

## Supplementary Information

### **Integrated transcriptomic and metabolomic analyses reveal the effects of callose deposition and multihormone signal transduction pathways on the tea plant-*Colletotrichum camelliae* interaction**

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**Supplementary Table S1 The quality of RNA-seq**

sample	Raw reads	Clean reads	Clean bases(G)	Error rate	Q20	Q30	GC %	Total map
T12h_1	49815466	49071720	7.36	0.03	97.48	93.02	43.52	44601778 (90.89%)
T12h_2	50831572	50251972	7.54	0.03	97.26	92.52	43.49	45525862 (90.6%)
T12h_3	56809808	56148184	8.42	0.03	97.6	93.32	43.66	51151888 (91.1%)
C12h_1	55864712	55334744	8.3	0.03	97.6	93.28	43.94	50593522 (91.43%)
C12h_2	45645770	45095710	6.76	0.03	97.25	92.51	43.73	40942481 (90.79%)
C12h_3	52341694	51820590	7.77	0.03	97.49	93.04	44.08	47385295 (91.44%)
T24h_1	51352088	50779830	7.62	0.03	97.22	92.48	44.11	45981203 (90.55%)
T24h_2	49478520	48820672	7.32	0.03	97.36	92.78	43.97	44309471 (90.76%)
T24h_3	56215976	55542038	8.33	0.03	97.15	92.25	44.24	50531894 (90.98%)
C24h_1	48074970	47315864	7.1	0.03	97.42	92.87	44.24	43099261 (91.09%)
C24h_2	49773122	49051488	7.36	0.03	97.58	93.23	44.11	44694606 (91.12%)
C24h_3	52282844	51442668	7.72	0.03	97.54	93.19	44.27	46805276 (90.99%)
T72h_1	47426446	46557026	6.98	0.03	97.14	92.28	44.47	40140793 (86.22%)
T72h_2	50975512	50026170	7.5	0.03	97.4	92.9	44.04	44201743 (88.36%)
T72h_3	48841340	48073218	7.21	0.03	97.22	92.44	44.31	42628791 (88.67%)
C72h_1	51330228	50127660	7.52	0.03	97.37	92.77	43.8	45542894 (90.85%)
C72h_2	71651004	70494396	10.57	0.03	97.71	93.74	44.03	64269666 (91.17%)
C72h_3	61622244	60832450	9.12	0.03	97.78	93.87	43.95	55464598 (91.18%)

Supplementary Table S2 Significantly differentially expressed genes (DEGs) in different time points

Supplementary Table S3 List of enriched Gene Ontology terms identified from all DEGs

**Supplementary Table S4 The top 35 GO terms are listed based on the number of assigned DEGs and P value**

GOID	Ontology	Term	Number in input list (q)	Number in the reference list (m)	q/m (%)	P-value
Upregulated genes (12 hpi)						
GO:0051716	BP	cellular response to stimulus	30	2587	1.16	0.000148
GO:0043207	BP	response to external biotic stimulus	23	1502	1.53	5.47E-05
GO:0051707	BP	response to other organism	23	1502	1.53	5.47E-05
GO:0009725	BP	response to hormone	19	1757	1.08	0.0203
GO:0033554	BP	cellular response to stress	18	1162	1.55	0.00054
GO:0006955	BP	immune response	13	748	1.74	0.00371
GO:0042594	BP	response to starvation	11	346	3.18	0.000139
GO:0009620	BP	response to fungus	10	557	1.80	0.0178
GO:0010243	BP	response to organonitrogen compound	9	445	2.02	0.0165
GO:0015706	BP	nitrate transport	6	206	2.91	0.0277
GO:0001666	BP	response to hypoxia	5	100	5.00	0.0101
GO:0017076	MF	purine nucleotide binding	10	605	1.65	0.0283
GO:0030554	MF	adenyl nucleotide binding	10	448	2.23	0.00405
GO:0004601	MF	peroxidase activity	8	100	8.00	1.56E-05
GO:0001067	MF	regulatory region nucleic acid binding	4	21	19.05	0.000494
GO:0051716	BP	cellular response to stimulus	30	2587	1.16	0.000148
Upregulated gene (24 hpi)						
GO:0010243	BP	response to organonitrogen compound	74	445	16.63	1.18E-34
GO:0051716	BP	cellular response to stimulus	181	2587	7.00	1.8E-32
GO:0043207	BP	response to external biotic stimulus	124	1502	8.26	1.43E-27
GO:0051707	BP	response to other organism	124	1502	8.26	1.43E-27
GO:0006955	BP	immune response	80	748	10.70	3.84E-24
GO:0009725	BP	response to hormone	125	1757	7.11	5.47E-22
GO:0070887	BP	cellular response to chemical stimulus	105	1312	8.00	5.84E-22
GO:0033554	BP	cellular response to stress	97	1162	8.35	1.81E-21
GO:0009404	BP	toxin metabolic process	40	225	17.78	2.35E-19
GO:0046942	BP	carboxylic acid transport	43	276	15.58	1.35E-18
GO:0006865	BP	amino acid transport	41	252	16.27	2.1E-18
GO:0015711	BP	organic anion transport	43	298	14.43	2.49E-17
GO:0098754	BP	detoxification	37	226	16.37	1.15E-16
GO:0015706	BP	nitrate transport	34	206	16.50	2.13E-15
GO:0044248	BP	cellular catabolic process	101	1535	6.58	3.44E-15
GO:0072657	BP	protein localization to membrane	44	377	11.67	2.5E-14
GO:0080135	BP	regulation of cellular response to stress	44	388	11.34	7.23E-14
GO:0050776	BP	regulation of immune response	45	428	10.51	5.42E-13
GO:0042446	BP	hormone biosynthetic process	61	741	8.23	6.84E-13

GO:0048585	BP	negative regulation of response to stimulus	41	370	11.08	1.52E-12
GO:0042445	BP	hormone metabolic process	64	819	7.81	1.58E-12
GO:2000377	BP	regulation of reactive oxygen species metabolic process	30	207	14.49	5.03E-12
GO:0051193	BP	regulation of cofactor metabolic process	30	209	14.35	6.49E-12
GO:0009651	BP	response to salt stress	61	785	7.77	8.32E-12
GO:0009723	BP	response to ethylene	39	355	10.99	8.47E-12
GO:0009617	BP	response to bacterium	52	607	8.57	1.47E-11
GO:0016310	BP	phosphorylation	64	868	7.37	2.05E-11
GO:0052542	BP	defense response by callose deposition	17	62	27.42	3.71E-11
GO:0034976	BP	response to endoplasmic reticulum stress	38	358	10.61	4.94E-11
GO:0009595	BP	detection of biotic stimulus	21	106	19.81	6.37E-11
GO:0031348	BP	negative regulation of defense response	33	278	11.87	7.84E-11
GO:0009620	BP	response to fungus	48	557	8.62	9.96E-11
GO:0006970	BP	response to osmotic stress	61	841	7.25	1.47E-10
GO:0071944	CC	cell periphery	176	3735	4.71	6.98E-13
GO:0004601	MF	peroxidase activity	21	100	21.00	1.97E-11
Upregulated gene (72 hpi)						
GO:0051716	BP	cellular response to stimulus	610	2587	23.58	1.58E-81
GO:0010243	BP	response to organonitrogen compound	208	445	46.74	2.81E-80
GO:0033554	BP	cellular response to stress	347	1162	29.86	6.85E-71
GO:0034976	BP	response to endoplasmic reticulum stress	157	358	43.85	1.91E-55
GO:0006955	BP	immune response	238	748	31.82	3.3E-53
GO:0043207	BP	response to external biotic stimulus	368	1502	24.50	4.28E-51
GO:0051707	BP	response to other organism	368	1502	24.50	4.28E-51
GO:0006865	BP	amino acid transport	116	252	46.03	2.58E-43
GO:0046942	BP	carboxylic acid transport	122	276	44.20	2.71E-43
GO:0015711	BP	organic anion transport	122	298	40.94	4.47E-39
GO:0009404	BP	toxin metabolic process	97	225	43.11	3.78E-33
GO:0098754	BP	detoxification	96	226	42.48	3.67E-32
GO:0009725	BP	response to hormone	356	1757	20.26	2.1E-30
GO:0070887	BP	cellular response to chemical stimulus	287	1312	21.88	7.38E-30
GO:0015833	BP	peptide transport	247	1084	22.79	2.95E-28
GO:0035966	BP	response to topologically incorrect protein	121	370	32.70	1.01E-27
GO:0016310	BP	phosphorylation	210	868	24.19	1.77E-27
GO:0006986	BP	response to unfolded protein	79	188	42.02	5.3E-26
GO:0052542	BP	defense response by callose deposition	43	62	69.35	1.97E-25
GO:0009617	BP	response to bacterium	161	607	26.52	2.01E-25
GO:0072657	BP	protein localization to membrane	118	377	31.30	3.95E-25
GO:0044248	BP	cellular catabolic process	307	1535	20.00	5.7E-25
GO:0006970	BP	response to osmotic stress	199	841	23.66	1.05E-24
GO:0050776	BP	regulation of immune response	127	428	29.67	1.1E-24

GO:0080135	BP	regulation of cellular response to stress	118	388	30.41	6.46E-24
GO:0045184	BP	establishment of protein localization	218	975	22.36	1.11E-23
GO:0009651	BP	response to salt stress	186	785	23.69	4.1E-23
GO:0015824	BP	proline transport	45	74	60.81	4.98E-23
GO:0009723	BP	response to ethylene	109	355	30.70	1.95E-22
GO:0071944	CC	cell periphery	761	3735	20.37	2E-72
GO:0012505	CC	endomembrane system	380	1675	22.69	3.43E-44
GO:0051740	MF	ethylene binding	7	5	140.00	0
GO:1901265	MF	nucleoside phosphate binding	219	839	26.10	8.06E-34
GO:0000166	MF	nucleotide binding	219	839	26.10	8.06E-34
GO:0017076	MF	purine nucleotide binding	155	605	25.62	8.92E-23
Downregulated gene (12 hpi)						
GO:0015979	BP	photosynthesis	21	403	5.21	1.14E-09
GO:0009657	BP	plastid organization	16	406	3.94	9.79E-06
GO:0006733	BP	oxidoreduction coenzyme metabolic process	16	427	3.75	1.76E-05
GO:0006091	BP	generation of precursor metabolites and energy	18	605	2.98	6.19E-05
GO:0044283	BP	small molecule biosynthetic process	28	1384	2.02	8.06E-05
GO:0017144	BP	drug metabolic process	20	831	2.41	0.000261
GO:0070838	BP	divalent metal ion transport	10	210	4.76	0.000385
GO:0051186	BP	cofactor metabolic process	21	935	2.25	0.000387
GO:0006790	BP	sulfur compound metabolic process	18	712	2.53	0.000405
GO:0006732	BP	coenzyme metabolic process	16	585	2.74	0.000537
GO:0071214	BP	cellular response to abiotic stimulus	9	173	5.20	0.000538
GO:0104004	BP	cellular response to environmental stimulus	9	173	5.20	0.000538
GO:0055082	BP	cellular chemical homeostasis	11	308	3.57	0.00136
GO:0019725	BP	cellular homeostasis	11	325	3.38	0.00212
GO:0019637	BP	organophosphate metabolic process	21	1095	1.92	0.00273
GO:0048731	BP	system development	37	2640	1.40	0.00273
GO:0006796	BP	phosphate-containing compound metabolic process	28	1749	1.60	0.003
GO:0043933	BP	protein-containing complex subunit organization	14	546	2.56	0.00304
GO:0022900	BP	electron transport chain	6	93	6.45	0.00457
GO:0006081	BP	cellular aldehyde metabolic process	12	431	2.78	0.00473
GO:0048506	BP	regulation of timing of meristematic phase transition	4	30	13.33	0.00504
GO:0048510	BP	regulation of timing of transition from vegetative to reproductive phase	4	30	13.33	0.00504
GO:0006793	BP	phosphorus metabolic process	28	1837	1.52	0.00611
GO:0031323	BP	regulation of cellular metabolic process	34	2462	1.38	0.00669
GO:0048367	BP	shoot system development	21	1241	1.69	0.0114

GO:0034765	BP	regulation of ion transmembrane transport	6	117	5.13	0.0127
GO:0010155	BP	regulation of proton transport	5	77	6.49	0.0145
GO:1904062	BP	regulation of cation transmembrane transport	5	79	6.33	0.0161
GO:0000302	BP	response to reactive oxygen species	9	317	2.84	0.025
GO:0031975	CC	envelope	30	902	3.33	1.14E-09
GO:0044422	CC	organelle part	57	3130	1.82	2.92E-09
GO:0009986	CC	cell surface	3	14	21.43	0.00953
GO:0008187	MF	poly-pyrimidine tract binding	4	19	21.05	0.00106
GO:0008266	MF	poly(U) RNA binding	4	19	21.05	0.00106
GO:0003727	MF	single-stranded RNA binding	4	40	10.00	0.0127
Downregulated genes (24 hpi)						
GO:0006796	BP	phosphate-containing compound metabolic process	165	1749	9.43	4.96E-40
GO:0006793	BP	phosphorus metabolic process	169	1837	9.20	1.05E-39
GO:0016043	BP	cellular component organization	219	2961	7.40	8.85E-38
GO:0044237	BP	cellular metabolic process	398	7935	5.02	1.7E-33
GO:0009657	BP	plastid organization	72	406	17.73	5.12E-33
GO:0006081	BP	cellular aldehyde metabolic process	74	431	17.17	5.14E-33
GO:0006996	BP	organelle organization	162	1947	8.32	1.43E-32
GO:0015979	BP	photosynthesis	71	403	17.62	2.29E-32
GO:0005975	BP	carbohydrate metabolic process	120	1281	9.37	6.34E-28
GO:0019637	BP	organophosphate metabolic process	106	1095	9.68	1.44E-25
GO:0006790	BP	sulfur compound metabolic process	82	712	11.52	2.32E-24
GO:0006091	BP	generation of precursor metabolites and energy	74	605	12.23	1.75E-23
GO:0006733	BP	oxidoreduction coenzyme metabolic process	62	427	14.52	1.86E-23
GO:1901564	BP	organonitrogen compound metabolic process	262	4863	5.39	2.06E-23
GO:0051186	BP	cofactor metabolic process	93	935	9.95	3.69E-23
GO:0006732	BP	coenzyme metabolic process	70	585	11.97	1.31E-21
GO:0048367	BP	shoot system development	101	1241	8.14	7.74E-19
GO:0006725	BP	cellular aromatic compound metabolic process	192	3385	5.67	1.79E-18
GO:0043933	BP	protein-containing complex subunit organization	61	546	11.17	2.64E-17
GO:0016310	BP	phosphorylation	78	868	8.99	9.94E-17
GO:0009311	BP	oligosaccharide metabolic process	37	210	17.62	1.31E-16
GO:0046483	BP	heterocycle metabolic process	174	3083	5.64	2.66E-16
GO:1901576	BP	organic substance biosynthetic process	247	5060	4.88	3.44E-16
GO:0000226	BP	microtubule cytoskeleton organization	38	238	15.97	1.35E-15
GO:0090698	BP	post-embryonic plant morphogenesis	56	511	10.96	1.68E-15
GO:0010073	BP	meristem maintenance	41	284	14.44	2.76E-15

GO:0009658	BP	chloroplast organization	38	251	15.14	7.74E-15
GO:0009653	BP	anatomical structure morphogenesis	116	1769	6.56	9.73E-15
GO:0044283	BP	small molecule biosynthetic process	98	1384	7.08	2.42E-14
GO:0043085	BP	positive regulation of catalytic activity	25	115	21.74	2.62E-13
GO:0044422	CC	organelle part	199	3130	6.36	4.47E-25
GO:0071944	CC	cell periphery	203	3735	5.44	1.31E-17
GO:0031975	CC	envelope	76	902	8.43	8.66E-15
GO:0030554	MF	adenyl nucleotide binding	57	448	12.72	9.32E-19
GO:0017076	MF	purine nucleotide binding	60	605	9.92	1.14E-14
Downregulated gene (72 hpi)						
GO:0009657	BP	plastid organization	175	406	43.10	1.21E-76
GO:0006081	BP	cellular aldehyde metabolic process	179	431	41.53	2.79E-75
GO:0006796	BP	phosphate-containing compound metabolic process	395	1749	22.58	4.17E-74
GO:0006793	BP	phosphorus metabolic process	405	1837	22.05	6.81E-73
GO:0006996	BP	organelle organization	417	1947	21.42	2.71E-71
GO:0016043	BP	cellular component organization	536	2961	18.10	3.21E-66
GO:0051186	BP	cofactor metabolic process	258	935	27.59	3.45E-65
GO:0044237	BP	cellular metabolic process	1063	7935	13.40	2E-63
GO:0019637	BP	organophosphate metabolic process	269	1095	24.57	9.58E-57
GO:0015979	BP	photosynthesis	142	403	35.24	7.12E-49
GO:0046483	BP	heterocycle metabolic process	498	3083	16.15	2.08E-45
GO:0006725	BP	cellular aromatic compound metabolic process	531	3385	15.69	6.29E-45
GO:0009658	BP	chloroplast organization	103	251	41.04	3.71E-42
GO:0006733	BP	oxidoreduction coenzyme metabolic process	135	427	31.62	2.38E-40
GO:0061024	BP	membrane organization	92	214	42.99	1.38E-39
GO:1901564	BP	organonitrogen compound metabolic process	671	4863	13.80	1.07E-38
GO:0048367	BP	shoot system development	254	1241	20.47	3.37E-38
GO:0005975	BP	carbohydrate metabolic process	257	1281	20.06	4.12E-37
GO:0006732	BP	coenzyme metabolic process	154	585	26.32	1.91E-35
GO:0006790	BP	sulfur compound metabolic process	172	712	24.16	1.51E-34
GO:0009311	BP	oligosaccharide metabolic process	81	210	38.57	1.01E-30
GO:1901576	BP	organic substance biosynthetic process	662	5060	13.08	1.08E-30
GO:0051656	BP	establishment of organelle localization	57	107	53.27	1.72E-30
GO:0006091	BP	generation of precursor metabolites and energy	147	605	24.30	1.16E-29
GO:0048731	BP	system development	401	2640	15.19	1.35E-29
GO:0007275	BP	multicellular organism development	489	3539	13.82	1.02E-26
GO:0009791	BP	post-embryonic development	338	2169	15.58	1.54E-26
GO:0090698	BP	post-embryonic plant morphogenesis	126	511	24.66	5.77E-26
GO:0044422	CC	organelle part	572	3130	18.27	5.79E-73

GO:0044464	CC	cell part	2107	21711	9.70	5.92E-29
GO:0031975	CC	envelope	186	902	20.62	5.63E-28
GO:0000166	MF	nucleotide binding	184	839	21.93	3.69E-31
GO:1901265	MF	nucleoside phosphate binding	184	839	21.93	3.69E-31
GO:0030554	MF	adenyl nucleotide binding	122	448	27.23	2.1E-29
GO:0017076	MF	purine nucleotide binding	146	605	24.13	3.96E-29

Supplementary Table S5 List of the differentially expressed metabolites (DEMs) in different time points

**Supplementary Table S6 qRT-PCR validation primers**

Gene ID	Primer	Sequence (5'→3')
TEA026913	Forward (F)	TCGGGTTTCTTCATCCCTAGAC
	Reverse (R)	CGTACCATTGGACAGTAGTGGA
novel.17836	F	ATGCACTCGAAGGACCAATC
	R	GTCGACTAAGTTGTGCCATACC
TEA012289	F	GCAAGCGACCAAGTTTATGG
	R	CTCTCTCTACTCGTCTGATCTC
TEA025907	F	CCACATGGTTGAGCCTAGAA
	R	CAAGATCCGCATGGTTCTCT
TEA019216	F	GAGGCGCTCTGTAACATCTA
	R	CCAAGGAAGTGGTCAGTGTA
TEA001041	F	GAAACGGGACATGGTGATAGAG
	R	CAGAACGTGCCTCAACATCT
TEA030190	F	CGGCTGATAAGGCAAAGGAA
	R	ACTCGAGGTAGTGGGAATCA
TEA026494	F	GACAGGTCATCCAGAGACAATC
	R	CTGGAACACCAAGTCCTGATAG
TEA011776	F	CGGTAGGTCATGGTGACAAG
	R	TTGGTTCGAGCAATGGTAGG
TEA004708	F	GAAACTGATGCAGGGCTTCT
	R	GGGATGAACCATGGCTAACA



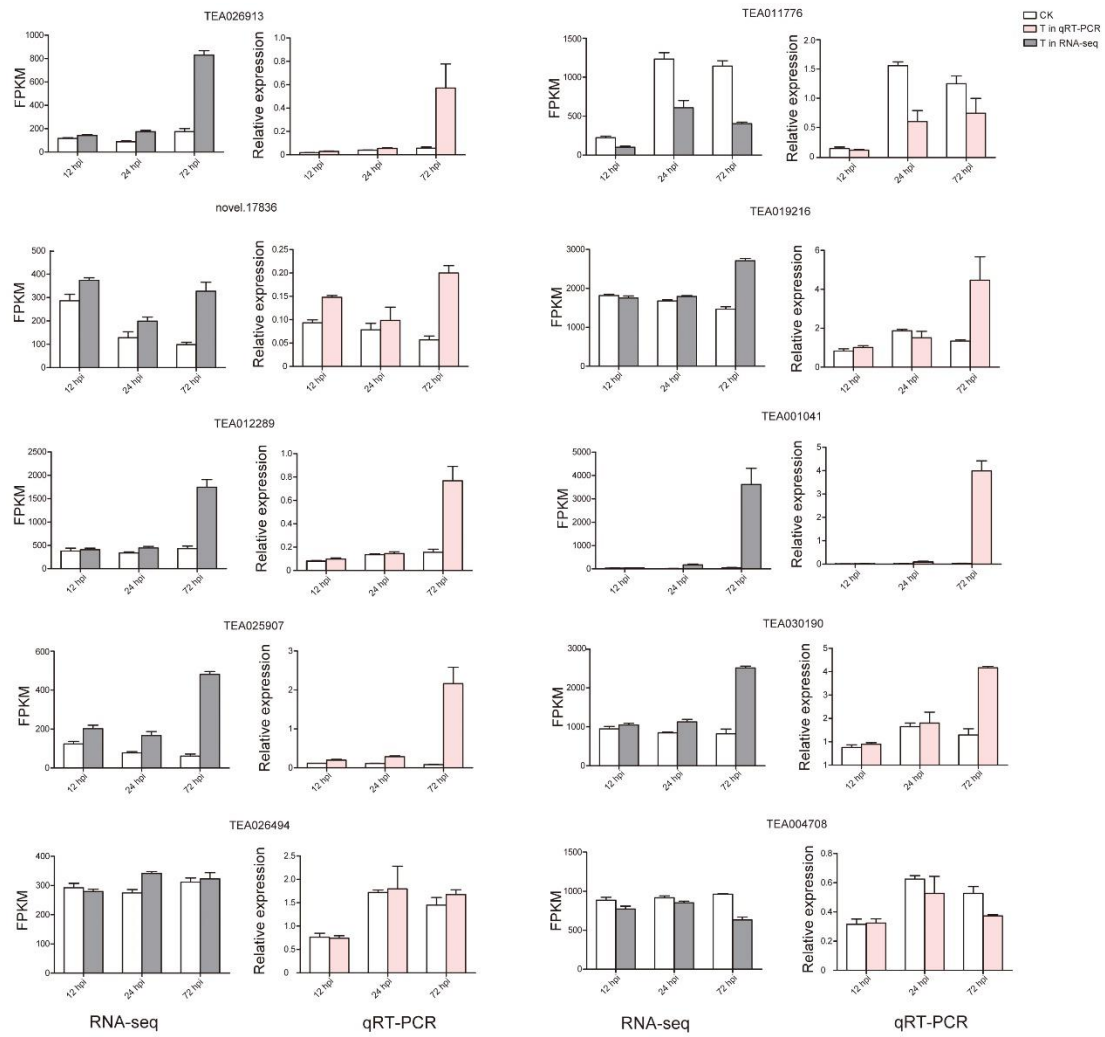


Figure S1 Expression profile comparisons between the RNA-Seq and qRT-PCR data