

Supplementary Table S1. Primer sequences for qPCR

Primer name	sequence(5'→3')
Gln1;1-RF (Ishiyama et al. 2004)	CATCAACCTAACCTCTCAGACTCCACT
Gln1;1-RR (Ishiyama et al. 2004)	ACTTCAGCTGCAACATCAGGGTTGCTA
Gln1;2-RF (Ishiyama et al. 2004)	TGTTAACCTTGACATCTCAGACAACAGT
Gln1;2-RR (Ishiyama et al. 2004)	ACTTCAGCAATAAACATCAGGGTTAGCA
Gln1;3-RF (Ishiyama et al. 2004)	CGTTAACCTAACCTCACCGATGCCACC
Gln1;3-RR (Ishiyama et al. 2004)	TCCTCCTTGGCAACGTCGGGGTGGCTG
NADH-GOGAT_F	ATCGTCATTTCCGCTGTT
NADH-GOGAT_R	TTGCTCTCACAAACCACAAGC
GLN2_F	CACCAAACCTTACTCTGACAGG
GLN2_R	CACTATCTCACCAAGGTGCTTG
qGLU1_forward (Takabayashi et al. 2016)	TTGGGACAGGATGTTGTTGA
qGLU1_reverse (Takabayashi et al. 2016)	GCCTTCACCCAGAAAGACAA
qGLU2_forward (Takabayashi et al. 2016)	GCTGGGATGACAGGTGGATTG
qGLU2_reverse (Takabayashi et al. 2016)	AAGCTGTGTTGTCCCAC TGG
AT3G55410_F	AGGATGTCGAACGAGGAACA
AT3G55410_R	TAACCCAATT CGAACCCAAG
UBQ2_F (Ishiyama et al. 2004)	CCAAGATCCAGGACAAAGAAGGA
UBQ2_R (Ishiyama et al. 2004)	TGGAGACGAGCATAACACTTGC

Supplementary Table S3. List of differentially expressed genes at 15 DAS in F1 hybrid ($\log_2\text{FC} \geq 0.58$, $\text{FDR} < 0.05$)

44 up-regulated genes and 22 down-regulated genes overlapped between two comparison of microarray data (F1 vs Col and F1 vs C24) . Number of biological replicates = 3.

number of genes	Arity Element	Locus Identifier	hapZFCF1C00	hapZFCF1C00A	Annotations
Regulated genes in P1 hybrid (names CDS from both parents)					
2	203011_Δ	AT5G17500	2.37	2.07	
3	203012_Δ	AT5G17501	0.45	0.35	Encodes a member of the ZTFP1 (polymerase Select subunit B) or E3BP (E3BP) transcription factor family (TFIIB1). The protein contains one TFIIB1 domain.
4	203013_Δ	AT5G06800	1.38	0.92	VQ-motif-containing protein domain (AnnotateIT)
5	203014_Δ	AT5G06801	1.39	0.93	Encodes an AIFM2-type transcription factor. It is a member of the AIFM2 transcription factor family. It is also a member of the AIFM2 transcription factor subfamily.
6	203015_Δ	AT5G11960	1.35	0.93	Encodes a member of the E3BP (polymerase Select subunit B) or E3BP (E3BP) transcription factor family. The protein contains one E3BP domain.
7	203016_Δ	AT5G11961	2.30	2.12	Encodes a member of the E3BP (polymerase Select subunit B) or E3BP (E3BP) transcription factor family. The protein contains one E3BP domain. This is also a member of the E3BP subfamily including ATBPI-1, ATBPI-2, AND ATBPI-3, involved in regulating nucleic acid structure and the response to cold stress.
8	203017_Δ	AT5G11962	2.30	2.12	Encodes a member of the E3BP (polymerase Select subunit B) or E3BP (E3BP) transcription factor family. The protein contains one E3BP domain. This is also a member of the E3BP subfamily including ATBPI-1, ATBPI-2, AND ATBPI-3, involved in regulating nucleic acid structure and the response to cold stress.
9	203018_Δ	AT5G11963	0.93	0.65	The gene encodes a protein that contains E3BP domains.
10	203019_Δ	AT5G11964	0.93	0.65	The gene encodes a protein with E3BP domains, including Box-C4H1, and, as a consequence, undergoes conformational change. E3BP expression occurs in all major organs, and transcript levels are increased by ~ 5-10 fold in plants subjected to heat, darkness, heat, cold, hydrogen peroxide, abscisic acid, and indole-3-acetic acid. However, E3BP protein accumulation changes were not detectable. The positive CDS24 regulatory region confers responsive expression at sites of mechanical stress, in regions undergoing growth, in vascular tissues, and in stem and floral organs, and in leaves, trichomes, and hydathodes. CDS24 underpinning transgenesis are mediated by RNAi inhibition of germination and seedling growth, and have enhanced tolerance to Cu(II), malathion and Cd(II), and bigC2. At5g11964 also regulates stress-tolerance.
11	203020_Δ	AT5G22705	1.32	0.66	At5g22705 also regulates stress-tolerance.
12	203021_Δ	AT5G22706	1.32	0.66	At5g22706 also regulates stress-tolerance.
13	203022_Δ	AT5G22740	0.79	0.46	Hypothetical protein domain (AnnotateIT)
14	203023_Δ	AT5G22740	1.65	1.47	Encodes a member of the PDRS transcription factor gene family. Expresses in response to abiotic stress and early in seedling root development. Interacts with ARF17 and regulates the expression of some auxin-response genes.
15	203024_Δ	AT5G22741	1.33	1.09	At5g22741 also regulates stress-tolerance.
16	203025_Δ	AT5G22742	1.33	1.09	At5g22742 also regulates stress-tolerance.
17	203026_Δ	AT5G22743	2.40	2.32	Encodes a member of the NPPY MP subfamily.
18	203027_Δ	AT5G22745	2.29	1.15	Encodes a member of the NPPY MP subfamily. It is also a member of the NPPY MP transcription factor 1, AT5G22746 (CYP14), AT5G22747 (CYP15). Has NPPY dehydrogenase activity. Also plays a role in plant defense responses.
19	203028_Δ	AT5G22746	1.60	1.90	BTW and TGA domain. Located in promoter and intron of At5g22745. Roots and seeds.
20	203029_Δ	AT5G22747	0.88	0.53	BTW and TGA domain. Located in promoter and intron of At5g22745. Roots and seeds.
21	203030_Δ	AT5G22780	3.02	2.02	BTW and TGA domain. It is also a C4H-domain transcription factor of auxin-regulated gene expression and interacts with CRL1.
22	203031_Δ	AT5G22781	2.33	1.24	BTW and TGA domain. It is also a C4H-domain transcription factor of auxin-regulated gene expression and interacts with CRL1.
23	203032_Δ	AT5G22810	1.32	1.12	Hypothetical protein domain (AnnotateIT)
24	203033_Δ	AT5G22816	1.61	1.00	The gene encodes a protein that contains BTW domain. It is also a BTW domain. The protein is well-conserved.
25	203034_Δ	AT5G22817	3.38	4.64	BTW and TGA domain. It is also a BTW domain. The protein is well-conserved.
26	203035_Δ	AT5G22836	2.66	0.79	Transcription initiation site P1-P2-Luciferase reporter gene construct (AnnotateIT)
27	203036_Δ	AT5G22837	1.45	0.79	BTW and TGA domain. It is also a BTW domain. The protein is well-conserved.
28	203037_Δ	AT5G22870	4.05	4.25	BTW and TGA domain. It is also a BTW domain. The protein is well-conserved.
29	203038_Δ	AT5G22871	2.00	1.25	BTW and TGA domain. It is also a BTW domain. The protein is well-conserved.
30	203039_Δ	AT5G22885	2.11	1.45	Part of a complex that binds to the auxin response element (ARE) of the auxin-induced gene (AuxR). The sequence is similar to SDR1. Participates in auxin signaling pathway. Has IAA10-like activity in ABA.
31	203040_Δ	AT5G22890	0.89	0.81	Encodes a member of protein MAAT (MIAA10-ACAS10-MAAT). Separating regulatory sequences. The sequence is similar to SDR1. Participates in auxin signaling pathway. Has IAA10-like activity in ABA.
32	203041_Δ	AT5G22891	0.89	0.71	Encodes a member of protein MAAT (MIAA10-ACAS10-MAAT). Separating regulatory sequences. The sequence is similar to SDR1. Participates in auxin signaling pathway. Has IAA10-like activity in ABA.
33	203042_Δ	AT5G22905	1.60	2.01	Participates in auxin signaling pathway by a role of auxin-induced gene (AuxR). The sequence is similar to SDR1. Participates in auxin signaling pathway. Has IAA10-like activity in ABA.
34	203043_Δ	AT5G22906	4.47	3.00	Participates in auxin signaling pathway by a role of auxin-induced gene (AuxR). The sequence is similar to SDR1. Participates in auxin signaling pathway. Has IAA10-like activity in ABA.
35	203044_Δ	AT5G22940	2.49	1.51	Pathogen-inducible factor. Binds At5g22940 to DNA. Transcription complex with Ghd7 and SDR1 and SDR10. Coexpression with At5g22940 leads to smaller At5g22940 and SDR1 complex. At5g22940 and SDR10 have partially induced roles in response to the hemispherical bacterial pathogen <i>Pseudomonas syringae</i> and the necrotrophic bacterial pathogen <i>Bacillus cereus</i> , while At5g22940 playing a more important role than the other two. The SDR10 is well-conserved module.
36	203045_Δ	AT5G22941	1.34	1.46	Pathogen-inducible factor. Binds At5g22941 to DNA. Transcription complex with Ghd7 and SDR1 and SDR10. Coexpression with At5g22941 leads to smaller At5g22941 and SDR1 complex. At5g22941 and SDR10 have partially induced roles in response to the hemispherical bacterial pathogen <i>Pseudomonas syringae</i> and the necrotrophic bacterial pathogen <i>Bacillus cereus</i> , while At5g22941 playing a more important role than the other two. The SDR10 is well-conserved module.
37	203046_Δ	AT5G22945	0.79	0.78	Pathogen-inducible factor P1-P2-Luciferase reporter gene construct (AnnotateIT)
38	203047_Δ	AT5G22946	1.33	1.33	Pathogen-inducible factor P1-P2-Luciferase reporter gene construct (AnnotateIT)
39	203048_Δ	AT5G22947	1.88	1.88	Pathogen-inducible factor. Ghd7 and SDR1 and SDR10. Coexpression with At5g22947 leads to smaller At5g22947 and SDR1 complex. At5g22947 and SDR10 have partially induced roles in response to the hemispherical bacterial pathogen <i>Pseudomonas syringae</i> and the necrotrophic bacterial pathogen <i>Bacillus cereus</i> , while At5g22947 playing a more important role than the other two. The SDR10 is well-conserved module.
40	203049_Δ	AT5G22948	1.88	1.88	Pathogen-inducible factor. Ghd7 and SDR1 and SDR10. Coexpression with At5g22948 leads to smaller At5g22948 and SDR1 complex. At5g22948 and SDR10 have partially induced roles in response to the hemispherical bacterial pathogen <i>Pseudomonas syringae</i> and the necrotrophic bacterial pathogen <i>Bacillus cereus</i> , while At5g22948 playing a more important role than the other two. The SDR10 is well-conserved module.
41	203050_Δ	AT5G22949	1.88	1.88	Pathogen-inducible factor. Ghd7 and SDR1 and SDR10. Coexpression with At5g22949 leads to smaller At5g22949 and SDR1 complex. At5g22949 and SDR10 have partially induced roles in response to the hemispherical bacterial pathogen <i>Pseudomonas syringae</i> and the necrotrophic bacterial pathogen <i>Bacillus cereus</i> , while At5g22949 playing a more important role than the other two. The SDR10 is well-conserved module.
42	203051_Δ	AT5G22970	3.35	2.80	Fatty and hydroxyl ester hydrolase (AnnotateIT)
43	203052_Δ	AT5G22971	0.84	1.44	Encodes a member of fatty ester hydrolase, related to KRM1. MIAA10-ACAS10-MIAA10. Specifically interacts with Phosphatidylethanolamine N-acyltransferase (PEMT). Encodes a protein that catalyzes phosphatidylethanolamine.
44	203053_Δ	AT5G22972	2.13	2.13	Encodes a member of fatty ester hydrolase, related to KRM1. MIAA10-ACAS10-MIAA10. Specifically interacts with Phosphatidylethanolamine N-acyltransferase (PEMT).
45	203054_Δ	AT5G22973	1.42	1.42	Encodes a member of fatty ester hydrolase, related to KRM1. MIAA10-ACAS10-MIAA10. Specifically interacts with Phosphatidylethanolamine N-acyltransferase (PEMT).
46	203055_Δ	AT5G22974	0.77	0.65	Encodes a member of fatty ester hydrolase, related to KRM1. MIAA10-ACAS10-MIAA10. Specifically interacts with Phosphatidylethanolamine N-acyltransferase (PEMT).
Regulated genes in P1 hybrid (names CDS from both parents)					
number of genes	Arity Element	Locus Identifier	hapZFCF1C00	hapZFCF1C00A	Annotations
1	203056_Δ	AT5G06555	-0.40	-0.34	Encodes a member of protein kinase CK2. The gene is located in three distinct loci but on the conserved genome and is transposed to make it easier to handle.
2	203057_Δ	AT5G06556	-0.98	-0.98	Encodes a member of protein kinase CK2.
3	203058_Δ	AT5G06557	-0.98	-0.77	Encodes a member of protein kinase CK2.
4	203059_Δ	AT5G06558	-0.98	-0.98	Encodes a member of protein kinase CK2.
5	203060_Δ	AT5G06559	-0.77	-0.79	Encodes the catalytic subunit of the At5g06559 kinase (CK2alpha) complex in plants. The complex catalyzes the phosphorylation of α/β tubulin and γ-tubulin.
6	203061_Δ	AT5G06560	-0.98	-0.98	Encodes the catalytic subunit of the At5g06560 kinase (CK2alpha) complex in plants. The complex catalyzes the phosphorylation of α/β tubulin and γ-tubulin.
7	203062_Δ	AT5G06561	-1.17	-1.02	AT5g06561 is a kinase.
8	203063_Δ	AT5G22480	-0.58	-1.04	AT5g22480 is a kinase.
9	203064_Δ	AT5G22481	-0.58	-0.58	AT5g22481 is a kinase.
10	203065_Δ	AT5G22482	-0.58	-0.58	AT5g22482 is a kinase.
11	203066_Δ	AT5G22483	-0.58	-0.58	AT5g22483 is a kinase.
12	203067_Δ	AT5G22486	-0.77	-0.65	Encodes CK2α1b kinase (CK2α1b).

Supplementary Table S4. Significant GO term of the differentially expressed genes in F1 hybrid

Significantly up- or down-regulated genes between F1 hybrid and parents was described in Supplemental table 2.

agriGO (bioinfo.cau.edu.cn/agriGO/) was used for singular enrichment analysis(SEA) of the differentially expressed genes in the F1 hybrid.

Ontology; P = Biological process, F = Molecular function, C = Cellular component.

Significant GO term of the up-regulated genes in F1 Hybrid

GO term	Ontology	Description	Number in input list	Number in BG/Ref	FDR
GO:0010200	P	response to chitin	8	134	1.4E-08
GO:0010243	P	response to organonitrogen compound	8	166	3.7E-08
GO:1901698	P	response to nitrogen compound	8	264	8.3E-07
GO:0009611	P	response to wounding	6	217	0.00009
GO:1901700	P	response to oxygen-containing compound	12	1557	0.00019
GO:0010033	P	response to organic substance	12	2023	0.0021
GO:0009719	P	response to endogenous stimulus	11	1732	0.0022
GO:0042221	P	response to chemical	14	2853	0.0025
GO:0001071	F	nucleic acid binding transcription factor activity	11	1730	0.0003
GO:0003700	F	transcription factor activity, sequence-specific DNA binding	11	1729	0.0003

Significant GO term of the down-regulated genes in F1 Hybrid

GO term	Ontology	Description	Number in input list	Number in BG/Ref	FDR
GO:0006810	P	transport	6	2391	0.0017
GO:0051234	P	establishment of localization	6	2406	0.0017
GO:0051179	P	localization	6	2517	0.0017
GO:0044435	C	plastid part	6	1455	0.00053
GO:0044434	C	chloroplast part	6	1419	0.00053
GO:0009536	C	plastid	8	4213	0.0014
GO:0009507	C	chloroplast	8	4148	0.0014
GO:0032991	C	macromolecular complex	6	2658	0.0062
GO:0043234	C	protein complex	5	1834	0.0083
GO:0044446	C	intracellular organelle part	7	4882	0.016
GO:0044422	C	organelle part	7	4894	0.016