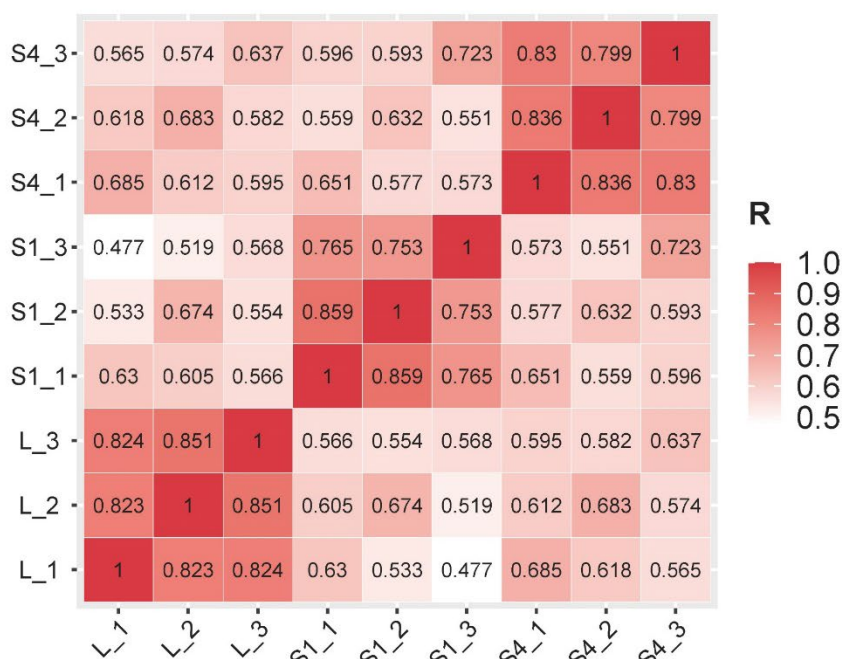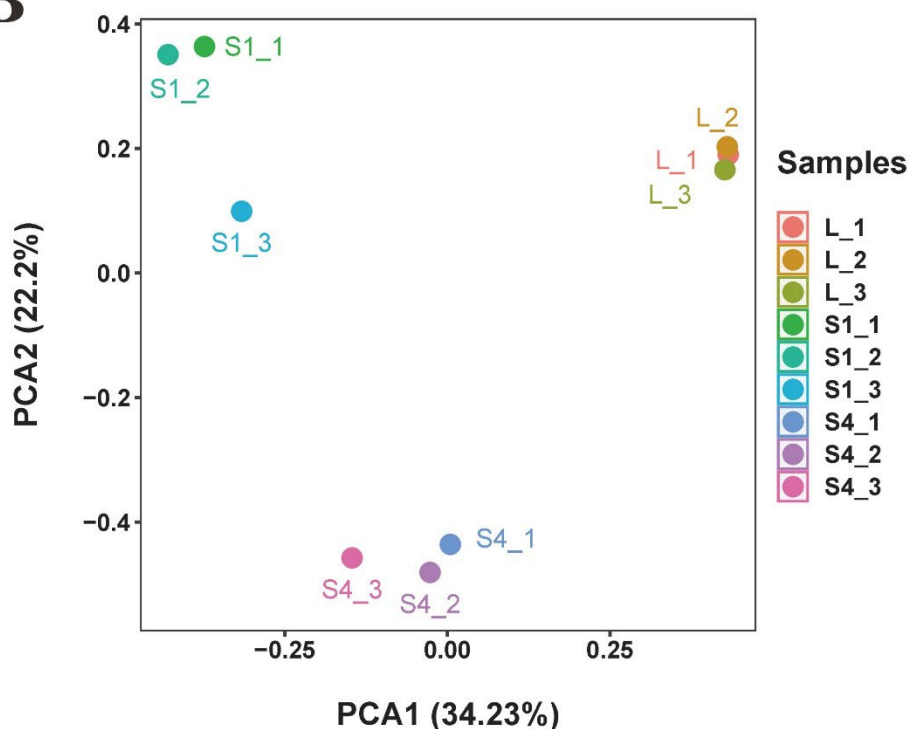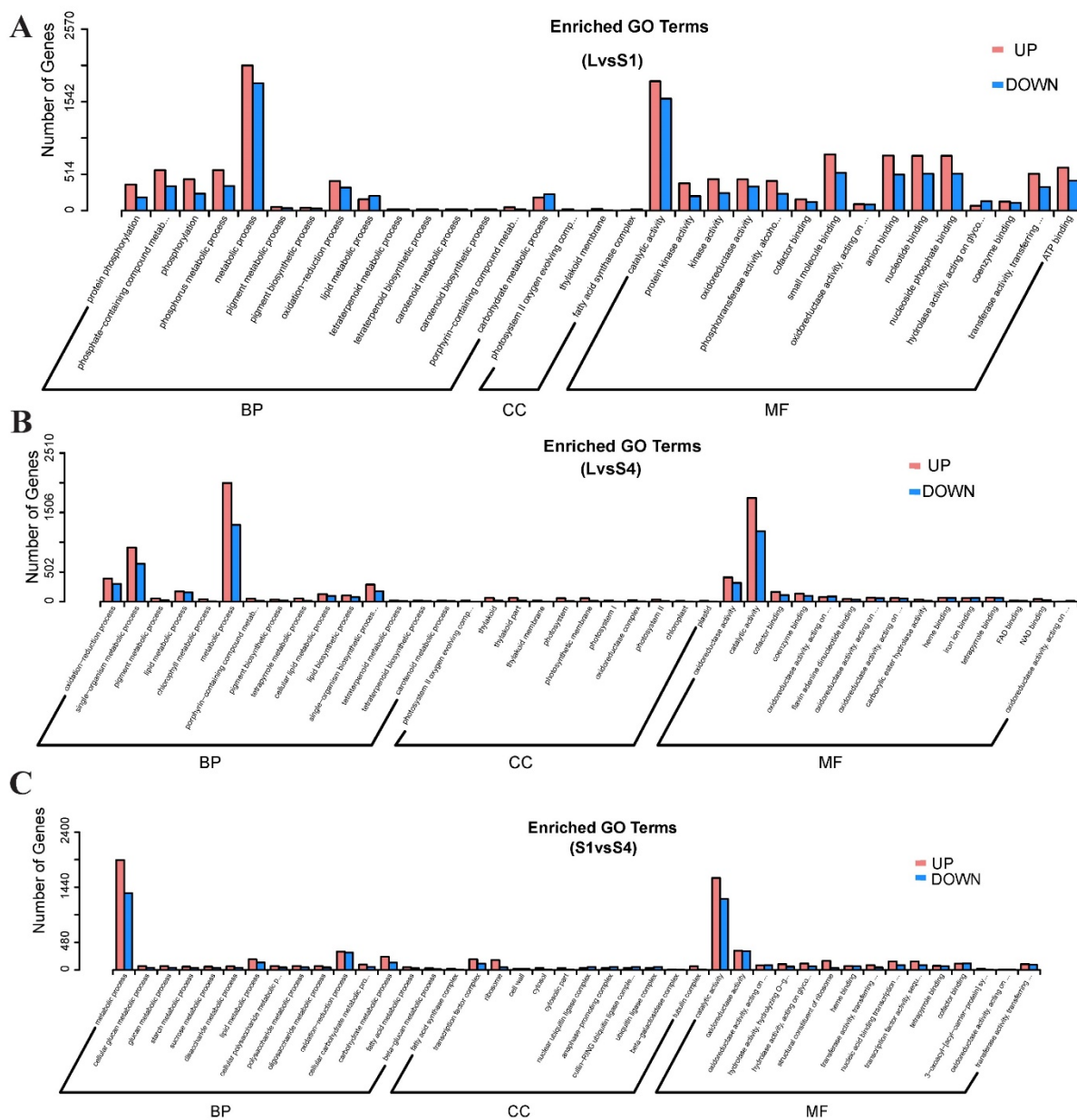**A**

Correlation Heatmap

B

PCA Analysis
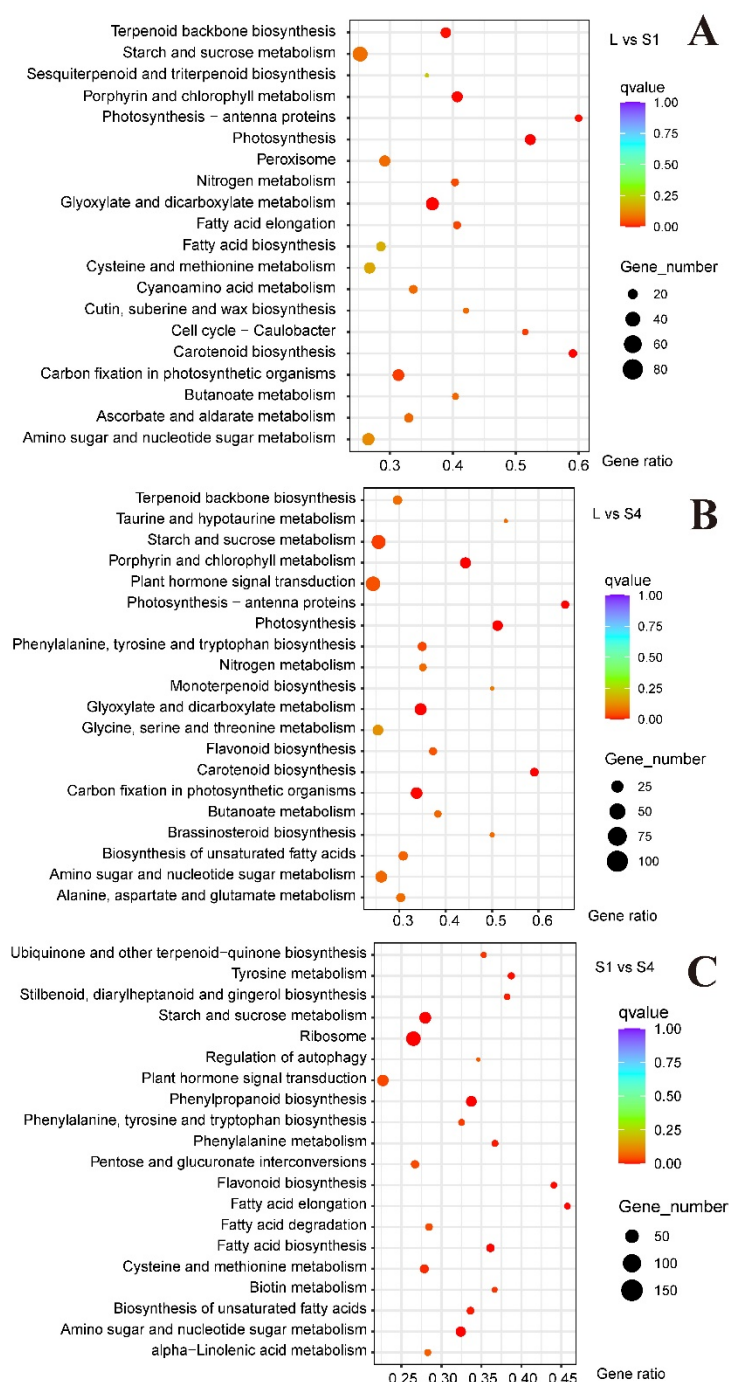

Figure S1 Correlation and PCA analysis of samples

A: Correlation analysis of samples; B: Principal Component Analysis of samples
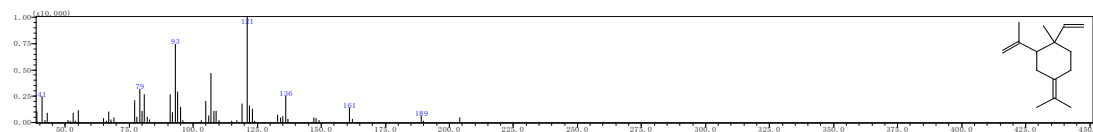
Figure S2. GO enrichment analysis of DEGs.
A: L vs S1; B: L vs S4; C: S1 vs S4

Figure S3 KEGG enrichment analysis of DEGs.

A: L vs S1; B: L vs S4; C: S1 vs S4.

Elixene   C15H24   204

beta.-copaene   C15H24   204
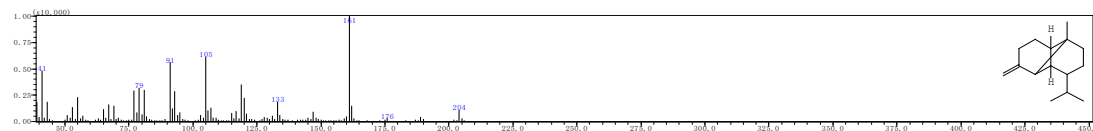
beta.-Caryophyllen   C15H24   204
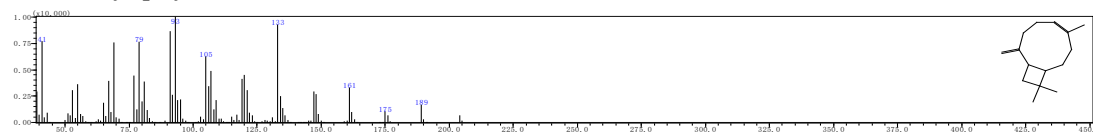
(E)-.beta.-Famesene   C15H24   204
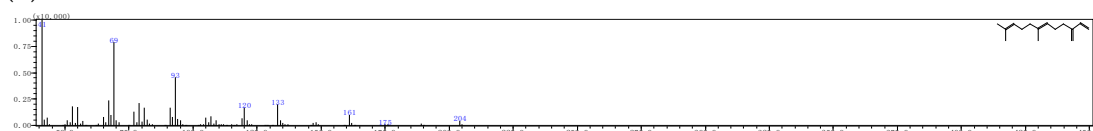
alpha.-Bergamotene   C15H24   204
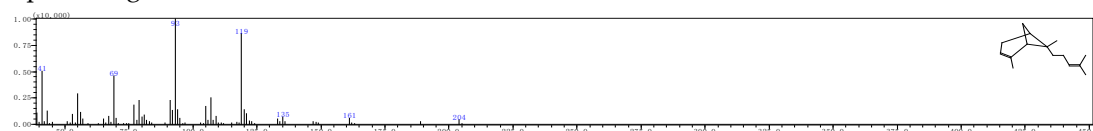
Germacrene D   C15H24   204
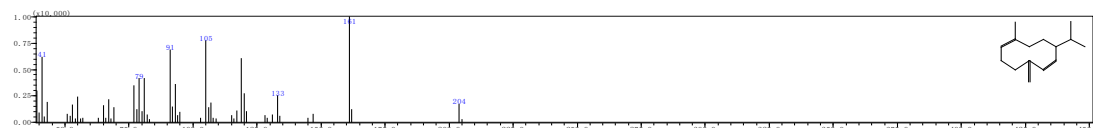
alpha.-Farnesene   C15H24   204
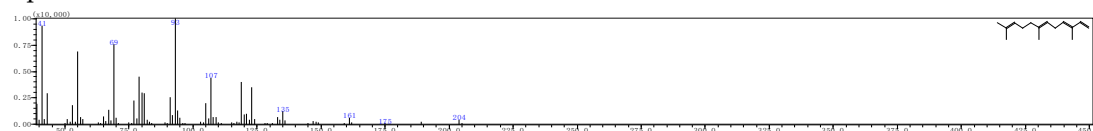
Figure S4 The mass spectrograms of pyrethrins

Cinerin I   C20H28O3 316

Jasmolin I   C21H30O3 330

Pyrethrin I   C21H28O3 328

Unknown 1

Cinerin II   C21H28O5 360

Jasmolin II   C22H30O5 374

Pyrethrin II   C22H30O5 374

Unknown 2
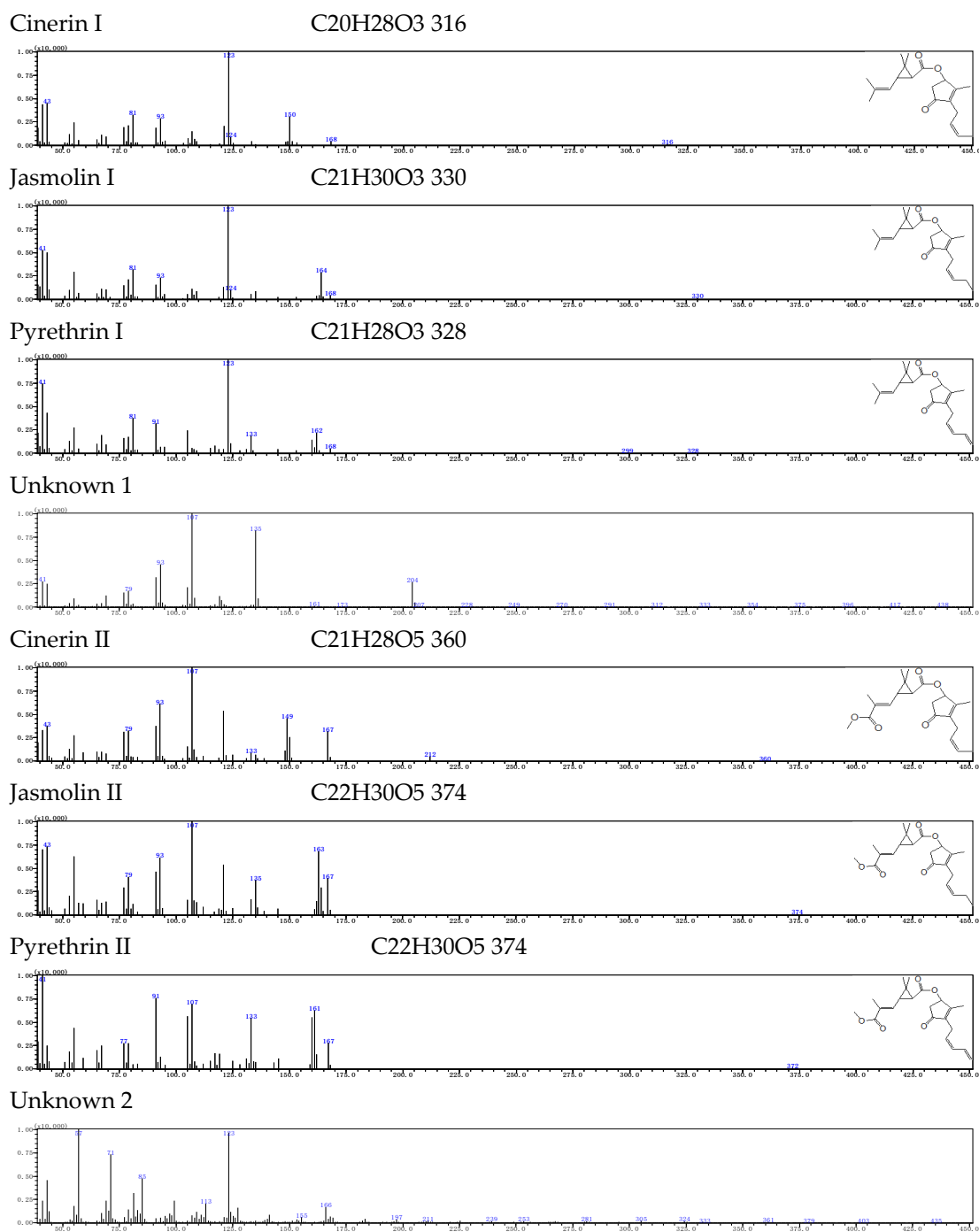
Figure S5 The mass spectrograms of volatile terpenes

Table S1. Summary of Illumina HiSeq™ 4000 sequencing data

Sample	Raw reads	Clean reads	Clean bases(bp)	Error(%)	Q20(%)	Q30(%)	GC content(%)
L_1	51087630	48713978(95.35%)	7.31G	0.03	97.95	93.77	43.05
L_2	44783836	43123200(96.29%)	6.47G	0.03	97.88	93.59	43.38
L_3	45877880	43562156(94.95%)	6.53G	0.03	97.68	93.15	43.13
S1_1	47513258	45032560(94.78%)	6.75G	0.03	97.76	93.31	42.31
S1_2	46556522	45149940(96.98%)	6.77G	0.03	97.91	93.65	42.29
S1_3	43845892	42370462(96.63%)	6.36G	0.03	97.72	93.23	42.09
S4_1	45180438	44016074(97.42%)	6.6G	0.03	97.84	93.51	42.37
S4_2	43971966	42554940(96.78%)	6.38G	0.03	97.88	93.54	42.37
S4_3	46138630	43929062(95.21%)	6.59G	0.03	97.97	93.75	41.99

Q20: Percentage of bases that account for more than 20 of Phred values. Phred=-10log10(e).

Q30: Percentage of bases that account for more than 30 of Phred values.Phred=-10log10(e).

GC content: The sum of base G and C accounts for the percentage of total base number.

Table S2. qRT-PCR primer

Primer	Primer sequence (5'to3')
DFR_RT_F	ATGCCACCATTCATCAATTAGC
DFR_RT_R	CCTCCGAACATCTCCTCCAA
CHS_RT_F	GGCTGATTACCAACTCACCAA
CHS_RT_R	TCGTTAGGACCACGGAATGT
ANS_RT_F	TCCAACTCTTCTACGACAACCA
ANS_RT_R	TCCTAACCTTCTCCTTATTCACAAG
GLIP_RT_F	CGATGAACTTACTAGACTACACAA
GLIP_RT_R	AAGGACCACTACCGCAACAT
ADH_RT_F	GGTGAATGTGGACAATGCT
ADH_RT_R	CGGACCATGTGGAGCAACT
CDS_RT_F	TTCTCCTCTCACTACGACATTGA
CDS_RT_R	ACAGAATAGCCTCGGACCATC
JMH_RT_F	TTTGTTGCGGATCTTTGGC
JMH_RT_R	GTCTTCCTGATCATGAGAATTGG
MT_RT_F	TTCATTCCTCAACCAGCCTACA
MT_RT_R	ACTATTTCGATAGAGCGTGATT
bHLH1_RT_F	TTCTGATACCACGGCTACTA
bHLH1_RT_R	GCCAGACAATCCTTGATGAT
CHH_RT_F	CCACGTGTATGTAGGGAGCAATGC
CHH_RT_R	CAGGATCAGTTGAACATGCGAAAG
ALDH_RT_F	CATTCCGCTACTTTGCTGGTGC
ALDH_RT_R	TCCAAGGAATGATGTGTCCAACTAC
PYS_RT_F	CTACAAGGTGCCCCCAAAGA
PYS_RT_R	TGATGACGGCTCCAAGGTAGA