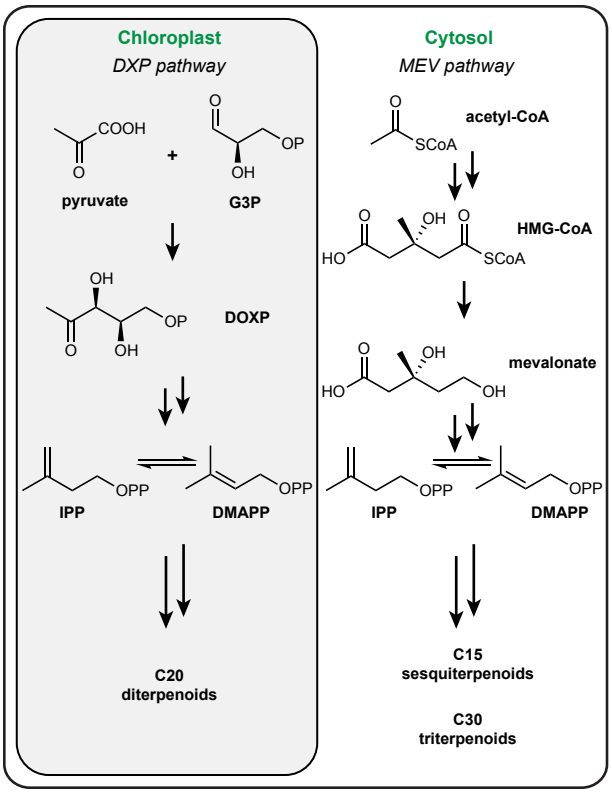
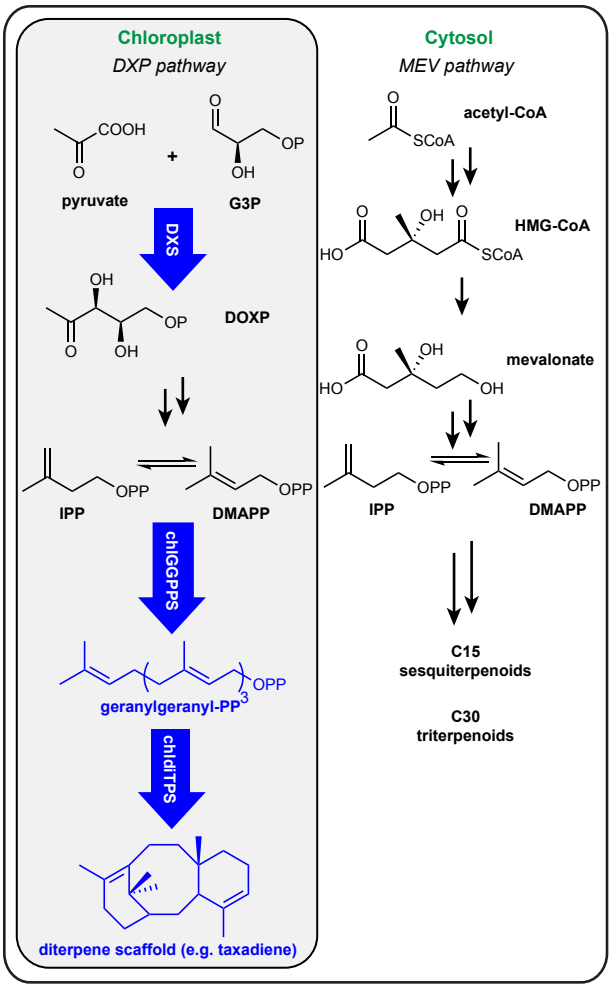
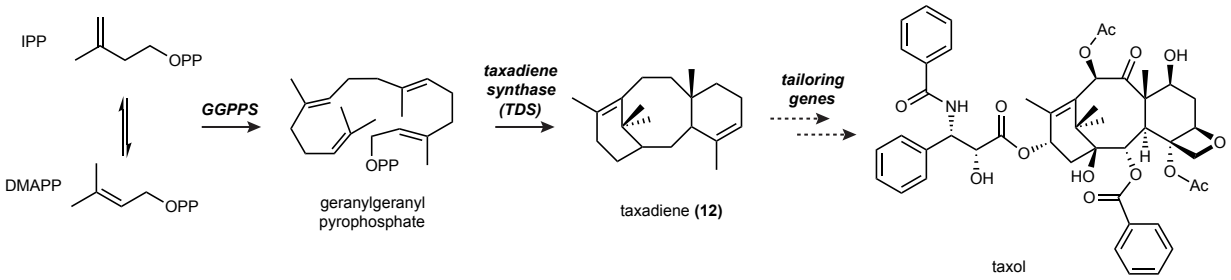


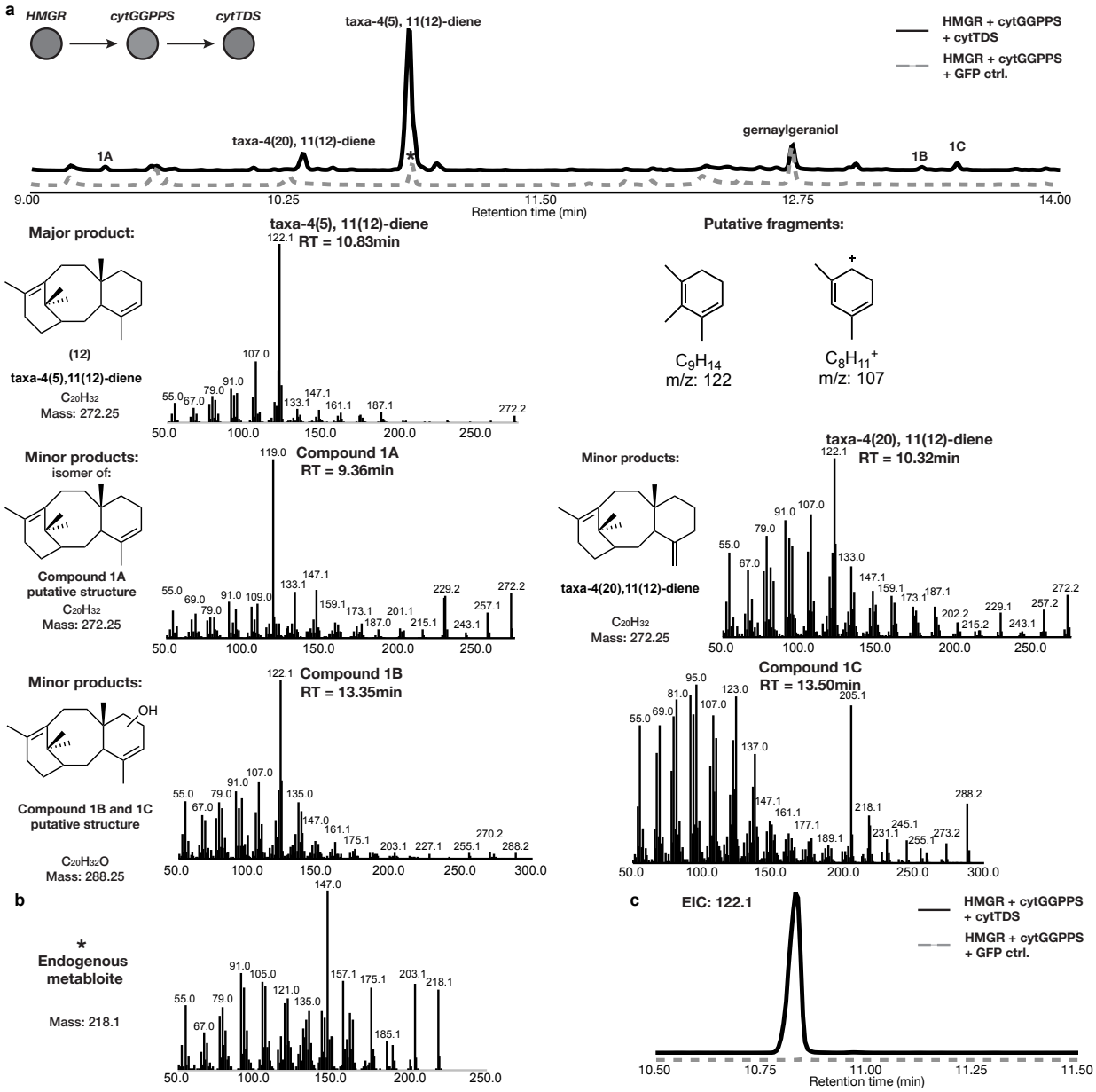
Supplementary Figure 1. Terpenoid biosynthesis in a plant cell can proceed via the chloroplast localized DXP pathway and the cytosol localized MEV pathway. G3P, glyceraldehyde 3-phosphate; DOXP, 1-deoxy-D-xylulose-5-phosphate synthase; IPP, isopentyl pyrophosphate; DMAPP, dimethylallyl pyrophosphate; HMG-CoA, 3-hydroxy-3-methylglutaryl-CoA.



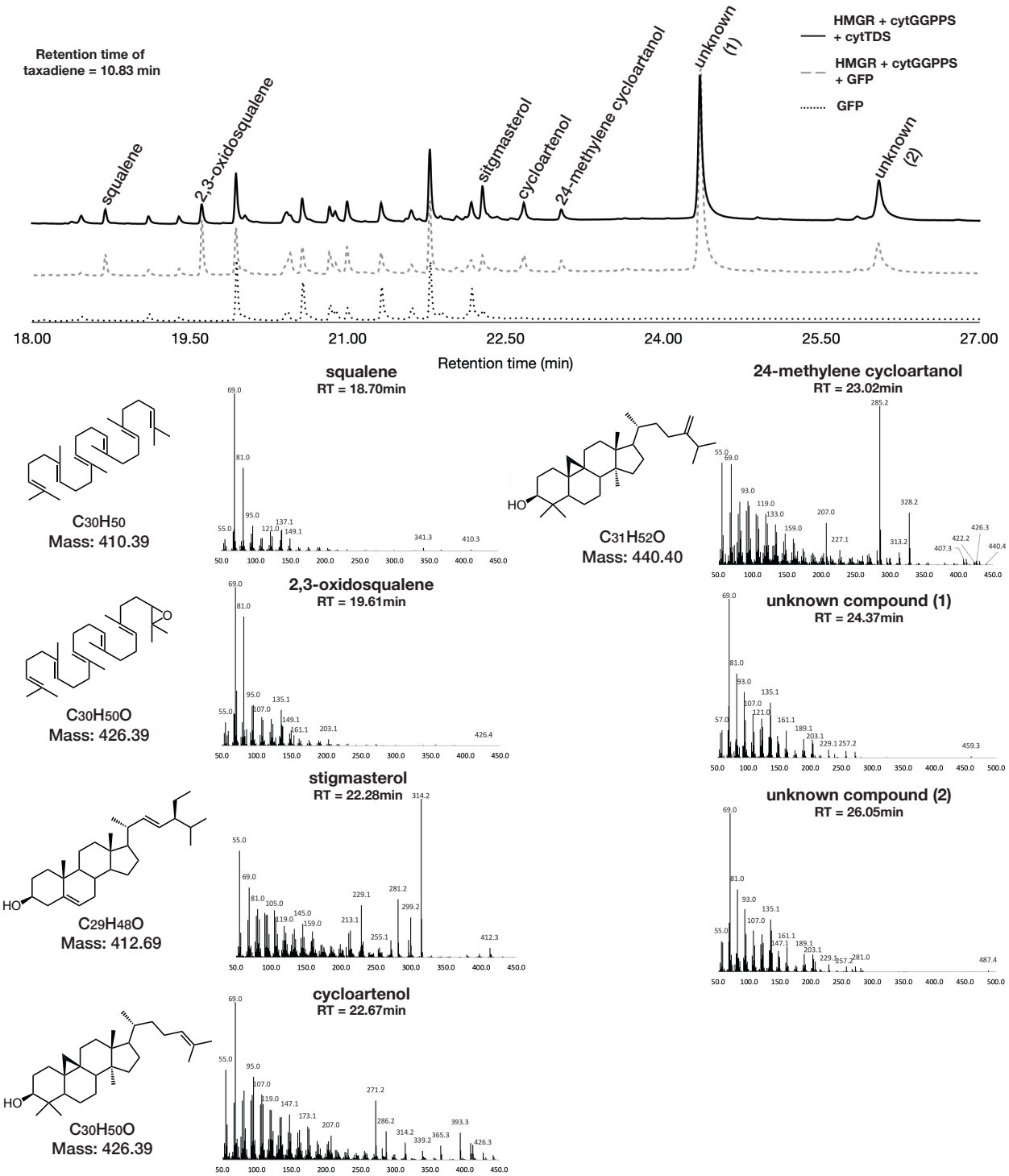
Supplementary Figure 2. Yield improvement of diterpenoids through the chloroplastic, DXP pathway requires overexpression of rate limiting gene DXS. Arrows in blue represent chloroplast localized and overexpressed genes.. G3P, glyceraldehyde 3-phosphate; DXS, 1-deoxy-D-xylulose-5-phosphate synthase; DOXP, 1-deoxy-D-xylulose-5-phosphate synthase; IPP, isopentyl pyrophosphate; DMAPP, dimethylallyl pyrophosphate; chlGGPPS, chloroplastic geranylgeranyl pyrophosphate synthase; chldiTPS, chloroplastic diterpene synthase(s); HMG-CoA, 3-hydroxy-3-methylglutaryl-CoA;



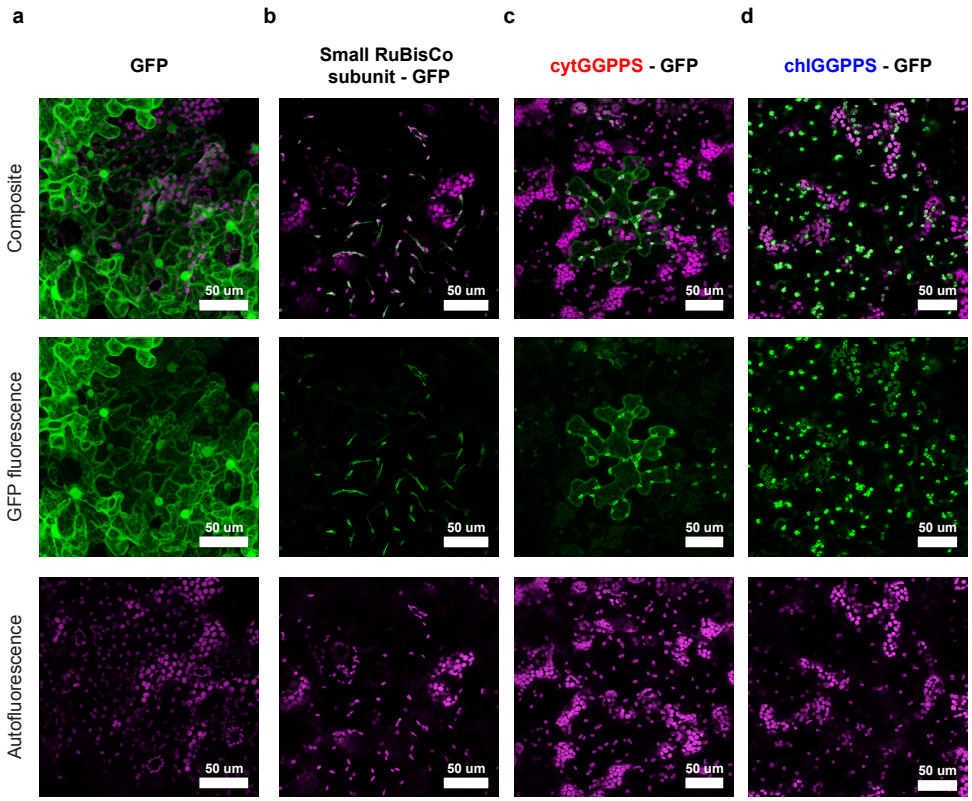
Supplementary Figure 3. Simplified taxol biosynthetic pathway



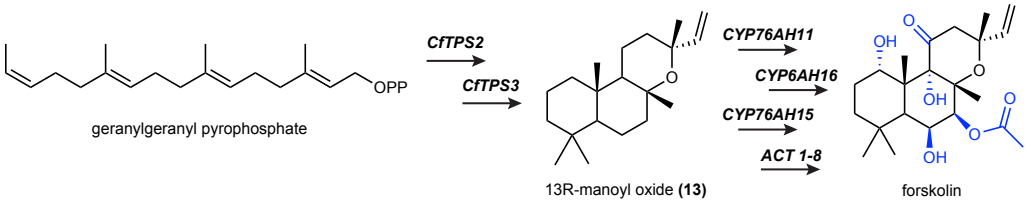
Supplementary Figure 4: Characterization of intermediates from overexpression of *cytTDS* via MEV engineering. (a) GC-MS total ion chromatogram (TIC) and MS spectra of products from overexpression of *HMGR*, *cytGGPPS* and *cytTDS* in *N. benthamiana*. Representative TICs are shown. Five products with m/z corresponding to diterpene derived scaffolds were observed upon expression of *cytTDS*. Identified products corresponded to **12**, isomer, taxadiene-4(20), 11(12)-diene, and three minor taxadiene-derived scaffolds[57]. Putative ion structures for **12** were assigned as reference. Putative structures are preliminary and based on predicted formulas combined with analysis of fragment ions observed in MS spectra. An endogenous metabolite co-eluting with taxadiene was identified (* in the TIC). **(b)** MS spectra of endogenous metabolite. **(c)** GC-MS extracted ion chromatogram (EIC) using m/z = 122.1, corresponding an abundant fragment found in the MS of **12**, confirmed that **12** is only present upon *TDS* expression.



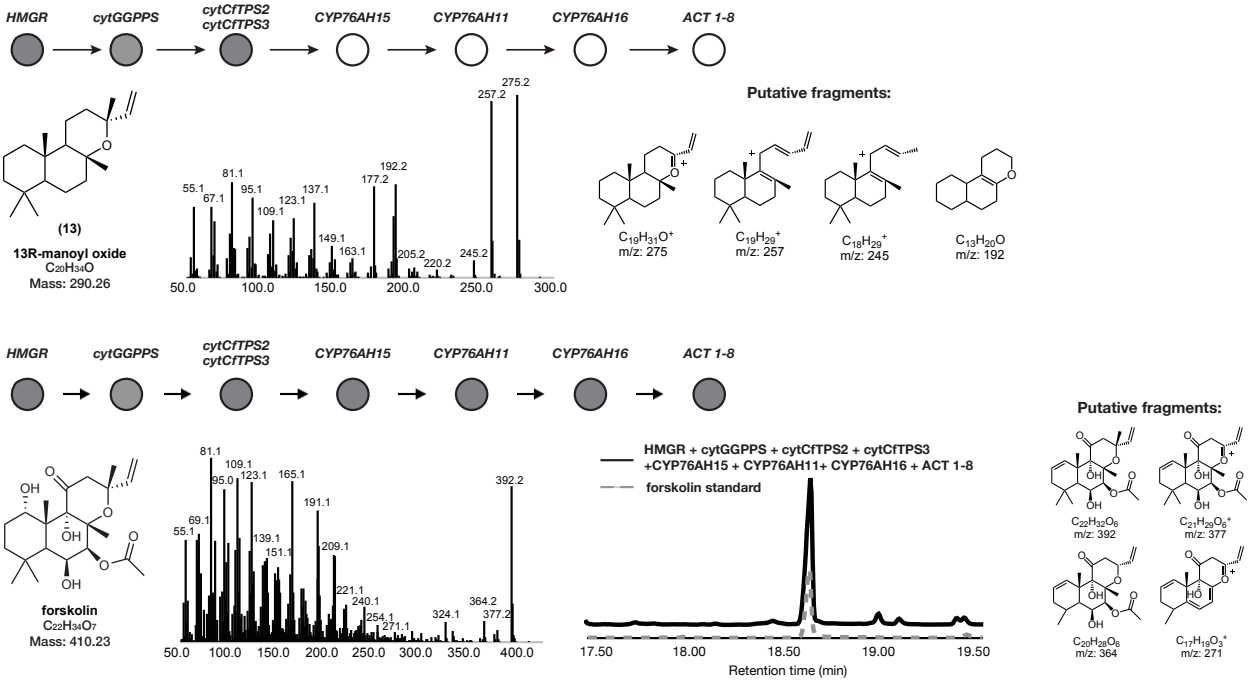
Supplementary Figure 5: Overexpression of *cytGGPPS* and *HMGR* alters endogenous triterpenoid metabolism. GC-MS total ion chromatogram (TIC) and MS spectra of triterpenoid derived products observed in *N. benthamiana*. Overexpression of *cytGGPPS* and *HMGR* results in the accumulation of endogenous phytosterols in leaf extracts independent of co-expression with *cytTDS*. Assignments for labeled peaks was done via comparison against MS spectra from previous reports[58].



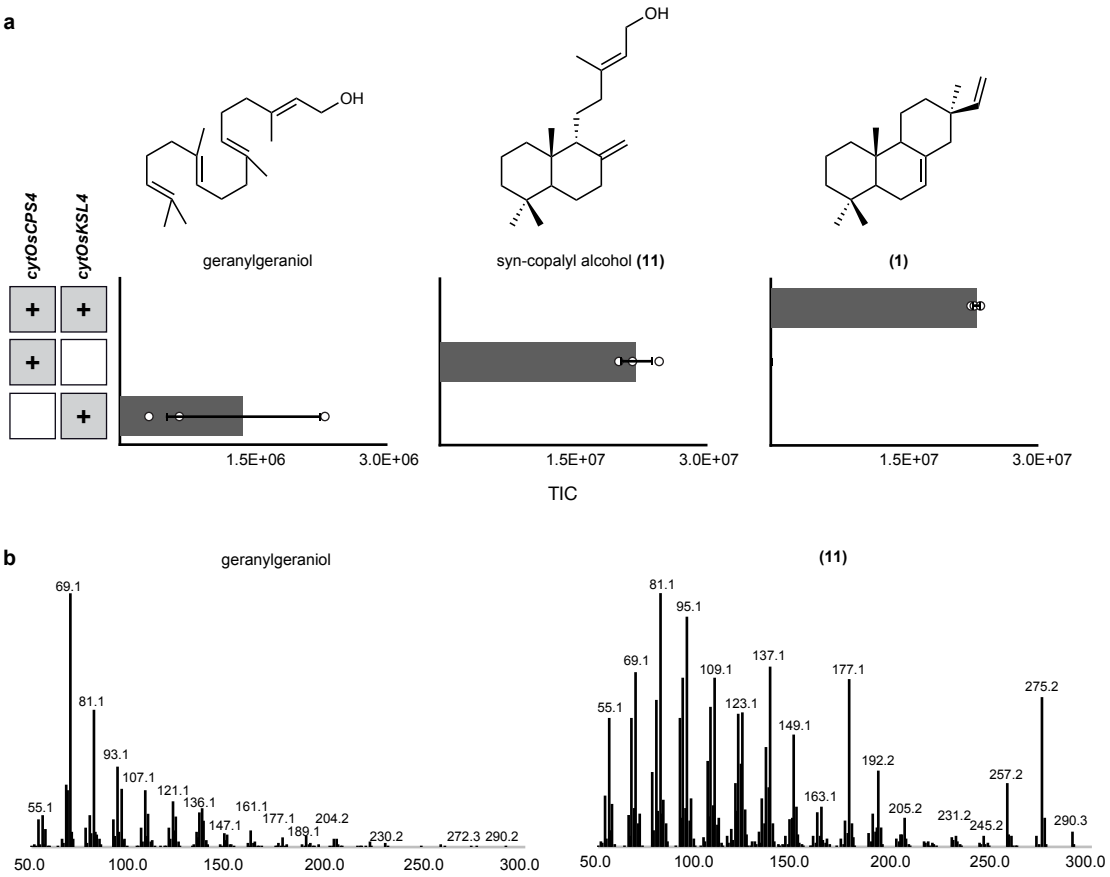
Supplementary Figure 6: Subcellular localization of overexpressed cytGGPPS-GFP and chlGGPPS-GFP fusion proteins and controls in *N. benthamiana*. (a) GFP localization and a **(b)** GFP fusion construct of the small subunit of RuBisCo indicate respective cytosolic and plastid localization. **(c)** Partial cytosolic localization of cytGGPPS-GFP was observed via the truncation of the predicted chloroplast transit peptide of GGPPS. **(d)** chlGGPPS-GFP overexpression resulted in plastid localization. Images of subcellular localization were chosen. All images show z-stacks of maximum intensity projections scaled to the same intensity range for GFP fluorescence (green; 488nm excitation, 500 - 550 emission), chlorophyll autofluorescence (magenta; 488nm excitation, 650nm excitation, 650 – 700 emission) and the two channel composite. Images are representative of three biological replicates repeated over two independent experiments.



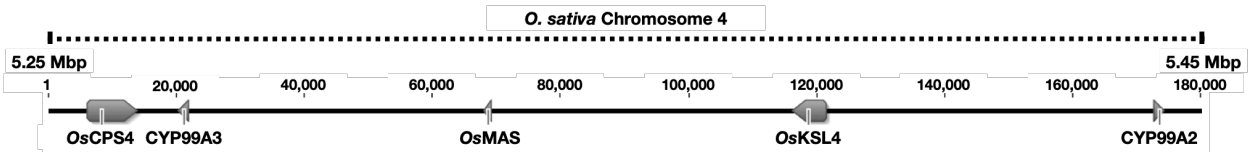
Supplementary Figure 7: Previously established forskolin biosynthetic pathway.



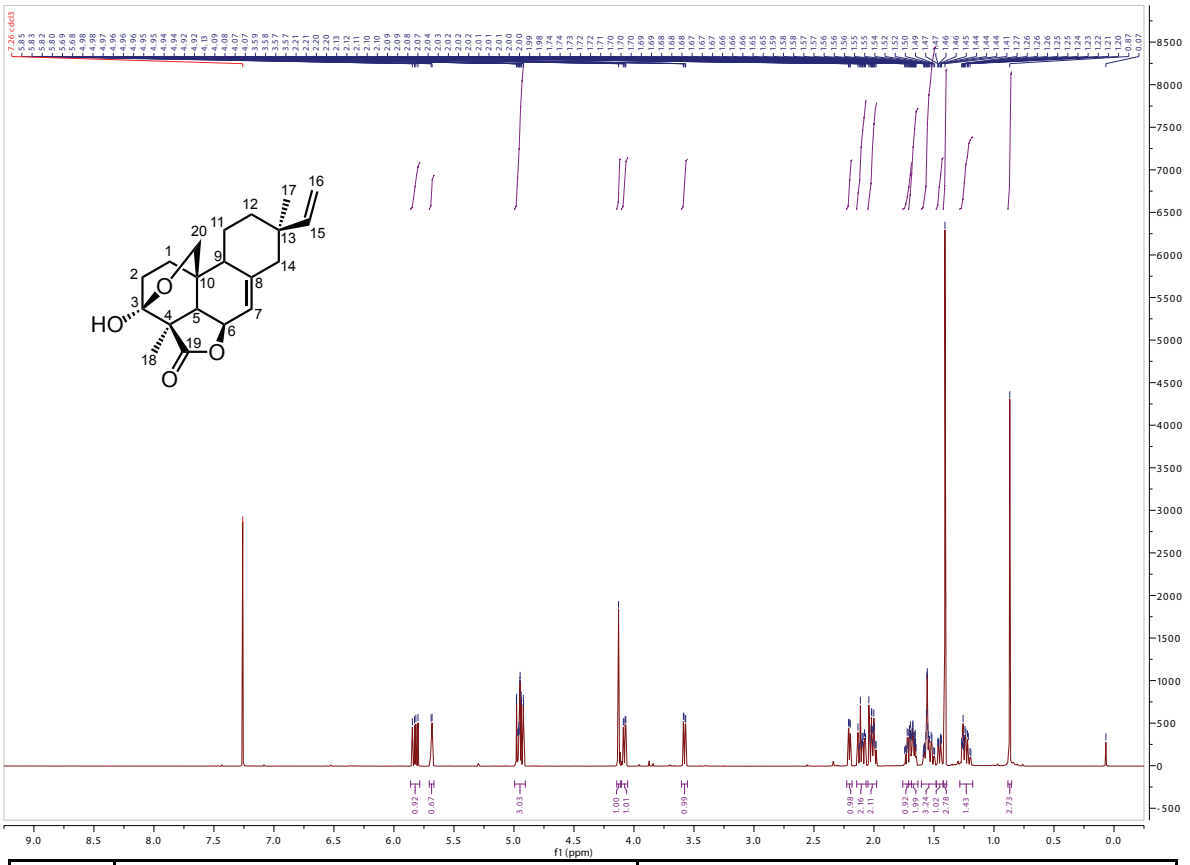
Supplementary Figure 8: MS spectra of 13R-manoyl oxide and forskolin. Putative ion structures for both products were assigned as reference.



Supplementary Figure 9: Characterization and yields of pathway intermediates upon overexpression of either *cytOsCPS4* or *cytOsKSL4* via cytosolic engineering. (a) Average GC-MS ion abundances of syn-pimaradiene precursors after overexpression of indicated genes via cytosolic engineering. Values and error bars represent the mean and the standard deviation of biological triplicates. **(b)** MS spectra of geranylgeraniol and **11**.



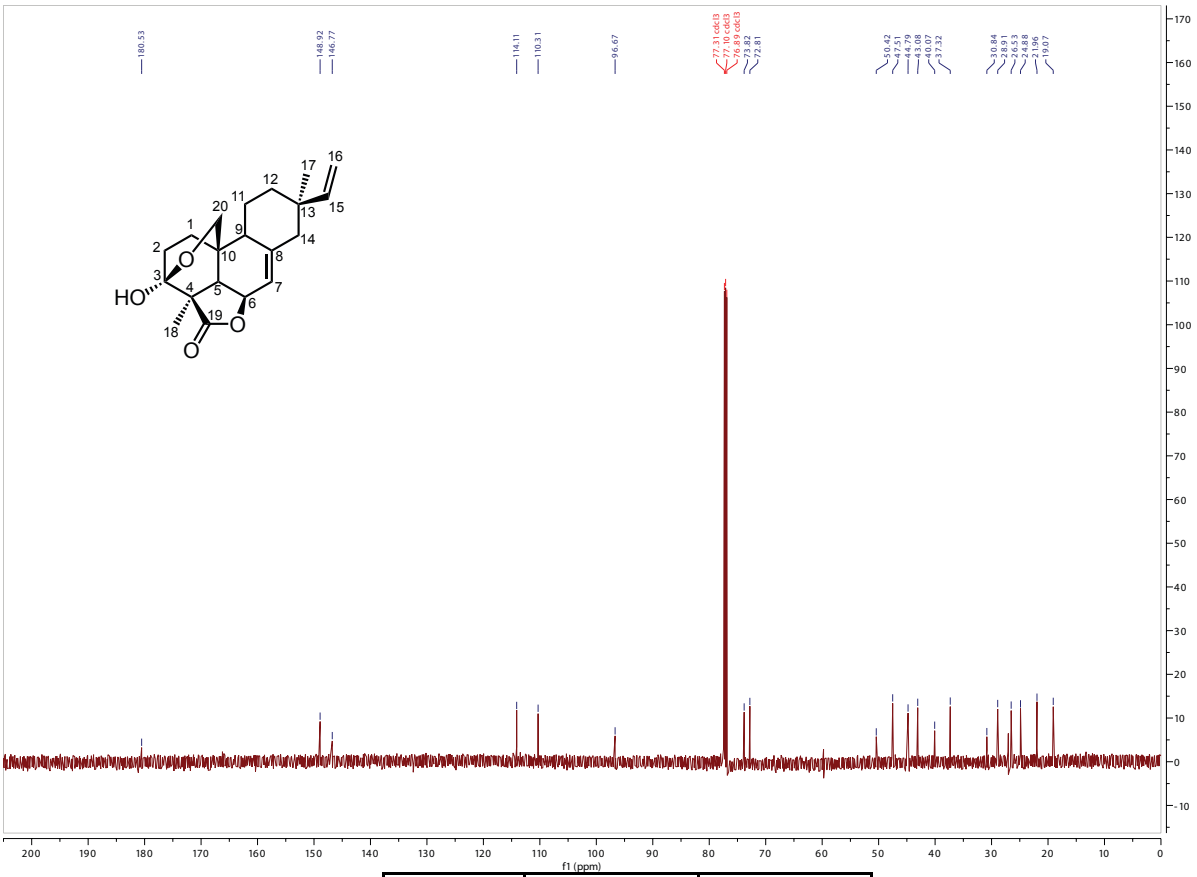
Supplementary Figure 10: Depiction of momilactone gene cluster on *Oryza sativa* chromosome 4. *Os*CPS4, *Os*KSL4, CYP99A3 and *Os*MAS have previously been directly implicated in momilactone biosynthesis.



Proton	^{1}H assignments (this study)			^{1}H assignments[10]		
	Shift (ppm)	*Multiplicity*	*Coupling (Hz)*	*Shift (ppm)*	*Multiplicity*	*Coupling (Hz)*
3-OH	4.13	bS			Not reported	
5-H	2.2	dd	6.8 and 2.1	2.2	dd	7.1 and 2.1
6-H	4.96	bd	4.3	4.94	dd	7.1 and 4.5
7-H	5.69	d	4.9	5.68	d	4.5
9 - H	1.76 - 1.69	m			Not reported	
15-H	5.82	dd	17.4 and 10.8	5.83	dd	17.6 and 10.5
16-H_A	4.93	dd	10.7 and 1.0	4.92	dd	10.5 and 1.2
16-H_B	4.96	dd	17.4 and 1.0	4.95	dd	17.6 and 1.2
17-H_3	0.87	S		0.87	S	
18-H_3	1.41	S		1.4	S	
20-H_A	3.58	dd	9.2 and 2.1	3.55	dd	9.0 and 2.1
20-H_B	4.08	dd	9.2 and 3.4	4.07	bd	9.0

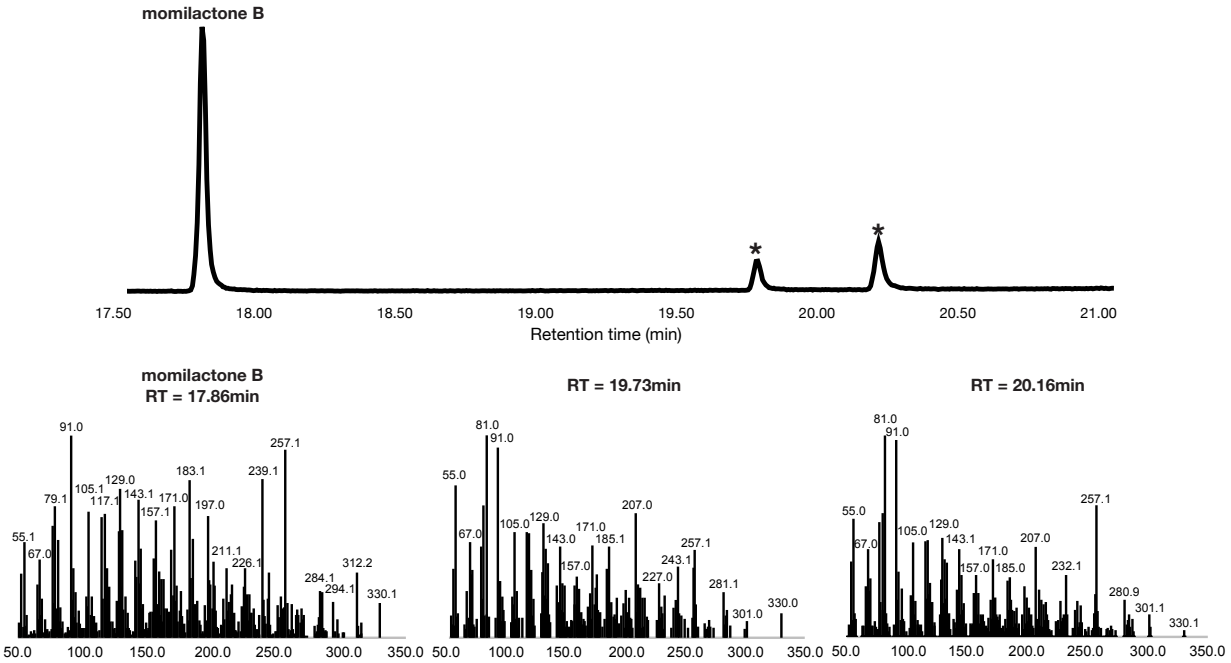
^{1}H NMR (600 MHz, Chloroform-*d*) δ 5.82 (dd, *J* = 17.4, 10.8 Hz, 1H), 5.69 (d, *J* = 4.9 Hz, 1H), 4.96 (dd, *J* = 17.4, 1.0 Hz, 1H), 4.96 (bd, 1H), 4.93 (dd, *J* = 10.7, 1.0 Hz, 1H), 4.13 (bs, 1H), 4.08 (dd, *J* = 9.2, 3.4 Hz, 1H), 3.58 (dd, *J* = 9.2, 2.1 Hz, 1H), 2.20 (dd, *J* = 6.8, 2.1 Hz, 1H), 2.14 – 2.07 (m, 2H), 2.05 – 1.98 (m, 2H), 1.76 – 1.69 (m, 1H), 1.71 – 1.63 (m, 2H), 1.60 – 1.48 (m, 2H), 1.48 – 1.42 (m, 1H), 1.41 (s, 3H), 1.28 – 1.18 (m, 1H), 0.87 (s, 3H).

Supplementary Figure 11: ^{1}H NMR spectra of momilactone B in $CDCl_3$ isolated from *N. benthamiana*.



Carbon #	^{13}C δ ppm	^{13}C δ ppm[10]
1	28.91	28.82
2	26.53	26.45
3	96.67	96.59
4	50.42	50.36
5	43.08	43.02
6	73.82	73.78
7	114.11	114.00
8	146.77	146.70
9	44.79	44.65
10	30.84	30.76
11	24.88	24.81
12	37.32	37.25
13	40.07	39.98
14	47.51	47.44
15	148.92	148.83
16	110.31	110.18
17	21.96	21.90
18	19.07	18.99
19	180.53	180.52
20	72.81	72.74

Supplementary Figure 12: ^{13}C NMR spectra of momilactone B in $CDCl_3$ isolated from *N. benthamiana*.



Supplementary Figure 13: TIC from purified momilactone B from large scale isolation in *N. benthamiana*. Two impurities were not separable by silica-gel chromatography. Based on MS fragmentation patters, these impurities possibly correspond to structural isomers of momilactone B or the ring-opened form of the lactol.

Supplementary Table 1: List of potential momilactone biosynthetic gene candidates.

	Name	Family	Gene ID	Chromosome	Rank				
					Bait: ***Os*CPS4**	*Bait:* **CYP99A3**	*Bait:* ***Os*MAS**	*Bait:* **CYP99A2**	*Bait:* ***Os*KSL4**
1	**CYP99A3**	P450	Os04g0178400	4*	3	N/A	76	26	271
2	**CYP701A8**	P450	Os06g0569500	6	4	6	89	7	154
3	CYP99A2	P450	Os04g0180400	4*	8	28	33	N/A	98
4	CYP701A9	P450	Os06g0568600	6	22	39	69	49	323
5	CYP71Z8	P450	Os10g0439800	10	31	84	7	18	230
6	CYP71Z5	P450	Os02g0529800	2	55	77	165	32	175
7	CYP94E3	P450	Os05g0382500	5	94	210	14	58	281
8	**CYP76M14**	P450	Os01g0561600	1	172	338	67	135	409
9	**CYP76M8**	P450	Os02g0569400	2^	620	581	882	273	4
10	CYP76M5	P450	Os02g0569000	2^	341	249	711	194	72
11	2-ODD candidate #1	2-ODD	Os09g0245500	9	48	12	232	139	503
12	2-ODD candidate #2	2-ODD	Os04g0662600	4	245	464	88	136	306
13	SDR candidate #1	SDR	Os07g0664000	7	16	27	42	89	558
14	***Os*MAS**	SDR	Os04g0179200	4*	17	69	N/A	22	309
15	SDR candidate #2	SDR	Os07g0663700	7	66	158	20	43	24
16	***Os*CPS4**	Terpene synthase	Os04g0178300	4*	N/A	3	19	8	243
17	*Os*KSL8	Terpene synthase	Os11g0474800	11	47	81	112	102	447
18	*Os*KSL7	Terpene synthase	Os02g0570400	2^	111	61	332	68	103
19	***Os*KSL4**	Terpene synthase	Os04g0179700	4*	386	392	532	125	N/A

List is ranked via Pearson's correlation coefficient between genes present in the momilactone biosynthetic cluster and biosynthetic candidates. Potential biosynthetic genes shown correspond only to genes belonging to CYP, 2-ODD, SDR, and terpene synthase families. Gene names in bold correspond to genes involved in momilactone biosynthesis. A * or a ^ indicate genes present in either the momilactone gene cluster or the phytocassane gene cluster.

Supplementary Table 2: Yields of diterpenoid products engineered in this study**.**

Pathway	Compound	Compound use for standard	MEV Eng.		DXP Eng.		Plants	Plant weight (g)	Isolated (mg)	Isolated yield	
			mg/g FW	mg/g DW[1]	mg/g FW	mg/g DW[1]				ug/g FW	ug/g DW[1]
taxane biosynthesis	taxadiene **(12)**	5a-taxadiene-ol	0.13 ± 0.03	1.27 ± 0.31	0.02 ± 0.00	0.20 ± 0.03	-	-	-		-
momilactone biosynthesis	syn-pimaradiene **(1)**	GGOH	0.13 ± 0.06	1.32 ± 0.57	0.01 ± 0.01	0.13 ± 0.07	-	-	-		-
	(6)	momilactone B	0.06 ± 0.01	0.63 ± 0.10	-	-	-	-	-		-
	momilactone A **(8)**	momilactone B	0.03 ± 0.02	0.28 ± 0.15	-	-	-	-	-		-
	(7)	momilactone B	0.01 ± 0.01	0.12 ± 0.07	-	-	-	-	-		-
	momilactone B	momilactone B	0.02 ± 0.01	0.17 ± 0.08	-	-	80	216	3.6	16.7	167
forskolin biosynthesis	13-R-manoyl oxide **(13)**	GGOH	0.67 ± 0.07	6.67 ± 0.69	0.06 ± 0.01	0.57 ± 0.13	-	-	-		-
	forskolin	forskolin	0.13 ± 0.03	1.27 ± 0.26	0.02 ± 0.01	0.19 ± 0.09	-	-	-		-

[1]Fresh to dry weight calculations correspond to typically observed ~90% weight loss after lyophillization of *N. benthamiana* leaves.

Supplementary Table 3: Germination efficiency of *A. thaliana* seeds (n=100).

Time days	**DMSO** mock	**SA** 1 mM	**momilactone B**		
			2.5 uM	12.5 uM	60 uM
0	0%	0%	0%	0%	0%
3	99%	0%	0%	0%	0%
5	99%	0%	97%	0%	0%
7	99%	0%	97%	0%	0%
10	99%	0%	97%	81%	0%

Supplementary Table 4: List of PCR primer pairs used in this study.

Purpose	Name		Primer Sequence (5' to 3')
Metabolic engineering	HMGR	Fwd	ATTCTGCCCAAATTCGCGACCGGT**ATGAAGAAAAAGCAAGCTGG**
		Rev	GAAACCAGAGTTAAAGGCCTCGAG**TCATGTTGTTGTTGTTGTCGTTGTCG**
	chlGGPPS	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	GAAACCAGAGTTAAAGGCCTCGAG**TCAGTTTTGCCTGAATGCAATG**
	cytGGPPS	Fwd	ATTCTGCCCAAATTCGCGACCGGT**ATGGCTTCCTATCAAGAATGC**
		Rev	GAAACCAGAGTTAAAGGCCTCGAG**TCAGTTTTGCCTGAATGCAATG**
	DXS	Fwd	ATTCTGCCCAAATTCGCGACCGGT**ATGGCTTCTTCTGCATTTGC**
		Rev	GAAACCAGAGTTAAAGGCCTCGAG**TCAAAACAGAGCTTCCCTTGG**
Taxane biosynthesis	chlTDS	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	GAAACCAGAGTTAAAGGCCTCGAG**TCATACTTGAATTGGATCAATATAAACTTTTC**
	cytTDS	Fwd	ATTCTGCCCAAATTCGCGACCGGT**ATGGTAATGATGAGCAGCAG**
		Rev	GAAACCAGAGTTAAAGGCCTCGAG**TCATACTTGAATTGGATCAATATAAACTTTTC**
Forskolin biosynthesis	chl*Cf*TPS2	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
	(22-773)cyt*Cf*TPS2	Fwd	ATTCTGCCCAAATTCGCGACCGGT**ATGAACAGCAATAAAAGGCAGTC**
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
	(46-773)cyt*Cf*TPS2	Fwd	ATTCTGCCCAAATTCGCGACCGGT**ATGGTTGCAAGTCTGGATGCG**
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
	chl*Cf*TPS3	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
	(23-598)cyt*Cf*TPS3	Fwd	ATTCTGCCCAAATTCGCGACCGGT**ATGTCTGCAGCTGTTAAATGC**
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
	(38-598)cyt*Cf*TPS3	Fwd	ATTCTGCCCAAATTCGCGACCGGT**ATGGGAATCTTGCCAGTCCACC**
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
	CYP76AH15	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
	CYP76AH11	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
	CYP76AH16	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
	ACT 1-8	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
Momilactone biosynthesis	chl*Os*CPS4	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
	cyt*Os*CPS4	Fwd	ATTCTGCCCAAATTCGCGACCGGT**ATGCCGCCGTACCCGGCC**
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
	chl*Os*KSL4	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
	cyt*Os*KSL4	Fwd	ATTCTGCCCAAATTCGCGACCGGT**ATGGCGGTGATGTCGTCCTG**
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
	CYP99A3	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	GAAACCAGAGTTAAAGGCCTCGAG

Purpose	Name	Primer Sequence	
Momilactone biosynthesis	**CYP76M8**	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
	***Os*MAS**	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
	CYP76M14	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
	CYP701A8	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
Momilactone biosynthesis gene candidates	**CYP99A2**	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
	CYP701A9	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
	CYP71Z8	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
	CYP71Z5	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
	CYP94E3	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
	CYP76M5	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
	2-ODD candidate #1	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
	2-ODD candidate #2	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
	SDR candidate #1	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
	SDR candidate #2	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	GAAACCAGAGTTAAAGGCCTCGAG
GFP fusion constructs	**GFP**	Fwd	*GGTTCGGGAAGC***ATGACTAGCAAAGGAGAAGAAC**
		Rev	GAAACCAGAGTTAAAGGCCTCGAG**TTATTTGTATAGTTCATCCATGCC**
	Gibson overlaps chlTDS-GFP	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	**GTTCTTCTCCTTTGCTAGTCAT***GCTTCCCGAACC***TACTTGAATTGGATCAATATAAAC**
	Gibson overlaps cytTDS-GFP	Fwd	ATTCTGCCCAAATTCGCGACCGGT**ATGGTAATGATGAGCAGCAG**
		Rev	**GTTCTTCTCCTTTGCTAGTCAT***GCTTCCCGAACC***TACTTGAATTGGATCAATATAAAC**
	Gibson overlaps chlGGPPS-GFP	Fwd	ATTCTGCCCAAATTCGCGACCGGT
		Rev	**GTTCTTCTCCTTTGCTAGTCAT***GCTTCCCGAACC***GTTTTGCCTGAATGCAATGTAATC**
	Gibson overlaps cytGGPPS-GFP	Fwd	ATTCTGCCCAAATTCGCGACCGGT**ATGGCTTCCTATCAAGAATGC**
		Rev	**GTTCTTCTCCTTTGCTAGTCAT***GCTTCCCGAACC***GTTTTGCCTGAATGCAATGTAATC**
	Gibson overlaps Small RuBisCo subunit - GFP	Fwd	ATTCTGCCCAAATTCGCGACCGGT**ATGGCTTCCTCTATGCTCTCTTCC**
		Rev	**GTTCTTCTCCTTTGCTAGTCAT***GCTTCCCGAACC***TTCGGAATCGGTAAGGTCAGG**

[1]Nucleotides emphazised in **bold** represent those which hybridize to the gene of interest. Nucleotides emphasized in *italics* represent those which hybridize to the four peptide linker used to link fusion protein constructs. All other nucleotides consist of the 5' overlaps designed for Gibson assembly with pEAQ-HT vector. Gene accession numbers and IDs can be found in Supplementary Table 5.

Supplementary Table 5: Accession numbers and gene IDs used in this study.

Name	Organism	Gene ID / Accession	Reference
HMGR	*Nicotiana tabacum*	AT1G76490.1 / AY488113	51
GGPPS	*Taxus canadensis*	AF081514	60
DXS	*Arabidopsis thalaina*	AT4G15560.1 / BT002340	52
TDS	*Taxus brevifolia*	U48796	38
***Cf*TPS2**	*Plectranthus barbatus*	KF444507	42
***Cf*TPS3**	*Plectranthus barbatus*	KF444508	
CYP76AH15	*Plectranthus barbatus*	KT382358	20
CYP76AH11	*Plectranthus barbatus*	KT382349	
CYP76AH16	*Plectranthus barbatus*	KT382359	
ACT 1-8	*Plectranthus barbatus*	KT382363	
***Os*CPS4**	*Oryza sativa*	Os04g0178300 / AB066270	25, 26
***Os*KSL4**	*Oryza sativa*	Os04g0179700 / AB126934	27, 28
CYP99A3	*Oryza sativa*	Os04g0178400 / AK071864	29
CYP76M8	*Oryza sativa*	Os02g0569400 / XM_015768144.1	30
***Os*MAS**	*Oryza sativa*	Os04g0179200 / XM_015778721.1	32
CYP76M14	*Oryza sativa*	Os01g0561600 / XM_015773010.1	This study
CYP701A8	*Oryza sativa*	Os06g0569500 / XM_015785419.1	43
CYP99A2	*Oryza sativa*	Os04g0180400 / XM_015778482.1	-
CYP701A9	*Oryza sativa*	Os06g0568600 / XM_015786143.1	-
CYP71Z8	*Oryza sativa*	Os10g0439800 / XM_015759387.1	-
CYP71Z5	*Oryza sativa*	Os02g0529800 / XM_015768673.1	-
CYP94E3	*Oryza sativa*	Os05g0382500 / XM_015782035.1	-
CYP76M5	*Oryza sativa*	Os02g0569000 / XM_015768639.1	30
2-ODD candidate #1	*Oryza sativa*	Os09g0245500 / XM_015755150.1	-
2-ODD candidate #2	*Oryza sativa*	Os04g0662600 / XM_015779149.1	59
SDR candidate #1	*Oryza sativa*	Os07g0664000 / XM_015790180.1	-
SDR candidate #2	*Oryza sativa*	Os07g0663700 / XM_015791272.1	-
Small RuBisCo subunit	*Arabidopsis thaliana*	RBCS1A / AT1G67090.1	-

Supplementary Table 6: Chloroplast transit peptide predictions using ChloroP and LOCALIZER.

Gene	Chloroplast transit peptide residues	
	ChloroP	LOCALIZER
GGPPS	(1 - 18)	(1 - 41)
TDS	(1 - 58)	(1 - 51)
***Cf*TPS2**	(1 -45)	(1 - 21)
***Cf*TPS3**	(1 - 37)	(1 - 22)
***Os*CPS4**	(1 - 56)	(1 - 52)
***Os*KSL4**	(1 - 81)	(1 - 73)

[1] Cells in gray indicate the truncated gene variant used in this study.

Supplementary Table 7: Table of Pfam numbers used to find momilactone biosynthetic genes

Family	Pfam #	ID
CYP450s	PF00067	p450
2-ODDs	PF03171	2OG-FeII_Oxy
	PF13532	2OG-FeII_Oxy 2
	PF13640	2OG-FeII_Oxy 3
	PF13661	2OG-FeII_Oxy 4
	PF13759	2OG-FeII_Oxy 5
	PF10014	2OG-Fe_Oxy_2
	PF16870	OxoGdeHyase_C
SDRs	PF00106	Adh_short
Terpene synthase	PF01397	Terpene_synth
	PF03936	Terpene_synth_C
Other PFAMs	PF01370	Epimerase
	PF01073	3Beta_HSD