Supplementary Information

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

Seema Meena[1#], Sarma Rajeev Kumar[1#], Varun Dwivedi[1#], Anup Kumar Singh[1], Chandan S. Chanotiya[2], Md. Qussen Akhtar[3], Krishna Kumar[1], Ajit Kumar Shasany[3], and Dinesh A. Nagegowda[1*]

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	Leaves	antimicrobial	2
6,7-hydroxy-3-methylcarbazole			
3e(1e-hydroxy ethyl)-7-hydroxy-1-isobenzofuranone	Stem bark	antibacterial, antidibetic	3, 4
3,3'-[oxybis(methylene)]bis99-methoxy-9H-carbazole)			
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	antibacterial, 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
Murrafoline-I	-	cytotoxicity against HL-60 cells	19
Murrayacine	Stem bark	-	25
Murrayacinine	Leaves	antioxidant, antimicrobial, antidiabetic	8

Murrayanine/1-Methoxy-9H-carbazole-3-carbaldehyde	Leaf & Stem bark	antimicrobial, neuroprotective, antiinflammatory	6, 37, 38
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'-dimethyl-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.

Abbriviation: TNAT-Total number of annotated transcripts.

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**

Table S4. Trancripts for prenyltransferase gene family with unknown function identified in *M. koenigii* 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_Confidence_0.188_Length_747	160	4.60446	hypothetical protein CICLE_v10020293mg	*Citrus clementina*	protein prenylation; protein prenyltransferase activity
Locus_10147_Transcript_11/11_Confidence_0.062_Length_747	158	4.54691	hypothetical protein CICLE_v10020293mg	*Citrus clementina*	protein prenylation; protein prenyltransferase activity
Locus_10147_Transcript_7/11_Confidence_0.438_Length_1027	255	5.33764	hypothetical protein CICLE_v10020293mg	*Citrus clementina*	protein prenylation; protein prenyltransferase activity
Locus_10147_Transcript_8/11_Confidence_0.250_Length_1218	250	4.41237	hypothetical protein CICLE_v10020293mg	*Citrus clementina*	protein prenylation; protein prenyltransferase activity
Locus_10311_Transcript_1/5_Confidence_0.667_Length_1420	1801	27.265	hypothetical protein CICLE_v10011942mg	*Citrus clementina*	integral component of membrane; prenyltransferase activity
Locus_10311_Transcript_2/5_Confidence_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_0.484_Length_1409	2635	40.2021	prenyltransferase	*Populus trichocarpa*	NA
Locus_7997_Transcript_1/5_Confidence_0.833_Length_689	513	16.0058	prenyltransferase	*Populus trichocarpa*	NA
Locus_7997_Transcript_2/5_Confidence_0.667_Length_651	485	16.0155	prenyltransferase	*Populus trichocarpa*	NA
Locus_7997_Transcript_3/5_Confidence_0.500_Length_617	433	15.0863	prenyltransferase	*Populus trichocarpa*	NA
Locus_7997_Transcript_4/5_Confidence_0.667_Length_1435	493	7.38541	prenyltransferase	*Populus trichocarpa*	NA
Locus_7997_Transcript_5/5_Confidence_0.167_Length_1577	543	7.40197	prenyltransferase	*Populus trichocarpa*	NA

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

Transcript ID	**Read count**	**FPKM**	**Gene name**	**Organism**	**GO term**
Locus_14513_Transcript_1/1_Confidence_0.000_Length_1760	281	3.4322	Methyltransferase	*Theobroma cacao*	NA
Locus_30864_Transcript_1/1_Confidence_0.000_Length_272	13	1.02743	Methyltransferase	*Ajellomyces dermatitidis* ATCC 18188	NA
Locus_22721_Transcript_1/1_Confidence_0.000_Length_836	57	1.46571	Methyltransferase family protein, putative	*Theobroma cacao*	NA
Locus_22721_Transcript_1/1_Confidence_0.000_Length_836	57	1.46571	Methyltransferase family protein, putative	*Theobroma cacao*	NA
Locus_4840_Transcript_10/28_Confidence_0.343_Length_2009	670	7.16926	Methyltransferase family protein isoform 2	*Theobroma cacao*	NA
Locus_4840_Transcript_11/28_Confidence_0.314_Length_1923	639	7.14333	Methyltransferase family protein isoform 2	*Theobroma cacao*	NA
Locus_4840_Transcript_13/28_Confidence_0.171_Length_569	370	13.9788	Methyltransferase family protein isoform 2	*Theobroma cacao*	NA
Locus_4840_Transcript_14/28_Confidence_0.171_Length_572	367	13.7927	Methyltransferase family protein isoform 2	*Theobroma cacao*	NA
Locus_4840_Transcript_17/28_Confidence_0.343_Length_2125	633	6.4036	Methyltransferase family protein isoform 2	*Theobroma cacao*	NA
Locus_4840_Transcript_18/28_Confidence_0.114_Length_685	334	10.4818	Methyltransferase family protein isoform 2	*Theobroma cacao*	NA
Locus_4840_Transcript_24/28_Confidence_0.314_Length_1107	451	8.75807	Methyltransferase family protein isoform 2	*Theobroma cacao*	NA
Locus_4840_Transcript_25/28_Confidence_0.086_Length_1392	453	6.99582	Methyltransferase family protein isoform 2	*Theobroma cacao*	NA
Locus_4840_Transcript_22/28_Confidence_0.171_Length_701	163	4.99861	Methyltransferase family protein isoform 4	*Theobroma cacao*	NA
Locus_4840_Transcript_23/28_Confidence_0.171_Length_1126	203	3.87558	Methyltransferase family protein isoform 4	*Theobroma cacao*	NA
Locus_7879_Transcript_2/3_Confidence_0.400_Length_919	530	12.3977	PREDICTED: putative methyltransferase At1g22800-like	*Citrus sinensis*	NA

Locus_14985_Transcript_1/4_Confidence_0.500_Length_570	115	4.33713	PREDICTED: putative methyltransferase At1g22800-like	*Citrus sinensis*	NA
Locus_14985_Transcript_2/4_Confidence_0.333_Length_540	108	4.29942	PREDICTED: putative methyltransferase At1g22800-like	*Citrus sinensis*	NA
Locus_14985_Transcript_3/4_Confidence_0.500_Length_595	105	3.7936	PREDICTED: putative methyltransferase At1g22800-like	*Citrus sinensis*	NA
Locus_14985_Transcript_4/4_Confidence_0.000_Length_660	108	3.5177	PREDICTED: putative methyltransferase At1g22800-like	*Citrus sinensis*	NA
Locus_2014_Transcript_6/12_Confidence_0.067_Length_199	18	1.94446	PREDICTED: uncharacterized methyltransferase WBSCR22-like	*Cucumis sativus*	NA
Locus_10007_Transcript_1/7_Confidence_0.333_Length_1091	1975	38.9154	PREDICTED: uncharacterized methyltransferase At1g78140, chloroplastic-like isoform X1	*Citrus sinensis*	NA
Locus_10007_Transcript_3/7_Confidence_0.667_Length_1604	2196	29.4312	PREDICTED: uncharacterized methyltransferase At1g78140, chloroplastic-like isoform X1	*Citrus sinensis*	NA
Locus_10007_Transcript_4/7_Confidence_0.583_Length_1709	2172	27.321	PREDICTED: uncharacterized methyltransferase At1g78140, chloroplastic-like isoform X1	*Citrus sinensis*	NA
Locus_10007_Transcript_5/7_Confidence_0.583_Length_1694	2034	25.8117	PREDICTED: uncharacterized methyltransferase At1g78140, chloroplastic-like isoform X1	*Citrus sinensis*	NA
Locus_10007_Transcript_6/7_Confidence_0.417_Length_1064	639	12.9104	PREDICTED: uncharacterized methyltransferase At1g78140, chloroplastic-like isoform X1	*Citrus sinensis*	NA
Locus_10007_Transcript_7/7_Confidence_0.250_Length_1604	2199	29.4714	PREDICTED: uncharacterized methyltransferase At1g78140, chloroplastic-like isoform X1	*Citrus sinensis*	NA
Locus_10007_Transcript_2/7_Confidence_0.167_Length_670	1309	41.9995	PREDICTED: uncharacterized methyltransferase At1g78140, chloroplastic-like isoform X2	*Citrus sinensis*	NA
Locus_2847_Transcript_10/29_Confidence_0.289_Length_2063	6881	71.7021	PREDICTED: uncharacterized methyltransferase At2g41040, chloroplastic-like	*Citrus sinensis*	NA
Locus_2847_Transcript_11/29_Confidence_0.200_Length_1165	3223	59.4722	PREDICTED: uncharacterized methyltransferase At2g41040, chloroplastic-like	*Citrus sinensis*	NA
Locus_2847_Transcript_12/29_Confidence_0.222_Length_1205	4544	81.0645	PREDICTED: uncharacterized methyltransferase At2g41040, chloroplastic-like	*Citrus sinensis*	NA
Locus_2847_Transcript_2/29_Confidence_0.133_Length_948	2382	54.0148	PREDICTED: uncharacterized methyltransferase At2g41040, chloroplastic-like	*Citrus sinensis*	NA
Locus_2847_Transcript_3/29_Confidence_0.222_Length_936	5215	119.773	PREDICTED: uncharacterized methyltransferase At2g41040, chloroplastic-like	*Citrus sinensis*	NA
Locus_2847_Transcript_4/29_Confidence_0.267_Length_1039	5481	113.403	PREDICTED: uncharacterized methyltransferase At2g41040, chloroplastic-like	*Citrus sinensis*	NA

Locus_2847_Transcript_5/29_Confidence_0.289_Length_1204	5877	104.932	PREDICTED: uncharacterized methyltransferase At2g41040, chloroplastic-like	*Citrus sinensis*	NA
Locus_2847_Transcript_6/29_Confidence_0.289_Length_1973	6640	72.347	PREDICTED: uncharacterized methyltransferase At2g41040, chloroplastic-like	*Citrus sinensis*	NA
Locus_2847_Transcript_7/29_Confidence_0.289_Length_1952	5393	59.3923	PREDICTED: uncharacterized methyltransferase At2g41040, chloroplastic-like	*Citrus sinensis*	NA
Locus_2847_Transcript_9/29_Confidence_0.311_Length_1294	6120	101.671	PREDICTED: uncharacterized methyltransferase At2g41040, chloroplastic-like	*Citrus sinensis*	NA

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_Length_523
	Locus_2658_Transcript_7/69_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
CYP72	**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**

	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

	Locus_2658_Transcript_45/69_Confidence_0.111_Length_1318
	Locus_2658_Transcript_46/69_Confidence_0.064_Length_1329
	Locus_2658_Transcript_40/69_Confidence_0.082_Length_1401
	Locus_2658_Transcript_42/69_Confidence_0.111_Length_1401
	Locus_3026_Transcript_2/74_Confidence_0.064_Length_1006
	Locus_2658_Transcript_6/69_Confidence_0.058_Length_424
	Locus_37046_Transcript_1/1_Confidence_0.833_Length_338
CYP84	**Locus_19681_Transcript_1/1_Confidence_0.000_Length_1840**
	Locus_11698_Transcript_1/1_Confidence_0.000_Length_841
	Locus_17506_Transcript_1/1_Confidence_0.000_Length_401
CYP85	**Locus_25051_Transcript_1/1_Confidence_0.000_Length_246**
CYP86	**Locus_2860_Transcript_4/16_Confidence_0.273_Length_758**
	Locus_19470_Transcript_1/1_Confidence_0.000_Length_901
CYP87	**Locus_11181_Transcript_10/17_Confidence_0.130_Length_381**
	Locus_11181_Transcript_13/17_Confidence_0.174_Length_1410
	Locus_11181_Transcript_12/17_Confidence_0.174_Length_1415
	Locus_11181_Transcript_11/17_Confidence_0.174_Length_1410
	Locus_11181_Transcript_14/17_Confidence_0.130_Length_1372
	Locus_11181_Transcript_15/17_Confidence_0.043_Length_1338
CYP88	**Locus_6215_Transcript_5/5_Confidence_0.000_Length_1741**
	Locus_6215_Transcript_4/5_Confidence_0.125_Length_2038
CYP89	**Locus_2860_Transcript_5/16_Confidence_0.273_Length_726**
	Locus_2860_Transcript_6/16_Confidence_0.273_Length_812
	Locus_2860_Transcript_7/16_Confidence_0.318_Length_904
	Locus_2860_Transcript_15/16_Confidence_0.273_Length_828
	Locus_2860_Transcript_8/16_Confidence_0.545_Length_1268
	Locus_2860_Transcript_11/16_Confidence_0.318_Length_1035
	Locus_2860_Transcript_13/16_Confidence_0.500_Length_1358
	Locus_2860_Transcript_10/16_Confidence_0.500_Length_1354
	Locus_2860_Transcript_16/16_Confidence_0.227_Length_1370

	Locus_2860_Transcript_14/16_Confidence_0.545_Length_1446
	Locus_2860_Transcript_9/16_Confidence_0.636_Length_1462
	Locus_2860_Transcript_12/16_Confidence_0.500_Length_1444
	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
CYP90	**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

	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
	Locus_9437_Transcript_4/8_Confidence_0.538_Length_2054
	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
	Locus_1182_Transcript_8/17_Confidence_0.548_Length_1872
	Locus_1182_Transcript_13/17_Confidence_0.516_Length_1872
	Locus_1182_Transcript_12/17_Confidence_0.516_Length_1909
	Locus_1182_Transcript_14/17_Confidence_0.484_Length_1909
	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
CYP707	**Locus_1174_Transcript_1/1_Confidence_0.000_Length_1127**
	Locus_12634_Transcript_1/1_Confidence_0.000_Length_1613
CYP708	**Locus_11181_Transcript_17/17_Confidence_0.000_Length_513**
	Locus_5093_Transcript_1/4_Confidence_0.600_Length_457
CYP709	**Locus_10475_Transcript_4/11_Confidence_0.312_Length_909**
	Locus_10475_Transcript_8/11_Confidence_0.438_Length_2605
CYP712	**Locus_6868_Transcript_4/14_Confidence_0.400_Length_671**
	Locus_16293_Transcript_1/1_Confidence_0.000_Length_1727
CYP714	**Locus_10475_Transcript_6/11_Confidence_0.438_Length_2115**
CYP716	**Locus_6034_Transcript_2/15_Confidence_0.120_Length_502**

	Locus_25282_Transcript_1/1_Confidence_0.000_Length_1460
	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/ http://blast.uthsc.edu /blast.cgi**	**Bio catnet CYPED v6.0/ https://cyped.biocatnet.de/ workbench/blast**	**NCBI**	**TAIR**
Locus_7540_Transcript_1/1_Confidence_0.000_Length_1583	CYP51G1/CYP51A2	Cyp51/PREDICTED: sterol 14-demethylase-like	PREDICTED: obtusifoliol 14-alpha demethylase [*Citrus sinensis*]	putative obtusifoliol 14-alpha demethylase involved in sterol biosynthesis
Locus_2312_Transcript_4/9_Confidence_0.417_Length_2270	CYP71B34	PREDICTED: cytochrome P450 71B37-like|cytochrome P450	PREDICTED: cytochrome P450 71B34-like [*Citrus sinensis*]	CYP71B2/secondary metabolite biosynthetic process
Locus_2312_Transcript_3/9_Confidence_0.458_Length_2289	CYP71B34	PREDICTED: cytochrome P450 71B37-like|cytochrome P450	PREDICTED: cytochrome P450 71B34-like [*Citrus sinensis*]	CYP71B2/secondary metabolite biosynthetic process
Locus_2312_Transcript_1/9_Confidence_0.458_Length_2300	CYP71B34	PREDICTED: cytochrome P450 71B37-like|cytochrome P450	PREDICTED: cytochrome P450 71B34-like [*Citrus sinensis*]	CYP71B2/secondary metabolite biosynthetic process

Locus_11455_Transcript_1/1_Confidence_0.000_Length_1818	CYP71B35	hypothetical protein	PREDICTED: cytochrome P450 71A1-like [*Citrus sinensis*]	CYP71B22
Locus_9283_Transcript_1/2_Confidence_0.333_Length_1824	CYP721	PREDICTED: cytochrome P450 734A1-like	PREDICTED: cytochrome P450 734A1-like [*Citrus sinensis*]	CYP721A1
Locus_2093_Transcript_4/5_Confidence_0.333_Length_2108	CYP74B2	hydroperoxide lyase [*Citrus jambhiri*]	fatty acid hydroperoxide lyase [*Citrus sinensis*]	CYP74B2, HPL1, HYDROPEROXIDE LYASE 1/sterol metabolic process
Locus_11826_Transcript_1/4_Confidence_0.714_Length_2049	CYP74A	CYP74A	allene oxide synthase [*Citrus sinensis*]	ALLENE OXIDE SYNTHASE, AOS, CYP74A, CYTOCHROME P450 74A, DDE2, DELAYED DEHISCENCE 2/defense response, defense response to fungus, epoxygenase 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_4/4_Confidence_0.143_Length_2049	CYP74A	CYP74A	allene oxide synthase [*Citrus sinensis*]	ALLENE OXIDE SYNTHASE, AOS, CYP74A, CYTOCHROME P450 74A, DDE2, DELAYED DEHISCENCE 2/defense response, defense response to fungus, epoxygenase 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_2/4_Confidence_0.714_Length_2061	CYP74A	CYP74A	allene oxide synthase [*Citrus sinensis*]	ALLENE OXIDE SYNTHASE, AOS, CYP74A, CYTOCHROME P450 74A, DDE2, DELAYED DEHISCENCE 2/defense response, defense response to fungus, epoxygenase 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_Confidence_0.429_Length_1919	CYP74A	CYP74A	allene oxide synthase [*Citrus sinensis*]	ALLENE OXIDE SYNTHASE, AOS, CYP74A, CYTOCHROME P450 74A, DDE2, DELAYED DEHISCENCE 2/defense response, defense response to fungus, epoxygenase 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_Confidence_0.500_Length_1727	CYP75B1	cytochrome P450 71A1-like	PREDICTED: cytochrome P450 71A1-like [*Citrus sinensis*]	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_1/4_Confidence_0.750_Length_1728	CYP75B1	cytochrome P450 71A1-like	PREDICTED: cytochrome P450 71A1-like [*Citrus sinensis*]	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_4/4_Confidence_0.000_Length_1652	CYP75B1	cytochrome P450 71A1-like	PREDICTED: cytochrome P450 71A1-like [*Citrus sinensis*]	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_Confidence_0.250_Length_1653	CYP75B1	cytochrome P450 71A1-like	PREDICTED: cytochrome P450 71A1-like [*Citrus sinensis*]	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_Confidence_0.000_Length_1803	CYP75B1	PREDICTED: flavonoid 3-monooxygenase-like	PREDICTED: flavonoid 3'-monooxygenase [*Citrus sinensis*]	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_Confidence_0.750_Length_1779	CYP76C4	CYP76B	PREDICTED: geraniol 8-hydroxylase-like isoform X3 [*Citrus sinensis*]	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 [*Citrus sinensis*]	CCT2, PHOSPHORYLCHOLINE CYTIDYLYLTRANSFERASE2
Locus_5093_Transcript_3/4_Confidence_0.400_Length_2576	CYP79B3	NADPH--cytochrome P450 reductase	PREDICTED: NADPH--cytochrome P450 reductase isoform X1 [*Citrus sinensis*]	P450 REDUCTASE 2/phenylpropanoid general pathway
Locus_5093_Transcript_2/4_Confidence_0.600_Length_2353	CYP79B3	NADPH--cytochrome P450 reductase	PREDICTED: NADPH--cytochrome P450 reductase isoform X1 [*Citrus sinensis*]	P450 REDUCTASE 2/phenylpropanoid general pathway

Locus_2612_Transcript_3/4_Confidence_0.333_Length_1908	CYP81K2	CYP81K	PREDICTED: cytochrome P450 81D11-like [*Citrus sinensis*]	CYP81K2/defense response to other organism, indole glucosinolate metabolic process,oxidation-reduction process, secondary metabolite biosynthetic process
Locus_1752_Transcript_1/7_Confidence_0.111_Length_1903	CYP81D8	cytochrome P450 81D1-like	PREDICTED: isoflavone 3'-hydroxylase-like [*Citrus sinensis*]	CYP81D5/defense response to other organism, indole glucosinolate metabolic process, oxidation-reduction process, secondary metabolite biosynthetic process
Locus_1752_Transcript_2/7_Confidence_0.111_Length_2104	CYP81D8	cytochrome P450 81D1-like	PREDICTED: isoflavone 3'-hydroxylase-like [*Citrus sinensis*]	CYP81D5/defense response to other organism, indole glucosinolate metabolic process, oxidation-reduction process, secondary metabolite biosynthetic process
Locus_1752_Transcript_6/7_Confidence_0.333_Length_1763	CYP81D8	CYP81E	PREDICTED: isoflavone 2'-hydroxylase-like isoform X1 [*Citrus sinensis*]	CYP81D5/defense response to other organism, indole glucosinolate metabolic process, oxidation-reduction process, secondary metabolite biosynthetic process
Locus_1752_Transcript_5/7_Confidence_0.444_Length_1767	CYP81D8	isoflavone 2'-hydroxylase-like isoform X1/CYP81E	PREDICTED: isoflavone 2'-hydroxylase-like isoform X1 [*Citrus sinensis*]	CYP81D5/defense response to other organism, indole glucosinolate metabolic process, oxidation-reduction process, secondary metabolite biosynthetic process
Locus_2616_Transcript_4/5_Confidence_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_Confidence_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_Confidence_0.250_Length_1851	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_2/5_Confidence_0.375_Length_1915	CYP82C4	CYP82G	PREDICTED: cytochrome P450 82C4-like [*Ziziphus jujuba*]	CYP82C4/cellular response to iron ion, oxidation-reduction process, secondary metabolite biosynthetic process
Locus_2096_Transcript_1/9_Confidence_0.182_Length_1978	CYP82C4	cytochrome P450 82C4-like	PREDICTED: cytochrome P450 CYP82D47-like [*Citrus sinensis*]	CYP82C3/oxidation-reduction process, secondary metabolite biosynthetic process
Locus_2096_Transcript_2/9_Confidence_0.091_Length_1980	CYP82C4	cytochrome P450 82C4-like	PREDICTED: cytochrome P450 CYP82D47-like [*Citrus sinensis*]	CYP82C3/oxidation-reduction process, secondary metabolite biosynthetic process
Locus_2006_Transcript_25/27_Confidence_0.321_Length_1534	CYP82C4/C2/C3	cytochrome P450 82C4-like	cytochrome P450 82A3-like isoform X2 [*Citrus sinensis*]	CYP71B37
Locus_3026_Transcript_71/74_Confidence_0.050_Length_1496	CYP83A2	CYP83B	PREDICTED: cytochrome P450 83B1-like [*Citrus sinensis*]	CYP71B5/ cellular response to ethylene stimulus, cellular response to iron ion, cellular response to nitric oxide, oxidation-reduction process, secondary metabolite biosynthetic process
Locus_3026_Transcript_67/74_Confidence_0.135_Length_2218	CYP83A2	CYP83B	PREDICTED: cytochrome P450 83B1-like [*Citrus sinensis*]	CYP71B5/ cellular response to ethylene stimulus, cellular response to iron ion, cellular response to nitric oxide, oxidation-reduction process, secondary metabolite biosynthetic process
Locus_3026_Transcript_62/74_Confidence_0.135_Length_2050	CYP83A2	CYP83B	PREDICTED: cytochrome P450 83B1-like [*Citrus sinensis*]	CYP71B5/ cellular response to ethylene stimulus, cellular response to iron ion, cellular response to nitric oxide, oxidation-reduction process, secondary metabolite biosynthetic

				process
Locus_19681_Transcript_1/1_Confidence_0.000_Length_1840	CYP84A1	CYP84A	PREDICTED: cytochrome P450 84A1 [*Citrus sinensis*]	CYP84A1, CYTOCHROME P450 84A1, FAH1, FERULIC ACID 5-HYDROXYLASE 1/lignin biosynthetic process, oxidation-reduction process, phenylpropanoid biosynthetic process, response to UV-B
Locus_10238_Transcript_1/1_Confidence_0.333_Length_1883	CYP89A5	PREDICTED: cytochrome P450 89A2-like	PREDICTED: cytochrome P450 89A2-like [*Citrus sinensis*]	CYP89A3/ oxidation-reduction process, secondary metabolite biosynthetic process
Locus_7472_Transcript_1/3_Confidence_0.400_Length_2057	CYP90C1	3-epi-6-deoxocathasterone 23-monooxygenase-like isoform X1	PREDICTED: 3-epi-6-deoxocathasterone 23-monooxygenase isoform X1 [*Citrus sinensis*]	CYP90B1, DWARF 4, DWF4, PARTIALLY SUPPRESSING COI1 INSENSITIVITY TO JA 1, PSC1, SAV1, SHADE AVOIDANCE 1, SNP2, SUPPRESSOR OF NPH4 2/ brassinosteroid biosynthetic process, brassinosteroid homeostasis, jasmonic acid mediated signaling pathway, leaf development, leaf shaping, oxidation-reduction process, response to brassinosteroid, response to jasmonic acid, sterol metabolic process, unidimensional cell growth

Locus_9617_Transcript_5/6_Confidence_0.571_Length_1910	CYP90D1	CYP90D	PREDICTED: 3-epi-6-deoxocathasterone 23-monooxygenase [*Citrus sinensis*]	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 catalyse 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_4/6_Confidence_0.571_Length_1919	CYP90D1	CYP90D	PREDICTED: 3-epi-6-deoxocathasterone 23-monooxygenase [*Citrus sinensis*]	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 catalyse 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_3/6_Confidence_0.571_Length_2005	CYP90D1	CYP90D	PREDICTED: 3-epi-6-deoxocathasterone 23-monooxygenase [*Citrus sinensis*]	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 catalyse 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_Confidence_0.714_Length_2014	CYP90D1	CYP90D	PREDICTED: 3-epi-6-deoxocathasterone 23-monooxygenase [*Citrus sinensis*]	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 catalyse 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_2871_Transcript_1/2_Confidence_0.750_Length_1863	CYP94D2	PREDICTED: cytochrome P450 94A1-like	PREDICTED: cytochrome P450 94A1-like [*Citrus sinensis*]	CYP94B1/CYP86C1

Locus_2871_Transcript_2/2_Confidence_0.250_Length_1867	CYP94D2	PREDICTED: cytochrome P450 94A1-like	PREDICTED: cytochrome P450 94A1-like [*Citrus sinensis*]	CYP94B1/CYP86C1
Locus_2424_Transcript_1/1_Confidence_0.000_Length_1734	CYP94D2	PREDICTED: cytochrome P450 94A1-like	PREDICTED: cytochrome P450 94A1-like [*Citrus sinensis*]	CYP94B1/CYP86C1
Locus_3183_Transcript_7/23_Confidence_0.452_Length_1677	CYP96A10	-	PREDICTED: peptidyl-prolyl cis-trans isomerase CYP37, chloroplastic isoform X1 [*Citrus sinensis*]	Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein
Locus_11035_Transcript_1/1_Confidence_0.000_Length_1723	CYP96A10	CYP86B	PREDICTED: alkane hydroxylase MAH1 [*Vitis vinifera*]	CYP96A9/CYP96A8
Locus_6410_Transcript_15/23_Confidence_0.556_Length_4023	CYP97A3	CYP97B	cytochrome P450 [*Citrus unshiu*]	CYP97A3, LUT5, LUTEIN DEFICIENT 5/carotenoid biosynthetic process, oxidation-reduction process, xanthophyll biosynthetic process
Locus_6410_Transcript_16/23_Confidence_0.593_Length_4842	CYP97A3	CYP97B	cytochrome P450 [*Citrus unshiu*]	CYP97A3, LUT5, LUTEIN DEFICIENT 5/carotenoid biosynthetic process, oxidation-reduction process, xanthophyll biosynthetic process
Locus_6410_Transcript_20/23_Confidence_0.593_Length_4735	CYP97A3	CYP97B	cytochrome P450 [*Citrus unshiu*]	CYP97A3, LUT5, LUTEIN DEFICIENT 5/carotenoid biosynthetic process, oxidation-reduction process, xanthophyll biosynthetic process
Locus_6410_Transcript_21/23_Confidence_0.556_Length_4876	CYP97A3	CYP97B	cytochrome P450 [*Citrus unshiu*]	CYP97A3, LUT5, LUTEIN DEFICIENT 5/carotenoid biosynthetic process, oxidation-reduction process, xanthophyll biosynthetic process

Locus_19973_Transcript_1/1_Confidence_0.000_Length_1735	CYP98A3	PREDICTED: cytochrome P450 98A2-like	PREDICTED: cytochrome P450 98A2 [*Citrus sinensis*]/p-coumaryl-CoA 3'-hydroxylase [Populus alba x Populus grandidentata	CYP98A3/encodes coumarate 3-hydroxylase (C3H), a P450-dependent monooxygenase. coumarin biosynthetic process, flavonoid biosynthetic process, lignin biosynthetic process, oxidation-reduction process, phenylpropanoid biosynthetic process
Locus_22762_Transcript_5/5_Confidence_0.000_Length_1642	CYP702A6/A5/A1/A2	CYP702A6	PREDICTED: cytochrome P450 708A2-like [*Camelina sativa*]	CYP702A6/A5/A1/A2 involved in brassinosteroid biosynthetic process, brassinosteroid homeostasis, multicellular organism development, oxidation-reduction process, sterol metabolic process
Locus_22762_Transcript_2/5_Confidence_0.571_Length_1702	CYP702A6/A5/A1/A2	CYP702A6	PREDICTED: cytochrome P450 708A2-like [*Camelina sativa*]	CYP702A6/A5/A1/A2 involved in brassinosteroid biosynthetic process, brassinosteroid homeostasis, multicellular organism development, oxidation-reduction process, sterol metabolic process
Locus_15761_Transcript_1/1_Confidence_0.000_Length_1304	CYP706A4	-	PREDICTED: 8-hydroxygeraniol dehydrogenase-like [*Citrus sinensis*]	CAD6/CAD6
Locus_12215_Transcript_6/8_Confidence_0.500_Length_2092	CYP706A4	CYP706A	PREDICTED: geraniol 8-hydroxylase [*Ricinus communis*]	CYP706A4/oxidation-reduction process, secondary metabolite biosynthetic process
Locus_12215_Transcript_7/8_Confidence_0.250_Length_2079	CYP706A4	CYP706A	PREDICTED: geraniol 8-hydroxylase [*Ricinus communis*]	CYP706A4/oxidation-reduction process, secondary metabolite biosynthetic process
Locus_12215_Transcript_8/8_Confidence_0.083_Length_1862	CYP706A4	CYP706A	PREDICTED: geraniol 8-hydroxylase [*Ricinus communis*]	CYP706A4/oxidation-reduction process, secondary metabolite biosynthetic process

Locus_12634_Transcript_1/1_Confidence_0.000_Length_1613	CYP707A4	CYP707A/abscisic acid 8'-hydroxylase 3-like precursor	abscisic acid 8'-hydroxylase 3-like precursor [*Citrus sinensis*]	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
Locus_10475_Transcript_8/11_Confidence_0.438_Length_2605	CYP709B2	cytochrome P450 78A9-like isoform X3	PREDICTED: cytochrome P450 4C1-like isoform X3 [*Citrus sinensis*]	CCT2, PHOSPHORYLCHOLINE CYTIDYLYLTRANSFERASE2
Locus_16293_Transcript_1/1_Confidence_0.000_Length_1727	CYP712A1	PREDICTED: cytochrome P450 93A1-like	PREDICTED: 3,9-dihydroxypterocarpan 6A-monooxygenase [*Citrus sinensis*]	CYP712A1/ oxidation-reduction process, secondary metabolite biosynthetic process
Locus_10475_Transcript_6/11_Confidence_0.438_Length_2115	CYP714A1	cytochrome P450 78A9-like isoform X1	PREDICTED: cytochrome P450 3A31-like isoform X1 [*Citrus sinensis*]	CCT2, PHOSPHORYLCHOLINE CYTIDYLYLTRANSFERASE2
Locus_3941_Transcript_3/6_Confidence_0.556_Length_1774	CYP734A1 old name CYP72B1	PREDICTED: cytochrome P450 734A1-like	PREDICTED: cytochrome P450 CYP749A22-like [*Citrus sinensis*]	DUF2
Locus_3941_Transcript_3/6_Confidence_0.556_Length_1774	CYP734A1 old name CYP72B2	PREDICTED: cytochrome P450 734A1-like	PREDICTED: cytochrome P450 CYP749A22-like [*Citrus sinensis*]	DUF2

Table S7: Localization prediction of MkTPSs using different software tools

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

A	Other characterized Sabinene synthases	MkTPS1
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%
B	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	CTTATGGACCGTGGGGGATATATTCG	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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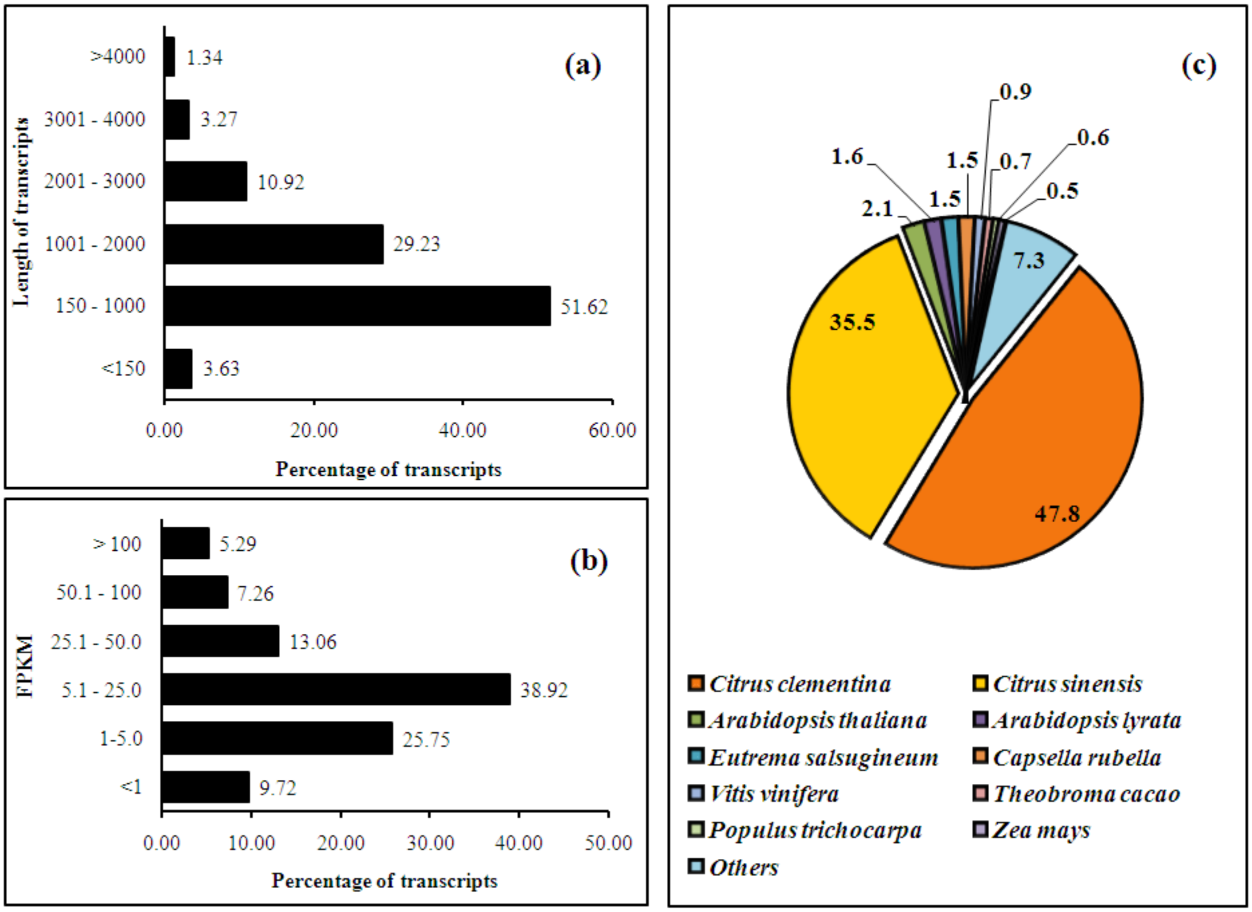


Figure S1. a) Length distribution of total assembled transcripts in *M. koenigii*, b) FPKM distribution of assembled transcripts with length ≥ 150 bp, c) Organismal distribution of *M. koenigii* transcripts annotated according to NCBI BLASTX top hits.

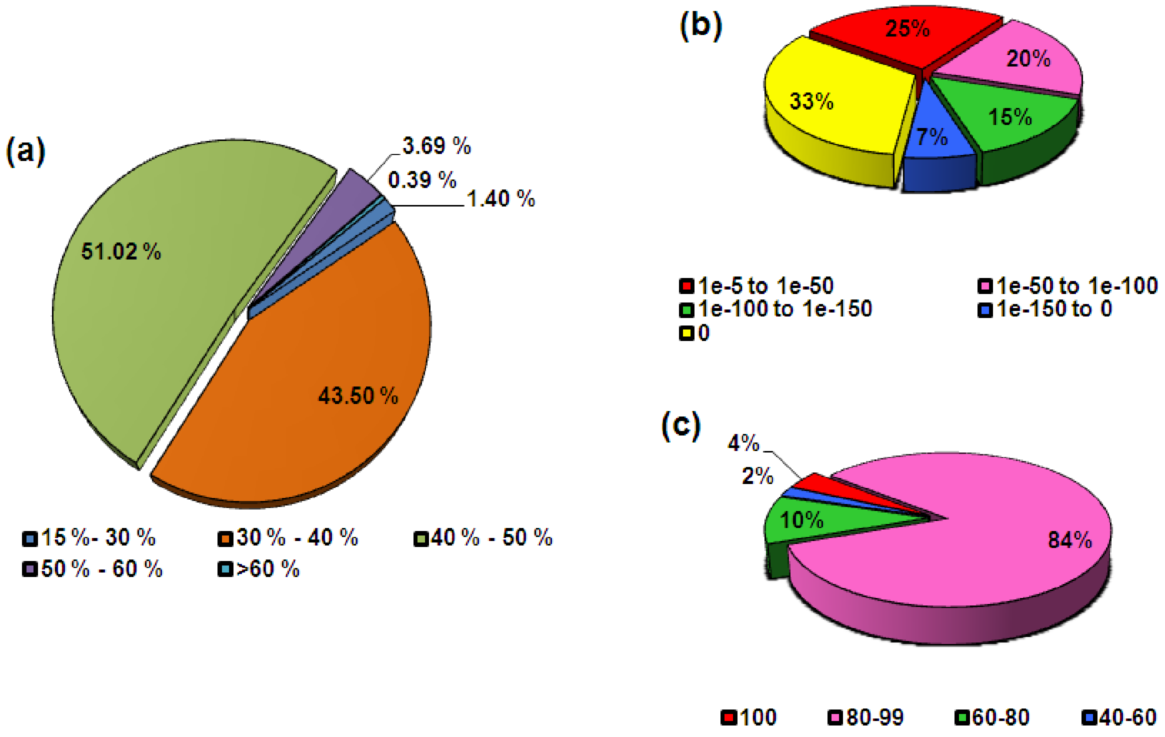


Figure S2. a) GC % distribution of assembled transcripts with length ≥150bp, b) E-value distribution of assembled transcripts with length ≥150bp and FPKM ≥1, balstx against NCBI nr database and (c) Similarity score distribution of blastx results against NCBI nr database

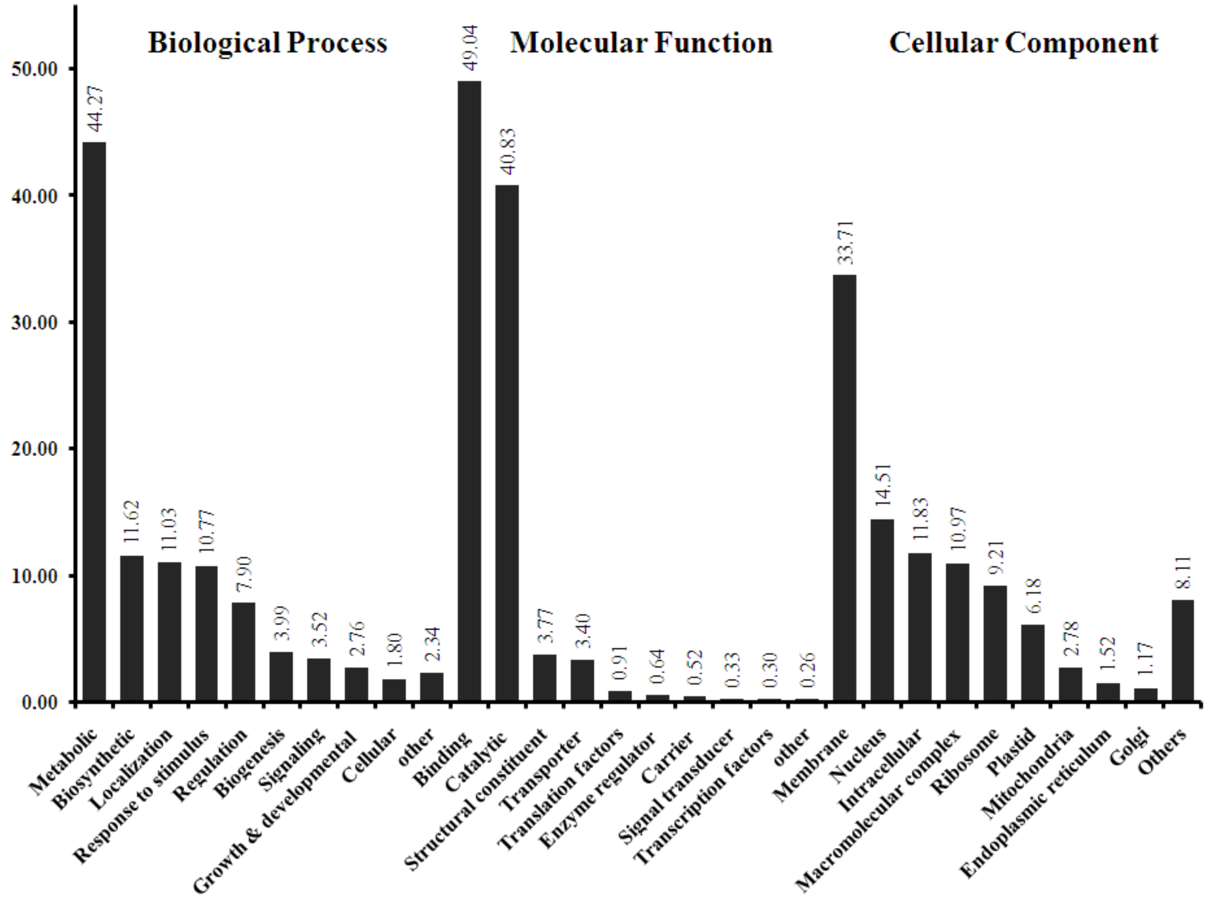


Figure S3. Gene ontology classification as derived from Uniprot annotation: Gene ontology has 3 main categories including Biological processes, Molecular function, Cellular component

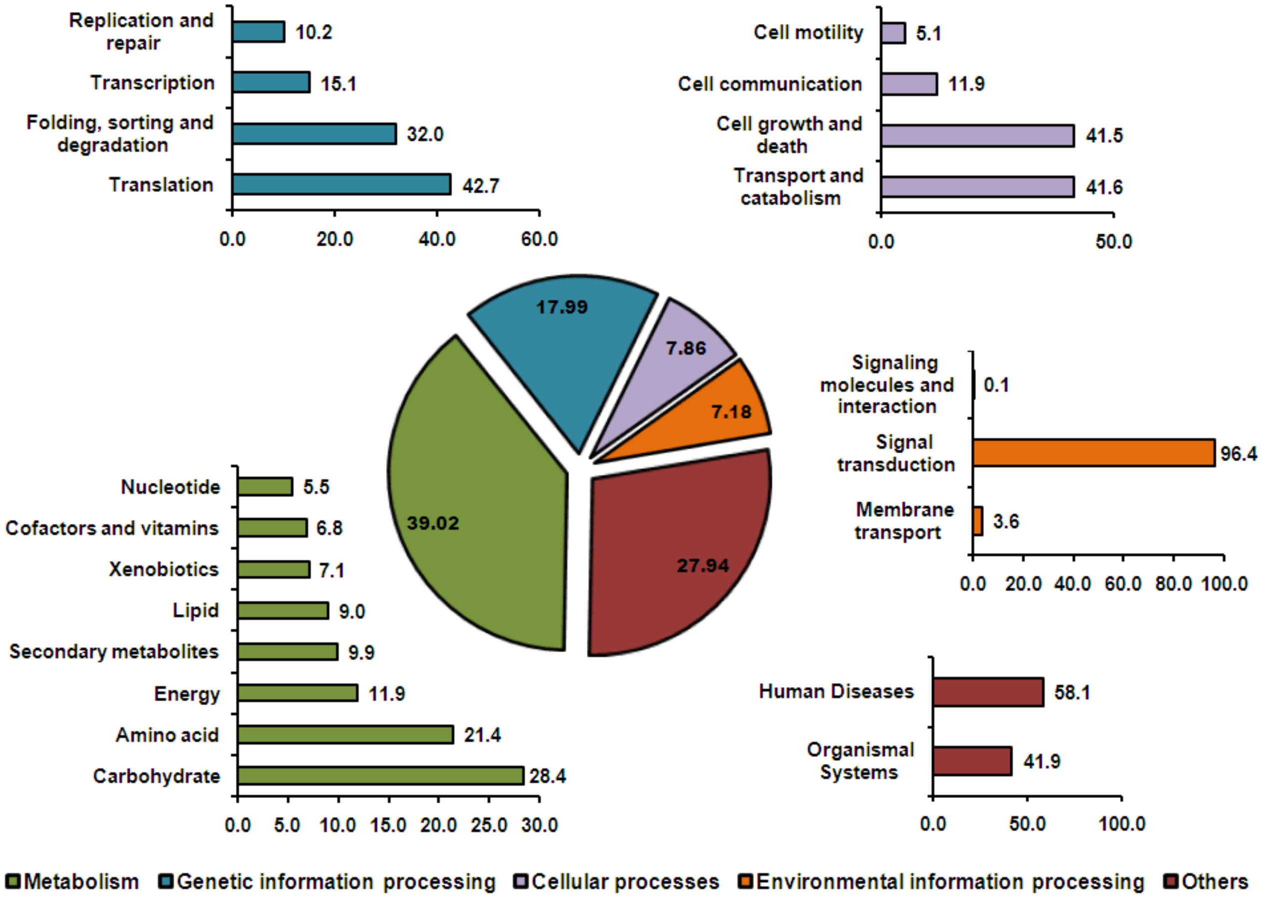


Figure S4. KEGG Orthology (KO) classification and distribution of transcripts identified by KASS into 5 main categories and their sub-categories.

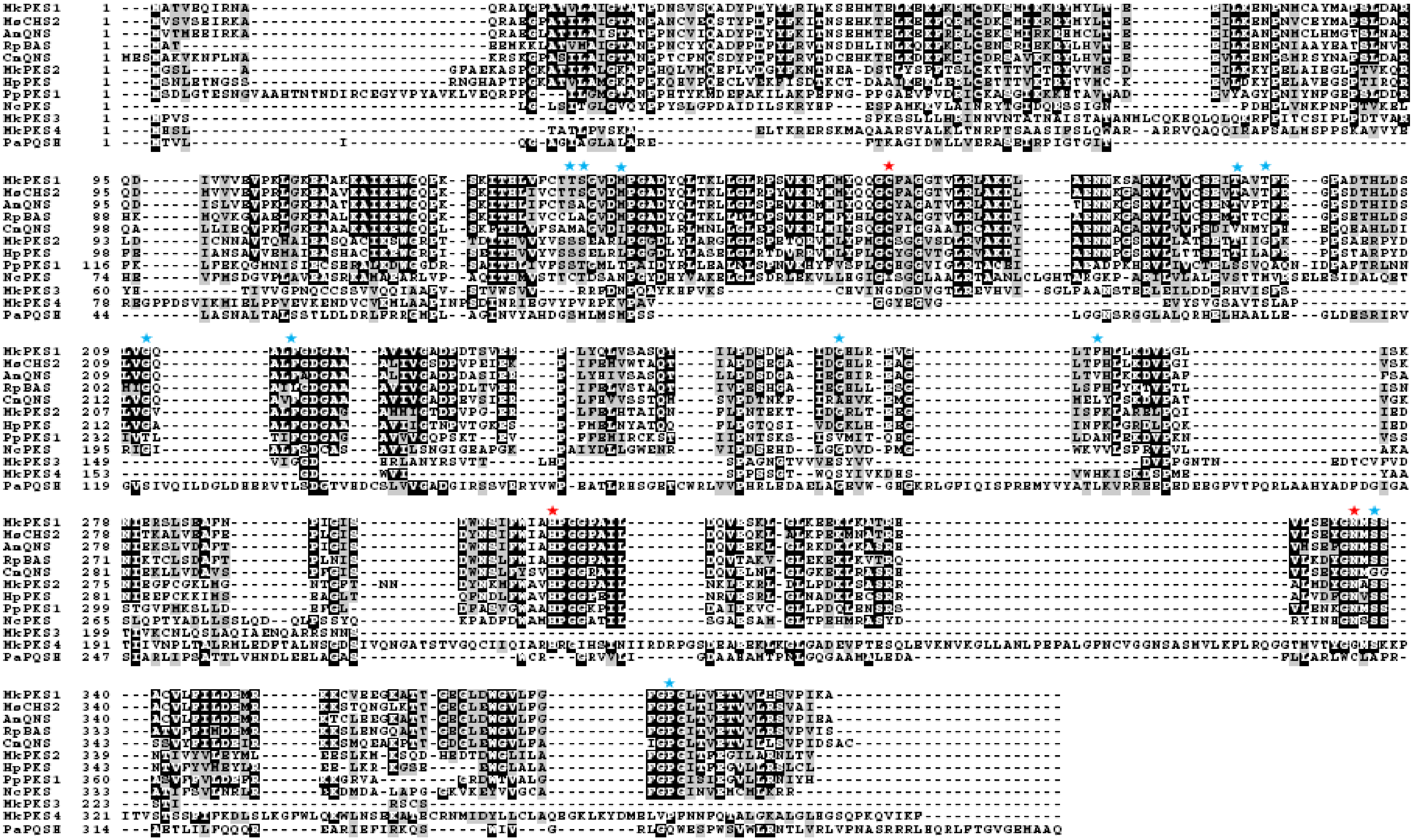

MkPKS1
MsCHS2
AnQNS
RpBAS
CnQNS
MkPKS2
HpPKS
PpPKS1
NcPKS
MkPKS3
MkPKS4
PaPQSH

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 (Q9I0Q0); 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.

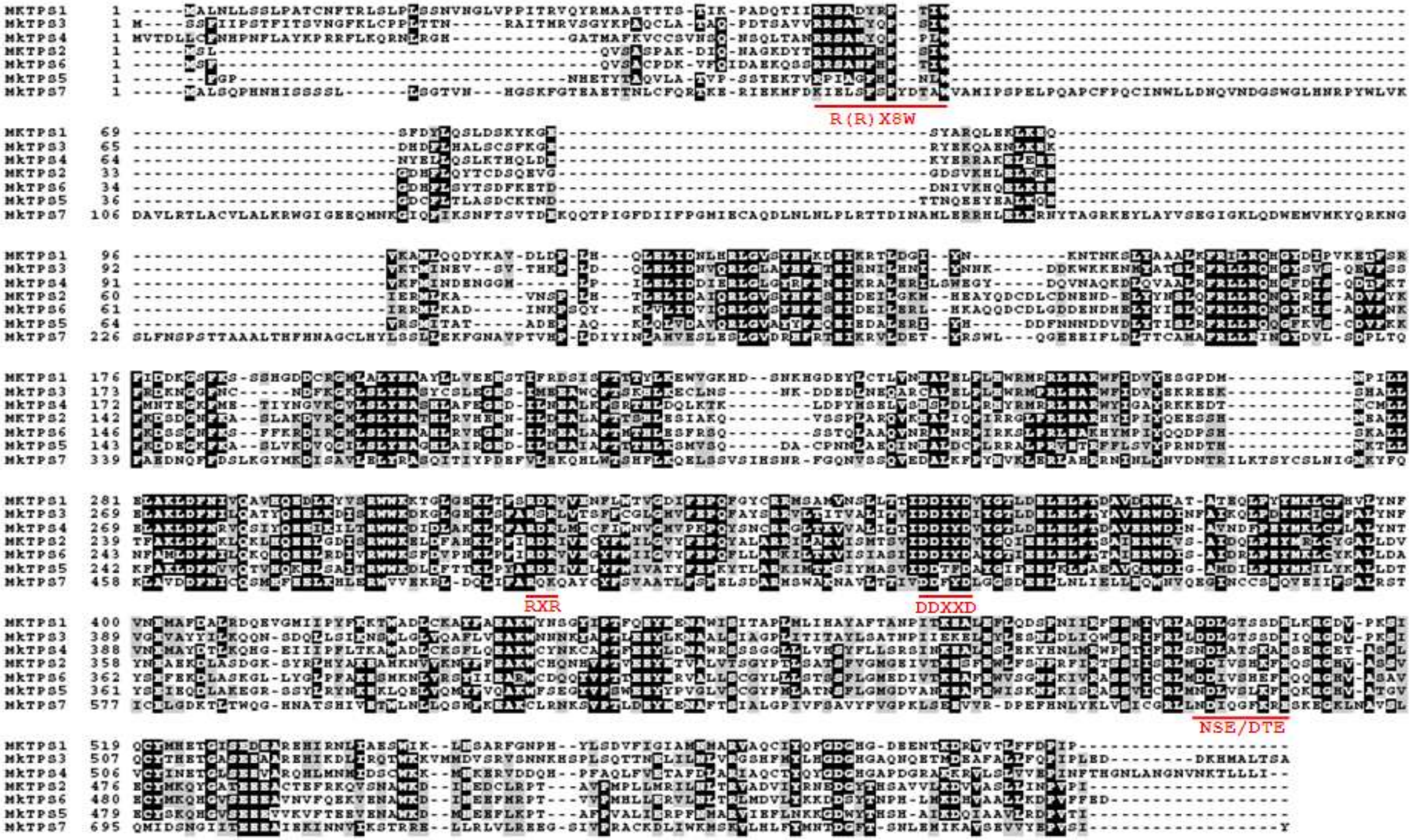


Figure S6. Multiple sequence alignment of full length MkTPSs. The conserved catalytic motifs are marked in red. Alignment was built using MAFFT 7.271 and BOXSHADE 3.21.

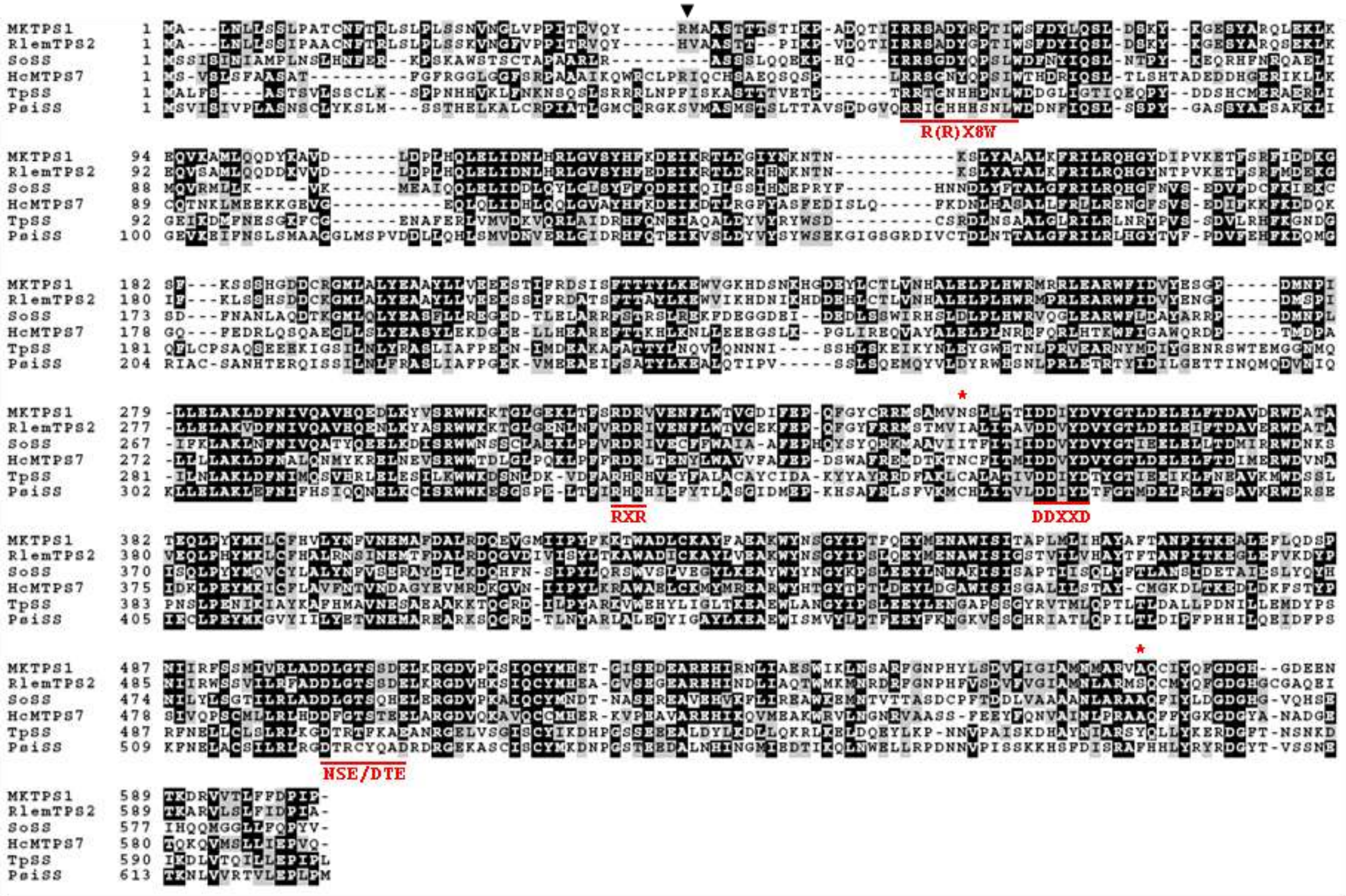

MKTPS1
RlemTPS2
SoSS
HcMTPS7
TpSS
PsiSS
R(R)X8W
RXR
DDXXD
NSE/DTE

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”, Arg-rich “RXR” and “R(R)X8W” motif, as well as a NSE/DTE motif are underlined in red. Cleavage site is marked with arrowhead.

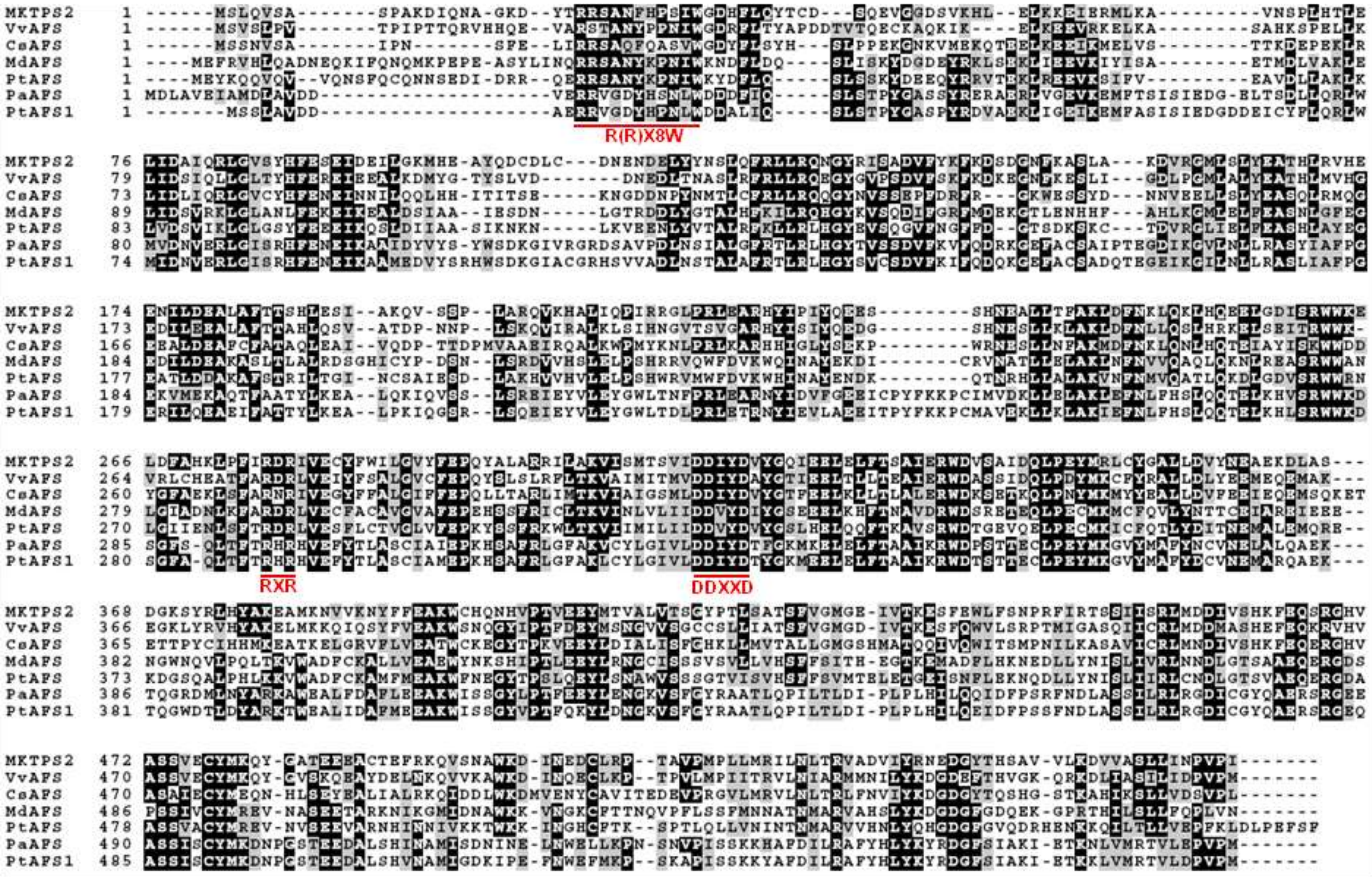

MKTPS2
VvAFS
CsAFS
MdAFS
PtAFS
PaAFS
PtAFS1
R(R)X8W
RXR
DDXXD

Fig. S8. Sequence relatedness of MkTPS2 with other characterized α-farnesene synthases. CsAFS, Cucumis sativus E,E-alpha-farnesene 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.

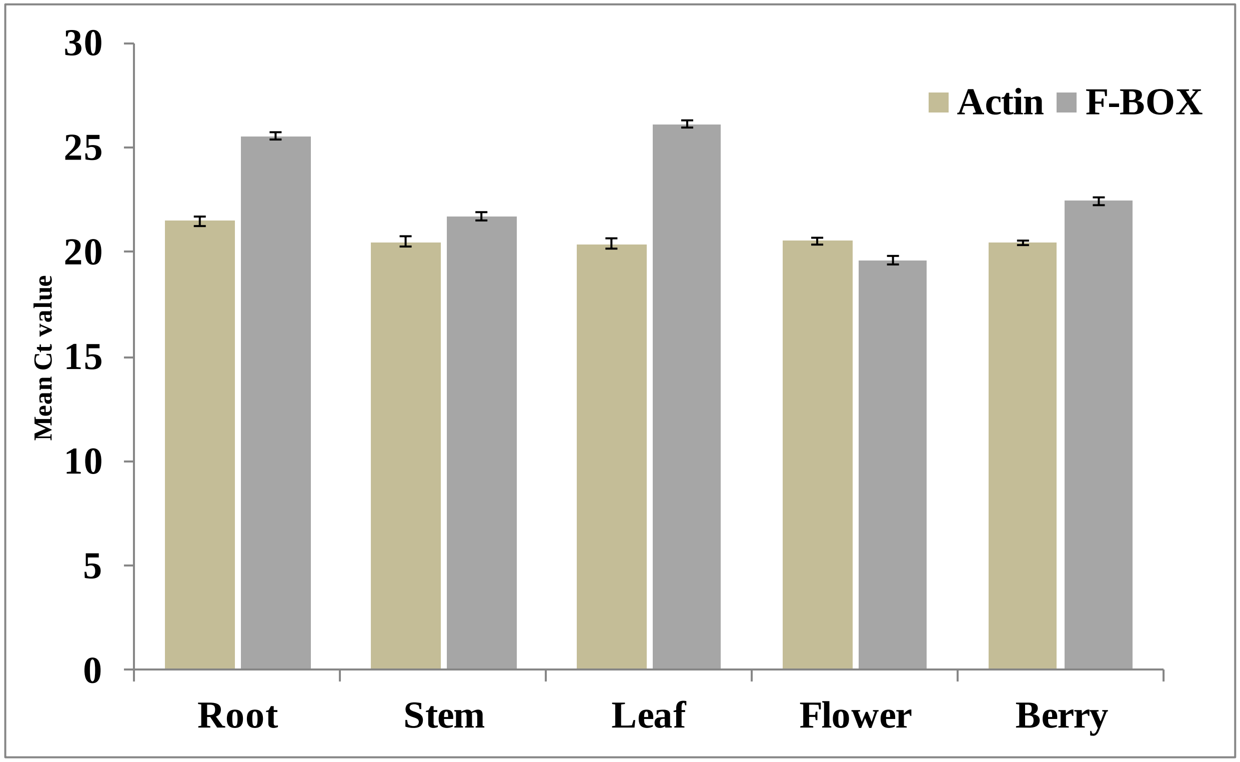


Fig. S9. Expression profiling of reference genes in *M. koenigii* - Mk Actin and Mk F-BOX were used to check the stability in different tissues of M. *koenigii*

Chromatogram of Standard Mixture – Expanded view

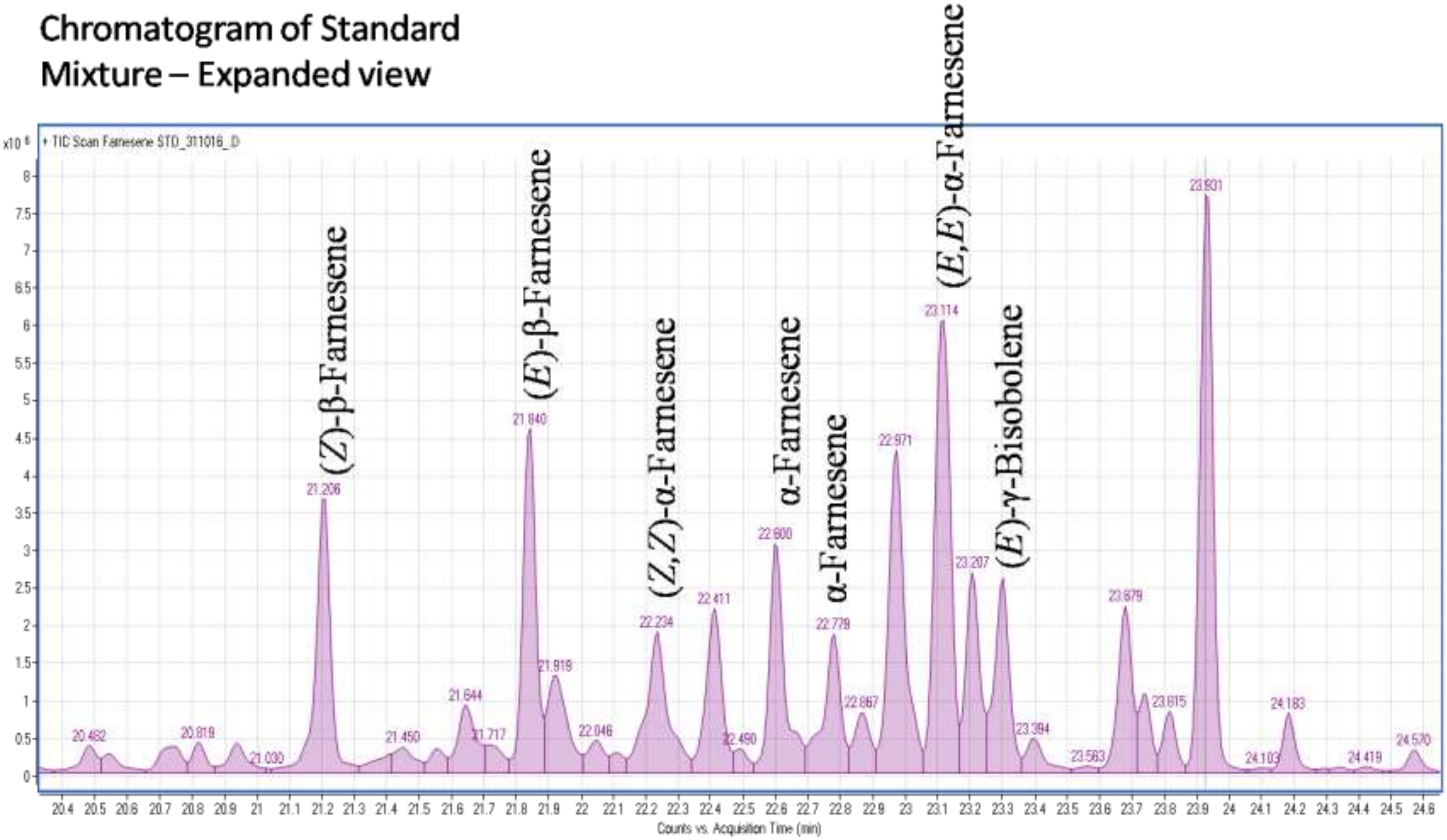
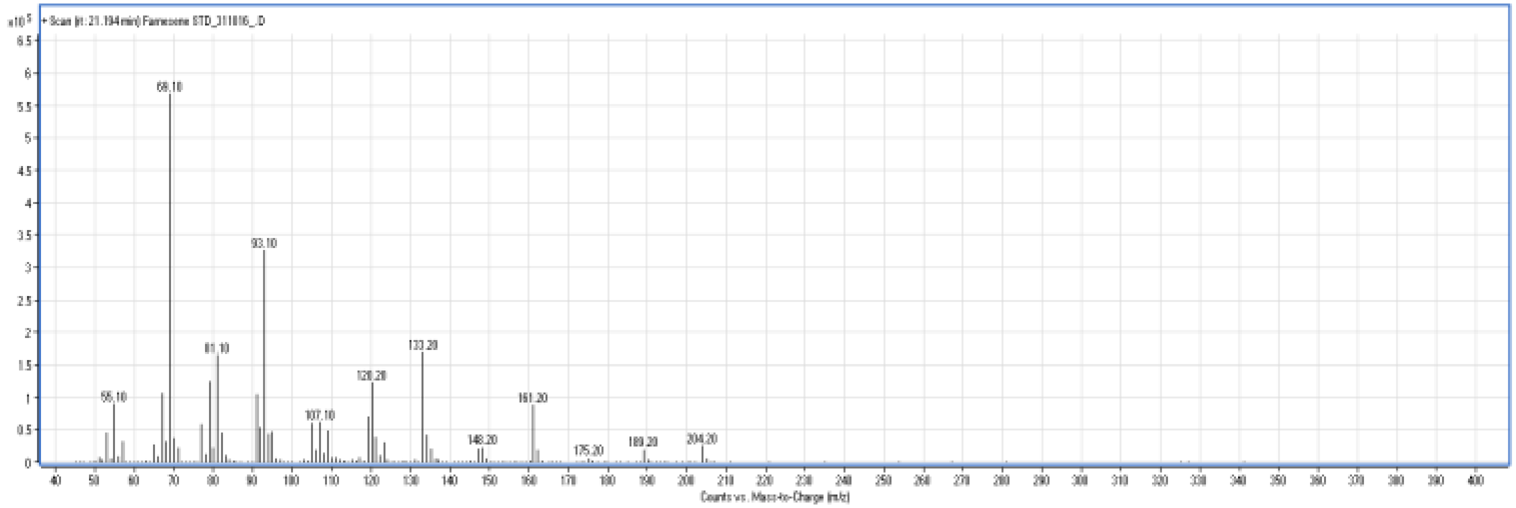


Fig. S10. GC-MS chromatogram of farnesene standard mixture and the respective mass spectra of individual geometric isomers.

(*Z*)-β-Farnesene



(*E*)-β-Farnesene

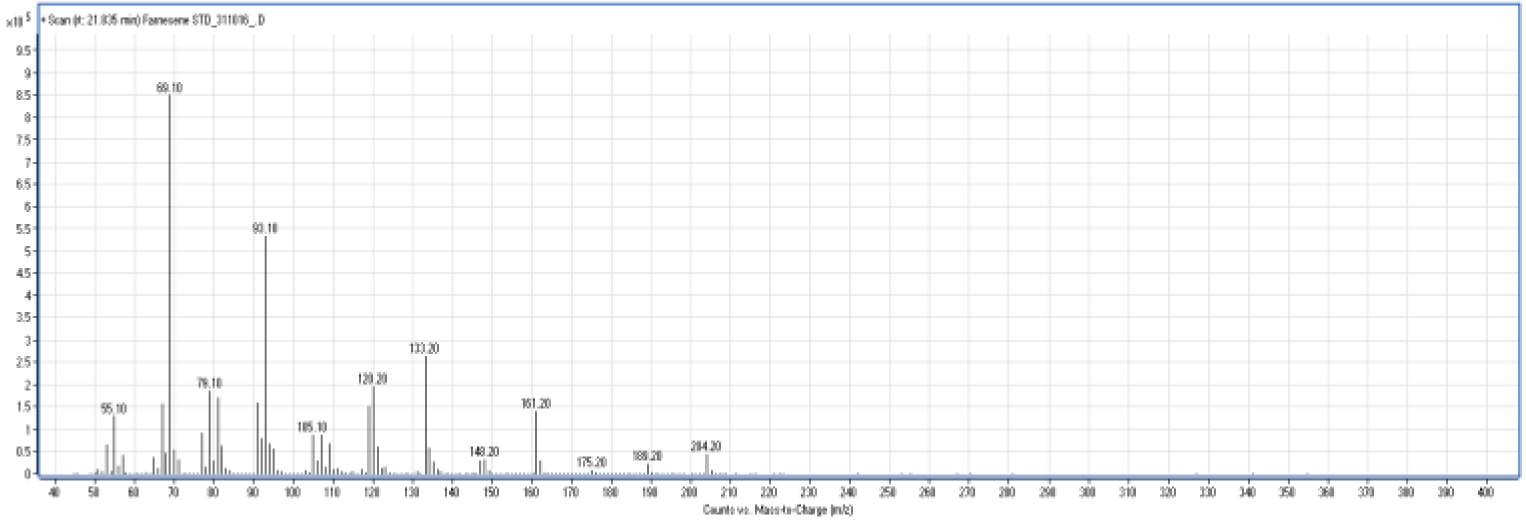
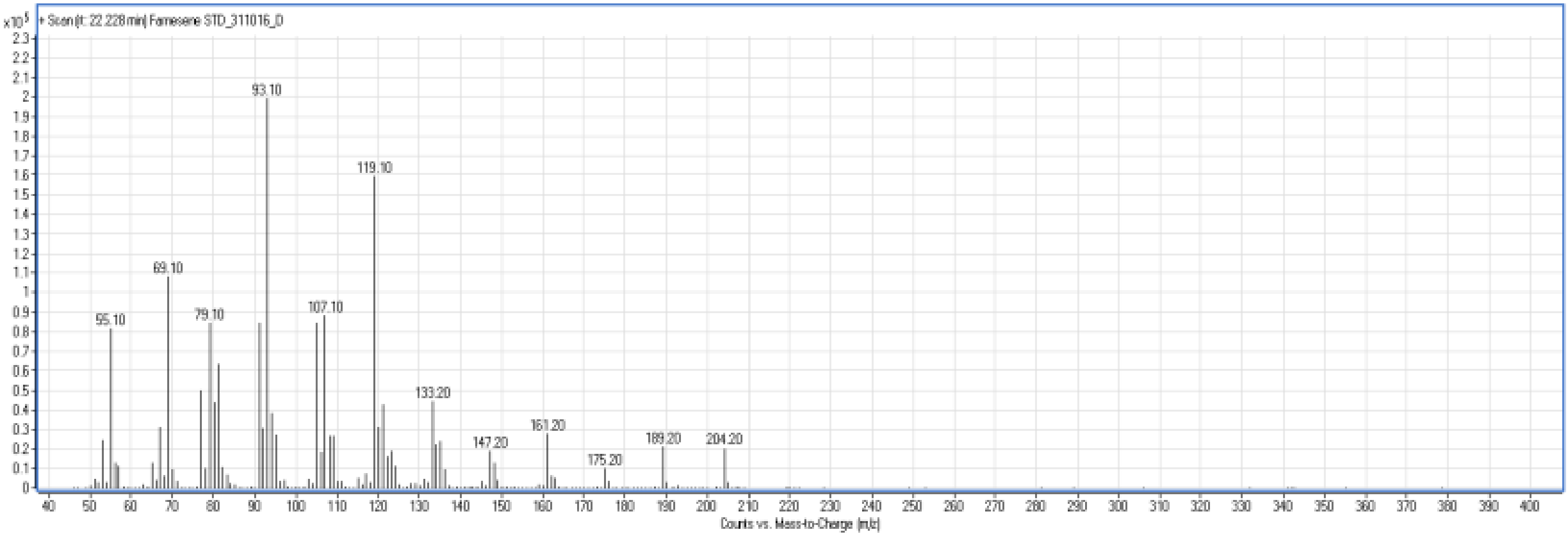


Fig. S10. Cont…

(Z,Z)-α-Farnesene



α-Farnesene

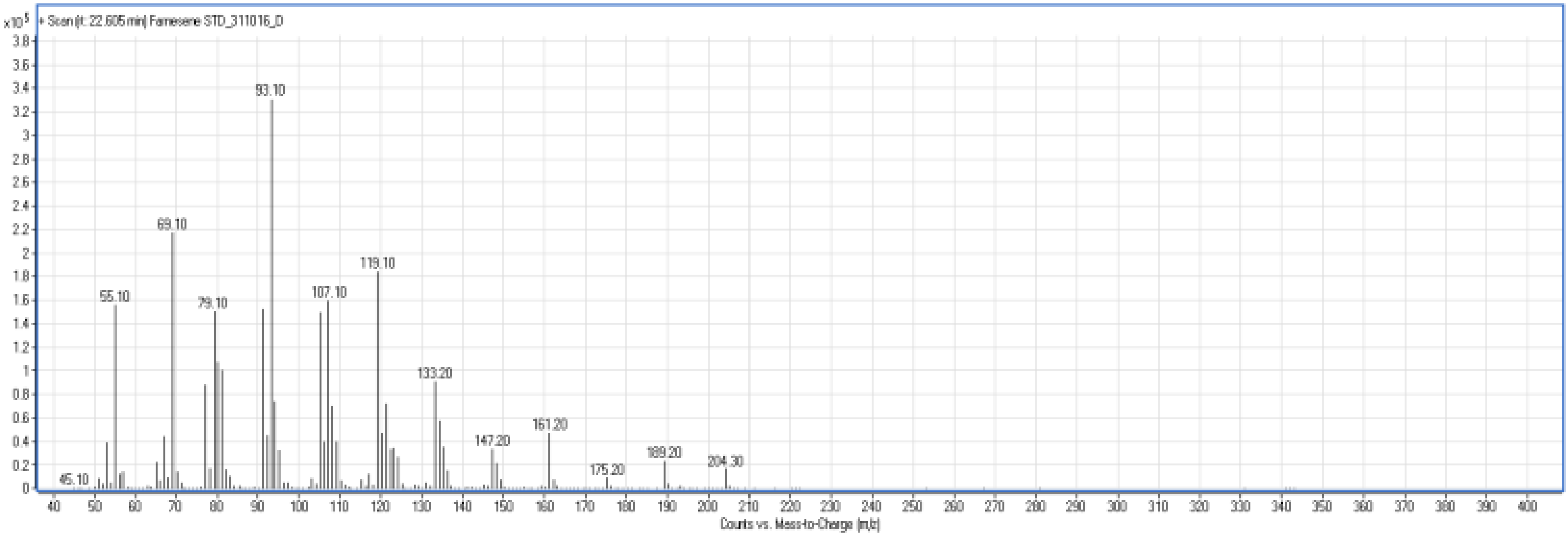
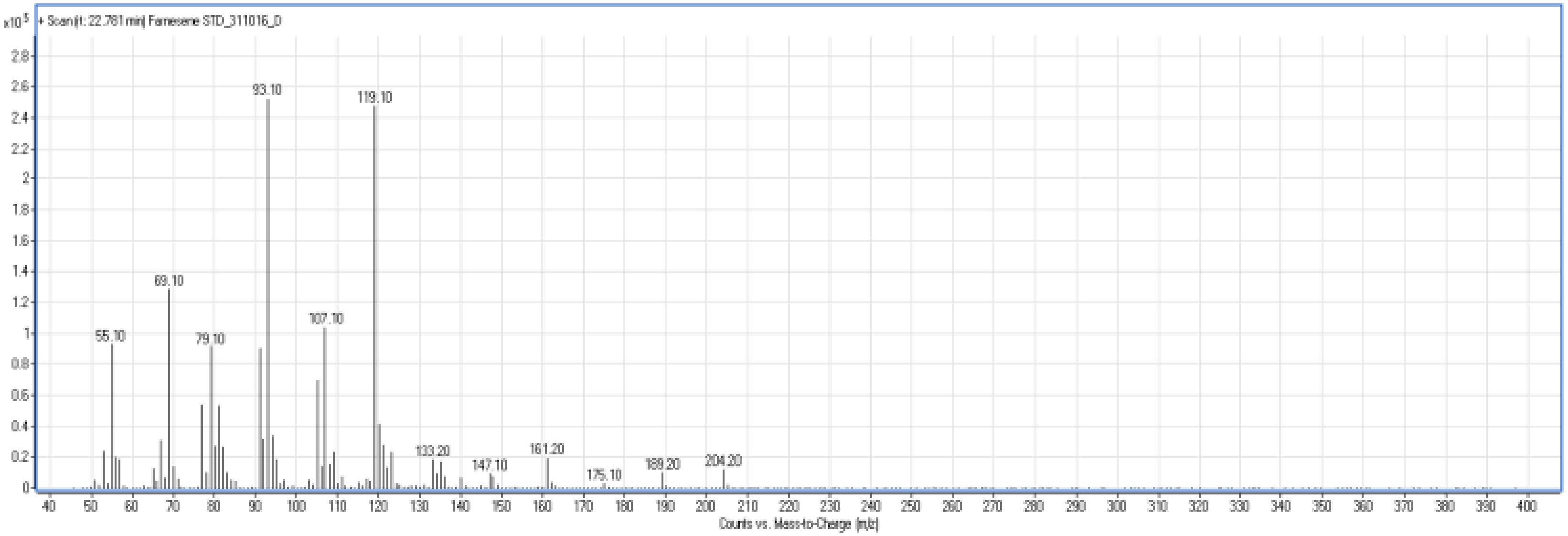


Fig. S10. Cont…

α-Farnesene



(*E*,*E*)-α-Farnesene

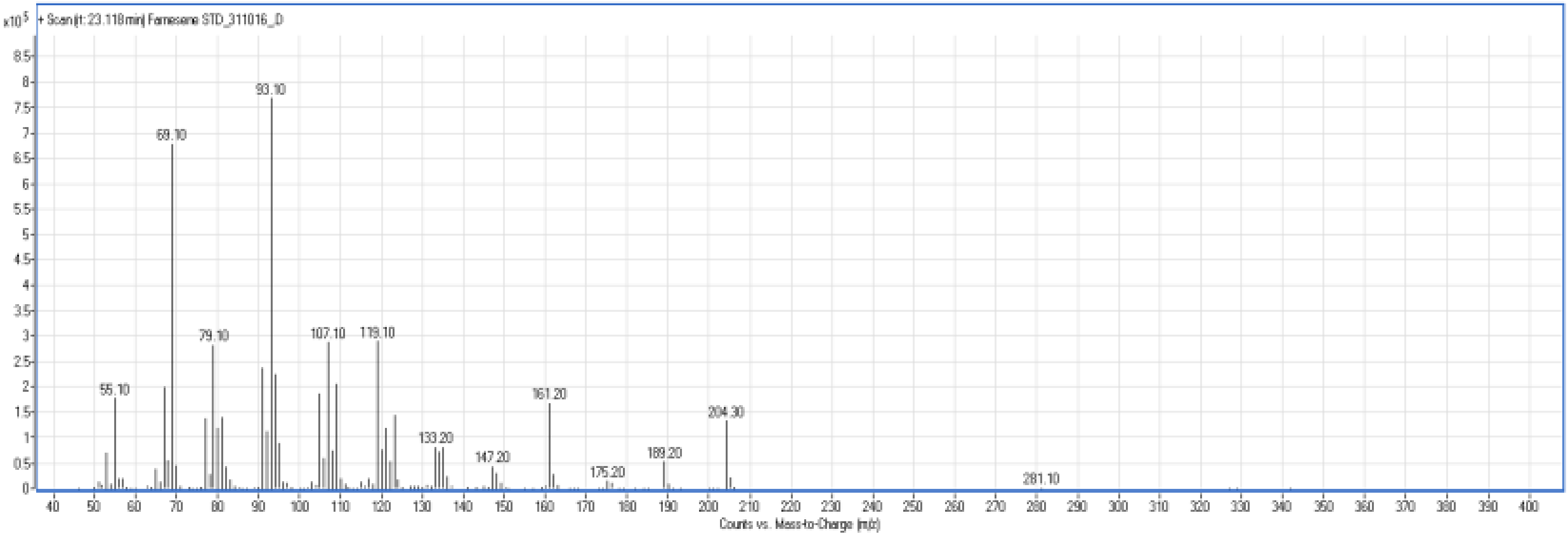


Fig. S10. Cont…

(*E*)-γ-Bisobolene

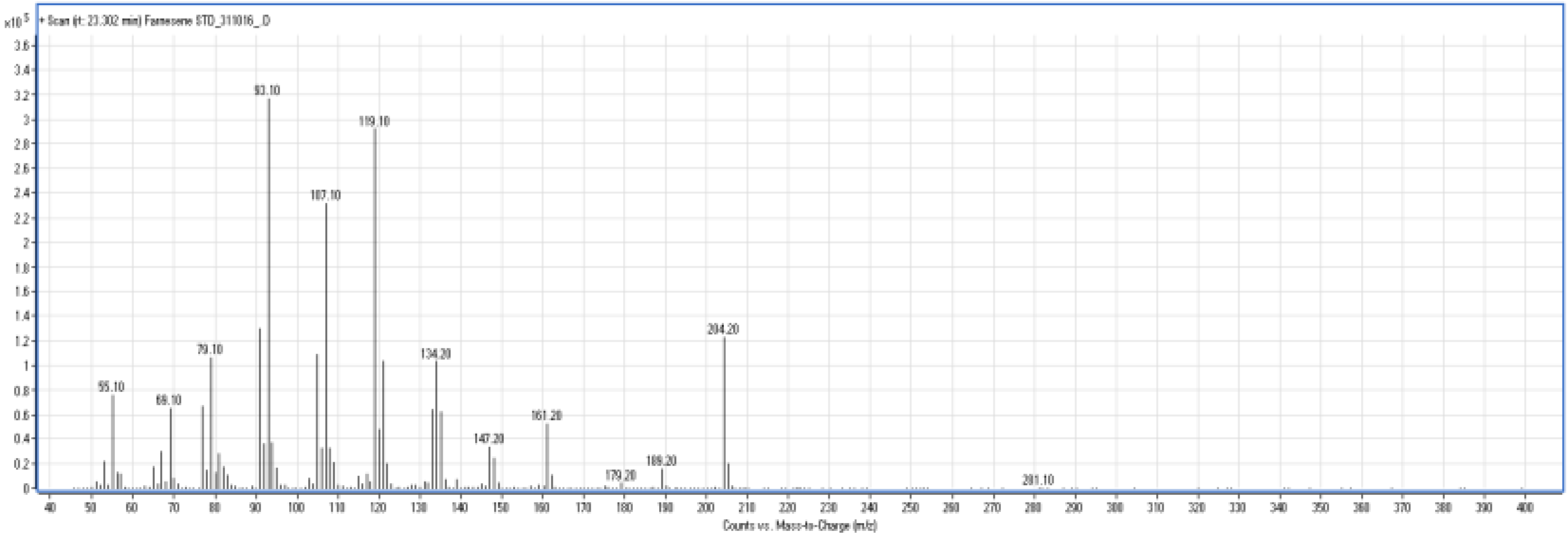


Fig. S10. Cont…

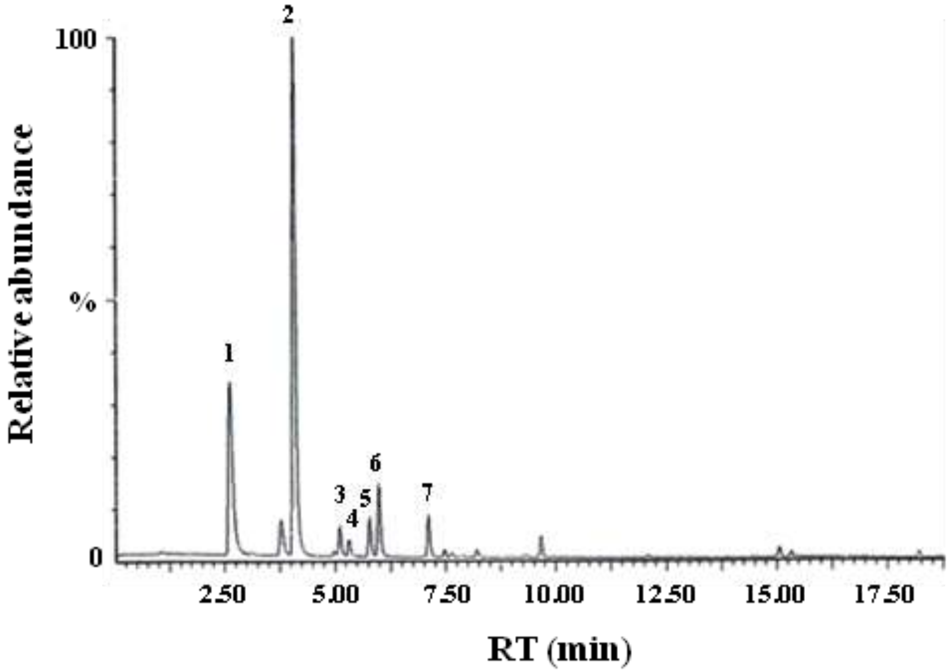


Fig. S11. Headspace volatile analysis of *M. koenigii* leaves by GC-MS. Peaks: 1, α-pinene; 2, sabinene; 3, β-myrcene; 4, α-terpinene; 5, limonene; 6, β-phellandrene; and 7, γ-terpinene.

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); ClCHS, *Curcuma longa* chalcone synthase (BAQ35543); ClDCS, *C. longa* diketide CoA synthase (C0SVZ5); ClCURS1, *C. longa* curcumin synthase 1 (C0SVZ6); EcFABH, *Escherichia coli* K-12 beta-ketoacyl-ACP synthase III (P0A6R0); Gh2PS, *Gerbera hybrida* 2-pyrone synthase (P48391); GhCHS1, *G. hybrida* naringenin-chalcone synthase 1 (P48390); GmBPS, *Garcinia mangostana* benzophenone synthase (AEI27291); HaBPS, *Hypericum androsaemum* benzophenone synthase (Q8SAS8); HpOKS, *H. perforatum* octaketide synthase (ACF37207); HpPKS, *H. perforatum* polyketide synthase (ABP98922); HmSTS, *Hydrangea macrophylla* stilbenecarboxylate 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 (Q9I0Q0); 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 (Q54240); VvTHS1, *Vitis vinifera* resveratrol synthase 1 (P28343); ZmCHS2, *Zea mays* chalcone synthase 2 (P24825).

Accession numbers used in Figure 4

AbLIMS, *Abies grandis* (-)-4*S*-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 synthase10 (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); ClLIMS2, *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 (BAD27257); CuLIS, *C. unshiu* linalool synthase (BAP75559); CuβOCS, *C. unshiu* (*E*)-β-ocimene synthase (BAD91046); CuγTPNS, *C. unshiu* γ-terpinene synthase (BAD27259); 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); Pp*ent*-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); PtαFS 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).