

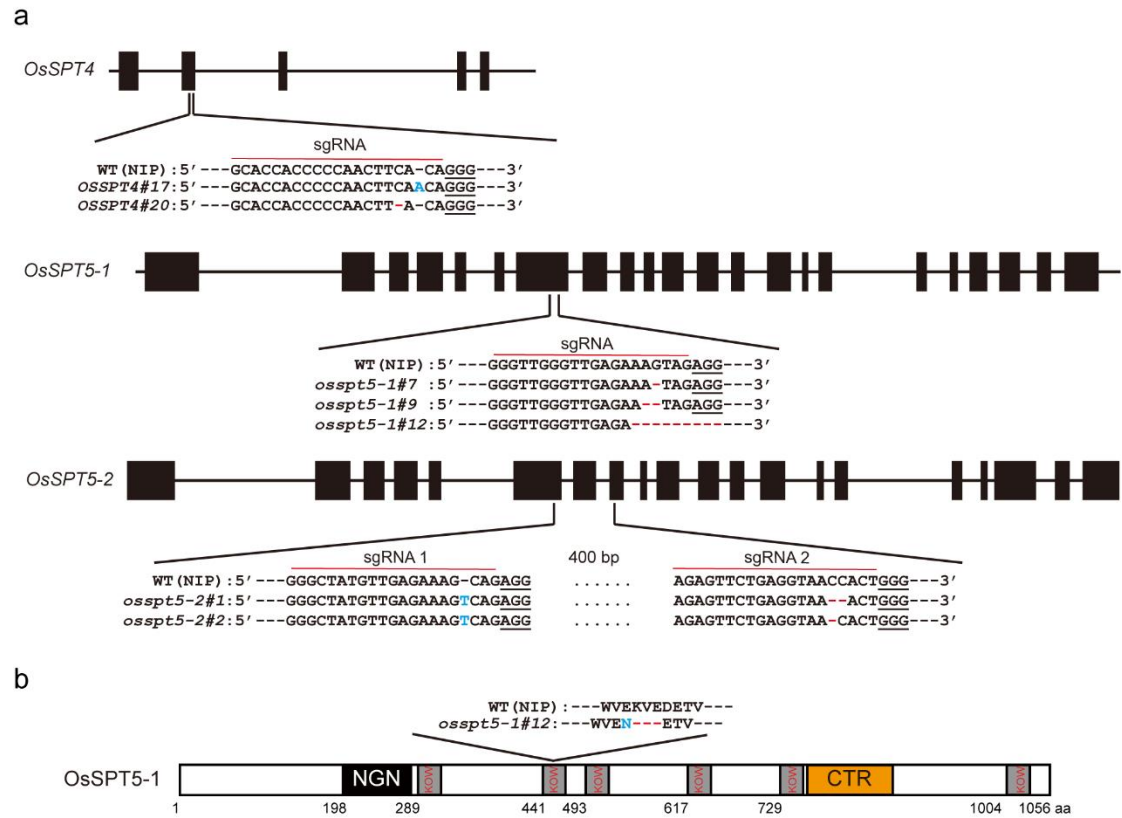


Figure S1. Schematic diagram of the mutation details of *osspt4*, *osspt5-1*, and *osspt5-2* mutant lines in T0 generation. (a) Exons and introns of the two genes are represented by black rectangles and lines, respectively. Sequence alignment near the target site of these three genes is also shown. Protospacer adjacent motif (PAM) sequences are underlined in black. The inserted and deleted bases are presented in blue and red, respectively. (b) Schematic diagram of conserved domains in OsSPT5-1. The predicted OsSPT5-1 protein sequence near the target site in WT and *osspt5-1#12* is also shown.

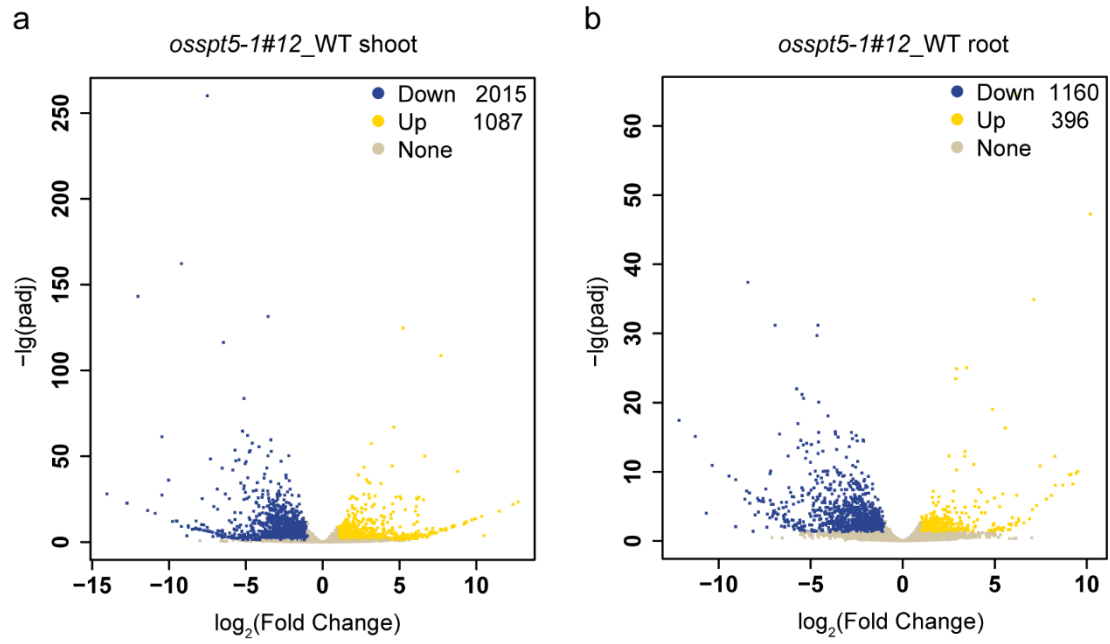


Figure S2. Volcano plot based on the $\log_2$ fold change values of the differentially expressed genes (DEGs) between shoot tissues (a) and root (b) of *osspt5-1#12* and WT. The yellow and blue dots represent the upregulated and downregulated DEGs, respectively.

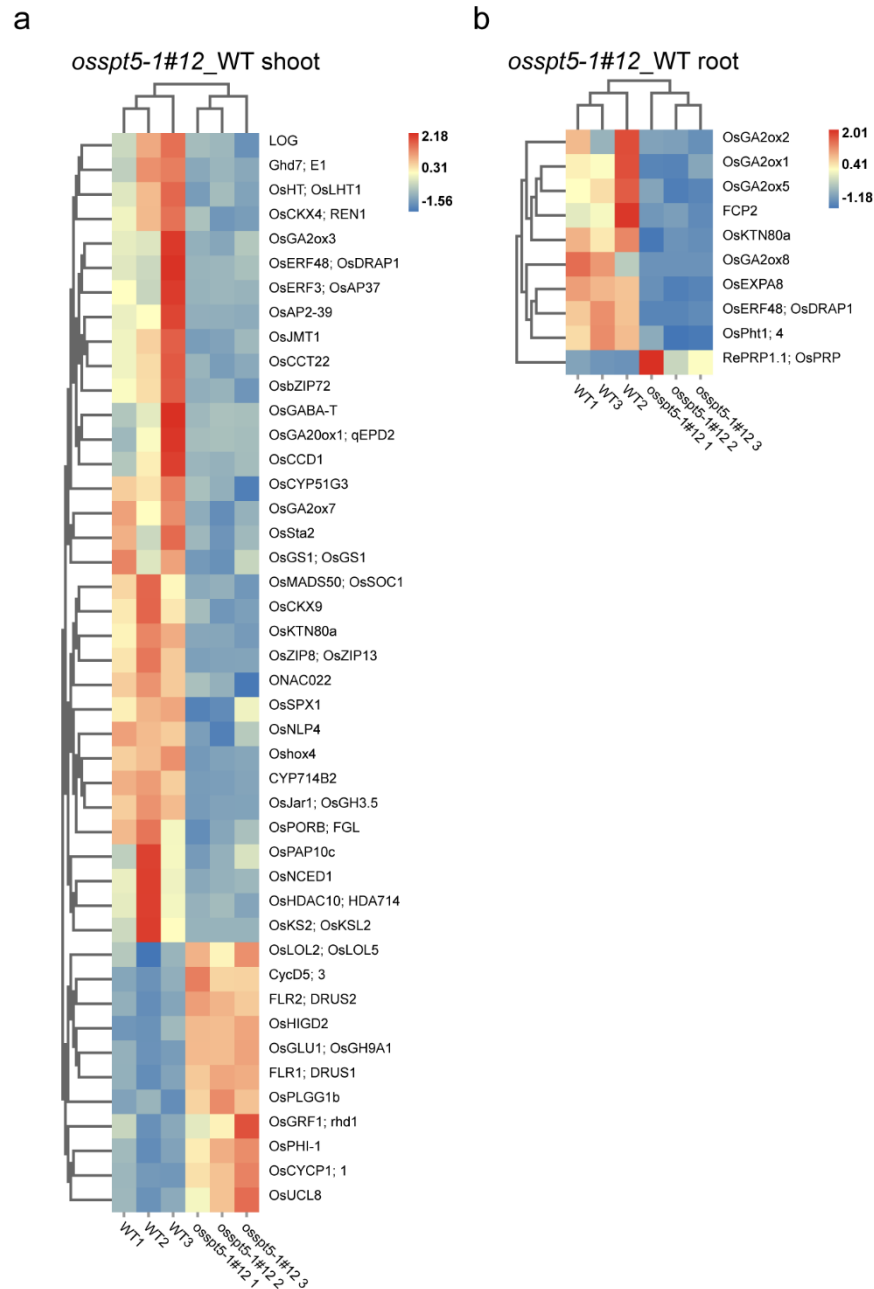


Figure S3. Heat map of DEGs between *osspt5-1#12* and WT associated with plant height in shoot tissues (a) and root development in the root (b). The FPKM value of each gene was calculated with a logarithm for normalization. The heatmap represents the highest (red) to lowest (blue) expression level for each gene.

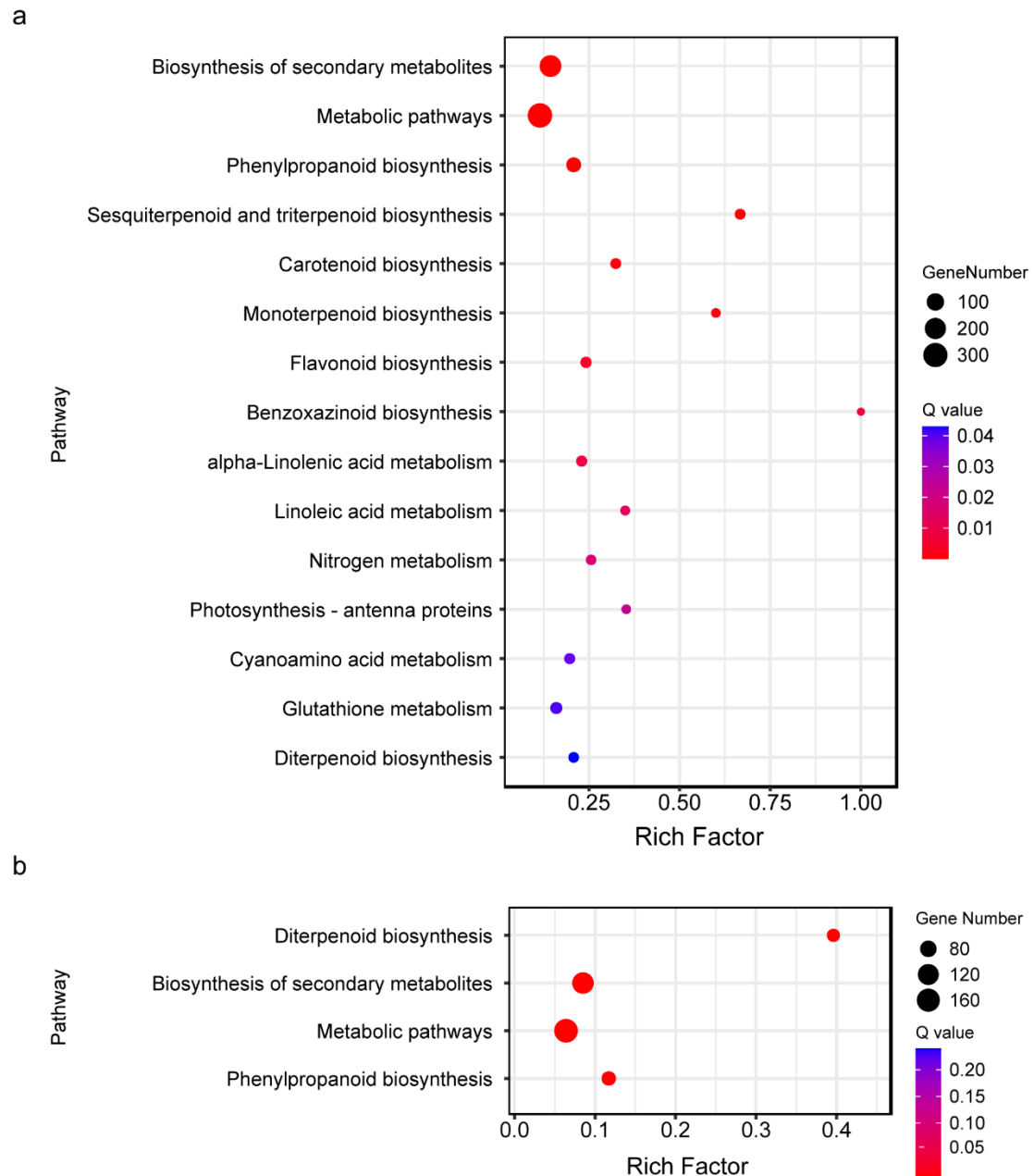


Figure S4. Enriched KEGG pathways associated with the identified DEGs in shoot tissues (a) and the root (b) between *osspt5-1#12* and WT.

Table S1. Primers used in this study.

Primer Name	Sequence (5'-3')	Purpose
OsUBQ-qF	GACAACGTGAAGGCGAAGA	qRT-PCR
OsUBQ-qR	CACCAGGTGGAGTGTGGAC	qRT-PCR
OsIAA9-qF	GGACCTGTGGTCACCTACGA	qRT-PCR
OsIAA9-qR	CAGATCGTGCAAAATCATCC	qRT-PCR
OsIAA18-qF	AAGAATGTGGGAAGGAGCTAACG	qRT-PCR
OsIAA18-qR	ATGGTGGTGAGGGACAGCAT	qRT-PCR
LOG-qF	CCTGGGCCCCAACTAGGAATC	qRT-PCR
LOG-qR	GCAGTTGGAGCCGAGATGAT	qRT-PCR
OsCKX4-qF	TCCAAAGATGGTGCGGTGG	qRT-PCR
OsCKX4-qR	CTGGGTCCTGTGGCTTGAAC	qRT-PCR
OsCKX9-qF	TGGAAATTGTGACTGGAAGAGGT	qRT-PCR
OsCKX9-qR	AGCCACCTTACCATTTTGGGA	qRT-PCR
OsKOS1-qF	ACAAGGAGGACACCATGCAG	qRT-PCR
OsKOS1-qR	CTTCCTCTGGGCTTGAGGTG	qRT-PCR
OsGA20ox1-qF	TACGCCAGCAGCTTCACGG	qRT-PCR
OsGA20ox1-qR	TCCATCAGCTCCAGCGACA	qRT-PCR
PHYA-qF	GCAAAGGAGTCCCAGCAGAT	qRT-PCR
PHYA-qR	AGAAGCAAGTTCGACGCTGA	qRT-PCR
OsARF23-qF	CACCAGGTGCTACTGAATGG	qRT-PCR
OsARF23-qR	CATCCACTCCTTCTTAGGACC	qRT-PCR
LOGL3-qF	TGACCCCCGAGATAATCGGA	qRT-PCR
LOGL3-qR	GCCATCTCAGCCTTCCTCTG	qRT-PCR
OsGA2ox2-qF	GGAGTACAAGAGGACCATGTAC	qRT-PCR
OsGA2ox2-qR	CTATTCATGGTCGTCATCGTCC	qRT-PCR
OsGA2ox5-qF	TACAAGAGCGTGAGCACAG	qRT-PCR
OsGA2ox5-qR	GTAGGAGGGGCAGAGGAAGA	qRT-PCR
OsKOS2-qF	ACAGGAATGGCTTTACCGGG	qRT-PCR
OsKOS2-qR	TTGGTAGGTCCTCCTCGGTC	qRT-PCR
PHYC-qF	GAGGGCCTTGGCCTTTACAT	qRT-PCR
PHYC-qR	GACGAGCTCTCTGATTCCCG	qRT-PCR
OsSPT5-1-proF	GTCGACGGAGAGGACGAGATGGGGTAAAG	GUS vector construction
OsSPT5-1-proR	GTCGACGGCGGATTTTTCGGCGGCTAGGT	GUS vector construction
OsSPT5-1-terF	GAGCTCATATGGTGATTTTGGCCAAACTG	GUS vector construction
OsSPT5-1-terR	GAATTCCGGAGGAAGAAGACAACGAGGAG	GUS vector construction
OsSPT5-1-Y2H-F	GGCCATGGAGGCCATGGCTCGCCGCGCCCCG CGACG	Y2H vector construction
OsSPT5-1-Y2H-R	CCCGGTCAACTCGCCAGTTTGGCCAAAAT CACC	Y2H vector construction

OsSPT5-1-KOW-F	CATATGCAAGCTTTGGCTAGTAAACTGG	Y2H vector construction
OsSPT5-1-KOW-R	GAATTCTTATTTTACTAGGACAACCTTCTG	Y2H vector construction
APO2-Y2H-F	CATATGGATCCCAACGATGCCT	Y2H vector construction
APO2-Y2H-R	GAATTCTTAGAACAAGGGCGGC	Y2H vector construction
OsSPT5-1-BiFC-F	CCATGGACACCGAATTCTGCCTCGTACCTTC CTGGTACACCTGGTGGTCAACCGATGACTC	BiFC vector construction
OsSPT5-1-BiFC-R	TCTAGATTAACTCGCCAGTTTGGCCAAAAT CACCATATCTAAGATCTTGACTTCGTATGTG	BiFC vector construction
APO2-BiFC-F	AAGCTTATGGATCCCAACGATGCCTT	BiFC vector construction
APO2-BiFC-R	GGTACCTTAGAACAAGGGCGGCGGGAG	BiFC vector construction
OsSPT4mF	AGGAGAGAGAGAGAGAGAAG	mutant detection
OsSPT4mR	CTTTTCGCTTCTTATCGGTC	mutant detection
OsSPT5-1mF	ATCGTGTGCTGTTTTCGTTT	mutant detection
OsSPT5-1mR	CATGTTCTTTTGTCGTGTCA	mutant detection
OsSPT5-2mF	CAAATAGGAAAAAAGGGCAC	mutant detection
OsSPT5-2mR	GACCCTAACGACATCCTTT	mutant detection

Table S2. DEGs related to plant hormone pathways in shoot tissues.

Plant hormone	Gene Number	Name	WT FPKM	osspt5-1#12 FPKM	Log2 Fold Change	P value	padj	Up/Down	annotation
Auxin	Os03g0162000	<i>OsCOW1</i>	0.96	0.32	-1.74	0.000206369	0.002342453	down	biosynthesis
	Os07g0671500	<i>OsGH3-11</i>	2.15	5.49	1.23	0.001385679	0.011667874	up	signaling
	Os01g0190300	<i>OsIAA2</i>	14.56	6.14	-1.39	3.53216E-11	1.78258E-09	down	signaling
	Os02g0805100	<i>OsIAA9</i>	1.51	4.28	1.36	0.006757419	0.040995974	up	signaling
	Os05g0523300	<i>OsIAA18</i>	8.26	26.53	1.55	8.34204E-11	4.02427E-09	up	signaling
	Os01g0768333	<i>OsSAUR2</i>	27.92	11.17	-1.45	2.67285E-05	0.00040539	down	signaling
	Os02g0512000	<i>OsSAUR10</i>	0.37	2.85	2.80	5.47292E-06	0.000100683	up	signaling
	Os02g0643800	<i>OsSAUR11</i>	1.58	0.56	-1.63	0.008522738	0.048638453	down	signaling
	Os06g0671600	<i>OsSAUR26</i>	1.38	0.18	-3.10	0.004853086	0.031654624	down	signaling
	Os09g0437400	<i>OsSAUR38</i>	0.26	1.62	2.50	0.005493201	0.034899844	up	signaling
	Os01g0919800	<i>OsPIN5a</i>	14.82	6.85	-1.28	0.000342028	0.003615295	down	transport
	Os05g0447200	<i>OsAUX3</i>	1.03	0.39	-1.57	0.008315694	0.04786021	down	transport
GA	Os04g0612000	<i>OsKS2</i>	0.25	0.00	-5.86	0.000550046	0.005393551	down	biosynthesis
	Os03g0856700	<i>OsGA20ox1</i>	11.08	4.47	-1.47	0.005652591	0.035658202	down	biosynthesis
	Os01g0612700	<i>OsLOL2</i>	2.92	6.65	1.06	0.001914336	0.015211116	up	biosynthesis
	Os06g0569500	<i>OsKOS1</i>	101.71	44.23	-1.34	0.00559631	0.035393314	down	biosynthesis
	Os03g0719800	<i>PHYA</i>	5.66	17.73	1.51	9.7273E-16	8.80654E-14	up	biosynthesis
	Os03g0333200	<i>FLR1</i>	19.96	48.20	1.13	2.11414E-11	1.10672E-09	up	biosynthesis
	Os01g0769700	<i>FLR2</i>	14.94	71.05	2.13	1.72002E-10	7.93552E-09	up	biosynthesis
	Os01g0757200	<i>OsGA2ox3</i>	14.04	5.20	-1.58	0.000113717	0.001409393	down	metabolism
	Os01g0209700	<i>OsGA2ox7</i>	0.63	0.09	-3.09	0.004503732	0.029892208	down	metabolism
	Os03g0332100	<i>CYP714B2</i>	12.63	1.22	-3.54	4.65103E-31	1.75649E-28	down	metabolism
	Os02g0776900	<i>OsGRF1</i>	3.09	9.41	1.49	0.002439536	0.018373664	up	signaling

	Os04g0610400	OsAP2-39	6.67	2.35	-1.65	6.68708E-05	0.000889798	down	signaling
	Os09g0470500	Oshox4	18.71	3.73	-2.48	5.8458E-22	9.48096E-20	down	signaling
CK	Os01g0588900	LOG	146.95	56.00	-1.55	5.39811E-05	0.000740168	down	biosynthesis
	Os01g0940000	OsCKX4	17.39	6.44	-1.59	9.9506E-07	2.21426E-05	down	metabolism
	Os05g0374200	OsCKX9	1.38	0.36	-2.11	0.000300272	0.003225516	down	metabolism
	Os02g0830200	OsRR3	1.73	5.26	1.45	0.006348352	0.039092719	up	signaling
	Os04g0673300	OsRR6	8.32	4.60	-1.02	0.007948336	0.046262044	down	signaling
ABA	Os02g0704000	OsNCED1	14.48	1.89	-3.13	3.56525E-09	1.3182E-07	down	biosynthesis
	Os03g0645900	OsNCED3	1.03	0.11	-3.40	0.007724147	0.045286217	down	biosynthesis
	Os12g0617400	OsNCED5	0.32	0.00	-5.14	0.007189093	0.042900872	down	biosynthesis
	Os04g0610400	OsAP2-39	6.67	2.35	-1.65	6.68708E-05	0.000889798	down	biosynthesis
	Os01g0343100	OsRab16A	0.18	0.00	-5.08	0.002946521	0.021355765	down	signaling
	Os02g0112900	OsGABA-T	0.83	0.05	-4.28	0.002113482	0.016437775	down	signaling
	Os03g0133000	ONAC022	9.74	4.73	-1.19	0.000185045	0.002126895	down	signaling
	Os03g0297600	OsPYL4	10.36	33.57	1.51	0.000675755	0.006373262	up	signaling
	Os06g0683400	OsCCD1	101.07	19.77	-2.52	2.1028E-06	4.32563E-05	down	signaling
BR	Os03g0227700	OsDWARF4	8.82	1.94	-2.33	9.66396E-12	5.28937E-10	down	biosynthesis
	Os05g0211100	OsCYP51G3	15.22	5.23	-1.68	3.56713E-05	0.000519849	down	biosynthesis
	Os07g0650600	OsBLE2	136.85	50.34	-1.60	4.15515E-10	1.82468E-08	down	signaling
ETH	Os05g0149400	OsACO5	55.09	23.08	-1.41	1.0418E-05	0.000178607	down	biosynthesis
	Os01g0797600	OsERF3	79.89	33.20	-1.40	5.21099E-05	0.000717862	down	signaling
	Os08g0408500	OsERF48	52.03	9.75	-2.56	7.60839E-07	1.749E-05	down	signaling
	Os03g0183000	OsLG3	39.07	139.04	1.69	9.8545E-19	1.20608E-16	up	signaling
	Os07g0673900	OsHIGD2	22.58	63.43	1.34	3.70437E-08	1.13738E-06	up	signaling

	Os05g0155200	<i>OsERS2</i>	4.52	1.47	-1.79	9.90451E-10	4.07844E-08	down	signaling
JA	Os03g0225900	<i>OsAOS2</i>	24.82	55.26	1.01	0.002127127	0.016505061	up	biosynthesis
	Os05g0102000	<i>OsJMT1</i>	11.51	5.02	-1.35	3.43667E-06	6.66558E-05	down	biosynthesis
	Os06g0314600	<i>OsJMT1</i>	14.08	2.08	-2.93	5.34714E-13	3.47314E-11	down	biosynthesis
	Os05g0586200	<i>OsJar1</i>	92.01	27.68	-1.89	5.72628E-22	9.34443E-20	down	biosynthesis

Table S3. DEGs related to plant hormone pathways in the root.

Plant hormone	Gene Number	Name	WT FPKM	osspt5-1#12 FPKM	Log2 Fold Change	P value	padj	Up/Down	annotation
Auxin	Os03g0162000	<i>OsCOW1</i>	2.27	0.48	-2.34	6.08478E-09	8.77721E-07	down	biosynthesis
	Os01g0190300	<i>OsIAA2</i>	13.80	4.18	-1.86	1.69995E-08	2.15457E-06	down	signaling
	Os03g0742900	<i>OsIAA13</i>	18.47	53.44	1.38	0.000908874	0.019562869	up	signaling
	Os11g0523800	<i>OsARF23</i>	46.64	24.25	-1.05	0.00051239	0.012473594	down	signaling
	Os01g0924966	<i>OsSAUR3</i>	6.92	0.46	-4.04	1.25745E-10	2.71329E-08	down	signaling
	Os01g0802700	<i>OsPIN9</i>	1.04	0.14	-3.03	0.000666929	0.015409595	down	transport
	Os12g0614600	<i>OsPID</i>	0.69	0.08	-3.26	0.002884259	0.047006947	down	transport
GA	Os06g0569500	<i>OsKOS1</i>	54.68	8.67	-2.87	0.000273036	0.007648812	down	biosynthesis
	Os06g0568600	<i>OsKOS2</i>	46.06	1.83	-4.75	1.97701E-13	8.1933E-11	down	biosynthesis
	Os04g0612000	<i>OsKS2</i>	2.35	0.14	-4.17	1.51062E-07	1.43421E-05	down	biosynthesis
	Os03g0719800	<i>PHYA</i>	9.54	29.78	1.52	1.72647E-06	0.000118001	up	biosynthesis
	Os03g0752100	<i>PHYC</i>	11.82	31.21	1.28	3.28833E-06	0.000203931	up	biosynthesis
	Os05g0482400	<i>EUI1</i>	3.37	0.55	-2.72	0.000562718	0.013466559	down	biosynthesis
	Os05g0158600	<i>OsGA2ox1</i>	2.02	0.36	-2.62	1.47817E-07	1.40852E-05	down	metabolism
	Os01g0332200	<i>OsGA2ox2</i>	2.08	0.27	-3.01	0.000345371	0.009126802	down	metabolism
	Os07g0103500	<i>OsGA2ox5</i>	3.58	0.32	-3.52	0.000158148	0.004945017	down	metabolism
	Os05g0560900	<i>OsGA2ox8</i>	0.33	0.00	-5.59	0.00090329	0.019555546	down	metabolism
CK	Os03g0109300	<i>LOGL3</i>	15.87	2.35	-2.82	0.000601466	0.014211463	down	biosynthesis
	Os05g0311801	<i>OsIPT3</i>	11.13	1.74	-2.72	0.000272581	0.007644274	down	biosynthesis
	Os07g0129700	<i>d6</i>	14.73	3.56	-2.15	2.57612E-06	0.000164853	down	metabolism
	Os11g0143300	<i>OsRR9</i>	11.83	33.23	1.35	0.000560355	0.01344697	up	signaling
	Os04g0587500	<i>OsPUP13</i>	0.97	0.25	-2.06	0.003144346	0.049845612	down	transport

ABA	Os01g0343100	<i>OsRab16A</i>	3.50	0.65	-2.55	0.0001168	0.003950172	down	signaling
	Os05g0226900	<i>RePRP1.1</i>	52.77	132.68	1.25	0.00256347	0.043069265	up	signaling
BR	Os03g0227700	<i>OsDWARF4</i>	20.43	5.52	-2.00	1.54846E-07	1.45952E-05	down	biosynthesis
ETH	Os03g0727600	<i>OsACS1</i>	2.10	0.54	-2.06	0.001003286	0.021090826	down	biosynthesis
	Os11g0186900	<i>OsACO4</i>	30.34	2.52	-3.61	1.43375E-05	0.000717121	down	biosynthesis
	Os08g0408500	<i>OsERF48</i>	54.54	19.05	-1.65	1.37532E-10	2.91937E-08	down	signaling
	Os08g0508700	<i>OsEIL4</i>	3.44	0.89	-2.12	9.23697E-06	0.000498281	down	signaling
	Os10g0390800	<i>EBL1</i>	6.65	3.25	-1.17	0.000969566	0.02053074	down	signaling
SL	Os04g0550600	<i>OsCCD7</i>	0.79	2.92	1.78	0.000984697	0.020783714	up	biosynthesis
JA	Os05g0586200	<i>OsJar1</i>	89.72	23.16	-2.06	3.22592E-05	0.001394798	down	signaling
