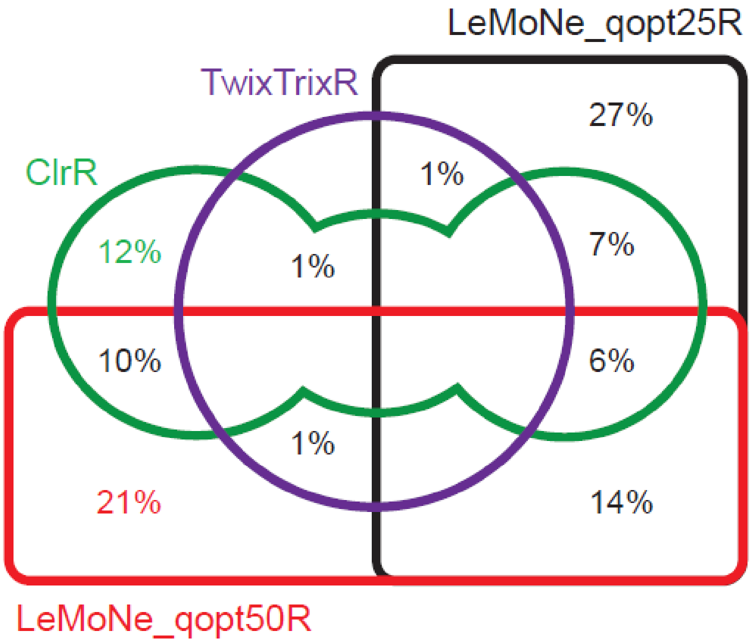
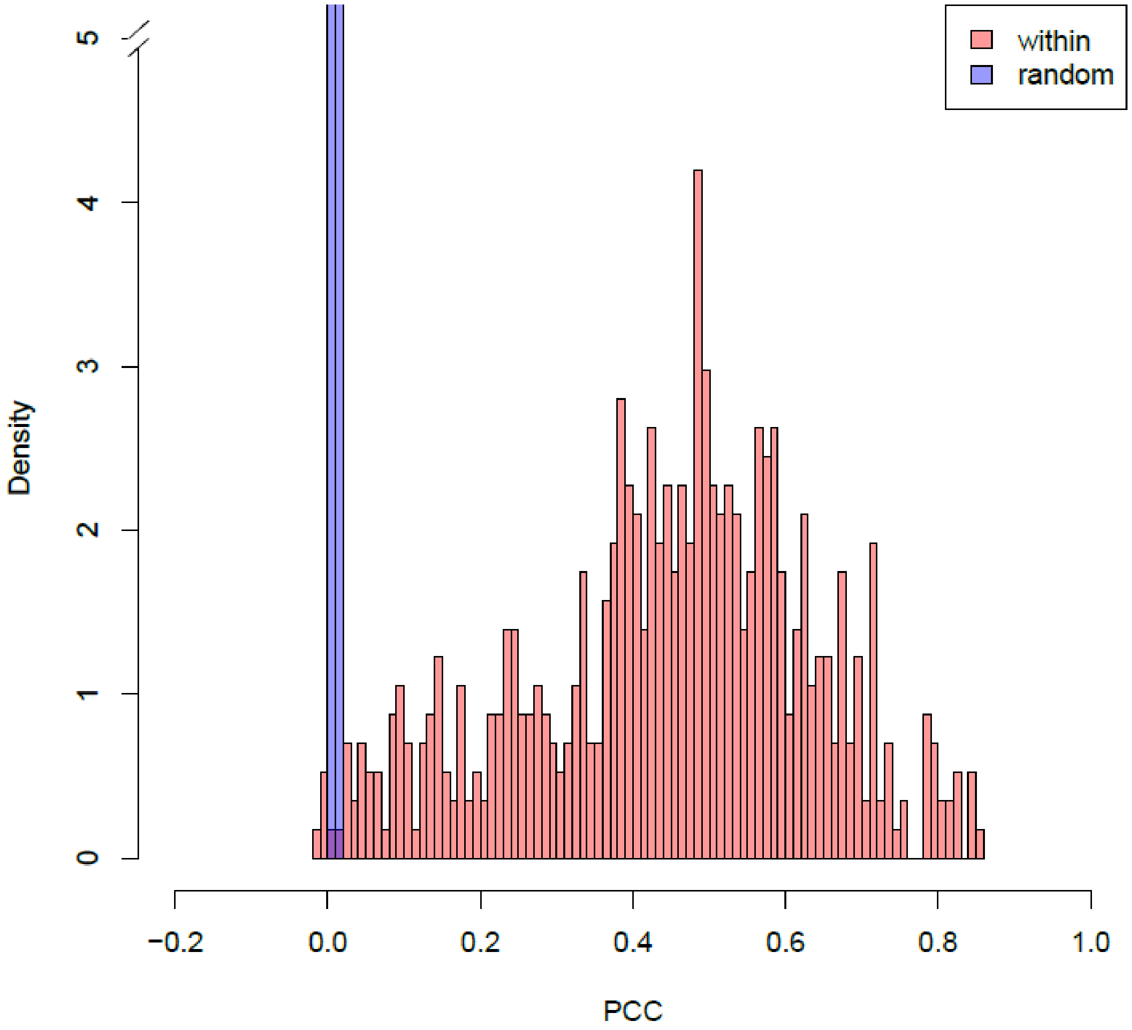
Supplemental Figures

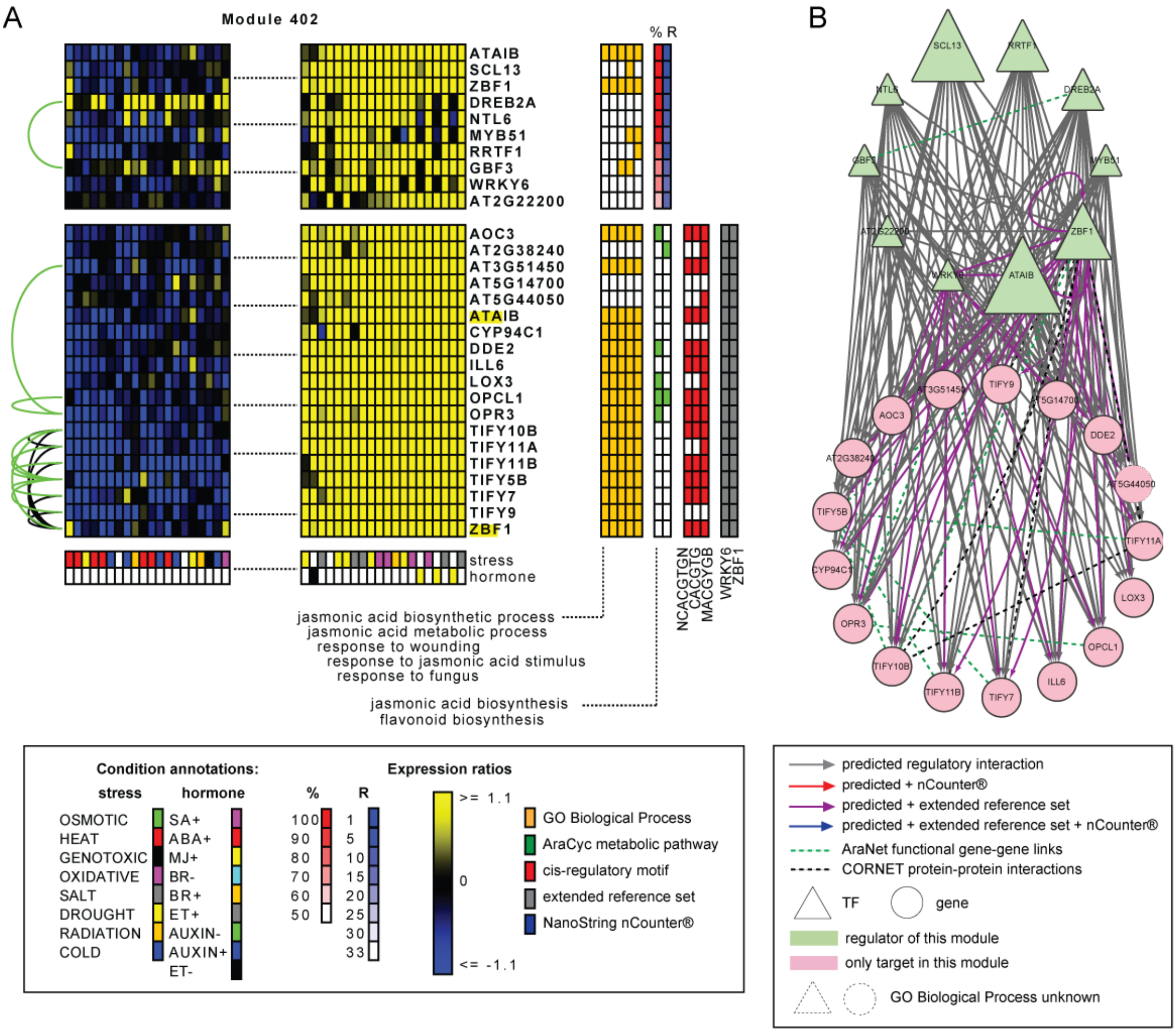


Supplemental Figure 1. Venn-diagram illustrating the percentage of the top 200,014 predictions of the rank aggregation ensemble predicted by each of the four network inference solutions and their overlap.



Supplemental Figure 2. Histograms of the Pearson Correlation Coefficient (PCC) on the expression profile ratios within modules of the abiotic stress GRN and within random modules.

pink = modules of the abiotic stress GRN (average PCC = 0.45), purple = random modules where the 10,350 genes were randomly distributed 1000 times in modules of the same size as the abiotic stress module GRN (average PCC = 0.01), Wilcoxon p-value < 2.2e-16.

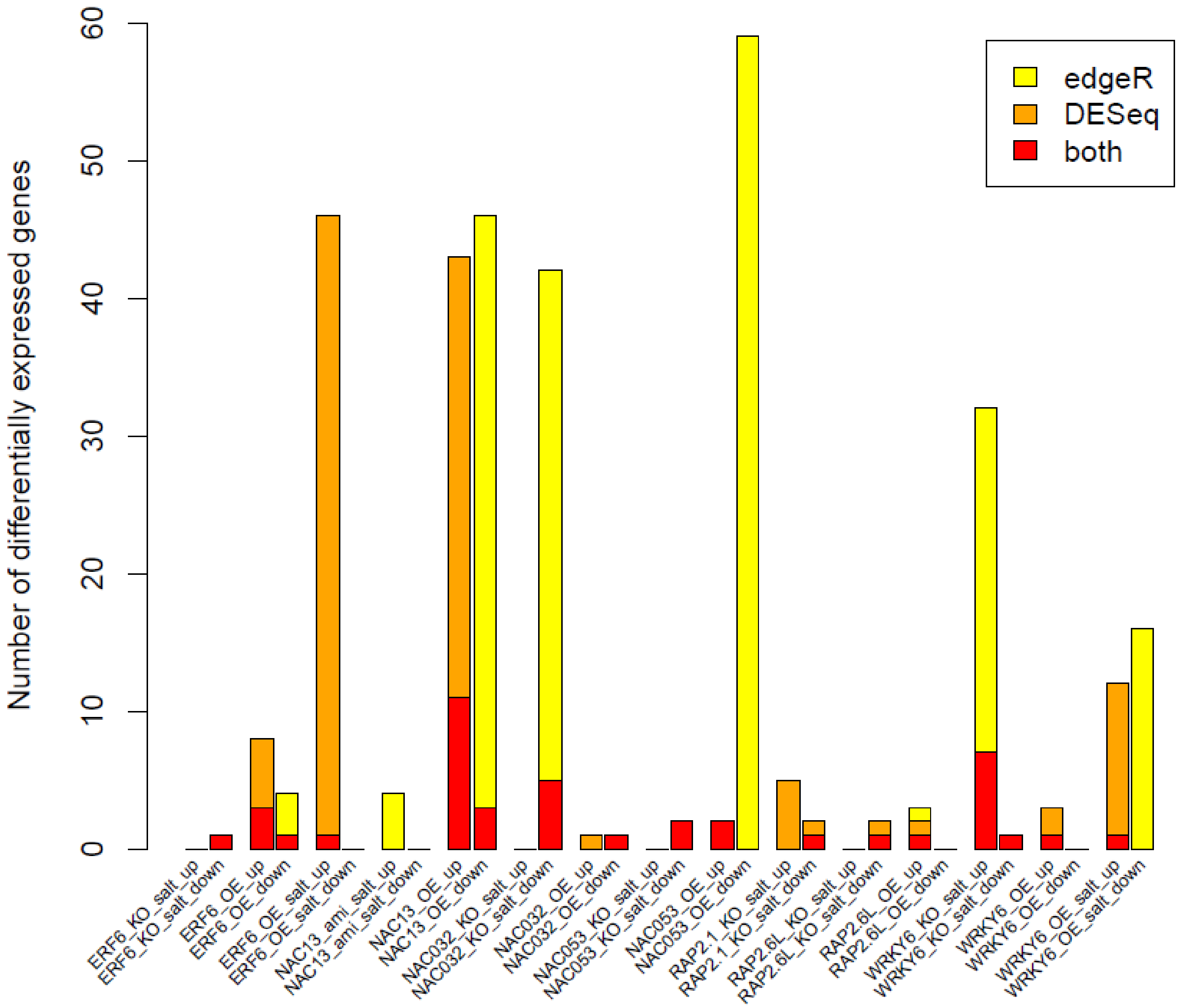


Supplemental Figure 3. Literature-based evidence for the biological relevance of the abiotic stress module GRN: module 402 was implicated in jasmonic acid biosynthesis.

Interpretation is as in **Figure 2.**

(A) Illustrations by ModuleViewer (see text) were modified to display only the 20 most up- and downregulated conditions. Upper block = $\log_2$ expression ratios of regulatory TFs ordered by rank, lower block = $\log_2$ expression ratios of coregulated target genes. Blocks on the right indicate functional coherence: top 5 BINGO GO Biological Process enrichment, top 5 AraCyc metabolic pathway enrichment, cis-regulatory motif enrichment, true positives in extended reference set and true positives from the nCounter® experiments. The regulating TFs are ranked by the percentage of the genes in the module they are predicted to regulate (%) and their average rank over the module interactions (R). It is also indicated if the TFs have the GO Biological Process annotation that is enriched in the module. Abiotic stress conditions are annotated according to abiotic stress or/and hormone treatment (SA = salicylic acid, ABA = abscisic acid, MJ = methyl jasmonate, BR = brassinosteroids, ET = ethylene, AUXIN = auxin). Arrows on the left: green = AraNet links, black = CORNET experimental protein-protein interaction links.

(B) Network illustrations by Cytoscape. The size of the regulating TF node is proportional to the average rank of this regulator in the module i.e. the importance of the TF for the module. Edges are colored if the predictions were validated by the extended reference set (purple), nCounter® experiments (red) or both (blue). Dotted node borders indicate module genes (including TFs) that lack a known GO Biological Process annotation.

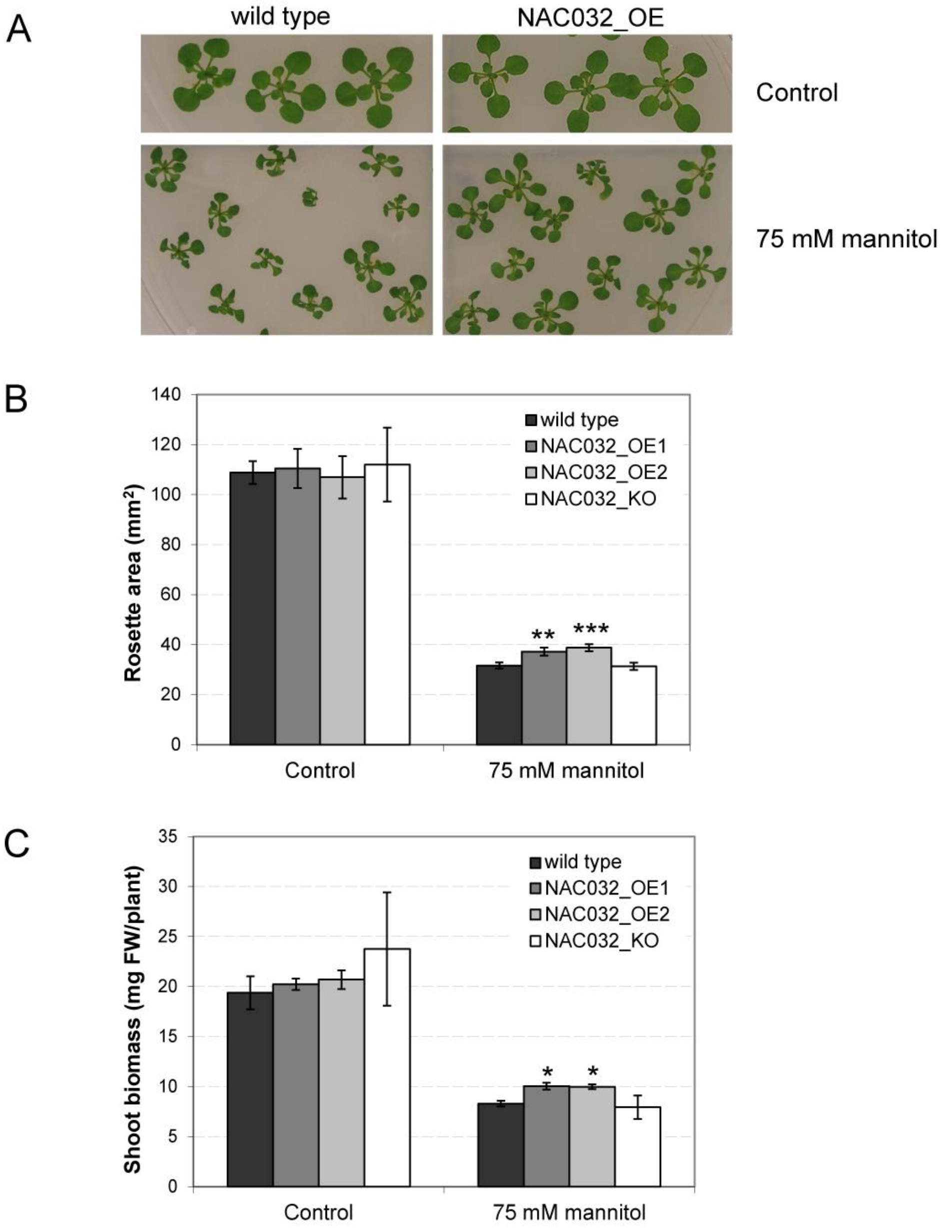


Supplemental Figure 4. Number of differentially expressed genes in the different TF perturbation experiments analyzed by nCounter® and considered statistically significant by edgeR, DESeq or both.

Transcript changes of 92 predicted target genes, 7 selected TFs and 10 housekeeping genes were quantified by nCounter® in gain- and loss-of-function mutations of 7 TFs upon 12 h salt stress treatment, in a total of 15 times three biological replicate experiments. We detected 335 times significant differential expression (FDR-corrected p-value < 0.1) in the different transgenic lines: 104 times by DESeq only, 188 times by edgeR only and 43 times by both methods. up = upregulated targets, down = downregulated targets.

Supplemental Figure 5. Visualization of all the predictions in the abiotic stress GRN for the 102 selected genes in the nCounter® experiments.

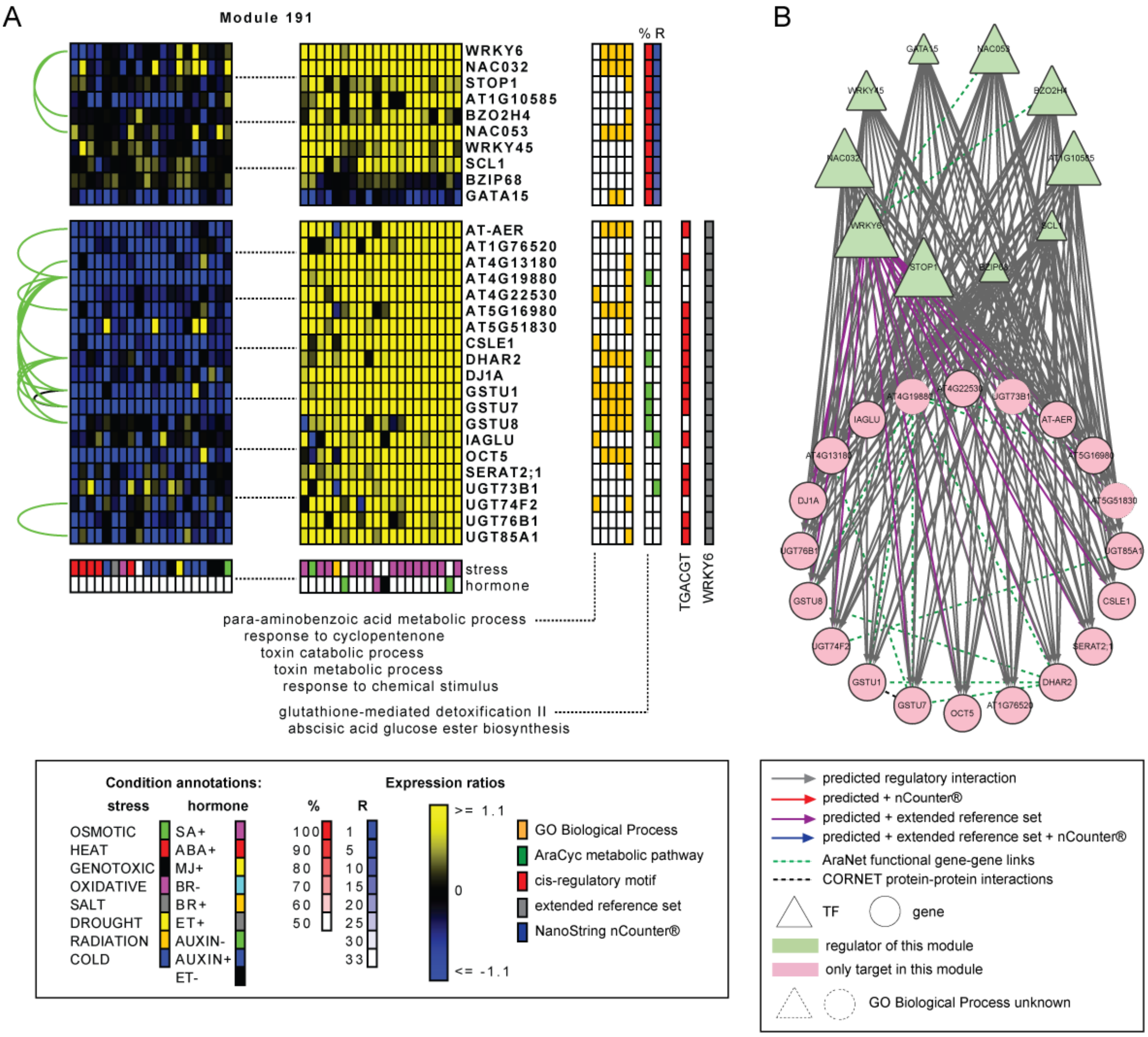
Only a limited number of regulatory interactions for the 102 selected genes in the nCounter® experiments had been reported before: validated by nCounter® experiments in this study (red), inferred in the extended reference set (green), known from the reference set of previously reported protein-DNA and regulatory interactions (blue), inferred in the extended reference set + nCounter® experiments (orange), known from the reference set + nCounter® experiments (cyan) and only predicted in this study (grey).



Supplemental Figure 6. Osmotic stress resistance phenotype of NAC032 overexpression plants.

(A) Wild-type and NAC032 overexpression (NAC032_OE) plants grown for 17 days on normal MS medium (Control) and on MS medium supplemented with 75 mM mannitol.

(B) and **(C)** Average rosette area and shoot fresh biomass (FW, fresh weight) of wild-type, NAC032_OE and NAC032 knockout (NAC032_KO) plants under control and mannitol stress conditions (n = 25 plants for control conditions, n = 75 plants for mannitol stress conditions). Error bars represent standard errors. Asterisks indicate significant differences from wild type (Student's t test; * $P<0.05$, ** $P<0.01$, and *** $P<0.001$).



Supplemental Figure 7. Module 191 was involved in detoxification processes of the oxidative stress response.

Interpretation is as in **Figure 2** and **Supplemental Figure 3.**

(A) Illustrations by ModuleViewer (see text) were modified to display only the 20 most up- and downregulated conditions. Upper block = $\log_2$ expression ratios of regulatory TFs ordered by rank, lower block = $\log_2$ expression ratios of coregulated target genes. Blocks on the right indicate functional coherence: top 5 BINGO GO Biological Process enrichment, top 5 AraCyc metabolic pathway enrichment, cis-regulatory motif enrichment, true positives in extended reference set and true positives from the nCounter® experiments. The regulating TFs are ranked by the percentage of the genes in the module they are predicted to regulate (%) and their average rank over the module interactions (R). It is also indicated if the TFs have the GO Biological Process annotation that is enriched in the module. Abiotic stress conditions are annotated according to abiotic stress or/and hormone treatment (SA = salicylic acid, ABA = abscisic acid, MJ = methyl jasmonate, BR = brassinosteroids, ET = ethylene, AUXIN = auxin). Arrows on the left: green = AraNet links, black = CORNET experimental protein-protein interaction links.

(B) Network illustrations by Cytoscape. The size of the regulating TF node is proportional to the average rank of this regulator in the module i.e. the importance of the TF for the module. Edges are colored if the predictions were validated by the extended reference set (purple), nCounter® experiments (red) or both (blue). Dotted node borders indicate module genes (including TFs) that lack a known GO Biological Process annotation.

Supplemental Tables

Supplemental Table 1. Number of interactions by source and type of experiment of the reference sets of known protein-DNA and regulatory interactions.

These reference sets contained regulatory interactions for 15% of TFs in the predictions. From the known reference set, which we compiled from literature and databases, two additional reference sets were created. The extended reference set in addition consists of all possible indirect paths between TFs and target genes, i.e. the hidden paths in the known reference set. The direct reference set comprises only the interactions for which there was evidence of both binding between a TF and its target gene and regulatory effect of a TF on transcription of its target gene.

Number of interactions	**Source**	**Type**
157	Y1H_Brady	binding
614	literature_ChIP	binding + effect on transcription
555	AtRegNet_confirmed	binding + effect on transcription
92	AtRegNet_confirmed|CORNET_TF	binding + effect on transcription
1	AtRegNet_confirmed|literature_microarray	binding + effect on transcription
30	literature_ChIP|CORNET_TF	binding + effect on transcription
15	literature_microarray|literature_ChIP	binding + effect on transcription
6102	AtRegNet_unconfirmed	effect on transcription
466	AtRegNet_unconfirmed|CORNET_TF	effect on transcription
5	AtRegNet_unconfirmed|literature_microarray	effect on transcription
35540	CORNET_TF	effect on transcription
8329	literature_microarray	effect on transcription
422	literature_microarray|CORNET_TF	effect on transcription
183111	hidden_paths_inferred_step_1	effect on transcription
396151	hidden_paths_inferred_step_2	effect on transcription
157478	hidden_paths_inferred_step_3	effect on transcription

789068	extended reference set (known + hidden)
52328	known reference set
1307	direct reference set

Supplemental Table 2. Properties of the 5% most connected TFs in the abiotic stress gene regulatory network and the 5% TFs that regulate most modules, which are defined as “hubs” in the network.

The selected TFs in the nCounter® system are also included and indicated in bold (NAC053, RAP2.6L and ERF6 are not hubs by definition). Dotted lines indicate borders of hubs based on individual targets and module targets. Out-degree = number of target genes, Out-degree module network = number of modules, TF family = TF family according to PlantTFDB, GO* = specific GO annotation for “response to stress” (R) or “response to abiotic stimulus” (X).

Locus identifier	Symbol	Out-degree	Out-degree module network	TF family	GO*
AT3G22780	TSO1	1874	89	CPP	RX
AT3G44750	HDT1	1306	53	C2H2	
AT5G61420	PMG1	1249	38	MYB	R
AT3G11020	DREB2B	1177	40	ERF	RX
AT1G22985	CRF7	1073	38	ERF	
AT4G36540	BEE2	1034	35	bHLH	
AT4G17230	SCL13	951	30	GRAS	R
AT1G62300	**WRKY6**	**936**	**23**	**WRKY**	**R**
AT1G54830	NF-YC3	901	20	NF-YC	
AT4G01460	AT4G01460	890	29	bHLH	
AT1G48000	MYB112	839	21	MYB	RX
AT2G34710	PHB-1D	809	30	HD-ZIP	RX
AT1G12860	SCRM2	796	19	bHLH	RX
AT3G15500	NAC3	784	26	NAC	RX
AT5G62020	HSFB2A	781	31	HSF	R
AT3G58120	BZIP61	779	26	bZIP	R
AT2G23320	WRKY15	775	21	WRKY	R
AT5G16540	ZFN3	763	24	C3H	
AT5G03740	HDT3	724	26	C2H2	RX
AT3G60630	LOM2	720	14	GRAS	
AT1G33240	GTL1	718	29	Trihelix	RX
AT5G22290	NAC089	709	24	NAC	
AT1G32870	**NAC13**	**706**	**25**	**NAC**	**RX**
AT2G46270	GBF3	693	20	bZIP	RX
AT2G24790	COL3	687	18	DBB	X
AT1G69780	ATHB13	685	18	HD-ZIP	
AT1G42990	BZIP60	662	23	bZIP	RX
AT2G28450	AT2G28450	655	25	C3H	
AT2G47190	MYB2	632	25	MYB	RX
AT1G07530	SCL14	629	25	GRAS	

AT1G49010	AT1G49010	628	17	MYB	RX
AT3G30260	AGL79	626	18	MIKC	
AT5G08330	TCP11	609	22	TCP	R
AT1G14410	WHY1	607	25	Whirly	R
AT5G46690	BHLH071	602	22	bHLH	
AT2G18300	HBI1	590	19	bHLH	
AT1G49560	AT1G49560	587	18	G2-like	
AT1G18570	MYB51	585	28	MYB	RX
AT1G43700	VIP1	581	28	bZIP	R
AT5G06110	AT5G06110	575	14	MYB_related	
AT1G77570	AT1G77570	570	22	HSF	
AT5G29000	PHL1	560	15	G2-like	
AT2G01060	AT2G01060	557	27	G2-like	
AT5G04340	ZAT6	551	15	C2H2	
AT4G01550	NTM2	550	9	NAC	
AT2G43000	NAC042	544	13	NAC	RX
AT4G17810	AT4G17810	537	18	C2H2	
AT1G49480	RTV1	536	19	B3	
AT1G20980	SPL1R2	536	13	SBP	R
AT3G23690	AT3G23690	532	15	bHLH	
AT3G49530	NTL6	529	28	NAC	RX
AT1G53230	TCP3	528	9	TCP	R
AT4G30935	WRKY32	525	18	WRKY	
AT3G19290	AREB2	522	12	bZIP	RX
AT3G22170	FHY3	511	9	FAR1	X
AT1G50600	SCL5	507	12	GRAS	
AT1G22590	AGL87	501	17	M-type	
AT4G18880	HSFA4A	499	17	HSF	RX
AT1G46768	**RAP2.1**	**497**	**8**	**ERF**	**RX**
AT2G16720	MYB7	497	5	MYB	RX
AT5G58010	LRL3	494	20	bHLH	
AT3G18100	MYB4R1	494	10	MYB	
AT2G21240	BPC4	492	25	BBR/BPC	
AT2G46680	HB-7	487	17	HD-ZIP	RX
AT4G14770	TCX2	486	14	CPP	
AT5G06960	TGA5	447	19	bZIP	RX
AT2G20280	AT2G20280	485	18	C3H	
AT1G20700	WOX14	484	18	WOX	
AT3G21175	ZML1	397	18	GATA	
AT1G80840	WRKY40	389	18	WRKY	RX
AT3G06740	GATA15	470	17	GATA	
AT1G77450	**NAC032**	**463**	**17**	**NAC**	
AT3G24050	GATA1	399	17	GATA	
AT2G28160	FRU	394	17	bHLH	R
AT3G06490	MYB108	387	17	MYB	RX
AT3G14180	ASIL2	383	17	Trihelix	
AT3G10500	**NAC053**	**468**	**14**	**NAC**	**RX**
AT5G13330	**RAP2.6L**	**356**	**11**	**ERF**	**RX**
AT4G17490	**ERF6**	**255**	**7**	**ERF**	**RX**

Supplemental Table 3. Known cis-regulatory motifs from the PLACE, AGRIS and ATCOECIS databases and some additional cis-regulatory motifs from literature, which are listed below, were searched in 1 kb *Arabidopsis* promoters.
Motif name, description and references are provided.

Motif	**Motif description**	**References**
TTNCGTA	NAC binding site	(Olsen et al., 2005)
WKNCGTR	NAC binding site	(Olsen et al., 2005)
TTGCGTGT	NAC binding site	(Olsen et al., 2005)
AGGGATG	NAC binding site	(Duval et al., 2002)
ACACGCATGT	NAC binding site	(Tran et al., 2004)
CTTGNNNNNCA[A,C]G	MDM motif - NAC13/NAC53	(De Clercq et al., 2013)
VGAATAW	KAN1 binding site	(Merelo et al., 2013)
CATGTG	ANAC019/ANAC055/ANAC072	(Tran et al., 2004)
T[A,C,G]CGT[A,G]	ATAF1 binding site	(Jensen et al., 2013)
TT[A,C,G]CGT	ATAF1 binding site	(Jensen et al., 2013)
CACTNNATTNTCAC	ZFHD binding site	(Tran et al., 2007b)
CACGCGC	FHY3/FAR1 binding site	(Ouyang et al., 2011)
CCAATC	GPIR1/GPIR2 binding site	(Waters et al., 2009)
GAANNTTC	HSE element (HSFA2 e.d.)	(Barros et al., 1992)
TGCCGT(7N)ACG	JUB1/NAC042 binding site	(Wu et al., 2012)
RRYGCCGT	JUB1/NAC042 binding site	(Wu et al., 2012)
KTCCAG	WRKY6 (ARE-arsenate repression element)	(Castrillo et al., 2013)
CCAATNNNNNNNNNCCACG	ERSE-I (ER stress)	(Liu and Howell, 2010)
ATTGGNCCACG	ERSE-II (ER stress)	(Liu and Howell, 2010)
GATGACGTGK	XBP1-BS (ER stress)	(Liu and Howell, 2010)
GCCG[A,C]C	ERF6 binding site	(Wang et al., 2013)

Supplemental Table 4. Known cis-regulatory motifs for the tested TFs present in 1 kb promoters of nCounter® target genes.

(A) The different cis-regulatory motifs and their description for the NAC transcription factors NAC13, NAC032 and NAC053; the DREB transcription factor RAP2.1; the ERF transcription factors RAP2.6L and ERF6; and the WRKY transcription factor WRKY6.

Motif	**Description**
AACCGACAA	DRE-like promoter motif
AACCGACAT	DRE-like promoter motif
AACCGACCA	DRE-like promoter motif
AACCGACGA	DRE-like promoter motif
AACCGACTT	DRE-like promoter motif
ACCGAC	DRE2 core found in maize (Z.M.) rab17 gene promoter; DBF1 and DBF2 bound to DRE2
ACCGAGA	DRE1 core found in maize (Z.M.) rab17 gene promoter; DRE1 was protected, in in vivo footprinting, by a protein in embryos specifically, but in leaves, was protected when was treated with ABA and drought
AGCCGACAA	DRE-like promoter motif
AGCCGACCA	DRE-like promoter motif
AGGGATG	NAC binding site
CATGTG	ANAC019/ANAC055/ANAC072
CTGACY	W box identified in the region between -125 and -69 of a tobacco class I basic chitinase gene CHN48; NtWRKY1, NtWRKY2 and NtWRKY4 bound to W box; Y=C/T
CTTGNNNNNCAMG	MDM motif - NAC13/NAC53
GACCGACAT	DRE-like promoter motif
GACCGACGT	DRE-like promoter motif
GACCGACTA	DRE-like promoter motif
GCCGCC	GCC-box, ethylene response factor binding site
GCCGAC	ERF6-specific GCC-box
GGCCGACAA	DRE-like promoter motif
GGCCGACAT	DRE-like promoter motif
GTCGAC	Preferred sequence for AP2 transcriptional activator HvCBF2 of barley; Core CRT/DRE motif; HvCBF2 bound to a (G/a)(T/c)CGAC core motif
KTCCAG	WRKY6 (ARE - arsenate repression element)
TACCGACAA	DRE-like promoter motif
TACCGACAT	Binding site of DREB1 and DREB2: Binding site of *Arabidopsis* CBF1(C-repeat/DRE binding factor); DRE-like promoter motif
TACCGACCT	DRE-like promoter motif
TACCGACGA	DRE-like promoter motif
TACCGACTT	DRE-like promoter motif
TGACT	SUSIBA2 bind to W-box element in barley iso1 (encoding isoamylase1) promoter
TGACY	W box found in the promoter region of a transcriptional repressor ERF3 gene in tobacco; Y=C/T

TGCCGACAT	DRE-like promoter motif
TGCCGACGA	DRE-like promoter motif
TGCCGACGT	DRE-like promoter motif
TGCCGACTT	DRE-like promoter motif
TTGACT	W-box promoter motif
TTGAC	W-box found in promoter of *Arabidopsis thaliana* (A.t.) NPR1 gene; Located between +70 and +79 in tandem; They were recognized specifically by salicylic acid (SA)-induced WRKY DNA binding proteins
TTGCGTGT	NAC binding site
TTNCGTA	NAC binding site
TTTGACY	WB box; WRKY proteins bind specifically to the DNA sequence motif (T)(T)TGAC(C/T), which is known as the W box; Found in amylase gene in sweet potato, alpha-Amy2 genes in wheat, barley, and wild oat, PR1 gene in parsley, and a transcription factor gene in *Arabidopsis*; Y=C/T
WKNCGTR	NAC binding site

(B) The detected cis-regulatory motifs by dna-pattern, RSA tools, in the region 1 kb upstream of translation start sites or in the intergenic region if the adjacent upstream gene is located within a smaller distance.

ERF6-specific GCC-box (ERF6), GCC-box (ERF6, RAP2.6L), DRE (RAP2.1), NAC (NAC13, NAC032, NAC053), MDM (NAC13, NAC053), W-box (WRKY6) and ARE (WRKY6). Motifs were counted separately on the D and R strand, the possible double counting of the palindromic MDM motif has been corrected for.

nCounter® gene	Motif(count) in promoter
AGD13	DRE(2)_W-box(4)_
AKR4C8	NAC(3)_W-box(4)_
ALDH7B4	NAC(4)_W-box(4)_
AT1G02270	DRE(1)_NAC(3)_W-box(1)_
AT1G04560	ARE(1)_DRE(1)_NAC(1)_W-box(5)_
AT1G13990	NAC(3)_
AT1G21790	DRE(3)_ERF6 GCC-box(1)_W-box(3)_
AT1G23710	ARE(1)_MDM(1)_NAC(5)_W-box(12)_
AT1G25400	DRE(2)_GCC-box(1)_NAC(5)_W-box(2)_
AT1G27200	DRE(2)_ERF6 GCC-box(1)_NAC(2)_W-box(3)_
AT1G28190	W-box(3)_
AT1G31750	NAC(2)_W-box(2)_
AT1G64890	ARE(1)_DRE(1)_NAC(3)_W-box(3)_
AT1G68620	ARE(1)_NAC(3)_W-box(6)_
AT1G69890	ARE(1)_DRE(1)_NAC(6)_W-box(3)_
AT1G71530	ERF6 GCC-box(1)_W-box(3)_
AT1G74870	MDM(2)_NAC(2)_W-box(3)_
AT2G21640	DRE(1)_MDM(1)_NAC(1)_W-box(2)_
AT2G35480	ERF6 GCC-box(1)_GCC-box(1)_MDM(1)_NAC(2)_W-box(2)_
AT2G42560	DRE(1)_ERF6 GCC-box(1)_NAC(4)_W-box(5)_
AT3G04000	ARE(1)_NAC(4)_W-box(5)_
AT3G25870	DRE(2)_ERF6 GCC-box(1)_NAC(1)_W-box(1)_
AT3G26910	ARE(1)_NAC(2)_W-box(10)_
AT3G27210	NAC(7)_W-box(3)_
AT3G50910	ARE(1)_NAC(8)_W-box(4)_
AT3G51890	NAC(4)_W-box(3)_
AT3G55760	DRE(1)_ERF6 GCC-box(1)_NAC(1)_W-box(3)_
AT3G55940	DRE(1)_ERF6 GCC-box(1)_NAC(1)_W-box(4)_
AT4G01870	NAC(4)_W-box(4)_
AT4G15610	DRE(2)_NAC(7)_W-box(5)_
AT4G16680	MDM(1)_NAC(3)_W-box(3)_
AT4G24160	DRE(2)_ERF6 GCC-box(1)_NAC(3)_W-box(3)_
AT4G29780	NAC(2)_W-box(6)_
AT4G31830	ARE(1)_NAC(1)_W-box(2)_
AT5G09570	ARE(1)_MDM(1)_NAC(2)_W-box(6)_
AT5G12010	NAC(3)_W-box(2)_

AT5G13200	DRE(1)_ERF6 GCC-box(1)_W-box(3)_
AT5G27760	NAC(1)_W-box(1)_
AT5G27930	NAC(1)_W-box(2)_
AT5G42570	DRE(3)_ERF6 GCC-box(1)_GCC-box(1)_NAC(2)_W-box(8)_
AT5G43450	W-box(2)_
AT5G61820	ARE(1)_DRE(1)_NAC(3)_W-box(3)_
ATACS6	MDM(1)_NAC(2)_W-box(2)_
ATADF5	DRE(2)_ERF6 GCC-box(2)_NAC(4)_W-box(4)_
BAC2	NAC(3)_W-box(6)_
BGLU11	ARE(1)_NAC(2)_W-box(3)_
CAF1A	NAC(2)_W-box(8)_
CAX3	NAC(5)_W-box(6)_
CAX7	ARE(1)_NAC(3)_W-box(2)_
CBP20	NAC(2)_
CHIC	DRE(1)_ERF6 GCC-box(1)_MDM(1)_NAC(9)_W-box(4)_
CKA2	NAC(1)_W-box(3)_
CNGC20	ARE(1)_NAC(2)_W-box(7)_
CRF6	GCC-box(1)_MDM(2)_NAC(2)_W-box(6)_
CYP81D8	MDM(1)_W-box(6)_
DGK1	W-box(2)_
DIC2	NAC(1)_W-box(3)_
EMB1624	NAC(1)_W-box(3)_
ERF6	DRE(1)_NAC(2)_W-box(3)_
GSTU24	W-box(3)_
GSTU25	NAC(2)_W-box(3)_
GSTU4	DRE(1)_NAC(3)_W-box(2)_
GSTU9	NAC(3)_W-box(4)_
HIPP26	ARE(2)_DRE(2)_NAC(1)_W-box(7)_
HSR3	MDM(2)_NAC(2)_W-box(6)_
HVA22B	NAC(3)_W-box(4)_
INT2	NAC(1)_W-box(4)_
LEA4-2	DRE(1)_NAC(5)_W-box(4)_
LSR2	ARE(1)_NAC(2)_W-box(6)_
NAC032	GCC-box(1)_NAC(5)_W-box(2)_
NAC053	ARE(2)_NAC(3)_W-box(4)_
NAC13	NAC(1)_W-box(3)_
NADP-ME1	ARE(1)_NAC(1)_W-box(1)_
NDB2	DRE(1)_MDM(1)_NAC(4)_W-box(5)_
NDB4	ERF6 GCC-box(1)_W-box(1)_
NFXL1	NAC(5)_W-box(6)_
NFYA5	ARE(2)_W-box(3)_
NSP5	ARE(1)_NAC(4)_W-box(1)_
PAP18	DRE(1)_NAC(2)_W-box(4)_
PGP4	ARE(1)_MDM(1)_NAC(6)_W-box(4)_
PMAT1	DRE(1)_NAC(2)_W-box(4)_
PPDK	ARE(1)_NAC(5)_W-box(3)_
PUB23	NAC(4)_W-box(8)_
RAP2.1	ARE(1)_DRE(3)_ERF6 GCC-box(1)_NAC(3)_W-box(1)_

RAP2.6L	ARE(1)_GCC-box(1)_NAC(2)_W-box(4)_
RD17	ARE(1)_DRE(1)_NAC(1)_W-box(4)_
RHA1A	NAC(2)_W-box(4)_
RPN1A	NAC(2)_W-box(4)_
SAP12	ARE(1)_DRE(2)_NAC(5)_W-box(3)_
SERPIN1	DRE(2)_NAC(1)_W-box(9)_
ST1	MDM(1)_NAC(1)_W-box(3)_
SUFE2	GCC-box(1)_NAC(2)_W-box(1)_
SZF1	ARE(1)_W-box(7)_
UGT73B5	ARE(1)_NAC(1)_W-box(2)_
UGT74E2	MDM(1)_NAC(5)_W-box(6)_
UGT87A2	DRE(1)_NAC(2)_W-box(9)_
WCOR413-LIKE	ARE(1)_DRE(3)_ERF6 GCC-box(1)_NAC(3)_W-box(4)_
WRKY6	NAC(1)_W-box(4)_
ZFAR1	DRE(1)_W-box(4)_
ZIFL1	DRE(1)_NAC(5)_W-box(6)_

Supplemental Table 5. ChIP and perturbed TF expression profiling experiments from literature used in the reference sets.

ChIP combined with perturbed TF expression profiling **(A)** and only perturbed TF expression profiling **(B)**.

ChIP experiments		**References**
AT1G46768	RAP2.1	(Dong and Liu, 2010)
AT1G69120	AP1	(Kaufmann et al., 2010)
AT2G20570	GLK1	(Waters et al., 2009)
AT3G22170	FHY3	(Ouyang et al., 2011)
AT4G37650	SHR	(Sozzani et al., 2010)
AT5G16560	KAN1	(Merelo et al., 2013)
AT5G60690	REV	(Brandt et al., 2012)

Microarray TF perturbation experiments		**References**
AT1G01720	ATAF1	(Jensen et al., 2008)
AT1G32640	ZBF1/MYC2	(Abe et al., 2003)
AT1G35515	MYB8/HOS10	(Zhu et al., 2005, 2010a)
AT1G43160	RAP2.6	(Zhu et al., 2010b)
AT1G46768	RAP2.1	(Dong and Liu, 2010)
AT1G52890	NAC019	(Tran et al., 2004)
AT1G69600	ZHD11	(Tran et al., 2007a)
AT2G01500	WOX6/HOS9	(Zhu et al., 2004)
AT2G23320	WRKY15	(Vanderauwera et al., 2012)
AT2G26150	HSFA2	(Nishizawa et al., 2006; Schramm et al., 2006; Ogawa et al., 2007)
AT2G30250	WRKY25	(Jiang and Deyholos, 2009)
AT2G46310	CRF5	(Rashotte et al., 2006)
AT2G47190	MYB2	(Abe et al., 2003)
AT3G15500	NAC3/ANAC055	(Tran et al., 2004)
AT3G61630	CRF6	(Rashotte et al., 2006)
AT4G11140	CRF1	(Rashotte et al., 2006)
AT4G23750	TMO3	(Rashotte et al., 2006)
AT4G25470	FTQ4/DREB1C	(Fowler and Thomashow, 2002; Vogel et al., 2005)
AT4G25480	DREB1A	(Fowler and Thomashow, 2002; Maruyama et al., 2004)
AT4G25490	DREB1B	(Fowler and Thomashow, 2002)
AT4G27410	RD26/ANAC072	(Fujita et al., 2004; Tran et al., 2004)
AT4G28110	MYB41	(Cominelli et al., 2008)
AT5G03720	HSFA3	(Yoshida et al., 2008)
AT5G05410	DREB2A	(Sakuma et al., 2006)
AT5G07690	PMG2/MYB29	(Hirai et al., 2007)
AT5G53290	CRF3	(Rashotte et al., 2006)
AT5G57390	PLT5/CHO1	(Yamagishi et al., 2009)
AT5G61420	PMG1/MYB28	(Hirai et al., 2007)

AT3G29035	NAC3/ANAC059	(Balazadeh et al., 2011)
AT5G39610	ANAC092	(Balazadeh et al., 2010)
AT2G40950	bZIP17	(Liu et al., 2007)
AT3G51960	bZIP24	(Yang et al., 2009)
AT1G42990	bZIP60	(Fujita et al., 2007)
AT1G56650	PAP1	(Dare et al., 2008)
AT3G47640	PYE1	(Long et al., 2010)
AT2G20570	GLK1	(Waters et al., 2009)
AT2G47460	MYB12/PFG1	(Stracke et al., 2007)
AT2G43000	NAC042	(Wu et al., 2012)
AT1G62300	WRKY6	(Kasajima et al., 2010; Castrillo et al., 2013)
AT3G10800	BZIP28	(Liu and Howell, 2010)
AT2G28160	FIT1	(Colangelo and Guerinot, 2004)
AT5G13330	RAP2.6L	(Liu et al., 2012)
AT4G17490	ERF6	(Moffat et al., 2012; Dubois et al., 2013; Meng et al., 2013; Sewelam et al., 2013)

Supplemental Table 6. Sequence of primers used to clone the coding sequence of *NAC032* and *ERF6*.

Primer	Sequence
NAC032-FW	AAAAAAGCAGGC TCCACCATGATGAAATCTGGGGCTGATTTGC
NAC032-RV	AGAAAGCTGGGTCTCAGAAAGTTCCCTGCCTAACC
ERF6-FW	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGCTACACCAAACGAAG
ERF6-RV	GGGGACCACTTTGTACAAGAAAGCTGGGTATCAAACAACGGTCAATTGTG

Supplemental Table 7. SALK T-DNA insertion lines used in this study as knockout lines.

Gene	KO line
NAC053	SALK_009578C
NAC032	SALK_012253
ERF6	SALK_030723
RAP2.1	SALK_092889C
RAP2.6L	SALK_051006C
WRKY6	SALK_012997

Supplemental Table 8. Accession numbers of the genes mentioned in this study.

Locus identifier	Symbol
AT1G49720	*ABF1*
AT1G63100	*AT1G63100*
AT1G01720	*ATAF1*
AT2G46510	*ATAIB*
AT4G36540	*BEE2*
AT5G04150	*BHLH101*
AT3G23210	*BHLH34*
AT3G18290	*BTS*
AT5G49450	*BZIP1*
AT1G42990	*BZIP60*
AT3G61630	*CRF6*
AT2G28160	*FIT1*
AT4G36920	*FLO2*
AT1G23020	*FRO3*
AT2G46270	*GBF3*
AT4G34590	*GBF6*
AT3G61890	*HB-12*
AT2G46680	*HB-7*
AT2G26150	*HSFA2*
AT3G17609	*HYH*
AT4G15550	*IAGLU*
AT5G11510	*MYB3R-4*
AT1G18570	*MYB51*
AT1G52890	*NAC019*
AT1G77450	*NAC032*
AT2G43000	*NAC042*
AT3G10500	*NAC053*
AT1G32870	*NAC13*
AT3G49530	*NTL6*
AT3G56980	*ORG3*
AT1G06570	*PDS1*
AT2G47460	*PFG1*
AT5G49330	*PFG3*
AT3G47640	*PYE*
AT1G46768	*RAP2.1*
AT5G13330	*RAP2.6L*
AT4G27410	*RD26*
AT1G07530	*SCL14*
AT5G18830	*SPL7*
AT2G03760	*ST1*
AT3G55980	*SZF1*
AT5G06950	*TGA2*
AT5G06960	*TGA5*
AT3G12250	*TGA6*

AT4G34138	*UGT73B1*
AT2G15490	*UGT73B4*
AT2G15480	*UGT73B5*
AT1G05680	*UGT74E2*
AT2G43820	*UGT74F2*
AT1G05560	*UGT75B1*
AT1G05560	*UGT75B1*
AT2G23320	*WRKY15*
AT5G24110	*WRKY30*
AT1G80840	*WRKY40*
AT1G62300	*WRKY6*
AT5G13080	*WRKY75*
AT1G32640	*ZBF1*
AT5G13750	*ZIFL1*
AT1G51600	*ZML2*

Supplemental Data Sets

Supplemental Data Set 1. Microarray compendium from which expression profile ratios (perturbation over control) in 199 different abiotic stress conditions were calculated.

Conditions were annotated by specific stress or hormone treatment if applicable. Control experiments are indicated. Description, database ID and reference of the studies are provided. *In Excell file online.*

Supplemental Data Set 2. The abiotic stress gene regulatory network: predictions, rank, symbolic names, individual methods and module number. *In Excell file online.*

Supplemental Data Set 3. Overview of the 572 modules of coregulated genes, their functional coherence and the biological relevance of their predicted TFs.

The number of genes in the module, their regulators (sorted by the percentage of genes they target in the module and their average rank over the module interactions), the number of genes with a known GO Biological Process annotation, the five most enriched GO Biological Process annotations, the five most enriched AraCyc metabolic pathways, whether the module genes (STRESS) and the predicted regulators (REGSTRESS) are respectively enriched or annotated with a specific GO annotation for “response to stress” (R) or “response to abiotic stimulus” (X), enriched cis-regulatory motifs (type), correspondence of the motif with respectively the module function or the predicted regulators, presence of heterodimers, true positives (TP) from the extended reference set of known and hidden protein-DNA and regulatory interactions, TP from the nCounter® experiments and additional remarks are provided. *In Excell file online.*

Supplemental Data Set 4. Overview of the 289 nCounter® experimental interactions.

The perturbed TF, target gene, experimental condition (OE = overexpression, KO = knockout, ami = amiRNA knockdown, D = DESeq, E = EdgeR, 0.05 or 0.1 significance level), individual methods of inference, final rank in the average rank ensemble, indirectly predicted by a path of length 2, known regulatory or protein-DNA interactions or their hidden paths from the extended reference set, interaction predicted in the module network, presence of relevant cis-regulatory motifs for the perturbed TF, interactions with large expression change and interactions confirmed by ChIP are indicated. Methods and rank of nCounter® interactions that were predicted by the individual reverse-engineering methods, but did not make it into the abiotic stress GRN, hence outside the top 200,014 (corresponding to rank > 73629), are indicated in grey. *In Excell file online.*

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