

Table S1. Primer sequences used to validate RNA-Sequencing results of trees grown waterlogging treatment versus control after transplanting

Gene	Forward primer	Reverse primer
TRINITY_DN85415_c0_g2_i1	TCATGGAGAGAAGCCAGGGC	GAACACCCGCGCATATGCTC
TRINITY_DN86343_c3_g1_i11	GCCTGCAAAGAGTGTGTTTCAG	CCTTGGAGGAGCTGTAAGGC
TRINITY_DN81275_c0_g2_i3	ACCCAAAGTACCCGGTTCCG	ATGTGGGTCGGGAGGATTGG
TRINITY_DN89101_c0_g1_i4	ACACACTCATGCCCCCTGGTC	CAACTGTGTGAAAGCCCCGC
TRINITY_DN85313_c0_g1_i5	CCCATGGAAAATGCTGGGGC	CCCGAGCCAAAACAGATGCC
TRINITY_DN78260_c0_g1_i5	CTGCATGTGGAGGCTGTTGC	TGGGCAGTCCAGTCTCCAAC
TRINITY_DN82177_c1_g1_i9	TAGAGTGGCCGCGGAGAAAG	GTGGCTCGGCACATTCAACC
TRINITY_DN89267_c1_g1_i6	TTTATGGAAGCCGTGCACGC	CGAGCGTGACGTGATGAAGC
TRINITY_DN79247_c0_g1_i10	TGTCCGAGGTGGTGTGGATG	ATCCGGACGTGGCAGGTTAG
F-box	TATTATTGTTGCAGGTGGGTT	AGAATGTTGAAGTTCGGCTAT

Table S2.Gene ontology (GO) analysis of transplant stress

	GO biological process complete	Gene	FDR
TC vs C and TW vs W up	lignan biosynthetic process (GO:0009807)	4	4.49E-03
	lignan metabolic process (GO:0009806)	4	4.45E-03
	osmosensory signaling pathway (GO:0007231)	3	2.93E-02
	positive regulation of cell wall organization or biogenesis (GO:1903340)	4	1.17E-02
	positive regulation of secondary cell wall biogenesis (GO:1901348)	4	1.16E-02
	lignin biosynthetic process (GO:0009809)	17	6.01E-11
	plant-type primary cell wall biogenesis (GO:0009833)	10	3.62E-06
	glucuronoxylan biosynthetic process (GO:0010417)	4	2.33E-02
	glucuronoxylan metabolic process (GO:0010413)	4	2.31E-02
	cuticle development (GO:0042335)	11	1.97E-06
	phenylpropanoid biosynthetic process (GO:0009699)	29	5.64E-17
	lignin metabolic process (GO:0009808)	18	2.40E-10
	L-phenylalanine biosynthetic process (GO:0009094)	4	2.87E-02
	erythrose 4-phosphate/phosphoenolpyruvate family amino acid biosynthetic process (GO:1902223)	4	2.85E-02
	regulation of secondary cell wall biogenesis (GO:2000652)	15	1.64E-08
	mitotic cytokinesis (GO:0000281)	12	1.46E-06
	xyloglucan metabolic process (GO:0010411)	17	4.41E-09
	phenylpropanoid metabolic process (GO:0009698)	32	3.45E-17
	cell wall pectin metabolic process (GO:0052546)	8	3.69E-04
	aromatic amino acid family biosynthetic process, prephenate pathway (GO:0009095)	4	4.17E-02
	L-phenylalanine metabolic process (GO:0006558)	6	4.71E-03
	erythrose 4-phosphate/phosphoenolpyruvate family amino acid metabolic process (GO:1902221)	6	4.68E-03
	regulation of cell wall organization or biogenesis (GO:1903338)	15	1.03E-07
	cellulose biosynthetic process (GO:0030244)	15	1.01E-07
	regulation of lignin biosynthetic process (GO:1901141)	4	4.97E-02
	syncytium formation (GO:0006949)	4	4.95E-02
	multidimensional cell growth (GO:0009825)	10	5.74E-05
	cytoskeleton-dependent cytokinesis (GO:0061640)	15	3.42E-07
	cellulose metabolic process (GO:0030243)	15	3.35E-07
	suberin biosynthetic process (GO:0010345)	5	2.23E-02
	response to mechanical stimulus (GO:0009612)	5	2.21E-02
	xylan biosynthetic process (GO:0045492)	9	3.23E-04
	plant-type secondary cell wall biogenesis (GO:0009834)	25	1.01E-11
	cell wall polysaccharide metabolic process (GO:0010383)	39	4.99E-18
	beta-glucan biosynthetic process (GO:0051274)	15	7.46E-07
	hemicellulose metabolic process (GO:0010410)	27	2.20E-12
	regulation of phenylpropanoid metabolic process (GO:2000762)	6	1.15E-02

beta-glucan metabolic process (GO:0051273)	15	2.03E-06
pectin biosynthetic process (GO:0045489)	11	1.56E-04
plant-type cell wall biogenesis (GO:0009832)	50	4.87E-21
cell wall polysaccharide biosynthetic process (GO:0070592)	18	2.30E-07
cell wall macromolecule catabolic process (GO:0016998)	6	1.91E-02
cell wall macromolecule metabolic process (GO:0044036)	40	2.38E-16
cellular glucan metabolic process (GO:0006073)	37	6.81E-15
secondary metabolite biosynthetic process (GO:0044550)	32	7.76E-13
cellular component macromolecule biosynthetic process (GO:0070589)	18	3.80E-07
cell wall macromolecule biosynthetic process (GO:0044038)	18	3.73E-07
glucan metabolic process (GO:0044042)	37	1.43E-14
xylan metabolic process (GO:0045491)	12	1.20E-04
very long-chain fatty acid metabolic process (GO:0000038)	7	1.08E-02
cellular polysaccharide metabolic process (GO:0044264)	56	5.22E-22
microtubule-based movement (GO:0007018)	10	9.42E-04
cell wall biogenesis (GO:0042546)	74	6.28E-29
protein complex oligomerization (GO:0051259)	9	2.58E-03
plant-type cell wall loosening (GO:0009828)	6	2.90E-02
cellular polysaccharide biosynthetic process (GO:0033692)	32	1.13E-11
pectin metabolic process (GO:0045488)	26	1.99E-09
cortical microtubule organization (GO:0043622)	8	7.33E-03
galacturonan metabolic process (GO:0010393)	26	2.18E-09
polysaccharide biosynthetic process (GO:0000271)	38	9.92E-14
polysaccharide metabolic process (GO:0005976)	76	7.18E-28
glucan biosynthetic process (GO:0009250)	19	1.40E-06
response to hydrogen peroxide (GO:0042542)	11	1.15E-03
plant-type cell wall organization or biogenesis (GO:0071669)	74	1.48E-25
cytokinesis (GO:0000910)	24	7.84E-08
plant-type cell wall modification (GO:0009827)	9	6.88E-03
cellular carbohydrate biosynthetic process (GO:0034637)	34	6.17E-11
microtubule cytoskeleton organization (GO:0000226)	24	1.48E-07
cortical cytoskeleton organization (GO:0030865)	9	8.21E-03
cytoplasmic microtubule organization (GO:0031122)	8	1.61E-02
seed coat development (GO:0010214)	7	3.20E-02
cell wall organization (GO:0071555)	40	3.29E-12
cell wall organization or biogenesis (GO:0071554)	124	9.21E-40
cell wall modification (GO:0042545)	22	1.48E-06
carbohydrate biosynthetic process (GO:0016051)	45	1.91E-13
polysaccharide catabolic process (GO:0000272)	18	2.60E-05
microtubule-based process (GO:0007017)	29	1.84E-08
cellular carbohydrate metabolic process (GO:0044262)	59	2.26E-17

regulation of cellular component biogenesis (GO:0044087)	18	3.38E-05
pectin catabolic process (GO:0045490)	12	2.11E-03
plant-type cell wall organization (GO:0009664)	21	6.16E-06
spindle organization (GO:0007051)	8	2.77E-02
external encapsulating structure organization (GO:0045229)	42	2.45E-11
fatty acid biosynthetic process (GO:0006633)	15	6.44E-04
response to brassinosteroid (GO:0009741)	11	1.13E-02
carbohydrate metabolic process (GO:0005975)	104	2.70E-24
cytoskeleton organization (GO:0007010)	29	4.28E-06
cell division (GO:0051301)	43	6.24E-09
flavonoid metabolic process (GO:0009812)	12	1.78E-02
response to gibberellin (GO:0009739)	11	3.12E-02
carbohydrate catabolic process (GO:0016052)	20	9.48E-04
mitotic cell cycle process (GO:1903047)	17	5.03E-03
fatty acid metabolic process (GO:0006631)	20	2.24E-03
monocarboxylic acid biosynthetic process (GO:0072330)	20	2.57E-03
response to reactive oxygen species (GO:0000302)	13	3.16E-02
regionalization (GO:0003002)	17	1.28E-02
cellular response to oxygen levels (GO:0071453)	18	9.84E-03
secondary metabolic process (GO:0019748)	59	1.72E-08
mitotic cell cycle (GO:0000278)	19	9.18E-03
cell cycle process (GO:0022402)	43	2.89E-06
response to chitin (GO:0010200)	22	4.44E-03
cellular response to hypoxia (GO:0071456)	17	1.99E-02
cell growth (GO:0016049)	38	3.71E-05
cellular response to decreased oxygen levels (GO:0036294)	17	2.13E-02
cell cycle (GO:0007049)	46	4.50E-06
pattern specification process (GO:0007389)	20	1.94E-02
response to heat (GO:0009408)	20	1.99E-02
growth (GO:0040007)	84	2.64E-10
response to oxidative stress (GO:0006979)	40	1.06E-04
carboxylic acid biosynthetic process (GO:0046394)	38	2.79E-04
response to oxygen levels (GO:0070482)	21	2.27E-02
response to hypoxia (GO:0001666)	20	3.30E-02
developmental growth (GO:0048589)	63	3.86E-06
organic acid biosynthetic process (GO:0016053)	40	2.14E-03
response to temperature stimulus (GO:0009266)	49	3.22E-04
response to organic cyclic compound (GO:0014070)	46	7.43E-04
cell morphogenesis (GO:0000902)	27	2.53E-02
developmental growth involved in morphogenesis (GO:0060560)	25	4.23E-02
tissue development (GO:0009888)	100	2.07E-08

response to cold (GO:0009409)	26	4.91E-02
cellular component biogenesis (GO:0044085)	102	2.23E-08
plant organ morphogenesis (GO:1905392)	48	1.77E-03
plant epidermis development (GO:0090558)	34	1.48E-02
lipid metabolic process (GO:0006629)	68	4.61E-05
anatomical structure morphogenesis (GO:0009653)	83	4.14E-06
lipid biosynthetic process (GO:0008610)	40	9.17E-03
organic cyclic compound biosynthetic process (GO:1901362)	48	4.13E-03
response to osmotic stress (GO:0006970)	45	7.83E-03
aromatic compound biosynthetic process (GO:0019438)	42	1.47E-02
response to fungus (GO:0009620)	49	7.51E-03
response to wounding (GO:0009611)	40	2.39E-02
small molecule biosynthetic process (GO:0044283)	44	1.50E-02
cellular lipid metabolic process (GO:0044255)	47	1.27E-02
cellular component organization or biogenesis (GO:0071840)	171	5.02E-10
response to hormone (GO:0009725)	116	5.88E-06
hormone-mediated signaling pathway (GO:0009755)	43	4.49E-02
response to endogenous stimulus (GO:0009719)	117	6.87E-06
cellular response to hormone stimulus (GO:0032870)	53	1.73E-02
cell differentiation (GO:0030154)	56	1.32E-02
cellular developmental process (GO:0048869)	63	6.51E-03
cellular response to endogenous stimulus (GO:0071495)	54	2.00E-02
cellular response to chemical stimulus (GO:0070887)	92	4.21E-04
response to organic substance (GO:0010033)	157	2.00E-07
organic substance biosynthetic process (GO:1901576)	139	2.14E-06
cellular response to organic substance (GO:0071310)	69	5.83E-03
response to lipid (GO:0033993)	86	1.18E-03
response to bacterium (GO:0009617)	55	2.46E-02
carboxylic acid metabolic process (GO:0019752)	68	9.26E-03
biosynthetic process (GO:0009058)	146	2.02E-06
response to oxygen-containing compound (GO:1901700)	134	1.55E-05
organic acid metabolic process (GO:0006082)	88	4.73E-03
plant organ development (GO:0099402)	83	8.65E-03
oxoacid metabolic process (GO:0043436)	82	8.37E-03
organic substance catabolic process (GO:1901575)	77	1.53E-02
cellular biosynthetic process (GO:0044249)	119	6.38E-04
response to external biotic stimulus (GO:0043207)	102	3.34E-03
response to other organism (GO:0051707)	102	3.31E-03
response to biotic stimulus (GO:0009607)	102	3.30E-03
biological process involved in interspecies interaction between organisms (GO:0044419)	102	3.44E-03
small molecule metabolic process (GO:0044281)	117	1.05E-03

	response to chemical (GO:0042221)	204	1.12E-06
	defense response (GO:0006952)	98	9.24E-03
	developmental process (GO:0032502)	232	1.27E-07
	defense response to other organism (GO:0098542)	84	2.88E-02
	cellular component organization (GO:0016043)	113	5.00E-03
	anatomical structure development (GO:0048856)	210	2.39E-06
	response to stress (GO:0006950)	205	1.55E-05
	response to external stimulus (GO:0009605)	114	1.37E-02
	multicellular organism development (GO:0007275)	162	3.38E-03
	response to abiotic stimulus (GO:0009628)	150	1.37E-02
	response to stimulus (GO:0050896)	337	2.15E-07
	multicellular organismal process (GO:0032501)	168	1.12E-02
	organic substance metabolic process (GO:0071704)	349	6.04E-07
	cellular process (GO:0009987)	522	3.33E-14
	metabolic process (GO:0008152)	376	1.39E-06
	cellular metabolic process (GO:0044237)	290	1.39E-02
	primary metabolic process (GO:0044238)	268	2.91E-02
	nitrogen compound metabolic process (GO:0006807)	151	9.42E-03
	heterocycle metabolic process (GO:0046483)	40	5.53E-05
	organonitrogen compound biosynthetic process (GO:1901566)	19	1.50E-02
	cellular nitrogen compound metabolic process (GO:0034641)	31	6.44E-11
	establishment of localization in cell (GO:0051649)	7	2.23E-02
	nucleobase-containing compound metabolic process (GO:0006139)	18	4.91E-09
	cellular nitrogen compound biosynthetic process (GO:0044271)	10	3.39E-05
	protein transport (GO:0015031)	4	3.90E-02
	intracellular transport (GO:0046907)	5	5.18E-03
	intracellular protein transport (GO:0006886)	3	3.37E-02
	regulation of transcription by RNA polymerase II (GO:0006357)	3	2.64E-02
	cellular amide metabolic process (GO:0043603)	4	1.36E-03
	ncRNA processing (GO:0034470)	2	2.92E-02
	nucleic acid metabolic process (GO:0090304)	8	1.14E-11
	ncRNA metabolic process (GO:0034660)	2	5.20E-03
	gene expression (GO:0010467)	5	2.43E-12
	RNA metabolic process (GO:0016070)	4	5.52E-10
	generation of precursor metabolites and energy (GO:0006091)	1	1.15E-02
	RNA processing (GO:0006396)	2	2.14E-06
	amide biosynthetic process (GO:0043604)	1	1.56E-04
	peptide metabolic process (GO:0006518)	1	1.14E-04
GO molecular fuction		Gene	FDR
TC vs C and TW vs W up	raffinose alpha-galactosidase activity (GO:0052692)	4	5.53E-03
	alpha-galactosidase activity (GO:0004557)	4	5.37E-03

xyloglucan:xyloglucosyl transferase activity (GO:0016762)	12	2.98E-07
cellulose synthase activity (GO:0016759)	13	9.56E-08
hydroquinone:oxygen oxidoreductase activity (GO:0052716)	6	2.51E-03
very-long-chain 3-ketoacyl-CoA synthase activity (GO:0102756)	8	1.80E-04
cellulose synthase (UDP-forming) activity (GO:0016760)	9	4.60E-05
xylan 1,4-beta-xylosidase activity (GO:0009044)	4	4.68E-02
galactosidase activity (GO:0015925)	8	7.64E-04
oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor (GO:0016682)	7	4.01E-03
glucuronosyltransferase activity (GO:0015020)	6	1.94E-02
oxidoreductase activity, acting on diphenols and related substances as donors (GO:0016679)	7	6.90E-03
O-acetyltransferase activity (GO:0016413)	10	7.34E-04
lactoperoxidase activity (GO:0140825)	13	1.06E-04
microtubule motor activity (GO:0003777)	10	1.58E-03
microtubule binding (GO:0008017)	27	1.98E-09
glucosyltransferase activity (GO:0046527)	29	7.69E-10
tubulin binding (GO:0015631)	27	5.65E-09
polysaccharide binding (GO:0030247)	13	6.17E-04
O-acyltransferase activity (GO:0008374)	16	1.41E-04
cytoskeletal motor activity (GO:0003774)	10	9.96E-03
peroxidase activity (GO:0004601)	14	7.44E-04
hexosyltransferase activity (GO:0016758)	46	7.45E-13
oxidoreductase activity, acting on peroxide as acceptor (GO:0016684)	14	1.20E-03
hydrolase activity, hydrolyzing O-glycosyl compounds (GO:0004553)	45	1.28E-11
pectinesterase activity (GO:0030599)	10	2.64E-02
acyltransferase activity, transferring groups other than amino-acyl groups (GO:0016747)	36	8.72E-09
antioxidant activity (GO:0016209)	14	5.22E-03
hydrolase activity, acting on glycosyl bonds (GO:0016798)	47	1.71E-10
protein self-association (GO:0043621)	12	1.71E-02
acyltransferase activity (GO:0016746)	36	7.69E-08
carbohydrate binding (GO:0030246)	20	3.67E-04
oxidoreductase activity, acting on CH-OH group of donors (GO:0016614)	21	2.30E-04
acetyltransferase activity (GO:0016407)	12	2.25E-02
glycosyltransferase activity (GO:0016757)	58	4.51E-12
cytoskeletal protein binding (GO:0008092)	30	4.65E-06
UDP-glycosyltransferase activity (GO:0008194)	28	1.58E-05
UDP-glucosyltransferase activity (GO:0035251)	13	2.35E-02
oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor (GO:0016616)	16	7.04E-03
carboxylic ester hydrolase activity (GO:0052689)	20	2.10E-03
signaling receptor activity (GO:0038023)	16	3.44E-02
molecular transducer activity (GO:0060089)	18	3.50E-02

	oxidoreductase activity (GO:0016491)	79	7.86E-06
	transferase activity (GO:0016740)	168	6.41E-10
	hydrolase activity (GO:0016787)	126	1.87E-06
	catalytic activity (GO:0003824)	372	5.84E-23
	nucleic acid binding (GO:0003676)	67	2.56E-02
	RNA binding (GO:0003723)	16	1.72E-04
	catalytic activity, acting on a nucleic acid (GO:0140640)	5	5.38E-03
	GO cellular component	Gene	FDR
TC vs C and TW vs W up	microtubule end (GO:1990752)	4	3.77E-03
	cellulose synthase complex (GO:0010330)	3	2.10E-02
	microtubule plus-end (GO:0035371)	3	2.07E-02
	cortical microtubule, transverse to long axis (GO:0010005)	6	3.04E-04
	cell surface (GO:0009986)	4	2.05E-02
	cortical microtubule cytoskeleton (GO:0030981)	14	1.99E-07
	cortical microtubule (GO:0055028)	13	7.25E-07
	cortical cytoskeleton (GO:0030863)	14	3.38E-07
	cytoplasmic microtubule (GO:0005881)	14	4.51E-07
	kinesin complex (GO:0005871)	7	1.14E-03
	microtubule (GO:0005874)	31	7.49E-12
	supramolecular polymer (GO:0099081)	31	4.09E-11
	polymeric cytoskeletal fiber (GO:0099513)	31	3.75E-11
	supramolecular fiber (GO:0099512)	31	3.46E-11
	microtubule associated complex (GO:0005875)	10	1.07E-03
	phragmoplast (GO:0009524)	10	1.15E-03
	microtubule cytoskeleton (GO:0015630)	38	2.45E-12
	plant-type cell wall (GO:0009505)	69	1.05E-22
	cell wall (GO:0005618)	69	5.66E-22
	external encapsulating structure (GO:0030312)	70	9.62E-22
	cell cortex (GO:0005938)	16	4.53E-05
	cytoskeleton (GO:0005856)	40	1.81E-10
	secretory vesicle (GO:0099503)	18	9.66E-05
	supramolecular complex (GO:0099080)	31	1.46E-07
	spindle (GO:0005819)	8	4.69E-02
	apoplast (GO:0048046)	28	3.41E-06
	anchored component of plasma membrane (GO:0046658)	15	3.34E-03
	intrinsic component of plasma membrane (GO:0031226)	24	6.75E-05
	trans-Golgi network (GO:0005802)	21	1.89E-03
	endosome (GO:0005768)	28	6.63E-04
	cytoplasmic vesicle (GO:0031410)	49	1.73E-06
	intracellular vesicle (GO:0097708)	49	1.77E-06
	plasmodesma (GO:0009506)	59	1.08E-07

	cell-cell junction (GO:0005911)	59	1.03E-07
	symplast (GO:0055044)	59	9.81E-08
	anchoring junction (GO:0070161)	59	9.38E-08
	cell junction (GO:0030054)	59	8.99E-08
	anchored component of membrane (GO:0031225)	20	1.32E-02
	Golgi apparatus subcompartment (GO:0098791)	23	6.47E-03
	extracellular region (GO:0005576)	195	3.29E-24
	cell periphery (GO:0071944)	220	4.05E-27
	vesicle (GO:0031982)	50	1.83E-05
	Golgi apparatus (GO:0005794)	69	4.92E-07
	plasma membrane (GO:0005886)	156	1.55E-11
	endomembrane system (GO:0012505)	107	3.24E-05
	membrane (GO:0016020)	193	2.99E-05
	cellular anatomical entity (GO:0110165)	708	6.09E-04
	intracellular anatomical structure (GO:0005622)	543	4.88E-04
	intracellular organelle (GO:0043229)	469	1.10E-07
	organelle (GO:0043226)	469	6.37E-08
	intracellular membrane-bounded organelle (GO:0043231)	460	4.69E-08
	membrane-bounded organelle (GO:0043227)	460	2.21E-08
	nucleus (GO:0005634)	242	4.57E-03
	chloroplast (GO:0009507)	108	4.22E-02
	organelle membrane (GO:0031090)	22	1.04E-02
	envelope (GO:0031975)	16	6.41E-03
	organelle envelope (GO:0031967)	16	6.31E-03
	mitochondrion (GO:0005739)	51	3.13E-12
	protein-containing complex (GO:0032991)	27	7.52E-12
	transferase complex (GO:1990234)	6	7.22E-03
	nuclear lumen (GO:0031981)	6	6.26E-05
	intracellular organelle lumen (GO:0070013)	7	6.36E-06
	membrane-enclosed lumen (GO:0031974)	7	6.18E-06
	organelle lumen (GO:0043233)	7	6.01E-06
	catalytic complex (GO:1902494)	6	2.81E-08
	nuclear protein-containing complex (GO:0140513)	4	1.05E-05
	intracellular protein-containing complex (GO:0140535)	3	1.06E-04
	membrane protein complex (GO:0098796)	2	4.03E-04
	ubiquitin ligase complex (GO:0000151)	1	3.96E-02
	ribosome (GO:0005840)	1	6.87E-03
	nucleoplasm (GO:0005654)	1	2.75E-03
GO biological process complete		Gene	FDR
TC vs C and TW vs W down	reductive pentose-phosphate cycle (GO:0019253)	6	2.23E-05
	photosynthesis, dark reaction (GO:0019685)	6	2.89E-05

carbon fixation (GO:0015977)	6	3.47E-05
photosynthesis, light harvesting in photosystem I (GO:0009768)	7	1.86E-05
negative regulation of photosynthesis (GO:1905156)	4	5.57E-03
negative regulation of photosynthesis, light reaction (GO:0043155)	3	3.76E-02
photoinhibition (GO:0010205)	3	3.71E-02
plant-type primary cell wall biogenesis (GO:0009833)	6	3.81E-04
photosynthesis, light harvesting (GO:0009765)	7	2.84E-04
mitotic cytokinesis (GO:0000281)	6	2.39E-03
response to high light intensity (GO:0009644)	9	3.19E-05
translational elongation (GO:0006414)	5	1.04E-02
gibberellin metabolic process (GO:0009685)	4	5.05E-02
response to low light intensity stimulus (GO:0009645)	4	4.98E-02
cellulose biosynthetic process (GO:0030244)	7	1.37E-03
amide transport (GO:0042886)	5	2.18E-02
cellulose metabolic process (GO:0030243)	7	2.38E-03
response to far red light (GO:0010218)	5	2.68E-02
photosynthesis (GO:0015979)	21	7.01E-10
beta-glucan biosynthetic process (GO:0051274)	7	3.50E-03
xenobiotic detoxification by transmembrane export across the plasma membrane (GO:1990961)	5	3.09E-02
xenobiotic export from cell (GO:0046618)	5	3.04E-02
cellular aldehyde metabolic process (GO:0006081)	5	2.99E-02
photosynthesis, light reaction (GO:0019684)	14	1.57E-06
cytoskeleton-dependent cytokinesis (GO:0061640)	6	1.45E-02
beta-glucan metabolic process (GO:0051273)	7	5.69E-03
xenobiotic transport (GO:0042908)	5	4.92E-02
glucan biosynthetic process (GO:0009250)	11	9.32E-05
export across plasma membrane (GO:0140115)	7	8.82E-03
response to toxic substance (GO:0009636)	12	3.82E-04
detoxification (GO:0098754)	10	2.67E-03
cellular glucan metabolic process (GO:0006073)	12	1.29E-03
generation of precursor metabolites and energy (GO:0006091)	23	1.26E-06
glucan metabolic process (GO:0044042)	12	1.47E-03
cellular polysaccharide biosynthetic process (GO:0033692)	11	3.98E-03
carbohydrate biosynthetic process (GO:0016051)	19	1.71E-05
cellular carbohydrate biosynthetic process (GO:0034637)	13	1.32E-03
inorganic ion transmembrane transport (GO:0098660)	11	7.89E-03
response to cold (GO:0009409)	23	4.81E-06
polysaccharide biosynthetic process (GO:0000271)	11	1.42E-02
ion transmembrane transport (GO:0034220)	12	1.72E-02

	cation transport (GO:0006812)	12	1.85E-02
	cellular polysaccharide metabolic process (GO:0044264)	13	1.38E-02
	transmembrane transport (GO:0055085)	31	5.33E-06
	response to light intensity (GO:0009642)	13	3.06E-02
	cellular carbohydrate metabolic process (GO:0044262)	16	1.41E-02
	response to temperature stimulus (GO:0009266)	29	5.22E-05
	ion transport (GO:0006811)	18	7.86E-03
	chemical homeostasis (GO:0048878)	17	2.21E-02
	homeostatic process (GO:0042592)	18	2.51E-02
	small molecule biosynthetic process (GO:0044283)	24	1.40E-02
	cellular macromolecule biosynthetic process (GO:0034645)	24	2.05E-02
	regulation of biological quality (GO:0065008)	28	1.56E-02
	biosynthetic process (GO:0009058)	75	1.44E-06
	response to light stimulus (GO:0009416)	45	1.37E-03
	response to radiation (GO:0009314)	45	2.45E-03
	cellular biosynthetic process (GO:0044249)	63	4.00E-05
	organic substance biosynthetic process (GO:1901576)	68	2.10E-05
	response to lipid (GO:0033993)	41	8.72E-03
	phosphorus metabolic process (GO:0006793)	38	5.06E-02
	response to abiotic stimulus (GO:0009628)	81	3.48E-05
	response to oxygen-containing compound (GO:1901700)	58	7.35E-03
	response to chemical (GO:0042221)	94	3.80E-05
	response to hormone (GO:0009725)	46	5.09E-02
	small molecule metabolic process (GO:0044281)	52	2.87E-02
	response to organic substance (GO:0010033)	62	1.91E-02
	cellular metabolic process (GO:0044237)	148	1.93E-06
	response to stress (GO:0006950)	88	5.72E-03
	response to stimulus (GO:0050896)	154	1.98E-06
	metabolic process (GO:0008152)	169	4.50E-06
	cellular process (GO:0009987)	215	1.69E-06
	organic substance metabolic process (GO:0071704)	139	2.24E-02
GO molecular fuction		Gene	FDR
TC vs C and TW vs W down	pigment binding (GO:0031409)	2	4.36E-02
	omega-6 fatty acid desaturase activity (GO:0045485)	2	4.28E-02
	glyceraldehyde-3-phosphate dehydrogenase (NAD+) (non-phosphorylating) activity (GO:0043878)	3	1.68E-02
	translation elongation factor activity (GO:0003746)	5	5.39E-04
	calcium:cation antiporter activity (GO:0015368)	3	2.93E-02
	chlorophyll binding (GO:0016168)	7	2.06E-05
	cellulose synthase (UDP-forming) activity (GO:0016760)	6	2.14E-04

aldehyde dehydrogenase [NAD(P)+] activity (GO:0004030)	3	4.17E-02
aldehyde dehydrogenase (NAD+) activity (GO:0004029)	3	4.09E-02
salicylic acid binding (GO:1901149)	5	2.67E-03
cellulose synthase activity (GO:0016759)	6	8.35E-04
mannan synthase activity (GO:0051753)	4	2.58E-02
beta-1,4-mannosyltransferase activity (GO:0019187)	4	2.52E-02
glucuronosyltransferase activity (GO:0015020)	4	2.74E-02
quercetin 7-O-glucosyltransferase activity (GO:0080044)	7	7.26E-04
quercetin 3-O-glucosyltransferase activity (GO:0080043)	7	1.53E-03
UDP-glucosyltransferase activity (GO:0035251)	15	1.31E-07
amide transmembrane transporter activity (GO:0042887)	5	3.59E-02
xenobiotic transmembrane transporter activity (GO:0042910)	6	1.77E-02
glucosyltransferase activity (GO:0046527)	15	3.56E-06
secondary active transmembrane transporter activity (GO:0015291)	17	8.63E-06
UDP-glycosyltransferase activity (GO:0008194)	18	5.43E-06
proton transmembrane transporter activity (GO:0015078)	10	2.73E-03
copper ion binding (GO:0005507)	11	1.66E-03
antiporter activity (GO:0015297)	10	5.90E-03
active ion transmembrane transporter activity (GO:0022853)	12	2.34E-03
tetrapyrrole binding (GO:0046906)	19	5.14E-05
inorganic cation transmembrane transporter activity (GO:0022890)	17	5.20E-04
cation transmembrane transporter activity (GO:0008324)	18	4.54E-04
mRNA binding (GO:0003729)	43	5.93E-10
hexosyltransferase activity (GO:0016758)	15	2.46E-03
inorganic molecular entity transmembrane transporter activity (GO:0015318)	23	4.73E-05
active transmembrane transporter activity (GO:0022804)	21	2.11E-04
ion transmembrane transporter activity (GO:0015075)	24	1.14E-04
oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen (GO:0016705)	15	8.20E-03
iron ion binding (GO:0005506)	12	3.67E-02
transmembrane transporter activity (GO:0022857)	43	1.56E-07
transporter activity (GO:0005215)	44	1.75E-07
RNA binding (GO:0003723)	49	1.32E-07
protein serine/threonine kinase activity (GO:0004674)	23	2.11E-03
glycosyltransferase activity (GO:0016757)	18	1.64E-02
oxidoreductase activity (GO:0016491)	43	3.68E-06
transition metal ion binding (GO:0046914)	32	9.80E-04
protein kinase activity (GO:0004672)	25	2.69E-02
metal ion binding (GO:0046872)	37	4.80E-03
cation binding (GO:0043169)	37	8.13E-03

	ion binding (GO:0043167)	56	1.69E-03
	catalytic activity (GO:0003824)	154	3.92E-10
	heterocyclic compound binding (GO:1901363)	93	8.11E-05
	organic cyclic compound binding (GO:0097159)	93	1.12E-04
	transferase activity (GO:0016740)	61	1.92E-02
	nucleic acid binding (GO:0003676)	63	1.78E-02
	binding (GO:0005488)	152	9.12E-04
	GO cellular component	Gene	FDR
TC vs C and TW vs W down	PSII associated light-harvesting complex II (GO:0009517)	4	1.41E-04
	thylakoid light-harvesting complex (GO:0009503)	4	2.82E-04
	light-harvesting complex (GO:0030076)	4	2.74E-04
	photosystem I reaction center (GO:0009538)	3	1.18E-02
	photosystem I (GO:0009522)	6	1.77E-05
	stromule (GO:0010319)	8	1.58E-06
	chloroplast thylakoid membrane protein complex (GO:0098807)	5	5.64E-04
	photosystem (GO:0009521)	10	4.14E-07
	photosystem II (GO:0009523)	6	5.49E-04
	plastoglobule (GO:0010287)	7	2.66E-04
	chloroplast thylakoid membrane (GO:0009535)	24	6.30E-10
	plastid thylakoid membrane (GO:0055035)	24	7.09E-10
	apoplast (GO:0048046)	20	3.55E-08
	thylakoid membrane (GO:0042651)	24	2.47E-09
	photosynthetic membrane (GO:0034357)	24	2.87E-09
	thylakoid (GO:0009579)	34	8.39E-13
	chloroplast thylakoid (GO:0009534)	27	6.70E-10
	plastid thylakoid (GO:0031976)	27	5.99E-10
	plastid membrane (GO:0042170)	26	7.98E-09
	chloroplast envelope (GO:0009941)	29	8.42E-09
	plastid envelope (GO:0009526)	39	7.14E-11
	chloroplast stroma (GO:0009570)	28	1.06E-06
	plant-type vacuole (GO:0000325)	30	4.85E-07
	plastid stroma (GO:0009532)	28	1.57E-06
	organelle subcompartment (GO:0031984)	38	7.39E-08
	envelope (GO:0031975)	42	3.64E-08
	organelle envelope (GO:0031967)	42	3.40E-08
	vacuole (GO:0005773)	31	3.55E-05
	plant-type cell wall (GO:0009505)	15	2.04E-02
	cell wall (GO:0005618)	15	2.81E-02
	organelle membrane (GO:0031090)	42	4.43E-06

external encapsulating structure (GO:0030312)	15	3.71E-02
membrane (GO:0016020)	123	1.88E-16
plasma membrane (GO:0005886)	74	8.01E-09
plasmodesma (GO:0009506)	21	3.77E-02
cell-cell junction (GO:0005911)	21	3.68E-02
symplast (GO:0055044)	21	3.60E-02
anchoring junction (GO:0070161)	21	3.51E-02
cell junction (GO:0030054)	21	3.44E-02
cell periphery (GO:0071944)	84	1.73E-09
cytosol (GO:0005829)	61	1.59E-06
plastid (GO:0009536)	105	1.15E-07
chloroplast (GO:0009507)	97	7.49E-07
cytoplasm (GO:0005737)	204	5.70E-05
nucleus (GO:0005634)	70	1.08E-06
nuclear protein-containing complex (GO:0140513)	1	2.40E-02

Letters show control (100% natural precipitation; C); waterlogging, (30 % additional precipitation; W) during 2018-2020 and trees were transplanted in October, 2020. Samples collected in A, 2021 and classified trees grown at control (TC) and waterlogging hardening treatment (TW). The GO terms associated with Fisher's exact test with FDR corrected P-value < 0.05.

Table S3.Gene ontology (GO) analysis of differences control (TC vs C) and waterlogging hardening treatment (TWvsW) before and after transplanting

	GO biological process complete	Gene	FDR
TC vs C up	protein homooligomerization (GO:0051260)	4	2.28E-02
	jasmonic acid biosynthetic process (GO:0009695)	4	2.15E-02
	long-chain fatty acid biosynthetic process (GO:0042759)	4	3.66E-02
	response to oxidative stress (GO:0006979)	17	9.33E-03
	response to fatty acid (GO:0070542)	16	1.36E-02
	response to wounding (GO:0009611)	21	1.88E-03
	cellular response to oxygen-containing compound (GO:1901701)	23	8.17E-03
	response to water (GO:0009415)	24	8.78E-03
	cellular catabolic process (GO:0044248)	19	4.33E-02
	response to acid chemical (GO:0001101)	24	1.11E-02
	response to water deprivation (GO:0009414)	21	3.37E-02
	response to oxygen-containing compound (GO:1901700)	57	2.87E-07
	response to salt (GO:1902074)	24	2.86E-02
	cellular response to chemical stimulus (GO:0070887)	33	6.74E-03
	response to abiotic stimulus (GO:0009628)	69	3.06E-07
	response to inorganic substance (GO:0010035)	32	2.28E-02
	response to external stimulus (GO:0009605)	45	1.97E-03
	response to chemical (GO:0042221)	72	1.64E-06
	cellular response to stimulus (GO:0051716)	51	1.69E-03
	response to stress (GO:0006950)	76	2.03E-06
	response to organic substance (GO:0010033)	59	5.23E-04
	response to stimulus (GO:0050896)	119	7.32E-11
	cellular process (GO:0009987)	133	2.46E-02
TC vs C down	monocarboxylic acid catabolic process (GO:0072329)	6	3.86E-02
	plant organ senescence (GO:0090693)	13	3.49E-02
	secondary metabolite biosynthetic process (GO:0044550)	14	2.96E-02
	peptide metabolic process (GO:0006518)	20	7.77E-03
	translation (GO:0006412)	18	1.90E-02
	peptide biosynthetic process (GO:0043043)	18	2.00E-02
	transmembrane transport (GO:0055085)	30	7.74E-04
	amide metabolic process (GO:0043603)	22	1.31E-02
	response to water deprivation (GO:0009414)	32	7.22E-03
	response to acid chemical (GO:0001101)	35	8.00E-03
	response to water (GO:0009415)	33	1.18E-02
	response to salt (GO:1902074)	34	2.03E-02
	response to stress (GO:0006950)	95	1.32E-02
	cellular metabolic process (GO:0044237)	153	5.04E-04
	metabolic process (GO:0008152)	185	5.18E-04

TW vs W up	organic substance metabolic process (GO:0071704)	164	3.19E-02
	cellular process (GO:0009987)	216	6.83E-04
	syncytium formation (GO:0006949)	6	5.89E-03
	acylglycerol biosynthetic process (GO:0046463)	7	1.12E-02
	neutral lipid biosynthetic process (GO:0046460)	7	1.11E-02
	stomatal lineage progression (GO:0010440)	6	2.48E-02
	lactone biosynthetic process (GO:1901336)	6	2.46E-02
	regulation of jasmonic acid mediated signaling pathway (GO:2000022)	11	4.60E-04
	triglyceride biosynthetic process (GO:0019432)	6	2.79E-02
	acylglycerol metabolic process (GO:0006639)	8	7.69E-03
	neutral lipid metabolic process (GO:0006638)	8	7.61E-03
	triglyceride metabolic process (GO:0006641)	7	1.70E-02
	stomatal complex morphogenesis (GO:0010103)	7	2.67E-02
	microtubule-based movement (GO:0007018)	11	2.37E-03
	plant-type cell wall loosening (GO:0009828)	7	3.39E-02
	regulation of mitotic cell cycle phase transition (GO:1901990)	9	1.23E-02
	stomatal complex development (GO:0010374)	15	3.15E-04
	mitotic cell cycle phase transition (GO:0044772)	8	2.59E-02
	cell cycle phase transition (GO:0044770)	8	3.16E-02
	regulation of mitotic cell cycle (GO:0007346)	11	1.07E-02
	plant-type cell wall modification (GO:0009827)	10	1.82E-02
	phenylpropanoid biosynthetic process (GO:0009699)	14	2.87E-03
	plant epidermis morphogenesis (GO:0090626)	15	2.09E-03
	phenylpropanoid metabolic process (GO:0009698)	17	9.58E-04
	mitotic cell cycle process (GO:1903047)	25	3.62E-05
	mitotic cell cycle (GO:0000278)	31	4.52E-06
	hemicellulose metabolic process (GO:0010410)	13	3.95E-02
	cell wall polysaccharide metabolic process (GO:0010383)	19	1.01E-02
	plant-type cell wall organization (GO:0009664)	19	1.14E-02
	flavonoid metabolic process (GO:0009812)	16	2.96E-02
	plant-type cell wall biogenesis (GO:0009832)	28	1.54E-03
	cell wall modification (GO:0042545)	17	2.94E-02
	cell wall macromolecule metabolic process (GO:0044036)	21	1.53E-02
	cell wall biogenesis (GO:0042546)	42	3.55E-05
	microtubule-based process (GO:0007017)	22	1.22E-02
	external encapsulating structure organization (GO:0045229)	36	2.84E-04
	polysaccharide biosynthetic process (GO:0000271)	24	7.65E-03
	carbohydrate biosynthetic process (GO:0016051)	34	5.06E-04
	regulation of cell cycle (GO:0051726)	22	1.52E-02
	secondary metabolite biosynthetic process (GO:0044550)	33	1.21E-03

cell wall organization (GO:0071555)	29	2.63E-03
plant-type cell wall organization or biogenesis (GO:0071669)	51	1.50E-05
cell cycle (GO:0007049)	66	4.20E-07
cell cycle process (GO:0022402)	55	6.22E-06
shoot system morphogenesis (GO:0010016)	22	2.10E-02
regulation of cell communication (GO:0010646)	41	3.42E-04
regulation of signal transduction (GO:0009966)	39	6.14E-04
anatomical structure formation involved in morphogenesis (GO:0048646)	25	1.51E-02
regulation of signaling (GO:0023051)	40	4.80E-04
floral whorl development (GO:0048438)	20	3.54E-02
response to wounding (GO:0009611)	80	3.48E-08
cell wall organization or biogenesis (GO:0071554)	86	1.24E-08
unidimensional cell growth (GO:0009826)	35	2.11E-03
response to oxygen levels (GO:0070482)	29	1.20E-02
response to hypoxia (GO:0001666)	28	1.55E-02
lipid metabolic process (GO:0006629)	119	5.14E-11
protein phosphorylation (GO:0006468)	45	6.12E-04
lipid biosynthetic process (GO:0008610)	68	4.48E-06
cell morphogenesis (GO:0000902)	45	6.88E-04
response to decreased oxygen levels (GO:0036293)	28	1.87E-02
polysaccharide metabolic process (GO:0005976)	40	2.37E-03
carbohydrate metabolic process (GO:0005975)	81	8.81E-07
cell division (GO:0051301)	41	2.25E-03
response to salt stress (GO:0009651)	55	2.16E-04
organic hydroxy compound metabolic process (GO:1901615)	29	2.48E-02
plant organ senescence (GO:0090693)	25	4.65E-02
response to osmotic stress (GO:0006970)	80	3.02E-06
regulation of defense response (GO:0031347)	66	6.42E-05
phosphorylation (GO:0016310)	55	6.19E-04
developmental growth involved in morphogenesis (GO:0060560)	37	2.08E-02
defense response to bacterium (GO:0042742)	77	7.15E-05
plant epidermis development (GO:0090558)	44	1.08E-02
regulation of response to stress (GO:0080134)	71	2.12E-04
cell growth (GO:0016049)	44	1.71E-02
leaf development (GO:0048366)	38	4.14E-02
reproductive shoot system development (GO:0090567)	39	3.50E-02
response to bacterium (GO:0009617)	93	4.50E-05
anatomical structure morphogenesis (GO:0009653)	116	1.67E-06
response to jasmonic acid (GO:0009753)	45	2.09E-02
tissue development (GO:0009888)	133	3.72E-07
cellular developmental process (GO:0048869)	96	5.50E-05

cellular response to lipid (GO:0071396)	54	1.09E-02
response to alcohol (GO:0097305)	86	2.54E-04
defense response to other organism (GO:0098542)	149	6.97E-08
response to fatty acid (GO:0070542)	46	2.56E-02
developmental growth (GO:0048589)	73	1.25E-03
defense response (GO:0006952)	169	1.15E-08
growth (GO:0040007)	91	1.83E-04
response to fungus (GO:0009620)	76	9.87E-04
cell differentiation (GO:0030154)	86	3.65E-04
phyllome development (GO:0048827)	56	1.08E-02
response to abscisic acid (GO:0009737)	76	1.01E-03
response to external biotic stimulus (GO:0043207)	172	1.17E-08
response to other organism (GO:0051707)	172	1.05E-08
response to biotic stimulus (GO:0009607)	172	9.78E-09
defense response to fungus (GO:0050832)	59	8.42E-03
biological process involved in interspecies interaction between organisms (GO:0044419)	172	1.02E-08
cellular response to oxygen-containing compound (GO:1901701)	80	9.33E-04
secondary metabolic process (GO:0019748)	50	2.45E-02
response to lipid (GO:0033993)	174	1.31E-08
monocarboxylic acid metabolic process (GO:0032787)	44	4.50E-02
regulation of response to stimulus (GO:0048583)	93	4.00E-04
cellular lipid metabolic process (GO:0044255)	69	6.67E-03
response to external stimulus (GO:0009605)	198	8.75E-09
response to organic cyclic compound (GO:0014070)	58	2.24E-02
phosphorus metabolic process (GO:0006793)	92	1.01E-03
phosphate-containing compound metabolic process (GO:0006796)	89	1.36E-03
response to temperature stimulus (GO:0009266)	80	3.81E-03
shoot system development (GO:0048367)	94	1.73E-03
response to endogenous stimulus (GO:0009719)	163	3.62E-06
response to hormone (GO:0009725)	161	4.86E-06
cellular response to hormone stimulus (GO:0032870)	66	2.32E-02
cellular response to endogenous stimulus (GO:0071495)	68	2.10E-02
response to stress (GO:0006950)	338	1.78E-14
response to water deprivation (GO:0009414)	72	1.88E-02
developmental process (GO:0032502)	358	2.06E-15
anatomical structure development (GO:0048856)	332	2.39E-13
response to oxygen-containing compound (GO:1901700)	198	5.51E-07
cellular response to chemical stimulus (GO:0070887)	122	6.22E-04
response to acid chemical (GO:0001101)	79	1.70E-02
response to water (GO:0009415)	77	1.88E-02
organic acid metabolic process (GO:0006082)	123	7.10E-04

cellular response to organic substance (GO:0071310)	92	1.13E-02
plant organ development (GO:0099402)	125	1.42E-03
oxoacid metabolic process (GO:0043436)	114	3.28E-03
response to light stimulus (GO:0009416)	122	1.80E-03
response to abiotic stimulus (GO:0009628)	263	2.45E-08
carboxylic acid metabolic process (GO:0019752)	86	2.43E-02
signal transduction (GO:0007165)	122	2.37E-03
response to radiation (GO:0009314)	127	1.71E-03
post-embryonic development (GO:0009791)	130	1.63E-03
response to organic substance (GO:0010033)	251	1.96E-07
regulation of developmental process (GO:0050793)	87	2.59E-02
signaling (GO:0023052)	125	2.86E-03
response to salt (GO:1902074)	80	4.08E-02
multicellular organismal process (GO:0032501)	274	9.12E-08
response to inorganic substance (GO:0010035)	121	6.11E-03
response to chemical (GO:0042221)	287	5.16E-08
multicellular organism development (GO:0007275)	252	1.15E-06
small molecule metabolic process (GO:0044281)	164	8.67E-04
organic substance catabolic process (GO:1901575)	102	2.47E-02
reproductive structure development (GO:0048608)	109	2.09E-02
reproductive system development (GO:0061458)	109	2.09E-02
cell communication (GO:0007154)	133	6.97E-03
reproduction (GO:0000003)	143	4.24E-03
developmental process involved in reproduction (GO:0003006)	122	1.55E-02
response to stimulus (GO:0050896)	510	2.52E-15
system development (GO:0048731)	206	3.84E-04
reproductive process (GO:0022414)	139	1.17E-02
catabolic process (GO:0009056)	115	4.10E-02
cellular response to stimulus (GO:0051716)	197	9.90E-04
protein modification process (GO:0036211)	130	4.75E-02
cellular process (GO:0009987)	739	1.40E-17
biological regulation (GO:0065007)	409	1.42E-05
regulation of biological process (GO:0050789)	386	9.74E-05
regulation of cellular process (GO:0050794)	324	1.50E-03
organic substance biosynthetic process (GO:1901576)	260	1.10E-02
primary metabolic process (GO:0044238)	444	8.40E-05
organic substance metabolic process (GO:0071704)	541	1.05E-06
biosynthetic process (GO:0009058)	269	2.92E-02
metabolic process (GO:0008152)	573	3.55E-06
cellular metabolic process (GO:0044237)	443	1.54E-03
biological_process (GO:0008150)	1038	2.34E-02

	cellular nitrogen compound metabolic process (GO:0034641)	136	2.92E-02
	RNA metabolic process (GO:0016070)	70	9.40E-03
	gene expression (GO:0010467)	28	7.70E-08
	mRNA metabolic process (GO:0016071)	6	3.73E-02
	RNA processing (GO:0006396)	10	5.43E-04
	amide biosynthetic process (GO:0043604)	6	3.96E-03
	ncRNA metabolic process (GO:0034660)	5	8.16E-03
	ncRNA processing (GO:0034470)	4	2.50E-02
	RNA modification (GO:0009451)	3	2.92E-02
	ribosome biogenesis (GO:0042254)	2	1.42E-02
	ribonucleoprotein complex biogenesis (GO:0022613)	2	1.70E-03
	translation (GO:0006412)	2	1.14E-04
	peptide biosynthetic process (GO:0043043)	2	8.27E-05
	peptide metabolic process (GO:0006518)	2	3.23E-05
TW vs W down	oligopeptide transport (GO:0006857)	5	2.42E-02
	peptide transport (GO:0015833)	5	2.32E-02
	immune response (GO:0006955)	13	3.88E-02
	defense response to bacterium (GO:0042742)	46	4.31E-05
	phosphorylation (GO:0016310)	31	3.79E-03
	response to bacterium (GO:0009617)	54	4.53E-05
	transmembrane transport (GO:0055085)	33	3.77E-02
	response to external biotic stimulus (GO:0043207)	94	3.55E-07
	response to other organism (GO:0051707)	94	1.78E-07
	response to biotic stimulus (GO:0009607)	94	1.24E-07
	biological process involved in interspecies interaction between organisms (GO:0044419)	94	1.55E-07
	defense response to other organism (GO:0098542)	79	5.85E-06
	phosphate-containing compound metabolic process (GO:0006796)	48	9.81E-03
	defense response (GO:0006952)	85	1.88E-05
	response to external stimulus (GO:0009605)	104	4.89E-07
	phosphorus metabolic process (GO:0006793)	48	1.80E-02
	protein metabolic process (GO:0019538)	111	2.37E-03
	response to oxygen-containing compound (GO:1901700)	89	2.55E-02
	cellular response to stimulus (GO:0051716)	99	1.73E-02
	response to stress (GO:0006950)	148	1.37E-04
	organonitrogen compound metabolic process (GO:1901564)	146	2.51E-03
	response to chemical (GO:0042221)	128	1.79E-02
	response to stimulus (GO:0050896)	227	4.47E-05
	primary metabolic process (GO:0044238)	221	2.90E-04
	organic substance metabolic process (GO:0071704)	263	5.88E-05
	nitrogen compound metabolic process (GO:0006807)	191	2.78E-02
	cellular metabolic process (GO:0044237)	218	8.44E-03

metabolic process (GO:0008152)	277	1.71E-04
cellular process (GO:0009987)	333	5.19E-06

Letters show control (100% natural precipitation; C); waterlogging, (30 % additional precipitation; W) during 2018-2020 and trees were transplanted in October, 2020. Samples collected in A, 2021 and classified trees grown at control (TC) and waterlogging hardening treatment (TW). The GO terms associated with Fisher's exact test with FDR corrected P-value < 0.05.

Table S4. Description of up-regulated secondary metabolites genes under waterlogging hardening after transplanting

Gene name	Locus	description	biological process
CAD9	AT4G39330	Probable cinnamyl alcohol dehydrogenase 9	phenylpropanoid biosynthetic process
DTX41	AT3G59030	Protein DETOXIFICATION 41	phenylpropanoid biosynthetic process
MYB3	AT1G22640	Transcription factor MYB3	phenylpropanoid biosynthetic process
LDOX	AT4G22880	Leucoanthocyanidin dioxygenase	phenylpropanoid biosynthetic process
UGT72B1	AT4G01070	UDP-glycosyltransferase 72B1	phenylpropanoid biosynthetic process
PAL4	AT3G10340	Phenylalanine ammonia-lyase 4	phenylpropanoid biosynthetic process
BAN	AT1G61720	Anthocyanidin reductase	flavonoid biosynthetic process
CHI1	AT3G55120	Chalcone--flavanone isomerase 1	flavonoid biosynthetic process
RNS1	AT2G02990	Ribonuclease 1	flavonoid biosynthetic process
DTX41	AT3G59030	Protein DETOXIFICATION 41	flavonoid biosynthetic process
LDOX	AT4G22880	Leucoanthocyanidin dioxygenase	flavonoid biosynthetic process
DFRA	AT5G42800	Dihydroflavonol 4-reductase	flavonoid biosynthetic process
ABCG29	AT3G16340	ABC transporter G family member 29	regulation of lignin biosynthetic process