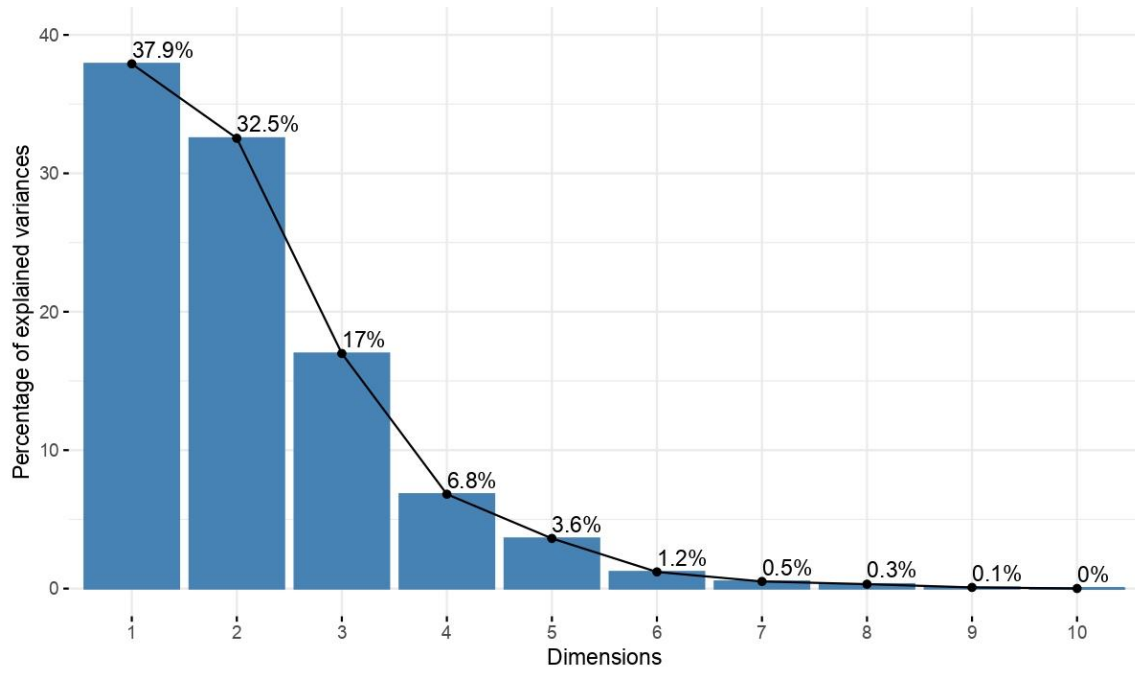
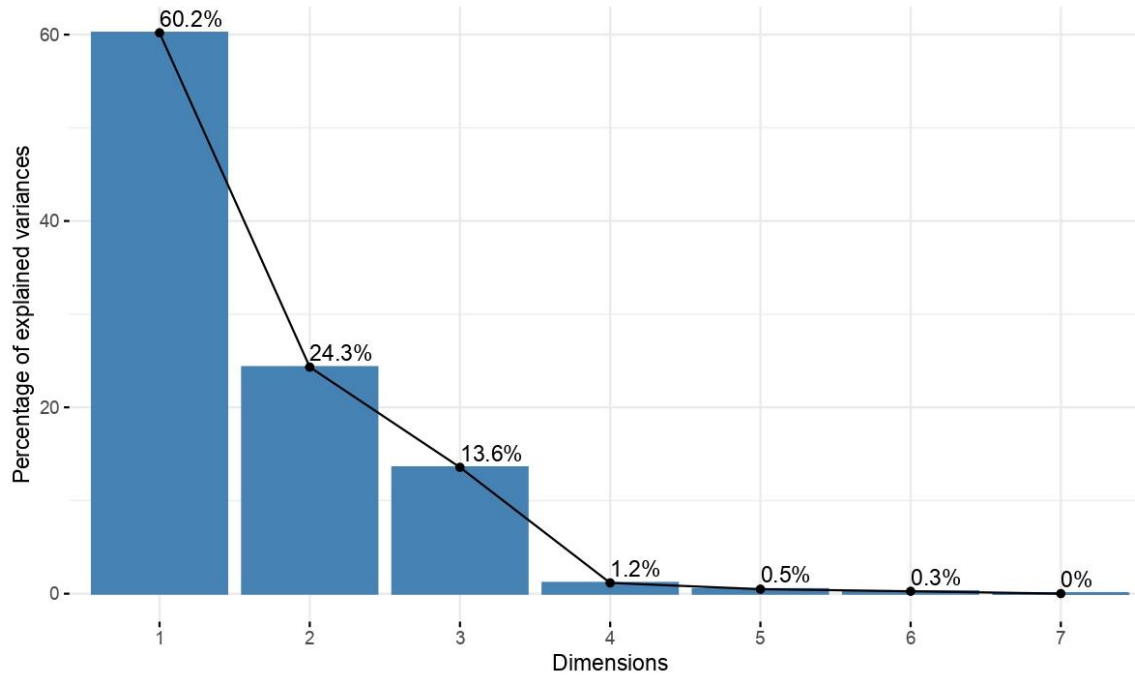


## Supplementary Information

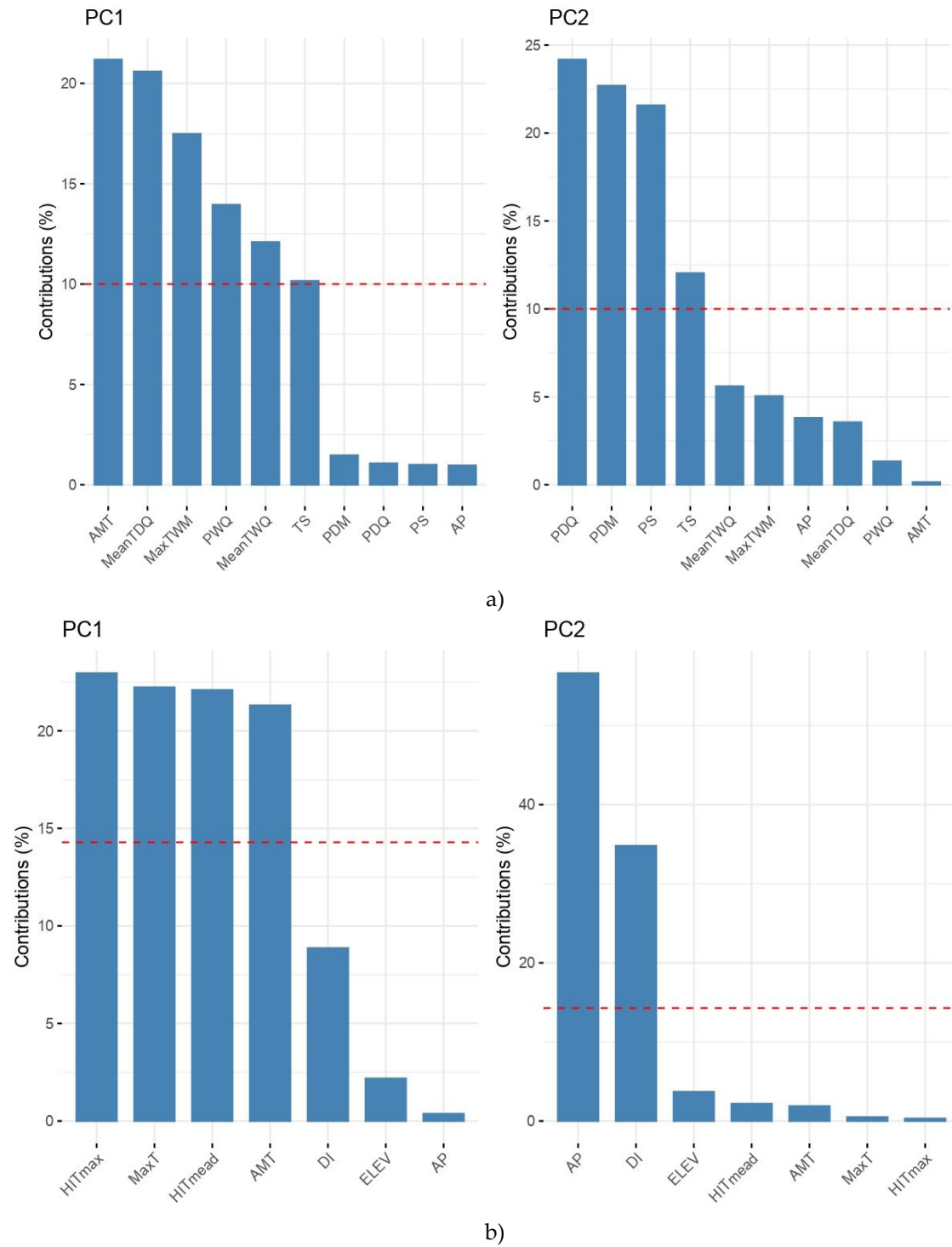


a)



b)

**Figure S1.** Contributions to the total variation of each component for the evaluated variables in the PCA. a) Bioclimatic variables related to aridity; b) Temperature related variables, calculated indices, AP, and ELEV.



**Figure S2.** Contributions to component principals 1 and 2 for the evaluated variables in the PCA. a) Bioclimatic variables related to aridity; b) Temperature related variables, calculated indices, AP, and ELEV.

Table S1. Detection of associated SNPs for seven climatic variables.

Var	Chr	No.	SNP	Physical position (bp)	<i>P-value</i>	SNPs	Genes
AMT	1A	1	108825112 F 0-19:T>A-19:T>A	277825486	6.60E-09	2	1
		2	108891114 F 0-33:A>G-33:A>G	388440316	5.89E-09		1
	1D	3	108739422 F 0-31:T>A-31:T>A	2113561	1.49E-06	1	1
	2D	4	108968402 F 0-23:C>T-23:C>T	79989524	9.63E-07	1	2
	3D	5	107698139 F 0-48:C>T-48:C>T	97153088	4.42E-07	2	1
		6	108308207 F 0-18:G>A-18:G>A	546672913	2.49E-07		2
	4D	7	109431634 F 0-54:G>A-54:G>A	370691683	5.90E-10	1	3
	5D	8	108305241 F 0-68:A>G-68:A>G	379130055	1.29E-06	1	1
						Total	12
MaxT	1A	1	108825112 F 0-19:T>A-19:T>A	277825486	8.02E-08	2	1
		2	108891114 F 0-33:A>G-33:A>G	388440316	1.32E-16		1
	3A	3	106510612 F 0-30:C>T-30:C>T	502971897	2.05E-07	3	2
		4	108476623 F 0-32:T>A-32:T>A	507114154	4.55E-07		2
	5D	5	108028914 F 0-20:A>G-20:A>G	574516154	1.86E-07	1	2
		6	109431634 F 0-54:G>A-54:G>A	370691683	1.09E-16		3
	6A	7	108652995 F 0-58:G>C-58:G>C	528660566	1.50E-08	1	1
	6D	8	109126792 F 0-49:C>T-49:C>T	5854616	1.23E-06	1	2
	7A	9	108582786 F 0-49:T>G-49:T>G	143959936	1.95E-12	2	2
		10	108830300 F 0-9:T>G-9:T>G	64789408	3.05E-10		2
	7B	11	109126469 F 0-35:G>A-35:G>A	662017143	8.41E-07	2	2
		12	107878167 F 0-16:G>A-16:G>A	107522176	1.30E-06	1	2
						Total	22
AP	1A	1	108256081 F 0-24:C>G-24:C>G	588647447	1.25E-07	1	1
	2A	2	109058266 F 0-7:C>T-7:C>T	640221452	1.32E-07	1	2
	2B	3	107797386 F 0-11:T>G-11:T>G	91596926	1.14E-09	2	1
		4	107593284 F 0-50:T>A-50:T>A	768567114	3.32E-07		1
	4A	5	108145069 F 0-52:C>A-52:C>A	714179675	1.02E-06	1	2
	5B	6	109305833 F 0-34:C>G-34:C>G	526249013	1.56E-06	1	1
	6B	7	109177937 F 0-11:A>G-11:A>G	223441723	1.81E-07	2	1
		8	109523315 F 0-24:C>T-24:C>T	269818400	1.26E-06		0
						Total	9
PS	1D	1	107874524 F 0-37:G>C-37:G>C	485539732	1.89E-07	1	3
	2A	2	108020469 F 0-43:T>C-43:T>C	711971015	1.78E-08	2	2
		3	108514047 F 0-10:A>C-10:A>C	729345577	3.13E-08		2
	2B	4	107794074 F 0-23:T>C-23:T>C	76022529	9.09E-08	2	2
		5	109021888 F 0-34:T>C-34:T>C	795754781	1.02E-07		1
	3B	6	108953425 F 0-21:A>G-21:A>G	50526285	1.78E-06	3	1
		7	107601308 F 0-23:G>A-23:G>A	741467423	1.38E-09		0
		8	108516380 F 0-24:T>C-24:T>C	758205945	5.53E-10		1

Table S1. Continued.

Var	Chr	No.	SNP	Physical position (bp)	<i>P</i> -value	SNPs	Genes
PS	4B	9	106772473 F 0-11:T>G-11:T>G	39759168	4.41E-07	1	1
	5A	10	107001591 F 0-37:T>C-37:T>C	619468262	3.81E-07	1	2
	5B	11	108348543 F 0-58:A>G-58:A>G	548120559	2.48E-08	2	1
		12	109119258 F 0-68:T>C-68:T>C	577227418	4.69E-09		2
	6B	13	109354013 F 0-58:A>G-58:A>G	485290761	2.50E-08	1	2
	7A	14	108619258 F 0-17:C>T-17:C>T	552606647	1.35E-08	1	1
	7B	15	108981313 F 0-8:C>T-8:C>T	650581291	5.17E-08	1	1
						Total	22
HITmead	1A	1	108891114 F 0-33:A>G-33:A>G	388440316	9.11E-18	1	1
	1B	2	108853213 F 0-26:C>T-26:C>T	201700273	4.52E-07	1	1
	1D	3	107880401 F 0-66:C>T-66:C>T	413939387	1.53E-07	1	2
	2B	4	107488994 F 0-17:T>C-17:T>C	29129965	1.44E-08	1	3
	3B	5	108146856 F 0-65:T>A-65:T>A	764282419	2.77E-07	1	1
	3D	6	107698139 F 0-48:C>T-48:C>T	97153088	1.25E-08	1	1
	4A	7	109242168 F 0-13:A>G-13:A>G	598521397	4.39E-08	1	2
	4B	8	108145974 F 0-24:T>C-24:T>C	56276689	3.44E-07	1	1
		9	109363420 F 0-34:G>A-34:G>A	62303691	1.34E-08		2
	4D	10	108773963 F 0-37:C>T-37:C>T	97959582	1.59E-06	3	2
		11	109431634 F 0-54:G>A-54:G>A	370691683	1.50E-08		3
	5B	12	109240982 F 0-38:G>C-38:G>C	68925700	2.02E-12	2	1
		13	108773279 F 0-51:C>T-51:C>T	530916378	8.04E-07		2
	7A	14	107178221 F 0-24:T>G-24:T>G	628906923	1.54E-06	1	2
						Total	24
HITmax	1A	1	108825112 F 0-19:T>A-19:T>A	277825486	8.48E-09	2	1
		2	108891114 F 0-33:A>G-33:A>G	388440316	1.94E-11		1
	2B	3	108024073 F 0-47:C>T-47:C>T	38321752	3.81E-09	1	2
	3A	4	108476623 F 0-32:T>A-32:T>A	507114154	1.68E-08	2	2
		5	108028914 F 0-20:A>G-20:A>G	574516154	7.31E-11		2
	3B	6	109122135 F 0-40:A>G-40:A>G	535641207	9.91E-07	1	1
	3D	7	108308207 F 0-18:G>A-18:G>A	546672913	4.37E-07	2	2
		8	109610030 F 0-20:C>T-20:C>T	575639014	6.69E-08		2
	4A	9	109242168 F 0-13:A>G-13:A>G	598521397	1.94E-09	1	2
	4D	10	109431634 F 0-54:G>A-54:G>A	370691683	4.78E-09	1	3
	6D	11	108582786 F 0-49:T>G-49:T>G	143959936	1.42E-09	1	2
						Total	20
DI	2B	1	108980638 F 0-33:T>C-33:T>C	584134131	2.76E-08	1	1
	2D	2	107489027 F 0-34:C>T-34:C>T	302776397	1.41E-07	1	1
	5B	3	109305833 F 0-34:C>G-34:C>G	526249013	4.31E-07	1	1
	7A	4	108206445 F 0-49:C>A-49:C>A	67617920	5.04E-08	2	1
		5	107952026 F 0-63:G>C-63:G>C	498861613	3.70E-07		1
	7D	6	109035950 F 0-29:C>T-29:C>T	88318125	1.89E-07	1	1
							6

Table S2. Other genes and proteins identified by GEA with seven climatic variables.

Chr	SNP	Gene	Variable	Protein	Function
<b>Morphological responses</b>					
2B	107488994 F 0-17:T>C-17:T>C	TraesCS2B02G060700	HITmead	Fbox ( <i>FBX</i> ).	Regulation of multiple developmental processes.
2B	108980638 F 0-33:T>C-33:T>C	TraesCS2B02G410500	DI	Ovate Family Proteins ( <i>OFP</i> ).	Morphological regulation in response to stress signals.
4B	106772473 F 0-11:T>G-11:T>G	TraesCS4B02G051500	PS	Transcription factor SCREAM2 ( <i>SCRM2</i> ).	Constitutive stomatal differentiation in the epidermis.
4B	108145974 F 0-24:T>C-24:T>C	TraesCS4B02G064000	HITmead	Growth regulating factor 1 ( <i>GIF1</i> ).	Regulation of cell expansion in foliar tissues and cotyledons.
4D	108773963 F 0-37:C>T-37:C>T	TraesCS4D02G117100	HITmead	Fbox ( <i>FBX</i> ).	Regulation of multiple developmental processes.
6B	109177937 F 0-11:A>G-11:A>G	TraesCS6B02G190600	AP	ADP-ribosylation factor GTPase ( <i>AGD12</i> ).	Calcium-dependent proteins that affect gravitropism in <i>AT</i> .
6B	109354013 F 0-58:A>G-58:A>G	TraesCS6B02G269700	PS	Similar to OCL1 homeobox ( <i>ROC5</i> ).	Modulates the curling of the leaves.
<b>Responses to biotic stress</b>					
2A	108514047 F 0-10:A>C-10:A>C	TraesCS2A02G499400	PS	Pelota homolog ( <i>PELO</i> ).	Defense responses to bacteria.
3A	108028914 F 0-20:A>G-20:A>G	TraesCS3A02G329100	MaxT and HITmax	rRNA N-glycosidase ( <i>RIP</i> ).	Antibacterial and antifungal activity.
3B	108146856 F 0-65:T>A-65:T>A	TraesCS3B02G523300	HITmead	Disease resistance ( <i>NBS-LRR</i> ).	Disease resistance genes in plants.
3D	109610030 F 0-20:C>T-20:C>T	TraesCS3D02G475300	HITmax	Protein LIFEGUARD 4 ( <i>LFG4</i> ).	Defense response to pathogens.
4A	108145069 F 0-52:C>A-52:C>A	TraesCS4A02G447200	AP	Disease resistance ( <i>NBS-LRR</i> ).	Disease resistance genes in plants.
5B	108773279 F 0-51:C>T-51:C>T	TraesCS5B02G349800	HITmead	Flavin-containing monooxygenase ( <i>FMO</i> ).	Defense response to pathogens.
5B	109119258 F 0-68:T>C-68:T>C	TraesCS5B02G400100	PS	Cyclic nucleotide-gated ion channel 2 ( <i>CNGC2</i> ).	Defense response to pathogens.
<b>Photosynthesis</b>					
2A	108020469 F 0-43:T>C-43:T>C	TraesCS2A02G467700	PS	(S)-2-hydroxy-acid oxidase ( <i>GLO1</i> ).	Photorespiration and regulation of photosynthesis.
2D	108968402 F 0-23:C>T-23:C>T	TraesCS2D02G136200	AMT	Magnesium-chelatase subunit, chloroplastic ( <i>CHLH</i> ).	Chlorophyll biosynthesis.
4D	109363420 F 0-34:G>A-34:G>A	TraesCS4D02G086900	HITmead	Rieske (2Fe-2S) domain ( <i>PSB33</i> ).	Assembly and stabilization of the PSII.
5D	107001591 F 0-37:T>C-37:T>C	TraesCS5A02G437100	PS	Photosystem II reaction center L ( <i>psbL</i> ).	The PSII core proteins.
7A	108830300 F 0-9:T>G-9:T>G	TraesCS7A02G107200	MaxT	Gamma carbonic anhydrase 1 ( $\gamma$ CA1).	Photorespiration.
7D	109035950 F 0-29:C>T-29:C>T	TraesCS7D02G138100	DI	Cytochrome b6-f complex subunit 5 ( <i>PETG</i> ).	Electron transfer between PSII and PSI.

Table S2. Continued.

Chr	SNP	Gene	Variable	Protein	Function
<b>Flowering</b>					
1A	108891114 F 0-33:A>G-33:A>G	TraesCS1A02G220300	AMT, MaxT, HITmead and HITmax.	CONSTANS-like ( <i>COL</i> ).	Regulation of floral development.
2A	109058266 F 0-7:C>T-7:C>T	TraesCS2A02G390500	AP	Casein kinase II subunit beta ( <i>CK2</i> ).	Circadian Regulation.
2B	107488994 F 0-17:T>C-17:T>C	TraesCS2B02G059500	HITmead	Flowering promoting factor 1 ( <i>FPP1</i> ).	Control of flowering time.
3B	108953425 F 0-21:A>G-21:A>G	TraesCS3B02G081800	PS	Adenylyl-sulfate kinase ( <i>APK</i> ).	Circadian Regulation.
<b>Nutrient assimilation</b>					
2A	109058266 F 0-7:C>T-7:C>T	TraesCS2A02G390800	AP	Metal-nicotianamine transporter ( <i>YSL1</i> ).	Iron uptake and transport.
3A	108028914 F 0-20:A>G-20:A>G	TraesCS3A02G329700	MaxT and HITmax	Purple acid phosphatase ( <i>PAP</i> ).	Nutritional deficiencies.
7B	107878167 F 0-16:G>A-16:G>A	TraesCS7B02G093800	MaxT	Starch synthase, chloroplastic/amyloplastic ( <i>wSs2a-3</i> ).	Starch biosynthesis.