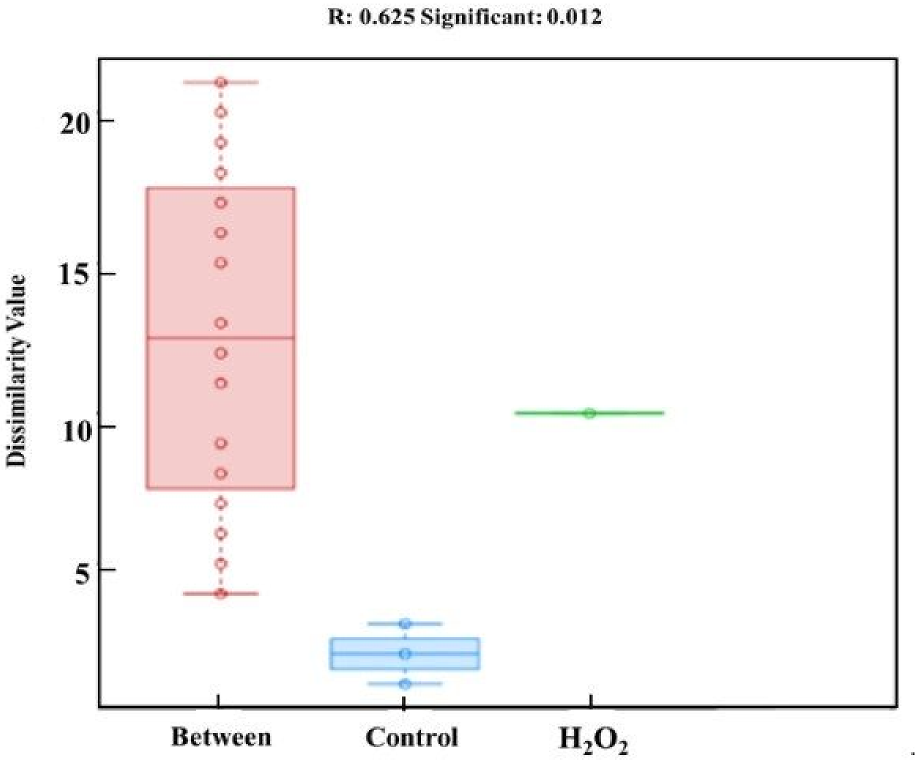

Figure S1. Comparison of the intra-group differences in the expression levels of genes in the control and the H_2O_2-elicited sample.

Table S2. Statistics of the transcriptomic analysis

Table S2A. Gene mapping statistics

	Control-1	**Control-2**	**Control-3**	**H_2O_2-1**	**H_2O_2-2**
Total reads	47,069,028 (100.00%)	54,373,304 (100.00%)	52,032,746 (100.00%)	50,900,752 (100.00%)	44,998,414 (100.00%)
Total mapped	44,554,976 (94.66%)	51,334,599 (94.41%)	48,978,449 (94.13%)	47,979,752 (94.26%)	42,798,219 (95.11%)
Multiple mapped	42,690,974 (90.70%)	49,096,450 (90.30%)	46,06,961 (89.96%)	45,968,784 (90.31%)	40,947,436 (91.00%)
Uniquely mapped	1,864,002 (3.96%)	2,238,149 (4.12%)	2,171,488 (4.17%)	2,010,968 (3.95%)	1,850,783 (4.11%)
Reads map to '+'	942,404 (2.00%)	1,130,786 (2.08%)	1,096,968 (2.11%)	1,017,238 (2.00%)	932,389 (2.07%)
Reads map to '-'	921,598 (1.96%)	1,107,363 (2.04%)	1,074,520 (2.07%)	993,730 (1.95%)	918,394 (2.04%)
Non-splice reads	1,864,002 (3.96%)	2,238,149 (4.12%)	2,171,488 (4.17%)	2,010,968 (3.95%)	1,850,783 (4.11%)
Splice reads	0 (0.00%)	0 (0.00%)	0 (0.00%)	0 (0.00%)	0 (0.00%)
Reads mapped in proper pairs	1,694,950 (3.60%)	2,036,422 (3.75%)	1,984,254 (3.81%)	1,828,442 (3.59%)	1,674,742 (3.72%)

Total reads: The number of reads after quality inspection (clean data)

Total mapped: The number of reads that can be matched to the reference sequence

Multiple mapped: The number of reads with multiple matching positions on the reference sequence

Unique mapped: The number of reads with only one matching position on the reference sequence

Reads map to '+', Reads map to '-': The number of reads mapped to the sense (+) or the nonsense (-) strands on the reference sequence (only the Unique Mapped reads are investigated)

Non splice reads: The number of reads that match the sequence of a single exon

Splice reads: The number of reads that overlap two exons (also known as junction reads)

Reads mapped in proper pairs: The number of two end reads matching to reference sequence at the same time.

Table S2B. Gene assembly statistics

	No.	**>=500bp**	**>=1000bp**	**N50**	**N90**	**Maximum length**	**Minimum length**	**Total length**	**Average length**
Transcript	120,623	85,543	73,702	5,368	1,712	28,619	201	343,306,921	2,846
Unigene	34,512	9,384	5,470	3,310	271	28,619	201	31,328,723	908

Table S4. Potential biosynthetic genes involved in antrodin C production

Gene ID	Protein ID	Query cover (%)	E value	Percent identity (%)	Predicted Function	Matching gene name
TRINITY_DN12797_c0_g1	gi|598002407	97	3.00E-70	36.69	WD40	poxJ/paeD
TRINITY_DN19315_c0_g1	gi|758349692	96	2.00E-93	42.05	Branched chain amino acid aminotransferase	poxL/paeG
TRINITY_DN12945_c0_g4	gi|597935992	90	2.00E-49	23.21	Nonribosomal peptide synthetases (NRPS)	poxE/paeO
TRINITY_DN12960_c2_g1	gi|1023204788	93	2.00E-25	25.78	Cytochrome P450	poxC/paeM
TRINITY_DN12230_c0_g1	gi|1023270917	91	1.00E-15	22.16	Cytochrome P450	poxM/paeH
TRINITY_DN12021_c0_g1	gi|1023274070	31	2.00E-09	26.98	Cytochrome P450	poxD/paeN