

# Supplementary Tables: The genomic basis for short-term evolution of environmental adaptation in maize

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Table S1: Quality control filtering of MaizeSNP50 data.

Step	Filter Criterion	Markers <sup>a</sup>
1	Total Markers Pre-filter	56,110
2	Inconsistent Between Replicated Samples	141
3	GenTrain Score < 0.6	4467
4	Missing Data $\geq$ 20%	1385
5	Unknown Map Location <sup>b</sup>	499
6	Redundant Markers	141
7	Monomorphic Markers	1825
8	< 2 Genotype Classes	35
9	No Heterozygous Genotypes	102

<sup>a</sup>Filtering based on B73 AGPv2 map.

Table S2: Subsets of MaizeSNP50 markers used for different analyses.

Set	Map Filter	Feature Filter	No. Markers	Analysis
A	AGPv2	Total SNPs post quality control	47,518 <sup>a</sup>	–
B	AGPv2	Minor allele count $\geq 12$	44,445	Diversity summary statistics
C	AGPv2	PZA/PZE markers; No missing data; Minor Allele Count $\geq 12$ ; Shared with 553 external samples <sup>b</sup>	9348	PHATE
D	AGPv2	PZA/PZE markers; No missing data; Minor allele count $\geq 12$ ; Inter-marker distances $> 0.05$ cM	3213	STRUCTURE ( $g_0$ )
E	AGPv2	PZA/PZE markers; No missing data; Minor allele count $\geq 12$ ; Inter-marker distances $> 0.05$ cM	3718	STRUCTURE (ancestry of $g_2$ individuals given $g_0$ subpopulations)
F	AGPv4	PZA/PZE markers; No missing data; Minor Allele Count $\geq 12$	8894	Genome-wide and chromosome-specific genomic relationship matrices
G	AGPv4	PZA/PZE markers; No missing data; Minor Allele Count $\geq 12$	7572	SIM <sup>-</sup> genomic relationship matrices
H	AGPv4	PZA/PZE markers; No missing data; Minor Allele Count $\geq 12$	1322	SIM <sup>+</sup> genomic relationship matrices
I	AGPv4	$g_0$ -specific minor allele count $\geq 12$	33,533	LD (all pairwise within chromosomes – $g_0$ )
J	AGPv4	$g_2$ -specific minor allele count $\geq 12$	26,975	LD (all pairwise within chromosomes – $g_2$ )
K	AGPv4	$g_4$ -specific minor allele count $\geq 12$	26,655	LD (all pairwise within chromosomes – $g_4$ )
L	AGPv4	$g_6$ -specific minor allele count $\geq 12$	28,009	LD (all pairwise within chromosomes – $g_6$ )
M	AGPv4	$g_8$ -specific minor allele count $\geq 12$	28,718	LD (all pairwise within chromosomes – $g_8$ )
N	AGPv4	$g_{10}$ -specific minor allele count $\geq 12$	28,492	LD (all pairwise within chromosomes – $g_{10}$ )
O	AGPv4	PZA/PZE markers; No missing data; $g_0$ -specific minor allele count $\geq 12$	5925	LD (all pairwise between chromosomes – $g_0$ )
P	AGPv4	PZA/PZE markers; No missing data; $g_2$ -specific minor allele count $\geq 12$	4017	LD (all pairwise between chromosomes – $g_2$ )
Q	AGPv4	PZA/PZE markers; No missing data; $g_4$ -specific minor allele count $\geq 12$	3948	LD (all pairwise between chromosomes – $g_4$ )
R	AGPv4	PZA/PZE markers; No missing data; $g_6$ -specific minor allele count $\geq 12$	4364	LD (all pairwise between chromosomes – $g_6$ )
S	AGPv4	PZA/PZE markers; No missing data; $g_8$ -specific minor allele count $\geq 12$	4595	LD (all pairwise between chromosomes – $g_8$ )
T	AGPv4	PZA/PZE markers; No missing data; $g_{10}$ -specific minor allele count $\geq 12$	4589	LD (all pairwise between chromosomes – $g_{10}$ )
U	AGPv4	No missing data; Minor allele count $\geq 12$	38,296	LD (sequential pairs – all generations)
V	AGPv4	Minor allele count $\geq 12$	43,628	SIM; Bayenv; FITR
W	AGPv4	Minor Allele Count $\geq 12$ ; Minimum of five phenotyped individuals per genotypic class	43,403	GWA

<sup>a</sup>The total number of QC markers includes 47,515 SNPs from the MaizeSNP50 chip (Table S1) plus three *ZmCCT10*-associated markers that were separately assayed.

<sup>b</sup>External refers to samples from Ganai *et al.* (2011) PLoS One 6:e28334.

Table S3: Admixture proportions estimated at  $K = 6$  for samples from  $g_0$ .

Sample name	Sample ID	1	2	3	4	5	6	Max proportion
C0_062314_043	39	0.28	0.01	0.05	0.23	0.17	0.27	1
C0_062314_054	50	0.74	0.01	0.00	0.17	0.06	0.03	1
C0_168_1	100	0.81	0.01	0.04	0.12	0.02	0.01	1
C0_062314_038	34	0.89	0.00	0.00	0.11	0.00	0.00	1
C0_062314_080	73	0.89	0.00	0.00	0.10	0.00	0.01	1
C0_062314_044	40	0.90	0.01	0.00	0.09	0.00	0.00	1
C0_164_3	90	0.92	0.00	0.00	0.07	0.00	0.00	1
C0_062314_055	51	0.92	0.00	0.00	0.07	0.00	0.00	1
C0_062314_015	13	0.92	0.00	0.00	0.07	0.00	0.00	1
C0_062314_096	86	0.94	0.00	0.00	0.06	0.00	0.00	1
C0_062314_061	57	0.96	0.00	0.00	0.04	0.00	0.00	1
C0_062314_046	42	0.99	0.00	0.00	0.00	0.00	0.00	1
C0_165_1	93	0.99	0.00	0.00	0.00	0.00	0.00	1
C0_168_2	101	1.00	0.00	0.00	0.00	0.00	0.00	1
C0_062314_077	71	1.00	0.00	0.00	0.00	0.00	0.00	1
C0_062314_010	8	1.00	0.00	0.00	0.00	0.00	0.00	1
C0_062314_094	84	0.00	0.51	0.00	0.49	0.00	0.00	2
C0_062314_050	46	0.00	0.55	0.00	0.45	0.00	0.00	2
C0_062314_023	20	0.00	1.00	0.00	0.00	0.00	0.00	2
C0_062314_067	63	0.00	1.00	0.00	0.00	0.00	0.00	2
C0_062314_095	85	0.00	1.00	0.00	0.00	0.00	0.00	2
C0_062314_037	33	0.00	1.00	0.00	0.00	0.00	0.00	2
C0_062314_090	80	0.00	1.00	0.00	0.00	0.00	0.00	2
C0_062314_042	38	0.00	1.00	0.00	0.00	0.00	0.00	2
C0_062314_070	65	0.00	1.00	0.00	0.00	0.00	0.00	2
C0_062314_084	76	0.00	1.00	0.00	0.00	0.00	0.00	2
C0_062314_002	1	0.00	1.00	0.00	0.00	0.00	0.00	2
C0_062314_018	15	0.00	1.00	0.00	0.00	0.00	0.00	2
C0_062314_025	22	0.00	1.00	0.00	0.00	0.00	0.00	2
C0_062314_028	25	0.00	1.00	0.00	0.00	0.00	0.00	2
C0_062314_036	32	0.00	1.00	0.00	0.00	0.00	0.00	2
C0_062314_051	47	0.00	1.00	0.00	0.00	0.00	0.00	2
C0_062314_034	30	0.00	0.95	0.00	0.05	0.00	0.00	2
C0_062314_021	18	0.01	0.56	0.00	0.03	0.37	0.03	2
C0_062314_053	49	0.10	0.51	0.05	0.18	0.14	0.03	2
C0_062314_072	67	0.46	0.52	0.00	0.02	0.00	0.00	2
C0_166_2	97	0.00	0.00	1.00	0.00	0.00	0.00	3
C0_062314_035	31	0.00	0.00	1.00	0.00	0.00	0.00	3
C0_062314_047	43	0.00	0.00	1.00	0.00	0.00	0.00	3
C0_062314_057	53	0.00	0.00	1.00	0.00	0.00	0.00	3
C0_062314_059	55	0.00	0.00	1.00	0.00	0.00	0.00	3
C0_062314_064	60	0.00	0.00	1.00	0.00	0.00	0.00	3
C0_165_3	95	0.00	0.00	1.00	0.00	0.00	0.00	3
C0_166_1	96	0.00	0.00	1.00	0.00	0.00	0.00	3
C0_062314_005	4	0.00	0.41	0.51	0.08	0.00	0.00	3
C0_062314_074	69	0.00	0.00	1.00	0.00	0.00	0.00	3
C0_062314_066	62	0.00	0.00	0.98	0.01	0.00	0.00	3
C0_062314_016	14	0.38	0.00	0.61	0.00	0.00	0.00	3
C0_062314_060	56	0.39	0.00	0.53	0.07	0.00	0.01	3
C0_062314_092	82	0.47	0.00	0.53	0.00	0.00	0.00	3
C0_062314_014	12	0.00	0.00	0.00	1.00	0.00	0.00	4
C0_062314_027	24	0.00	0.00	0.00	1.00	0.00	0.00	4
C0_062314_056	52	0.00	0.00	0.00	1.00	0.00	0.00	4
C0_062314_058	54	0.00	0.00	0.00	1.00	0.00	0.00	4
C0_062314_082	74	0.00	0.00	0.00	1.00	0.00	0.00	4

Table S3: continued from previous page.

Sample name	Sample ID	1	2	3	4	5	6	Max proportion
C0_062314_087	78	0.00	0.00	0.00	1.00	0.00	0.00	4
C0_062314_097	87	0.00	0.00	0.00	1.00	0.00	0.00	4
C0_062314_031	28	0.00	0.35	0.00	0.65	0.00	0.00	4
C0_062314_062	58	0.00	0.36	0.00	0.64	0.00	0.00	4
C0_062314_024	21	0.00	0.38	0.00	0.62	0.00	0.00	4
C0_062314_004	3	0.00	0.38	0.00	0.62	0.00	0.00	4
C0_062314_073	68	0.00	0.39	0.00	0.61	0.00	0.00	4
C0_164_1	88	0.00	0.39	0.00	0.61	0.00	0.00	4
C0_062314_039	35	0.00	0.42	0.00	0.58	0.00	0.00	4
C0_062314_048	44	0.00	0.42	0.00	0.58	0.00	0.00	4
C0_062314_065	61	0.00	0.43	0.00	0.57	0.00	0.00	4
C0_171_1	105	0.00	0.46	0.00	0.54	0.00	0.00	4
C0_062314_012	10	0.00	0.46	0.00	0.54	0.00	0.00	4
C0_062314_041	37	0.00	0.47	0.00	0.53	0.00	0.00	4
C0_164_5	92	0.00	0.48	0.00	0.52	0.00	0.00	4
C0_164_2	89	0.00	0.48	0.00	0.52	0.00	0.00	4
C0_062314_049	45	0.00	0.48	0.00	0.52	0.00	0.00	4
C0_062314_093	83	0.00	0.49	0.00	0.51	0.00	0.00	4
C0_166_3	98	0.00	0.49	0.00	0.51	0.00	0.00	4
C0_062314_009	7	0.00	0.49	0.00	0.51	0.00	0.00	4
C0_062314_068	64	0.00	0.49	0.00	0.51	0.00	0.00	4
C0_062314_063	59	0.00	0.50	0.00	0.50	0.00	0.00	4
C0_169_2	103	0.02	0.00	0.00	0.69	0.29	0.00	4
C0_167_2	99	0.04	0.00	0.06	0.68	0.14	0.07	4
C0_062314_083	75	0.10	0.00	0.04	0.68	0.09	0.09	4
C0_062314_086	77	0.39	0.01	0.00	0.59	0.01	0.00	4
C0_062314_040	36	0.39	0.00	0.00	0.61	0.00	0.00	4
C0_062314_011	9	0.42	0.01	0.00	0.57	0.00	0.00	4
C0_169_1	102	0.42	0.00	0.00	0.58	0.00	0.00	4
C0_062314_020	17	0.00	0.00	0.00	0.27	0.73	0.00	5
C0_062314_022	19	0.00	0.00	0.00	0.27	0.72	0.00	5
C0_062314_052	48	0.00	0.00	0.00	0.25	0.75	0.00	5
C0_165_2	94	0.00	0.03	0.00	0.21	0.76	0.00	5
C0_164_4	91	0.00	0.00	0.00	0.25	0.74	0.00	5
C0_062314_030	27	0.01	0.00	0.00	0.22	0.77	0.00	5
C0_169_3	104	0.13	0.01	0.01	0.21	0.37	0.27	5
C0_062314_033	29	0.00	0.00	0.00	0.00	0.00	1.00	6
C0_062314_013	11	0.00	0.00	0.00	0.01	0.00	0.99	6
C0_062314_006	5	0.00	0.00	0.00	0.00	0.00	0.99	6
C0_062314_003	2	0.01	0.00	0.00	0.10	0.00	0.88	6
C0_062314_026	23	0.06	0.00	0.01	0.17	0.03	0.73	6
C0_062314_088	79	0.09	0.01	0.00	0.08	0.00	0.83	6
C0_062314_019	16	0.09	0.02	0.00	0.12	0.00	0.77	6
C0_062314_078	72	0.10	0.01	0.03	0.11	0.00	0.76	6
C0_062314_071	66	0.13	0.04	0.00	0.13	0.05	0.64	6
C0_062314_045	41	0.14	0.01	0.00	0.08	0.02	0.75	6
C0_062314_029	26	0.17	0.00	0.00	0.16	0.07	0.59	6
C0_062314_091	81	0.20	0.04	0.01	0.13	0.06	0.55	6
C0_062314_007	6	0.22	0.02	0.02	0.24	0.13	0.37	6
C0_062314_076	70	0.24	0.08	0.08	0.14	0.12	0.34	6

Table S4: Comparison of the proportion of individuals in each subpopulation of  $g_0$  to the corresponding subpopulation admixture proportion in  $g_2$ .

Subpopulation	Proportion of $g_0$ individuals in subpopulation <sup>a</sup>	Mean proportion of ancestry for $g_2$ individuals <sup>a</sup>
1	0.15	0.13
2	0.19	0.22
3	0.13	0.07
4	0.32	0.42
5	0.07	0.06
6	0.13	0.10

<sup>a</sup>The two vectors are highly correlated and not significantly different ( $t = -0.07$ ;  $p = 0.945$ ).

Table S5: Regions of the genome identified by kernel regression analysis of SIM test results.

Region	Chr	AGPv4-left	AGPv4-right	cM-left	cM-right	SIM <sup>+</sup> <sup>a</sup>
1	1	140265874	141784033	89.49	89.51	6
2	1	232258157	235649350	135.40	137.75	31
3	1	271957876	274610467	160.53	162.40	32
4	2	80486563	82278954	73.53	73.71	14
5	2	167628942	168147089	82.51	82.59	4
6	2	210883668	212206641	109.33	110.76	10
7	3	115123631	118593844	59.00	59.27	22
8	4	39269834	43845553	51.19	52.15	25
9	4	99643728	108146674	57.85	58.08	14
10	4	189093568	192689956	98.49	102.35	24
11	4	230198325	231781194	114.31	114.66	13
12	5	68261863	71509380	64.55	65.32	22
13	5	85945163	90344713	68.44	69.27	34
14	5	111272484	113207281	70.52	70.62	10
15	5	119329575	124643535	70.94	71.22	11
16	5	135998724	143453372	71.81	72.20	46
17	5	149166680	151756778	72.49	72.91	19
18	6	138083969	139243488	51.93	52.59	33
19	7	153336525	155503321	80.64	82.70	19
20	8	42896269	58359331	45.41	50.04	117
21	9	29355770	36335089	43.00	43.40	55
22	9	39449354	51050725	43.57	44.23	101
23	9	68801309	91882695	45.23	46.53	184
24	9	105916829	107329955	49.90	50.49	8
25	9	116149304	126635638	54.17	59.38	81
26	10	58200959	62904445	37.46	37.74	41
27	10	80774127	80878696	39.32	39.34	1
28	10	89308334	90682008	40.98	41.25	9
29	10	134353483	136247228	59.14	61.32	22

<sup>a</sup>Number of SIM<sup>+</sup> markers ( $q < 0.01$ ) within each of the 29 SIM<sup>+</sup><sub>regions</sub>.

Table S6: Additive, dominance and residual genetic variance component estimates per chromosome.

Chr	Additive variance (chr) <sup>a</sup>	Dominance variance (chr)	Additive variance (sans chr)	Dominance variance (sans chr)	Residual genetic variance	No. Markers <sup>b</sup>	SIM <sup>+</sup> <sup>c</sup>
1	4.8	2.4	22.3	3.1	0.0	1525	976
2	0.0	0.0	27.2	5.4	0.0	1241	538
3	4.1	0.7	23.6	4.3	0.0	1140	623
4	2.3	0.1	25.2	5.0	0.0	1244	692
5	2.3	0.0	25.1	5.2	0.0	1023	793
6	0.7	0.0	27.0	5.2	0.0	786	277
7	2.0	0.0	25.6	5.0	0.0	825	436
8	2.0	4.9	25.7	0.0	0.0	906	501
9	4.3	0.0	23.6	5.0	0.0	766	775
10	8.1	2.3	21.0	3.1	0.0	742	504

<sup>a</sup>Additive and dominance variances estimated from the fitted **G** and **D** matrices respectively, constructed with markers from the corresponding chromosome (“chr”) and the remaining chromosomes (“sans chr”).

<sup>b</sup>Number of markers in SNP set F (Table S2) used to estimate chromosome-specific genetic variances.

<sup>c</sup>Number of SIM<sup>+</sup> markers.

Table S7: Markers significantly associated with phenotypic variation in flowering time identified by genome-wide association tests under a 10% FDR threshold.

Marker	Chr	AGPv4	SIM ( $q$ )	FITR (BPP) <sup>a</sup>	GWA ( $q$ )	Minor Allele <sup>b,c</sup>	Beta <sup>d</sup>	Additive effect <sup>e</sup>
PZE.101091520	1	85,230,603	0.1072	0	0.0758	G	-0.0166	4.2
PZE.101162348	1	208,360,266	0.0044	0	0.0060	A	-0.0133	-1.4
PZE.102146567	2	199,515,336	0.0724	0	0.0296	G	-0.0151	4.6
PZE.104005434	4	1,474,971	0.0355	0	0.0758	G	0.0139	-4.5
PZE.104069513	4	141,309,604	0.0285	0	0.0758	A	-0.0135	2.5
PZE.105112537	5	173,406,538	0.2925	0	0.0178	A	-0.0047	10.2
SYN38278	5	205,090,726	0.4219	0	0.0178	A	-0.0050	7.9
SYN29958	7	136,246,166	0.2116	0	0.0701	G	0.0136	-2.0
PZE.108080696	8	141,126,129	0.2832	0	0.0758	A	-0.0029	8.4
ZmCCT10_CACTA	10	94,435,768	0.0000	0	0.0001	D	-0.0190	12.3
PZE.110050177	10	94,908,997	0.0021	0	0.0130	A	-0.0192	6.3
PZE.110055163	10	106,558,205	0.0571	0	0.0701	A	-0.0107	7.8

<sup>a</sup>FITR bootstrap proportion.

<sup>b</sup>Reference allele for estimated effect in table.

<sup>c</sup>D: "deletion" (lack of insertion) allele at the presence-absence causal variant of *ZmCCT10*.

<sup>d</sup>Slope in allele frequency change.

<sup>e</sup>Given the estimated allele effect for PZE.101162348, the slope in allele frequency change across generations has the unexpected sign.



Table S8: The candidate gene for flowering time nearest to each GWA<sup>+</sup> marker in S7 Table.

Marker	Chr	AGPv4	Nearest gene	Distance from marker (bp) <sup>a</sup>
PZE.101091520	1	85,230,603	CCT(ghd7-like) (Zm00001d029885)	-6,987,083
PZE.101162348	1	208,360,266	SPY (Zm00001d031938)	-885,523
PZE.102146567	2	199,515,336	FT (Zm00001d006116)	-454,929
PZE.104005434	4	1,474,971	CCT(ghd7-like) (Zm00001d049347)	-25,840,962
PZE.104069513	4	141,309,604	TOC1 (Zm00001d051114)	-2,558,009
PZE.105112537	5	173,406,538	CRY1 (Zm00001d016915)	-6,349,176
SYN38278	5	205,090,726	CIB1 (Zm00001d017777)	-1,323,207
SYN29958	7	136,246,166	AtDOF{1.6,3.4,5.8} (Zm00001d020837)	1,892,764
PZE.108080696	8	141,126,129	rap2.7 (Zm00001d010987)	5,113,282
ZmCCT10_CACTA	10	94,435,768	CCT(ghd7-like) (Zm00001d024909)	-2,499
PZE.110050177	10	94,908,997	CCT(ghd7-like) (Zm00001d024909)	-475,728
PZE.110055163	10	106,558,205	COP9 (Zm00001d025407)	11,125,411

<sup>a</sup>Negative and positive values indicate gene locations that are upstream and downstream respectively of the associated variant.