

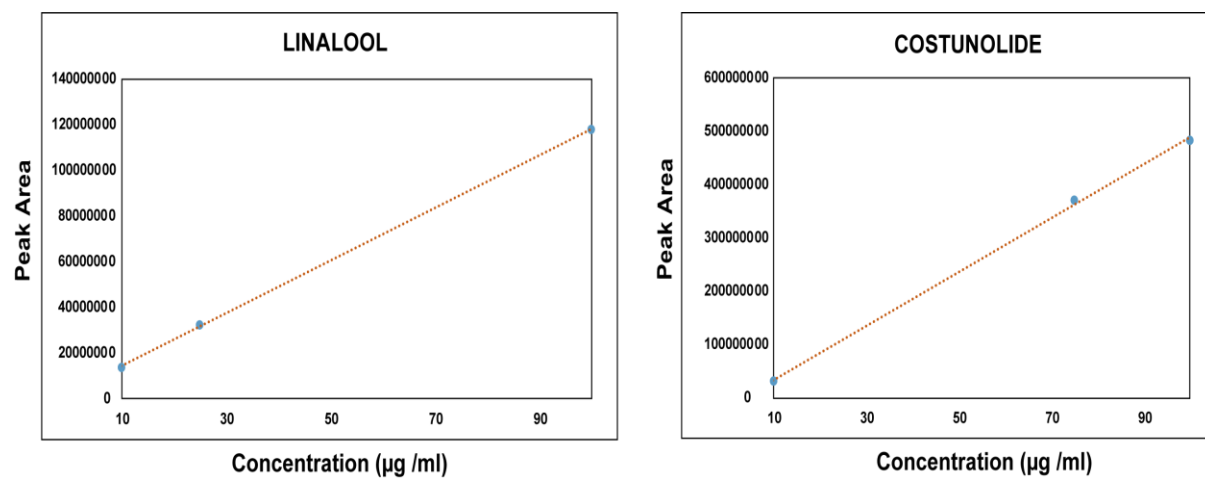
Supplementary Table 1. List of MEP and MVA gene name, accession number, plant source, full-length, qPCR primer sequences and gene products.

Pathways	Gene name	Accession number	Plant source	Primer Name	Full length sequence (5' to 3')	Size (bp)	qPCR sequence (5' to 3')	Size (bp)
MEP	1-deoxy-D-xylulose-5-phosphate synthase (DXS)	EU650419	<i>Nicotiana tabacum</i>	DXS_FP	ATGGCGCTGAATTTGCTG	1212	GCAGACAAGTATCACGGAGTAG	99
				DXS_RP	TTATACAAGAGCTGGACTAAAACC		CTCCGCAAAGTACGTCGTATAG	
	1-deoxy-D-xylulose 5-phosphate reductoisomerase (DXR)	DQ839130	<i>Nicotiana tabacum</i>	DXR_FP	ATGGCGCTGAATTTGCTG	1816	CCTACAGTGGCTGCCATAAA	94
				DXR_RP	TTATACAAGAGCTGGACTAAAACC		GCGCAAGAGGAAGAACAAATG	
	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (CMK)	KJ159923	<i>Nicotiana tabacum</i>	CMK_FP	ATGGCTTCTTGTAATTTCTAAG	1029	TCTGGTGAGATCGGTTCTGATA	100
				CMK_RP	CTAAGAATTATCAAAAGATCCGG		GTATGGGCGATGGGATATCTTG	
	Isopentenyl-diphosphate isomerase	AB049815	<i>Nicotiana tabacum</i>	IDI_FP	ATGTCGCTGACAACTACG	1753	GCAACGATCAGCAACAAAGG	106
				IDI_RP	TTAAGTCAATTTGTGGA		CCCAAGAGCATTCTCC	

	(IDI)				TGGTTT		TCAAT	
	Geranyl pyrophospha te synthase (GGPS)	KF977582	<i>Nicotiana tabacum</i>	GPPS_FP	ATGCTATTTGCAAGGGG	1468	GTACCAGGCAGCAGT GTATAG	93
				GPPS_RP	CTATTTTGTCTTGTGAT GACTC		GTCGTGTGTCAGCATC ATCTA	
	Linalool synthase (LIS)	U58314	<i>Clarkia breweri</i>	LIS_FP	ATGCAGCTCATAACAAA TTTCTC	1474	CTGCGGAACTATACAG GGATTC	108
				LIS_RP	TTAACTGAAACATAGTT TGATGTTG		CACGGATTTCGTCGTC ATCTAA	
MVA	Acetoacetyl- CoA-thiolase (AAT)	AF364059	<i>Arabidopsis thaliana</i>	AAT_FP	ATGGCCCATACATCAGA ATCTG	1212	TTTGGCAGAAGCAAGGA AGG	103
				AAT_RP	TCAAAGGAGCTCAAGA ACTAGAG		TCCCATCCCACAGTCGT TATAG	
	Hydroxy-3- methylglutar yl-CoA reductase (HMGR)	LC015758	<i>Nicotiana benthamiana</i>	HMGR_F P	ATGGACGTTCCCGGAG ATC	1816	CGTGCAGATACCTGTTG GAATA	100
				HMGR_R P	TTAGGAGGATGCCTTTG TGACATC		TGGTGCTAGCCACTAAA CATC	
	Farnesyl pyrophospha te synthase (FPS)	NM117823	<i>Arabidopsis thaliana</i>	FPS_FP	ATGAGTGTGAGTTGTTG TTGTAG	1029	TACGCGGAGGGAAGCTA AA	109
				FPS_RP	CTACTTCTGCCTCTTGTA GATCT		CCAAGAGCACATGAGA GGAAAG	

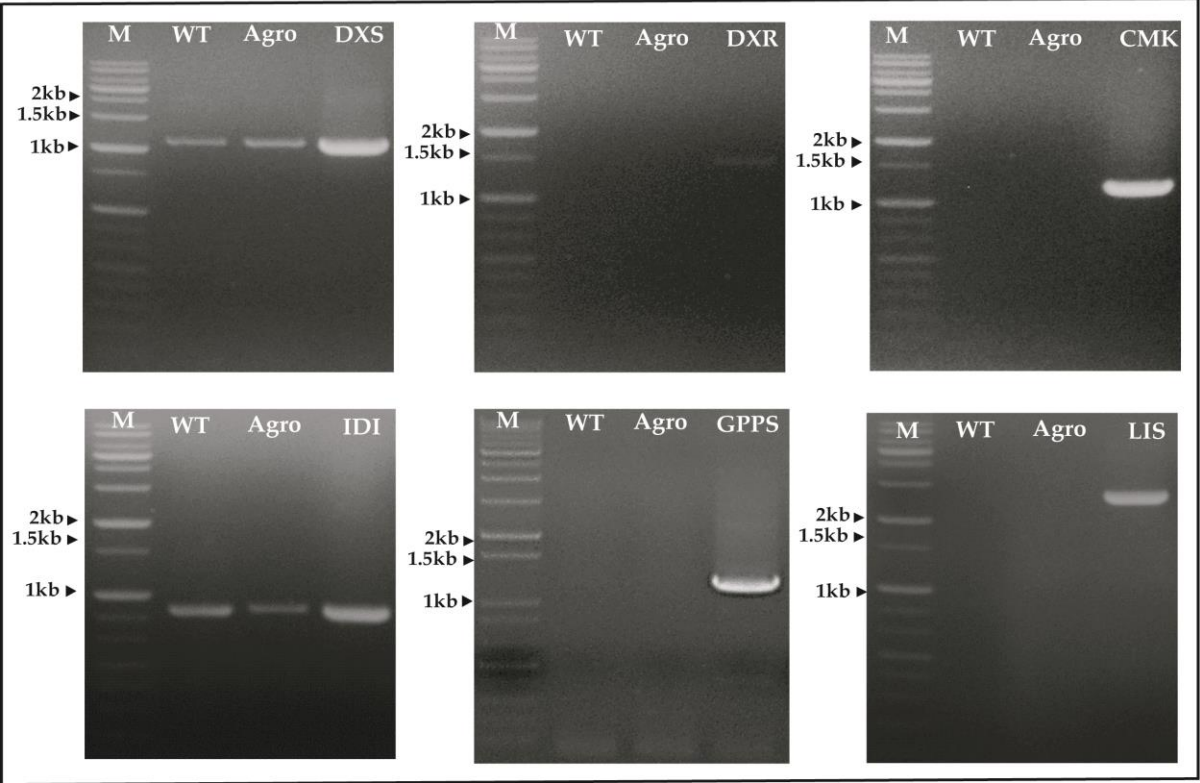
	Germacrene A synthase (GAS)	AF497999	<i>Cichorium intybus</i>	GAS_FP	ATGGCTCTCGTTAGAAA CAA	1753	ATTCCAACAATCCGTCC CTTAC	101
				GAS_RP	TCAGTTTTCGAGACTCG GTGGA		TGATACGTGCCCCGAGAG TAATA	
	Germacrene A oxidase (GAO)	GU256644	<i>Cichorium intybus</i>	GAO_FP	ATGGAGCTCTCACTCAC TAC	1468	AGGGCTAGGCTAACCAG TAT	120
				GAO_RP	TTAAAAACTTGGTACGA GTATCAA		CCGTAGCAACACATCGA GAA	
	Costunolide synthase (COS)	HQ439599	<i>Lactuca sativa</i>	COS_FP	ATGGAGCCTCTCACCAT CG	1474	CAAAGCCGTTGTTCTGG ATATG	123
				COS_RP	CTAGGACTTGAGGATCG GGA		CTCACTTCTTCTTGCT CTCT	

Supplementary figure 1: Linalool and costunolide linearity graph with three point-injection.

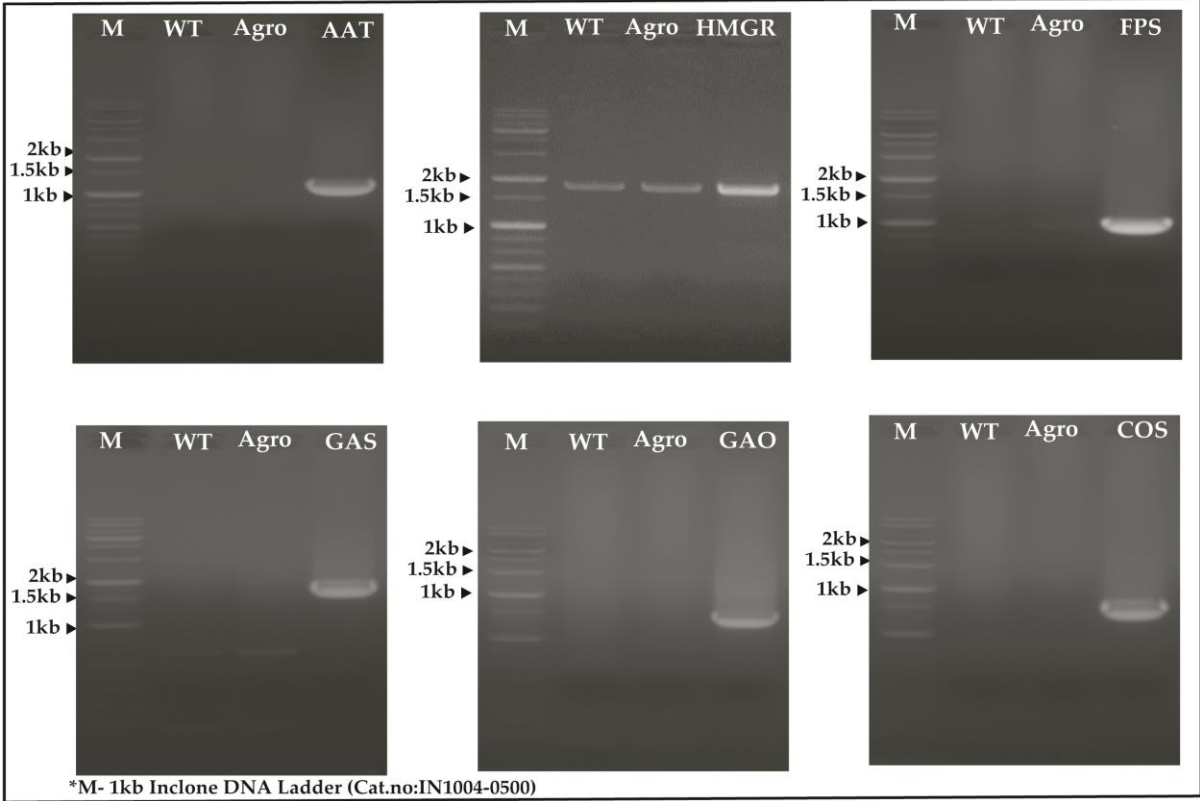


Supplementary figure 2: Full-length RT-PCR analysis for MEP and MVA pathway gene expression analysis.

MEP



MVA



Supplementary Table 2. List of MoClo golden gate vector promoter and terminator

Promoter/Terminator	Full name
CaMV35S-D	Promoter (double), 35s (Cauliflower Mosaic Virus) + 5'UTR, Ω (Tobacco Mosaic Virus)
SIRbcl-5U	Promoter and 5'UTR, RbcS2 (<i>S. lycopersicum</i>)
ProG10-90	Promoter G10-90 (strong, constitutive in <i>Arabidopsis</i>)
CaMV35S-L	promoter (0.4 kb), 35s (Cauliflower Mosaic Virus) + 5'UTR, Ω (Tobacco Mosaic Virus)
AtUBQ-10	GGAG_Pro-AtuNos_5U-TMV_AATG promoter, nos, (<i>Agrobacterium tumefaciens</i>) + 5'UTR, Ω (Tobacco Mosaic Virus)
AtRPS5a	~ 1700 bp upstream of <i>Arabidopsis</i> RPS5a (At3g11940) (strong, constitutive promoter in <i>Arabidopsis</i>)
CaMV35S-Ter	3'UTR, polyadenylation signal/terminator, 35s (Cauliflower Mosaic Virus)
AtuNos-Ter	3'UTR, polyadenylation signal/terminator, nos (<i>A. tumefaciens</i>)

Supplementary Table 3: Linalool and costunolide metabolite concentration in individual and combinatorial constructs

Pathway	Constructs	Metabolite concentration (ng/mg)
MEP (Linalool-Individual and Combinatorial)	WT	38.84
	Agro	41.00
	DXS	77.43
	DXR	70.73
	CMK	32.61
	GPPS	19.04
	IDI	23.99
	LIS	70.85
	DXS+LIS	63.47
	DXR+LIS	69.99
	DXS+DXR+LIS	94.55
MVA (Costunolide-Individual and Combinatorial)	WT	0.00
	Agro	0.00
	AAT	14.87
	HMGR	48.71
	FPS	24.73
	GAS	36.02
	GAO	23.86
	COS	10.48
	FPS+COS	16.93
	HMGR+COS	33.89
	HMGR+FPS+COS	40.63
	GAS+GAO+COS	64.84
	HMGR+GAO+GAS+GAO+COS	67.22
	AAT+HMGR+FPS+GAS+GAO+COS	94.18