Supplementary Information

Transcriptomic insight into terpenoid and carbazole-alkaloid biosynthesis, and functional characterization of two terpene synthases in curry tree (*Murraya koenigii* L.)

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Table S1. List of biologically active compounds isolated from different plant parts of *M. koenigii* and their respective biological properties.

Biologically active compound	Part	Biological activity	References
1,1'-Bis(2-hydroxy-3-methylcarbazole)/3,3'-Dimethyl-[1,1'-bi-9H-carbazole]- 2,2'-diol	Roots & Stem bark	-	1
1-formyl-3-methoxy-6-methyl carbazole 6,7-hydroxy-3-methylcarbazole	Leaves	antimicrobial	2
3e(1e-hydroxy ethyl)-7-hydroxy-1-is obenzofuranone 3,3'-[oxybis(methylene)]bis99-methoxy-9H-carbazole)	Stem bark	antibacterial, antidibetic	3, 4
3-methyl Carbazole	Roots	antimicrobial	5
8,8° '-biskoenigine (bisindole alkaloid)	Leaves	antiosteoporotic	6
9-Carbethoxy-3-methyl-9H-carbazole/Ethyl 3-methyl-9H-carbazole-9- carboxylate	Roots	antiinflammatory, antineoplastic	5
9-formyl-3-methylcarbazole	Roots	cytotoxic	5
Bicyclomahanimbicine	Leaves	antidiabetic, antioxidant, anticancer, antiulcer	7, 8
Bikoeniquinone-A (bisindole alkaloid)	Roots & Stem bark	-	1
Bikoeniquinonine (bisindole alkaloid)	Aerial part	antimicrobial	6, 9
Bismurrayaquinone-A	Roots & Stem bark	-	1
Bisgerayafolines A–C	Fruit pulp	antioxidant, anti- α -glucosidase, DNA binding, cytotoxic	10
Bismahanine	Leaves & Stem bark	antioxidant	1, 11
Bismahanimbinol	Fruit pulp	-	10
Bispyarafoline	Leaves & Fruit pulp	antioxidant	10, 11
Bismurrayafoline E	Leaves	antioxidant	10, 11
Bismurrayaquinone-A (bisindole alkaloid)	Roots & Stem bark	inotropic response (triphasic)	1, 12

Chrestifoline-A	Roots	cytotoxic	1
Curryangine/Mahanimbidine/Murrayazoline	Stem & Leaves	cytotoxic	13
Euchrestine-B	Leaves	antioxidant	10, 11
eustifoline-C	Roots	-	1
Curryanine/Murrayazolidine/Cyclomahanimbine (terpenoid alkaloid)	Leaves & Stem bark	antiinflammatory	7
Furostifoline	Stem	cytotoxic	13
Girinimbilol/mukoenine-A/2-Hydroxy-3-methyl-1-prenylcarbazole	Stem bark	anti-trichomonal	14, 15
Girinimbiol	Leaves	hypoglycaemic, hepatoprotective	16
Girinimbine/3,11-Dihydro-3,3,5-trimethyl-Pyrano(3,2-a)carbazole	Seeds, Leaves & stem bark	anti-trichomonal, hypoglycaemic, cytotoxic, antiplatelet agent	1, 15-17
Glycozoline	Roots	antibacterial	1
Isomahanine/Pyrafoline D/Pyrayafoline D	Leaves, Seeds & Fruits	antibacteria l, cytotoxicity against HL-60 cells	18, 19
isomurrayafoline-B	Stem bark	analgesic activity	1, 20
Isomurrayazoline	Stem bark	anti-amnesic, immunomodulatory	21, 22
Isomurrayazolinine	Stem bark	-	21
karapinchamines A & B	Leaves	melanogenesis	23
Koenigine	Leaves	antioxidant, radical-scavenging	2, 24
Koenimbidine/Koenidine/Koenigicine	Roots & Leaves	insecticidal, antidiabetic	25, 26
Koenimbine	Seeds, Leaves & Stem	anti-diarrhea, antiinflammatory, antimicrobial	27, 28
Koenine	Leaves, seeds	anti-diarrhea	27
Koenoline/1-Methoxy-9H-carbazole-3-methanol	Roots & Stem bark	anti-tumor	29
Kurryam	seeds	anti-diarrhea	27
Mahanimbicine/Isomahanimbine	Roots & Leaves	anticancer, antimicrobial, mosquitocidal, antiproliferative, wound healing, antioxidant	11, 30

Mahanimbine	Roots, Leaves, Stem bark & Seeds	antidiabetic, hypolipidemic, antimicrobial, mosquitocidal, antioxidant, antiinflammatory, antiproliferative, anti-diarrhea, antitumor, wound healing	11, 25, 27, 30, 31
Mahanimbinine (terpenoid alkaloid)	Leaves & Seeds	antioxidant, anti-microbial	7, 8
Mahanimbilol	Stem bark	antitrichomal	14, 15
Mahanimbinol/1-(3,7-Dimethyl-octa-2,6-dienyl)-3-methyl-9H-carbazol-2-ol	Stem bark	cytotoxic	1
Mahanimboline	Roots	anti-diarrhea, antibacterial	27
Mahanine	Leaves, Roots, Stem bark, Seeds & Fruit pulp	anticancer, antioxidant, antimicrobial, mosquitocidal, antiinflammatory, antiproliferative, anti-diarrhea, wound healing, radical scavenging, α -glucosidase inhibitory	10, 11, 19, 27, 30
Mukonal/2-Hydroxy-9H-carbazole-3-carboxaldehyde	Stem bark	antifungal	32, 33
Mukoeic acid	Stem bark	antioxidant	34
Mukolidine/3-Formyl-8-methoxycarbazole/6-Formyl-1-methoxycarbazole	Roots	-	35
Mukoline/6-Hydroxymethyl-1-methoxycarbazole	Roots	antibacterial	35
Mukonicine	Leaves	antioxidant	36
Mukonidine	Stem bark	-	10
Mukoenine-B/3-Formyl-1-geranyl-2-hydroxycarbazole	roots	-	1
Mukoenine-C/Murrayamine A	roots	-	1
Mukoenigatin	aerial part	-	9
Murrafoline -A, B, C, D, G, H	-	-	1
Murratolme-1	-	cytotoxicity against HL-60 cells	19
Murrayacine	Stem bark	- antioxidant antimicrobial	25
Murrayacinine	Leaves	antidiabetic	8

Murrayanine/1-Methoxy-9H-carbazole-3-carbaldehyde	Leaf & Stem	antimicrobial, neuroprotective,	6, 37, 38
	Dark	anunin anniatory	
Murrayadinal	aerial part	-	9
Murrayanol	Leaves & Seeds	antimicrobial, antioxidant, mosquitocidal, antiinflammatory, anticancer	18, 39
Murrayafoline-A	Stem bark & Roots	anticancer	1,40
Murrastifoline-F/1,1'-Dimethoxy-3,3'-dimethy1-4,9'-bi-9H-carbazole, 9CI	Roots	-	1
Murrayaquinone-A	Stem bark & Roots	anticancer	1,40
Murrayaquinone-B	Stem bark	-	1
Murrayaquinoline	Stem	cytotoxic	13
Murrayazolinine	Stem bark	cytotoxic	13
Murrayazolinol	Roots & Stem bark	-	41
O-methyl murrayamine A	Leaves	-	10, 11
O-methyl mahanine	Leaves & Fruit pulp	-	10, 11
O-methyl mukanol	Leaves & Fruit pulp		10, 11
Scopolin	Leaves	antiinflammatory, anti-dementia	38
Xanthotoxin	Seeds	used to treat psoriasis, eczema, vitiligo & some cutaneous lymphomas	42
Isobyakangelicol	Seeds	-	42
Phellopterin	Seeds	neuroprotective	42
Gosferol	Seeds	-	42
Neobyakangelicol	Seeds	-	42
Byakangelicol	Seeds	-	42
Byakangelicin	Seeds	Antidiabetic & anticataract	42
Isogosferol	Seeds	-	42

Table S2. Summary of RNA-Seq.

	Murraya koenigii
Total Number of HQ Reads	50311257 (50.31 Mb)
Number of paired-end reads after trimming/filtered	46517951(46.51 Mb)
Mean read quality (Phred score)	35.415
Number of bases (MB)	5081.44
Number of bases (Gb) after trimming	3.72
Mean read length (bp)	101
kmer size	41
Number of assembled transcripts	118,221
No. of transcripts with length >= 150 bp	113,931
Maximum transcript length (bp)	12,154
Mean GC % of transcripts	40.79
Number of transcripts with FPKM >= 1.0	102,857
N50 value	1733

Table S3: Annotation summary of M. koenigii leaf transcriptome.

Database	TNAT	Percentage(%)
NCBI	87,417	84.98
Uniprot	54,887	53.36
KEGG	30708	29.94
AGRIS	8261	8.03
Total transcripts	102857	100

Abbriviation: TNAT-Total number of annotated transcripts.

Table S4. Trancripts for prenyltransferase gene family with unknown function identified in *M. koenigü* leaf transcriptome.NA- Not annotated

Transcript ID	Read count	FPKM	Gene name	Organism	GO term
Locus_9584_Transcript_4/8_Confidence _0.333_Length_920	381	8.90259	hypothetical protein CICLE_v10000458mg	Citrus clementina	protein prenylation; protein prenyltransferase activity
Locus_10147_Transcript_10/11_Confide nce_0.188_Length_747	160	4.60446	hypothetical protein CICLE_v10020293mg	Citrus clementina	protein prenylation; protein prenyltransferase activity
Locus_10147_Transcript_11/11_Confide nce_0.062_Length_747	158	4.54691	hypothetical protein CICLE_v10020293mg	Citrus clementina	protein prenylation; protein prenyltransferase activity
Locus_10147_Transcript_7/11_Confiden ce_0.438_Length_1027	255	5.33764	hypothetical protein CICLE_v10020293mg	Citrus clementina	protein prenylation; protein prenyltransferase activity
Locus_10147_Transcript_8/11_Confiden ce_0.250_Length_1218	250	4.41237	hypothetical protein CICLE_v10020293mg	Citrus clementina	protein prenylation; protein prenyltransferase activity
Locus_10311_Transcript_1/5_Confidenc e_0.667_Length_1420	1801	27.265	hypothetical protein CICLE_v10011942mg	Citrus clementina	integral component of membrane; prenyltransferase activity
Locus_10311_Transcript_2/5_Confidenc e_0.667_Length_1494	1966	28.2887	hypothetical protein CICLE_v10011942mg	Citrus clementina	integral component of membrane; prenyltransferase activity
Locus_2984_Transcript_4/4_Confidence _0.222_Length_574	131	4.90613	hypothetical protein CICLE_v10020293mg	Citrus clementina	protein prenylation; protein prenyltransferase activity
Locus_565_Transcript_12/20_Confidence e_0.484_Length_1409 Locus_7997_Transcript_1/5_Confidence	2635	40.2021	prenyltransferase	Populus trichocarpa Populus	NA
	513	16.0058	prenyltransferase	trichocarpa Populus	NA
_0.667_Length_651 Locus_7997_Transcript_3/5_Confidence	485	16.0155	prenyltransferase	trichocarpa Populus	NA
_0.500_Length_617 Locus_7997_Transcript_4/5_Confidence	433	15.0863	prenyltransferase	trichocarpa Populus	NA
_0.667_Length_1435 Locus_7997_Transcript_5/5_Confidence	493	7.38541	prenyltransferase	trichocarpa Populus trichocarpa	
_0.10/_Lengui_13//	543	/.4019/	prenymansterase	тапосатра	INA

Table S5. Transcripts for methyltransferase gene family with unknown function identified in *M. koenigü* leaf transcriptome. NA- Not annotated.

Transcript ID	Read	FPKM	Gene name	Organism	GO
	count				term
Locus_14513_Transcript_1/1_Confid	281	3.4322	Methyltransferase	Theobroma cacao	NA
ence_0.000_Length_1760					
Locus_30864_Transcript_1/1_Confid	13	1.02/43	Methyltransferase	Ajellomyces	NA
ence_0.000_Length_2/2				dermatitidis AICC	
Loove 22721 Transprint 1/1 Confid	57	1 46571	Mathyltronafaraaa family matain mytatiya	18188 Theological and a second	NT A
Locus_22/21_Transcript_1/1_Contra	57	1.40371	Methyliransierase family protein, putative	Theobroma cacao	INA
Logue 22721 Transprint 1/1 Confid	57	1 46571	Mathyltransforasa family protain putativa	Theobroma og ogo	ΝA
ana 0.000 Longth 826	57	1.40371	Methylitansierase family protein, putative	Theobroma cacao	INA
Locus 4840 Transcript 10/28 Confi	670	7 16026	Methyltransferase family protein isoform 2	Theobroma cacao	NΛ
dence 0.343 Length 2009	070	7.10920	We dry it ansierase ranning protein isororm 2		INA
Locus 4840 Transcript 11/28 Confi	639	7 14333	Methyltransferase family protein isoform 2	Theobroma cacao	NA
dence 0.314 Length 1923	009	/11/000			1111
Locus 4840 Transcript 13/28 Confi	370	13.9788	Methyltransferase family protein isoform 2	Theobroma cacao	NA
dence 0.171 Length 569					
Locus_4840_Transcript_14/28_Confi	367	13.7927	Methyltransferase family protein isoform 2	Theobroma cacao	NA
dence_0.171_Length_572					
Locus_4840_Transcript_17/28_Confi	633	6.4036	Methyltransferase family protein isoform 2	Theobroma cacao	NA
dence_0.343_Length_2125					
Locus_4840_Transcript_18/28_Confi	334	10.4818	Methyltransferase family protein isoform 2	Theobroma cacao	NA
dence_0.114_Length_685					
Locus_4840_Transcript_24/28_Confi	451	8.75807	Methyltransferase family protein isoform 2	Theobroma cacao	NA
dence_0.314_Length_1107					
Locus_4840_Transcript_25/28_Confi	453	6.99582	Methyltransferase family protein isoform 2	Theobroma cacao	NA
dence_0.086_Length_1392	1.00	4 000 61		771 1	
Locus_4840_Transcript_22/28_Conf1	163	4.99861	Methyltransferase family protein isoform 4	Theobroma cacao	NA
dence_0.171_Length_701	202	2 07550		7T1 1	NT 4
Locus_4840_Transcript_23/28_Conf1	203	3.8/558	Methyltransferase family protein isoform 4	Theobroma cacao	NA
dence_0.1/1_Length_1126	520	10 2077	DDEDICTED, autotice and the line of	Citaria	NIA
Locus_/8/9_Transcript_2/3_Confide	530	12.3977	Attac22800 Litra	Curus sinensis	INA
nce_0.400_Lengtn_919			At1g22800-11Ke		

Locus_14985_Transcript_1/4_Confid	115	4.33713	PREDICTED: putative methyltransferase	Citrus sinensis	NA
ence_0.500_Length_570			At1g22800-like		
Locus_14985_Transcript_2/4_Confid	108	4.29942	PREDICTED: putative methyltransferase	Citrus sinensis	NA
ence_0.333_Length_540			At1g22800-like		
Locus_14985_Transcript_3/4_Confid	105	3.7936	PREDICTED: putative methyltransferase	Citrus sinensis	NA
ence_0.500_Length_595			At1g22800-like		
Locus_14985_Transcript_4/4_Confid	108	3.5177	PREDICTED: putative methyltransferase	Citrus sinensis	NA
ence_0.000_Length_660			At1g22800-like		
Locus_2014_Transcript_6/12_Confid	18	1.94446	PREDICTED: uncharacterized methyltransferase	Cucumis sativus	NA
ence_0.067_Length_199			WBSCR22-like		
Locus_10007_Transcript_1/7_Confid	1975	38.9154	PREDICTED: uncharacterized methyltransferase	Citrus sinensis	NA
ence_0.333_Length_1091			At1g78140, chloroplastic-like isoform X1		
Locus_10007_Transcript_3/7_Confid	2196	29.4312	PREDICTED: uncharacterized methyltransferase	Citrus sinensis	NA
ence_0.667_Length_1604			At1g78140, chloroplastic-like isoform X1		
Locus_10007_Transcript_4/7_Confid	2172	27.321	PREDICTED: uncharacterized methyltransferase	Citrus sinensis	NA
ence_0.583_Length_1709			At1g78140, chloroplastic-like isoform X1		
Locus_10007_Transcript_5/7_Confid	2034	25.8117	PREDICTED: uncharacterized methyltransferase	Citrus sinensis	NA
ence_0.583_Length_1694			At1g78140, chloroplastic-like isoform X1		
Locus_10007_Transcript_6/7_Confid	639	12.9104	PREDICTED: uncharacterized methyltransferase	Citrus sinensis	NA
ence_0.417_Length_1064			At1g78140, chloroplastic-like isoform X1		
Locus_10007_Transcript_7/7_Confid	2199	29.4714	PREDICTED: uncharacterized methyltransferase	Citrus sinensis	NA
ence_0.250_Length_1604			At1g78140, chloroplastic-like isoform X1		
Locus_10007_Transcript_2/7_Confid	1309	41.9995	PREDICTED: uncharacterized methyltransferase	Citrus sinensis	NA
ence_0.167_Length_670			At1g78140, chloroplastic-like isoform X2		
Locus_2847_Transcript_10/29_Confi	6881	71.7021	PREDICTED: uncharacterized methyltransferase	Citrus sinensis	NA
dence_0.289_Length_2063			At2g41040, chloroplastic-like		
Locus_2847_Transcript_11/29_Confi	3223	59.4722	PREDICTED: uncharacterized methyltransferase	Citrus sinensis	NA
dence_0.200_Length_1165			At2g41040, chloroplastic-like		
Locus_2847_Transcript_12/29_Confi	4544	81.0645	PREDICTED: uncharacterized methyltransferase	Citrus sinensis	NA
dence_0.222_Length_1205			At2g41040, chloroplastic-like		
Locus_2847_Transcript_2/29_Confid	2382	54.0148	PREDICTED: uncharacterized methyltransferase	Citrus sinensis	NA
ence_0.133_Length_948			At2g41040, chloroplastic-like		
Locus_2847_Transcript_3/29_Confid	5215	119.773	PREDICTED: uncharacterized methyltransferase	Citrus sinensis	NA
ence_0.222_Length_936			At2g41040, chloroplastic-like		
Locus_2847_Transcript_4/29_Confid	5481	113.403	PREDICTED: uncharacterized methyltransferase	Citrus sinensis	NA
ence_0.267_Length_1039			At2g41040, chloroplastic-like		

Locus_2847_Transcript_5/29_Confid	5877	104.932	PREDICTED: uncharacterized methyltransferase	Citrus sinensis	NA
ence_0.289_Length_1204			At2g41040, chloroplastic-like		
Locus_2847_Transcript_6/29_Confid	6640	72.347	PREDICTED: uncharacterized methyltransferase	Citrus sinensis	NA
ence_0.289_Length_1973			At2g41040, chloroplastic-like		
Locus_2847_Transcript_7/29_Confid	5393	59.3923	PREDICTED: uncharacterized methyltransferase	Citrus sinensis	NA
ence_0.289_Length_1952			At2g41040, chloroplastic-like		
Locus_2847_Transcript_9/29_Confid	6120	101.671	PREDICTED: uncharacterized methyltransferase	Citrus sinensis	NA
ence_0.311_Length_1294			At2g41040, chloroplastic-like		

Table S6a: Cytochrome P450 families identified in *M. koenigii* leaf transcriptome putatively involved in Secondary metabolic pathways

CYP Family	Locus
CYP51	Locus_7540_Transcript_1/1_Confidence_0.000_Length_1583
	Locus_31208_Transcript_1/2_Confidence_0.333_Length_398
CYP70	Locus_21790_Transcript_3/3_Confidence_0.000_Length_307
CYP71	Locus_2163_Transcript_6/11_Confidence_0.269_Length_721
	Locus_2163_Transcript_10/11_Confidence_0.385_Length_1465
	Locus_2163_Transcript_1/11_Confidence_0.269_Length_681
	Locus_7712_Transcript_6/10_Confidence_0.455_Length_726
	Locus_3183_Transcript_12/23_Confidence_0.129_Length_663
	Locus_2658_Transcript_11/69_Confidence_0.035_Length_241
	Locus_21900_Transcript_1/1_Confidence_0.000_Length_150
	Locus_16873_Transcript_1/2_Confidence_0.333_Length_467
	Locus_2312_Transcript_4/9_Confidence_0.417_Length_2270
	Locus_2312_Transcript_3/9_Confidence_0.458_Length_2289
	Locus_2312_Transcript_1/9_Confidence_0.458_Length_2300
	Locus_2312_Transcript_5/9_Confidence_0.208_Length_2261
	Locus_2312_Transcript_2/9_Confidence_0.458_Length_2411
	Locus_24492_Transcript_1/1_Confidence_0.000_Length_305
	Locus_9952_Transcript_4/4_Confidence_0.000_Length_910
	Locus_19197_Transcript_1/1_Confidence_0.000_Length_425
	Locus_3026_Transcript_55/74_Confidence_0.028_Length_342
	Locus_3356_Transcript_3/48_Confidence_0.074_Length_3952
	Locus_3356_Transcript_8/48_Confidence_0.037_Length_4106
	Locus_3356_Transcript_4/48_Confidence_0.025_Length_2472
	Locus_2658_Transcript_8/69_Confidence_0.053_Length_357
	Locus_2658_Transcript_9/69_Confidence_0.053_Length_391

Locus 2658 Transcript 37/69 Confidence 0.053 Longth 523
Locus_2658_Transcript_//69_Confidence_0.041_Length_593
Locus_2658_Transcript_41/69_Confidence_0.058_Length_938
Locus_37231_Transcript_1/1_Confidence_1.000_Length_220
Locus_2658_Transcript_1/69_Confidence_0.029_Length_667
Locus_2658_Transcript_2/69_Confidence_0.023_Length_352
Locus_2658_Transcript_3/69_Confidence_0.023_Length_456
Locus_2658_Transcript_10/69_Confidence_0.041_Length_299
Locus_2656_Transcript_2/3_Confidence_0.455_Length_813
Locus_2656_Transcript_1/3_Confidence_0.182_Length_447
Locus_2658_Transcript_52/69_Confidence_0.041_Length_228
Locus_2658_Transcript_64/69_Confidence_0.292_Length_3126
Locus_2658_Transcript_25/69_Confidence_0.135_Length_1122
Locus_2658_Transcript_67/69_Confidence_0.222_Length_3336
Locus_2658_Transcript_61/69_Confidence_0.251_Length_3206
Locus_2658_Transcript_4/69_Confidence_0.070_Length_321
Locus_2658_Transcript_5/69_Confidence_0.058_Length_288
Locus_3026_Transcript_52/74_Confidence_0.028_Length_578
Locus_3026_Transcript_53/74_Confidence_0.043_Length_732
Locus_11455_Transcript_1/1_Confidence_0.000_Length_1818
Locus_37069_Transcript_1/1_Confidence_0.667_Length_170
Locus_29371_Transcript_1/1_Confidence_0.000_Length_407
Locus_8228_Transcript_1/1_Confidence_0.000_Length_1766
Locus_7712_Transcript_7/10_Confidence_0.409_Length_670
Locus_7712_Transcript_10/10_Confidence_0.273_Length_1276
Locus_7712_Transcript_8/10_Confidence_0.500_Length_1274
Locus_2163_Transcript_4/11_Confidence_0.346_Length_684
Locus_7712_Transcript_2/10_Confidence_0.500_Length_852
Locus_7712_Transcript_1/10_Confidence_0.500_Length 850
Locus 2163 Transcript 5/11 Confidence 0.308 Length 699

Locus_7712_Transcript_9/10_Confidence_0.545_Length_965
Locus_7712_Transcript_5/10_Confidence_0.409_Length_1394
Locus_7712_Transcript_4/10_Confidence_0.500_Length_1392
Locus_2163_Transcript_2/11_Confidence_0.269_Length_830
Locus_2843_Transcript_18/18_Confidence_0.200_Length_3790
Locus_2843_Transcript_17/18_Confidence_0.533_Length_3870
Locus_1265_Transcript_5/69_Confidence_0.059_Length_929
Locus_1265_Transcript_2/69_Confidence_0.034_Length_581
Locus_1265_Transcript_61/69_Confidence_0.109_Length_1394
Locus_9283_Transcript_2/2_Confidence_0.000_Length_1221
Locus_1265_Transcript_37/69_Confidence_0.034_Length_515
Locus_1265_Transcript_46/69_Confidence_0.084_Length_866
Locus_1265_Transcript_43/69_Confidence_0.059_Length_847
Locus_27095_Transcript_1/1_Confidence_0.000_Length_405
Locus_1265_Transcript_41/69_Confidence_0.059_Length_637
Locus_1265_Transcript_39/69_Confidence_0.076_Length_637
Locus_1265_Transcript_35/69_Confidence_0.076_Length_649
Locus_1265_Transcript_36/69_Confidence_0.076_Length_675
Locus_1265_Transcript_40/69_Confidence_0.076_Length_759
Locus_1265_Transcript_1/69_Confidence_0.034_Length_831
Locus_1265_Transcript_3/69_Confidence_0.042_Length_839
Locus_1265_Transcript_56/69_Confidence_0.059_Length_554
Locus_1265_Transcript_66/69_Confidence_0.067_Length_424
Locus_1265_Transcript_4/69_Confidence_0.025_Length_580
Locus_1265_Transcript_55/69_Confidence_0.059_Length_918
Locus_1265_Transcript_51/69_Confidence_0.126_Length_961
Locus_1265_Transcript_33/69_Confidence_0.109_Length_1413
Locus_1265_Transcript_32/69_Confidence_0.118_Length_1569
Locus_23869_Transcript_1/1_Confidence_0.000_Length_221
Locus_27253_Transcript_1/1_Confidence_0.000_Length_396

	Locus_1265_Transcript_60/69_Confidence_0.025_Length_469
	Locus_1265_Transcript_57/69_Confidence_0.042_Length_1162
	Locus_1265_Transcript_63/69_Confidence_0.067_Length_424
	Locus_1265_Transcript_67/69_Confidence_0.050_Length_424
	Locus_1265_Transcript_65/69_Confidence_0.050_Length_670
	Locus_3026_Transcript_15/74_Confidence_0.043_Length_449
	Locus_3026_Transcript_14/74_Confidence_0.014_Length_449
	Locus_3026_Transcript_31/74_Confidence_0.014_Length_511
	Locus_3026_Transcript_27/74_Confidence_0.043_Length_757
	Locus_3026_Transcript_28/74_Confidence_0.035_Length_757
	Locus_1900_Transcript_12/104_Confidence_0.040_Length_1345
	Locus_1900_Transcript_13/104_Confidence_0.015_Length_919
	Locus_9283_Transcript_1/2_Confidence_0.333_Length_1824
CYP73	Locus_5435_Transcript_3/3_Confidence_0.000_Length_865
	Locus_5435_Transcript_2/3_Confidence_0.333_Length_1897
	Locus_5435_Transcript_1/3_Confidence_0.667_Length_1101
	Locus_25834_Transcript_1/1_Confidence_0.000_Length_811
	Locus_32754_Transcript_1/1_Confidence_0.000_Length_506
	Locus_30656_Transcript_1/1_Confidence_0.000_Length_217
	Locus_32312_Transcript_1/1_Confidence_0.000_Length_161
CYP74	Locus_2093_Transcript_5/5_Confidence_0.111_Length_1720
	Locus_2093_Transcript_4/5_Confidence_0.333_Length_2108
	Locus 2093 Transcript 3/5 Confidence 0.333 Length 2201
	Locus_2093_Transcript_2/5_Confidence_0.222_Length_998
	Locus_2093_Transcript_1/5_Confidence_0.111_Length_1136
	Locus 11826 Transcript 1/4 Confidence 0.714 Length 2049
	Locus 11826 Transcript 4/4 Confidence 0.143 Length 2049
	Locus 11826 Transcript 2/4 Confidence 0.714 Length 2061
	Locus 11826 Transcript 3/4 Confidence 0.429 Length 1919
CYP75	Locus 6034 Transcript 6/15 Confidence 0.600 Length 2103
CYP75	Locus_11826_Transcript_2/4_Confidence_0.714_Length_2061 Locus_11826_Transcript_3/4_Confidence_0.429_Length_1919 Locus_6034_Transcript_6/15_Confidence_0.600_Length_2103

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	Locus_31518_Transcript_1/1_Confidence_0.000_Length_381
	Locus_6034_Transcript_12/15_Confidence_0.320_Length_1242
	Locus_6034_Transcript_8/15_Confidence_0.560_Length_1504
	Locus_6034_Transcript_14/15_Confidence_0.280_Length_1817
	Locus_21489_Transcript_1/1_Confidence_0.000_Length_203
	Locus_16409_Transcript_3/4_Confidence_0.500_Length_1727
	Locus_16409_Transcript_1/4_Confidence_0.750_Length_1728
	Locus_16409_Transcript_4/4_Confidence_0.000_Length_1652
	Locus_16409_Transcript_2/4_Confidence_0.250_Length_1653
	Locus_11745_Transcript_2/2_Confidence_0.000_Length_1803
	Locus_11745_Transcript_1/2_Confidence_0.750_Length_1596
CYP76	Locus_384_Transcript_17/34_Confidence_0.068_Length_507
	Locus_384_Transcript_4/34_Confidence_0.095_Length_215
	Locus_384_Transcript_8/34_Confidence_0.027_Length_518
	Locus_22631_Transcript_1/1_Confidence_0.000_Length_257
	Locus_384_Transcript_22/34_Confidence_0.095_Length_540
	Locus_384_Transcript_23/34_Confidence_0.149_Length_679
	Locus_384_Transcript_27/34_Confidence_0.135_Length_683
	Locus_13518_Transcript_1/2_Confidence_0.750_Length_1779
	Locus_384_Transcript_5/34_Confidence_0.216_Length_664
	Locus_384_Transcript_6/34_Confidence_0.162_Length_731
	Locus_384_Transcript_11/34_Confidence_0.257_Length_846
	Locus_384_Transcript_10/34_Confidence_0.257_Length_854
	Locus_384_Transcript_3/34_Confidence_0.095_Length_461
	Locus_384_Transcript_12/34_Confidence_0.203_Length_846
	Locus_384_Transcript_14/34_Confidence_0.216_Length_910
	Locus_13518_Transcript_2/2_Confidence_0.000_Length_1850
	Locus_18083_Transcript_1/2_Confidence_1.000_Length_266
CYP78	Locus_12021_Transcript_1/1_Confidence_0.000_Length_564
	Locus_10475_Transcript_5/11_Confidence_0.500_Length_2157

	Locus_10475_Transcript_7/11_Confidence_0.188_Length_1295
	Locus_10475_Transcript_9/11_Confidence_0.125_Length_1785
	Locus_6692_Transcript_2/2_Confidence_0.333_Length_810
	Locus_6692_Transcript_1/2_Confidence_0.667_Length_803
	Locus_21638_Transcript_1/1_Confidence_0.000_Length_701
	Locus_12984_Transcript_1/1_Confidence_0.000_Length_728
CYP79	Locus_10851_Transcript_10/11_Confidence_0.476_Length_1586
	Locus_3183_Transcript_1/23_Confidence_0.065_Length_379
	Locus_5093_Transcript_3/4_Confidence_0.400_Length_2576
	Locus_5093_Transcript_2/4_Confidence_0.600_Length_2353
	Locus_22028_Transcript_1/1_Confidence_0.000_Length_297
CYP81	Locus_3183_Transcript_2/23_Confidence_0.032_Length_473
	Locus_6868_Transcript_3/14_Confidence_0.333_Length_492
	Locus_6868_Transcript_2/14_Confidence_0.400_Length_525
	Locus_6868_Transcript_1/14_Confidence_0.467_Length_850
	Locus_2612_Transcript_4/4_Confidence_0.000_Length_1036
	Locus_2612_Transcript_3/4_Confidence_0.333_Length_1908
	Locus_1752_Transcript_1/7_Confidence_0.111_Length_1903
	Locus_1752_Transcript_2/7_Confidence_0.111_Length_2104
	Locus_11470_Transcript_3/4_Confidence_0.571_Length_1398
	Locus_24190_Transcript_1/1_Confidence_0.000_Length_1129
	Locus_11470_Transcript_2/4_Confidence_0.429_Length_1398
	Locus_11470_Transcript_4/4_Confidence_0.000_Length_1398
	Locus_7159_Transcript_5/7_Confidence_0.667_Length_1917
	Locus_7159_Transcript_6/7_Confidence_0.500_Length_1917
	Locus_7159_Transcript_4/7_Confidence_0.250_Length_1327
	Locus_11470_Transcript_1/4_Confidence_0.286_Length_270
	Locus_7159_Transcript_2/7_Confidence_0.500_Length_1195
	Locus_7159_Transcript_3/7_Confidence_0.417_Length_1204
	Locus_7159_Transcript_1/7_Confidence_0.500_Length_1172

	Locus_1500_Transcript_8/8_Confidence_0.429_Length_2594
	Locus_1752_Transcript_6/7_Confidence_0.333_Length_1763
	Locus_1752_Transcript_5/7_Confidence_0.444_Length_1767
	Locus_1752_Transcript_3/7_Confidence_0.444_Length_3510
	Locus_12542_Transcript_1/9_Confidence_0.500_Length_580
CYP82	Locus_10475_Transcript_2/11_Confidence_0.188_Length_1306
	Locus_10475_Transcript_3/11_Confidence_0.062_Length_1602
	Locus_2006_Transcript_6/27_Confidence_0.283_Length_1221
	Locus_2006_Transcript_8/27_Confidence_0.264_Length_1352
	Locus_17484_Transcript_1/1_Confidence_0.000_Length_678
	Locus_2006_Transcript_16/27_Confidence_0.057_Length_380
	Locus_2006_Transcript_3/27_Confidence_0.189_Length_737
	Locus_2616_Transcript_5/5_Confidence_0.000_Length_1077
	Locus_2616_Transcript_4/5_Confidence_0.375_Length_1917
	Locus_2616_Transcript_1/5_Confidence_0.625_Length_1907
	Locus_2616_Transcript_3/5_Confidence_0.250_Length_1851
	Locus_2616_Transcript_2/5_Confidence_0.375_Length_1915
	Locus_2006_Transcript_12/27_Confidence_0.113_Length_628
	Locus_2006_Transcript_10/27_Confidence_0.226_Length_832
	Locus_2006_Transcript_11/27_Confidence_0.189_Length_672
	Locus_2096_Transcript_1/9_Confidence_0.182_Length_1978
	Locus_2096_Transcript_2/9_Confidence_0.091_Length_1980
	Locus_2006_Transcript_25/27_Confidence_0.321_Length_1534
	Locus_2006_Transcript_26/27_Confidence_0.226_Length_1571
	Locus_2006_Transcript_19/27_Confidence_0.396_Length_1572
	Locus_2006_Transcript_22/27_Confidence_0.358_Length_1572
	Locus_2006_Transcript_18/27_Confidence_0.396_Length_1565
	Locus_2006_Transcript_23/27_Confidence_0.396_Length_1641
	Locus_2006_Transcript_21/27_Confidence_0.396_Length_1659
	Locus_2006_Transcript_27/27_Confidence_0.113_Length_622

	Locus_2006_Transcript_4/27_Confidence_0.302_Length_1221
	Locus_2006_Transcript_2/27_Confidence_0.321_Length_1308
	Locus_16804_Transcript_1/1_Confidence_0.000_Length_905
	Locus_2006_Transcript_20/27_Confidence_0.340_Length_1572
	Locus_1496_Transcript_5/16_Confidence_0.625_Length_1627
	Locus_1496_Transcript_13/16_Confidence_0.583_Length_1641
	Locus_1496_Transcript_11/16_Confidence_0.625_Length_1641
	Locus_1496_Transcript_6/16_Confidence_0.542_Length_1627
	Locus_1496_Transcript_12/16_Confidence_0.500_Length_1641
	Locus_1496_Transcript_8/16_Confidence_0.625_Length_1695
	Locus_1496_Transcript_14/16_Confidence_0.542_Length_1709
	Locus_1496_Transcript_10/16_Confidence_0.542_Length_1811
	Locus_1496_Transcript_7/16_Confidence_0.625_Length_1626
	Locus_1496_Transcript_15/16_Confidence_0.333_Length_1640
	Locus_1496_Transcript_9/16_Confidence_0.583_Length_1575
	Locus_1496_Transcript_16/16_Confidence_0.000_Length_395
	Locus_1496_Transcript_3/16_Confidence_0.542_Length_1610
	Locus_1496_Transcript_4/16_Confidence_0.417_Length_1195
	Locus_1496_Transcript_1/16_Confidence_0.167_Length_828
	Locus_1496_Transcript_2/16_Confidence_0.042_Length_500
	Locus_2006_Transcript_5/27_Confidence_0.302_Length_1222
CYP83	Locus_3026_Transcript_71/74_Confidence_0.050_Length_1496
	Locus_3026_Transcript_67/74_Confidence_0.135_Length_2218
	Locus_3026_Transcript_62/74_Confidence_0.135_Length_2050
	Locus_13963_Transcript_5/5_Confidence_0.000_Length_1807
	Locus_13963_Transcript_4/5_Confidence_0.500_Length_1808
	Locus_13963_Transcript_1/5_Confidence_0.667_Length_1809
	Locus_13963_Transcript_3/5_Confidence_0.583_Length_1809
	Locus_13963_Transcript_2/5_Confidence_0.583_Length_1762
	Locus_2658_Transcript_36/69_Confidence_0.082_Length_1040

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	Locus_3183_Transcript_18/23_Confidence_0.419_Length_1290
	Locus_10238_Transcript_1/1_Confidence_0.333_Length_1883
	Locus_16923_Transcript_3/4_Confidence_0.400_Length_1016
	Locus_16923_Transcript_1/4_Confidence_0.400_Length_852
	Locus_16923_Transcript_2/4_Confidence_0.200_Length_955
	Locus_10856_Transcript_3/7_Confidence_0.091_Length_628
	Locus_4058_Transcript_7/12_Confidence_0.143_Length_555
СҮР90	Locus_296_Transcript_2/14_Confidence_0.200_Length_789
	Locus_296_Transcript_3/14_Confidence_0.333_Length_1223
	Locus_296_Transcript_14/14_Confidence_0.100_Length_1314
	Locus_296_Transcript_10/14_Confidence_0.300_Length_2127
	Locus_296_Transcript_13/14_Confidence_0.233_Length_2259
	Locus_296_Transcript_11/14_Confidence_0.367_Length_2384
	Locus_296_Transcript_7/14_Confidence_0.467_Length_2388
	Locus_296_Transcript_8/14_Confidence_0.433_Length_2415
	Locus_296_Transcript_9/14_Confidence_0.300_Length_1930
	Locus_296_Transcript_12/14_Confidence_0.100_Length_2867
	Locus_16943_Transcript_1/1_Confidence_0.000_Length_2055
	Locus_2919_Transcript_6/8_Confidence_0.200_Length_1003
	Locus_2919_Transcript_3/8_Confidence_0.400_Length_1573
	Locus_7472_Transcript_3/3_Confidence_0.000_Length_846
	Locus_7472_Transcript_1/3_Confidence_0.400_Length_2057
	Locus_7472_Transcript_2/3_Confidence_0.000_Length_1334
	Locus_21810_Transcript_1/1_Confidence_0.000_Length_535
	Locus_26673_Transcript_1/1_Confidence_0.000_Length_238
	Locus_9617_Transcript_5/6_Confidence_0.571_Length_1910
	Locus_9617_Transcript_4/6_Confidence_0.571_Length_1919

	Locus_9617_Transcript_3/6_Confidence_0.571_Length_2005
	Locus_9617_Transcript_1/6_Confidence_0.714_Length_2014
	Locus_9617_Transcript_6/6_Confidence_0.143_Length_2014
	Locus_9617_Transcript_2/6_Confidence_0.714_Length_2109
CYP94	Locus_2871_Transcript_1/2_Confidence_0.750_Length_1863
	Locus_2871_Transcript_2/2_Confidence_0.250_Length_1867
	Locus_2424_Transcript_1/1_Confidence_0.000_Length_1734
CYP96	Locus_2163_Transcript_3/11_Confidence_0.346_Length_520
	Locus_3183_Transcript_3/23_Confidence_0.323_Length_874
	Locus_3183_Transcript_4/23_Confidence_0.387_Length_879
	Locus_3183_Transcript_7/23_Confidence_0.452_Length_1677
	Locus_3183_Transcript_8/23_Confidence_0.516_Length_1682
	Locus_3183_Transcript_6/23_Confidence_0.387_Length_1020
	Locus_3183_Transcript_5/23_Confidence_0.452_Length_1025
	Locus_3183_Transcript_17/23_Confidence_0.452_Length_1117
	Locus_3183_Transcript_19/23_Confidence_0.452_Length_1113
	Locus_3183_Transcript_9/23_Confidence_0.581_Length_1828
	Locus_3183_Transcript_13/23_Confidence_0.581_Length_1920
	Locus_3183_Transcript_16/23_Confidence_0.516_Length_1878
	Locus_3183_Transcript_15/23_Confidence_0.548_Length_1990
	Locus_3183_Transcript_20/23_Confidence_0.581_Length_2078
	Locus_3183_Transcript_21/23_Confidence_0.419_Length_1275
	Locus_3183_Transcript_22/23_Confidence_0.581_Length_2081
	Locus_3183_Transcript_23/23_Confidence_0.290_Length_1288
	Locus_11035_Transcript_1/1_Confidence_0.000_Length_1723
	Locus_21546_Transcript_1/1_Confidence_0.000_Length_1236
	Locus_30147_Transcript_1/1_Confidence_0.000_Length_300
	Locus_12542_Transcript_7/9_Confidence_0.333_Length_577
CYP97	Locus_6410_Transcript_12/23_Confidence_0.370_Length_2302
	Locus_6410_Transcript_7/23_Confidence_0.407_Length_2315

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	Locus_6410_Transcript_10/23_Confidence_0.407_Length_2320
	Locus_6410_Transcript_13/23_Confidence_0.407_Length_2349
	Locus_6410_Transcript_14/23_Confidence_0.407_Length_2422
	Locus_6410_Transcript_15/23_Confidence_0.556_Length_4023
	Locus_6410_Transcript_16/23_Confidence_0.593_Length_4842
	Locus_6410_Transcript_18/23_Confidence_0.556_Length_4938
	Locus_6410_Transcript_3/23_Confidence_0.111_Length_928
	Locus_6410_Transcript_5/23_Confidence_0.111_Length_928
	Locus_6410_Transcript_4/23_Confidence_0.111_Length_933
	Locus_6410_Transcript_6/23_Confidence_0.222_Length_1366
	Locus_6410_Transcript_20/23_Confidence_0.593_Length_4735
	Locus_6410_Transcript_21/23_Confidence_0.556_Length_4876
	Locus_6410_Transcript_2/23_Confidence_0.148_Length_625
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	Locus_9437_Transcript_8/8_Confidence_0.154_Length_2219
	Locus_9437_Transcript_7/8_Confidence_0.692_Length_2201
	Locus_9437_Transcript_2/8_Confidence_0.538_Length_2553
	Locus_9437_Transcript_1/8_Confidence_0.308_Length_1777
	Locus_5217_Transcript_4/6_Confidence_0.222_Length_823
	Locus_5217_Transcript_5/6_Confidence_0.222_Length_827
	Locus_5217_Transcript_1/6_Confidence_0.667_Length_1286
	Locus_5217_Transcript_2/6_Confidence_0.667_Length_1290
	Locus_5217_Transcript_6/6_Confidence_0.111_Length_1187
	Locus_5217_Transcript_3/6_Confidence_0.444_Length_1361
	Locus_15204_Transcript_2/2_Confidence_0.400_Length_995
	Locus_15204_Transcript_1/2_Confidence_0.800_Length_757
	Locus_6410_Transcript_22/23_Confidence_0.370_Length_4847
CYP98	Locus_5966_Transcript_4/8_Confidence_0.333_Length_881
	Locus_5966_Transcript_3/8_Confidence_0.389_Length_884
	Locus_5966_Transcript_5/8_Confidence_0.389_Length_1106

	Locus_5966_Transcript_2/8_Confidence_0.389_Length_1805
	Locus_5966_Transcript_1/8_Confidence_0.389_Length_1808
	Locus_5966_Transcript_6/8_Confidence_0.389_Length_1808
	Locus_5966_Transcript_8/8_Confidence_0.056_Length_1768
	Locus_5966_Transcript_7/8_Confidence_0.111_Length_1065
	Locus_19973_Transcript_1/1_Confidence_0.000_Length_1735
CYP702	Locus_22762_Transcript_3/5_Confidence_0.143_Length_696
	Locus_22762_Transcript_5/5_Confidence_0.000_Length_1642
	Locus_22762_Transcript_2/5_Confidence_0.571_Length_1702
	Locus_11181_Transcript_8/17_Confidence_0.217_Length_376
	Locus_11181_Transcript_9/17_Confidence_0.217_Length_363
CYP704	Locus_21790_Transcript_1/3_Confidence_0.750_Length_416
	Locus_21790_Transcript_2/3_Confidence_0.500_Length_509
CYP705	Locus_2163_Transcript_7/11_Confidence_0.538_Length_1351
	Locus_2163_Transcript_8/11_Confidence_0.538_Length_1693
	Locus_2163_Transcript_11/11_Confidence_0.154_Length_678
	Locus_28508_Transcript_1/1_Confidence_0.000_Length_300
	Locus_3897_Transcript_2/3_Confidence_0.625_Length_792
	Locus_3897_Transcript_3/3_Confidence_0.500_Length_912
	Locus_3897_Transcript_1/3_Confidence_0.625_Length_922
	Locus_6868_Transcript_5/14_Confidence_0.200_Length_287
	Locus_5093_Transcript_4/4_Confidence_0.000_Length_680
	Locus_17870_Transcript_2/3_Confidence_0.200_Length_1007
CYP706	Locus_9265_Transcript_3/3_Confidence_0.167_Length_360
	Locus_9265_Transcript_2/3_Confidence_0.500_Length_466
	Locus_9265_Transcript_1/3_Confidence_0.333_Length_466
	Locus_22720_Transcript_1/1_Confidence_0.000_Length_304
	Locus_1182_Transcript_2/17_Confidence_0.516_Length_1813
	Locus_1182_Transcript_3/17_Confidence_0.484_Length_1813
	Locus_1182_Transcript_1/17_Confidence_0.516_Length_1817

Locus_1182_Transcript_4/17_Confidence_0.516_Length_1813
Locus_1182_Transcript_11/17_Confidence_0.452_Length_1872
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Locus_1182_Transcript_7/17_Confidence_0.484_Length_1870
Locus_1182_Transcript_10/17_Confidence_0.484_Length_1852
Locus_1182_Transcript_6/17_Confidence_0.581_Length_1909
Locus_1182_Transcript_15/17_Confidence_0.484_Length_1929
Locus_1182_Transcript_5/17_Confidence_0.581_Length_1969
Locus_1182_Transcript_9/17_Confidence_0.613_Length_2028
Locus_18372_Transcript_1/1_Confidence_0.000_Length_284
Locus_14353_Transcript_1/1_Confidence_0.000_Length_1114
Locus_15761_Transcript_1/1_Confidence_0.000_Length_1304
Locus_1182_Transcript_16/17_Confidence_0.226_Length_866
Locus_12215_Transcript_6/8_Confidence_0.500_Length_2092
Locus_12215_Transcript_7/8_Confidence_0.250_Length_2079
Locus_12215_Transcript_8/8_Confidence_0.083_Length_1862
Locus_28066_Transcript_1/1_Confidence_0.000_Length_559
Locus_1174_Transcript_1/1_Confidence_0.000_Length_1127
Locus_12634_Transcript_1/1_Confidence_0.000_Length_1613
Locus_11181_Transcript_17/17_Confidence_0.000_Length_513
Locus_5093_Transcript_1/4_Confidence_0.600_Length_457
Locus_10475_Transcript_4/11_Confidence_0.312_Length_909
Locus_10475_Transcript_8/11_Confidence_0.438_Length_2605
Locus_6868_Transcript_4/14_Confidence_0.400_Length_671
Locus_16293_Transcript_1/1_Confidence_0.000_Length_1727
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	Locus_7923_Transcript_2/4_Confidence_0.333_Length_1584
	Locus_7923_Transcript_1/4_Confidence_0.444_Length_1589
	Locus_7923_Transcript_3/4_Confidence_0.667_Length_1593
	Locus_7923_Transcript_4/4_Confidence_0.333_Length_1655
	Locus_22920_Transcript_1/1_Confidence_0.000_Length_236
	Locus_28257_Transcript_1/1_Confidence_0.000_Length_364
	Locus_24538_Transcript_1/1_Confidence_0.000_Length_786
	Locus_18277_Transcript_1/1_Confidence_0.000_Length_293
	Locus_6034_Transcript_9/15_Confidence_0.200_Length_706
	Locus_6034_Transcript_1/15_Confidence_0.360_Length_1151
	Locus_6034_Transcript_3/15_Confidence_0.320_Length_1151
	Locus_6034_Transcript_13/15_Confidence_0.360_Length_1496
	Locus_6034_Transcript_5/15_Confidence_0.400_Length_1811
	Locus_6034_Transcript_15/15_Confidence_0.040_Length_831
CYP721	Locus_10475_Transcript_1/11_Confidence_0.250_Length_749
	Locus_10475_Transcript_11/11_Confidence_0.000_Length_1062
CYP722	Locus_6868_Transcript_9/14_Confidence_0.467_Length_1899
CYP734	Locus_2860_Transcript_2/16_Confidence_0.227_Length_535
	Locus_3941_Transcript_5/6_Confidence_0.222_Length_1272
	Locus_3941_Transcript_1/6_Confidence_0.667_Length_1619
	Locus_3941_Transcript_3/6_Confidence_0.556_Length_1774
	Locus_3941_Transcript_2/6_Confidence_0.444_Length_669
	Locus_3941_Transcript_4/6_Confidence_0.111_Length_1852
	Locus_3941_Transcript_3/6_Confidence_0.556_Length_1774
	Locus_3941_Transcript_2/6_Confidence_0.444_Length_669
CYP735	Locus_20269_Transcript_1/1_Confidence_0.000_Length_720
	Locus_3780_Transcript_9/13_Confidence_0.462_Length_1358
	Locus_3780_Transcript_7/13_Confidence_0.500_Length_1389
	Locus_3780_Transcript_2/13_Confidence_0.462_Length_1291

Locus_3780_Transcript_8/13_Confidence_0.577_Length_1997
Locus_3780_Transcript_1/13_Confidence_0.269_Length_1024
Locus_3780_Transcript_10/13_Confidence_0.115_Length_1666
Locus_3780_Transcript_5/13_Confidence_0.231_Length_879
Locus_3780_Transcript_4/13_Confidence_0.231_Length_878
Locus_3780_Transcript_3/13_Confidence_0.269_Length_1519
Locus_3780_Transcript_6/13_Confidence_0.269_Length_1568

Table S6b: Putative nomenclature of identified *M. koenigii* full length genes encoding Cytochrome P450 using different public databases

Transcript ID	Nelson database/	Bio catnet CYPED v6.0/	NCBI	TAIR
	http://blast.uthsc.edu			
	/blast.cgi	https://cyped.biocatnet.de/		
	U	workbench/blast		
Locus_7540_Transcript_1/1_Co	CYP51G1/CYP51A2	Cyp51/PREDICTED: sterol	PREDICTED: obtusifoliol	putative obtusifoliol 14-alpha demethy lase
nfidence_0.000_Length_1583		14-demethy lase-like	14-alpha demethy lase	involved in sterol biosynthesis
			[Citrus sinensis]	
Locus_2312_Transcript_4/9_Co	CYP71B34	PREDICTED: cytochrome	PREDICTED: cytochrome	CYP71B2/secondary metabolite biosynthetic
nfidence_0.417_Length_2270		P450 71B37-like cytochrome	P450 71B34-like [Citrus	process
		P450	sinensis	
			-	
Locus_2312_Transcript_3/9_Co	CYP71B34	PREDICTED: cytochrome	PREDICTED: cytochrome	CYP71B2/secondary metabolite biosynthetic
nfidence_0.458_Length_2289		P450 71B37-like cytochrome	P450 71B34-like [Citrus	process
		P450	sinensis]	
Locus_2312_Transcript_1/9_Co	CYP71B34	PREDICTED: cytochrome	PREDICTED: cytochrome	CYP71B2/secondary metabolite biosynthetic
nfidence_0.458_Length_2300		P450 71B37-like cytochrome	P450 71B34-like [Citrus	process
_		P450	sinensis	-
			-	

Locus_11455_Transcript_1/1_C onfidence_0.000_Length_1818 Locus_9283_Transcript_1/2_Co nfidence_0.333_Length_1824	CYP71B35 CYP721	hypothetical protein PREDICTED: cytochrome P450 734A1-like	PREDICTED: cytochrome P450 71A1-like [<i>Citrus</i> <i>sinensis</i>] PREDICTED: cytochrome P450 734A1-like [<i>Citrus</i> <i>sinensis</i>]	CYP71B22 CYP721A1
Locus_2093_Transcript_4/5_Co nfidence_0.333_Length_2108	CYP74B2	hy droperoxide ly ase [<i>Citrus jambhiri</i>]	fatty acid hydroperoxide lyase [<i>Citrus sinensis</i>]	CYP74B2, HPL1, HYDROPEROXIDE LYASE 1/sterol metabolic process
Locus_11826_Transcript_1/4_C onfidence_0.714_Length_2049	CYP74A	CYP74A	allene oxide synthase [<i>Citrus sinensis</i>]	ALLENE OXIDE SYNTHASE, AOS, CYP74A, CYTOCHROME P450 74A, DDE2, DELA YED DEHISCENCE 2/defense response, defense response to fungus, epoxy genase P450 pathway, jasmonic acid biosynthetic process, oxidation-reduction process, oxylipin biosynthetic process, oxylipin biosynthetic process, oxylipin metabolic process, response to fungus, response to jasmonic acid, response to wounding, sterol metabolic process
Locus_11826_Transcript_4/4_C onfidence_0.143_Length_2049	CYP74A	CYP74A	allene oxide synthase [<i>Citrus sinensis</i>]	ALLENE OXIDE SYNTHASE, AOS, CYP74A, CYTOCHROME P450 74A, DDE2, DELAYED DEHISCENCE 2/defense response, defense response to fungus, epoxy genase P450 pathway, jasmonic acid biosynthetic process, oxidation-reduction process, oxylipin biosynthetic process

Locus_11826_Transcript_2/4_C	CYP74A	CYP74A	allene oxide synthase	ALLENE OXIDE SYNTHASE, AOS,
onfidenœ_0.714_Length_2061			[Citrus sinensis]	CYP74A, CYTOCHROME P450 74A, DDE2, DELAYED DEHISCENCE 2/defense response, defense response to fungus, epoxy genase P450 pathway, jasmonic acid biosynthetic process, oxidation-reduction process, oxylipin biosynthetic process, oxylipin metabolic process, response to fungus, response to jasmonic acid, response to wounding, sterol metabolic process
Locus_11826_Transcript_3/4_C	CYP74A	CYP74A	allene oxide synthase	ALLENE OXIDE SYNTHASE, AOS,
onfidenœ_0.429_Length_1919			[Citrus sinensis]	CYP74A, CYTOCHROM E P450 74A, DDE2, DELAYED DEHISCENCE 2/defense response, defense response to fungus, epoxy genase P450 pathway, jasmonic acid biosynthetic process, oxidation-reduction process, oxylipin biosynthetic process, oxylipin metabolic process, response to fungus, response to jasmonic acid, response to wounding, sterol metabolic process
Locus_16409_Transcript_3/4_C	CYP75B1	cytochrome P450 71A1-like	PREDICTED: cytochrome	CYP81H1/defense response to other organism,
onfidence_0.500_Length_1727			P450 71A1-like [<i>Citrus</i> sinensis]	indole glucosinolate metabolic process, oxidation-reduction process, secondary metabolite biosynthetic process OR CYP71B16/secondary metabolite biosynthetic process
Locus_16409_Transcript_1/4_C	CYP75B1	cytochrome P450 71A1-like	PREDICTED: cytochrome	CYP81H1/defense response to other organism,
onfidence_0.750_Length_1728			sinensis]	oxidation-reduction process, secondary metabolite biosynthetic process OR CYP71B16/secondary metabolite biosynthetic process

Locus_16409_Transcript_4/4_C onfidence_0.000_Length_1652	CYP75B1	cytochrome P450 71A1-like	PREDICTED: cytochrome P450 71A1-like [<i>Citrus</i> <i>sinensis</i>]	CYP81H1/defense response to other organism, indole glucosinolate metabolic process, oxidation-reduction process, secondary metabolite biosynthetic process OR CYP71B16/secondary metabolite biosynthetic process
Locus_16409_Transcript_2/4_C onfidence_0.250_Length_1653	CYP75B1	cytochrome P450 71A1-like	PREDICTED: cytochrome P450 71A1-like [<i>Citrus</i> <i>sinensis</i>]	CYP81H1/defense response to other organism, indole glucosinolate metabolic process, oxidation-reduction process, secondary metabolite biosynthetic process OR CYP71B16/secondary metabolite biosynthetic process
Locus_11745_Transcript_2/2_C onfidence_0.000_Length_1803	CYP75B1	PREDICTED: flavonoid 3- monooxy genase-like	PREDICTED: flavonoid 3'- monooxy genase [<i>Citrus</i> <i>sinensis</i>]	CYP75B1, CYTOCHROME P450 75B1, D501, TRANSPARENT TESTA 7, TT7/flavonoid biosynthetic process, oxidation- reduction process, response to UV, response to auxin, secondary metabolite biosynthetic process
Locus_13518_Transcript_1/2_C onfidence_0.750_Length_1779	CYP76C4	CYP76B	PREDICTED: geraniol 8- hy droxy lase-like isoform X3 [<i>Citrus sinensis</i>]	CYP71B20/defense response to other organism, oxidation-reduction process, secondary metabolite biosynthetic process
Locus_10475_Transcript_5/11_ Confidence_0.500_Length_2157	CYP78A9	cytochrome P450 78A9-like isoform	PREDICTED: cytochrome P450 3A31-like isoform X1 [<i>Citrus sinensis</i>]	CCT2, PHOSPHORYLCHOLINE CYTIDYLYLTRANSFERASE2
Locus_5093_Transcript_3/4_Co nfidence_0.400_Length_2576	СҮР79В3	NADPHcytochrome P450 reductase	PREDICTED: NADPH cytochrome P450 reductase isoform X1 [<i>Citrus</i> <i>sinensis</i>]	P450 REDUCTASE 2/pheny propanoid general pathway
Locus_5093_Transcript_2/4_Co nfidence_0.600_Length_2353	СҮР79В3	NADPHcytochrome P450 reductase	PREDICTED: NADPH cytochrome P450 reductase isoform X1 [<i>Citrus</i> <i>sinensis</i>]	P450 REDUCTASE 2/phenylpropanoid general pathway

Locus_2612_Transcript_3/4_Co nfidence_0.333_Length_1908 Locus_1752_Transcript_1/7_Co nfidence_0.111_Length_1903	CYP81K2 CYP81D8	CYP81K cytochrome P450 81D1-like	PREDICTED: cytochrome P450 81D11-like [<i>Citrus</i> <i>sinensis</i>] PREDICTED: isoflavone 3'-hy droxy lase-like [<i>Citrus</i> <i>sinensis</i>]	CYP81K2/defense response to other organism, indole glucosinolate metabolic process,oxidation-reduction process, secondary metabolite biosynthetic process CYP81D5/defense response to other organism, indole glucosinolate metabolic process, oxidation-reduction process, secondary metabolite biosynthetic process
Locus_1752_Transcript_2/7_Co nfidence_0.111_Length_2104	CYP81D8	cytochrome P450 81D1-like	PREDICTED: isoflavone 3'-hy droxy lase-like [<i>Citrus</i> <i>sinensis</i>]	CYP81D5/defense response to other organism, indole glucosinolate metabolic process, oxidation-reduction process, secondary metabolite biosynthetic process
Locus_1752_Transcript_6/7_Co nfidenœ_0.333_Length_1763	CYP81D8	CYP81E	PREDICTED: isoflavone 2'-hy droxy lase-like isoform X1 [<i>Citrus sinensis</i>]	CYP81D5/defense response to other organism, indole glucosinolate metabolic process, oxidation-reduction process, secondary metabolite biosynthetic process
Locus_1752_Transcript_5/7_Co nfidenœ_0.444_Length_1767	CYP81D8	isoflavone 2'-hydroxylase- like isoform X1/CYP81E	PREDICTED: isoflavone 2'-hy droxy lase-like isoform X1 [<i>Citrus sinensis</i>]	CYP81D5/defense response to other organism, indole glucosinolate metabolic process, oxidation-reduction process, secondary metabolite biosynthetic process
Locus_2616_Transcript_4/5_Co nfidence_0.375_Length_1917	CYP82C4	CYP82G	PREDICTED: cytochrome P450 82C4-like [Ziziphus jujuba]	CYP82C4/cellular response to iron ion, oxidation-reduction process, secondary metabolite biosynthetic process
Locus_2616_Transcript_1/5_Co nfidence_0.625_Length_1907	CYP82C4	CYP82G	PREDICTED: cytochrome P450 82C4-like [Ziziphus jujuba]	CYP82C4/cellular response to iron ion, oxidation-reduction process, secondary metabolite biosynthetic process

Locus_2616_Transcript_3/5_Co	CYP82C4	CYP82G	PREDICTED: cytochrome	CYP82C4/cellular response to iron ion,
nfidence_0.250_Length_1851			P450 82C4-like [Ziziphus	oxidation-reduction process, secondary
			jujuba]	metabolite biosynthetic process
Locus_2616_Transcript_2/5_Co	CYP82C4	CYP82G	PREDICTED: cytochrome	CYP82C4/cellular response to iron ion,
nfidence 0.375 Length 1915			P450 82C4-like [Ziziphus	oxidation-reduction process, secondary
			iuiubal	metabolite biosynthetic process
			Jugue al	
Locus 2096 Transcript 1/9 Co	CYP82C4	cytochrome P450 82C4-like	PREDICTED: cvtochrome	CYP82C3/oxidation-reduction process.
nfidence 0.182 Length 1978	0110201		P450 CYP82D47-like	secondary metabolite biosynthetic process
indence_0.102_1.engtin_1770			[Citrus sinonsis]	secondary metabolice biosynthetic process
Locus 2096 Transcript 2/9 Co	CVP82C4	cytochrome P450 82C4_like	PREDICTED: cytochrome	CYP82C3/oxidation-reduction process
nfidence 0.001 Length 1980	011 0204	cytoenionie 1 450 82e4-like	P450 CYP82D47-like	secondary metabolite biosynthetic process
Indence_0.071_12.lgtn_1700			[Citrus sinonsis]	secondary inclusione biosynthetic process
Locus 2006 Transcript 25/27	CVD82CA/C2/C3	outochrome P450 82C4 like	cytochrome P450 8243-	CVD71B37
Confidence 0.321 Length 1534	011 0204/02/03	cytoenionie 1 450 82e4-like	like isoform X2 [<i>Citrus</i>	
Confidence_0.521_fengtin_1554			sinongial	
			Smensis	
Locus_3026_Transcript_71/74_	CYP83A2	CYP83B	PREDICTED: cytochrome	CYP71B5/ cellular response to ethylene
Confidence 0.050 Length 1496			P450 83B1-like [Citrus	stimulus, cellular response to iron ion, cellular
0 _			sinensis]	response to nitric oxide, oxidation-reduction
			-	process, secondary metabolite biosynthetic
				process
Locus_3026_Transcript_67/74_	CYP83A2	CYP83B	PREDICTED: cytochrome	CYP71B5/ cellular response to ethylene
Confidence_0.135_Length_2218			P450 83B1-like [Citrus	stimulus, cellular response to iron ion, cellular
			sinensis]	response to nitric oxide, oxidation-reduction
				process, secondary metabolite biosynthetic
				process
Locus_3026_Transcript_62/74_	CYP83A2	CYP83B	PREDICTED: cytochrome	CYP71B5/ cellular response to ethylene
Confidence_0.135_Length_2050			P450 83B1-like [Citrus	stimulus, cellular response to iron ion, cellular
			sinensis]	response to nitric oxide, oxidation-reduction
				process, secondary metabolite biosynthetic

				process
Locus_19681_Transcript_1/1_C	CYP84A1	CYP84A	PREDICTED: cytochrome	CYP84A1, CYTOCHROME P450 84A1,
onfidence_0.000_Length_1840			sinonsis]	1/lignin biosynthetic process oxidation-
			sittensis	reduction process, pheny propanoid
				biosynthetic process, response to UV-B
Loong 10228 Transprint 1/1 C	CVD90 4 5	DDEDICTED: autochroma	DREDICTED: autochrome	$CVD_{20} \wedge 2/$ ovidation reduction process
onfidence 0.333 Longth 1883	CYP89A5	PREDICTED: cytochrome	PREDICTED: cytochrome P450 8942-like [<i>Citrus</i>	secondary metabolite biosynthetic process
onnuence_0.355_Lengtn_1885		1450 87A2-like	sinensis]	secondary metabolite biosynthesic process
			-	
Locus_7472_Transcript_1/3_Co	CYP90C1	3-epi-6-deoxocathasterone	PREDICTED: 3-epi-6-	CYP90B1, DWARF 4, DWF4, PARTIALLY
nfidence_0.400_Length_2057		23-monooxy genase-like	deoxocathasterone 23-	SUPPRESSING COI1 INSENSITIVITY TO
		isoform X I	monooxy genase isoform	JA 1, PSC1, SAV1, SHADE AVOIDANCE 1, SNP2 SUPPRESSOR OF NPH4 2/
			AI [Curus sinensis]	brassinosteroid biosynthetic process.
				brassinosteroid homeostasis, jasmonic acid
				mediated signaling pathway, leaf development,
				leaf shaping, oxidation-reduction process,
				response to brassmosteroid, response to
				unidimensional cell growth

Locus 9617 Transcript 5/6 Co	CVP90D1	CYP90D	PREDICTED: 3-eni-6-	CYP90D1/Encodes a cytochrome P-450 gene
nfidonce 0.571 Longth 1010	C 11 70D1		deoxocathasterone 23-	that is involved in brassingsteroid biosynthesis
indence_0.571_tengtin_1710			monooxy genase [<i>Citrus</i>	most likely in the conversion step of teasterone
			sinonsis]	(TE) to 3-dehydroteasterone (3DT) and/or 6-
			smensis	deovotessterone (6-deovoTE) to 6-deovo-3-
				dehydroteasterone (6-deoxo3DT); or the
				approximate of a state
				conversion of cathasterone $(C + T)$ to TE, and/or
				b-deoxocathasterone (b-deoxoC1) to b-
				deoxol E. Recently, CYP90D1 was shown to
				cataly se the C-23 hydroxy lation of several
				brassinosteroids (the enzyme has a broad
				specificity for 22-hydroxylated substrates).
				Member of the CYP90C CYP450 family.
				Similar to Cytochrome P450 90C1 (ROT3).
Locus_9617_Transcript_4/6_Co	CYP90D1	CYP90D	PREDICTED: 3-epi-6-	CYP90D1/Encodes a cytochrome P-450 gene
nfidenœ_0.571_Length_1919			deoxocathasterone 23-	that is involved in brassinosteroid biosynthesis,
			monooxy genase [Citrus	most likely in the conversion step of teasterone
			sinensis]	(TE) to 3-dehydroteasterone (3DT), and/or 6-
				deoxoteasterone (6-deoxoTE) to 6-deoxo-3-
				dehydroteasterone (6-deoxo3DT); or the
				dehydroteasterone (6-deoxo3DT); or the conversion of cathasterone (CT) to TE, and/or
				dehydroteasterone (6-deoxo3DT); or the conversion of cathasterone (CT) to TE, and/or 6-deoxocathasterone (6-deoxoCT) to 6-
				dehydroteasterone (6-deoxo3DT); or the conversion of cathasterone (CT) to TE, and/or 6-deoxocathasterone (6-deoxoCT) to 6- deoxoTE. Recently, CYP90D1 was shown to
				dehydroteasterone (6-deoxo3DT); or the conversion of cathasterone (CT) to TE, and/or 6-deoxocathasterone (6-deoxoCT) to 6- deoxoTE. Recently, CYP90D1 was shown to cataly se the C-23 hydroxylation of several
				dehydroteasterone (6-deoxo3DT); or the conversion of cathasterone (CT) to TE, and/or 6-deoxocathasterone (6-deoxoCT) to 6- deoxoTE. Recently, CYP90D1 was shown to cataly se the C-23 hydroxylation of several brassinosteroids (the enzy me has a broad
				dehydroteasterone (6-deoxo3DT); or the conversion of cathasterone (CT) to TE, and/or 6-deoxocathasterone (6-deoxoCT) to 6- deoxoTE. Recently, CYP90D1 was shown to cataly se the C-23 hydroxylation of several brassinosteroids (the enzyme has a broad specificity for 22-hydroxylated substrates).
				dehydroteasterone (6-deoxo3DT); or the conversion of cathasterone (CT) to TE, and/or 6-deoxocathasterone (6-deoxoCT) to 6- deoxoTE. Recently, CYP90D1 was shown to cataly se the C-23 hydroxylation of several brassinosteroids (the enzyme has a broad specificity for 22-hydroxylated substrates). Member of the CYP90C CYP450 family.
				dehydroteasterone (6-deoxo3DT); or the conversion of cathasterone (CT) to TE, and/or 6-deoxocathasterone (6-deoxoCT) to 6- deoxoTE. Recently, CYP90D1 was shown to cataly se the C-23 hydroxylation of several brassinosteroids (the enzy me has a broad specificity for 22-hydroxylated substrates). Member of the CYP90C CYP450 family. Similar to Cytochrome P450 90C1 (ROT3).

Locus 9617 Transcript 3/6 Co	CYP90D1	CYP90D	PREDICTED: 3-epi-6-	CYP90D1/Encodes a cytochrome P-450 gene
nfidenœ_0.571_Length_2005			deoxo cathasterone 23- monooxy genase [<i>Citrus</i> <i>sinensis</i>]	that is involved in brassinosteroid biosynthesis, most likely in the conversion step of teasterone (TE) to 3-dehydroteasterone (3DT), and/or 6- deoxoteasterone (6-deoxoTE) to 6-deoxo-3- dehydroteasterone (6-deoxo3DT); or the conversion of cathasterone (CT) to TE, and/or 6-deoxocathasterone (6-deoxoCT) to 6- deoxoTE. Recently, CYP90D1 was shown to cataly se the C-23 hydroxylation of several brassinosteroids (the enzyme has a broad specificity for 22-hydroxylated substrates). Member of the CYP90C CYP450 family. Similar to Cytochrome P450 90C1 (ROT3).
Locus_9617_Transcript_1/6_Co nfidenœ_0.714_Length_2014	CYP90D1	CYP90D	PREDICTED: 3-epi-6- deoxocathasterone 23- monooxy genase [<i>Citrus</i> <i>sinensis</i>]	CYP90D1/Encodes a cytochrome P-450 gene that is involved in brassinosteroid biosynthesis, most likely in the conversion step of teasterone (TE) to 3-dehydroteasterone (3DT), and/or 6- deoxoteasterone (6-deoxoTE) to 6-deoxo-3- dehydroteasterone (6-deoxo3DT); or the conversion of cathasterone (CT) to TE, and/or 6-deoxocathasterone (6-deoxoCT) to 6- deoxoTE. Recently, CYP90D1 was shown to cataly se the C-23 hydroxylation of several brassinosteroids (the enzy me has a broad specificity for 22-hydroxylated substrates). Member of the CYP90C CYP450 family. Similar to Cytochrome P450 90C1 (ROT3).
Locus_2871_Transcript_1/2_Co nfidenœ_0.750_Length_1863	CYP94D2	PREDICTED: cytochrome P450 94A1-like	PREDICTED: cytochrome P450 94A1-like [<i>Citrus</i> <i>sinensis</i>]	CYP94B1/CYP86C1

Locus_2871_Transcript_2/2_Co	CYP94D2	PREDICTED: cytochrome	PREDICTED: cytochrome	CYP94B1/CYP86C1
nfidenœ_0.250_Length_1867		P450 94A1-like	P450 94A1-like [<i>Citrus</i>	
			smensis	
Locus_2424_Transcript_1/1_Co	CYP94D2	PREDICTED: cytochrome	PREDICTED: cytochrome	CYP94B1/CYP86C1
nfidenœ_0.000_Length_1734		P450 94A1-like	P450 94A1-like [Citrus	
			sinensis]	
Locus_3183_Transcript_7/23_C	CYP96A10	-	PREDICTED: peptidyl-	Cyclophilin-like peptidyl-prolyl cis-trans
onfidenœ_0.452_Length_1677			prolyl cis-trans isomerase	isomerase family protein
			CYP37, chloroplastic	
			sinensis	
			Sitensis	
Locus_11035_Transcript_1/1_C	CYP96A10	CYP86B	PREDICTED: alkane	CYP96A9/CYP96A8
onfidence_0.000_Length_1723			hydroxylase MAH1 [Vitis	
			vinifera]	
Locus_6410_Transcript_15/23_	CYP97A3	СҮР97В	cytochrome P450 [Citrus	CYP97A3, LUT5, LUTEIN DEFICIENT
Confidence_0.556_Length_4023			unshiu]	5/carotenoid biosynthetic process, oxidation-
				reduction process, xanthophyll biosynthetic
				process
Locus_6410_Transcript_16/23_	CYP97A3	CYP97B	cytochrome P450 [Citrus	CYP97A3, LUT5, LUTEIN DEFICIENT
Confidence_0.593_Length_4842			unshiu]	5/carotenoid biosynthetic process, oxidation-
				reduction process, xanthophyll biosynthetic
				process
Locus_6410_Transcript_20/23_	CYP97A3	CYP97B	cytochrome P450 [Citrus	CYP97A3, LUT5, LUTEIN DEFICIENT
Confidence_0.593_Length_4735			unshiu]	5/carotenoid biosynthetic process, oxidation-
				reduction process, xanthophyll biosynthetic
				process
Locus_6410_Transcript_21/23_	CYP97A3	CYP97B	cytochrome P450 [Citrus	CYP97A3, LUT5, LUTEIN DEFICIENT
Confidence_0.556_Length_4876			unshiu]	5/carotenoid biosynthetic process, oxidation-
				reduction process, xanthophyll biosynthetic
				process
		1	1	

Locus_19973_Transcript_1/1_C	CYP98A3	PREDICTED: cytochrome	PREDICTED: cytochrome	CYP98A3/encodes coumarate 3-hydroxylase
onfidence_0.000_Length_1735		P450 98A2-like	P450 98A2 [Citrus	(C3H), a P450-dependent monooxy genase.
			sinensis]/p-coumaryl-CoA	coumarin biosynthetic process, flavonoid
			3'-hydroxylase [Populus	biosynthetic process, lignin biosynthetic
			alba x Populus	process, oxidation-reduction process,
			grandidentata	phenylpropanoid biosynthetic process
Locus 22762 Transcript 5/5 C	CVD702A6/A5/A1/A2	CVD70246	PREDICTED: cytochrome	$CVP702 \Delta 6/\Delta 5/\Delta 1/\Delta 2$ involved in
onfidence 0.000 Longth 1642	C 11 /02A0/AJ/A1/A2	C 11 702A0	P450 708 A 2-like	brassingsteroid biosynthetic process
onnuence_0.000_Lengui_1042			[Camelina sativa]	brassinosteroid homeostasis multicellular
				organism development oxidation-reduction
				process, starol metabolic process
				process, sector incrabolic process
Locus_22762_Transcript_2/5_C	CYP702A6/A5/A1/A2	CYP702A6	PREDICTED: cytochrome	CYP702A6/A5/A1/A2 involved in
onfidence 0.571 Length 1702			P450 708A2-like	brassinosteroid biosynthetic process,
0 _			[Camelina sativa]	brassinosteroid homeostasis, multicellular
				organism development, oxidation-reduction
				process, sterol metabolic process
Locus_15761_Transcript_1/1_C	CYP706A4	-	PREDICTED: 8-	CAD6/CAD6
onfidence_0.000_Length_1304			hy droxy geraniol	
			dehy drogenase-like [Citrus	
			sinensis]	
Locus_12215_Transcript_6/8_C	CYP706A4	CYP706A	PREDICTED: geraniol 8-	CYP/06A4/oxidation-reduction
onfidence_0.500_Length_2092			hydroxylase [<i>Ricinus</i>	process, secondary metabolite biosynthetic
			communis]	process
Locus_12215_Transcript_7/8_C	CYP706A4	CYP706A	PREDICTED: geraniol 8-	CYP706A4/oxidation-reduction
onfidence_0.250_Length_2079			hy droxy lase [Ricinus	process, secondary metabolite biosynthetic
			communis]	process
Locus_12215_Transcript_8/8_C	CYP706A4	CYP706A	PREDICTED: geraniol 8-	CYP706A4/oxidation-reduction
onfidence_0.083_Length_1862			hydroxylase [Ricinus	process, secondary metabolite biosynthetic
			communis]	process

Locus_12634_Transcript_1/1_C onfidence_0.000_Length_1613	СҮР707А4	CYP707A/abscisic acid 8'- hydroxylase 3-like precursor	abscisic acid 8'-hydroxylase 3-like precursor [<i>Citrus</i> <i>sinensis</i>]	CYP707A4/ ABA 8'-hydroxylase activity, involved in abscisic acid catabolic process, brassinosteroid biosynthetic process, brassinosteroid homeostasis, multicellular organism development, oxidation-reduction process, sterol metabolic process
Logue 10475 Trongorint 9/11	CVD700D2	autochrome D450 78 A0 lile	DDEDICTED, autochromo	CCT2 DUOSDUODVI CUOLINE
Locus_10475_1fanscript_8/11_	CYP709B2	cytochrome P450 78A9-like	PREDICTED: cytochrome	CVTIDNI VI TDANGEEDAGE2
Confidence_0.438_Length_2605		ISOIORM X3	P430 4C1-like Isolorili AS	CYTIDYLYLTKANSFERASE2
			[Citrus sinensis]	
Locus 16293 Transcript 1/1 C	CYP712A1	PREDICTED: cvtochrome	PREDICTED: 3.9-	CYP712A1/ oxidation-reduction process.
onfidence 0.000 Length 1727	011 / 12/11	P450 93A 1-like	dihydroxypterocarpan 6A-	secondary metabolite biosynthetic process
omidence_0.000_length_1/2/		1 450 75111 like	monooxy genase [<i>Citrus</i>	secondary metabolice biosynthetic process
			sinansis	
			Shiensis	
Locus_10475_Transcript_6/11_	CYP714A1	cytochrome P450 78A9-like	PREDICTED: cytochrome	CCT2, PHOSPHORYLCHOLINE
Confidence_0.438_Length_2115		isoform X1	P450 3A31-like isoform X1	CYTIDYLYLTRANSFERASE2
_			[Citrus sinensis]	
Locus_3941_Transcript_3/6_Co	CYP734A1 old name	PREDICTED: cytochrome	PREDICTED: cytochrome	DUF2
nfidenœ_0.556_Length_1774	CYP72B1	P450 734A1-like	P450 CYP749A22-like	
			[Citrus sinensis]	
Locus_3941_Transcript_3/6_Co	CYP734A1 old name	PREDICTED: cytochrome	PREDICTED: cytochrome	DUF2
nfidenœ_0.556_Length_1774	CYP72B2	P450 734A1-like	P450 CYP749A22-like	
			[Citrus sinensis]	

	ChlorpP	WoLF PSORT	Predotar	TargetP
MkTPS1	Chloroplast	Chloroplast	Plastid	Chloroplast
MkTPS2	none	cytosol	None	none
MkTPS3	Chloroplast	Chloroplast	possibly plastid	Chloroplast
MkTPS4	Chloroplast	Chloroplast	possibly plastid	Chloroplast
MkTPS5	none	cytosol	None	none
MkTPS6	none	cytosol/nucleus	None	none
MkTPS7	Chloroplast	cytosol/chloroplast	None	none

 Table S7: Localization prediction of MkTPSs using different software tools

Table S8: Identity and similarity score matrix of MkTPS1 and MkTPS2 with characterized A) Sabinene synthases and B) α -Farnesene synthases

	Other characterized Sabinene	MIZTDS 1
А	synthases	IVIKITSI
1	RlemTPS2	I- 80%, S-87%
2	SoSS	I- 43%, S-62%
3	HcMTPS7	I- 41%, S-60%
4	PsSS	I- 31%, S-47%
5	TpSS	I- 29%, S-51%
В	Other characterized α-Farnesene synthases (AFS)	MkTPS2
1	VvAFS	I- 54%, S-71%
2	CmAFS	I- 46%, S-5%6
3	CsAFS/BOCS	I- 45%, S-64%
4	VvAFS/BOCS	I- 38%, S-56%
5	RcAFS	I- 35%, S-55%
6	OfTPS4	I- 36%, S-53%
7	AtAFS/BOCS	I- 35%, S-55%
8	MdAFS1/BOCS	I- 35%, S-54%
9	PaAFS	I- 33%, S-53%
10	PtAFS	I- 32%, S-51%
11	PgXeTPS/bocs	I- 32%, S-52%
12	AdAFS/bocs	I- 26%, S-47%

Table S9. List of primers used in the study

Name	Sequence (5'-3')	Use
MKTPS1 F1	GCATATGGCTACTACTAAGCCTGCC	pet32a(+) cloning forward primer
MKTPS1 R1	CGCGGCCGCTGGAATGGGATCAAAAAATAAAG	pet32a(+) cloning reverse primer
MKTPS1 F2	GTCTAGAATGGCTCTCAATCTGCTCTCTTC	GFP cloning forward vector
MKTPS1 R2	CGGATCCGGCATACGATTCTCCCTTATA	GFP cloning reverse primer
MKTPS1 F3	CGCACATTAGTGAACCAT	internal sequencing
MKTPS1 F4	CTTATGGACCGTGGGGGGATATATTCG	internal sequencing
MKTPS1 R3	CCCCCACGGTCCATAAGAAATTCTC	internal sequencing
MKTPS2 F1	GCATATGTCTTTACAAGTTTCAGCCTC	pet32a(+) cloning forward primer
MKTPS2 R1	CGCGGCCGCTATCGGCACAGGATTAATAAGC	pet32a(+) cloning reverse primer
MKTPS2 F2	GTCTAGAATGTCTTTACAAGTTTCAGCCTC	GFP cloning forward vector
MKTPS2 R2	CGGATCCTGCATCAATCAATTCAAGTGCAT	GFP cloning reverse primer
MKTPS2 R3	CGGATCCTATCGGCACACCATTAATAAGC	internal sequencing
MKActin F	GTCAGGGACATGAAGGAAAAGC	Endogenous control for qPCR
MKActin R	TCTTGGAGGTCTCAAGCTCTTGT	Endogenous control for qPCR
MKF-BOX F	TCGCCACTGGGTTTGATGAT	Endogenous control for qPCR
MKF-BOX R	AACAAGGAACGCGGGAACTT	Endogenous control for qPCR
MKTPS1 RT F	TGGAGGATGCGAAGATTGG	TPS1 qPCR primer
MKTPS1 RTR	CATGTCCGGTCCACTTTCGT	TPS1 qPCR primer
MKTPS2 RTF	CCAACTGCTGTGCCAATGC	TPS2 qPCR primer
MKTPS2 RTR	GACATCTGCAACGCGTGTAAG	TPS2 qPCR primer

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Figure S1. a) Length distribution of total assembled transcripts in *M. koenigii*, b) FPKM distribution of assembled transcripts with length \geq 150 bp, c) Organismal distribution of *M. koenigii* transcripts annotated according to NCBI BLASTX top hits.



Figure S2. a) GC % distribution of assembled transcripts with length \geq 150bp, b) E-value distribution of assembled transcripts with length \geq 150bp and FPKM \geq 1, balstx against NCBI nr database and (c) Similarity score distribution of blastx results against NCBI nr database



Figure S3. Gene ontology classification as derived from Uniprot annotation: Gene ontology has 3 main categories including Biological processes, Molecular function, Cellular component



Metabolism
 Genetic information processing
 Cellular processes
 Environmental information processing
 Others

Figure S4. KEGG Orthology (KO) classification and distribution of transcripts identified by KASS into 5 main categories and their sub-categories.

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HDPES	342	343 - NEW FY VERY LAI- ER-LKR-MGSR- FUCLALA	
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D DOGT	214	314METLINFOODUEARIEFIRKOSÖIMGRUGOWRSPWSWWONTLVRLVPNASERRLKO	PLFTGVGRMAAO

Figure S5. Multiple sequence alignment of full length MkPKSs with characterized PKSIII. AmQNS, *Aegle marmelos* quinolone aynthase (AGE44110); CmQNS, *C. microcarpa* quinolone synthase (BAO05328); HpPKS, *H. perforatum* polyketide synthase (ABP98922); MsCHS2, *Medicago sativa* Chalcone synthase 2 (P30074); NcPKS, *Neurospora crassa* type III Pentaketide Synthase (3EUQ); PaPQSH, *P. aeruginosa* 2-heptyl-3-hydroxy-4(1H)-quinolone synthase (Q910Q0); PpPKS1, *Physcomitrella patens* 2'-oxoalkylresorcinol synthase (ABU87504); RpBAS, *R. palmatum* benzalacetone synthase (Q94FV7). The conserved catalytic triad (Cys-164, His-303, and Asn-336) is star marked in red and the active site residues (132, 133, 137, 194, 197, 211, 215, 256, 338, and 375) are star marked in blue (numbering in *M. sativa* CHS)Alignment was built using MAFFT 7.271 and BOXSHADE 3.21.

NKTPS1 MkTPS3 MkTPS4 MKTPS2 MkTPS6 MkTPS5 MkTPS7	1 CALNELSSLPATCNFTRESLPASSNVNGEVPPITRVQYRMAASTTTS - DIK - PADOTIIERSADYRF - TIM 1 MSSFIIPSTFITSVNGFKECPPETTNRAITHRVSGYKPDQCLA-DAG - PDTSAVVRESANYQF - SIT 1 MVTDLEGINHPNFLAYKPRRFEKQRMERGH
MKTPS1 MkTPS3 MkTPS4 MKTPS6 MkTPS5 MkTPS7	69 SFDT QSLDSKYKG SYARQLEK4XEQ 65 DHDT HALSCSFKG SYARQLEK4XEQ 64 NYBLQSLKTHQLD KYERAKSIED 33 CDHF QYTCDSQEVG GDSVKHLHARE 34 CDHF QYTSDFKETD DNIVKHQLAKE 36 CDCFTTLASDCKTND TTNQEEYEAAKQE 106 DAVLRTLACVLALKRWGI GEEQHNKCI QJIKSNFTSVTD KQQTPIGFDIIFPGMIECAQDLNLNLPLRTTDINAHLEREHLELK RNYTAGRKEYLAYVSEGIGKLQDWEMVHKYQRKNG
MKTPS1 MKTPS3 MKTPS4 MKTPS2 MKTPS6 MKTPS5 MKTPS7	96
MKTPS1 MKTP33 MKTP34 MKTP32 MKTP36 MKTP35 MKTP37	176 FILDEGSFES-SENGDECEGMAATTAAYALVEEGSTIPRDEISTTEYAEEWYGKHD-SNKHGDEYZCLUNEAYELVEENKERLEARWFIDYYESGPDM
MKTPS1 MKTPS3 MKTPS4 MKTPS2 MKTPS6 MKTPS5 MKTP37	281 ELAKLDYNIYCAVHOEDLXYYSENNKKTGUGSKUTTSEDRYVENYLLTYCDITEPOROYCERHSAMUNSULTTIDDIYDYYGTLDELELFTDAVDRWCAT-ATEOLYYNKLCFHYFYYP 269 ELAKLDYNIYCATYOBELNDISRWWDKGUGEKUS ARSELYTSFCGLCHYPHPORAYSRYLTITVALITYIDDIYDYYGTLDELELFTDAVBRWDINPAIKOLPOYNKICFFAYNP 269 ELAKLDYNRYCSIYOBEIRIITRWWRDIDDARCHFARDENE CFIMNYCHYPHPORAYSRYLTITVALITYIDDIYDYYGTLDELELFTDAVBRWDINPAIKOLPOYNKICFFAYNP 239 TFALDYNRYCSIYOBEIRIITRWWRSIDDIARCHFARDENE CFIMNYCHYPHPORAYSRYLTITVALITYIDDIYDYYGTLDELELFTDAVBRWDIN-AYNDFPIMKLCFHL 239 TFALDYNRYCSIYOBEIRIITRWWRSIDFFIRDIARCHFARDENE CFIMNYCHYPHPORALARFIJAKVISHTSYIDDIYDYYGTLDELELFTDAVBRWDIN-AYNDFPIMKLCFHL 243 NFANLDYNRYCKHORBIRDIYRWWSFDYNRUFTIDDIYDYYGTLBELELFTTAIERWDIS-AIDCHFYRKCYKALLDA 242 KFAKLDYNYCTYHOKSISAHIRWWRDLDFTITIPJARDENYEIYFWIYATYFFFKYTLARKIMTSIYMASVIDDIYDAYGTIELELFTTAIERWDIS-AIDRLPHYNKCYKALLDA 242 KFAKLDYNYCTYHOKSISAHIRWWRDLDFTITIPJARDENYEIYFWIYATYFFFKYTLARKIMTSIYMASVIDDIFDAYGIPSELKLPAEAVCRWDIG-ANDILPEYMKLLYKALDT 458 KLAYDDYNICCSMEFEDRHBISRWYSKRJ-DCUIFARORIYCYYFSYAATEFSELSDARNANAYTTIYDFYYDDIFYDIGGSDEELLNLIELEOWNYCGFINCCSEOYEIIFSAIRK
MKTPS1 MKTPS3 MKTPS4 MKTPS2 MKTP36 MKTP35 MKTP37	400 VNEMAFE AFROQUEVGMIIPYFERT AFFERT
MKTPS1 MKTPS3 MKTPS2 MKTPS6 MKTPS5 NKTPS7	519 OCTIMHETCISEDEAREHIRNLAESUIKLESARFGNPHYESDYFIGIAMEMALVAOCIOFOCHG-DEENTEREVTZFFDFIP

Figure S6. Multiple sequence alignment of full length MkTPSs. The conserved catalytic motifs are marked in red. Alignment was built using MAFFT 7.271 and BOXSHADE 3.21.

		▼
MKTPS1 RlemTPS2 SoSS HcMTPS7 TPSS PsiSS	1 1 1 1 1 1 1	MALNLESSLPATCNFTELSLPLSSNUNGLVPPITEVQYRMAASTTISTIKE-AEQTIIRESADYRPTIWSPDYLOSL-DEKYRGESYARQLEKLK MALNLESSIPAACNFTELSLPLSSKUNGEVPPITEVQYHVAASTT-PIKE-WQTIIRESADYRPTIWSPDYIOSL-DEKYRGESYARQSEKLE MSSIBINIAMPLNSHNPERRPSKAWSTSCTAPAARWRASSSLQQEKP-HQIRESGYQPSLWDFNYQSL-NTPYREGENERROAE MSSIBINIAMPLNSHNPERRPSKAWSTSCTAPAARWRASSSLQQEKP-HQIRESGYQPSLWDFNYQSL-NTPYREGENERROAE MSSIBINIAMPLNSHNPERRFSKAWSTSCTAPAARWR
		R (R) X8W
MKTPS1 RlemTPS2 SoSS HcMTPS7 TpSS PsiSS	94 92 88 99 92 100	EQVEANLOODYTANDLDPLHOLELIDNLHERLGVSYHFEDEIERTLDGIYNENTNESLYAAALEFRILROHGYDIPVEETFSEFIDDE EQVSAMLOODDEVUDLDPLHOLELIDNLHERLGVSYHFEDEIERTLDRIHMENTNESLYAAALEFRILROHGYNTPVEETFSEFIDDE MOVEMLLEVE
MKTPS1 RlemTPS2 SoSS HcMTPS7 TpSS PsiSS	182 180 173 178 181 204	SEKSSEHGDCCRGNLALYEAAYLLVEEESTIPRDSISFTTYLKEWVGKHDSNIHGDEYLCTLVNHALELPLHWRMRRLEARWFIDVYESGPDMNPI IFKLSEHSDDCKGNLALYEAAYLLVEESSIFRDATSFTTAYLKEWVIKHDNIKHDDEHLCTLVNHALELPLHWRMPRLEARWFIDVYENGPDMSPI SDPNANLAQDTKGNLQLYEASELLREGED-TLELARRFSTRSLREKPDEGGDEIDEDLESWIRHSLDLPLHWRVQGLEARWFIDAYARRPDMNPI GQPEDRLQSQAEGLLSLYEASYLEKDGEE-LLHEAREFTTKHLKNLLEEEGSLAPGLIREQVAYALELPLNRRPORLHTKWFIGAWQRDPTMDPA QELCPSAQSEEEKIGSILNLYRASLIAFPEEN-IMDEAKAFATTYLNQVLQNNNISSELSKEIKYNLEYGWETNLPRVEARNYMDIYGENRSWTEMGGNMC RIAC-SANHTERQISSILNLYRASLIAFPEEK-VMEBAEIFSATYLKEALQTIPVSSLSQEMQVVLDYRWESNLPRLETRTYDDILGETTINQMQDVEIC
MKTPS1 RlemTPS2 SoSS HcMTPS7 TPSS PsiSS	279 277 267 272 281 302	-LLELAKLDFNIVQAVHQEDLKYVSRWWKKTGLGEKLIFSRDRVVENFLWTVGDIFEP OFGYCRRMSAMVNSLLTIDDEYDVYGTLDELELFTDAVDRWDATA -LLELAKMDFNIVQAVHQENLKYASRWWKKTGLGENLNFVRDRIVENFLWTVGEKFEP OFGYFRRMSAMVNSLLTIDDEYDVYGTLDELELFTDAVDRWDATA -IFFLAKLNFNIVQAVHQENLKYASRWWKKTGLGENLNFVRDRIVENFLWTVGEKFEP OFGYFRRMSAMVNSLLTIDDEYDVYGTLDELELFTDAVERWDATA -IFFLAKLNFNIVQAVHQENLKYASRWWKSGLAEKLPFVRDRIVENFLWIVENFLWIVGFFANAAVIITFITIDDEYDVYGTLDELELFTDAVERWDATA -IFFLAKLNFNIVQAVHQENLKUSSCUAEKLPFVRDRIVENFLWIVENFLWAVVFAFEP DSWAFREMDTKINCFITMIDDYDVYGTLDELELFTDIMERWDVNA -LLLLAKLDFNARONYKRELNEVSRWWTDLGUPFFRDRITENYLWAVVFAFEP DSWAFREMDTKINCFITMIDDYDVYGTLDELELFTDIMERWDVNA -ILNLAKLDFNIMOSVERLELESILKWWKDSNLDK -VDFARHRHVEYFALACAYCIDA -KYYAYRRDFAKLCALATIVDDIYDTYGTHEIKLFNEAVKMWDSSI KLLELAKLEFNIFHSIQONELKCISRWWKESGSPE - LTFIRHRHIEFYTLASGIDMEF -KHSAFRLSFVKMCHLITVLDDIYDTFGTMDELRLFTSAVKRWDRSE
MKTPS1 RlemTPS2 SoSS HcMTPS7 TPSS PsiSS	382 380 370 375 383 405	TEOLPYYNKEGFHYLYNFVNEMAPDALEDOEVGMI I PYPEKTWADLCKAYPABAKWYNSGYI PTFOEYMENAWI SI TAPLMU HAYAFTANPITKBALEFLOD SE VEOLPHYNEUC FHALENSINEMTFDALEDOGVDI VISYLTKAWADHCKAYLVBAKWYNSGYI PSLOEYMENAWI SI GSTVI LVHAYTFTANPITKEGLEFVKDYS ISOLPYYMOVCYLALYNPVSBERAYDHLKDOHFN - SI PYLOESWVSLVEGYLXBAYWYN GYKPSLEEYLNNAKI SI SAPTII SOLPYTLANSIDETAI ESLYOY IDKLPEYNKICFLAVFNTVNDAGYEVMEDKGVN - II PYLERAWABLCKMYMEBARWYHTGYNPTLDEYLDGAWI SI SGALHISTAY - CMGKDLTKEDLDKFSTY PNSLPENIKI AYKAFHMAVNESABAAKKTOGEL - II PYLERAWABLCKMYMEBARWYHTGYNPTLDEYLDGAWI SI SGALHISTAY - CMGKDLTKEDLDKFSTY IDKLPEYNKICFLAVFNTVNDAGYEVMEDKGVN - II PYLERAWABLCKMYMEBARWYHTGYNPTLDEYLDGAWI SI SGALHISTAY - CMGKDLTKEDLDKFSTYF PNSLPENIKI AYKAFHMAVNESABAAKKTOGEL - II PYLERAWABLCKMYMEBARWYHTGYNPTLDEYLDGAWI SI SGALHISTAY - CMGKDLTKEDLDKFSTYF IDKLPEYNKGYY I TLYFTVNEMARBARKKTOGEL - II PYLERAWABLCKMYMEBARWYHTGYNPTGYNFSLEYLENGAPSSGYRVTMI OPTLTUDALLPDN ILLEMDYPS
MKTPS1 RlemTPS2 SoSS HcMTPS7 TPSS PsiSS	487 485 474 478 487 509	* NIIRFSSMIURLADDLGTSSDELKRGDVPKSIQCYMEET - GISEDEAREHIRNLIAESMIKLNSARPGNPHYLSDVFIGIAMMARVAQCIYQFGDGH GDEEN NIIRWSSVILPTADDLGTSBDELKRGDVPKSIQCYMEA - GVSEGEAREHINDLIAQTWMKMNRDRPGNPHFVSDVFVGIAMNLARMSQCMQCGDGHGCGAQEI NILYLSGTILRLADDLGTSQHELERGDVPKAIQCYMNDT - NASEREAVEHVIFLIREAMHEMNTVTTASDCPFTDDLVAAANLARMSQCMQPGDGHGCGAQEI SIVOPSCHLRLHDDFGTSTEELARGDVQKAVQCCMHER - KVPEAVAREHIKQVMEAKMEVLNGMEVASS - PEYFQNVAINLPBAAQFFYGKGDGYA - NADGE FFNELLCLSLRLKGDTRTFKAEANRGELVSGTSCYIKDHPGSSEEEALDYLKDLLQKKEVELGPDQEYLKP - NNVPAISKDHAYNTARSYQLLYKERDGFT - NSNKI KPNELACSILRLRGDTRCYQADRDRGEKASCISCYMKDNPGSTEEDALNHINGMIEDTINQLNWELLRPDNNVPISSKKHSPDISRAPHHLYRYRDGYT - VSSNE
MKTPS1 RlemTPS2 SoSS HcMTPS7 TPSS PsiSS	589 589 577 580 590 613	TEDRVYTEFDPIE- TRARVESEFIDFIA- IHQQMGGLEFQPYV- DQKQVMSLEIEFVQ- IEDEVTQTEBFIFL TENEVEFDEFM

Fig. S7. Amino acid alignment of MkTPS1 with other characterized sabinene synthases. Abbreviations with accession numbers: RlemTPS2, *Citrus jambhiri* (Rough lemon) sabinene synthase (BAF73933); HcMTPS7, *Hedychium coronarium* chloroplast monoterpene synthase (AHJ57305); PsSS, *Picea sitchensis* (+)-sabinene synthase (ADU85930);SoSS, *Salvia officinalis* sabinene synthase (O81193); TpSS, *Thuja plicata* sabinene synthase (AGO02736). The substrate binding, Asp-rich domain "DDXXD", Argrich "RXR" and "R(R)X8W" motif, as well as a NSE/DTE motif are underlined in red. Cleavage site is marked with arrowhead.

MKTPS2	1	WSLQVSASPAKDIQNA-GKDYTRRSANFHESINGDHELQYTCDSQEVGGDSVKHLELKKEIBRMLKAVNS	PHITE
VVAFS	1	MSVSEPUTPIPTTQRVHHQEVAESTANNPDNIKGEREITYAPDDTVTQECKAQKIKEKEEVRKELKASAHK	SPELEK
CSAFS	1	MSSNVSAIPNSFELINNSAOFQASVAGDYEFSYHSFPPEKGNKVMBKQTEELKEEIMELVSTTK	EPEKER
MdAFS	1	MEFRUH QADNEQKIFQNQMKPEPE-ASYLINQRRSANKKPNIKKNDEFDQSFISKYDGDEYRKLSEKTIEEVKIYISAETM	LVAKE
PtAFS	1	MEYKQQVQVVQNSFQCQNNSEDI-DRRQERRSANYKPNIWKYDFLQ <mark>SLS</mark> SKYDBEQYRRYTEKLREEVKSIFVEAV	LEAKEK
PaAFS	1	IDLAVEIAMDIAUDDVERRVGDUHSNLWDDDEICSLSTPYGASSYRERAERUVGEVREMFTSISIEDG-ELTS	LEOREW
PtAFS1	1	MSSTANDDAERRVGDHPNLWDDALIOSLSTPYGASPYRDVAEKLIGEIXEMPASISIEDGDDEICY	FORW
		D/D/YOW/	1000
		DIDAGA	1000
MKTPS2	76	MEAIORICVSYHTESEIDEIICKMHE-AYODCDLCDNENDELYYNSIOFRMIRONGYRISADVFYKFKDSDCNFKASLAKDVRCMISLYEN	HERVHE
VVAFS	79	IDSIQLICLTYHFEREIBEN KOMYG-TYSLVDDNEDLTNASIRFRILROEGYGWPSDVESKFKDKECNEKESLIGDLPCMLALYEN	HMVHC
CeAFS	73	ILLIORLEVCYHFENEINNILOOLHH-ITITSEKNGDDNPYNMTLCFRLLROOGYNVSSEPEDRFRCKWESSYDNNVEELSYEAS	QURMQC
MdAFS	89	IDSYRKICLANLFEREIXENDSIAAIBSDNLGTRDDLYGTALHERILROHGYKVSQDIEGREMDBRGTLENHHFAHLRCMUELFEAS	NGFEG
PtAFS	83	VESUIKLELESYBEELKQSEDIIAA-SIKNKNLKVBENLYVTALREKLLELEGYEVSQGVENGEPDETSDKSKCTEVRELTELFEAS	HAYEG
PaAFS	80	WDNYERLGISREFENEIKAAIDYWYS-YWSDKGIVRGRDSAVPDLNSIALGPRTLRLEGYTVSSDVEKVFODRKCEFACSAIPTEGDIKCVENLLRAS	YIAFPC
PtAFS1	74	EDNYERLEISRHFENELKAAMEDVYSRHWSDKGIACGRHSVVADLNSTALAFRTLRLHGYSVCSDVEKIFODOKCEFACSADOTEGEIKCIPNLLRAS	LIAFPG
MKTPS2	174	NEWDEALATTSHEESI - AKOV-SSP- MAROVKHAJIOTIRRGIDENBARHYIPINOEES SHNEAMTPAATDENKLOKTHEEEGDI	SRWWKE
VVAFS	173	dideealattahiosv - atdp-nnpiskoviralklsihngvtsvgarhyisiogedgshnesiikkaktdenllosihrkeisei	TRWWK-
CEAFS	166	BANDEAPCHARACHEAI VODP - TTDPMVAABIRQAKKWMYKNLPREKARHHIGLUSEKP WRNESIENPAKMDINKLONEHETEIAYI	SKWMDD
MdAFS	184	d e lo de a kas la la la degli cyp - den - - le sa du ve su e le se revowfdyk wol na lek di cevna t u e da ku en vo a o le kni rea	SRWWAN
PtAFS	177	ATTODAKANSERIETGI NCSAIESO TAKHEVHVIELESHWRVMWFDVKWHENAEENDK OTNRHEIAMANVNATLEKDEGDV	SRWWRN
PaAFS	184	KVMEKLQTTAATYLKEA - LQKIQVSS - ISRBIEYVLEYGULTNFPREARNYIDVFGEBICPYFKKPCIMVDKLIBLAKTEFNLFHSIONTELKHU	SRWWKD
PtAFS1	179	REFORMET ANTY KEA - LPKIQGER - ISOBIEYVIEYGWLTDLPRIETENYIEVLAEEITPYFKK PCMAVEKIIKIAKIEFNLFHSIOFTEIKHI	SRWWKD
0.11002-01002-01	1000		
MKTPS2	266	DFAHKLPFIRDRIVECYFWILGVYFBPQYALARRILAKVISMTSVIDDIYDVYGQIBBLELFTSAIERWDVSAIDQLPBYMRLCYGALLDVYNBAEKD	LAS
VVAFS	264	RLCHBATEARDRIVEIYFSAEGVCFEPQYBLSLRPLTKVAIMITMVDDIYDAYGTIBBLTULTEAIERWDASSIDQLPDYMKCPYRALLDLYBEMEQE	MAK
CBAFS	260	GFAEKLSFARNRIVEGYFFARGIFFEPOLLTARLIMTKVIAIGSMLDDIYDYGTFEELKLLTLALERWDXSETKOLPNYMKMYYEALLDVFEEIEOE	MSQKET
MdAFS	279	GIADNLKFARDRIVECFACAVGVAFEPEHSSFRICLTKVINLVIIIDDVYDIYGSEEELKHFTNAVDRWDSRBTEOLPECMKMCFQVLYNTTCEIARE	IEBE
PEAFS	270	<u>GIIENLSETRDREVESELCTVGEVFEPKYSSERKWLTKVIIMILIIDDWYDWYGSLHELQOFTKAVSRWDTGBVQELPECMKICEQTLYDITNBMALE</u>	MQRB
PaAFS	285	<u>iges - oltetrhrhvefytlasciaiepkhsafrigfakvcylgividdiydtegkmkelelftaaikrwdpstteclpeymkgvymapyncvnelalo</u>	AEK
PtAFS1	280	ioea - onte trebeve pyt lascia merkebasheg paxecy egived diver mesheve a faikend tstrech peven gvymapyd cvnemar	AEK
		RXB DDXXD	
MKTPS2	368	GKSYRLHYAKEAMKNVVKNYFFEAKWCHONHVPTVEEYMTVALVTSCYPTUSATSFVGMGE - IVWKESFEWLFSNPRFIRTSBIISRLMDDIVSHKFE	OSCOHV
VVAFS	300	GRLYRVHYANELMERGIGSIFVUARWSNOGYIPAPDEYMSNOVVSGCCSIDIATSEVGMGD-IVWRESFOWVLSRPTMIGASOTICRIMDDMASHEF	OKUVHV
CBAFS	365	TTTPICTHRMMEATKELGRVPLVGATWCKEGYTPKVERVPDIALIEPCHKLMMVTALLGMGSHMAHOOIVGWITSMPNILKASAVICKEMNDIVSHKP	OERCHV
MdAFS	384	GWNQVLPQLTEVWADFCKALLVLAEWYNKSHIPALEEYFRACCISSSVSVDLVHSYFSITH - EGYKEMADFLRKNEDLLYNISLIVKLNNDLGTSAA	OFFCODS
PEAPS	3/3	DGSOALPHLIKVMADFCKAMFMEAKWFNEGTTPBLOEVIS NAWVESSGTVISVHEMFEVMTELENGLISNFLEKNODLLYNISLIIKLCNDLGSVA	GERCIDA
PAAFS	380	CORDMUNIAR AND BALF DAFIE BAAKNISS OF UPP PERFILENCE VSFCIRAAT LOPILITEDI-PEPLAH LOOIDFPSRINDLASSILERUK OD LOGICA	RSCORE
PCAFSI	38T	OGWDINDINKAINSKEIDIESSENDIA	RSEREEQ
METDES	472	COUPERATION - CATERRED TO PROVIDE A TERMETER - TRENDITER TO TREAD A DUTRE A DUTRE A V - UT ROUMATER A VIEW A DUTRE	100
U. APG	470	CONFIGURATION CONFIGURATION TO PROVIDE TRANSPORTATION TO A DESTRUCT A DESTRUCT A DESTRUCT	
Cabpo	470		
MANDO	405	THE STREAM TRADE IS NOT AN A STREAM AND A TRADE AND A STREAM AND	
DEARC	470	I GUNAY DEV. NVGDINI DNATINI DNATNA - NDAGI I NVYF DOGFANAA IMAA MAAGHTADGDOGU GUDAU AFATALISHIF OMAYA.	CP
Dalles	490	i de la companya de la	
DEARCI	405	nen generale gelen in den ander over the "dink burge" or veroek and did af i rent i rend taket bit aver i veroek and average ave	
PCAPSI	485	TEFESTITE WAR STATES AND AND AND SUCCESSION AND AND AND AND AND AND AND AND AND AN	

Fig. S8. Sequence relatedness of MkTPS2 with other characterized α -farnesene synthases. CsAFS, Cucumis sativus E,E-alphafarnesene synthase (AAU05951); MdAFS, *Malus domestica* (*E*,*E*)- α -farnesene synthase (001280822); PtAFS, *Populus trichocarpa* α farnesene synthase (AEI52902); PaAFS, *Picea abies* (*E*,*E*)- α -farnesene synthase (AAS47697); PtAFS1, *Pinus taeda* α -farnesene synthase (AAO61226)VvAFS1, *Vitis vinifera* α -farnesene synthase (ADR74198); VvAFS2, *Vitis vinifera* (*E*,*E*) α -farnesene synthase (ADR7419). Asp-rich domain "DDXXD", Arg-rich "RXR" and "R(R)X8W" motif are underlined in red.



Fig. S9. Expression profiling of reference genes in *M. koenigii* - Mk Actin and Mk F-BOX were used to check the stability in different tissues of M. *koenigii*



Fig. S10. GC-MS chromatogram of farnesene standard mixture and the respective mass spectra of individual geometric isomers.

(Z)- β -Farnesene



(E)- β -Farnesene



Fig. S10. Cont...

(Z,Z)- α -Farnesene



α -Farnesene



Fig. S10. Cont...

α-Farnesene



(E,E)- α -Farnesene



Fig. S10. Cont...

(E)- γ -Bisobolene



Fig. S10. Cont...



Fig. S11. Headspace volatile analysis of *M. koenigii* leaves by GC-MS. Peaks: 1, α-pinene; 2, sabinene; 3, β-myrcene; 4, α-terpinene;
5, limonene; 6, β-phellandrene; and 7, γ-terpinene.

Accession numbers used in Figure 3

AaOKS1, Aloe arborescens octaketide synthase 1 (Q3L7F5); AaPCS, A. arborescens pentaketide chromone synthase (Q58VP7); AbDpgA, Amycolatopsis balhimycina dihydroxyphenylacetic acid synthase (CAC48378); AhSTS, Arachis hypogaea stilbene synthase (BAA78617); AmQNS, Aegle marmelos quinolone aynthase (AGE44110); AtCHS, Arabidopsis thaliana chalcone synthase (AAA32771); BsNCHS, Bacillus subtilis naringenin-chalcone synthase (AAA96613); CsCHS, Cannabis sativa chalcone synthase (AAL92879); CmACS, Citrus microcarpa acridone synthase (BAO05327); CmQNS, C. microcarpa quinolone synthase (BAO05328); CsPKSIIIB, C. sinensis polyketide synthase type III B (XP_006487398); CICHS, Curcuma longa chalcone synthase (BAQ35543); CIDCS, C. longa diketide CoA synthase (C0SVZ5); CICURS1, C. longa curcumin synthase 1 (C0SVZ6); EcFABH, Escherichia coli K-12 beta-ketoacyl-ACP synthase III (P0A6R0); Gh2PS, Gerbera hybrida 2pyrone synthase (P48391); GhCHS1, G. hybrida naringenin-chalcone synthase 1 (P48390); GmBPS, Garcinia mangostana benzophenone synthase (AEI27291); HaBPS, Hypericum and rosaemum benzophenone synthase (Q8SAS8); HpOKS, H. perforatum octaketide synthase (ACF37207); HpPKS, H. perforatum polyketide synthase (ABP98922); HmSTS, Hydrangea macrophylla stilbene carboxylate synthase (AAN76182); HsPKS1, Huperzia serrata chalcone synthase-like polyketide synthase 1 (ABI94386); MpSTCS, Marchantia polymorpha stilbene carboxylate synthase 2 (AAW30010); MsCHS2, Medicago sativa Chalcone synthase 2 (P30074); MtPKS1, Mycobacterium tuberculosis phenolpthiocerol synthesis type-I polyketide synthase (CEZ67477); NcPKS, Neurospora crassa type III Pentaketide Synthase (3EUQ); OsCHS1, Oryza sativa Chalcone synthase 1 (A2ZEX7); OsCUS, O. sativa Curcuminoid synthase (Q8LIL0); PaPQSD, Pseudomonas aeruginosa 2-heptyl-4(1H)-quinolone synthase (P20582); PaPQSH, P. aeruginosa 2-heptyl-3-hydroxy-4(1H)-quinolone synthase (Q910Q0); PBBS, Phalaenopsis sp. bibenzyl synthase (CAA56276); PiPKS, Plumbago indica polyketide synthase (BAF44539); PnVPS, Psilotum nudum valerophenone synthase (Q9SLX9); PpPKS1, Physcomitrella patens 2'-oxoalkylresorcinol synthase (ABU87504); PsCHS, Pisum sativum chalcone synthase

(BAA01512); PsCHS, *Pinus strobus* chalcone synthase (CAA06077); PsSBS, *P. strobus* stilbene synthase (CAA87013); RgACS2, *Ruta graveolens* acridone synthase 2 (Q9FSC0); RgCHS1, *R. graveolens* chalcone synthase 1 (Q9FSB9); RpALS, *Rheum palmatum* aloesone synthase (AAS87170); RpBAS, *R. palmatum* benzalacetone synthase (Q94FV7); SaBIS, *Sorbus aucuparia* biphenyl synthase (ABB89212); SbARS1, *Sorghum bicolor* alkylresorcinol synthase 1 (XM_002449699); SbARS2, *S. bicolor* alkylresorcinol synthase 2 (XM_002441794); ScTHNS, *Streptomyces coelicolor* 1,3,6,8-tetrahydroxynaphthalene synthase (Q9FCA7); SgTHNS, *Streptomyces griseus* 1,3,6,8-tetrahydroxynaphthalene synthase 1 (P28343); ZmCHS2, *Zea mays* chalcone synthase 2 (P24825).

Accession numbers used in Figure 4

AbLIMS, *Abies grandis* (-)-4S-limonene synthase (AAB70907); AaLIS, *Actinidia arguta* linalool synthase (ADD81294); AdGDS, *Actinidia deliciosa* germacrene-D synthase (AAX16121); *Antirrhinum majus* nerolidol/linalool synthase 1 (ABR24417); AtTPS02, *Arabidopsis thaliana* Terpene synthase 02 (POCJ43); AtTPS10, *A. thaliana* Terpene synthase 10 (Q9ZUH4); AmNES/LIS-1,; CsαPINS, *Cannabis sativa* (+)-α-pinene synthase (ABI21838); CJGES, *Citrus jambhiri* geraniol synthase (BAM29049); RlemTPS2, *C. jambhiri* sabinene synthase (BAF73933); RlemTPS4, C. *jambhiri* δ-elemene synthase (BAP74389); CjβPINS, *C. jambhiri* β- pinene synthase (BAF73933); CjuβFS, *C. junos* (*E*)-β-farnesene synthase (Q94JS8); CILIMS2, *C. limon* limonene synthase 2 (AAM53946); ClβPINS, *C. limon* (-)-β-pinene synthase (AAM53945); ClγTPNS, *C. limon* γ-terpinene synthase (Q8L5K4); CsiVLS, *C. sinensis* valencene synthase (NP_001275785); CudLIMS, *C. unshiu* limonene synthase (BAP75559); CuβOCS, *C. unshiu* (*E*)-β-ccimene synthase (BAD27257); CuLIS, *C. unshiu* linalool synthase (BAP75559); CuβOCS, *C. unshiu* (*E*)-β-ccimene synthase (BAD91046); CuγTPNS, *C. unshiu* γ-terpinene synthase (BAD27257); CbLIS2, *Clarkia breweri* linalool synthase 2 (AAD19840); CcLIS, *C. concinna* linalool synthase (AAD19839); Cmα-FS1, *Cucumis melo* α-farnesene synthase (B2KSJ6); CsαFS, *C. sativus* (E,E)-α-farnesene synthase (AAU05951); CmCPS, *Cucurbita maxima* copalyl diphosphate sythase (AAD04292); GaδCDS, *Gossypium arboreum* (+)-δ-cadinene synthase (AAB41259); HcMTPS7,

Hedychium coronarium chloroplast monoterpene synthase (AHJ57305); MdαFS, *Malus domestica* (*E*,*E*)-α-farnesene synthase (Q84LB2); MpβFS, *Mentha piperita* β-farnesene synthase (O48935); ObGES, *Ocimum basilicum* geraniol synthase (Q6USK1); OsKSL10, *Oryza sativa Ent*sandaracopimaradiene synthase (Q2QQJ5); OfTPS4, *Osmanthus fragrans* α-farnesene synthase (AMB57288); Ppent-KS, *Physcomitrella patens* (-)-*ent*-kaurene synthase (BAF61135); PaαBS, *Picea abies E-α*-bisabolene synthase (AAS47689); PaLIS, *P. abies* (-)-linalool synthase (AAS47693); PaαFS, *P. abies E,E-α*-farnesene synthase (AAS47697); PsLIMS, *P. sitchensis* (-)-limonene synthase (ABA86248); PsPINS, *P. sitchensis* pinene synthase (AAP72020); PsSS, *P. sitchensis* (+)-sabinene synthase (ADU85930); *Pinus sylvestris E-*β-farnesene synthase (ADH29869); PtaFS Psβ-FS, *Pinus taeda* α-farnesene synthase (AAO61226); Ptα-FS, *P. taeda* α-farnesene synthase (Q84KL5); PaIPS, *Populus alba* isoprene synthase (Q50L36); PtIPS, *P. tremuloides* isoprene synthase (Q7XAS7); Rcα-FS, *Ricinus communis* α-farnesene synthase (B9RXW0); SoSS, *Salvia officinalis* (+)-sabinene synthase (O81193); SrCPS, *Stevia rebaudiana* copalyl pyrophosphate synthase (AAB87091); TpSS, *Thuja plicata* sabinene synthase (AGO02736); Vvα-FS1, *Vitis vinifera* α-farnesene synthase (ADR74198); VvαFS2, *V. vinifera* α-farnesene/β-ocimene synthase (ADR74207); VvVLS, *V. vinifera* valencene synthase (Q6Q3H2).