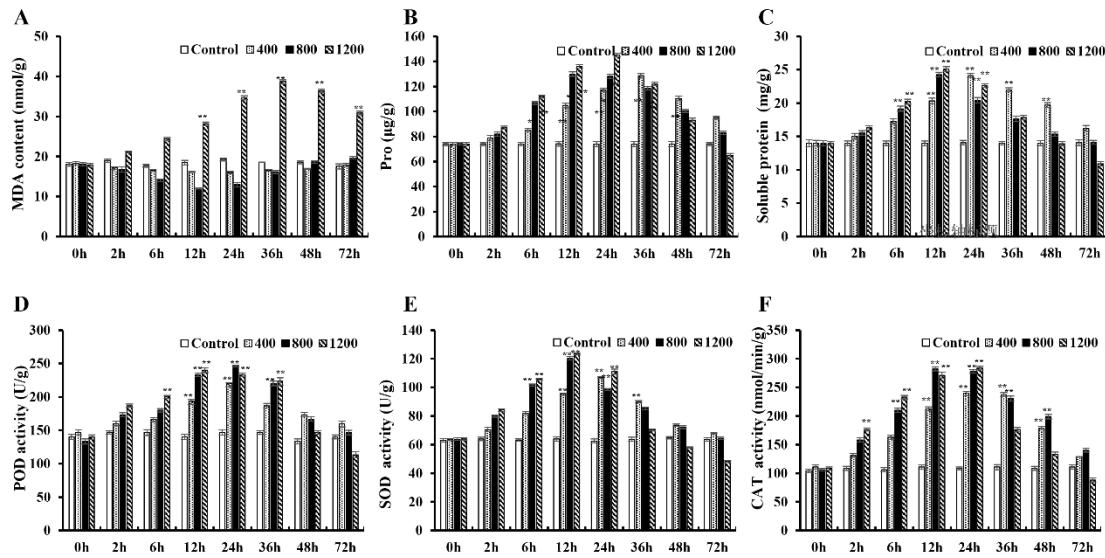
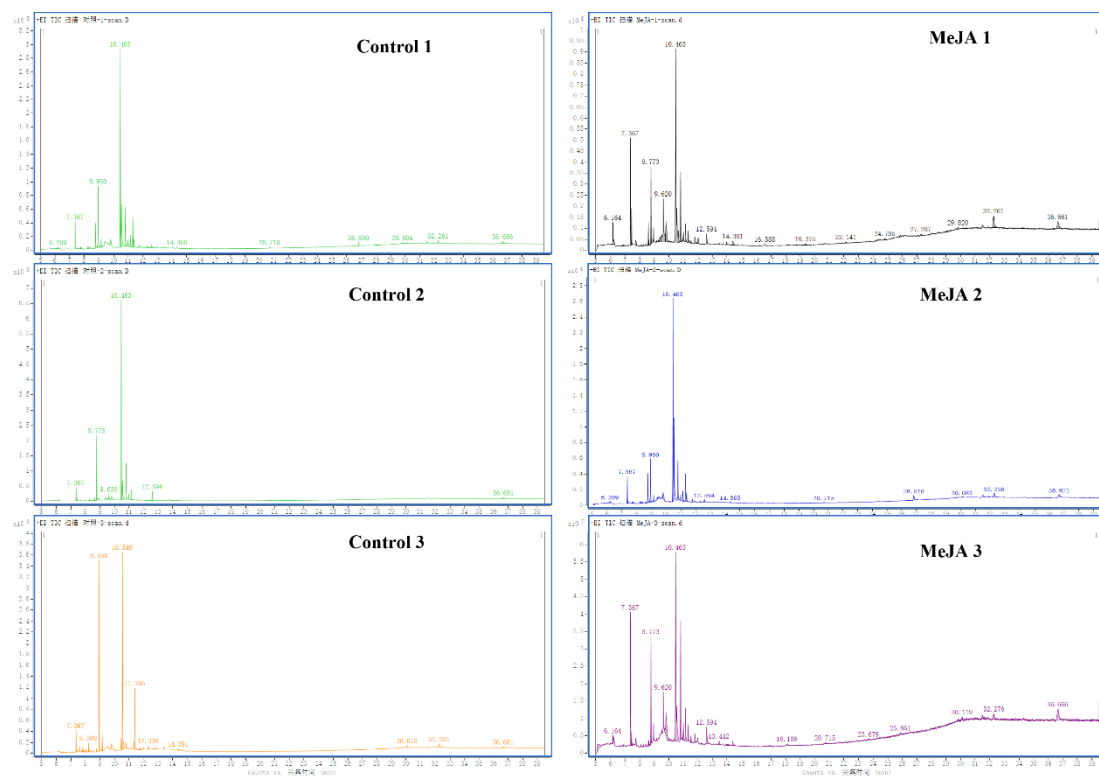


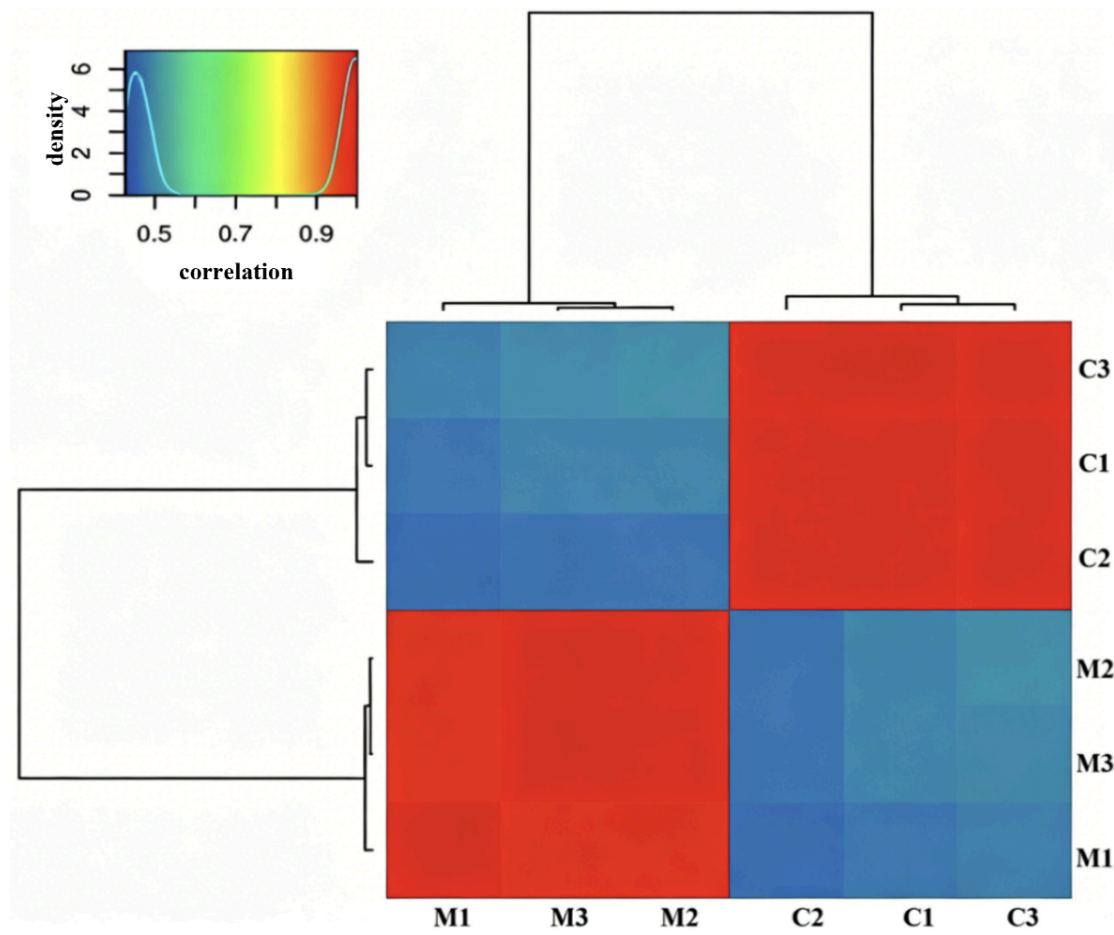
Additional files



Supplementary Figure 1 Changes of physiological index and chemical compounds in leaves of *D. fragrans* with different concentrations of MeJA treatment. A, MDA content. B, Pro content. C, Soluble protein content. D, POD activity. E, CAT activity. F, SOD activity. The treatment time is 0 h, 2 h, 6 h, 12 h, 24 h, 36 h, 48 h, 72 h, and MeJA concentrations are 400 µmol/L, 800 µmol/L, and 1200 µmol/L. (*P ≤ 0.05, **P ≤ 0.01, n=3)

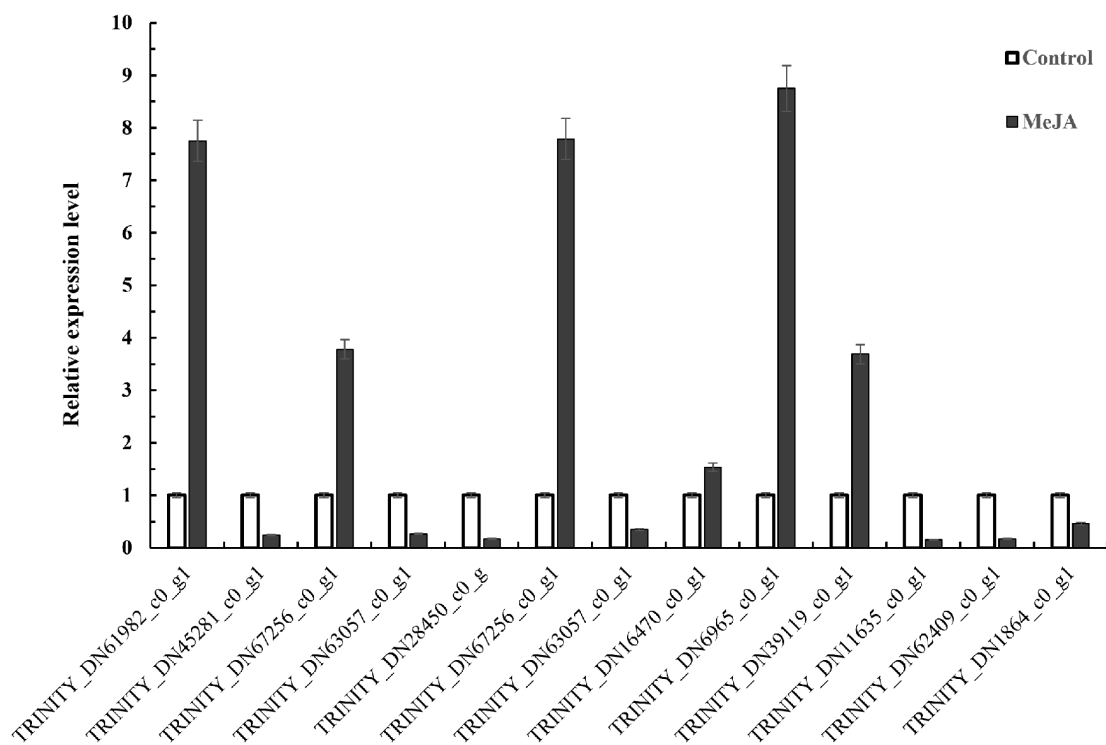


Supplemental Figure 2 spectrum of MeJA and Control group.



Supplementary Figure 3 Schematic diagram of correlation between samples.

Note: M1, M2 and M3 are 800 $\mu\text{mol/L}$ treatment with MeJA for 12 h; C1, C2 and C3 were control group.



Supplementary Figure 4 Results of qRT-PCR validation of DEGs

Supplementary Table 1 Relative standard deviation (RSD) of standard product nonyl acetate

Standard compound	Peak area1	Peak area2	Peak area3	Peak area4	Peak area5	Peak area6	RSD (%)
Acetic Acid	5354	52833	5263332	53827	52917	532184	0.86
n-Nonyl Ester	7974	563	5	461	426	73	

Supplementary Table 2 Recovery rate of nonyl acetate

	Peak area1	Peak area2	Peak area3	Rate of recovery	Concentration of Acetic Acid n-Nonyl Ester
control	5028634 2	5471874 8	4742420 9	95.57%	8.26µg/g
MeJA	6036057 5	4534905 4	4860817 9	96.76%	8.36µg/g

Supplementary Table 3 Frequency distribution of assembly length

Transcript length interval	<500bp	500-1k	1k-2k	>2k	Total
Number of transcripts	62,707	27,710	25,694	22,680	138,791

Supplementary Table 4 Assembly length distribution

Type	Min Length	Max Length	Mean Length	Median Length	N50	Total assembled bases
Isoform	188	17,692	1,069	577	1,936	148,394,536

Supplementary Table 5 Protein function analysis of DEGs related to terpenoid synthesis pathway

Gene IDs	Swiss-Prot_Id	Description	Species
TRINITY_DN319 75_c0_g1	sp Q80W54 FACE1 _MOUSE	CAAX prenyl protease 1 homolog	Mus musculus
TRINITY_DN164 70_c0_g1	sp Q5N8G1 ISPD_O RYSJ	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase, chloroplastic	Oryza sativa subsp. japonica
TRINITY_DN610 23_c0_g1	sp Q10132 IDI1_SC HPO	Isopentenyl-diphosphate Delta-isomerase	Schizosaccharom ycepombe
TRINITY_DN387 88_c0_g1	sp Q86SQ9 DHDDS _HUMAN	Dehydrodolichyl diphosphate synthase complex subunit DHDDS	Homo sapiens GN
TRINITY_DN115 23_c0_g1	sp Q0INZ4 SPS3_O RYSJ	Probable solanesyl-diphosphate synthase 3, chloroplastic (Fragment)	Oryza sativa subsp. japonica
TRINITY_DN885 93_c0_g1	sp Q6L8K7 THIL_Y ARLI	THIL_YARLI Acetyl-CoA acetyltransferase	Yarrowia lipolytica
TRINITY_DN133 16_c0_g1	sp P29057 HMDH1_ HEVBR	3-hydroxy-3-methylglutaryl -coenzyme A reductase 1	Hevea brasiliensis
TRINITY_DN696 5_c1_g1	sp P08836 FPPS_C HICK	Farnesyl pyrophosphate synthase	Gallus gallus
TRINITY_DN624 09_c0_g1	sp P08524 FPPS_YE AST	Farnesyl pyrophosphate synthase	Saccharomyces cerevisiae
TRINITY_DN693 1_c0_g1	sp Q3T0R7 THIM_ BOVIN	3-ketoacyl-CoA thiolase, mitochondrial	Bos taurus
TRINITY_DN386 24_c0_g1	sp Q8QZT1 THIL_ MOUSE	Acetyl-CoA acetyltransferase, mitochondrial	Mus musculus
TRINITY_DN851 45_c0_g1	sp Q12598 THIA_C ANTR	Acetyl-CoA acetyltransferase IA	sp Q12598 THIA_ CANTR
TRINITY_DN532 7_c0_g1	sp P54873 HMCS_A RATH	Hydroxymethylglutaryl-Co A synthase	Arabidopsis thaliana
TRINITY_DN854 67_c0_g1	sp Q8K2I1 FNTB_ MOUSE	Protein farnesyltransferase subunit beta	Mus musculus

TRINITY_DN630 57_c0_g1	sp P24521 ERG8_Y EAST	Phosphomevalonate kinase	Saccharomyces cerevisiae
TRINITY_DN262 21_c0_g1	sp Q9UQW6 THIL_ SCHPO	Acetyl-CoA acetyltransferase	Schizosaccharom yces pombe
TRINITY_DN208 6_c0_g1	sp Q9ZS34 CHLP_T OBAC	Geranylgeranyl diphosphate reductase, chloroplastic	Nicotiana tabacum
TRINITY_DN391 99_c0_g1	sp Q92235 FPPS_GI BFU	Farnesyl pyrophosphate synthase	Gibberella fujikuroi
TRINITY_DN621 43_c0_g1	sp Q4R4W5 IDI1_M ACFA	Isopentenyl-diphosphate Delta-isomerase 1	Macaca fascicularis
TRINITY_DN477 5_c0_g1	sp O23722 MVD1_ ARATH	Diphosphomevalonate decarboxylase MVD1, peroxisomal	Arabidopsis thaliana
TRINITY_DN587 7_c0_g1	sp Q9ZS34 CHLP_T OBAC	Geranylgeranyl diphosphate reductase, chloroplastic	Nicotiana tabacum
TRINITY_DN653 58_c0_g1	sp Q7S565 COQ1_N EUCR	Probable hexaprenyl pyrophosphate synthase, mitochondria	Neurospora crassa
TRINITY_DN311 37_c0_g1	sp Q8HXX4 ECHB_ MACFA	Trifunctional enzyme subunit beta, mitochondrial	Macaca fascicularis
TRINITY_DN129 64_c0_g1	sp Q5T2R2 DPS1_H UMAN	Decaprenyl-diphosphate synthase subunit 1	Homo sapiens
TRINITY_DN269 6_c0_g1	sp Q9C6T1 PMK_A RATH	Phosphomevalonate kinase, peroxisomal	Arabidopsis thaliana
TRINITY_DN221 58_c0_g1	sp P47154 STE24_Y EAST	CAAX prenyl protease 1	Saccharomyces cerevisiae
TRINITY_DN328 33_c0_g1	sp P29702 FNTA_B OVIN	Protein farnesyltransferase/geranylgera nyltransferase type-1 subunit alpha	Bos taurus
TRINITY_DN866 73_c0_g1	sp P54872 HMCSA_ DICDI	Hydroxymethylglutaryl-Co A synthase A	Dictyostelium discoideum
TRINITY_DN795 05_c0_g1	sp O60725 ICMT_H UMAN	Protein-S-isoprenylcysteine O-methyltransferase	Homo sapiens
TRINITY_DN647 96_c0_g1	sp Q8QZT1 THIL_ MOUSE	Acetyl-CoA acetyltransferase, mitochondrial	Mus musculus

TRINITY_DN284 34_c0_g1	sp P54870 HMCS2_ BLAGE	Hydroxymethylglutaryl-Co A synthase 2	Blattella germanica
TRINITY_DN116 35_c0_g1	sp Q92250 FPPS_N EUCR	Farnesyl pyrophosphate synthase	Neurospora crassa
TRINITY_DN183 38_c1_g1	sp P46086 KIME_A RATH	Mevalonate kinase	Arabidopsis thaliana
TRINITY_DN230 36_c0_g1	sp Q10132 IDI1_SC HPO	Isopentenyl-diphosphate Delta-isomerase	Schizosaccharom yces pombe
TRINITY_DN334 75_c0_g1	sp Q9U1H8 FACE2 _DROME	CAAX prenyl protease 2	Drosophila melanogaster
TRINITY_DN650 12_c0_g1	sp P54839 HMCS_Y EAST	sp P54839 HMCS_YEAST	Saccharomyces cerevisiae
TRINITY_DN944 0_c0_g1	sp Q01559 HMDH_ NICSY	3-hydroxy-3-methylglutaryl -coenzyme A reductase	Nicotiana sylvestris
TRINITY_DN619 82_c0_g1	sp Q86AG7 KIME_ DICDI	Mevalonate kinase	Dictyostelium discoideum
TRINITY_DN284 50_c0_g1	sp Q9UT88 ERG8_S CHPO	Probable phosphomevalonate kinase	chizosaccharomyc es pombe
TRINITY_DN388 42_c0_g1	sp Q9CQF9 PCYOX _MOUSE	Prenylcysteine oxidase	Mus musculus
TRINITY_DN387 16_c0_g1	sp O42641 IDI1_PH ARH	Isopentenyl-diphosphate Delta-isomerase	Phaffia rhodozyma
TRINITY_DN452 81_c0_g1	sp Q9R008 KIME_ MOUSE	Mevalonate kinase	Mus musculus
TRINITY_DN113 34_c0_g1	sp Q6NU46 THILA _XENLA	Acetyl-CoA acetyltransferase A, mitochondrial	Xenopus laevis
TRINITY_DN672 56_c0_g1	sp Q9C6T1 PMK_A RATH	Phosphomevalonate kinase, peroxisomal	Arabidopsis thaliana
TRINITY_DN253 17_c0_g1	sp Q94AS5 ICME_ ARATH	Isoprenylcysteine alpha-carbonyl methylesterase ICME	Arabidopsis thaliana
TRINITY_DN741 93_c0_g1	sp P54874 HMCS_S CHPO	Hydroxymethylglutaryl-Co A synthase	Schizosaccharom yces pombe
TRINITY_DN883 2_c2_g1	sp P56966 GGPPS_ BOVIN	Geranylgeranyl pyrophosphate synthase	Bos taurus

TRINITY_DN422 36_c0_g1	sp G9BIY1 MVD_G ANLU	Diphosphomevalonate decarboxylase	Ganoderma lucidum
TRINITY_DN861 63_c0_g1	sp Q86YH6 DLP1_ HUMAN	Decaprenyl-diphosphate synthase subunit 2	Homo sapiens
TRINITY_DN541 32_c0_g1	sp P0CT44 HMDH_ GIBFU	3-hydroxy-3-methylglutaryl -coenzyme A reductase	Gibberella fujikuroi
TRINITY_DN743 77_c0_g1	sp Q29RZ0 THIL_B OVIN	Acetyl-CoA acetyltransferase, mitochondrial	Bos taurus
TRINITY_DN534 45_c0_g1	sp Q9BWD1 THIC_ HUMAN	Acetyl-CoA acetyltransferase, cytosolic	Homo sapiens
TRINITY_DN186 4_c0_g1	sp P49351 FPPS1_L UPAL	Farnesyl pyrophosphate synthase 1	Lupinus albus
TRINITY_DN277 67_c0_g1	sp Q9UQW6 THIL_ SCHPO	Acetyl-CoA acetyltransferase	Schizosaccharom yces pombe
TRINITY_DN535 74_c0_g1	sp Q5U403 MVD1_ DANRE	Diphosphomevalonate decarboxylase	Danio rerio
TRINITY_DN639 76_c0_g1	sp Q41438 HMDH3 _SOLTU	3-hydroxy-3-methylglutaryl -coenzyme A reductase 3	Solanum tuberosum
TRINITY_DN737 _c0_g1	sp Q9FIK7 THIC2_ ARATH	Probable acetyl-CoA acetyltransferase, cytosolic 2	Arabidopsis thaliana
TRINITY_DN883 22_c0_g1	sp P54960 HMDH_ BLAGE	3-hydroxy-3-methylglutaryl -coenzyme A reductase	Blattella germanica
