

Supplementary Table S1 Full names of the specific internal–standard compounds for hormone quantification

substance		Corresponding internal standard information	
ABA	d6–ABA	Czech	034 2721
ABA–GE	d6–ABA	Czech	034 2721
ABA–ald	d6–ABA	Czech	034 2721
IAA–Glu	d5–IAA–Val	Czech	0311641
IAN	[2H4]INDOLE–3–ACETONITRILE	Czech	031 1852
IAA–Val–Me	d5–IAA–Val	Czech	0311641
OxIAA	d2–IAA	isoreag	R–30387–100 mg
IAA–Asp	[2H5]INDOLE–3–ACETYL–L–[15N] ASPARTIC ACID	Czech	031 1593
IAA–Val	d5–IAA–Val	Czech	0311641
IAM	[2H5]–IAM	IsoReag	IR–21912
TRA	Tryptamine– $\alpha,\alpha,\beta,\beta$ –d4 HCl	CDN	D1546
IAA–Ala	[2H5]INDOLE–3–ACETYL–L–[15N] ALANINE	Czech	031 1583
TRP	[2H5]–L–TRP	sigma	615862–500 mg
IAA–Phe	d5–IAA–Val	Czech	0311641
ICA	Indole–3–carboxylic Acid–d5	isoreag	IR–73457–25 mg
IAA–Glc	d2–IAA	isoreag	R–30387–100 mg
IAA	d2–IAA	isoreag	R–30387–100 mg
ICAld	Indole–3–carboxaldehyde–13C	TRC	1614992
MEIAA	d5–MEIAA	CDN	D–6165–10 mg
Indole	d2–IAA	isoreag	R–30387–100 mg
mT	d7–BAP	Czech	030 0221

K	d7-BAP	Czech	030 0221
iP7G	d6-iP9G	Czech	030 0231
tZOG	[2H5]trans-ZEATIN-O-GLUCOSIDE	Czech	030 5121
DHZROG	[2H7]DIHYDROZEATIN-O-GLUCOSIDE RIBOSIDE	Czech	030 0652
cZROG	15N4-cZ	Czech	0300321
mT9G	d6-iP9G	Czech	030 0231
BAP9G	d6-iP9G	Czech	030 0231
2MeSiP	d6-IP	Czech	030 0161
2MeScZR	[2H5]2-METHYLTHIO-trans-ZEATIN RIBOSIDE	Czech	030 5181
DHZ7G	d7-DHZOG	Czech	030 0642
IP	d6-IP	Czech	030 0161
IPR	d6-IPR	Czech	030 0171
tZ	d5-tZ	IsoReag	IR-35064
tZR	d5-tZ	IsoReag	IR-35064
iPRMP	d6-iP9G	Czech	030 0231
tZ9G	[2H5]trans-ZEATIN-O-GLUCOSIDE	Czech	030 5121
tZRMP	d6-iP9G	Czech	030 0231
GA20	[2H2]GIBBERELLIN A20	Czech	0322483
GA3	d2-GA4	Czech	0322531
GA4	d2-GA4	Czech	0322531
GA7	d2-GA4	Czech	0322531
GA9	d2-GA9	Czech	0322661
GA8	d2-GA4	Czech	0322531
GA5	d2-GA4	Czech	0322531
JA-Phe	d5-JA	SCRSTANDARD	D-6936
JA-Val	d5-JA	SCRSTANDARD	D-6936
OPC-4	d5-JA	SCRSTANDARD	D-6936
JA	d5-JA	SCRSTANDARD	D-6936

JA-ILE	d5-JA	SCRSTANDARD	D-6936
MEJA	d5-MEJA	IsoReag	IR-22054
OPDA	d5-JA	SCRSTANDARD	D-6936
12-OH-JA	d5-JA	SCRSTANDARD	D-6936
SA	d4-SA	isoreag	IR-30219-0.1 g
SAG	d4-SA	isoreag	IR-30219-0.1 g
Phe	N-(3-Indolylacetyl)-L-phenylalanine	Bide	BD9025-1 g
t-CA	trans-Cinnamic acid	Ron	R014152-5 g
2-Coumarate	2-Coumarate	TCI	C0394-5 G
MeSAG	2-Methoxycarbonylphenyl beta-D-glucopyranoside	Heya	B017320

Supplementary Table S2 Primer sequence for qRT-PCR

Gene name	Gene Locus ID	Primer-F	Primer-R
<i>Csβ-actin</i>	HD.01G0021100	TGAGGATATTCAGCCCCCTTG	GCCTGGGTCGACCTACAATA
<i>CsANS</i>	HD.09G0021230	CTTCAAGGGTATGGGAGCAA	CGTACTCAACTGTCGCAGGA
<i>CsSCPL</i>	HD.1307844	ACCAGGCTTTGATGGTGAAC	CATTGAAAGCAGAGCAACCA
<i>CsDFR</i>	HD.06G0036240	CACAGTTCGCGATCCTGATA	ACGTGGAAGACACCATGACA
<i>CsTCP</i>	HD.02G0007530	TGCGAGATGTGAGATTCAGG	AAATCAGGAGGAGCAGCAAA
<i>CsMYB-related</i>	HD.03G0018090	GCAGCTACATTCTGGCCTTC	AGTGCACACTGGCAACAGTC
<i>CsTIR1</i>	HD.01014854	ATAGCCCTTTTGGTGACGTG	TGGCATCTTCTTTGCAAGTG

Supplementary Table S3 Design of AsODNs sequences for *CsARF2*, *CsMYC2*, and *CsMYB80*

Gene	Primer-F	Primer-R
<i>CsARF2</i> (HD.14G0019970) –AsODNs	AGACAGTTGGAGGTCTTGCAAGGT	ACCTTGCAAGACCTCCAACGTCT
<i>CsMYC2</i> (HD.07G0018360)–AsODNs	AAACTGCAACGGAATCCAGT	ACTGGATTCCGTTGCAGTTT
<i>CsMYB80</i> (HD.08G0030520) –AsODNs	TACATTGCCCAACACGGAAC	GTTCCGTGTTGGGCAATGTA
<i>CsARF2</i> (HD.14G0019970)–qRT-PCR	GATTGGAGAATCAGCCGCACTT	GGAAGAGCAGGACAGACACTATGA
<i>CsMYC2</i> (HD.07G0018360)–qRT-PCR	GCTTGTGAAGACTCCACCAGTG	TCTTACCTCGTCAGCGTCCATC
<i>CsMYB80</i> (HD.08G0030520) – qRT-PCR	CGGTTACCCACAAGCCCTTCTC	TGCTGGTCTCCTGCCGTGTA
<i>CsSCPL16</i> (HD.1307844)–qRT-PCR	GCTCCTCTTCCTCCTAGTGCTCTT	GGCGTACCTCCCTCATACTCTGTT

Supplementary Table S4 Contents of endogenous phytohormone components in tea shoots of different treatment groups (ng·g⁻¹ FW)

Hormone category	Component	Ct-1	Ct-2	Ct-3	PAC-1	PAC-2	PAC-3	LS-1	LS-2	LS-3	P-L-1	P-L-2	P-L-3
GAs	GA5	8.56	8.86	8.71	4.28	4.69	3.81	7.04	8.34	8.05	5.41	5.20	5.00
	GA3	9.26	8.61	9.17	10.45	9.46	9.07	7.92	9.25	7.95	5.36	5.28	5.19
	GA4	2.59	2.37	1.97	1.58	2.07	2.10	0.00	0.00	0.00	2.08	1.23	2.30
	GA8	0.72	0.50	0.99	1.21	0.76	0.40	0.77	1.00	0.91	0.62	0.77	0.58
	GA9	1.20	1.38	1.18	1.13	1.20	1.50	1.48	1.32	0.64	0.00	0.00	0.00
	GA7	0.25	0.11	0.12	0.05	0.07	0.07	0.07	0.07	0.06	0.00	0.00	0.00
Auxins	TRA	6.64	6.70	6.05	7.29	6.90	6.72	6.23	6.67	7.28	7.74	7.29	6.89
	TRP	24918.61	23050.30	25574.56	30019.14	29476.25	30562.05	28693.38	28511.14	28328.73	25367.89	24645.25	26090.54

CTKs	IAA-Phe	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.05	0.05
	OxIAA	18.03	21.50	19.76	33.16	34.06	32.27	27.05	26.03	26.54	22.85	21.05	22.06
	IAA-Val-Me	0.00	0.00	0.00	0.00	0.00	0.00	0.36	0.20	0.35	0.18	0.08	0.11
	MEIAA	0.34	0.38	0.44	0.26	0.38	0.34	0.20	0.30	0.36	0.33	0.37	0.33
	IAM	8.79	6.42	7.61	8.23	8.07	7.27	7.40	8.61	9.83	10.54	10.43	10.58
	IAA-Ala	0.71	0.61	0.54	0.82	0.90	1.13	0.87	0.67	0.66	1.17	0.69	1.31
	IAA	61.04	61.68	62.31	57.91	57.15	56.38	44.69	46.12	45.80	61.72	60.56	61.14
	IAN	0.18	0.00	0.00	0.44	0.50	0.69	0.40	0.21	0.30	0.25	0.41	0.51
	IAA-Glc	4.39	4.99	5.73	4.71	5.42	4.76	3.14	3.98	4.07	5.29	4.51	4.39
	ICAld	4.92	5.62	4.42	4.58	5.84	6.46	5.51	6.49	5.99	4.14	4.13	5.28
	ICA	2.79	2.68	2.07	2.14	2.25	3.35	2.95	2.56	2.97	2.82	1.69	1.78
	Indole	6714.46	6883.42	6545.51	9152.95	9019.08	9286.83	9015.21	9283.11	8958.34	6820.87	6849.70	6878.53
	IAA-Asp	2.54	2.67	2.68	2.94	3.70	3.86	3.01	3.20	2.61	4.26	4.42	4.15
	BAP9G	0.35	0.21	0.17	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	mT	0.11	0.09	0.07	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	2MeSiP	0.00	0.00	0.00	0.07	0.06	0.06	0.00	0.00	0.00	0.00	0.00	0.00
	K	0.10	0.08	0.08	0.10	0.08	0.09	0.00	0.00	0.00	0.10	0.10	0.08
	2MeScZR	1.38	1.37	1.80	1.70	1.51	1.36	1.38	1.54	1.70	1.55	1.47	1.30
	DHZROG	1.72	1.72	1.94	2.24	2.14	2.08	1.90	1.83	2.06	1.87	1.94	1.89
	IP	0.14	0.17	0.17	0.20	0.21	0.23	0.19	0.21	0.26	0.16	0.07	0.10
	IPR	0.31	0.24	0.26	0.35	0.31	0.34	0.34	0.28	0.33	0.18	0.20	0.22
	iP7G	0.22	0.29	0.32	0.53	0.24	0.34	0.26	0.29	0.29	0.21	0.22	0.18
	tZ	0.39	0.42	0.35	0.39	0.47	0.48	0.41	0.39	0.38	0.41	0.39	0.43
	DHZ7G	0.06	0.06	0.06	0.08	0.08	0.08	0.07	0.05	0.07	0.08	0.07	0.06
	mT9G	0.36	0.39	0.43	0.30	0.47	0.37	0.36	0.37	0.59	0.33	0.39	0.39
	tZOG	4.43	4.62	4.94	4.79	4.36	4.58	3.73	3.56	3.87	3.30	3.15	3.17
	tZR	1.93	2.38	2.32	3.32	3.23	3.42	2.14	2.56	2.72	2.21	2.59	2.44
	tZRMP	17.34	17.29	25.81	37.46	24.77	25.76	20.76	22.85	23.91	28.24	31.38	28.00

	tZ9G	4.36	4.32	3.24	2.52	3.33	3.66	3.34	3.29	2.57	3.33	2.70	3.80
JAs	JA–Val	0.30	0.27	0.31	0.54	0.61	0.55	0.60	0.51	0.55	0.40	0.44	0.45
	MEJA	15.63	14.54	15.62	37.22	37.78	38.34	33.14	32.83	32.51	14.87	15.52	16.38
ABAs	ABA	569.49	529.20	549.35	437.99	458.38	417.61	403.94	416.71	429.48	459.39	458.56	539.64
	ABA–GE	540.11	552.70	527.53	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	ABA–ald	370.68	395.16	382.92	354.13	361.99	346.27	303.85	346.13	324.99	273.23	200.69	236.96
SAs	SAG	5059.09	5399.40	6662.41	4912.65	4918.47	4906.84	4738.97	4697.12	4655.28	4083.48	4170.06	4256.63
	SA	184.60	186.17	183.02	366.67	376.27	393.63	189.37	194.82	192.10	270.50	295.06	264.68
	MeSAG	145.15	125.45	135.30	136.65	144.93	128.37	268.91	276.54	284.18	147.46	154.94	162.41
	Phe	7808.63	7410.61	7845.33	8656.41	8582.13	8730.68	9251.65	9528.00	9478.59	8117.71	8520.86	8319.29
	t–CA	76.22	75.10	77.35	75.06	76.03	77.00	87.46	87.42	87.38	90.69	96.45	115.14
	2–Coumarate	0.00	0.00	0.00	260.68	261.19	260.17	267.72	270.31	269.02	307.85	315.83	311.84

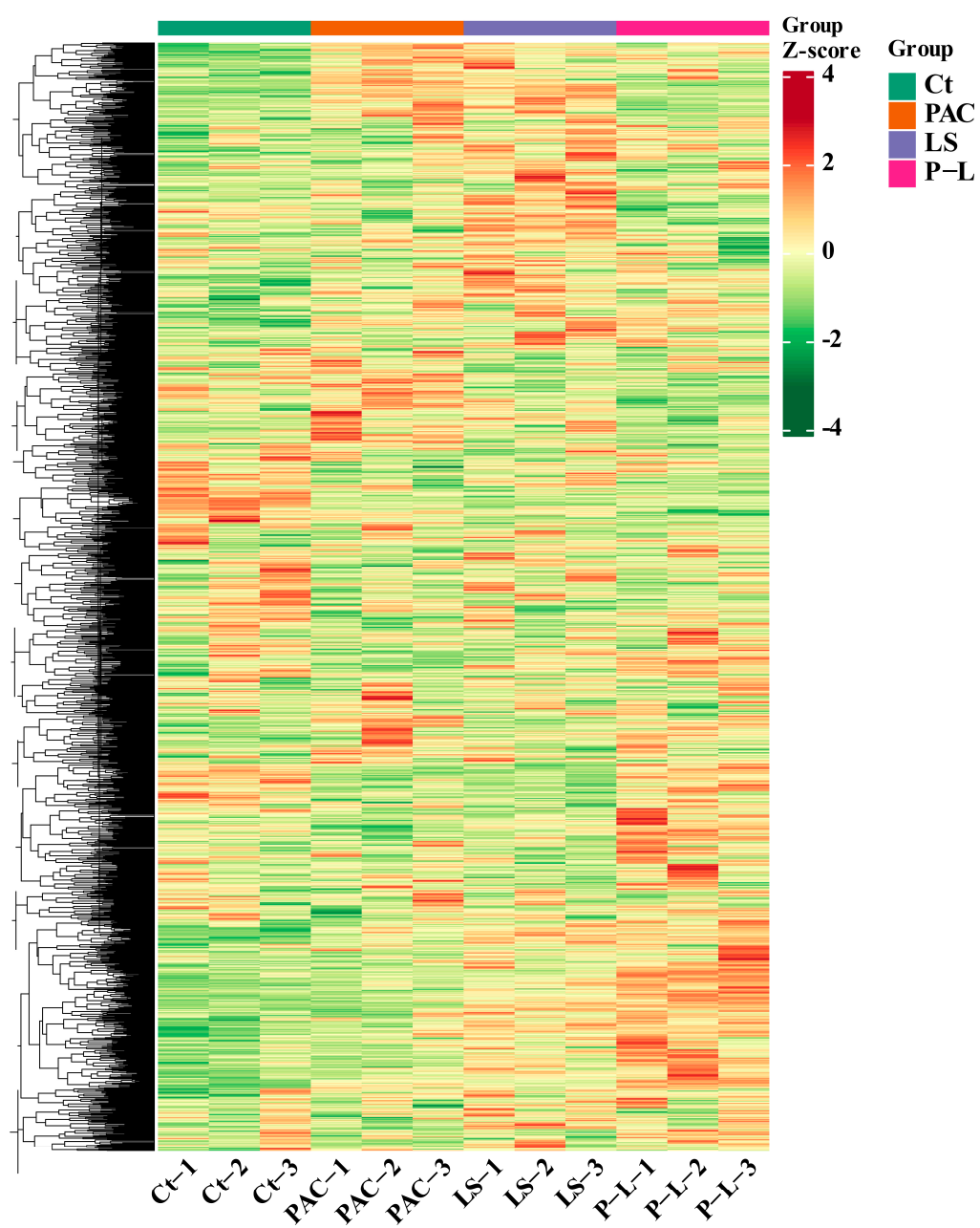


Figure S1 Cluster heatmap of all detected metabolites in tea shoots under different treatments

Supplementary Table S5 Quality evaluation of RNA-seq data

Sample	Raw Reads	Clean Reads	Clean Base (G)	Error Rate (%)	Q20(%)	Q30(%)	GC Content (%)
CK-1	49,882,136	47,889,524	7.18	0.03	97.66	93.23	45.61
CK-2	49,477,036	48,290,288	7.24	0.03	97.3	92.65	45.06
CK-3	53,013,374	51,798,202	7.77	0.03	97.35	92.76	45.09
PAC-1	51,895,474	50,643,510	7.6	0.03	97.42	92.92	45.13
PAC-2	52,079,078	50,984,822	7.65	0.03	97.25	92.56	45.16
PAC-3	47,254,870	46,304,574	6.95	0.03	97.34	92.71	45.07
LS-1	49,956,286	48,864,688	7.33	0.03	97.37	92.82	45.09
LS-2	51,253,944	50,209,048	7.53	0.03	97.11	92.14	45.05
LS-3	49,082,810	47,843,588	7.18	0.03	97.56	93.27	45.1
P-L-1	51,690,576	50,395,926	7.56	0.03	97.53	93.21	44.96
P-L-2	48,720,142	47,618,644	7.14	0.03	97.56	93.28	45.14
P-L-3	52,745,060	51,601,080	7.74	0.03	97.59	93.34	45.17

Note: Raw reads: the number of reads of the original sequencing data; Clean reads: the number of filtered reads; Clean bases: the number of Clean reads multiplied by the length of reads; Error rate: average error rate of sequencing base; Q20, Q30: the percentage of bases with sequencing quality greater than 99% and 99.9% in total bases; GC content: the percentage of the sum of G and C bases of Clean reads in total bases. CK: contrast; PAC: 50 μ mol $\cdot$ L⁻¹PAC for sample treatment; LS: 100 μ mol $\cdot$ L⁻¹LS treatment sample; P-L: 50 μ mol $\cdot$ L⁻¹PAC +100 μ mol $\cdot$ L⁻¹LS for sample treatment.

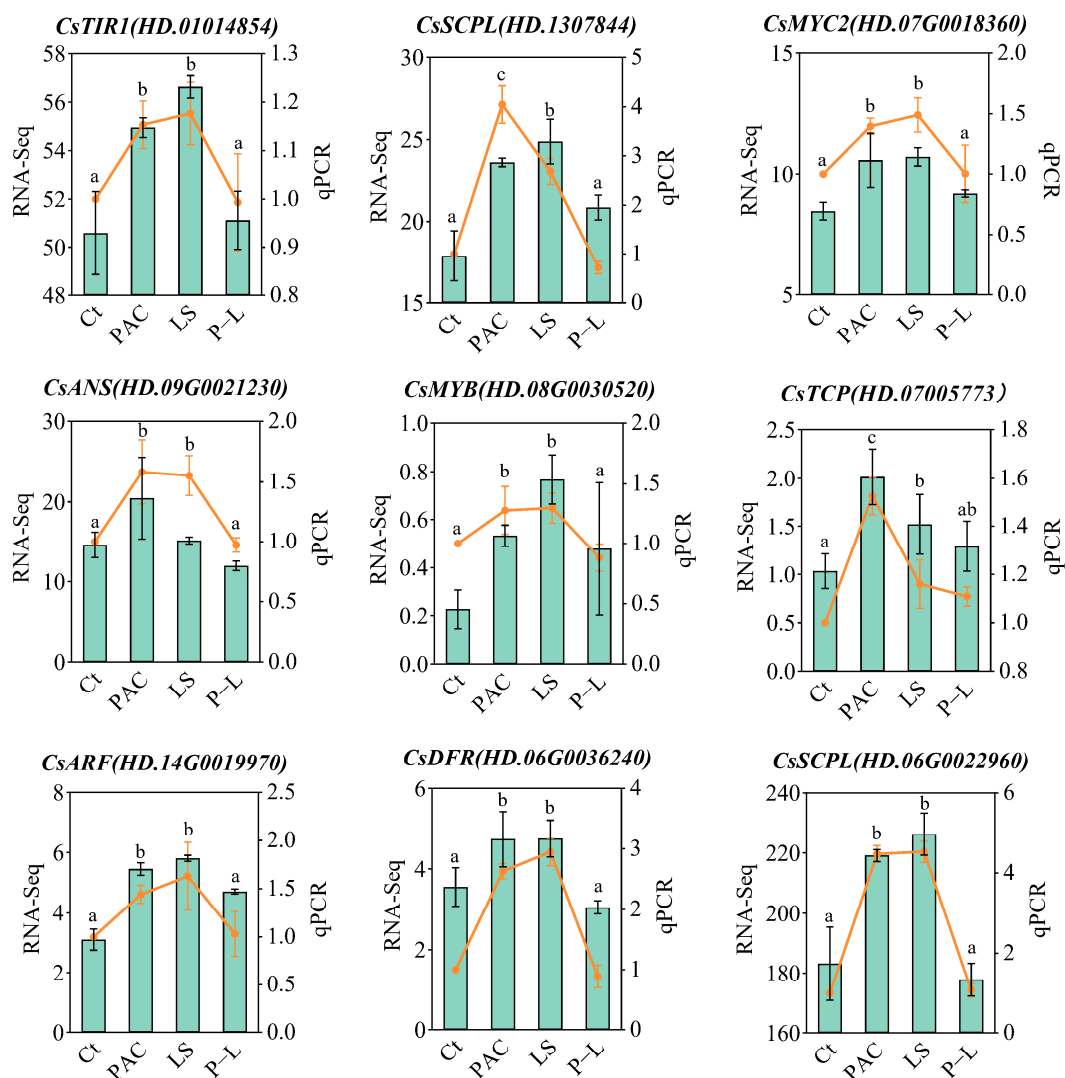


Figure S2 FPKM value and qRT-PCR relative expression of differentially expressed genes. The histogram represents the FPKM value of the differentially expressed genes, and the line chart represents the relative expression of qRT-PCR of the differentially expressed genes. Different lowercase letters represent significant differences in gene expression detected by qRT-PCR at the $p < 0.05$ level.

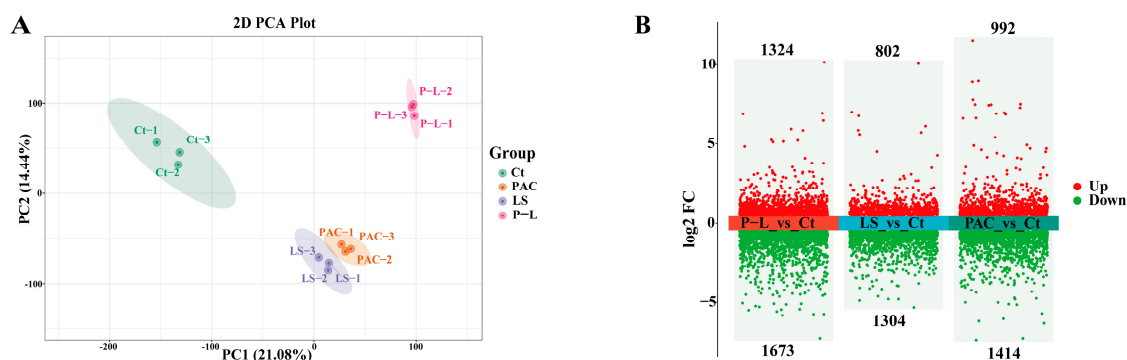


Figure S3 Transcriptome analysis of tea shoots. (A) PCA diagram of the overall sample. (B) Number of differentially expressed genes.

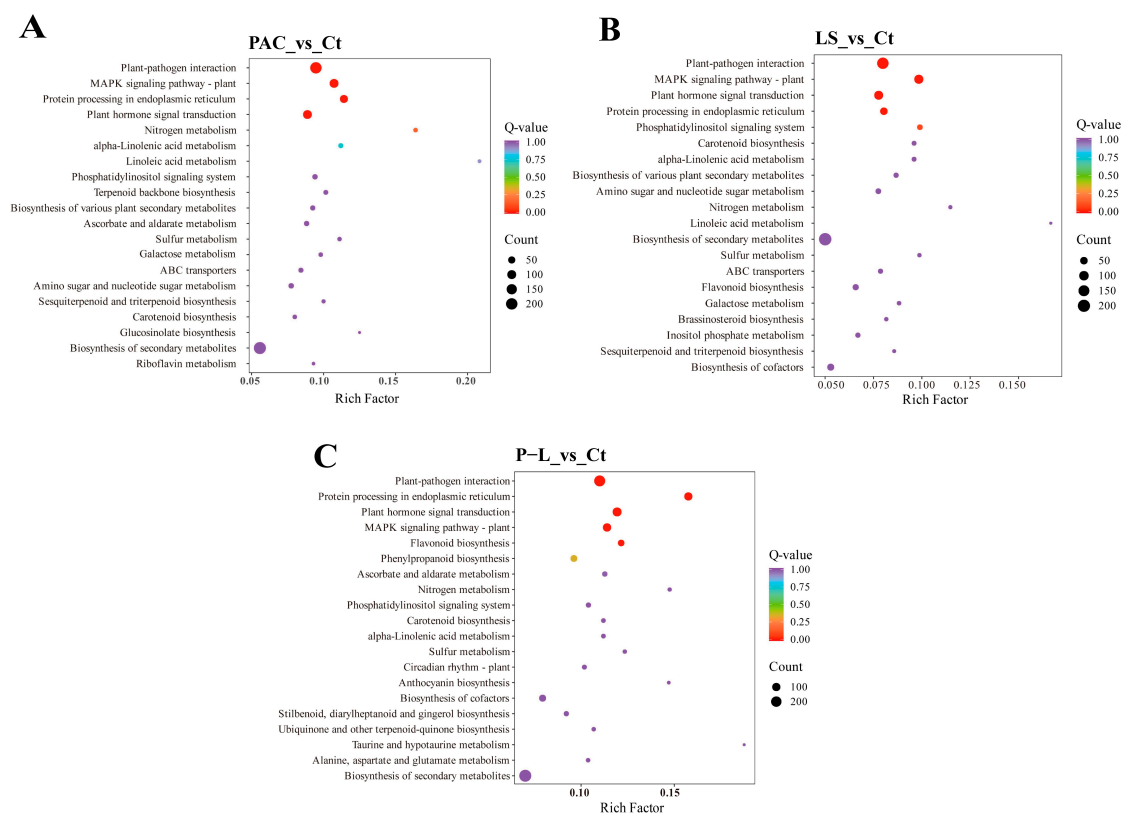


Figure S4 KEGG enrichment bubble diagram of differential genes in different treatment groups. (A) Enrichment analysis of PAC vs Ct. (B) Enrichment analysis of LS vs Ct. (C) Enrichment analysis of P-L vs Ct.

Supplementary Table S6 Transcription factor binding site of 4 structure genes

Motif id	TF	Target	Start	Stop	Strand	Score	p-Value	q-Value	Matched sequence
MP00617	<i>CsHB-WOX</i> (HD.01G0027770)	<i>CsSCPL</i> (HD.06G0022960)	222	231	+	13.4894	1.20×10^{-5}	0.144	aatcaatcat
MP00213	<i>CsMYB</i> (HD.01G0029900)	<i>CsSCPL</i> (HD.06G0022960)	1010	1020	-	13.0152	1.87×10^{-5}	0.0787	GATTTAGTTAT
MP00238	<i>CsZF-HD</i> (HD.01G0030230)	<i>CsSCPL</i> (HD.06G0022960)	257	267	-	12.0597	6.22×10^{-5}	0.483	ATATAATTAAT
MP00125	<i>CsC2H2</i> (HD.02G0015370)	<i>CsDFR</i> (HD.06G0036240)	1350	1369	+	11.0758	2.13×10^{-5}	0.12	aaaaaaaccacaaaaaaaaa
MP00422	<i>CsWRKY</i> (HD.02G0025310)	<i>CsSCPL</i> (HD.05G0027520)	506	518	+	13.2121	1.73×10^{-5}	0.229	aaaagtaatttt
MP00556	<i>CsERF</i> (HD.02G0032350)	<i>CsSCPL</i> (HD.06G0022960)	1828	1842	-	10.8182	3.38×10^{-5}	0.179	GTGGTGGTGGTGGTG
MP00408	<i>CsWRKY</i> (HD.02G0032820)	<i>CsSCPL</i> (HD.05G0027520)	506	518	-	10.7424	4.00×10^{-5}	0.577	AAAATTGACTTTT
MP00302	<i>CsAP2/ERF</i> (HD.02G0033890)	<i>CsSCPL</i> (HD.06G0022960)	1829	1849	-	27.2	6.13×10^{-11}	9.71E-07	GGTGGTGGTGGTGGTGGT GGT
MP00222	<i>CsMYB</i> (HD.03G0004660)	<i>CsSCPL</i> (HD.06G0022960)	405	417	+	12.5488	2.90×10^{-5}	0.361	atactttccgta
MP00320	<i>CsHD-ZIP</i> (HD.03G0018290)	<i>CsSCPL</i> (HD.06G0022960)	222	234	-	16.5909	1.16×10^{-6}	0.0136	TAAATGATTGATT
MP00081	<i>CsbHLH</i> (HD.03G0030020)	<i>CsSCPL</i> (HD.06G0022960)	1540	1549	-	15.7727	1.36×10^{-6}	0.0216	GGCCACGTGA
MP00570	<i>CsC2C2</i> (HD.04G0020440)	<i>CsSCPL</i> (HD.1307844)	1409	1422	-	16.2576	2.45×10^{-7}	0.00282	AAAAAAGTAAAAAA
MP00100	<i>CsbHLH</i> (HD.05G0001220)	<i>CsSCPL</i> (HD.06G0022960)	1701	1708	+	12.7865	4.39×10^{-5}	0.546	ccacgtgc
MP00090	<i>CsSBP</i> (HD.05G0006190)	<i>CsDFR</i> (HD.06G0036240)	1280	1295	+	13.4045	1.44×10^{-5}	0.133	aattttgtacaataaa
MP00179	<i>CsNAC</i> (HD.06G0029710)	<i>CsSCPL</i> (HD.05G0027520)	1897	1915	-	5.07576	9.80×10^{-5}	1	TTTATACTTGCAGCTGAC G
MP00064	<i>CsTCP</i> (HD.07005773)	<i>CsSCPL</i> (HD.06G0022960)	1430	1439	-	13.0204	1.22×10^{-5}	0.194	TGGGGTCCAC
MP00171	<i>CsWRKY</i> (HD.07G0003420)	<i>CsSCPL</i> (HD.05G0027520)	506	518	+	10.7424	5.73×10^{-5}	0.689	aaaagtaatttt
MP00248	<i>CsBESI</i> (HD.07G0006010)	<i>CsSCPL</i> (HD.06G0022960)	1699	1709	-	6.27273	7.75×10^{-5}	0.742	GGCACGTGGAT

MP00084	<i>CsbHLH</i> (HD.07G0018840)	<i>CsSCPL</i> (HD.06G0022960)	1701	1708	+	11.7349	5.38×10^{-5}	0.414	ccacgtgc
MP00334	<i>CsMYB</i> (HD.08G0000370)	<i>CsDFR</i> (HD.06G0036240)	870	884	+	12.2879	4.03×10^{-5}	0.569	ttggactgattaggt
MP00296	<i>CsMYB</i> (HD.08G0016970)	<i>CsSCPL</i> (HD.06G0022960)	314	334	+	17.0366	9.82×10^{-7}	0.00964	aaagatgaggataaaattgtg
MP00564	<i>CsMYB</i> ((HD.08G0030520)	<i>CsSCPL</i> (HD.1307844)	894	908	−	13.3939	1.58×10^{-5}	0.168	TTTAATTAGTTAAAC
MP00174	<i>CsGARP–G2</i> (HD.09G0017610)	<i>CsSCPL</i> (HD.06G0022960)	860	874	+	11.8571	4.88×10^{-5}	0.348	cgattaatattctct
MP00548	<i>CsAP2/ERF</i> (HD.09G0018910)	<i>CsSCPL</i> (HD.06G0022960)	1830	1850	+	17.5455	6.69×10^{-7}	0.0106	ccaccaccaccaccaccacca
MP00448	<i>CsWRKY</i> (HD.09G0022600)	<i>CsSCPL</i> (HD.05G0027520)	723	733	−	12.8939	2.68×10^{-5}	0.235	ATAAGTCAAAT
MP00162	<i>CsC2C2</i> (HD.10G0006870)	<i>CsSCPL</i> (HD.05G0027520)	1561	1571	−	12.6418	8.20×10^{-6}	0.107	CACTGCCACTG
MP00121	<i>CsNAC</i> (HD.10G0014670)	<i>CsDFR</i> (HD.06G0036240)	1709	1730	−	14.2273	4.18×10^{-6}	0.0579	TACGTGTTTCGGATCGTCA AATT
MP00139	<i>CsAP2/ERF</i> (HD.11G0005680)	<i>CsDFR</i> (HD.06G0036240)	966	982	−	13.4394	1.28×10^{-5}	0.135	AAGGTGAGTTATGTTGA
MP00160	<i>CsGARP–G2</i> (HD.11G0005710)	<i>CsSCPL</i> (HD.06G0022960)	862	872	−	11.3939	9.28×10^{-5}	1	AGAATATTAAT
MP00299	<i>CsWRKY</i> (HD.11G0020630)	<i>CsSCPL</i> (HD.06G0022960)	1795	1805	+	12.1667	4.54×10^{-5}	0.328	ataagtcaaaa
MP00306	<i>CsC2C2</i> (HD.11G0025110)	<i>CsSCPL</i> (HD.05G0027520)	37	43	−	13.2632	9.66×10^{-5}	0.114	TTGAAAA
MP00464	<i>CsWRKY</i> (HD.12G0001660)	<i>CsSCPL</i> (HD.05G0027520)	505	518	−	12.0455	2.86×10^{-5}	0.325	AAAATTGACTTTTT
MP00439	<i>CsNAC</i> (HD.12G0010900)	<i>CsSCPL</i> (HD.05G0027520)	1897	1911	−	13.9091	1.14×10^{-5}	0.168	TACTTGCAGCTGACG
MP00531	<i>CsWRKY</i> (HD.1400400)	<i>CsSCPL</i> (HD.05G0027520)	504	516	−	15.697	3.70×10^{-6}	0.0487	AATTGACTTTTTT
MP00280	<i>CsNAC</i> (HD.14G0005980)	<i>CsDFR</i> (HD.06G0036240)	1839	1857	−	10.803	5.57×10^{-5}	0.879	ATTTCTTACTTGTTAGGTT
MP00014	<i>CsGARP–G2</i> (HD.14G0011470)	<i>CsSCPL</i> (HD.1307844)	70	83	+	11.0161	5.70×10^{-5}	0.365	gtaagatttgatgt
MP00099	<i>CsbHLH</i> (HD.14G0017810)	<i>CsSCPL</i> (HD.06G0022960)	1701	1708	+	11.9355	5.38×10^{-5}	0.429	ccacgtgc
MP00251	<i>CsWRKY</i> (HD.15G0007590)	<i>CsSCPL</i> (HD.05G0027520)	504	518	−	13.4697	1.71×10^{-5}	0.239	AAAATTGACTTTTTT
MP00232	<i>CsHD–ZIP</i> (HD.15G0019350)	<i>CsSCPL</i> (HD.06G0022960)	255	265	+	13.8939	1.63×10^{-5}	0.166	tcattaattat

Supplementary Table S7 Prediction of hormone responsive elements in transcription factors

Gene	Hormone responsive elements	Elements Sequence	Elements Position	Base length of elements	DNA positive and negative strands	Function
<i>CsTCP19</i> (HD.07005773)	AuxRR-core	GGTCCAT	377	7	–	cis-acting regulatory element involved in Auxin responsiveness
<i>CsMYB80</i> (HD.08G0030520)	TGACG-motif	TGACG	1458	5	+	cis-acting regulatory element involved in the MeJA-responsiveness
<i>CsMYB80</i> (HD.08G0030520)	AuxRR-core	GGTCCAT	1655	7	+	cis-acting regulatory element involved in Auxin responsiveness
<i>CsMYB80</i> (HD.08G0030520)	CGTCA-motif	CGTCA	1458	5	–	cis-acting regulatory element involved in the MeJA-responsiveness