

Supplementary Materials for

Hotspots in the genomic architecture of field drought responses in wheat as breeding targets

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This PDF file includes:

Figs. S1 to S16
Tables S1 to S17

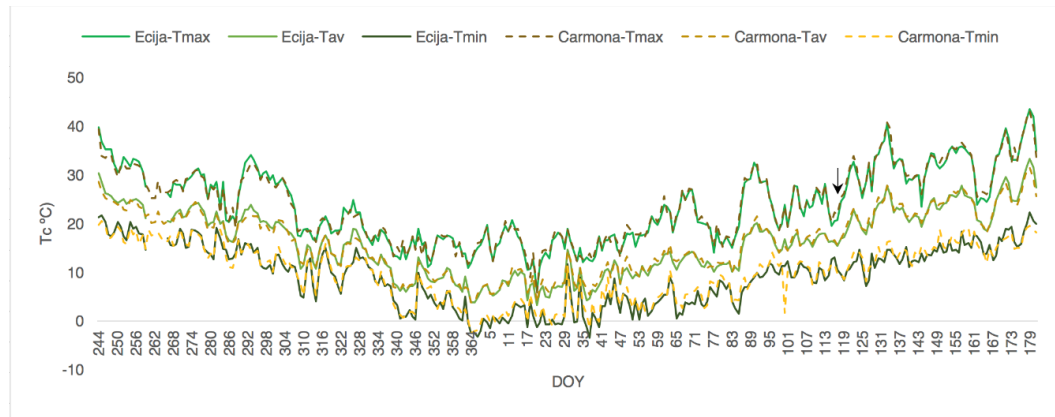
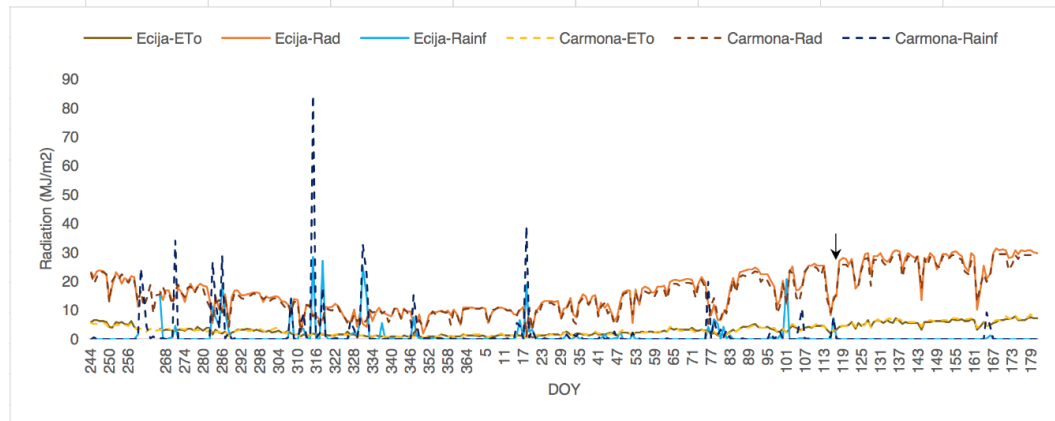
a**b**

Fig. S1. Weather characteristics of field sites used in this study. (a) Maximum (Tmax), average (Tav), and minimum (Tmin) daily temperature (°C) during the growing season at both trial sites (Carmona and Ecija). **(b)** Evapotranspiration (ETo, mm), solar radiation (MJ m⁻²), and rainfall (mm) for the same period. Arrows indicate the time of flight (on day of year (DOY) 120).

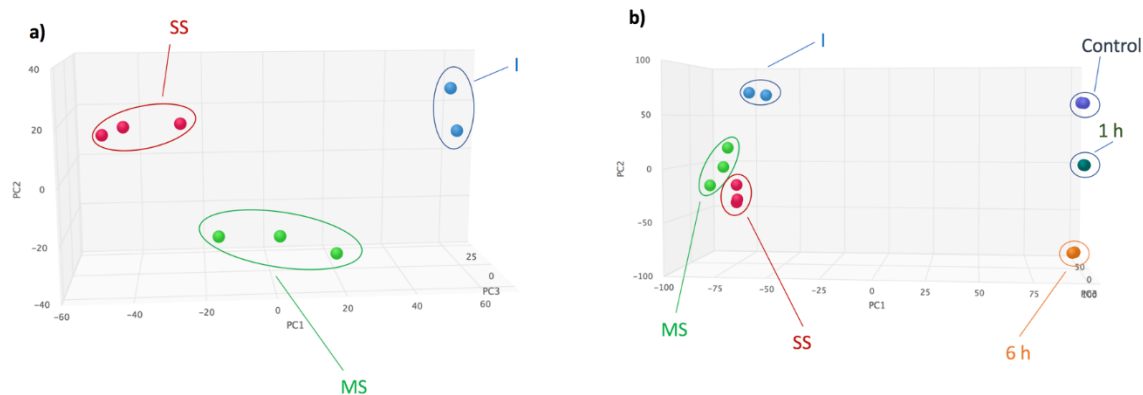


Fig. S2. Principal Component Analysis (PCA) of RNA-Seq data. (a) 3D PCA of RNA-Seq samples from this study. An interactive view can be accessed at http://galactus.uma.es/galvez/triticum/PCA3D_CS_best_pAdj.html (b) Integrated analysis of samples from this study and the previously published work on PEG-induced drought in wheat seedlings (SRA SRP04540; Liu et al. 2017). SS: Severe stress; MS: mild stress; I: Irrigated; 1 h: one hour PEG stress; 6 h: 6 h PEG stress. An interactive view can be accessed at http://galactus.uma.es/galvez/triticum/PCA3D_CS_shock_best_pAdj.html

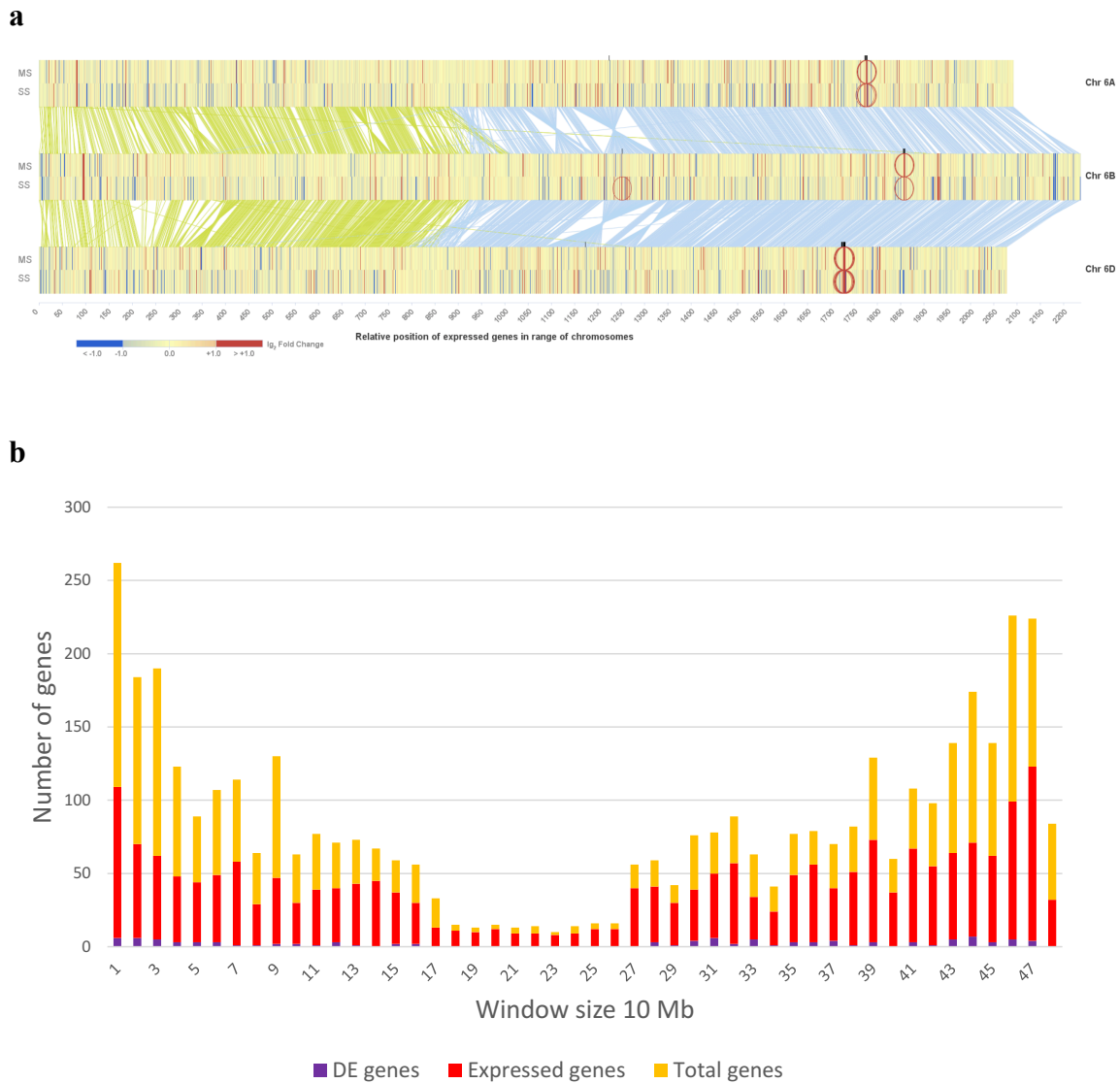


Fig. S3. Physical distribution of DE genes in group 6 chromosomes. (a) Gene expression map of differentially expressed genes under field drought conditions on group 6 chromosomes. Red circles indicate the physical position of *Dehydrin* genes. Green lines connect short arm homeologs, blue lines connect the long arm homeologs. MS: mild stress; SS: severe stress. **(b)** Physical position of DE HC on chromosome 6D. Expressed genes (red), DE genes (purple) and total genes (yellow) are shown per 10 Mb window.

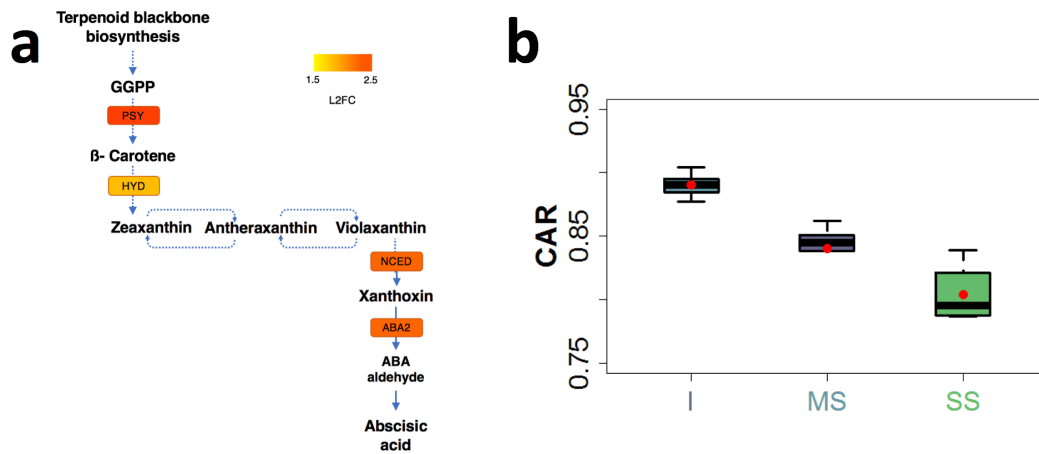


Fig. S4. Transcriptional changes reflect remote sensing physiological data. (A)

Response of genes in the carotenoid biosynthesis pathway to drought stress.

Overexpressed genes are shown in orange. **(B)** Chlorophyll Absorption Region (CAR) remote sensing trait corresponding to the three water status levels analyzed (I: irrigated; MS: mild stress; SS: severe stress). Boxplots include the median interquartile range and means (red dot).

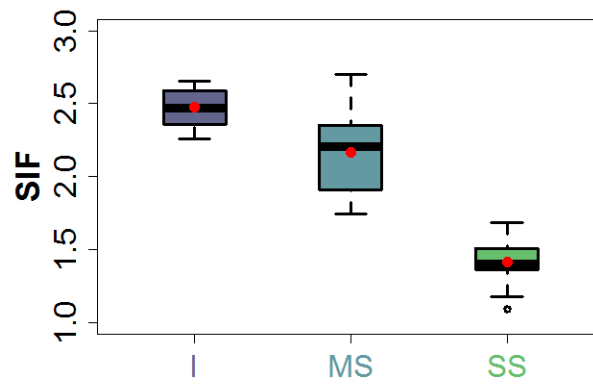


Fig. S5. Solar-induced chlorophyll Fluorescence (SIF) remote sensing trait. Boxplots include the median (bold horizontal line), 25-75 inter-quartiles range and means (red dots). Irrigated (I), mild stress (MS) and severe stress (SS).

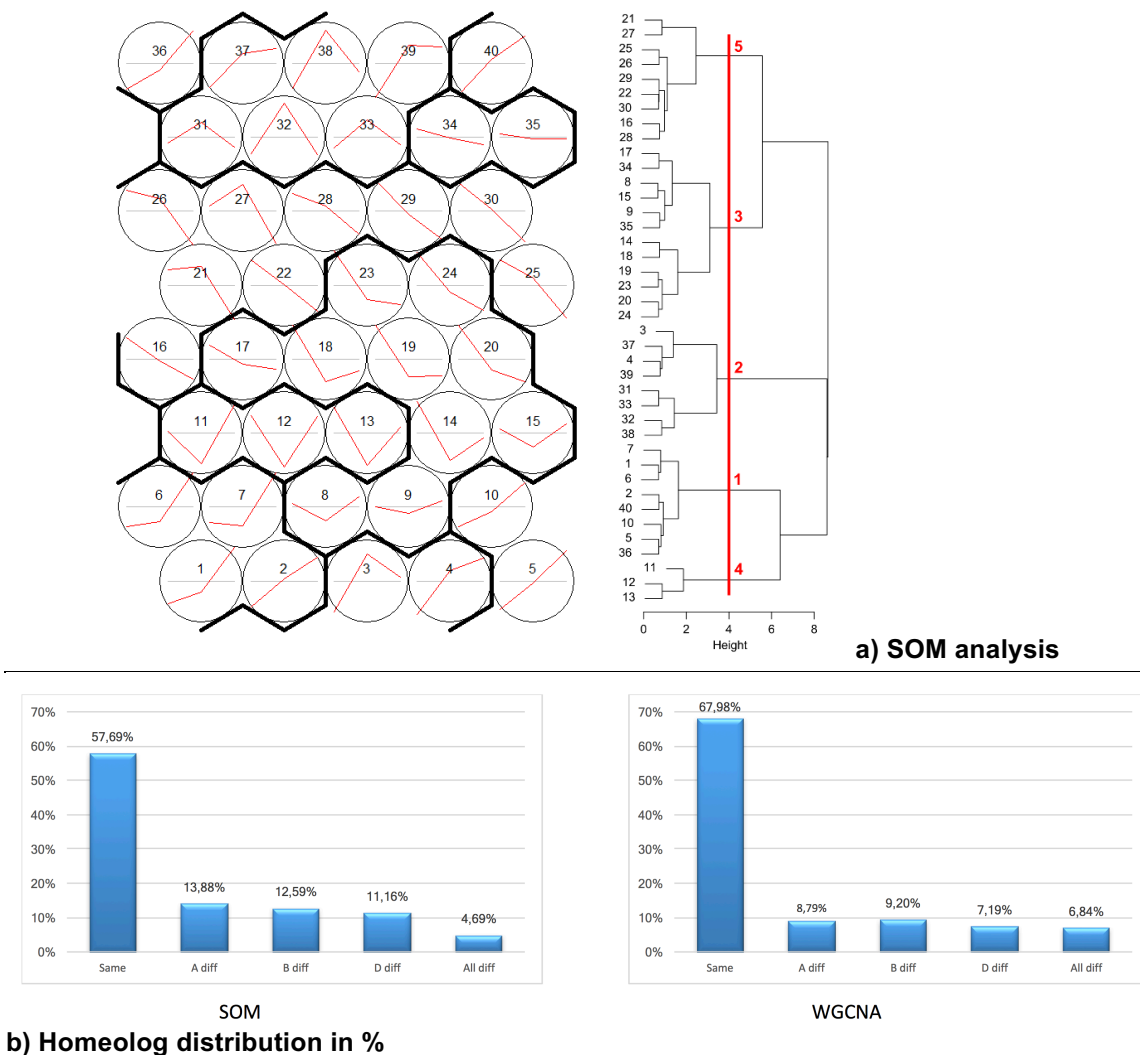


Fig S7. Self-organizing map modules. (a) SOM genes classified into 40 main patterns with a hierarchical organization which defines the five main SOM modules used in the analyses. (b) Distribution of homeologs in the five SOM modules (left) and in the 19 WGCNA modules (right). Left-hand bar shows the percentage of homeolog triads that are assigned to the same module; middle bars show the percentage of homeologs where one gene of the triad is assigned to a different module; right-hand bar show the percentage of homeolog triads where all genes are assigned to a different module.

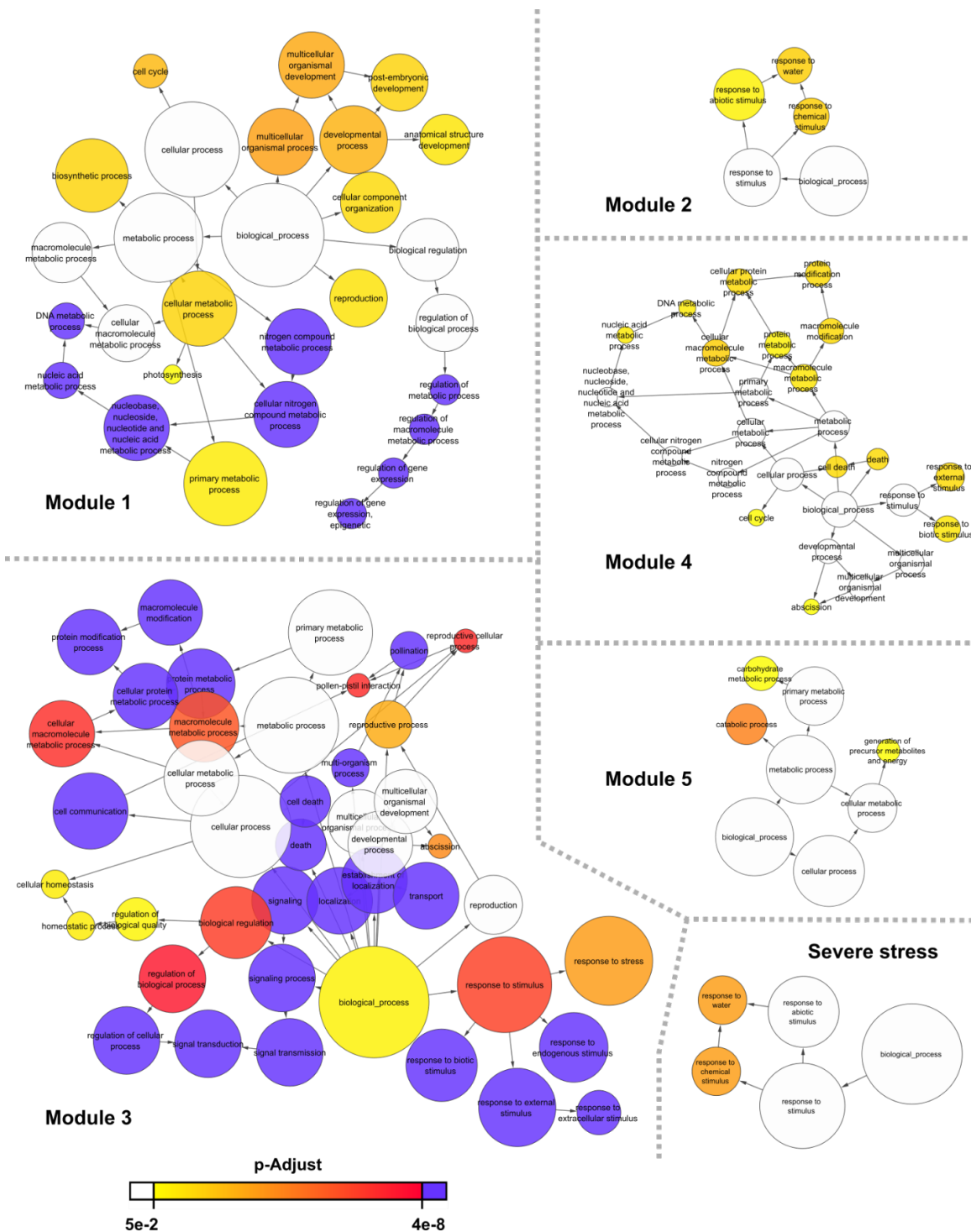


Fig. S8. GO Slim terms enrichment analysis of the five SOM modules and for all DE genes under severe stress. The size of a node is proportional to the number of genes annotated).

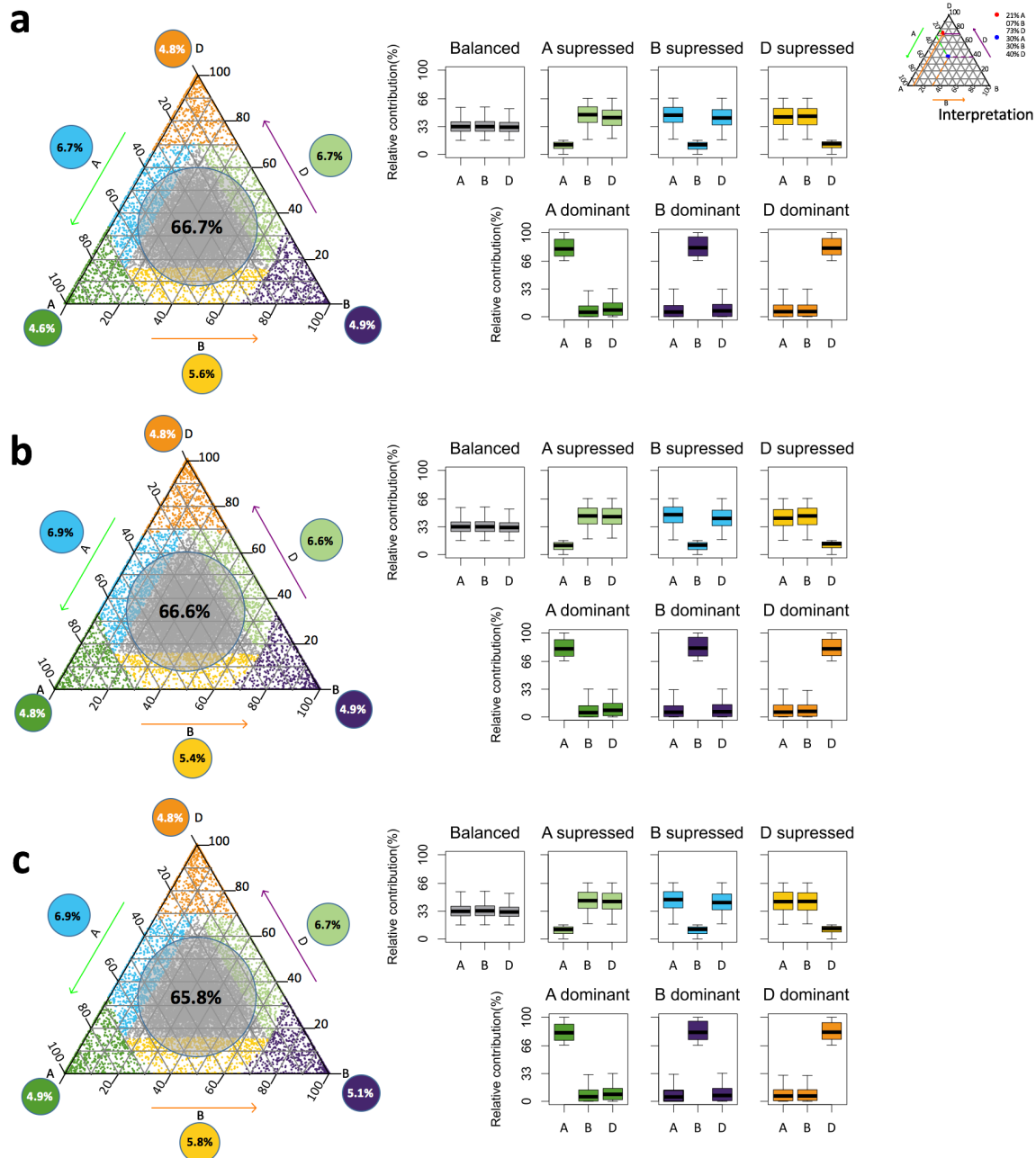


Fig. S9. Relative homoeolog expression bias in genome triads (TPM>0.5). (a) irrigated samples (13575 triads); (b) mild stressed samples (13904 triads), (c) severe stressed samples (13517 triads). Homoeolog triads are classified into 7 categories: (A, B, D)-dominant when the expression of a single homoeolog exceeds the 66%; (A, B, D)-suppressed when the expression of a single homoeolog is lower than 16%; and Balanced in any other case. Each triad is located in a spot corresponding to the percentage contribution of its constitutive genes, as shown in the Interpretation panel.

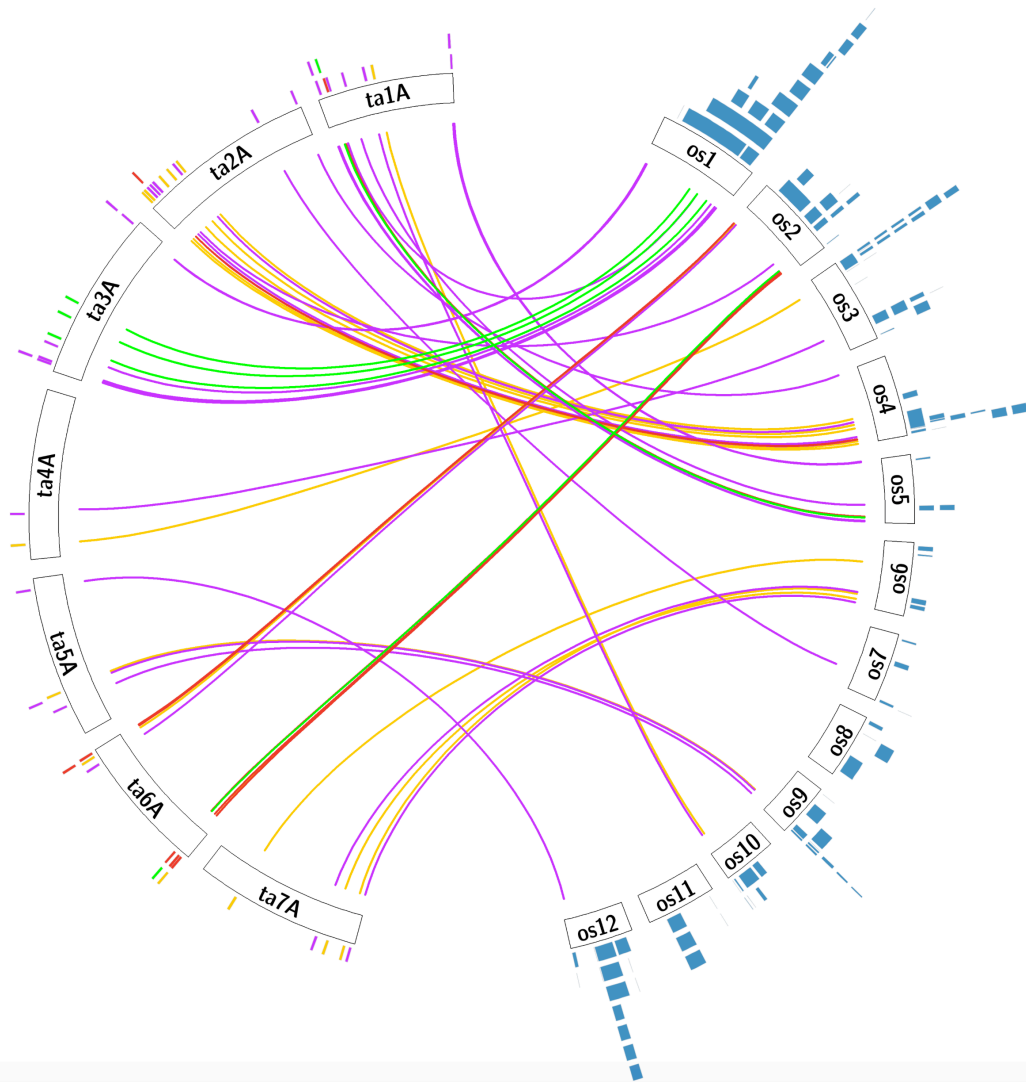


Fig. S10. Circos plot representing the relationship between wheat CoDReGs (ta, left) and rice drought QTL intervals (os; right). The seven chromosomes of the A genome are represented on the left-hand side and the twelve rice chromosomes are represented on the right-hand side. The CoDReGs location in the A subgenome is shown on the left of the wheat chromosomes. On the rice genome, the 111 QTL intervals related to drought-tolerance extracted from QTARO database (Yonemaru et al. 2010) are shown in blue. The clusters related to the SOM module 1 are marked in red; green for module 2; purple for module 3 and orange for module 5.

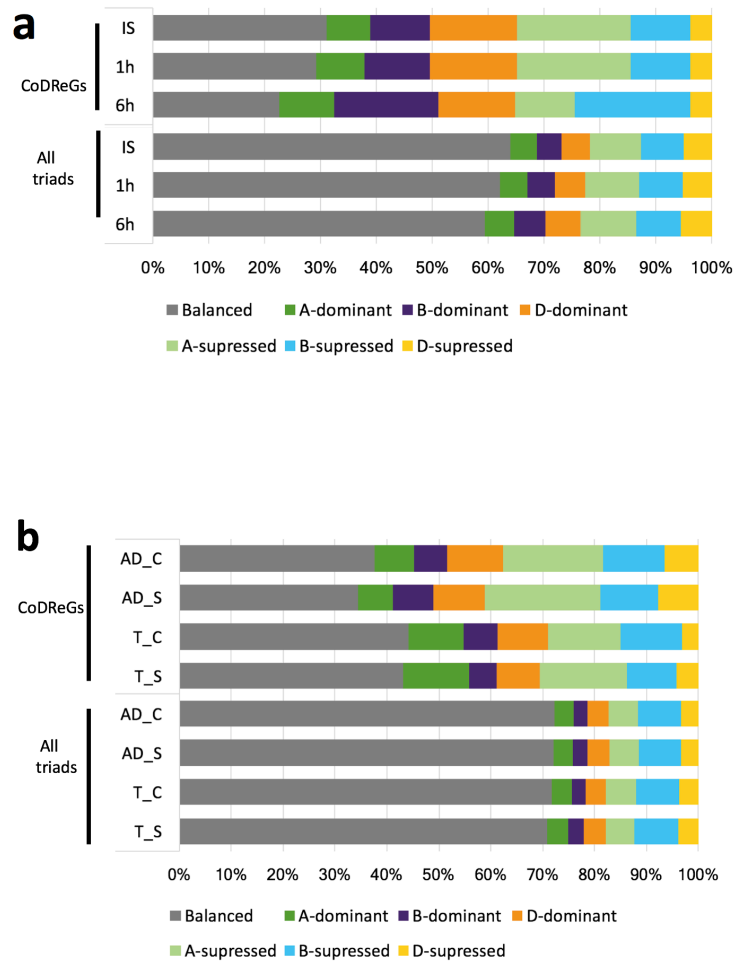


Fig. S11. Homeolog gene expression bias (corresponding to the seven classes categories described in Fig. S13) across the genome and CoDReGs, and the stress levels in **(a)** drought shock experiment in seedlings (Liu et al. 2017) and **(b)** rain shelter experiment in flag leaf (Ma et al. 2017).

K-segment	EKKGIMDKIKEKLPG
Inter-pattern	EDDGQGR
Y-segment	VDEYGNP
S-segment	SSSSS+

proteins have been truncated to show the initial amino acid sequence. The left side of the figure shows the chromosome assignment of each dehydrin.

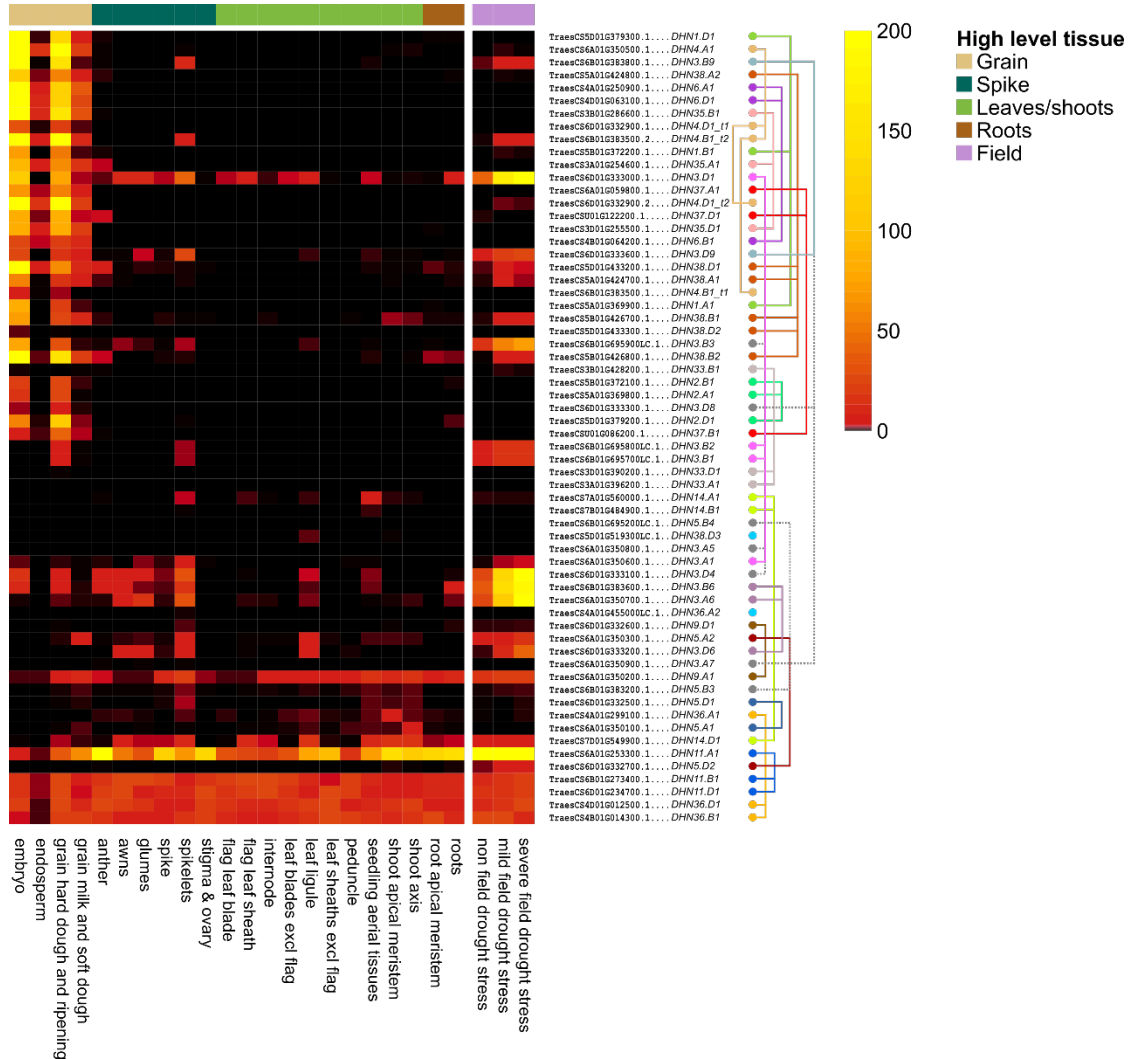


Figure S13. Dehydrin genes clustering. Figure is based on expression values of all available experiments at www.wheat-expression.com (left-clustering). The range of expression shown is 0 to 200 TPM; any TPM>200 has been set to 200. Columns indicate high level tissue grouping; the three non-clustered columns on the right represent the field samples. RefSeq1 gene IDs and their corresponding proposed gene names are shown. Colored lines connect homoeologs.

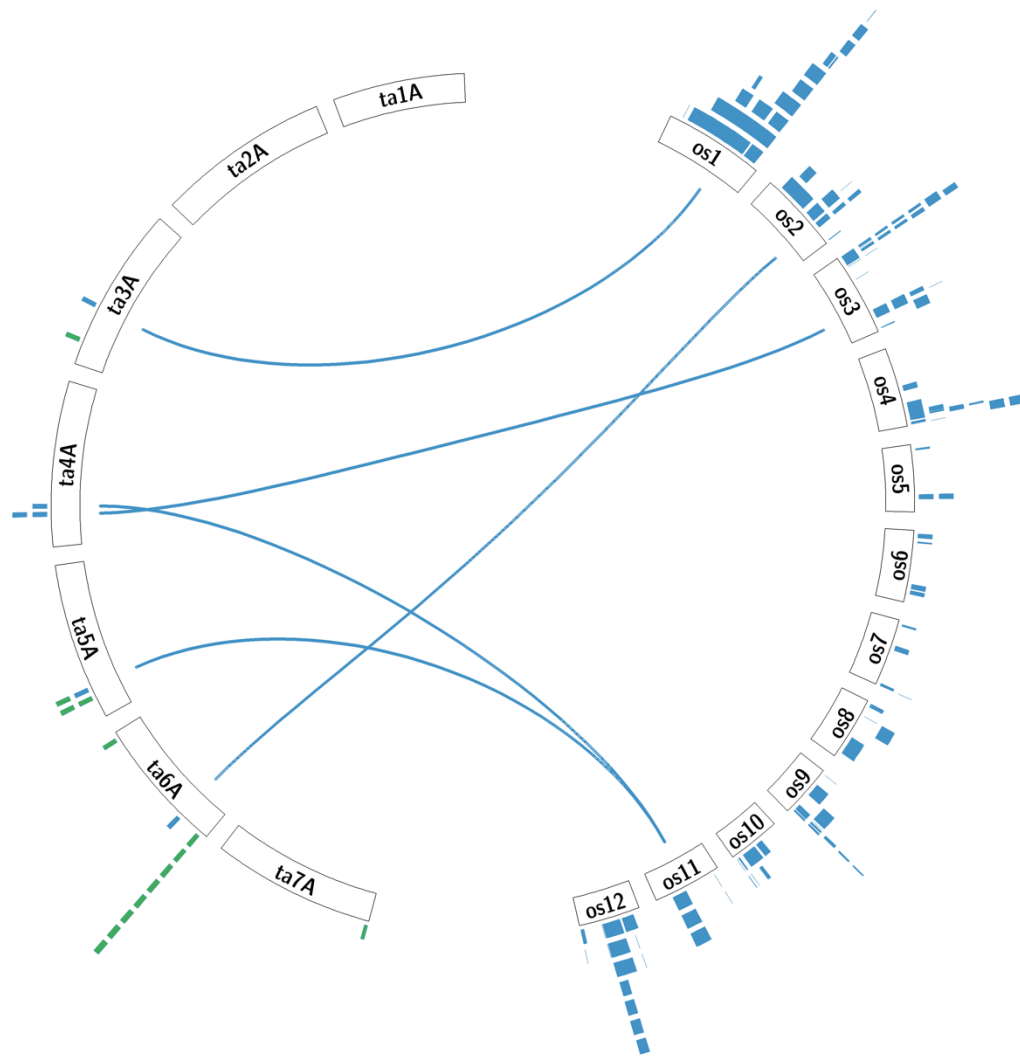


Figure S14. Syntenic relationships between dehydrin genes of wheat (ta; left) and rice (os; right). The seven chromosomes of the A genome are represented on the left-hand side and the twelve rice chromosomes are represented on the right-hand side. Ortholog (6) and non-ortholog (14) DHN genes located in wheat A subgenome are shown in blue and green, respectively. On the rice genome, the 111 QTL intervals related to drought-tolerance extracted from QTARO database (Yonemaru et al. 2010) are shown in blue. The blue lines between the two genomes represent the syntenic relationships of the DHNs.

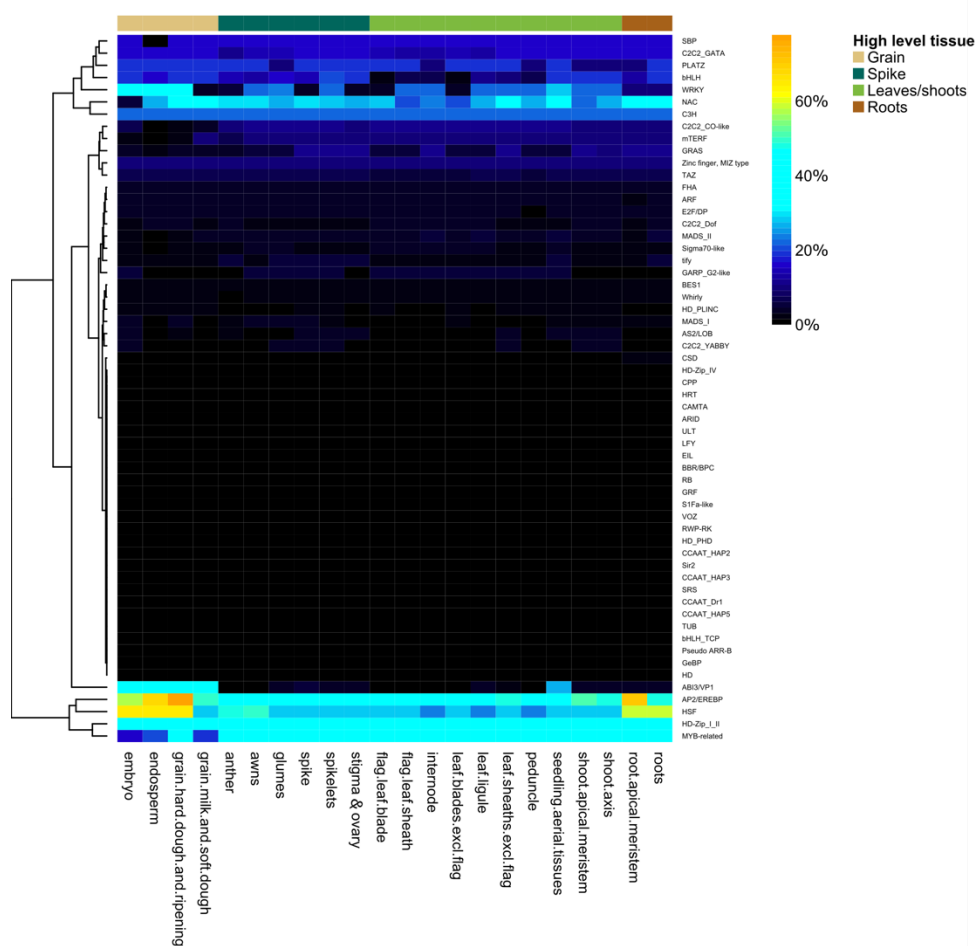


Fig. S15. The regulation of dehydrins by transcription factor families. The transcription factors which target dehydrins were predicted by genie3 analysis using the top 1 million edges (Ramírez-González et al. 2018). The percentage of high-confidence dehydrins regulated by each TF family are shown. Each row represents one TF family, with each column representing one tissue.

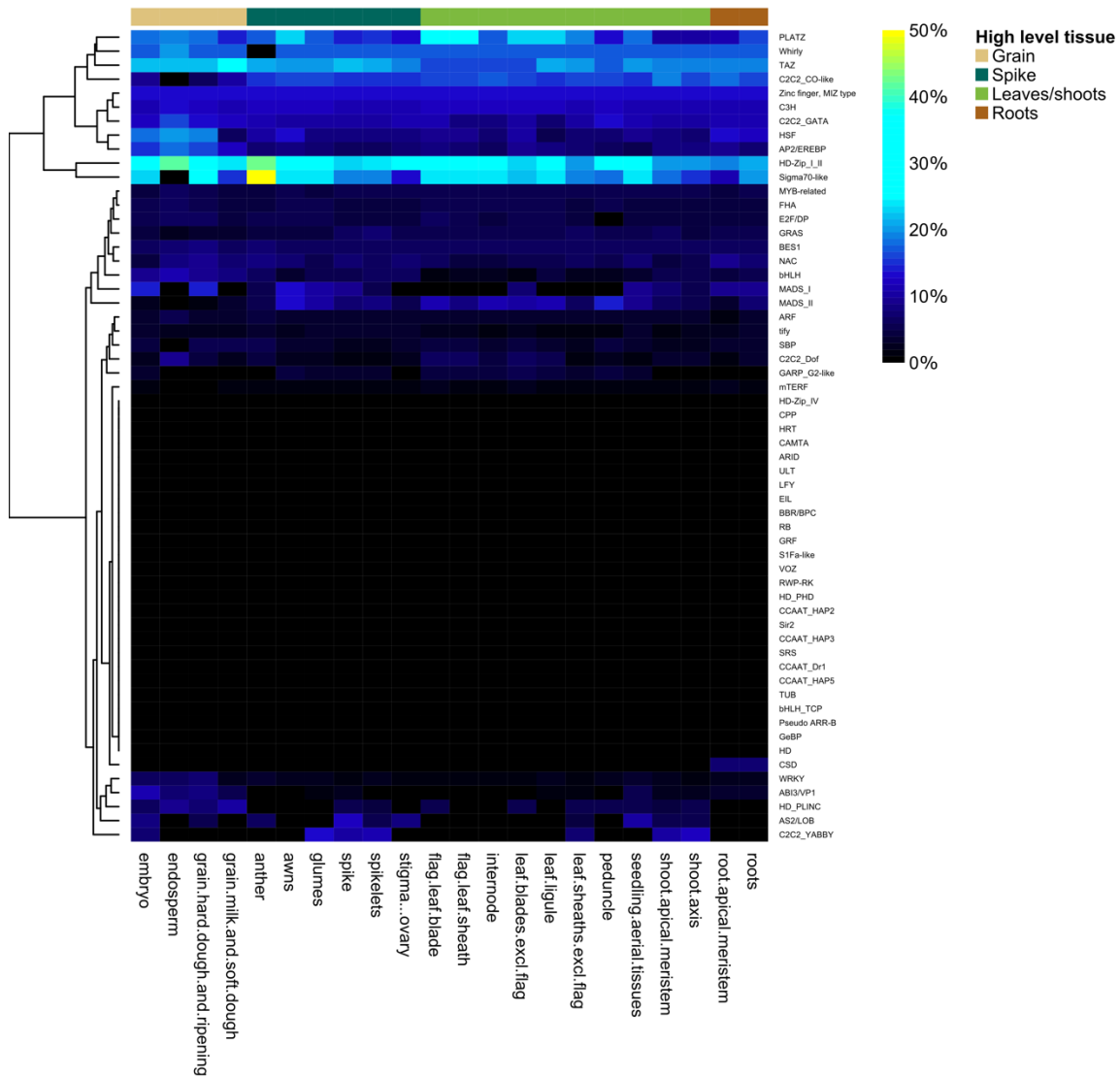


Fig. S16. TFs predicted to regulate dehydrins. The percentage of TFs which are predicted to regulate dehydrins by genie3 analysis using the top 1 million edges (Ramírez-González et al. 2018). Each row represents one TF family, with each column representing one tissue. Only TFs expressed ≥ 0.5 TPM were included in the analysis.

Table S1.

Analysis of variance results for remote sensing traits.

	Mean $\pm$ Stdev			ANOVA	
	<i>I</i>	<i>MS</i>	<i>SS</i>	F value	p-value
CWSI	0.13 $\pm$ 0.040	0.51 $\pm$ 0.074	0.64 $\pm$ 0.060	369.5	<2e-16
SIF	2.47 $\pm$ 0.124	2.16 $\pm$ 0.300	1.41 $\pm$ 0.146	174.5	<2e-16
TCARI₁₅₁₀	-0.25 $\pm$ 0.025	-0.15 $\pm$ 0.014	-0.10 $\pm$ 0.004	86.49	6.52e-06
CAR	0.89 $\pm$ 0.009	0.84 $\pm$ 0.022	0.80 $\pm$ 0.024	27.18	2.27e-05
PRI	-0.61 $\pm$ 0.040	-0.53 $\pm$ 0.040	-0.51 $\pm$ 0.030	11.71	0.00124

Table S2.

Differentially expressed (DE) and total gene distribution along chromosomal compartments (IWGSC 2018)¹².

	DE genes (HC/LC)	%	Total genes (HC/LC)	%
R1/R3	526 (471/55)	53.7 (48.1/5.6)	133,177 (57,116/76,061)	49.4 (21.2/28.2)
R2a/R2b	420 (380/40)	42.9 (38.8/4.1)	109,335 (46,582/62,753)	40.6 (17.3/23.3)
C	33 (28/5)	3.4 (2.9/0.5)	26,961 (7,092/19,869)	10.0 (2.6/7.4)
Total	979 (879/100)	100 (89.8/10.2)	269,473 (110,790/158,683)	100 (41.1/58.9)

Table S3.

Gene enrichment analysis in DE genes, ABD clusters, CoDReGs, dehydrin (DHN) and aquaporin (AQP) gene families.

	DE genes	Genes in CoDReGs	DE genes in CoDReGs	DHNs	DE DHNs*	AQPs	DE AQPs*	Wheat genome
Total N°. of genes R1/R3	526	647	45	48	12	73	4	133,177
Total N°. of genes R2a/R2b/C	453	268	8	12	1	89	4	136,296
	P = 0.007	P = 0	P = 2e-6	P = 0.001	P = 0.007			

P: Significant exact Fisher test P values are indicated for significant tests. Gene decrease is shown with a red cell, gene enrichment is shown with a blue cell.

*By any bioinformatic pipeline.

Table S4.

DGE analysis significance parameters for differentially expressed Glutamine Synthetase genes, Photosystem I genes, the Photosystem II regulator PsbQ and UDP-glucose-6-dehydrogenase. Significant values ($|\log_2FC|$, $\beta|>1.0$ and p-Adjust, Q-value<0.05) have been highlighted.

Gene name	Description	Field								PEG shock			
		Mild stress				Severe stress				One hour		Six hours	
		Kallisto		STAR		Kallisto		STAR		STAR		STAR	
		Beta	Q-Val	L2FC	p-Adj	Beta	Q-Val	L2FC	p-Adj	L2FC	p-Adj	L2FC	p-Adj
TraesCS6D01G383600L.C.2	Glutamine synthetase GS1c: DQ124211			-1.23	0.00			-1.03	0.00	-0.35	0.00	-0.39	0.00
TraesCS6D01G383600L.C.1	Glutamine synthetase GS1c: DQ124211	-0.88	0.01	-1.23	0.00	-0.75	0.02	-1.03	0.00	-0.35	0.00	-0.39	0.00
TraesCS6B01G500000L.C.1	Oxygen-evolving enhancer protein 3-2, chloroplastic. Photosystem II regulator PsbQ	1.06	0.22	1.32	0.11	1.61	0.00	1.99	0.00	-0.11	0.90	2.01	0.00
TraesCS3B01G667200L.C.1	Photosystem I iron-sulfur center	0.76	0.79	0.55		1.37	0.04	0.63		-1.06		0.21	0.90
TraesCS5A01G218200L.C.1	Photosystem I iron-sulfur center	-4.86	0.00			1.71	0.42			-0.22		-0.15	
TraesCS5A01G394900.1	UDP-glucose 6-dehydrogenase: UDPg	-0.48	1.00	-0.7	0.71	-1.24	0.25	-1.53	0.01	3.05	0.00	2.35	0.00
TraesCS5B01G399800.1	UDP-glucose 6-dehydrogenase: UDPg	-0.79	0.97	-0.8	0.64	-1.71	0.08	-1.97	0.00	3.37	0.00	1.50	0.00
TraesCS5D01G404300.1	UDP-glucose 6-dehydrogenase: UDPg	-0.83	1.00	-0.8	0.71	-1.75	0.24	-1.93	0.01	3.19	0.00	1.01	0.00

Table S5.

Comparative abundance of miRNA families between control, and stress-applied samples.

I: irrigated control; MS: mild stress; SS: severe stress.

	I	MS	SS
miR1117	16	14	9
miR1118	0	6	3
miR1120	10	9	11
miR1121	4	2	2
miR1122	24	39	33
miR1125	0	0	1
miR1127	32	17	21
miR1128	4	2	6
miR1130	43	59	55
miR1131	1	1	3
miR1135	7	3	6
miR1136	0	4	4
miR1137	4	15	12
miR1139	2	0	0
miR1436	22	41	38
miR1439	4	2	3
miR166	4	4	1
miR167	9	9	6
miR2275	2	2	2
miR397	0	0	3
miR398	6	3	3
miR437	1	0	1
miR5049	33	64	30
miR5062	4	4	5
miR5067	0	0	2
miR5070	3	2	0
miR5086	1	1	0
miR5174	4	2	5
miR5175	5	1	1
miR5180	5	4	1
miR5181	11	17	6
miR5200	15	0	3
miR530	15	11	11
miR5568	2	4	2
miR6197	4	3	8
miR9654	0	3	0
miR9666	1	0	0
miR9668	0	7	1
miR9673	1	1	4
miR9772	0	0	2
miR9776	1	0	0
miR9781	0	0	1
miR9782	3	3	3
miR9783	2	3	7

Table S6.

Gene targets of irrigated and drought stress-specific miRNAs.

miRNA	Target Transcript ID	Functional Annotation
Irrigated sample-specific miRNA targets		
miR1139-5p	TraesCS1B01G002300.1	Disease-resistance protein (TIR-NBS-LRR class)
miR1139-5p	TraesCS1A01G006700.1	Disease-resistance protein (TIR-NBS-LRR class) family
miR1139-5p	TraesCS1B01G002300.3	NBS-LRR-like resistance protein
miR1139-5p	TraesCS1B01G002300.2	Disease-resistance protein (TIR-NBS-LRR class)
miR9776-5p	TraesCS3B01G141300.1	ATP-dependent RNA helicase
Severe stress-specific miRNA targets		
miR397-5p	TraesCS1D01G044300.1	Laccase
miR397-5p	TraesCS1A01G043900.1	Laccase
miR397-5p	TraesCS1B01G056900.1	Laccase
miR397-5p	TraesCS1D01G283000.1	Laccase
miR397-5p	TraesCS1D01G044600.1	Laccase
miR397-5p	TraesCS2D01G209400.1	Laccase
miR397-5p	TraesCS3B01G393000.1	Laccase
miR397-5p	TraesCS3D01G354400.1	Laccase
miR397-5p	TraesCS3A01G360600.1	Laccase
miR397-5p	TraesCS2B01G233500.1	Laccase
miR397-5p	TraesCS2D01G209800.1	Laccase
miR397-5p	TraesCS2B01G233700.1	Laccase
miR9772-5p	TraesCS6D01G071900.1	F-box family protein-like protein
miR9772-5p	TraesCS3B01G076500.1	F-box family protein
miR9772-5p	TraesCS3A01G015900.1	F-box family protein
miR9772-5p	TraesCS3D01G013200.1	F-box family protein
miR397-3p	TraesCS5D01G435800.1	Aldehyde oxidase, putative
miR397-3p	TraesCS5A01G427700.1	Aldehyde oxidase, putative
miR397-5p	TraesCS4A01G096400.1	Laccase
miR397-5p	TraesCS4D01G208900.1	Laccase
miR9772-5p	TraesCS6D01G070800.1	F-box domain containing protein, expressed
miR9772-5p	TraesCS6D01G070800.2	F-box domain containing protein, expressed
miR9772-5p	TraesCS6D01G071500.2	F-box family protein
miR9772-5p	TraesCS6A01G073200.1	F-box family protein
miR9772-5p	TraesCS6B01G098200.1	F-box family protein
miR9772-5p	TraesCS6D01G071500.1	F-box family protein
miR9772-5p	TraesCSU01G133400.1	F-box family protein
miR9772-5p	TraesCSU01G042700.1	F-box family protein
miR9772-5p	TraesCSU01G217400.1	F-box family protein
miR9772-5p	TraesCS4A01G375300.1	Mitochondrial metalloendopeptidase OMA1
miR9772-5p	TraesCS3B01G075900.1	F-box family protein
miR397	TraesCS7A01G047900.1	Phosphatase 2C family protein, putative
miR397	TraesCS5B01G377800.1	Cysteine protease
Targets of miRNAs common in irrigated and mild stress		
miR5200-3p	TraesCS3A01G001500.1	Protein kinase
miR5200-3p	TraesCS3B01G000400.1	Protein kinase
Targets of miRNAs up-regulated in both stress conditions		
miR1122-3p	TraesCS4B01G160300.1	Thiol:disulfide interchange protein txIA
miR1122-3p	TraesCS7D01G131200.1	Disease-resistance protein (TIR-NBS-LRR class) family

miR1122-3p	TraesCS7A01G005800.1	Disease-resistance protein
miR1122-3p	TraesCS3D01G482500.1	Crossover junction endonuclease mus81
miR1122-3p	TraesCS5B01G444700.1	Pseudouridine synthase
miR1122-3p	TraesCS5D01G448100.1	Pseudouridine synthase
miR1122-3p	TraesCS5A01G441000.1	Pseudouridine synthase
miR1122-3p	TraesCS5D01G539200.1	Basic blue protein
miR1122-3p	TraesCS1B01G036500.1	ERD (Early-responsive to dehydration stress) family protein
miR1122-3p	TraesCS3A01G258800.2	Methyltransferase
miR1122-3p	TraesCS3D01G258900.1	Methyltransferase
miR1122-3p	TraesCS3B01G291700.1	Methyltransferase
miR1122-3p	TraesCS3A01G258800.1	Methyltransferase
miR1122-3p	TraesCS6B01G297100.1	F-box family protein
miR1122-3p	TraesCS6D01G245100.1	F-box family protein
miR1130-3p	TraesCS7A01G005800.1	Disease-resistance protein
miR1130-3p	TraesCS3D01G482500.1	Crossover junction endonuclease mus81
miR1130-3p	TraesCS2D01G248200.6	Receptor protein kinase-like protein
miR1130-5p	TraesCS5D01G261800.1	F-box family protein
miR1130-3p	TraesCS7D01G522300.1	Pm3-like disease resistance protein
miR1137-3p	TraesCS5B01G557400.1	Beta-fructofuranosidase, insoluble protein
miR1137-3p	TraesCS3B01G220700.1	Eukaryotic translation initiation factor 6
miR1137-3p	TraesCS3B01G220700.2	Eukaryotic translation initiation factor 6
miR1137-5p	TraesCS4B01G114400.1	Anthranilate synthase alpha subunit 2, chloroplastic
miR1436-3p	TraesCS3D01G482500.1	Crossover junction endonuclease mus81
miR1436-3p	TraesCS2D01G072600.1	Glycosyltransferase
miR1436-3p	TraesCS7A01G005800.1	Disease resistance protein
miR1436-3p	TraesCS2D01G578800.1	Shaggy-like protein kinase 41
Targets of miRNAs down-regulated in both stress conditions		
miR1127-3p	TraesCS2A01G360000.1	Cysteine-rich receptor-like protein kinase 41
miR1127-3p	TraesCS5B01G063100.1	F-box family protein
miR1127-5p	TraesCS7D01G293800.2	65-kDa microtubule-associated protein 6
miR1127-5p	TraesCS1D01G409900.1	Beta-adaptin-like protein
miR1127-5p	TraesCS3B01G610700.1	B3 domain-containing protein
miR1127-5p	TraesCS7D01G293800.1	65-kDa microtubule-associated-like protein
miR1127-5p	TraesCS6B01G449300.1	Smad/FHA domain protein
miR1127-3p	TraesCS2B01G056900.1	Histone acetyltransferase
miR1127-5p	TraesCS3A01G327800.1	Haloacid dehalogenase superfamily protein
miR1127-3p	TraesCS3B01G251400.1	StAR-related lipid transfer protein
miR1127-3p	TraesCS5B01G215200.1	Glucan synthase-like 10
miR1127-3p	TraesCS3B01G174800.1	Protein kinase family protein
miR1127-3p	TraesCS6B01G256600.1	RNA-binding protein
miR1127-3p	TraesCS5D01G023200.1	Serine/threonine-protein kinase
miR1127-3p	TraesCS1B01G466000.1	Leucine-rich repeat receptor-like protein kinase family protein
miR1127-5p	TraesCS6A01G380400.1	DEAD/DEAH box RNA helicase family protein
miR1127-5p	TraesCS2A01G017400.1	FACT complex subunit SPT16
miR1127-5p	TraesCS5D01G261800.1	F-box family protein
miR1127-5p	TraesCS1A01G065000.1	Importin subunit beta-1
miR1127-3p	TraesCS2D01G146600.1	Gibberellin receptor GID1a
miR1127-5p	TraesCS2B01G452200.5	Core-2/l-branching beta-1,6-N-acetylglucosaminyltransferase family protein
miR1127-3p	TraesCS1D01G409900.1	Beta-adaptin-like protein
miR1127-3p	TraesCS5B01G451800.1	Cactin
miR1127-3p	TraesCS4A01G492700.1	Glutaredoxin family protein, expressed
miR1127-3p	TraesCSU01G156500.2	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein, putative

miR1127-5p	TraesCS3A01G190300.12	Exportin-7
miR1127-5p	TraesCS3A01G190300.13	Exportin-7
miR1127-5p	TraesCS2D01G236200.6	Transcription factor
miR1127-5p	TraesCS5B01G013700.1	F-box protein
miR1127-5p	TraesCS2A01G131100.1	Disease-resistance protein (TIR-NBS-LRR class) family
miR5175-5p	TraesCS2A01G485700.2	Serine/threonine-protein kinase
miR5181-5p	TraesCS3B01G105100.1	DUF674 family protein

Table S7.

GO terms over-represented in miRNA targets which are unique to the severe stress samples. Universe consists of 1,516 target genes identified from the whole genome analysis (IWGSC 2018).

GO term	Number of genes in Severe Stress	Number of genes in universe	ontology	GO Description	p_adjust	percentage
GO:0016722	14	14	MF	oxidoreductase activity, oxidizing metal ions	0	100
GO:0046274	14	14	BP	lignin catabolic process	0	100
GO:0052716	14	14	MF	hydroquinone:oxygen oxidoreductase activity	0	100
GO:0005507	17	20	MF	copper ion binding	4.48E-09	85
GO:0055114	29	65	BP	oxidation-reduction process	4.56E-07	44.62
GO:0009698	13	15	BP	phenylpropanoid metabolic process	4.93E-07	86.67
GO:0016682	9	9	MF	oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor	1.78E-05	100
GO:0009809	10	15	BP	lignin biosynthetic process	0.0015	66.67
GO:0016491	19	48	MF	oxidoreductase activity	0.0018	39.58
GO:0004601	9	14	MF	peroxidase activity	0.0042	64.29
GO:0009832	9	14	BP	plant-type cell wall biogenesis	0.0068	64.29
GO:0010413	8	11	BP	glucuronoxylan metabolic process	0.0070	72.73
GO:0016209	8	12	MF	antioxidant activity	0.0075	66.67
GO:0051920	8	12	MF	peroxiredoxin activity	0.0075	66.67
GO:0009414	16	42	BP	response to water deprivation	0.0089	38.1
GO:0009561	9	16	BP	megagametogenesis	0.0122	56.25
GO:0030246	10	19	MF	carbohydrate binding	0.0122	52.63
GO:0045492	8	13	BP	xylan biosynthetic process	0.0233	61.54

Table S8.

Enrichment of GO slim terms in SOM network modules 1 and 3.

GO term	Number of genes in Network	Number of genes in universe	ontology	GO Description	p_adjust	percentage	Network Module
GO:0003676	211	441	MF	nucleic acid binding	2.99E-17	47.85	1
GO:0006139	301	721	BP	nucleobase-containing compound metabolic process	4.07E-15	41.75	1
GO:0006259	75	118	BP	DNA metabolic process	3.21E-13	63.56	1
GO:0040029	48	64	BP	regulation of gene expression, epigenetic	2.70E-12	75	1
GO:0003677	69	150	MF	DNA binding	0.00031	46	1
GO:0007275	305	897	BP	multicellular organism development	0.003297	34	1
GO:0007049	64	149	BP	cell cycle	0.006148	42.95	1
GO:0009791	220	642	BP	post-embryonic development	0.026352	34.27	1
GO:0009058	381	1179	BP	biosynthetic process	0.033668	32.32	1
GO:0003723	26	52	MF	RNA binding	0.036492	50	1
GO:0016043	252	753	BP	cellular component organization	0.036492	33.47	1
GO:0016301	262	443	MF	kinase activity	3.51E-27	59.14	3
GO:0009605	470	1003	BP	response to external stimulus	7.32E-20	46.86	3
GO:0009607	395	815	BP	response to biotic stimulus	5.43E-19	48.47	3
GO:0007154	442	939	BP	cell communication	6.07E-19	47.07	3
GO:0004872	138	212	MF	receptor activity	1.42E-18	65.09	3
GO:0004871	141	227	MF	signal transducer activity	2.16E-16	62.11	3
GO:0008219	185	336	BP	cell death	3.10E-14	55.06	3
GO:0006464	317	667	BP	cellular protein modification process	4.13E-13	47.53	3
GO:0000166	339	728	MF	nucleotide binding	1.08E-12	46.57	3
GO:0007165	340	748	BP	signal transduction	7.52E-11	45.45	3
GO:0009991	131	242	BP	response to extracellular stimulus	2.76E-09	54.13	3
GO:0019538	364	833	BP	protein metabolic process	5.36E-09	43.7	3
GO:0003824	663	1677	MF	catalytic activity	1.62E-08	39.53	3
GO:0006810	331	751	BP	transport	1.68E-08	44.07	3
GO:0009719	363	843	BP	response to endogenous stimulus	5.22E-08	43.06	3
GO:0016740	360	837	MF	transferase activity	5.22E-08	43.01	3
GO:0030246	46	66	MF	carbohydrate binding	1.30E-07	69.7	3
GO:0009856	90	159	BP	pollination	2.26E-07	56.6	3
GO:0005215	162	338	MF	transporter activity	1.34E-06	47.93	3
GO:0009875	27	34	BP	pollen-pistil interaction	2.65E-06	79.41	3
GO:0009838	29	44	BP	abscission	0.000472	65.91	3
GO:0005515	222	522	MF	protein binding	0.00071	42.53	3
GO:0006950	620	1632	BP	response to stress	0.001046	37.99	3
GO:0005102	29	49	MF	receptor binding	0.007335	59.18	3

Table S9.

Publicly available flag leaf and drought experiment RNA-Seq samples (www.wheat-expression.com; Borill et al. 2016) included for WGCNA analysis.

	Age	Stress-disease	Phenotype code	Sample IDs
(1)	Anther differentiation stage	Early drought	AD_S	SRR5383650, SRR5383900, SRR5383901
		None	AD_C	SRR5383933, SRR5383934, SRR5383935
	Tetrad stage	Late drought	T_S	SRR5383936, SRR5383938, SRR5383941
		None	T_C	SRR5383944, SRR5383945, SRR5383947
	Age	Stress-disease	Phenotype code	Sample IDs
(2)	7 days	6 hour PEG stress	PEG6	SRR1542409, SRR1542408
		1 hour PEG stress	PEG1	SRR1542407, SRR1542406
		None	IS	SRR1542405, SRR1542404
	Age	Stress-disease	Phenotype code	Sample IDs
(3)	Flag leaf stage	None	IP	Sample_61A, Sample_62A, Sample_63A, Sample_75A, Sample_77A, Sample_78A
	Full boot			Sample_94B, Sample_95A, Sample_96A
	30% spike			Sample_109A, Sample_110A, Sample_111B
	Ear emergence			Sample_127A, Sample_128A, Sample_129A
	Anthesis			Sample_166A, Sample_167A, Sample_168A
	Milk grain stage			Sample_175A, Sample_176A, Sample_177A
	Dough			Sample_202A, Sample_203A, Sample_204A
	Ripening			Sample_223B, Sample_225A, Sample_224A
	Age	Stress-disease	Phenotype code	Sample IDs
(4)	12 dpa	None	IP	SRR085459, SRR085458, SRR085457
	Age	Stress-disease	Phenotype code	Sample IDs
(5)	30 dpa	None	IP	SRR3068482
	25 dpa			SRR3068481
	15 dpa			SRR3068477
	anthesis			SRR3068439
	Ear emergence			SRR3068387

(1) Ma et al. 2017

(2) Liu et al. 2017

(3), (4), (5) Ramírez-González et al. 2018

Table S10.
CoDReGs' SOM module classification and annotation.

Module 1	
CoDReG 6 011 01	Acid beta-fructofuranosidase
CoDReG 6 581 01	Dehydrin
CoDReG 6 593 01	Serine-rich protein
CoDReG 1 544 01	Late embryogenesis abundant protein
CoDReG 6 005 01	Leucine-rich repeat receptor-like protein kinase family protein
CoDReG 6 559 01	1-Aminocyclopropane-1-carboxylate oxidase
CoDReG 2 735 01	Isoaspartyl peptidase/L-asparaginase
Module 2	
CoDReG 3 608 01	Laccase
CoDReG 3 508 01	Glycosyltransferase
CoDReG 3 438 01	GDSL esterase/lipase
CoDReG 6 562 01	Auxin-responsive family protein
CoDReG 1 549 01	Lipid transfer protein
Module 3	
CoDReG 2 590 01	Chitinase
CoDReG 1 002 01	Receptor protein kinase, putative
CoDReG 7 567 01	Glutamine dumper, putative
CoDReG 1 578 01	Receptor-like protein kinase, putative, expressed
CoDReG 1 582 01	ATP-dependent zinc metalloprotease FtsH
CoDReG 1 009 01	Receptor-like kinase
CoDReG 1 464 01	Transmembrane protein, putative (DUF1218)
CoDReG 2 734 01	Nuclease
CoDReG 2 702 01	Senescence-associated family protein (DUF581)
CoDReG 3 712 01	Beta-1,3-glucanase
CoDReG 5 569 01	Protein DETOXIFICATION
CoDReG 3 719 01	Protein kinase
CoDReG 1 374 01	Expansin protein
CoDReG 3 026 01	Receptor-like kinase
CoDReG 5 513 01	Glycosyltransferase
CoDReG 1 533 01	Glycosyltransferase
CoDReG 3 724 01	Protein DETOXIFICATION
CoDReG 3 644 01	DUF1685 family protein
CoDReG 7 721 01	Expansin-like protein
CoDReG 5 046 01	Kinase, putative
CoDReG 2 012 01	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
CoDReG 6 061 01	Chlorophyll a-b binding protein, chloroplastic
CoDReG 2 194 01	Cellulose synthase-like protein
CoDReG 3 024 01	Trypsin inhibitor
CoDReG 4 456 01	Germin-like protein
CoDReG 2 718 01	Anthocyanidin reductase
Module 5	
CoDReG 2 624 01	Phenylalanine ammonia-lyase
CoDReG 7 619 01	Xyloglucan endotransglucosylase/hydrolase
CoDReG 6 023 01	Peroxidase
CoDReG 6 592 01	Embryogenesis transmembrane protein-like
CoDReG 5 503 02	Beta-glucosidase
CoDReG 1 337 01	Glutathione S-transferase
CoDReG 7 182 01	Embryogenesis transmembrane protein
CoDReG 2 751 01	Heavy metal transport/detoxification superfamily protein
CoDReG 2 572 01	Amino acid transporter, putative
CoDReG 2 667 01	Glycosyltransferase
CoDReG 2 765 01	NAC domain-containing protein, putative
CoDReG 4 678 01	Arabinogalactan protein 5
CoDReG 7 694 01	Protein kinase

CoDReG genes syntenic with rice. Only the HC genes in the A genome are shown. Start pos.: Gene starting position at the RefSeqv1 pseudomolecule (IWGSC 2018); Chr: chromosome.

31

Table S12.

CoDReGs with syntenic positions with rice drought tolerance QTLs. Rice chromosomal positions (IRGSP 2017) are indicated. *: from the Q-TARO database (Yonemaru 2010)

CoDReG	Trait*	Trait category 1*	Trait category 2*	Chr	Start pos.	End pos.
CoDReG_1A_337_01	osmotic adjustment	Resistance or Tolerance	Drought tolerance	os10	21,384,897	21,932,522
CoDReG_1A_374_01	dry weight per plant	Resistance or Tolerance	Blast resistance	os10	21,624,625	21,629,868
	Percent sterility	Resistance or Tolerance	Drought tolerance	os10	21,474,732	21,503,768
CoDReG_1A_464_01	Salt-soluble storage proteins	Physiological trait	Eating quality	os5	22,309,016	25,730,022
	panicle or tiller no.per m2	Resistance or Tolerance	Drought tolerance	os5	22,309,016	24,371,958
CoDReG_1A_533_01	dwarf phenotype and leaves with abnormally rounded tip regions	Morphological trait	Dwarf	os1	29,747,390	29,878,594
	leaf rolling of culturing (LRC)	Resistance or Tolerance	Drought tolerance	os1	28,571,547	34,744,337
CoDReG_2A_590_01	Plant age in leaf number F-C	Morphological trait	Culm/leaf	os4	24,646,179	25,619,040
	root fresh weight	Resistance or Tolerance	Drought tolerance	os4	25,626,203	33,083,265
CoDReG_2A_624_01	root fresh weight	Resistance or Tolerance	Drought tolerance	os4	25,626,203	33,083,265
CoDReG_2A_667_01	Maximum new root length Average	Morphological trait	Root	os4	27,941,367	30,762,314
	root fresh weight	Resistance or Tolerance	Drought tolerance	os4	25,626,203	33,083,265
CoDReG_2A_702_01	bacterial blight resistance	Resistance or Tolerance	Bacterial blight resistance	os4	29,644,621	33,083,265
	panicle number per hill	Resistance or Tolerance	Drought tolerance	os4	29,644,621	31,356,186
CoDReG_2A_718_01	bacterial blight resistance	Resistance or Tolerance	Bacterial blight resistance	os4	32,036,440	32,061,259
	Plant height-control	Resistance or Tolerance	Drought tolerance	os4	31,648,882	32,246,967
CoDReG_2A_734_01	Basal root thickness	Resistance or Tolerance	Drought tolerance	os4	33,234,004	33,430,563
CoDReG_2A_735_01	Basal root thickness	Resistance or Tolerance	Drought tolerance	os4	33,234,004	33,430,563
CoDReG_2A_751_01	leaf drying	Resistance or Tolerance	Drought tolerance	os4	34,247,154	35,283,358
CoDReG_2A_765_01	Shoot weight low N condition	Resistance or Tolerance	Other soil stress tolerance	os4	35,277,669	35,283,358
	Biomass-control	Resistance or Tolerance	Drought tolerance	os4	35,277,669	35,283,358
CoDReG_3A_438_01	initial plant height	Resistance or Tolerance	Submergency tolerance	os1	26,419,476	29,360,353
	leaf rolling of culturing (LRC)	Resistance or Tolerance	Drought tolerance	os1	28,571,547	34,744,337
CoDReG_3A_508_01	dwarf phenotype and leaves with abnormally rounded tip regions	Morphological trait	Dwarf	os1	29,747,390	29,878,594
	leaf rolling of culturing (LRC)	Resistance or Tolerance	Drought tolerance	os1	28,571,547	34,744,337
CoDReG_3A_608_01	Yield(1998)	Morphological trait	Seed	os1	36,226,902	39,470,731
	Plant height	Resistance or Tolerance	Drought tolerance	os1	36,697,294	42,364,623
CoDReG_3A_644_01	cold tolerance at seedling stage (CTS)	Resistance or Tolerance	Cold tolerance	os1	38,490,966	39,646,396
	Plant height (Low N level, Soil culture , Maturity)	Resistance or Tolerance	Other soil stress tolerance	os1	36,697,294	42,364,623
CoDReG_3A_712_01	Tiller number	Morphological trait	Culm/leaf	os1	41,444,285	42,364,623
	leaf drying score	Resistance or Tolerance	Drought tolerance	os1	41,444,285	44,211,418
CoDReG_3A_719_01	panicle length	Morphological trait	Panicle/flower	os1	42,157,734	42,364,623
	Plant height	Resistance or Tolerance	Drought tolerance	os1	41,923,730	42,364,623
CoDReG_3A_724_01	panicle length	Morphological trait	Panicle/flower	os1	42,157,734	42,364,623
	Plant height	Resistance or Tolerance	Drought tolerance	os1	41,923,730	42,364,623
CoDReG_4A_678_01	Plant height	Morphological trait	Dwarf	os3	5,210,684	5,584,862
	lateral root number	Resistance or Tolerance	Drought tolerance	os3	5,758,005	5,758,498
CoDReG_5A_046_01	Lowest elongated internode	Resistance or Tolerance	Submergency tolerance	os12	25,203,610	26,368,115
	Drought score	Resistance or Tolerance	Drought tolerance	os12	26,277,931	27,748,876
CoDReG_5A_503_02	ABA accumulation	Resistance or Tolerance	Drought tolerance	os9	19,559,036	19,562,133
	maximum root length (non stress)	Resistance or Tolerance	Drought tolerance	os9	20,078,749	20,828,859
CoDReG_5A_513_01	maximum root length (non stress)	Resistance or Tolerance	Drought tolerance	os9	20,078,749	20,828,859
CoDReG_5A_569_01	Elongation of plant height	Morphological trait	Dwarf	os9	22,688,515	22,690,613
	Days to heading-control	Resistance or Tolerance	Drought tolerance	os9	21,313,734	22,021,406
CoDReG_7A_567_01	3rd internode length	Morphological trait	Dwarf	os6	25,794,136	25,797,291
	Penetrated root thickness	Resistance or Tolerance	Drought tolerance	os6	23,740,405	25,797,291
CoDReG_7A_619_01	Carbon isotope discrimination "	Physiological trait	Source activity	os6	29,477,181	29,477,319
	Panicles per plant	Resistance or Tolerance	Drought tolerance	os6	26,569,436	28,130,383
CoDReG_7A_696_01	Panicles per plant	Resistance or Tolerance	Drought tolerance	os6	26,569,436	28,130,383

Table S13.

Unbalanced triads enrichment in CoDReGs in irrigated (I), medium stress (MS) and severe stress (SS) levels.

	I		MS		SS	
	<i>All triads</i>	<i>CoDReGs</i>	<i>All triads</i>	<i>CoDReGs</i>	<i>All triads</i>	<i>CoDReGs</i>
<i>Unbalanced</i>	4468	70	4586	80	4565	77
<i>Balanced</i>	9008	29	9217	21	8856	19
		P=1e-5		P=1e-5		P=1e-5

P: Significant exact Fisher test P values are indicated for significant tests. Triads enrichment is shown with a blue cell. For all triads, genes with TPM>0.5 have been considered. For CoDReGs, genes with known TPM (TPM>0) have been considered.

Table S14.

Proposed nomenclature for RefSeqv1 dehydrin gene models

RefSeqv1 ID	Proposed name		RefSeqv1 ID	Proposed name	
TraesCS3A01G254600	DHN35	<i>DHN35-A1</i>	TraesCS6A01G253300	DHN11	<i>DHN11-A1</i>
TraesCS3B01G286600		<i>DHN35-B1</i>	TraesCS6B01G273400		<i>DHN11-B1</i>
TraesCS3D01G255500		<i>DHN35-D1</i>	TraesCS6D01G234700		<i>DHN11-D1</i>
TraesCS3A01G396200	DHN33	<i>DHN33-A1</i>	TraesCS6A01G350100	DHN5.1	<i>DHN5-A1</i>
TraesCS3B01G428200		<i>DHN33-B1</i>	TraesCS6D01G332500		<i>DHN5-D1</i>
TraesCS3D01G390200		<i>DHN33-D1</i>	TraesCS6A01G350200	DHN9.6	<i>DHN9-A1</i>
TraesCS4A01G250900	DHN6	<i>DHN6-A1</i>	TraesCS6D01G332600		<i>DHN9-D1</i>
TraesCS4B01G064200		<i>DHN6-B1</i>	TraesCS6A01G350300	DHN5.2	<i>DHN5-A2</i>
TraesCS4D01G063100		<i>DHN6-D1</i>	TraesCS6D01G332700		<i>DHN5-D2</i>
TraesCS4A01G455000LC	DHN36.2	<i>DHN36-A2</i>	TraesCS6B01G383200	DHN5.3	<i>DHN5-B3</i>
TraesCS4A01G299100	DHN36	<i>DHN36-A1</i>	TraesCS6B01G695200LC	DHN5.4	<i>DHN5-B4</i>
TraesCS4B01G014300		<i>DHN36-B1</i>	TraesCS6A01G350500	DHN4	<i>DHN4-A1</i>
TraesCS4D01G012500		<i>DHN36-D1</i>	TraesCS6B01G383500		<i>DHN4-B1</i>
TraesCS5A01G369800	DHN2	<i>DHN2-A1</i>	TraesCS6D01G332900		<i>DHN4-D1</i>
TraesCS5B01G372100		<i>DHN2-B1</i>	TraesCS6A01G350600	DHN3.1	<i>DHN3-A1</i>
TraesCS5D01G379200		<i>DHN2-D1</i>	TraesCS6B01G695700LC		<i>DHN3-B1</i>
TraesCS5A01G369900	DHN1	<i>DHN1-A1</i>	TraesCS6B01G695800LC		<i>DHN3-B2</i>
TraesCS5B01G372200		<i>DHN1-B1</i>	TraesCS6D01G333000		<i>DHN3-D1</i>
TraesCS5D01G379300		<i>DHN1-D1</i>	TraesCS6B01G695900LC	DHN3.3	<i>DHN3-B3</i>
TraesCS5A01G424700	DHN38	<i>DHN38-A1</i>	TraesCS6D01G333100	DHN3.4	<i>DHN3-D4</i>
TraesCS5A01G424800		<i>DHN38-A2</i>	TraesCS6A01G350800	DHN3.5	<i>DHN3-A5</i>
TraesCS5B01G426700		<i>DHN38-B1</i>	TraesCS6A01G350700	DHN3.6	<i>DHN3-A6</i>
TraesCS5B01G426800		<i>DHN38-B2</i>	TraesCS6B01G383600		<i>DHN3-B6</i>
TraesCS5D01G433200		<i>DHN38-D1</i>	TraesCS6D01G333200		<i>DHN3-D6</i>
TraesCS5D01G433300		<i>DHN38-D2</i>	TraesCS6A01G350900	DHN3.7	<i>DHN3-A7</i>
TraesCS5D01G519300LC	DHN38.3	<i>DHN38-D3</i>	TraesCS6D01G333300	DHN3.8	<i>DHN3-D8</i>
TraesCS6A01G059800	DHN37	<i>DHN37-A1</i>	TraesCS6B01G383800	DHN3.9	<i>DHN3-B9</i>
TraesCSU01G086200		<i>DHN37-B1</i>	TraesCS6D01G333600		<i>DHN3-D9</i>
TraesCSU01G122200		<i>DHN37-D1</i>	TraesCS7A01G560000	DHN14	<i>DHN14-A1</i>
			TraesCS7B01G484900		<i>DHN14-B1</i>
			TraesCS7D01G549900		<i>DHN14-D1</i>

Table S15.

Synteny of wheat dehydrin genes with rice, *Hordeum vulgare*, *Brachypodium distachyon* and *Sorghum bicolor*. Only the HC dehydrins in chromosome A are shown. 'Chr comp': Chromosome compartment as defined by IWGSC (2018). Start pos.: Gene start position at the RefSeqv1 pseudomolecule (IWGSC 2018); *: pseudomolecule percentile

<i>Triticum aestivum</i>					<i>Oryza sativa</i>			<i>Hordeum vulgare</i>			<i>Brachypodium distachyon</i>			<i>Sorghum bicolor</i>		
A genome gene model	Chr. Comp.	*	DHN name	Start pos. Chr	Gene	Start pos. Chr		Gene	Start pos. Chr		Gene	Start pos. Chr		Gene	Start pos. Chr	
TraesCS3A01G254600	R2B	63	DHN35-A1	476564123 3A	OS01T0702500-01	29123535 os1					BRADI2G47580.1	47975647 bd2		Sb03g032255.1	60688846 sb3	
TraesCS3A01G396200	R2B	86	DHN33-A1	643460238 3A				HORVU3Hr1G089300.1	628030631 hv3H							
TraesCS4A01G250900	R2B	76	DHN6-A1	562290028 4A												
TraesCS4A01G299100	R3	80	DHN36-A1	597754246 4A												
TraesCS5A01G369800	R3	80	DHN2-A1	569677464 5A				HORVU5Hr1G092100.1	587585373 hv5H							
TraesCS5A01G369900	R3	80	DHN1-A1	569683002 5A												
TraesCS5A01G424700	R3	86	DHN38-A1	610078630 5A				HORVU5Hr1G103460.2	616115076 hv5H							
TraesCS5A01G424800	R3	86	DHN38-A2	610184966 5A												
TraesCS6A01G059800	R1	5	DHN37-A1	31583758 6A				HORVU6Hr1G011050.1	19541242 hv6H							
TraesCS6A01G253300	R2B	76	DHN11-A1	468474016 6A	OS02T0669100-01	27165514 os2		HORVU6Hr1G064620.1	439397806 hv6H		BRADI3G51200.1	52299700 bd3		Sb04g032250.1	62251614 sb4	
TraesCS6A01G350100	R3	94	DHN5-A1	581982926 6A												
TraesCS6A01G350200	R3	94	DHN9-A1	582086404 6A												
TraesCS6A01G350300	R3	94	DHN5-A2	582092081 6A												
TraesCS6A01G350500	R3	94	DHN4-A1	582264814 6A				HORVU6Hr1G083980.1	553165574 hv6H							
TraesCS6A01G350600	R3	94	DHN3-A1	582511184 6A												
TraesCS6A01G350700	R3	94	DHN3-A6	582516403 6A												
TraesCS6A01G350800	R3	94	DHN3-A5	582630751 6A												
TraesCS6A01G350900	R3	94	DHN3-A7	582638141 6A												
TraesCS7A01G560000	R3	99	DHN14-A1	731882428 7A												

Table S16.

TFs predicted by genie3 to regulate dehydrins. The top 1 million edges from the genie3 network were used for this analysis (Ramírez-González et al. 2018).

TF_family	Number of TF from each family predicted to regulate		Percentage of TF from each family predicted to regulate		chisq (dehydrins vs all genes)	enriched for dehydrin targets
	dehydrins	all genes	dehydrins	all genes		
AP2/EREBP	38	352	16.7%	11.9%	0.00000	YES
NAC	31	255	13.6%	8.6%	0.00000	YES
MYB-related	29	498	12.7%	16.9%	0.00000	NO
ABI3/VP1	13	169	5.7%	5.7%	0.95317	NO
HD-Zip_I_II	13	56	5.7%	1.9%	0.00000	YES
bHLH	10	207	4.4%	7.0%	0.00000	NO
C3H	10	90	4.4%	3.0%	0.00002	YES
HSF	10	62	4.4%	2.1%	0.00000	YES
WRKY	9	252	3.9%	8.5%	0.00000	NO
MADS_II	8	107	3.5%	3.6%	0.73360	NO
C2C2_GATA	5	49	2.2%	1.7%	0.02358	YES
GRAS	5	86	2.2%	2.9%	0.01984	NO
AS2/LOB	4	60	1.8%	2.0%	0.28318	NO
C2C2_CO-like	4	27	1.8%	0.9%	0.00000	YES
Sigma70-like	4	18	1.8%	0.6%	0.00000	YES
TAZ	4	21	1.8%	0.7%	0.00000	YES
MADS_I	3	41	1.3%	1.4%	0.73277	NO
mTERF	3	85	1.3%	2.9%	0.00000	NO
PLATZ	3	32	1.3%	1.1%	0.22482	YES
ARF	2	61	0.9%	2.1%	0.00001	NO
C2C2_Dof	2	72	0.9%	2.4%	0.00000	NO
C2C2_YABBY	2	19	0.9%	0.6%	0.11300	YES
CSD	2	15	0.9%	0.5%	0.00483	YES
FHA	2	42	0.9%	1.4%	0.01227	NO
GARP_G2-like	2	65	0.9%	2.2%	0.00000	NO
tify	2	67	0.9%	2.3%	0.00000	NO
Zinc finger, MIZ type	2	15	0.9%	0.5%	0.00483	YES
BES1	1	13	0.4%	0.4%	0.98736	NO
CPP	1	25	0.4%	0.8%	0.01545	NO
E2F/DP	1	22	0.4%	0.7%	0.05260	NO
HD_PLINC	1	27	0.4%	0.9%	0.00657	NO
SBP	1	35	0.4%	1.2%	0.00018	NO
Whirly	1	6	0.4%	0.2%	0.00455	YES

Table S17.

NAC and AP2/EREBP TFs predicted to regulate dehydrins by top 1 million edges from genie3. Homoeologs are indicated in the same color.

TF	TF family	Arabidopsis orthologue(s)	Rice orthologue(s)	Arabidopsis function	Rice function
TraesCS1A01G263700	NAC	AT1G01720.1	LOC_Os05g34830	ATAF1 negative regulator of genes in drought stress https://doi.org/10.1007/s11240-009-9640-9	ABA responsive, increases drought tolerance https://doi.org/10.1007/s11240-009-9640-9
TraesCS1D01G194200	NAC	AT3G49530.1; AT1G54330.1; AT1G53810.1	LOC_Os10g42130	NAC062 ABA sensitive doi: 10.4161/psb.11083, mediates protein re-unknown	NAC062 ABA sensitive doi: 10.4161/psb.11083, mediates protein re-unknown
TraesCS1D01G263800	NAC	AT1G01720.1	LOC_Os05g34830	ATAF1 negative regulator of genes in drought stress https://doi.org/10.1007/s11240-009-9640-9	ABA responsive, increases drought tolerance https://doi.org/10.1007/s11240-009-9640-9
TraesCS2A01G101400	NAC	N/A	LOC_Os07g48550	N/A	ONAC069, ONAC015; pathogen resistance http://agris.fao.org/agris-search/search.do?recordID=KR2012003225
TraesCS2B01G118400	NAC	N/A	LOC_Os07g48550	N/A	ONAC069, ONAC015; pathogen resistance http://agris.fao.org/agris-search/search.do?recordID=KR2012003225
TraesCS2B01G118500	NAC	N/A	LOC_Os07g48550	N/A	ONAC069, ONAC015; pathogen resistance http://agris.fao.org/agris-search/search.do?recordID=KR2012003225
TraesCS2B01G627200	NAC	N/A	N/A	N/A	N/A
TraesCS2D01G576300	NAC	N/A	N/A	N/A	N/A
TraesCS3B01G271900	NAC	N/A	LOC_Os01g47670	N/A	unknown
TraesCS3D01G243900	NAC	N/A	LOC_Os01g47670	N/A	unknown
TraesCS3D01G467000	NAC	N/A	N/A	N/A	N/A
TraesCS4A01G242700	NAC	AT3G18400.1; AT5G53950.1	LOC_Os03g42630	CUC2 leaf shape doi: 10.1105/tpc.106.045617, NAC058 unknown	unknown
TraesCS4B01G027400	NAC	AT5G53950.1; AT3G18400.1	LOC_Os03g42630	CUC2 leaf shape doi: 10.1105/tpc.106.045617, NAC058 unknown	unknown
TraesCS4D01G071200	NAC	AT5G53950.1	LOC_Os03g42630	CUC2 leaf shape doi: 10.1105/tpc.106.045617	unknown
TraesCS5A01G482200	NAC	AT3G04070.1	N/A	NAC047/SHG regulates response to waterlogging doi: 10.1105/tpc.1 N/A	1 N/A
TraesCS5A01G467300	NAC	N/A	LOC_Os03g59730	N/A	unknown
TraesCS5B01G142100	NAC	AT3G04070.1	N/A	NAC047/SHG regulates response to waterlogging doi: 10.1105/tpc.1 N/A	N/A
TraesCS5B01G290200	NAC	N/A	LOC_Os09g33490	N/A	unknown
TraesCS5D01G148800	NAC	AT3G04070.1	N/A	NAC047/SHG regulates response to waterlogging doi: 10.1105/tpc.1 N/A	N/A
TraesCS7A01G152500	NAC	N/A	N/A	N/A	N/A
TraesCS7A01G209100	NAC	N/A	LOC_Os12g22940; LOC_Os09g36100	N/A	ONAC136, unknown
TraesCS7A01G1537300	NAC	N/A	N/A	N/A	N/A
TraesCS7A01G569100	NAC	N/A	N/A	N/A	N/A
TraesCS7A01G569300	NAC	N/A	N/A	N/A	N/A
TraesCS7B01G004900	NAC	N/A	N/A	N/A	N/A
TraesCS7B01G108900	NAC	N/A	LOC_Os12g22940; LOC_Os09g36100	N/A	ONAC136, unknown
TraesCS7B01G252100	NAC	N/A	N/A	N/A	N/A
TraesCS7D01G100400	NAC	N/A	N/A	N/A	N/A
TraesCS7D01G154200	NAC	N/A	N/A	N/A	N/A
TraesCS7D01G348100	NAC	N/A	N/A	N/A	N/A
TraesCS7D01G371800	NAC	N/A	N/A	N/A	N/A
TraesCS1A01G244800	AP2/EREBP	N/A	N/A	N/A	N/A
TraesCS1B01G246000	AP2/EREBP	N/A	N/A	N/A	N/A
TraesCS1B01G282300	AP2/EREBP	N/A	LOC_Os05g36100	N/A	unknown
TraesCS1B01G441300	AP2/EREBP	N/A	N/A	N/A	N/A
TraesCS1D01G244500	AP2/EREBP	N/A	N/A	N/A	N/A
TraesCS2A01G505600	AP2/EREBP	N/A	LOC_Os04g55970	N/A	unknown
TraesCS2A01G514200	AP2/EREBP	AT5G67180.1	LOC_Os04g55560	N/A	N/A
TraesCS2A01G514300	AP2/EREBP	AT5G67190.1; AT4G36900.1; AT2G23100.1	LOC_Os04g55520	TOE3 stem cell nice, DEAR2 DEAR3 CE1 closely related to DEAR1 inv unknown	unknown
TraesCS2B01G467400	AP2/EREBP	N/A	LOC_Os04g55970	N/A	unknown
TraesCS2D01G412400	AP2/EREBP	N/A	LOC_Os04g46460	N/A	OsDREB4-2 bind dehydration responsive element DOI: 10.1111/j.1744-7909.2005.00028.x
TraesCS2D01G506500	AP2/EREBP	N/A	LOC_Os04g55970	N/A	unknown
TraesCS3A01G099200	AP2/EREBP	N/A	LOC_Os01g07120	N/A	OSDREB2A improves drought tolerance doi: 10.1016/j.plaphy.2011.09.012
TraesCS3A01G238300	AP2/EREBP	N/A	LOC_Os01g46870	N/A	unknown
TraesCS3D01G099500	AP2/EREBP	N/A	N/A	N/A	N/A
TraesCS4A01G011600	AP2/EREBP	N/A	N/A	N/A	N/A
TraesCS4A01G123800	AP2/EREBP	N/A	LOC_Os03g19900	N/A	unknown
TraesCS4B01G180600	AP2/EREBP	N/A	LOC_Os03g19900	N/A	unknown
TraesCS4B01G292900	AP2/EREBP	N/A	N/A	N/A	N/A
TraesCS4D01G182100	AP2/EREBP	N/A	LOC_Os03g19900	N/A	unknown
TraesCS4D01G122500	AP2/EREBP	AT3G25790.1; AT1G13260.1; AT1G25100.1	N/A	EDF3, RAV1, RAV2, TEM1: RAV1 and RAV2 regulate abiotic stress resp	N/A
TraesCS5A01G310700	AP2/EREBP	N/A	LOC_Os09g35010	N/A	OsDREB1B confers drought tolerance DOI: 10.1007/s11103-008-9391-8
TraesCS5B01G313000	AP2/EREBP	N/A	LOC_Os09g35030	N/A	OsDREB1A increases drought tolerance DOI: 10.1046/j.1365-3113X.2003.01661.x AND directly induces expression of OsDhn1 https://link.springer.com/article/10.1007/s12374-012-0377-3
TraesCS5B01G481300	AP2/EREBP	N/A	N/A	N/A	N/A
TraesCS5D01G317500	AP2/EREBP	N/A	LOC_Os09g35010	N/A	OsDREB1B confers drought tolerance DOI: 10.1007/s11103-008-9391-8
TraesCS5D01G317600	AP2/EREBP	N/A	LOC_Os09g35010	N/A	OsDREB1B confers drought tolerance DOI: 10.1007/s11103-008-9391-8
TraesCS5D01G318100	AP2/EREBP	N/A	LOC_Os09g35020	N/A	ERF13, unknown
TraesCS5D01G318300	AP2/EREBP	N/A	LOC_Os09g35010	N/A	OsDREB1B confers drought tolerance DOI: 10.1007/s11103-008-9391-8
TraesCS6A01G243500	AP2/EREBP	N/A	LOC_Os02g43820	N/A	ERF95 unknown
TraesCS6A01G336300	AP2/EREBP	N/A	N/A	N/A	N/A
TraesCS6B01G126200	AP2/EREBP	N/A	LOC_Os02g43820	N/A	ERF95 unknown
TraesCS6B01G249600	AP2/EREBP	N/A	N/A	N/A	N/A
TraesCS7A01G057800	AP2/EREBP	N/A	LOC_Os06g03670	N/A	DREB1C, constitutive expr DOI: 10.1046/j.1365-3113X.2003.01661.x
TraesCS7B01G057500	AP2/EREBP	N/A	LOC_Os06g10780	N/A	unknown
TraesCS7D01G052500	AP2/EREBP	N/A	LOC_Os06g03670	N/A	DREB1C, constitutive expr DOI: 10.1046/j.1365-3113X.2003.01661.x
TraesCS7D01G052600	AP2/EREBP	N/A	LOC_Os06g03670	N/A	DREB1C, constitutive expr DOI: 10.1046/j.1365-3113X.2003.01661.x
TraesCS7D01G127600	AP2/EREBP	AT5G67190.1; AT4G36900.1; AT2G23100.1	LOC_Os06g07030	TOE3 stem cell nice, DEAR2 DEAR3 CE1 closely related to DEAR1 inv	N/A
TraesCS7D01G179600	AP2/EREBP	N/A	LOC_Os06g10780	N/A	unknown
TraesCS7D01G469200	AP2/EREBP	N/A	N/A	N/A	N/A

Supplementary material File SM1. SOM and WGCNA modules' gene IDs.