

Supplementary Tables

**Supplementary Table 1.** Sampled dehydrin sequences from grass species closely related to *Brachypodium*. The accession code and the protein name correspond to those indicated in Phytozome and Genbank. Asterisks indicate the original names of DHN genes. Outgroup DHN sequences orthologous to the corresponding *Brachypodium* Bdh genes are based on the analyses developed in this study; crosses indicate orthology information retrieved from Ensembl Plants and Phytozome.

<i>Panther familiy ortology</i>	<i>Bdhn</i>	<i>Aegilops tauschii</i>		<i>Hordeum vulgare</i>		<i>Oryza sativa</i>		<i>Sorghum bicolor</i>		<i>Triticum aestivum</i>		<i>Zea mays</i>	
		Accession	Name	Accession	Name	Accession	Name	Accession	Name	Accession	Name	Accession	Name
<i>ERD14</i>	<i>Bdhn 1 Bdhn 2</i>	AET6Gv20653900	DHNAtau 1	HORVU6Hr1G064620	DHNVul 8*	LOC_Os02g44870	DHNOsat 1†	Sobic.004G286600	DHNSbic 2*†	TraesCS6A02G253300	DHNTaes 1	GRMZM2G147014	DHNZmays 1†
										TraesCS6D02G234700	DHNTaes 2	GRMZM2G373522	DHNZmays 2†
										TraesCS6B02G273400	DHNTaes 3		
<i>SF23</i>	<i>Bdhn 3</i>	AET6Gv20864900	DHNAtau 4	HORVU6Hr1G084010	DHNVul 7*	LOC_Os11g26570	DHNOsat 2†	Sobic.009G116700	DHNSbic 3†	TraesCS6D02G332900	DHNTaes 4	Zm00001d010094	DHNZmays 3†
		AET6Gv20865700	DHNAtau5	HORVU6Hr1G084070	DHNVul 3*			Sobic.010G041900	DHNSbic 4†	TraesCS6D02G333200	DHNTaes 5		
		AET6Gv20866400	DHNAtau 6							TraesCS6D02G333300	DHNTaes 6		
		AET6Gv20866000	DHNAtau 7							TraesCS6D02G333600	DHNTaes 7		
										TraesCS6A02G350700	DHNTaes 8		

							TraesCS6B02G383500	DHNTaes 9		
							TraesCS6B02G383600	DHNTaes 10		
							TraesCS6D02G333100	DHNTaes 11		
							TraesCS6A02G350600	DHNTaes 12		
							TraesCS6A02G350800	DHNTaes 13		
<i>Bdhn 4</i> <i>Bdhn 5</i>	AET5Gv20866800	DHNAtau 2*	HORVU5Hr1G092120	DHNHvul1a*	LOC_Os11g26780	DHNOsat 3a†				
	AET5Gv20866700	DHNAtau 9	HORVU5Hr1G092160	DHNHvul 1b	LOC_Os11g26790	DHNOsat 3b†				
			HORVU5Hr1G092100	DHNHvul 2a*						
			HORVU5Hr1G092150	DHNHvul 2b						
<i>SF14</i>    <i>Bdhn 7</i> <i>Bdhn 8</i>							TraesCS5A02G424700	DHNTaes 14		
							TraesCS5A02G424800	DHNTaes 15		
							TraesCS5B02G426700	DHNTaes 16		
							TraesCS5B02G426800	DHNTaes 17		
							TraesCS5D02G433200	DHNTaes 18		
							<i>TraesCS5D02G433300</i>	<i>DHNTaes 19</i>		
<i>SF19</i>	<i>Bdhn 6</i>	AET4Gv20132600	DHNAtau 3*						GRMZM2G052364	DHNZmays 4†

										GRMZM2G098750	DHNZmays 5†
<i>XEROI</i>	<i>Bdhn 9</i>	AET3Gv20620600	DHNAtau 8			LOC_Os01g50700	DHNOsat 4	Sobic.003G270200	DHNSbic 5		
<i>HIRD11</i>	<i>Bdhn 10</i>			AY681974	DHNHvul 13*	LOC_Os03g45280	DHNOsat 13	Sobic.001G149500	DHNSbic 10	GRMZM2G169372	DHNZmays 10a
										GRMZM2G448511	DHNZmays 10b

**Supplementary Table 2.** Molecular traits of *Brachypodium Bdhn* proteins. No. aa, number of aminoacids; Mwt, molecular weight; pI, isoelectric point; Instability index; GRAVY, grand hydrophathicity average index. Abbreviations of species and reference genomes: BD, *B. distachyon* Bd21; BHD, *B. hybridum* D-subgenome ABR113; BS, *B. stacei* ABR114; BHS, *B. hybridum* S-subgenome ABR113; BSY, *B. sylvaticum* Ain1.

<i>Bdhn</i>	No. aa					Mwt (Kda)					pI					Instability index					GRAVY				
	BD	BHD	BS	BHS	BSY	BD	BHD	BS	BHS	BSY	BD	BHD	BS	BHS	BSY	BD	BHD	BS	BHS	BSY	BD	BHD	BS	BHS	BSY
<i>Bdhn1a</i>	252	252	259	259	252	27506.5	27575.6	28096.2	28096.2	27255.3	5.24	5.30	5.54	5.54	5.30	58.09	60.80	58.20	58.20	61.23	-1.17	-1.18	-1.16	-1.16	-1.09
<i>Bdhn1b</i>					252					27354.4					5.42					55.47					-1.11
<i>Bdhn2</i>	254	254	252	252	258	27504.6	27490.6	27304.4	27352.5	28032.2	5.24	5.24	5.30	5.30	5.37	64.07	63.54	65.46	64.41	61.02	-1.04	-1.04	-1.10	-1.12	-1.13
<i>Bdhn3</i>	163	163	160	160	162	16348.6	16348.6	16153.4	15978.2	16107.3	9.13	9.13	7.17	6.79	8.87	15.43	15.43	17.31	18.55	14.94	-1.07	-1.07	-1.03	-1.00	-1.03
<i>Bdhn4</i>	107					11015.2					9.40					47.63					-1.24				
<i>Bdhn5</i>	143	143	132	132	145	14468.8	14469.8	13518.8	13504.8	14730.0	8.86	8.86	9.16	9.16	8.07	28.95	28.95	30.08	29.44	32.68	-1.05	-1.05	-1.08	-1.08	-1.06
<i>Bdhn6</i>	395	395	362	363	423	37817.7	37751.5	34828.3	35013.6	40262.1	9.03	9.05	8.53	8.55	8.06	8.01	7.75	12.31	9.67	7.23	-0.67	-0.69	-0.76	-0.76	-0.67
<i>Bdhn7</i>	183	183	181	181	180	18455.9	18429.9	18340.8	18340.8	18203.7	9.25	9.25	9.05	9.05	9.25	18.26	17.79	21.10	21.10	16.35	-1.10	-1.08	-1.14	-1.14	-1.03
<i>Bdhn8</i>	157	157	169	169	172	16125.5	16125.5	17248.6	17226.6	17528.0	9.07	9.07	9.05	9.05	9.33	21.05	21.05	22.31	22.76	29.13	-1.15	-1.15	-1.12	-1.12	-1.12
<i>Bdhn9</i>	226	226	206	206	222	23501.6	23532.6	21570.5	21570.5	22965.1	5.79	5.68	5.99	5.99	6.06	43.84	41.28	42.75	42.75	41.40	-0.80	-0.83	-0.94	-0.94	-0.83
<i>Bdhn10</i>	100	102	107	107	102	11313.5	11515.6	12109.3	12109.3	11529.7	7.23	6.87	7.25	7.25	6.87	41.87	43.14	42.39	42.39	43.14	-2.15	-2.15	-2.19	-2.19	-2.15

**Supplementary Table 3.** Chromosomal location of *Bdhn* genes across the four studied *Brachypodium* species and genomes. Chr, chromosome number (*B. distachyon* Bd21: Bd1-Bd5; *B. hybridum* ABR113 subgenome D: Bd1-Bd5; *B. stacei* ABR114: Bs1-Bs10; *B. hybridum* ABR113 subgenome S: Bs1-Bs10; *B. sylvaticum* Ain-1: Bsy1-Bsy9). The highest density of dehydrin genes were found in the syntenic chromosomes Bd3 and Bd4 (*Bdhn2*, *Bdhn4*, *Bdhn5*, *Bdhn6*, *Bdhn7*, *Bdhn8*), Bs4 (*Bdhn2*, *Bdhn6*, *Bdhn7*), the equivalent *B. hybridum* D and S subgenomic chromosomes (except *Bdhn4*), and Bsy4 (*Bdhn2*, *Bdhn6*, *Bdhn7*, *Bdhn8*). Lengths and positions correspond to the respective reference genomes.

		<i>Bdhn1a</i>	<i>Bdhn1b</i>	<i>Bdhn2</i>	<i>Bdhn3</i>	<i>Bdhn4</i>	<i>Bdhn5</i>	<i>Bdhn6</i>	<i>Bdhn7</i>	<i>Bdhn8</i>	<i>Bdhn9</i>	<i>Bdhn10</i>
<i>B. distachyon</i>	<b>Chr</b>	Bd5		Bd3	Bd1	Bd 4	Bd 4	Bd 4	Bd 3	Bd 3	Bd 2	Bd 1
Bd21	<b>Length</b>	28630136		59640145	75071545	48594894	48594894	48594894	59640145	59640145	59130575	75071545
	<b>from</b>	14358126		52061272	33400971	26400080	26401854	22188216	45300502	45290875	47751383	10098645
	<b>to</b>	14359531		52062769	33402000	26400807	26402677	22189942	45301669	45291925	47757368	10100931
	<b>direction</b>	forward		forward	reverse	reverse	reverse	forward	reverse	forward	forward	reverse
<i>B. hybridum</i> D	<b>Chr</b>	Bd5		Bd3	Bd1		Bd 4	Bd 4	Bd3	Bd3	Bd 2	Bd 1
ABR113	<b>Length</b>	28673805		59422649	73190849		48381198	48381198	59422649	59422649	59597844	73190849
	<b>from</b>	14493652		51909664	32658384		25616401	21335117	45017036	45007503	47969138	9743153
	<b>to</b>	14494867		51910828	32659379		25617226	21336708	45018083	45008367	47975373	9743841
	<b>direction</b>	forward		forward	reverse		reverse	forward	reverse	forward	forward	reverse
<i>B. stacei</i>	<b>Chr</b>	Bs9		Bs4	Bs7		Bs5	Bs5	Bs4	Bs4	Bs1	Bs2
ABR114	<b>Length</b>	20576529		24645555	20893312		23048618	23048618	24645555	24645555	30086066	27792411
	<b>from</b>	9210852		6997868	14026099		3806913	6372578	13156720	13537514	10860306	18652003
	<b>to</b>	9212190		6999029	14026708		3849990	6374159	13157693	13538422	10866472	18652813
	<b>direction</b>	forward		reverse	forward		forward	reverse	forward	forward	reverse	forward
<i>B. hybridum</i> S	<b>Chr</b>	Bs9		Bs4	Bs7		Bs5	Bs5	Bs4	Bs4	Bs1	Bs2
ABR113	<b>Length</b>	21007308		25447193	21638549		23591727	23591727	25447193	25447193	30608744	28346489
	<b>from</b>	7214663		7269373	14706419		3849103	7640493	13819476	13842937	10890765	19034663

	<b>to</b>	7216004		7270541	14707427		3849990	7642071	13820451	13843854	10897704	19035490
	<b>direction</b>	forward		reverse	forward		forward	forward	forward	reverse	reverse	forward
<i>B. sylvaticum</i>	<b>Chr</b>	Bsy9	Bsy9	Bsy4	Bsy7		Bsy5	Bsy4	Bsy4	Bsy4	Bsy1	Bsy2
Ain-1	<b>Lenght</b>	31923712	31923712	38747968	22318590		48035605	38747968	38747968	38747968	52666873	42817455
	<b>from</b>	13763612	14190187	9798501	14062257		26543391	21623366	19478535	19507464	17853540	25255158
	<b>to</b>	13765006	14191050	9799643	14062972		26543956	21625489	19479154	19508169	17853540	25256158
	<b>direction</b>	forward	reverse	reverse	forward		reverse	forward	forward	reverse	reverse	forward

**Supplementary Table 4.** Sampling origins of the four studied *Brachypodium* species and of 54 ecotypes of *B. distachyon*. All samples were used in the comparative genomic analysis of the dehydrin genes. Asterisks indicate *B. distachyon* accessions additionally used in the dehydrin expression and drought-response phenotypic traits changes analyses (32 ecotypes). Diamonds indicate accessions additionally used in the phylogenetic signal analysis (30 ecotypes).

Species	accession	longitude	latitude	Locality
<i>B.stacei</i>	ABR114	38.682846	1.398957	Spain: Balearic isles, Formentera, Torrent
<i>B.hybridum</i>	ABR113	38.782993	-9.250488	Portugal: Lisboa, Belas
<i>B.sylvaticum</i>	Ain1	36.768235	8.707878	Tunisia: Ain-Draham
<i>B.distachyon</i>	ABR2*♦	3,3000	43,6500	France: Herault, Octon
<i>B.distachyon</i>	ABR3*♦	0,0731	42,1805	Spain: Huesca, Aisa
<i>B.distachyon</i>	ABR4*♦	0,7168	42,2627	Spain: Huesca, Aren
<i>B.distachyon</i>	ABR5*♦	-0,5800	42,5810	Spain: Huesca, Jaca, Banaguas
<i>B.distachyon</i>	ABR6*♦	-2,2030	42,5810	Spain: Navarra, Los Arcos
<i>B.distachyon</i>	ABR8*♦	11,3197	43,3146	Italy: Siena
<i>B.distachyon</i>	ABR9	14,4895	46,0609	Croatia: Ljubjana
<i>B.distachyon</i>	Adi10*♦	38,3523	38,7707	Turkey: Adiyaman
<i>B.distachyon</i>	Adi12*♦	38,3523	38,7707	Turkey: Adiyaman
<i>B.distachyon</i>	Adi2*♦	38,3523	38,7707	Turkey: Adiyaman
<i>B.distachyon</i>	Arn1	0,7299	42,2565	Spain: Huesca, Arén
<i>B.distachyon</i>	Bd1_1*♦	28,2510	38,4170	Turkey: Manisa
<i>B.distachyon</i>	Bd18_1*♦	33,7300	39,3678	Turkey: Kaman
<i>B.distachyon</i>	Bd2_3*♦	44,4031	33,7609	Irak: Al Mansuriya
<i>B.distachyon</i>	Bd21_3*♦	44,5350	36,7660	Irak: near Salakudin
<i>B.distachyon</i>	Bd29_1	33,5639	44,5153	Ukraine: Krimea
<i>B.distachyon</i>	Bd3_1*♦	44,5350	36,7660	Irak: Al Mansuriya
<i>B.distachyon</i>	BdTR10C*♦	31,8849	37,7782	Turkey: Konya Province
<i>B.distachyon</i>	BdTR11A	31,8849	37,7782	Turkey: Konya Province
<i>B.distachyon</i>	BdTR11G*♦	27,4770	41,4220	Turkey: Kirklareli
<i>B.distachyon</i>	BdTR11I*♦	28,0402	39,7382	Turkey: Balikesir, Karakaya
<i>B.distachyon</i>	BdTR12C*	34,6503	39,7482	Turkey: Saray, Yozgat province
<i>B.distachyon</i>	BdTR13a*♦	32,4324	39,7565	Turkey: Ankara
<i>B.distachyon</i>	BdTR13C*	32,9881	39,4129	Turkey: Ankara
<i>B.distachyon</i>	BdTR1i*♦	28,5830	38,0930	Turkey: Aydin
<i>B.distachyon</i>	BdTR2B*♦	31,3311	40,0821	Turkey: Karahisarkozlu
<i>B.distachyon</i>	BdTR2G*♦	32,9850	40,3940	Turkey: Ankara
<i>B.distachyon</i>	BdTR3C*♦	32,9630	36,7830	Turkey: Balkusan
<i>B.distachyon</i>	BdTR5i*♦	32,9854	40,3936	Turkey: Cubuk
<i>B.distachyon</i>	BdTR7A	34,6500	39,7480	Turkey: Yozgat

<i>B.distachyon</i>	BdTR8i	34,0714	37,1885	Turkey: Berendi
<i>B.distachyon</i>	BdTR9K*♦	30,7886	39,7530	Turkey: Eskisehir
<i>B.distachyon</i>	Bis1*♦	41,0151	37,8735	Turkey: Bismil
<i>B.distachyon</i>	Foz1	-1,3050	42,6370	Spain: Navarra, Foz de Lumbier
<i>B.distachyon</i>	Gaz8	37,3910	37,1280	Turkey: Gaziantep
<i>B.distachyon</i>	Jer1	0,0120	42,0550	Spain: Huesca, Adahuesca
<i>B.distachyon</i>	Kah1*♦	38,5330	37,7340	Turkey: Kahta
<i>B.distachyon</i>	Kah5*♦	38,5330	37,7340	Turkey: Kahta
<i>B.distachyon</i>	Koz1*♦	41,6100	38,1520	Turkey: Kozluk
<i>B.distachyon</i>	Koz3*♦	41,6100	38,1520	Turkey: Kozluk
<i>B.distachyon</i>	Luc1	-0,8930	42,6100	Spain: Huesca, Berdun
<i>B.distachyon</i>	Mig3	-0,2050	42,1470	Spain: Huesca, Ibieca, San Miguel de Foces
<i>B.distachyon</i>	Mon3	-0,2090	41,6520	Spain: Zaragoza, Castejón de Monegros
<i>B.distachyon</i>	Mur1	0,8770	42,0980	Spain: Lleida, Castillo de Mur
<i>B.distachyon</i>	Per1	-1,7500	42,7370	Spain: Navarra, Puerto del Perdon
<i>B.distachyon</i>	S8iiC	0,1440	41,6054	Spain: Huesca, Zaidín
<i>B.distachyon</i>	Sig2	-1,0150	42,6130	Spain: Zaragoza, Sigüés
<i>B.distachyon</i>	Tek2	26,9310	41,0850	Turkey: Tekirdag
<i>B.distachyon</i>	Tek4	27,5191	41,0112	Turkey: Tekirdag



**Supplementary Table 5.** Topological congruence tests between **(a)** the *B. distachyon* nuclear species tree (Gordon et al. 2017) and **(b)** the *B. distachyon* plastome tree (Sancho et al. 2018) versus the *B. distachyon* dehydrin *Bdhn* tree. Test(s) were performed for significance of likelihood-score differences. KH: Kishino-Hasegawa test using normal approximation, two-tailed test. SH: Shimodaira-Hasegawa test using RELL bootstrap (one-tailed test). AU: Shimodaira Approximately Unbiased test. Values for KH/SH/AU tests are P values for the null hypothesis of no difference between trees. \*the null hypothesis is accepted. Number of bootstrap replicates = 1,000,000.

		KH test					SH		
a)		-lnL	Diff'-lnL	s.d.	T	P	SH-test	wtd-SH	AU
Tree1= Brachy nuclear tree (best)	46255.5731	(best)							
Tree2= Brachy <i>Bdhn</i> tree	54391.9775	8136.40442	202.241	40.231	<0.0001*	0.0000*	0.0000*	~0*	
Tree1=Brachy <i>Bdhn</i> tree (best)	5898.89581	(best)							
Tree2=Brachy nuclear tree	6170.77777	271.88196	59.738	4.551	<0.0001*	0.0000*	0.0000*	~0*	
		* P < 0.05							
(b)									
Tree1= Brachy plastome tree (best)	1442.4868	(best)							
Tree2= Brachy <i>Bdhn</i> tree	2334.75366	892.26686	52.856	16.881	<0.0001*	0.0000*	0.0000*	~0*	
Tree1= Brachy <i>Bdhn</i> tree (best)	5898.89581	(best)							
Tree2= Brachy plastome tree	6268.97012	370.07431	91.549	4.042	0.0001*	0.0003*	0.0003*	~0*	
		* P < 0.05							

**Supplementary table 6.** *Brachypodium distachyon* climate data. **(a)** Values of 19 current climate parameters retrieved from worldclim for the sampled localities of the studied *B. distachyon* ecotypes. Climate, climatic class of the *B. distachyon* ecotypes classified according to their PCA1 values (cold:> 2.5; mesic: (-2.5) – (2.5); warm: < - 2.5; see Supplementary Figure S5). **(b)** PCA1 and PCA2, coordinate values of the first and second PCA axes obtained from the climate PC analysis.

**(a)**

ecotype	longitude	latitude	altitude	bio1	bio2	bio3	bio4	bio5	bio6	bio7	bio8	bio9	bio10	bio11	bio12	bio13	bio14	bio15	bio16	bio17	bio18	bio19	PCA1	Climate
ABR2	3.3	43.65	265	13.3	10	3.7	577.4	27.9	1.3	26.6	9.9	20.8	20.8	6	707	85	29	23	218	126	126	188	2.5793	Cold
ABR3	0.07311	42.1805	798	10.1	10	3.8	566.4	24.6	-1.5	26.1	12.1	3	17.5	3	688	79	40	18	206	143	162	143	4.8611	Cold
ABR4	0.7168	42.26265	932	9.9	9.5	3.6	582.3	24.2	-1.6	25.8	11.8	2.6	17.4	2.6	873	96	53	18	262	176	227	176	5.6901	Cold
ABR5	-0.58	42.581	986	8.7	9.8	3.9	540.9	22.6	-2.4	25	10.5	15.8	15.8	2	842	90	48	15	237	177	184	208	5.3953	Cold
ABR6	-2.203	42.581	557	12.1	10.1	3.9	557.9	26.6	0.9	25.7	8.8	19.3	19.3	5.1	668	71	36	18	191	131	131	174	3.4004	Cold
ABR8	11.319695	43.314569	300	13.7	9	3.4	600.3	28.7	2.5	26.2	10.5	21.6	21.6	6.4	757	101	29	29	262	117	117	203	2.1759	Mesic
Adi10	38.352277	38.770694	839	13.6	9.8	2.7	936.7	33.4	-2.8	36.2	12.2	25.3	25.3	1.3	459	63	2	57	172	13	25	161	-1.7567	Mesic
Adi12	38.352277	38.770694	839	13.6	9.8	2.7	936.7	33.4	-2.8	36.2	12.2	25.3	25.3	1.3	459	63	2	57	172	13	25	161	-1.7567	Mesic
Adi2	38.352277	38.770694	839	13.6	9.8	2.7	936.7	33.4	-2.8	36.2	12.2	25.3	25.3	1.3	459	63	2	57	172	13	25	161	-1.7567	Mesic
Bd1-1	28.251	38.417	644	13.8	11.5	3.8	660.1	30.2	0.7	29.5	5.6	22	22.4	5.6	698	146	8	72	360	38	39	360	-0.5973	Mesic
Bd18-1	33.730025	39.36784	1057	10.4	10.9	3.4	747.4	27.4	-4.3	31.7	0.4	19.4	19.6	0.4	445	63	6	48	161	29	49	161	0.7309	Mesic
Bd2-3	44.403075	33.760883	40	22.7	15.2	3.8	877.5	43.7	4.5	39.2	12.7	33.7	33.7	11.3	171	31	0	86	88	0	0	87	-5.7177	Warm
Bd21ctrl	44.535	36.766	1089	15	12.1	3.1	961.1	36	-2.8	38.8	3.6	27	27	2.6	728	136	0	86	385	3	3	349	-3.5166	Warm
Bd21-3	44.535	36.766	1089	15	12.1	3.1	961.1	36	-2.8	38.8	3.6	27	27	2.6	728	136	0	86	385	3	3	349	-3.5166	Warm
Bd3-1	44.535	36.766	1089	15	12.1	3.1	961.1	36	-2.8	38.8	3.6	27	27	2.6	728	136	0	86	385	3	3	349	-3.5166	Warm
Bd30-1	-3.558733	36.990489	810	14.7	11.4	3.8	603.2	31.7	2.2	29.5	8.4	22.9	22.9	7.5	467	63	5	54	181	24	24	175	-0.4576	Mesic
BdTR10c	31.884911	37.778233	1448	9.4	11.5	3.5	750	27.2	-5.6	32.8	-0.3	18.6	18.9	-0.3	522	77	10	49	209	36	52	209	0.8878	Mesic
BdTR11g	27.477	41.422	89	13	11.3	3.7	666.2	29.5	-0.3	29.8	6.2	20.9	21.5	4.5	598	78	18	37	227	74	86	202	1.0333	Mesic
BdTR11i	28.040197	39.738164	229	13.7	10.9	3.7	683.7	29.8	0.5	29.3	7	21.9	22.4	5	652	108	11	56	284	48	49	282	0.0435	Mesic
BdTR1i	28.583	38.093	956	12.6	11.5	3.7	697.5	29.7	-0.9	30.6	3.9	21.3	21.6	3.9	748	146	10	68	376	43	49	376	-0.2852	Mesic
BdTR2b	31.331114	40.082097	894	10.9	10.5	3.4	714.2	27.4	-2.9	30.3	1.5	19.6	19.8	1.5	488	61	17	34	159	60	85	159	1.5604	Mesic
BdTR2g	32.985	40.394	1531	7.3	10.5	3.3	722	23.9	-7.1	31	-2.4	16	16.2	-2.4	623	84	20	42	221	67	97	221	2.6038	Cold
BdTR5i	32.985367	40.393647	1531	7.3	10.5	3.3	722	23.9	-7.1	31	-2.4	16	16.2	-2.4	623	84	20	42	221	67	97	221	2.6038	Cold
BdTR9k	30.788631	39.75295	900	10.7	11	3.5	729.1	27.8	-3.5	31.3	9.8	19.5	19.8	1.1	419	52	11	37	136	45	67	134	1.1200	Mesic
Bis1	41.015083	37.876556	608	16.5	13.1	3.3	928.6	38.9	-0.6	39.5	9.7	28.3	28.3	4.5	548	83	1	70	237	6	10	219	-3.6626	Warm
Kah1	38.533	37.734	657	16.9	11	2.9	914.8	37.3	0.6	36.7	5.3	28.6	28.6	5.3	586	108	1	77	291	7	10	291	-3.5423	Warm
Kah5	38.533	37.734	657	16.9	11	2.9	914.8	37.3	0.6	36.7	5.3	28.6	28.6	5.3	586	108	1	77	291	7	10	291	-3.5423	Warm
Koz1	41.61	38.152	819	15.3	12.1	3	951.9	37.2	-2.1	39.3	8.3	27.4	27.4	3.1	703	104	1	69	303	10	10	283	-3.2693	Warm
Koz3	41.61	38.152	819	15.3	12.1	3	951.9	37.2	-2.1	39.3	8.3	27.4	27.4	3.1	703	104	1	69	303	10	10	283	-3.2693	Warm
RON2	-0.963	42.781	956	8.9	9.9	3.9	539.5	22.9	-2.2	25.1	3.1	16	16	2.2	952	101	52	16	274	190	190	257	5.4782	Cold

(b)

Variable contribution	PCA1	PCA2
bio1	7.04157791	2.8336316
bio2	5.1431788	0.23831544
bio3	3.59658313	1.20932109
bio4	7.92629573	0.71530785
bio5	9.29173338	0.57639096
bio6	0.48821208	6.97369089
bio7	8.7044993	0.30756729
bio8	0.03627953	10.374377
bio9	8.12122146	0.14333639
bio10	9.05581757	0.73901616
bio11	1.08408395	6.54349079
bio12	2.28358537	11.4483415
bio13	0.23276403	18.6365656
bio14	8.64758564	0.05494295
bio15	9.03019188	1.48194295
bio16	0.49621767	18.6220566
bio17	8.61189114	0.08756497
bio18	9.14009127	0.07915297
bio19	1.06819015	18.9349869

**Supplementary Table 7.** *Brachypodium distachyon* dehydrin expression data. Filtered and normalized transcripts per million (TPM) values of annotated dehydrins. Only four dehydrin genes (*Bdhn1a*, *Bdhn2*, *Bdhn3*, *Bdhn7*) were expressed in leaves of 31-days grown plants. Plants were subjected to drought (W: watered, D: Drought) and temperature (C: Cold, H: Hot) stress conditions (see text). Code indicates the sampling code used in the RNAseq analysis.

Drought (D)						Watered (W)					
Code	accession	<i>Bdhn1a</i>	<i>Bdhn2</i>	<i>Bdhn3</i>	<i>Bdhn7</i>	Code	accession	<i>Bdhn1a</i>	<i>Bdhn2</i>	<i>Bdhn3</i>	<i>Bdhn7</i>
BA030_HD_ABR2	ABR2	309,6	207,4	131,8	21	BA053_HW_ABR2	ABR2	199,6	27,2	5,3	1
BA101_HD_ABR2	ABR2	150,4	142,4	278,7	19	BA085_HW_ABR2	ABR2	143,6	67,5	39,1	3,6
BA366_CD_ABR2	ABR2	181,8	183,1	227,7	26,6	BA145_HW_ABR2	ABR2	132,7	36,5	0	1,7
BA439_CD_ABR2	ABR2	214,9	135,5	51,5	11	BA403_CW_ABR2	ABR2	163,6	53	30,2	2,9
BA006_HD_ABR3	ABR3	304,9	182,2	32,1	10,7	BA447_CW_ABR2	ABR2	120,5	52	26	4,7
BA103_HD_ABR3	ABR3	197,7	326	738,2	75,7	BA096_HW_ABR3	ABR3	248,9	29,4	8,5	3,8
BA418_CD_ABR3	ABR3	328,3	116,6	43,9	9,4	BA146_HW_ABR3	ABR3	132,4	13,2	3,3	0
BA465_CD_ABR3	ABR3	224,2	51,4	65,3	22,3	BA413_CW_ABR3	ABR3	193,5	46,6	26,9	1,8
BA038_HD_ABR4	ABR4	299,5	76,8	7,3	2,4	BA419_CW_ABR3	ABR3	205,1	69,4	10,1	1,3
BA170_HD_ABR4	ABR4	226,2	194,7	164,3	37,6	BA040_HW_ABR4	ABR4	109,5	27,1	1,2	0
BA368_CD_ABR4	ABR4	270,3	65,9	15,7	15,7	BA043_HW_ABR4	ABR4	230,1	35,3	7,3	3,7
BA521_CD_ABR4	ABR4	192,6	96,3	61,4	4,7	BA477_CW_ABR4	ABR4	594,4	80,7	5,8	2,7
BA024_HD_ABR5	ABR5	335,1	298,2	62,4	17	BA508_CW_ABR4	ABR4	143,5	50,5	5,8	3,2
BA104_HD_ABR5	ABR5	234,1	580,1	681,7	92,8	BA161_HW_ABR5	ABR5	143,9	33,7	7,6	2,4
BA454_CD_ABR5	ABR5	188,7	55,4	140,2	45	BA479_CW_ABR5	ABR5	418	55,8	3,9	0,4
BA522_CD_ABR5	ABR5	217,7	279,5	46,2	21,9	BA502_CW_ABR5	ABR5	254,8	23,3	9,4	6,1
BA037_HD_ABR6	ABR6	333,5	130,4	147,8	13,5	BA123_HW_ABR6	ABR6	357,3	39,7	3,6	10,8
BA099_HD_ABR6	ABR6	281,5	397,3	2175,5	102,5	BA153_HW_ABR6	ABR6	340,4	26,1	3,9	3,9
BA416_CD_ABR6	ABR6	289	199,9	778,6	33,6	BA437_CW_ABR6	ABR6	258,1	26,1	4,4	2,5
BA523_CD_ABR6	ABR6	256,7	90,5	300,3	16,6	BA452_CW_ABR6	ABR6	308,2	18,1	3,1	2,6
BA100_HD_ABR8	ABR8	298,2	144,7	199,2	63,3	BA008_HW_ABR8	ABR8	224,6	36,4	4,2	0
BA143_HD_ABR8	ABR8	379,6	336,2	262,1	112	BA138_HW_ABR8	ABR8	128,8	21,1	3,5	0
BA415_CD_ABR8	ABR8	502,2	312,7	177,6	84,1	BA360_CW_ABR8	ABR8	249	35,8	5,6	1,7
BA506_CD_ABR8	ABR8	940,2	644,1	285,3	251,7	BA517_CW_ABR8	ABR8	292,4	23,1	3,3	2,3
BA049_HD_Adi10	Adi10	440	197,7	215,9	112,4	BA067_HW_Adi10	Adi10	632,4	37,3	1,7	0,4
BA052_HD_Adi10	Adi10	357,1	249,5	258,2	64,7	BA105_HW_Adi10	Adi10	415,9	49,3	8,4	3,1
BA478_CD_Adi10	Adi10	820,4	1251,9	1961,7	462	BA428_CW_Adi10	Adi10	841,2	51	8,7	6,5
BA513_CD_Adi10	Adi10	1020,1	2043,2	2431,9	692,5	BA520_CW_Adi10	Adi10	341,2	20,1	8,1	2,9
BA036_HD_Adi12	Adi12	558	751,2	290,8	59,5	BA041_HW_Adi12	Adi12	339	81,9	4,9	2,4
BA140_HD_Adi12	Adi12	377,1	260,2	133	56,5	BA044_HW_Adi12	Adi12	396,1	43,2	0	0
BA455_CD_Adi12	Adi12	778,7	840	1104,1	330	BA407_CW_Adi12	Adi12	193,2	96	30,9	13,7
BA525_CD_Adi12	Adi12	240,8	515,5	466,2	113,3	BA423_CW_Adi12	Adi12	746,4	53,9	11,2	1,7

BA050_HD_Adi2	Adi2	458,9	161,7	37,1	11	BA176_HW_Adi2	Adi2	402,2	68	5	3,8
BA094_HD_Adi2	Adi2	396,1	457,9	318,7	55,9	BA357_CW_Adi2	Adi2	489,2	36,5	1,1	3,2
BA500_CD_Adi2	Adi2	528,3	913,4	957	123,8	BA468_CW_Adi2	Adi2	398,6	65,7	4	2
BA509_CD_Adi2	Adi2	456,6	405,1	463,1	64,5	BA354_CW_Bd1-1	Bd1-1	390,9	46,9	8,1	1,5
BA025_HD_Bd1-1	Bd1-1	475,8	282,7	88,6	27,7	BA496_CW_Bd1-1	Bd1-1	320	17,6	14,4	4
BA051_HD_Bd1-1	Bd1-1	352,8	22	3,3	2,2	BA060_HW_Bd18-1	Bd18-1	239,9	21,8	5	0
BA122_HD_Bd1-1	Bd1-1	235,1	42,5	53,7	4,5	BA063_HW_Bd18-1	Bd18-1	278,7	16,2	2,8	0,9
BA442_CD_Bd1-1	Bd1-1	369,3	70,6	42	14,3	BA375_CW_Bd18-1	Bd18-1	160,7	14,5	6,9	0,8
BA475_CD_Bd1-1	Bd1-1	582,4	352,4	578,5	79,5	BA446_CW_Bd18-1	Bd18-1	266,7	14,6	6,3	0
BA093_HD_Bd18-1	Bd18-1	464,3	392	257,2	138,3	BA069_HW_Bd21	Bd21	324,2	24,3	1,3	0,7
BA453_CD_Bd18-1	Bd18-1	1009,6	704,2	564	207,5	BA112_HW_Bd21	Bd21	363,1	70	24	5,7
BA056_HD_Bd21	Bd21	292,8	125	23,5	12,3	BA386_CW_Bd21	Bd21	183,1	24,9	2,4	1
BA163_HD_Bd21	Bd21	249,1	129,2	28,3	45,6	BA456_CW_Bd21	Bd21	330	59,6	37,8	6
BA459_CD_Bd21	Bd21	440,2	148,4	65,8	36,5	BA054_HW_Bd21-3	Bd21-3	307,6	25,8	9,4	1,8
BA499_CD_Bd21	Bd21	325,3	52,3	4,7	2,9	BA171_HW_Bd21-3	Bd21-3	276,1	26,2	18,8	0,7
BA097_HD_Bd21-3	Bd21-3	478,7	621,3	567	243,4	BA458_CW_Bd21-3	Bd21-3	288,6	25,4	14,7	2
BA111_HD_Bd21-3	Bd21-3	452,8	647	487,3	145,7	BA086_HW_Bd2-3	Bd2-3	181,2	37,4	5	2,1
BA430_CD_Bd21-3	Bd21-3	966,8	1402	1464,4	692,9	BA114_HW_Bd2-3	Bd2-3	422,7	54,3	0	0
BA512_CD_Bd21-3	Bd21-3	503,2	539,2	266,5	103,9	BA487_CW_Bd2-3	Bd2-3	327	82,5	6,9	3
BA023_HD_Bd2-3	Bd2-3	531,4	253	121,1	16,7	BA492_CW_Bd2-3	Bd2-3	542,5	48,5	3,8	4,9
BA088_HD_Bd2-3	Bd2-3	635,6	173,8	50,8	38,3	BA005_HW_Bd30-1	Bd30-1	266,2	37,1	5	3
BA353_CD_Bd2-3	Bd2-3	291,6	40,1	6,9	1,9	BA018_HW_Bd30-1	Bd30-1	244,7	20,3	2,5	0,4
BA494_CD_Bd2-3	Bd2-3	550,1	341,3	200,5	60,2	BA417_CW_Bd30-1	Bd30-1	504,7	32,9	8,1	2,9
BA079_HD_Bd30-1	Bd30-1	353,5	492,1	287	76,5	BA474_CW_Bd30-1	Bd30-1	444,6	44	7,3	2,9
BA162_HD_Bd30-1	Bd30-1	198,6	406,5	439,7	73,3	BA007_HW_Bd3-1	Bd3-1	321,4	34,7	4,6	1,5
BA425_CD_Bd30-1	Bd30-1	1005,9	1632,6	2616,2	685,5	BA012_HW_Bd3-1	Bd3-1	287,1	46,4	2,6	2,2
BA481_CD_Bd30-1	Bd30-1	396,7	515,6	283,3	55,5	BA429_CW_Bd3-1	Bd3-1	477,4	43	20,9	0
BA166_HD_Bd3-1	Bd3-1	316,4	405,3	1017,8	55,9	BA434_CW_Bd3-1	Bd3-1	256,1	46,6	10	7,2
BA398_CD_Bd3-1	Bd3-1	441,6	446,3	730,1	78	BA119_HW_BdTR10c	BdTR10c	196,7	36,9	0	0
BA422_CD_Bd3-1	Bd3-1	427,5	544,5	3386,7	854,4	BA131_HW_BdTR10c	BdTR10c	232	65	25,5	0
BA121_HD_BdTR10c	BdTR10c	242,1	214,3	471,6	66,8	BA384_CW_BdTR10c	BdTR10c	223	29,9	1,3	0
BA173_HD_BdTR10c	BdTR10c	380,8	122,7	284,2	82	BA436_CW_BdTR10c	BdTR10c	177,4	56,1	7,1	3,5
BA421_CD_BdTR10c	BdTR10c	603,2	483	1912,7	439,9	BA021_HW_BdTR11g	BdTR11g	320,5	63	6,2	1,4
BA440_CD_BdTR10c	BdTR10c	415,4	490,6	1028,6	187,7	BA032_HW_BdTR11g	BdTR11g	547	46,8	9,1	2,9
BA059_HD_BdTR11g	BdTR11g	452,4	370,4	615,1	63,5	BA406_CW_BdTR11g	BdTR11g	373,6	78,3	51,5	22,4
BA090_HD_BdTR11g	BdTR11g	590,1	645,2	1214,5	215,9	BA493_CW_BdTR11g	BdTR11g	314,6	49,3	3,6	2,1
BA397_CD_BdTR11g	BdTR11g	479,7	522,4	607	65,4	BA042_HW_BdTR11i	BdTR11i	274,4	30,1	2,8	2,1

BA510_CD_BdTR11g	BdTR11g	466,4	280,8	135,7	37,8	BA148_HW_BdTR11i	BdTR11i	230,3	39,3	4,2	1,4
BA102_HD_BdTR11i	BdTR11i	483,9	567,1	981,6	139,8	BA377_CW_BdTR11i	BdTR11i	258,1	27,6	4	2,2
BA128_HD_BdTR11i	BdTR11i	505,6	651	1554,8	175,1	BA526_CW_BdTR11i	BdTR11i	443,8	72,9	8,3	5,2
BA408_CD_BdTR11i	BdTR11i	708,1	680,3	833,4	135,7	BA022_HW_BdTR13a	BdTR13a	345,6	79,5	5,7	0
BA450_CD_BdTR11i	BdTR11i	429,9	314,4	305,8	46,7	BA174_HW_BdTR13a	BdTR13a	324	45,8	2,6	2,6
BA361_CD_BdTR12c	BdTR12c	297,8	37	9,7	5,8	BA371_CW_BdTR13a	BdTR13a	213,6	23,8	6,7	0
BA061_HD_BdTR13a	BdTR13a	382	213,3	110,5	41,8	BA405_CW_BdTR13a	BdTR13a	310,6	30,7	14,6	3,8
BA144_HD_BdTR13a	BdTR13a	369,6	249,2	130,1	69,2	BA070_HW_BdTR1i	BdTR1i	274,8	23,6	2,5	0
BA394_CD_BdTR13a	BdTR13a	363,5	160	95,3	31,8	BA155_HW_BdTR1i	BdTR1i	375,1	48,1	5,9	3,8
BA460_CD_BdTR13a	BdTR13a	1347,2	930,2	735,4	270,3	BA469_CW_BdTR1i	BdTR1i	409,4	34,5	9	3,3
BA108_HD_BdTR1i	BdTR1i	639,7	788	1133,3	488,1	BA486_CW_BdTR1i	BdTR1i	348,4	78,2	5,4	2,6
BA134_HD_BdTR1i	BdTR1i	315,7	191,5	199,9	73,1	BA115_HW_BdTR2b	BdTR2b	348,7	11,1	0	0
BA457_CD_BdTR1i	BdTR1i	579,7	591,8	246,9	79	BA133_HW_BdTR2b	BdTR2b	270,5	58,2	6,4	3,9
BA480_CD_BdTR1i	BdTR1i	796,6	989,7	1329,2	364,4	BA378_CW_BdTR2b	BdTR2b	259,5	14,5	3,5	1,2
BA003_HD_BdTR2b	BdTR2b	874,2	662,1	896,5	314,5	BA503_CW_BdTR2b	BdTR2b	377,6	73,2	10,9	2,1
BA091_HD_BdTR2b	BdTR2b	658,5	524,5	502,4	140	BA107_HW_BdTR2g	BdTR2g	475,5	44,3	3,2	4,4
BA389_CD_BdTR2b	BdTR2b	299,5	213,3	177,2	58,6	BA167_HW_BdTR2g	BdTR2g	401,5	36,3	7,7	3,3
BA472_CD_BdTR2b	BdTR2b	320,5	222,3	168,1	32,5	BA445_CW_BdTR2g	BdTR2g	334,5	41,6	5,2	4,2
BA124_HD_BdTR2g	BdTR2g	784,1	1119	2009,5	616,6	BA527_CW_BdTR2g	BdTR2g	594,9	48,9	7,4	2,5
BA165_HD_BdTR2g	BdTR2g	402,6	473,2	1420,3	511,6	BA071_HW_BdTR3c	BdTR3c	349,4	22	2,1	1,4
BA364_CD_BdTR2g	BdTR2g	1009,2	1135,3	2063,8	712,3	BA129_HW_BdTR3c	BdTR3c	227,6	38,8	2,6	2,6
BA369_CD_BdTR2g	BdTR2g	806,3	537,8	578,2	230,2	BA362_CW_BdTR3c	BdTR3c	368,9	105,8	162,7	53,3
BA073_HD_BdTR3c	BdTR3c	432,8	335,1	402,5	61,8	BA427_CW_BdTR3c	BdTR3c	234,2	75,7	8,1	3,9
BA172_HD_BdTR3c	BdTR3c	676,9	752,3	1712,3	351,6	BA160_HW_BdTR5i	BdTR5i	258,8	48,1	3,3	0,4
BA370_CD_BdTR3c	BdTR3c	542,5	585,9	354,6	53,6	BA372_CW_BdTR5i	BdTR5i	119,9	23,4	9,3	1,5
BA424_CD_BdTR3c	BdTR3c	985,9	1131,8	1662	310,6	BA464_CW_BdTR5i	BdTR5i	455,1	38,7	6,5	5,2
BA065_HD_BdTR5i	BdTR5i	358,7	296	254,4	57,5	BA113_HW_BdTR9k	BdTR9k	270,8	55,8	0	0
BA082_HD_BdTR5i	BdTR5i	366,7	390,6	459,3	80,5	BA125_HW_BdTR9k	BdTR9k	282,5	32,3	5,4	2,7
BA470_CD_BdTR5i	BdTR5i	367,3	369,8	607	94	BA383_CW_BdTR9k	BdTR9k	309,8	41,3	2,6	0,4
BA473_CD_BdTR5i	BdTR5i	345,6	298,7	254,6	50,9	BA515_CW_BdTR9k	BdTR9k	0	0	0	0
BA002_HD_BdTR9k	BdTR9k	377,8	193,6	54,1	21,5	BA118_HW_Bis1	Bis1	252,7	32,8	2,3	0
BA033_HD_BdTR9k	BdTR9k	400,2	201,3	104,5	29,4	BA156_HW_Bis1	Bis1	577,5	32,3	10,6	1,1
BA363_CD_BdTR9k	BdTR9k	514,8	390,2	585,7	209,9	BA385_CW_Bis1	Bis1	237,8	29,9	3,4	1,7
BA410_CD_BdTR9k	BdTR9k	454,2	259,8	136,3	52,7	BA390_CW_Bis1	Bis1	276,9	51,3	4,2	0,6
BA110_HD_Bis1	Bis1	606,4	739,8	1165,4	357,5	BA147_HW_Kah1	Kah1	167,3	41,4	3,1	0
BA142_HD_Bis1	Bis1	544,7	393,2	352,6	133,2	BA169_HW_Kah1	Kah1	218	68,9	8,6	1,5
BA373_CD_Bis1	Bis1	455,8	282,8	276,4	64,5	BA356_CW_Kah1	Kah1	135	47,9	3	0,8

BA519_CD_Bis1	Bis1	288,5	152,2	181,6	43,3
BA046_HD_Kah1	Kah1	251,7	91,2	14,7	1,5
BA168_HD_Kah1	Kah1	184,9	185,4	223,9	41
BA382_CD_Kah1	Kah1	552,3	517,7	470,1	81,4
BA495_CD_Kah1	Kah1	552,7	775	912,6	139,7
BA048_HD_Kah5	Kah5	401,4	219,2	144,2	44,3
BA095_HD_Kah5	Kah5	386,8	648,6	480,8	58,5
BA401_CD_Kah5	Kah5	444,7	708	526,8	88,6
BA489_CD_Kah5	Kah5	498,2	867	776	154,1
BA127_HD_Koz1	Koz1	337,2	319,5	341,6	41,9
BA132_HD_Koz1	Koz1	377,6	429,1	638,9	75,8
BA395_CD_Koz1	Koz1	458,4	415,4	127,4	27
BA507_CD_Koz1	Koz1	505,3	585,8	388	84,8
BA081_HD_Koz3	Koz3	523,6	592,8	892,7	120
BA388_CD_Koz3	Koz3	1094,8	1066,9	5661,6	1244,7
BA467_CD_Koz3	Koz3	1201,8	1447,1	4545,9	1203
BA089_HD_Koz-3	Koz3	773,9	1189,3	2664,1	681,1
BA035_HD_Ron2	Ron2	1429,9	1947,5	1398,8	364,2
BA379_CD_Ron	Ron2	264	166	74,8	15,9
BA432_CD_Ron2	Ron2	274,6	254,9	202,5	41,2

BA420_CW_Kah1	Kah1	254,1	46,2	11,5	3,2
BA047_HW_Kah5	Kah5	280,1	28,2	5,6	0,9
BA158_HW_Kah5	Kah5	268,7	128,5	16	3,1
BA399_CW_Kah5	Kah5	351,8	34	19,5	7,3
BA482_CW_Kah5	Kah5	315,1	30,4	5,6	2
BA141_HW_Koz1	Koz1	323,6	22,5	1	1
BA157_HW_Koz1	Koz1	353	68,7	9,5	0,6
BA501_CW_Koz1	Koz1	415,6	43,4	4,3	2,9
BA511_CW_Koz1	Koz1	397,2	79,4	31,8	10,6
BA057_HW_Koz3	Koz3	325,3	18,2	1,3	0
BA074_HW_Koz3	Koz3	435,3	20,5	2	1,1
BA411_CW_Koz3	Koz3	283,6	28,8	15,3	3,7
BA484_CW_Koz3	Koz3	332,2	47,8	9,3	2,3
BA026_HW_Ron2	Ron2	218	122,8	15,3	1,7
BA151_HW_Ron2	Ron2	350,5	38,4	7	1,5
BA409_CW_Ron2	Ron2	296,4	36,6	73,2	32,9
BA431_CW_Ron2	Ron2	259,2	15,4	6,5	4

**Supplementary Table 8.** Summary statistics of dehydrin *Bdhn1a*, *Bdhn2*, *Bdhn3* and *Bdhn7* gene expressions under dry (D) vs watered (W) conditions and comparative differential expression (DE) tests in *B. distachyon* ecotypes. (a) Kruskal-Wallis rank tests (D vs W) for each *Bdhn* gene. (b) Wilcoxon pairwise tests of normalized TPM values across ecotypes, p-values were adjusted with the Benjamini–Hochberg (BH) procedure, controlling the false discovery rate, to correct for multiple comparisons; n. s., non significant, p≤ 0.05\* significant values are highlighted in bold.

(a)

Var	<i>Bdhn1a</i>	<i>Bdhn2</i>	<i>Bdhn3</i>	<i>Bdhn7</i>
t-test	123.74	179.98	178.8	175.02
df	63	63	63	63
p-value	7.69E-06	3.38E-13	5.10E-15	1.75E-12

(b)

Ecotype	<i>Bdhn1a</i>			<i>Bdhn2</i>			<i>Bdhn3</i>			<i>Bdhn7</i>		
	D	W	W-test	D	W	W-test	D	W	W-test	D	W	W-test
ABR2	214.175	159.875	n.s	<b>167.1</b>	<b>46.05</b>	*	<b>172.425</b>	<b>18.65</b>	*	<b>19.4</b>	<b>2.3</b>	*
ABR3	263.775	215.833	n.s	169.05	48.467	n.s	219.875	15.167	n.s	29.525	2.3	n.s
ABR4	247.15	269.375	n.s	108.425	48.4	n.s	<b>62.175</b>	<b>5.025</b>	*	15.1	2.4	n.s
ABR5	252.633	272.233	n.s	311.233	37.6	n.s	294.767	6.967	n.s	51.6	2.967	n.s
ABR6	290.175	302.233	n.s	<b>204.525</b>	<b>23.433</b>	*	850.55	3.8	n.s	41.55	3	n.s
ABR8	530.05	255.333	n.s	359.425	31.767	n.s	231.05	4.367	n.s	127.775	1.333	n.s
Adi10	659.4	532.767	n.s	935.575	40.133	n.s	1216.925	8.4	n.s	332.9	4.167	n.s
Adi12	488.65	418.675	n.s	<b>591.725</b>	<b>68.75</b>	*	<b>498.525</b>	<b>11.75</b>	*	<b>139.825</b>	<b>4.45</b>	*
Adi2	461.1	430	n.s	511	56.733	n.s	437.6	3.367	n.s	63.567	3	n.s
Bd1_1	414.3	355.45	n.s	152.35	32.25	n.s	45.95	11.25	n.s	14.95	2.75	n.s
Bd18-1	736.95	259.3	n.s	548.1	19	n.s	410.6	3.9	n.s	172.9	0.45	n.s
Bd21-3	632.767	290.767	n.s	890.1	25.8	n.s	839.567	14.3	n.s	360.667	1.5	n.s
Bd21ctrl	326.85	300.1	n.s	113.725	44.7	n.s	30.575	16.375	n.s	24.325	3.35	n.s
Bd2-3	502.175	368.35	n.s	202.05	55.675	n.s	94.825	3.925	n.s	29.275	2.5	n.s
Bd30-1	488.675	365.05	n.s	<b>761.7</b>	<b>33.575</b>	*	<b>906.55</b>	<b>5.725</b>	*	<b>222.7</b>	<b>2.3</b>	*
Bd3-1	395.167	361.967	n.s	465.367	41.367	n.s	1711.533	9.367	n.s	329.433	1.233	n.s
BdTR10c	410.375	200.2	n.s	327.65	43	n.s	924.275	4.2	n.s	194.1	1.75	n.s
BdTR11g	497.15	388.925	n.s	<b>454.7</b>	<b>59.35</b>	*	<b>643.075</b>	<b>17.6</b>	*	<b>95.65</b>	<b>7.2</b>	*
BdTR11i	531.875	325.433	n.s	553.2	43.533	n.s	918.9	5.033	n.s	124.325	3.167	n.s



BdTR13a	697.567	298.45	n.s	434.5	44.95	n.s	313.733	7.4	n.s	114.633	1.6	*
BdTr1i	582.925	351.925	n.s	640.25	46.1	*	727.325	5.7	*	251.15	2.425	*
BdTR2b	538.175	318.55	n.s	405.55	43.85	n.s	436.05	7.2	n.s	136.4	1.65	n.s
BdTR2g	750.55	451.6	n.s	816.325	42.775	*	1517.95	5.875	*	517.675	3.6	*
BdTR3c	659.525	317.5	n.s	701.275	67.833	n.s	1032.85	57.633	n.s	194.4	19.533	n.s
BdTR5i	364.233	277.933	n.s	352.133	36.733	n.s	440.233	6.367	n.s	77.333	2.367	n.s
BdTR9k	436.75	197.433	n.s	261.225	24.533	n.s	220.15	2.667	n.s	78.375	1.033	n.s
Bis1	450.233	364.067	n.s	391.6	37.833	n.s	541.133	6.067	n.s	155.1	1.133	n.s
Kah1	385.4	202.367	n.s	392.325	54.333	n.s	405.325	7.7	n.s	65.9	1.833	n.s
Kah5	432.775	303.925	*	610.7	55.275	*	481.95	11.675	*	86.375	3.325	*
Koz1	481.85	388.6	n.s	500.6	63.833	n.s	257.7	15.2	n.s	55.9	4.7	n.s
Koz3	898.525	344.1	*	1074.025	28.825	*	3441.075	6.975	*	812.2	1.775	*
RON2	656.167	288.3	n.s	789.467	65.933	n.s	558.7	31.833	n.s	140.433	12.033	n.s

**Supplementary Table 9.** Linear model (lm) regression analysis for comparative differential gene expressions of dehydrin *Bdhn* genes in the studied *B. distachyon* ecotypes. W (watered) and D (dry) conditions. Significant p-values ( $p \leq 0.001$ \*\*\*).

W+D	<i>Bdhn1a ~ Bdhn2</i>	<i>Bdhn1a ~ Bdhn3</i>	<i>Bdhn1a ~ Bdhn7</i>	<i>Bdhn2 ~ Bdhn3</i>	<i>Bdhn2 ~ Bdhn7</i>	<i>Bdhn3 ~ Bdhn7</i>
Median	-11.12	-14.77	-14.05	-68.64	-72.05	-37.35
Residual standard error:	134.6	169.5	156.3	220.8	210.7	237
F-statistic:	368	148.3	214.6	344.9	401	1840
p-value:	< 2.20E-16***	< 2.20E-16***	< 2.20E-16***	< 2.20E-16***	< 2.20E-16***	< 2.20E-16***

**Supplementary Table 10.** Comparative analysis of dehydrin genes showing upregulated expression under drought compared to watered conditions in *Brachypodium distachyon* and *Triticum aestivum*. Orthology between the differentially expressed genes in the two species was retrieved through Ensembl Plants using BioMart and Blast searches using orthologies previously established in Galvez et al. (2019) (§).

<i>Brachypodium distachyon</i>			<i>Triticum aestivum</i>			
Gene name	RefSeq.v3.0 Name	Ref.Seqv3.1 Name	Original gene name	Gene name in Supplementary Table 1	RefSeq v2.1 Name	Differentially expressed genes under drought conditions (Galvez et al. 2019)
<i>Bdhn1</i>	BRADI_5g10860v3	Bradi5g10860	DHN11-A1	DHNTaes 1	TraesCS6A02G253300	Mild stress
<i>Bdhn2</i>	BRADI_3g51200v3	Bradi3g51200	DHN11-B1	DHNTaes 3	TraesCS6B02G273400	
			DHN11-D1	DHNTaes 2	TraesCS6D02G234700	
<i>Bdhn3</i>	BRADI_1g37410v3	Bradi1g37410	DHN4-B1	DHNTaes 9	TraesCS6B02G383500	Severe Stress
			DHN4-D1	DHNTaes 4	TraesCS6D02G332900	Severe Stress
			DHN3-A1	DHNTaes 12	TraesCS6A02G350600	Mild stress
			DHN3-A5	DHNTaes 13	TraesCS6A02G350800	
			DHN3-A6	DHNTaes 8	TraesCS6A02G350700	Mild stress
			DHN3-B6	DHNTaes 10	TraesCS6B02G383600	Mild stress
			DHN3-D6	DHNTaes 5	TraesCS6D02G333200	Severe Stress
			DHN3-D4	DHNTaes 11	TraesCS6D02G333100	Severe Stress
			DHN3-D8	DHNTaes 6	TraesCS6D02G333300	
			DHN3-D9	DHNTaes 7	TraesCS6D02G333600	Severe Stress
<i>Bdhn7</i>	BRADI_3g43870v3	Bradi3g43870	DHN38-A1	DHNTaes 14	TraesCS5A02G424700	
			DHN38-B1	DHNTaes 16	TraesCS5B02G426700	Severe Stress
			DHN38-D1§	DHNTaes 18§	TraesCS5D01G433200	
			DHN38-A2	DHNTaes 15	TraesCS5A02G424800	
			DHN38-B2§	DHNTaes 17§	TraesCS5B01G426800	Severe Stress
			DHN38-D2	DHNTaes 19	TraesCS5D02G433300	

**Supplementary Table 11.** Summary statistics of 12 drought-response phenotypic traits [leaf\_rwc (relative water content in leaf); leaf\_wc (water content in leaf); lma (leaf mass per área); pro (leaf proline content); abvrgd (above ground biomass); blwgrd (below ground biomass); ttlmass (total mass); rmr (root mass ratio); delta13c (carbon isotope, a proxy for lifetime integrated WUE); leafc (leaf carbon content); leafn (leaf nitrogen content); cn (leaf carbon/nitrogen ratio)] in dry (D) vs watered (W) *Brachypodium distachyon* plants. (a) Kruskal-Wallis rank tests (W vs D) for each phenotypic trait. (b) comparative pairwise Wilcoxon tests in the studied *B. distachyon* ecotypes; p-values were adjusted with the Benjamini–Hochberg (BH) procedure, controlling the false discovery rate, to correct for multiple comparisons; n, number of replicates. n. s., non significant, \*p≤ 0.05\*; significant values are highlighted in bold.

(a)

Var	Leaf_rwc	Leaf_wc	Lma	Pro	abvgrd	blwgrd	ttlmas	rmr	WUE	leafC	LeafN	C:N
t-test	197.24	172.97	166.68	189.78	190.61	161.24	181.31	192.97	192.67	169.61	188.34	188.8
df	63	63	63	63	63	63	63	63	63	63	63	63
p-value	9.46E-16***	3.42E-12***	2.62E-11***	1.24E-14***	9.32E-15***	1.47E-10***	2.17E-13***	4.15E-15***	4.60E-15***	1.02E-11***	2.02E-14***	7.32E-15***

(b)

Ecotype	n	leaf_rwc			leafwc			lma			pro			abvgrd			blwgrd		
		D	W	W-test	D	W	W-test	D	W	W-test	D	W	W-test	D	W	W-test	D	W	W-test
ABR2	4	95.92	99.09	*	275.41	327.41	*	31.09	27.07	*	39.54	17.51	*	82.39	82.83	n.s	54.70	39.94	n.s
ABR3	4	95.91	99.23	*	325.50	341.29	n.s	24.83	23.35	n.s	18.48	9.26	*	94.28	113.30	n.s	57.44	52.51	n.s
ABR4	4	96.62	99.44	*	312.84	357.86	*	28.94	27.19	n.s	15.44	8.76	*	53.93	63.83	*	32.19	29.34	*
ABR5	3	95.28	100.14	n.s	309.74	355.00	n.s	27.51	23.67	n.s	12.79	7.68	n.s	83.10	84.11	n.s	55.12	33.31	n.s
ABR6	4	95.07	99.73	*	300.31	334.41	*	27.93	25.84	*	24.37	10.16	*	72.96	80.03	n.s	40.48	30.95	*
ABR8	4	94.01	99.09	*	327.95	359.65	n.s	30.93	27.92	*	25.45	8.00	*	112.43	172.49	*	33.23	40.93	*
Adi10	4	92.50	99.49	*	333.21	372.90	*	28.86	24.35	*	54.79	10.94	*	133.87	225.64	*	67.65	80.73	n.s
Adi12	4	92.10	99.41	*	291.01	322.88	*	29.34	26.69	*	30.06	10.47	*	141.38	168.85	*	70.54	57.79	*
Adi2	3	94.99	97.91	n.s	282.54	307.59	n.s	28.99	25.70	n.s	40.57	8.61	n.s	102.75	161.41	n.s	55.39	49.99	n.s
Bd1-1	2	96.65	99.49	n.s	318.06	340.96	n.s	27.89	26.05	n.s	22.48	8.68	n.s	69.95	70.85	n.s	32.68	28.03	n.s
Bd18-1	2	92.46	98.01	n.s	305.47	330.20	n.s	29.18	26.35	n.s	26.56	9.00	n.s	127.49	166.53	n.s	60.50	52.55	n.s
Bd21ctrl	4	94.72	98.53	*	348.66	370.79	n.s	29.95	28.19	n.s	16.88	7.80	*	104.63	104.94	n.s	48.95	34.90	*
Bd21-3	3	88.24	99.96	n.s	300.78	333.15	n.s	34.40	29.66	n.s	46.00	7.99	n.s	132.92	166.58	n.s	76.00	57.59	n.s
Bd2-3	4	94.68	99.54	*	301.70	323.22	n.s	29.30	27.49	*	24.56	7.18	*	109.68	142.81	*	52.55	48.69	n.s
Bd30-1	4	91.94	98.74	*	290.94	360.88	*	29.98	24.18	*	39.52	8.27	*	108.47	150.05	*	55.83	70.51	*
Bd3-1	3	87.95	98.93	*	314.60	346.29	*	30.34	26.74	*	39.47	11.38	*	147.08	202.11	*	64.45	66.88	n.s
BdTR10c	4	92.18	99.85	n.s	292.36	346.45	n.s	28.54	24.40	n.s	62.13	9.26	n.s	122.84	179.83	n.s	54.84	78.85	n.s
BdTR11g	4	92.67	99.17	*	303.40	348.85	*	30.29	28.51	n.s	26.36	6.46	*	118.32	162.40	*	58.96	59.50	n.s
BdTR11i	4	92.16	98.87	*	301.41	356.48	*	31.49	26.81	*	44.23	7.77	*	123.81	151.69	*	54.83	57.03	n.s

BdTR13a	3	<b>94.01</b>	<b>99.13</b>	*	<b>298.81</b>	<b>335.52</b>	*	<b>30.04</b>	<b>28.16</b>	*	<b>20.39</b>	<b>7.56</b>	*	<b>101.63</b>	<b>130.20</b>	*	50.92	49.18	n.s
BdTR1i	4	<b>91.62</b>	<b>98.50</b>	*	<b>291.95</b>	<b>310.40</b>	*	<b>27.84</b>	<b>25.64</b>	*	<b>42.46</b>	<b>11.32</b>	*	<b>132.79</b>	<b>172.05</b>	*	67.58	65.85	n.s
BdTR2b	4	90.58	99.16	n.s	286.28	334.79	n.s	30.04	25.59	n.s	32.55	9.08	n.s	135.43	184.43	n.s	69.31	74.33	n.s
BdTR2g	4	<b>88.23</b>	<b>99.03</b>	*	<b>275.58</b>	<b>321.83</b>	*	<b>30.19</b>	<b>25.78</b>	*	<b>54.82</b>	<b>10.80</b>	*	141.09	152.06	n.s	78.53	55.90	n.s
BdTR3c	4	<b>91.01</b>	<b>99.87</b>	*	<b>287.62</b>	<b>335.43</b>	*	<b>29.31</b>	<b>24.88</b>	*	<b>29.50</b>	<b>8.46</b>	*	106.26	174.36	n.s	58.46	55.66	n.s
BdTR5i	3	92.84	98.68	n.s	292.29	324.81	n.s	31.54	26.77	n.s	42.44	9.39	n.s	97.23	141.26	n.s	62.53	64.18	n.s
BdTR9k	4	<b>95.21</b>	<b>98.97</b>	*	303.20	315.82	n.s	27.63	28.14	n.s	<b>19.61</b>	<b>14.46</b>	*	133.27	151.78	n.s	58.40	51.30	n.s
Bisl	3	93.77	98.41	n.s	300.90	329.00	n.s	29.34	25.63	n.s	21.24	7.71	n.s	97.16	113.62	n.s	45.96	41.93	n.s
Kah1	4	<b>94.02</b>	<b>99.23</b>	*	315.47	334.60	n.s	29.18	28.18	n.s	<b>31.07</b>	<b>9.33</b>	*	<b>109.04</b>	<b>136.56</b>	*	<b>55.51</b>	<b>48.92</b>	*
Kah5	4	<b>93.11</b>	<b>98.86</b>	*	311.66	343.46	n.s	27.96	26.56	n.s	<b>33.53</b>	<b>7.36</b>	*	<b>122.20</b>	<b>161.41</b>	*	48.54	50.30	n.s
Koz1	2	95.95	99.58	n.s	332.48	335.81	n.s	26.64	26.38	n.s	16.15	7.35	n.s	82.20	135.72	n.s	56.78	46.36	n.s
Koz3	4	<b>85.40</b>	<b>99.62</b>	*	<b>310.63</b>	<b>366.61</b>	*	<b>30.12</b>	<b>23.45</b>	*	<b>44.27</b>	<b>5.49</b>	*	122.40	167.18	n.s	62.03	56.69	n.s
RON2	3	94.61	99.50	n.s	335.71	366.35	n.s	27.23	24.52	n.s	30.60	7.88	n.s	93.14	133.44	n.s	63.23	62.31	n.s

Ecotype	n	ttlmass			rmr			WUE			leafc			leafn			cn		
		D	W	W-test	D	W	W-test	D	W	W-test	D	W	W-test	D	W	W-test	D	W	W-test
ABR2	4	137.09	122.76	n.s	<b>38.89</b>	<b>33.48</b>	*	<b>11.32</b>	<b>10.27</b>	*	-31.00	-31.29	n.s	<b>397.18</b>	<b>394.22</b>	*	<b>35.17</b>	<b>39.21</b>	*
ABR3	4	151.72	165.80	n.s	<b>37.51</b>	<b>31.32</b>	*	12.01	9.45	n.s	<b>-30.66</b>	<b>-31.50</b>	*	<b>401.27</b>	<b>389.46</b>	*	<b>33.47</b>	<b>41.64</b>	*
ABR4	4	86.11	93.11	n.s	<b>37.90</b>	<b>31.43</b>	*	<b>11.37</b>	<b>9.41</b>	*	-30.98	-31.69	n.s	<b>402.26</b>	<b>397.76</b>	*	<b>35.51</b>	<b>42.42</b>	*
ABR5	3	138.14	117.42	n.s	39.48	27.78	n.s	10.80	9.06	n.s	-31.21	-32.05	n.s	397.90	389.95	n.s	37.03	43.31	n.s
ABR6	4	113.44	110.98	n.s	<b>35.52</b>	<b>27.32</b>	*	<b>11.77</b>	<b>9.26</b>	*	<b>-31.30</b>	<b>-31.93</b>	*	<b>404.47</b>	<b>389.55</b>	*	<b>34.51</b>	<b>42.18</b>	*
ABR8	4	<b>145.65</b>	<b>213.41</b>	*	<b>23.44</b>	<b>19.36</b>	*	12.49	11.39	n.s	<b>-31.33</b>	<b>-31.58</b>	*	393.03	383.02	n.s	31.77	34.08	n.s
Adi10	4	<b>201.51</b>	<b>305.91</b>	*	<b>33.44</b>	<b>26.40</b>	*	<b>12.53</b>	<b>12.19</b>	*	<b>-30.84</b>	<b>-31.58</b>	*	397.39	388.03	n.s	31.74	32.45	n.s
Adi12	4	211.91	226.64	n.s	<b>33.45</b>	<b>24.94</b>	*	<b>12.47</b>	<b>10.13</b>	*	<b>-30.34</b>	<b>-31.28</b>	*	<b>400.60</b>	<b>390.93</b>	*	<b>32.22</b>	<b>38.80</b>	*
Adi2	3	158.14	211.40	n.s	34.89	23.65	n.s	12.80	11.38	n.s	-30.63	-31.27	n.s	396.23	389.55	n.s	31.17	34.69	n.s
Bd1-1	2	102.62	98.88	n.s	32.62	28.27	n.s	12.27	8.92	n.s	-30.71	-31.69	n.s	396.41	386.51	n.s	32.63	43.38	n.s
Bd18-1	2	188.09	219.08	n.s	31.97	23.64	n.s	12.44	11.16	n.s	-30.57	-31.84	n.s	407.79	397.53	n.s	32.83	36.54	n.s
Bd21ctrl	4	<b>153.58</b>	<b>139.84</b>	*	<b>31.91</b>	<b>25.87</b>	*	<b>12.58</b>	<b>9.82</b>	*	<b>-30.22</b>	<b>-31.43</b>	*	<b>403.73</b>	<b>388.69</b>	*	<b>32.31</b>	<b>39.63</b>	*
Bd21-3	3	208.92	224.17	n.s	35.09	25.19	n.s	11.57	11.10	n.s	-31.03	-31.93	n.s	396.29	389.81	n.s	34.28	35.17	n.s
Bd2-3	4	<b>162.12</b>	<b>191.49</b>	*	<b>32.24</b>	<b>25.42</b>	*	12.63	10.64	n.s	<b>-30.73</b>	<b>-31.27</b>	*	<b>394.31</b>	<b>381.89</b>	*	<b>31.43</b>	<b>36.48</b>	*
Bd30-1	4	<b>164.29</b>	<b>220.57</b>	*	34.51	32.28	n.s	<b>11.14</b>	<b>10.05</b>	*	<b>-31.16</b>	<b>-32.11</b>	*	<b>386.45</b>	<b>376.32</b>	*	<b>34.98</b>	<b>37.58</b>	*
Bd3-1	3	<b>211.52</b>	<b>268.99</b>	*	<b>31.01</b>	<b>24.91</b>	*	<b>13.24</b>	<b>10.75</b>	*	<b>-30.66</b>	<b>-32.08</b>	*	<b>394.78</b>	<b>387.37</b>	*	<b>29.94</b>	<b>36.25</b>	*
BdTR10c	4	177.68	258.67	n.s	31.05	30.12	n.s	13.38	11.49	n.s	-30.71	-31.65	n.s	402.76	390.60	n.s	30.43	34.09	n.s
BdTR11g	4	<b>177.28</b>	<b>221.90</b>	*	<b>33.12</b>	<b>26.75</b>	*	<b>12.31</b>	<b>11.47</b>	*	<b>-31.34</b>	<b>-32.07</b>	*	401.69	391.18	n.s	32.85	34.58	n.s
BdTR11i	4	<b>178.64</b>	<b>208.72</b>	*	<b>31.09</b>	<b>27.21</b>	*	<b>12.52</b>	<b>10.94</b>	*	<b>-31.11</b>	<b>-31.91</b>	*	399.66	384.59	n.s	32.06	36.11	n.s
BdTR13a	3	<b>152.54</b>	<b>179.38</b>	*	<b>33.35</b>	<b>27.44</b>	*	<b>11.89</b>	<b>10.37</b>	*	-31.26	-32.08	n.s	<b>399.54</b>	<b>393.72</b>	*	<b>33.74</b>	<b>38.07</b>	*

BdTR1i	4	200.37	237.90	n.s	<b>33.23</b>	<b>26.66</b>	*	<b>12.99</b>	<b>11.00</b>	*	<b>-30.33</b>	<b>-31.11</b>	*	<b>401.43</b>	<b>389.86</b>	*	<b>31.01</b>	<b>35.67</b>	*
BdTR2b	4	204.81	258.75	n.s	33.70	28.43	n.s	12.36	9.81	n.s	-30.46	-31.97	n.s	402.35	396.22	n.s	32.69	40.70	n.s
BdTR2g	4	219.62	207.97	n.s	<b>35.40</b>	<b>27.05</b>	*	<b>12.52</b>	<b>12.08</b>	*	-30.43	-31.05	n.s	397.63	392.77	n.s	31.94	33.34	n.s
BdTR3c	4	<b>164.73</b>	<b>230.02</b>	*	<b>35.42</b>	<b>24.14</b>	*	<b>13.88</b>	<b>11.71</b>	*	<b>-30.84</b>	<b>-31.73</b>	*	<b>404.11</b>	<b>392.73</b>	*	<b>29.21</b>	<b>33.63</b>	*
BdTR5i	3	159.77	205.44	n.s	38.12	30.36	n.s	12.04	10.29	n.s	-31.08	-31.94	n.s	400.25	389.96	n.s	33.50	38.15	n.s
BdTR9k	4	191.67	203.08	n.s	<b>31.27</b>	<b>25.03</b>	*	<b>12.35</b>	<b>10.09</b>	*	<b>-30.75</b>	<b>-31.74</b>	*	<b>405.45</b>	<b>385.74</b>	*	<b>33.06</b>	<b>38.39</b>	*
Bis1	3	143.08	155.54	n.s	33.24	27.64	n.s	12.22	10.28	n.s	-31.34	-32.29	n.s	400.67	391.98	n.s	32.82	38.27	n.s
Kah1	4	164.55	185.48	n.s	<b>33.74</b>	<b>26.03</b>	*	<b>12.89</b>	<b>9.85</b>	*	<b>-30.89</b>	<b>-31.79</b>	*	<b>402.98</b>	<b>390.96</b>	*	<b>31.44</b>	<b>39.79</b>	*
Kah5	4	<b>170.74</b>	<b>211.70</b>	*	<b>28.57</b>	<b>23.54</b>	*	<b>12.54</b>	<b>10.60</b>	*	<b>-30.50</b>	<b>-31.22</b>	*	<b>403.40</b>	<b>393.09</b>	*	<b>32.24</b>	<b>37.22</b>	*
Koz1	2	138.98	182.08	n.s	40.08	25.48	n.s	12.58	10.89	n.s	-31.28	-31.70	n.s	404.89	397.19	n.s	32.45	36.64	n.s
Koz3	4	184.43	223.87	n.s	<b>33.05</b>	<b>25.26</b>	*	<b>13.20</b>	<b>11.25</b>	*	<b>-30.74</b>	<b>-31.80</b>	*	<b>405.07</b>	<b>393.25</b>	*	<b>30.73</b>	<b>35.26</b>	*
RON2	3	157.49	195.76	n.s	38.91	31.37	n.s	11.70	10.03	n.s	-30.61	-31.32	n.s	404.26	396.07	n.s	35.48	39.74	n.s

**Supplementary Table 12.** Linear model (lm) regression analysis for comparative *Brachypodium distachyon* *Bdhn* gene expressions and drought-induced phenotypic trait changes under total watered (W) and dry (D) conditions. Significant p-values (p≤ 0.05\*; 0.01\*\*; 0.001\*\*\*).

traits	<i>Bdhn1a</i>				<i>Bdhn2</i>				<i>Bdhn3</i>				<i>Bdhn7</i>			
	median	Std error	F-statistic	p-value	median	Std error	F-statistic	p-value	median	Std error	F-statistic	p-value	median	Std error	F-statistic	p-value
leaf_rwc	-34.83	196.9	51.03	1.227E-11 ***	-41.95	265.3	169.3	<2E-16***	-8.7	564.8	136.8	<2E-16***	-4.23	145.1	129.7	<2E-16***
leaf_wc	-49.32	213.2	10.19	0.001609**	-70.69	321.3	43.09	3.51E-10***	-166.9	682.3	22.33	4.02E-06***	-43.52	174.8	16.68	2.32E-05***
lma	-54.08	213.8	9.029	0.0025955 **	-96.58	321.2	43.25	3.28E-10***	-188	689.2	17.37	4.38E05***	-46.48	175.3	17.44	4.22E-05***
pro	-46.12	210.7	15.82	9.36E-05***	-93.89	308.5	66.03	2.85E-14***	-127.6	649.7	47.99	4.37E-11***	-30.73	166.5	43.91	2.47E-10***
abvgrd	-53.51	217.9	0.1635	0.6864	-136.1	346.7	4.911	0.0277*	-270.9	713.4	1.055	0.30554	-71.82	181.8	0.08986	0.765
blwgrd	-40.97	208.7	20.63	9.07E-06***	-72.33	333.1	24.22	1.65E-06***	-165.2	687	18.89	2.09E-05***	-38.5	173	23.87	1.95E-06***
ttlmass	-52.88	216.7	2.607	0.1078	-175	350.4	0.1187	0.73078	-293.4	714.8	0.1826	0.6695	-58.21	181.3	1.305	0.255
rnr	-35.02	213.1	10.56	0.001331**	-77.24	313.3	56.99	1.06E-12***	-152.7	674.7	27.97	2.90E-07***	-41.8	174	20.85	8.16E-06***
WUE	-129.55	206.2	26.68	5.26E-07***	-52.93	308	66.88	2.04E-14***	-122.5	664.9	35.53	9.50E-09***	-31.64	167.8	39.49	1.67E-09***
leafC	-39.98	210.7	15.95	8.80E-05***	-90.2	323.7	39.07	2E-09***	-183.4	682.8	21.94	4.85E-06***	-50.17	175.8	15.87	9.14E-05***
leafN	-42.83	199.8	43.07	3.54E-10***	-62.2	311.9	59.54	3.77E-13***	-160.7	658.5	40.66	1.E-09***	-44.7	169	36.01	7.69E-09***
CN	-40.24	198.4	46.9	6.93E-11***	-58.73	307.7	67.44	1.64E-14***	-131.6	652.1	45.95	1.04E-10***	-33.83	168	39.09	1.98E-09***

**Supplementary Table 13.** Phylogenetic signal of dehydrin gene expressions under watered (W) and dry (D) conditions, drought-induced phenotypic traits changes and climate niche variation assessed in **(a)** the *B. distachyon* nuclear-SNP tree and **(b)** the *B. distachyon* *Bdhn* tree using the *phylosig* option of the *phytools* R package. Blomberg’s K and Pagel’s lambda values close to one indicate phylogenetic signal and values close to zero phylogenetic independence. K, p-values based on 1000 randomizations; lambda, p-values based on the Likelihood Ratio test. Significant and marginal significant values are highlighted in bold.

**(a)**

<i>Bdhn</i> gene	Treatment	K	P-value	lambda( $\lambda$ )	logL( $\lambda$ )	LR( $\lambda=0$ )	P-value
<i>Bdhn1aW</i>	W	0.00207548	0.579	6.6113E-05	-170094	-9.01E-04	1
<i>Bdhn2W</i>		0.00467069	0.235	6.6113E-05	-111372	-9.77E-04	1
<i>Bdhn3W</i>		0.00236035	0.553	6.6113E-05	-90.2705	-1.13E-03	1
<i>Bdhn7W</i>		0.00162038	0.695	6.6113E-05	-59.9152	-1.39E-03	1
<i>Bdhn1aD</i>	D	0.0038235	0.317	6.6113E-05	-194.936	-1.03E-03	1
<i>Bdhn2D</i>		0.00311909	0.364	6.6113E-05	-209.636	-1.03E-03	1
<i>Bdhn3D</i>		0.00257041	0.71	6.6113E-05	-237.428	-1.06E-03	1
<i>Bdhn7D</i>		0.00137242	0.753	6.6113E-05	-196.53	-1.04E-03	1



	Drought						Watered					
Phenotypic trait	K	P-value (based on 1000 randomizations)	lambda( $\lambda$ )	logL( $\lambda$ )	LR( $\lambda=0$ )	P-value	K	P-value	lambda( $\lambda$ )	logL( $\lambda$ )	LR( $\lambda=0$ )	P-value
leaf_rwc	0.00595303	0.202	0.8240433	-70.83287	-71.94764	0.1353942	0.00633355	0.137	6.6113E-05	-21.1366	-21.1361	1
leaf_wc	0.0191719	0.029	0.5318181	-129.0792	-129.2025	0.6194317	0.00601205	0.142	0.712778	-124.3118	-124.641	0.4171331
lma	0.00655413	0.198	0.4014225	-60.3207	-60.04825	1	<b>0.0127346</b>	<b>0.067</b>	0.5672695	-53.1973	-54.02652	0.1978138
pro	0.00178069	0.645	6.61128E-05	-118.2053	-118.2048	1	0.00751385	0.279	6.6113E-05	-65.7397	-65.73915	1
<b>abvrgd</b>	<b>0.0548587</b>	<b>0.005</b>	<b>0.9862024</b>	<b>-132.3802</b>	<b>-137.5324</b>	<b>0.00132712</b>	0.00982265	0.118	<b>0.9056281</b>	<b>-143.4905</b>	<b>-147.2048</b>	<b>0.00641901</b>
blwgrd	0.00799846	0.135	0.6778591	-112.6454	-113.232	0.2787568	0.00503958	0.192	0.372553	-117.8161	-117.602	1
<b>ttlmass</b>	<b>0.0254584</b>	<b>0.02</b>	<b>0.9586421</b>	<b>-144.0437</b>	<b>-147.1176</b>	<b>0.01315614</b>	0.00760606	0.15	<b>0.8313881</b>	<b>-153.3088</b>	<b>-155.4348</b>	<b>0.0392068</b>
rmr	0.0117638	0.1	<b>0.8587116</b>	<b>-71.60054</b>	<b>-74.00027</b>	<b>0.02846858</b>	<b>0.0198041</b>	<b>0.031</b>	<b>0.8500612</b>	<b>-65.57032</b>	<b>-69.23347</b>	<b>0.00679529</b>
<b>delta13c</b>	<b>0.0206935</b>	<b>0.023</b>	0.5455282	-9.438273	-9.102205	1	0.00079528	0.921	6.6113E-05	-9.565582	-9.565045	1
leafc	0.00564166	0.206	6.61128E-05	-86.81046	-86.80988	1	0.00344133	0.413	6.6113E-05	-84.79111	-84.79067	1
<b>leafn</b>	<b>0.0127895</b>	<b>0.066</b>	<b>0.8379002</b>	<b>-52.22653</b>	<b>-57.04403</b>	<b>0.00190906</b>	0.00111356	0.809	0.6412875	-71.1111	-72.40537	0.1076397
<b>cn</b>	<b>0.015233</b>	<b>0.051</b>	<b>0.8350859</b>	<b>-24.49639</b>	<b>-28.06983</b>	<b>0.00750945</b>	0.00101427	0.842	0.6145648	-35.11085	-36.01121	0.1796235

Climate trait	K	p-value	lambda( $\lambda$ )	logL( $\lambda$ )	LR( $\lambda=0$ )	p-value
PCA1	0.0201727	0.024	0.905784	-70.641	12.567	0.000392627

(b)

<i>Bdhn</i> gene	Treatment	K	p-value	lambda( $\lambda$ )	logL( $\lambda$ )	LR( $\lambda=0$ )	p-value
<i>Bdhn</i> 1aW	W	0.231879	0.142	0.782475	-175.48	1.121	0.289703
<i>Bdhn</i> 2W		<b>0.34558</b>	<b>0.017</b>	<b>0.759422</b>	<b>-112.036</b>	<b>6.78197</b>	<b>0.00920834</b>
<i>Bdhn</i> 3W		0.10957	0.603	6.64306E-05	-93.2539	0.00063134	1
<i>Bdhn</i> 7W		<b>0.433394</b>	<b>0.031</b>	<b>0.97584</b>	<b>-60.2457</b>	<b>3.42969</b>	<b>0.0640339</b>
<i>Bdhn</i> 1aD	D	0.308794	0.051	0.502054	-194.065	0.710376	0.399319
<i>Bdhn</i> 2D		0.211919	0.176	6.64306E-05	-208.371	0.00063094	1
<i>Bdhn</i> 3D		<b>0.433425</b>	<b>0.064</b>	<b>0.951732</b>	<b>-234.916</b>	<b>4.48918</b>	<b>0.0341101</b>
<i>Bdhn</i> 7D		0.379302	0.083	0.917646	-195.278	1.74672	0.18629

Phenotypic trait	K	p-value	lambda( $\lambda$ )	logL( $\lambda$ )	LR( $\lambda=0$ )	p-value
leaf_rwcW	0.00633355	0.137	6.61E-05	-21.1366	-21.1361	1
leaf_wcW	0.00601205	0.142	0.712778	-124.3118	-124.641	0.4171331
lmaW	0.0127346	0.067	0.5672695	-53.1973	-54.02652	0.1978138
proW	0.00751385	0.279	6.61E-05	-65.7397	-65.73915	1
<b>abvrgdW</b>	<b>0.00982265</b>	<b>0.118</b>	<b>0.9056281</b>	<b>-143.4905</b>	<b>-147.2048</b>	<b>0.006419007</b>
blwgrdW	0.00503958	0.192	0.372553	-117.8161	-117.602	1
ttlmassW	0.00760606	0.15	0.8313881	-153.3088	-155.4348	0.0392068
<b>rmrW</b>	<b>0.0198041</b>	<b>0.031</b>	<b>0.8500612</b>	<b>-65.57032</b>	<b>-69.23347</b>	<b>0.006795293</b>
WUE_W	0.00079528	0.921	6.61E-05	-9.565582	-9.565045	1
leafcW	0.00344133	0.413	6.61E-05	-84.79111	-84.79067	1
<b>leafnW</b>	<b>0.00111356</b>	<b>0.809</b>	<b>0.6412875</b>	<b>-71.1111</b>	<b>-72.40537</b>	<b>0.1076397</b>
<b>cnW</b>	<b>0.00101427</b>	<b>0.842</b>	<b>6.15E-01</b>	<b>-35.11085</b>	<b>-36.01121</b>	<b>0.1796235</b>
<b>leaf_rwcD</b>	<b>0.00595303</b>	<b>0.202</b>	<b>0.8240433</b>	<b>-70.83287</b>	<b>-71.94764</b>	<b>0.1353942</b>
leaf_wcD	0.0191719	0.029	0.5318181	-129.0792	-129.2025	0.6194317
lmaD	0.00655413	0.198	0.4014225	-60.3207	-60.04825	1
proD	0.00178069	0.645	6.61E-05	-118.2053	-118.2048	1
<b>abvrgdD</b>	<b>0.0548587</b>	<b>0.005</b>	<b>0.9862024</b>	<b>-132.3802</b>	<b>-137.5324</b>	<b>0.001327115</b>
blwgrdD	0.00799846	0.135	0.6778591	-112.6454	-113.232	0.2787568
ttlmassD	0.0254584	0.02	0.9586421	-144.0437	-147.1176	0.01315614
rmrD	0.0117638	0.1	0.8587116	-71.60054	-74.00027	0.02846858
WUE_D	0.0206935	0.023	0.5455282	-9.438273	-9.102205	1

leafcD	0.00564166	0.206	6.61E-05	-86.81046	-86.80988	1
leafnD	0.0127895	0.066	0.8379002	-52.22653	-57.04403	0.001909058
cnD	0.015233	0.051	0.8350859	-24.49639	-28.06983	0.007509447

Climate trait	K	p-value	lambda( $\lambda$ )	logL( $\lambda$ )	LR( $\lambda$ =0)	p-value
PCA1	0.462712	0.005	0.753963	-72.2802	9.38246	0.00219071