-54</sup>
	XP_011071842.2	4-hydroxybenzoate geranyltransferase 2	<i>Sesamum indicum</i>	5e <sup>-52</sup>
c88362_g2_i5	XP_009401152.1	4-hydroxybenzoate polyprenyltransferase	<i>Musa acuminata</i> subsp. <i>Malaccensis</i>	3e <sup>-73</sup>
	XP_009794833.1	4-hydroxybenzoate geranyltransferase 2	<i>Nicotiana sylvestris</i>	1e <sup>-69</sup>
c88362_g2_i6	XP_015945685.1	4-hydroxybenzoate polyprenyltransferase	<i>Arachis duranensis</i>	2e <sup>-72</sup>
	XP_011071842.2	4-hydroxybenzoate geranyltransferase 2	<i>Sesamum indicum</i>	5e <sup>-70</sup>
c141373_g1_i1	XP_014756843.1	4-hydroxybenzoate polyprenyltransferase	<i>Brachypodium distachyon</i>	9e <sup>-39</sup>
	XP_008221044.1	4-hydroxybenzoate geranyltransferase 2	<i>Prunus mume</i>	3e <sup>-36</sup>