

Table S1 Transcriptome assembly results of *P. lactiflora*

Type	Number	Mean Length (bp)	N50
Transcript	147709	761	1217
Unigene	131366	825	1269

Table S2 Primers for cloning the ORFs of PLOSCs

Names	Sequence 5' to 3'
PITPS1	F: ATGTCTGTTTTAGGTCTGC R: TCAGCAAGGGTTTATGAG
PITPS2	F:ATGTCTGTCCAAGTCTCACCCG R:TCATACTGGGACAGGCTCTATG
PITPS3	F:ATGTCCGTTTTAGGTCTGC R:TCAGCAAGGGTTTATGAGC
PITPS4	F:ATGGCCTATTTCAATACCTC R:CTATAAAGATAAAGTTCCATACAAG
PITPS5	F:ATGATGAATCTGCGCCTTAC R:TCATTCTTTGCCTGATTTATTTAATAC
PITPS6	F:ATGTCTCTCCCTGTGTTAGAAAC R:TCATATTGGGATTGGATCAATTAG
PITPS7	F:ATGGCCTATTTCAATACCTC R:CTATAAAGATAAAGTTCCATACAAG
PITPS8	F:ATGTCTACTGAAGCTTCCGCTG R:TCATATTGCAAAATGATCAATGAG
PITPS9	F:CCATGTCTGTCCAAGTCCTGGCTTC R:TCAAGAGGTGTGATCCACTGGAAAAT
PITPS10	F:ATGGAAGTAGTTTCTTTCC R:TTATAGTACATTGATATGTTTACTT
PITPS11	F:ATGTCTGTCCAAGTCCCAGC R:TCATACTGGCACGGGGTC
PITPS12	F:ATGAGCCAGTATCTTCAGTGCATAG R:TTAATTAACATTAGTGTTACCAAAT
PITPS13	F:ATGTCAATTGGGAAGGAGAAGGCAG R:TCAGCCACACGTGCATAGTTGAG
PITPS14	F:ATGCAATTAAAGACGGGGC R:TCACATTGCAATAGGATCGG
PITPS15	F:ATGTCTACTGAAGCTTCCGCTG R:TCATATTGCAATATGATCAATGAG
PITPS16	F:ATGCAAACCAGCTATTCC R:TCATACTGGGACAGGCTC
PITPS17	F:ATGTCTTTCCAACCTCTCCACCAATG R:TCATATTGGAACAGGATCAATCAGC
PITPS18	F:ATGTCTGTTCAAGCTGCAACTGGTC R:TCACATTGCGATAGGATCGACCAC
PITPS19	F:ATGAAGCTTGCCAAAGTGGTGG R:TTAGGGAATGGGCTGAATGAGAAG
PITPS20	F:ATGGCCATTTGCTCTGTCAATTAC R:TTAGGGAATGGGTTGAATGAGAAG
PITPS21	F:ATGGCTACACGTCTGGTTG R:CTACATGGGAATGGGTTGAAAAAG

PITPS22	F:ATGTCTATTCATCAGCTTAC R:TTAAGGAATGGGTTGAATAAGTAG
PITPS23	F:ATGTATCTCTCCAACCCTAGCAACC R:TCATTAAGGACTGCATTTGC
PITPS24	F:ATGGAATCAACACAAATCACAAT R:TATTTAGAAACAATACCCACTCTTG
PITPS25	F:ATGAAGAGTTTGACCACGGAC R:TGTTTGACAAAGTTACATTCCTGTG
PITPS26	F:ATGGCCCTTCAACTTCTCTTC R:GCTAGTTTAGTGAAACAGGTTCCAC

Table S3 Primers for vector construction of PITPSs

Names	Sequence 5' to 3'
PITPS1	F: acgtcaaggagaaaaaaccccgatccATGTCTGTTTTAGGTCTGC R: tagtgagtcgtattacggatccTCAGCAAGGGTTTATGAG
PITPS2	F:acgtcaaggagaaaaaaccccgatccATGTCTGTCCAAGTCTCACCCG R:tagtgagtcgtattacggatccTCATACTGGGACAGGCTCTATG
PITPS3	F:acgtcaaggagaaaaaaccccgatccATGTCCGTTTTAGGTCTGC R:tagtgagtcgtattacggatccTCAGCAAGGGTTTATGAGC
PITPS4	F:acgtcaaggagaaaaaaccccgatccATGGCCTATTTCAATACCTC R:tagtgagtcgtattacggatccCTATAAAGATAAAGTTCCATACAAG
PITPS5	F:acgtcaaggagaaaaaaccccgatccATGATGAATCTGCGCCTTAC R:tagtgagtcgtattacggatccTCATTCTTTGCCTGATTTATTTAATAC
PITPS6	F:acgtcaaggagaaaaaaccccgatccATGTCTCTCCCTGTGTTAGAAAC R:tagtgagtcgtattacggatccTCATATTGGGATTGGATCAATTAG
PITPS7	F:acgtcaaggagaaaaaaccccgatccATGGCCTATTTCAATACCTC R:tagtgagtcgtattacggatccCTATAAAGATAAAGTTCCATACAAG
PITPS8	F:acgtcaaggagaaaaaaccccgatccATGTCTACTGAAGCTTCCGCTG R:tagtgagtcgtattacggatccTCATATTGCAAAATGATCAATGAG
PITPS9	F:acgtcaaggagaaaaaaccccgatccCCATGTCTGTCCAAGTCCTGGCTTC R:tagtgagtcgtattacggatccTCAAGAGGTGTGATCCACTGGAAAAT
PITPS10	F:acgtcaaggagaaaaaaccccgatccATGGAAGTAGTTTCTTTCC R:tagtgagtcgtattacggatccTTATAGTACATTGATATGTTTACTT
PITPS11	F:acgtcaaggagaaaaaaccccgatccATGTCTGTCCAAGTCCCAGC R:tagtgagtcgtattacggatccTCATACTGGCACGGGGTC
PITPS12	F:acgtcaaggagaaaaaaccccgatccATGAGCCAGTATCTTCAGTGCATAG R:tagtgagtcgtattacggatccTTAATTAACATTAGTGTTCAACCAAT
PITPS13	F:acgtcaaggagaaaaaaccccgatccATGTCAATTGGGAAGGAGAAGGCAG R:tagtgagtcgtattacggatccTCAGCCACACGTGCATAGTTGAG
PITPS14	F:acgtcaaggagaaaaaaccccgatccATGCAATTAAAGACGGGGC R:tagtgagtcgtattacggatccTCACATTGCAATAGGATCGG
PITPS15	F:acgtcaaggagaaaaaaccccgatccATGTCTACTGAAGCTTCCGCTG R:tagtgagtcgtattacggatccTCATATTGCAATATGATCAATGAG
PITPS16	F:acgtcaaggagaaaaaaccccgatccATGCAAACAGCTATTCC R:tagtgagtcgtattacggatccTCATACTGGGACAGGCTC
PITPS17	F:acgtcaaggagaaaaaaccccgatccATGTCTTTCCAACCTCTCCACCAATG R:tagtgagtcgtattacggatccTCATATTGGAACAGGATCAATCAGC
PITPS18	F:acgtcaaggagaaaaaaccccgatccATGTCTGTTCAAGCTGCAACTGGTC R:tagtgagtcgtattacggatccTCACATTGCGATAGGATCGACCAC
PITPS19	F:acgtcaaggagaaaaaaccccgatccATGAAGCTTGCCAAAGTGGTGG R:tagtgagtcgtattacggatccTTAGGGAATGGGCTGAATGAGAAG
PITPS20	F:acgtcaaggagaaaaaaccccgatccATGGCCATTTGCTCTGTCATTAC R:tagtgagtcgtattacggatccTTAGGGAATGGGTTGAATGAGAAG
PITPS21	F:acgtcaaggagaaaaaaccccgatccATGGCTACACGTCTGGTTG R:tagtgagtcgtattacggatccCTACATGGGAATGGGTTGAAAAAG

PITPS22	F:acgtcaaggagaaaaaaccccgatccATGTCTATTCATCAGCTTAC R:tagtgagtcgtattacggatccTTAAGGAATGGGTTGAATAAGTAG
PITPS23	F:acgtcaaggagaaaaaaccccgatccATGTATCTCTCCAACCCTAGCAACC R:tagtgagtcgtattacggatccTCATTAAGGACTGCATTTGC
PITPS24	F:acgtcaaggagaaaaaaccccgatccATGGAATCAACACAAATCACAAT R:tagtgagtcgtattacggatccTATTTAGAAACAATACCCACTCTTG
PITPS25	F:acgtcaaggagaaaaaaccccgatccATGAAGAGTTTGACCACGGAC R:tagtgagtcgtattacggatccTGTTTGACAAAGTTACATTCCTGTG
PITPS26	F:acgtcaaggagaaaaaaccccgatccATGGCCCTTCAACTTCTCTTC R:tagtgagtcgtattacggatccGCTAGTTTAGTGAAACAGGTTCCAC

Table S4 Primers for Qrt-PCR of PITPS21

Names	Sequence 5' to 3'
Actin	F: AGCTCATCGGTTGAGAAGAAGTAC
	R: ACATAGTTGATCCACCACTGAGAAC
PITPS21	F: GTTTGGGTTACGAGTTTGAGACAG
	R: GCCTCCTCCATGATGCTTTC

Table S5 The information of TPSs from representative characterized subfamily genes

Gene name	Gene Bank NO.	Species	Gene name	Gene Bank NO.
CbTPS1	WKW91725	<i>Cinnamomum burmanni</i>	AtTPS1	NP_193322
CoLIS-LL	AFK09265	<i>Cinnamomum osmophloeum</i>	AtTPS2	NP_193406
CtGES	Q8GUE4	<i>Cinnamomum tenuipile</i>	AtTPS3	NP_567511
LcTPS2	G0Y7D2	<i>Litsea cubeba</i>	AtTPS4	NP_564772
LiS-LINS	AXF50410	<i>Lavandula x intermedia</i>	AtTPS5	NP_179904
LpPIN	T1RR71	<i>Lavandula pedunculata</i>	AtTPS6	NP_177165
FaPIN	O23945	<i>Fragaria vesca</i>	AtTPS7	NP_193753
MdPIN	NP_001281061	<i>Malus domestica</i>	AtTPS8	NP_193754
CsLINS	AHC54051	<i>Coriandrum sativum</i>	AtTPS9	NP_193756
CsTPS35	QLC36840	<i>Cannabis sativa</i>	AtTPS10	NP_179998
LcTPS1	G0Y7D1	<i>Litsea cubeba</i>	AtTPS11	NP_199276
LnTPS1	AKQ19357	<i>Laurus nobilis</i>	AtTPS12	NP_193064
Cslis	QNI69163	<i>Camellia sinensis</i>	AtTPS14	NP_176361
Amlis	ABR24418	<i>Antirrhinum majus</i>	AtTPS15	NP_189564
ZpTPS3	BBD88590	<i>Zanthoxylum piperitum</i>	AtTPS16	NP_189555
PdTPS1	XP_034211271	<i>Prunus dulcis</i>	AtTPS17	NP_188067
CiCaMS	QNV69587	<i>Cinnamomum camphora</i>	AtTPS18	NP_188070
SBS	O81192	<i>Salvia officinalis</i>	AtTPS19	NP_188072
LaBPPS	AJW68082	<i>Lavandula angustifolia</i>	AtTPS21	NP_197784
PdBPPS	ATY48638	<i>Phyla dulcis</i>	AtTPS22	NP_174635
WvBPPS	AWW87313	<i>Wurfbainia villosa</i>	AtTPS23	NP_189210
PLPIN	KU187411	<i>Paeonia lactiflora</i>	AtTPS24	NP_189209
PpCPS/KS	XP_024380398	<i>Physcomitrium patens</i>	AtTPS25	NP_189587
AtEKS	NP_178064	<i>Arabidopsis thaliana</i>	AtTPS26	NP_176776

SrKS1	Q9XEH9	<i>Stevia rebaudiana</i>	AtTPS27	NP_189210
CmKS	XP_022968895	<i>Cucurbita maxima</i>	AtTPS28	NP_175312
AtKS	AAC39443	<i>Arabidopsis thaliana</i>	AtTPS29	NP_001319127
CcTPS2	QNV69588	<i>Cinnamomum camphora</i>	AtTPS30	NP_189746
LnTPS2	AKQ19358	<i>Laurus nobilis</i>		
ZpTPS1	BBD88588	<i>Zanthoxylum piperitum</i>		
SgTPS	UOW66203	<i>Sindora glabra</i>		
SmSTPS	F6M8H7	<i>Santalum murrayanum</i>		
SvTPS15	XP_049345898	<i>Solanum verrucosum</i>		
OvTPS3	E2E2N8	<i>Origanum vulgare</i>		
SsTPS12	XP_049379744	<i>Solanum stenotomum</i>		
SLTPS9	NP_001234055	<i>Solanum lycopersicum</i>		
ZaTPS	UJH94381	<i>Zanthoxylum ailanthoides</i>		
SLTPS31	NP_001239040	<i>Solanum lycopersicum</i>		
CbTPS1	QTW43990	<i>Cinnamomum burmanni</i>		
PmTPS2	AWK77755	<i>Persicaria minor</i>		
PdTPS2	QEE82240	<i>Prunus dulcis</i>		
AkTPS2	BBO53955	<i>Angelica keiskei</i>		
TwTPS	AWV55521	<i>Tripterygium wilfordii</i>		
GbTPS3	KAB2044572	<i>Gossypium barbadense</i>		

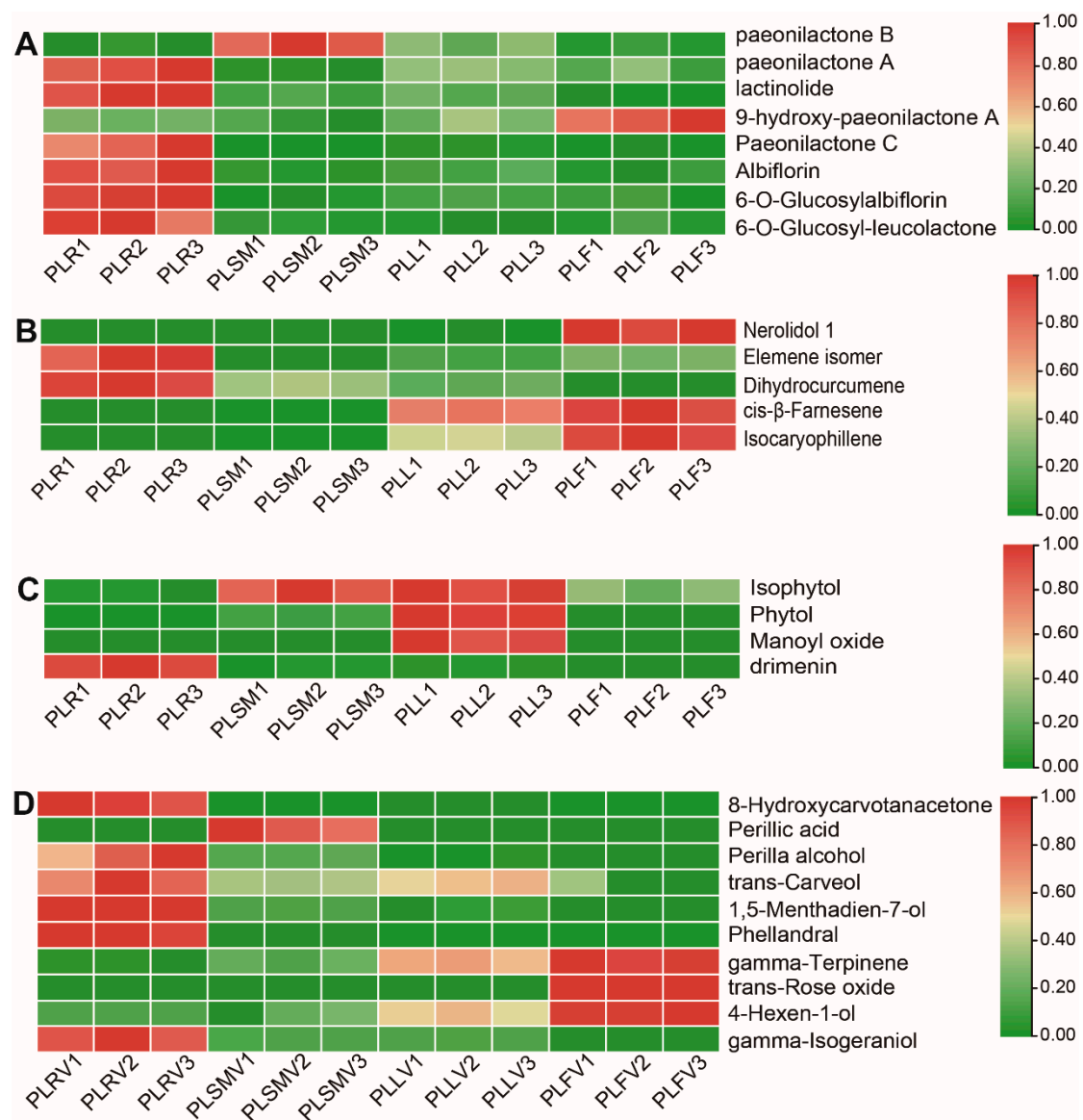


Figure S1 Metabolome results for different tissues of *P. lactiflora*. A: Heatmap analysis of *P. lactiflora* about different tissue parts of Non paeoniflorin derivatives. B: Heatmap analysis of *P. lactiflora* about different tissue parts of sesquiterpenoids. C: Heatmap analysis of *P. lactiflora* about different tissue parts of diterpenoids. C: Heatmap analysis of *P. lactiflora* about different tissue parts of Non Pinane Monoterpenoids.

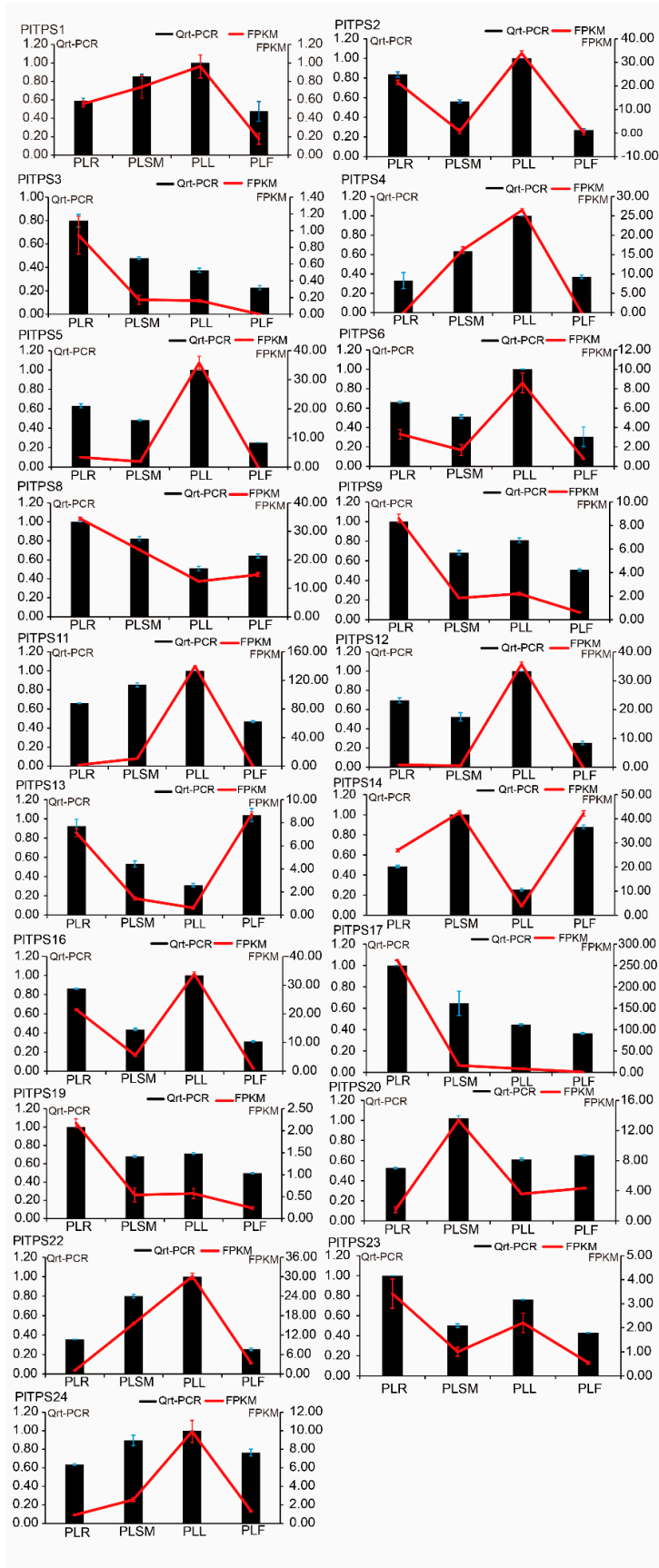


Figure S2 Relative expression level of *P. lactiflora* of PITPSs by RT-qPCR and the reads per kilobase million value from the *P. lactiflora* transcriptome.

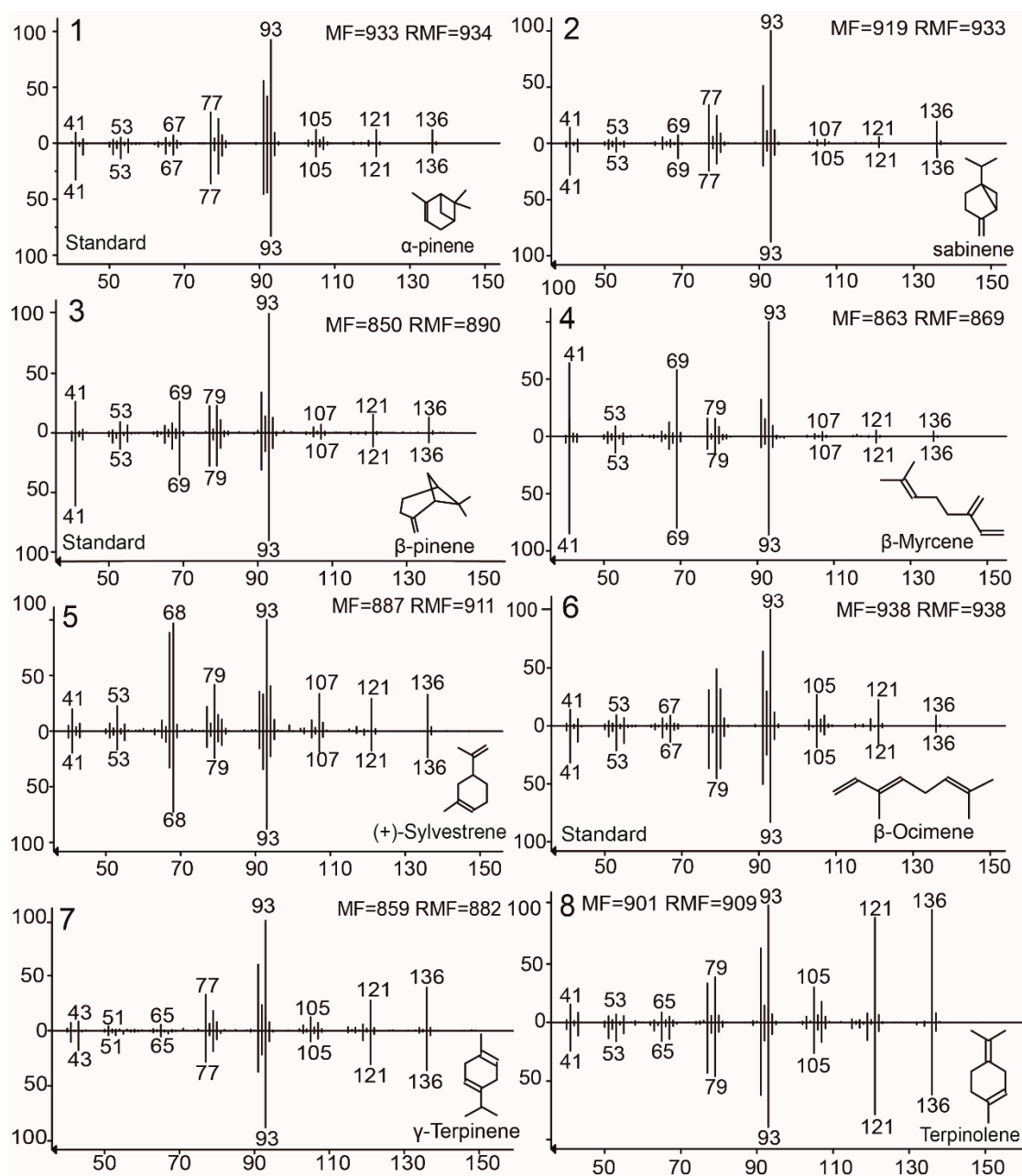


Figure S3 GC-MS analysis of *P. lactiflora* Class I terpene synthase in vitro assays with engineered yeast that can produce GPP. The m/z of products were matched with NIST mass spectral library for identification of a potential terpenes.

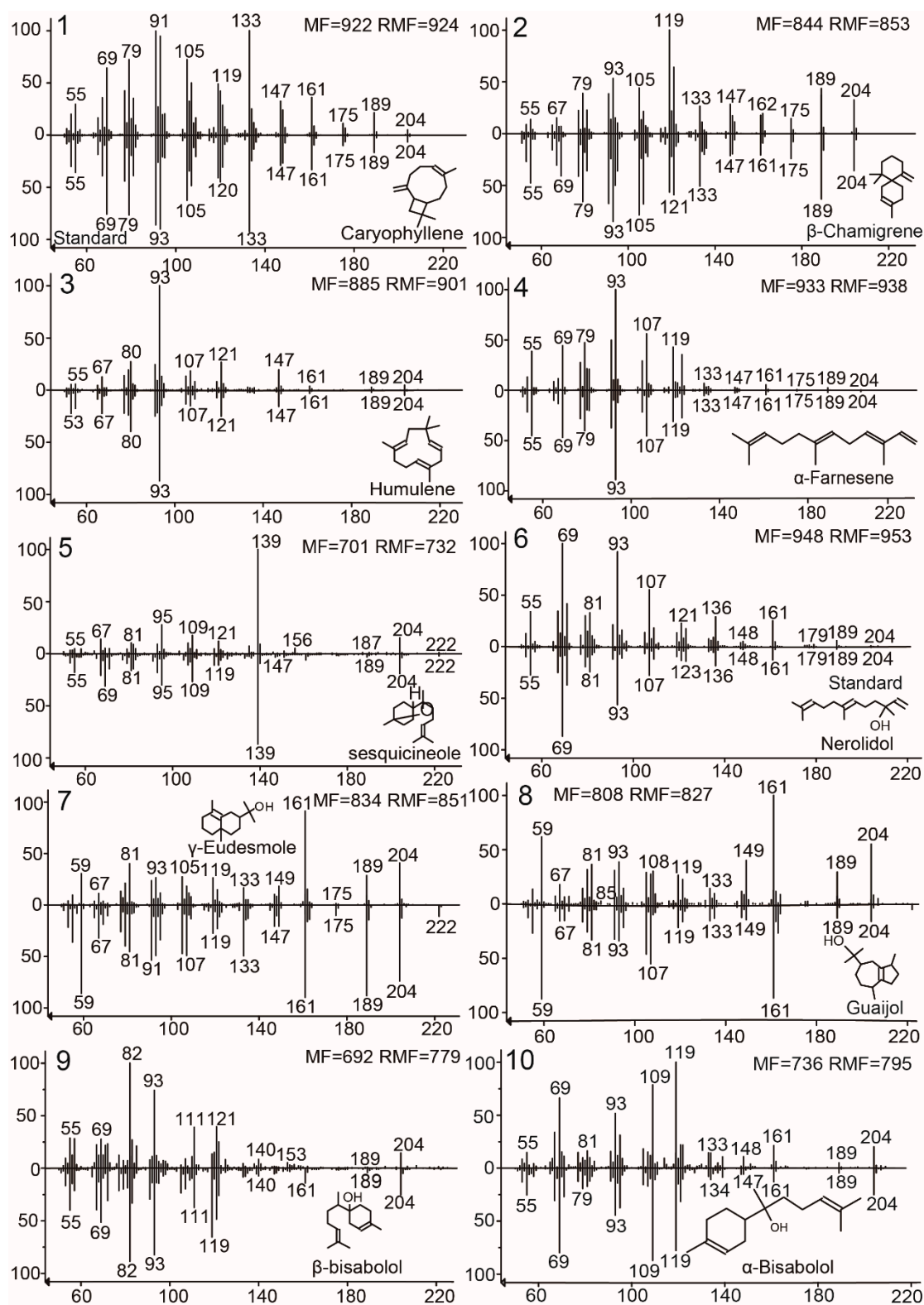


Figure S4 GC-MS analysis of *P. lactiflora* Class I terpene synthase in vitro assays with engineered yeast that can produce FPP. The m/z of products were matched with NIST mass spectral library for identification of a potential terpenes.