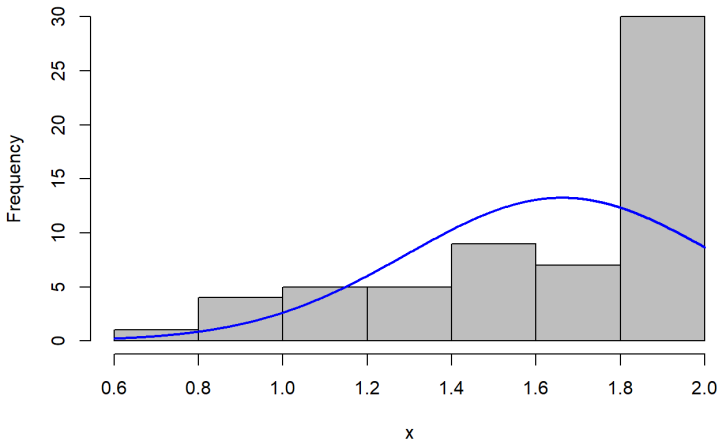
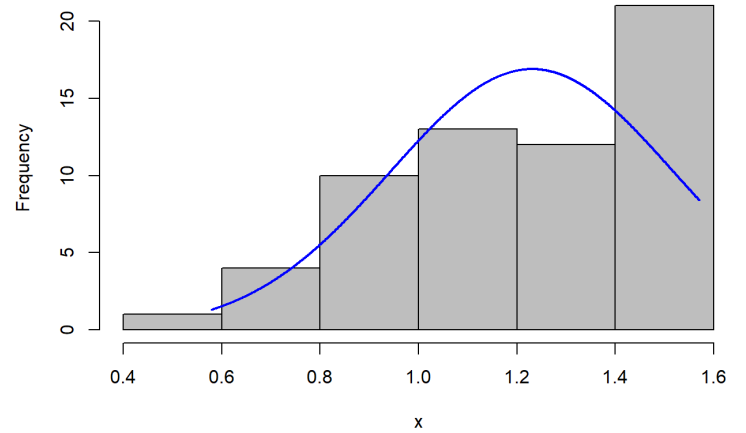


Supplemental Figures:

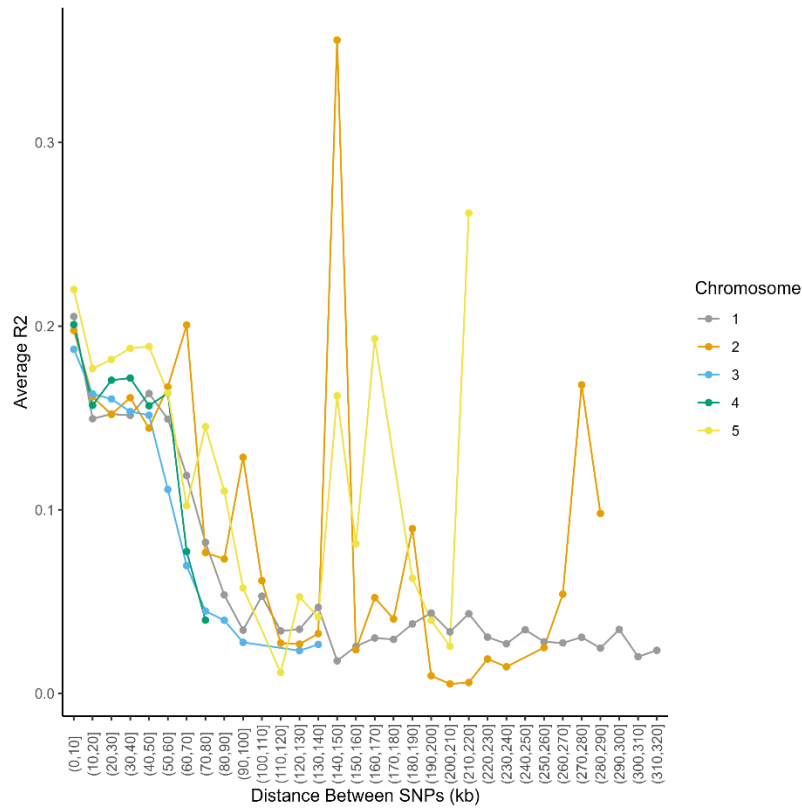
A: Short Stamen Number



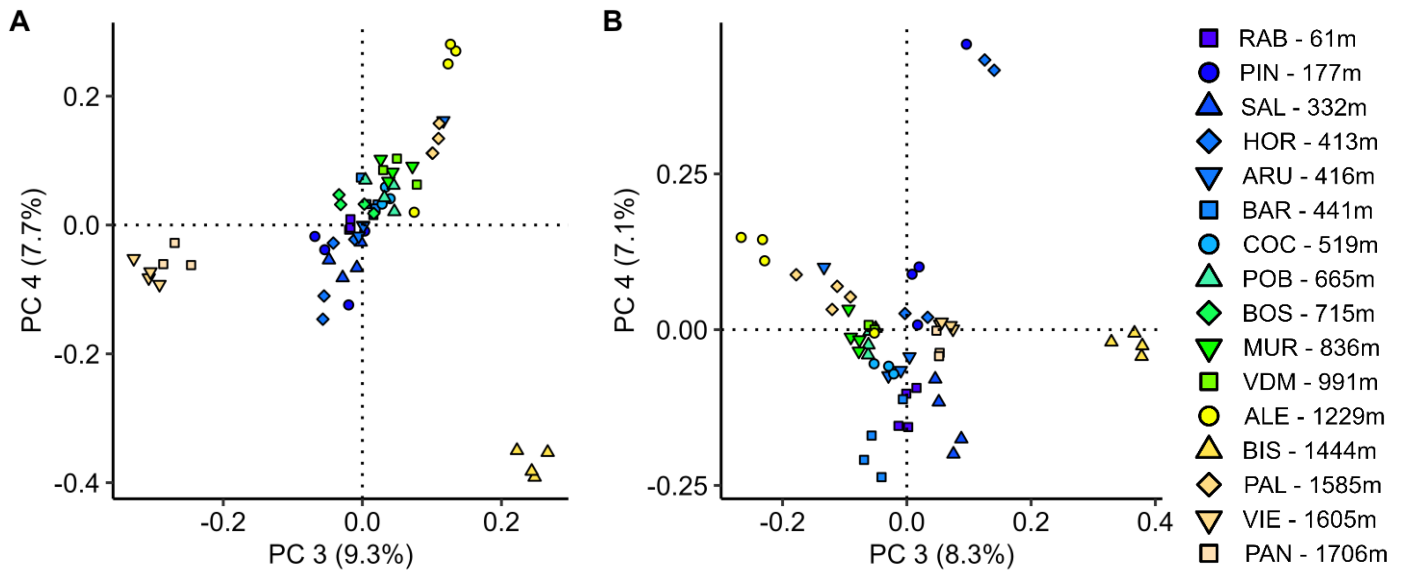
B: Arcsine(sqrt(short stamen number / 2))



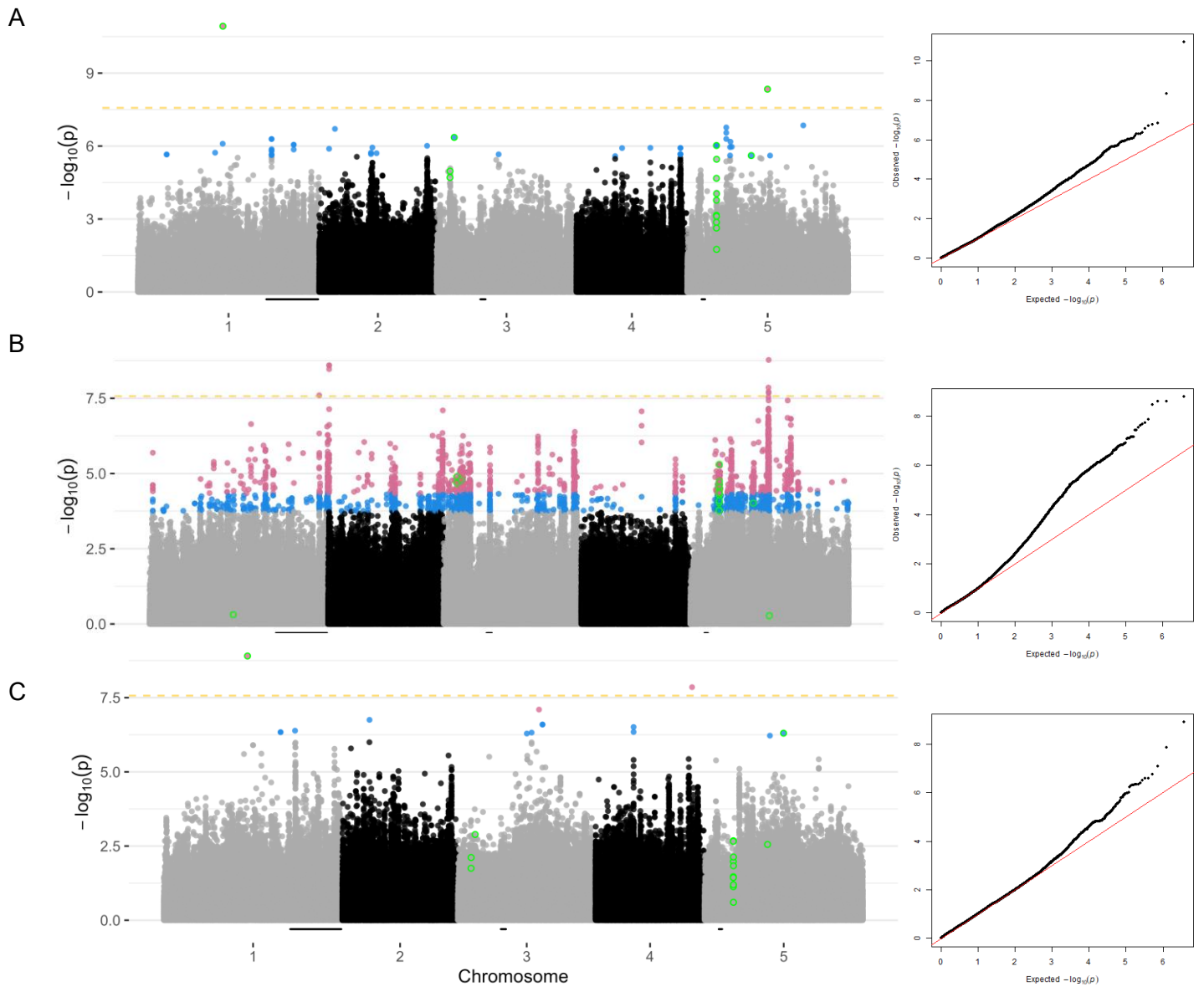
Supplemental Figure 1. Short stamen number is not normally distributed, even after transformation. Histogram of individual mean short stamen number without transformation (A) and after arcsine transformation (B).



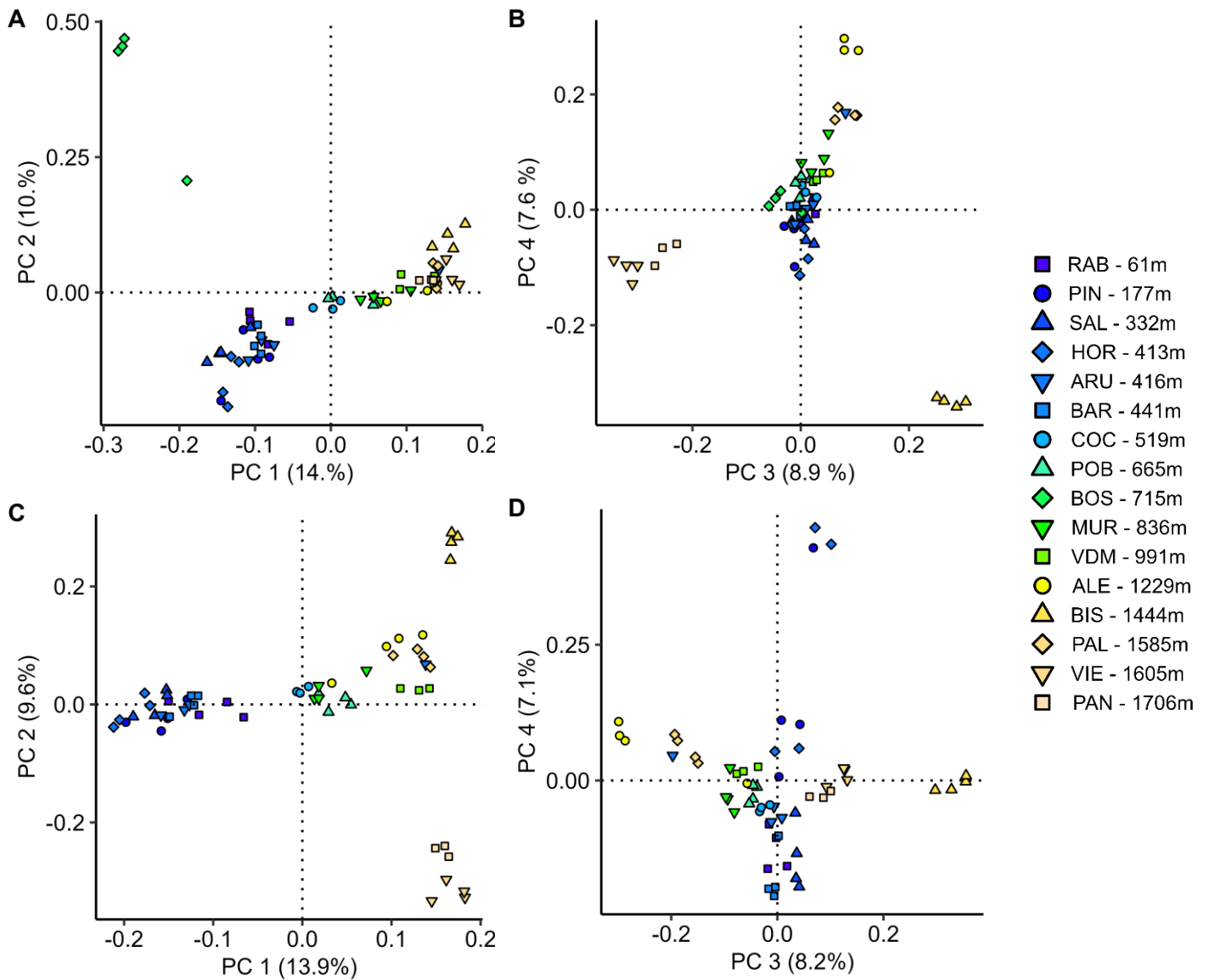
Supplemental Figure 2. Linkage Disequilibrium decay within each chromosome. LD decay calculated with plink. We estimated the first major drop in LD for all chromosomes around 50kb. X axis is 10kb windows from 0 to 320kb to bin the distance between SNPs..



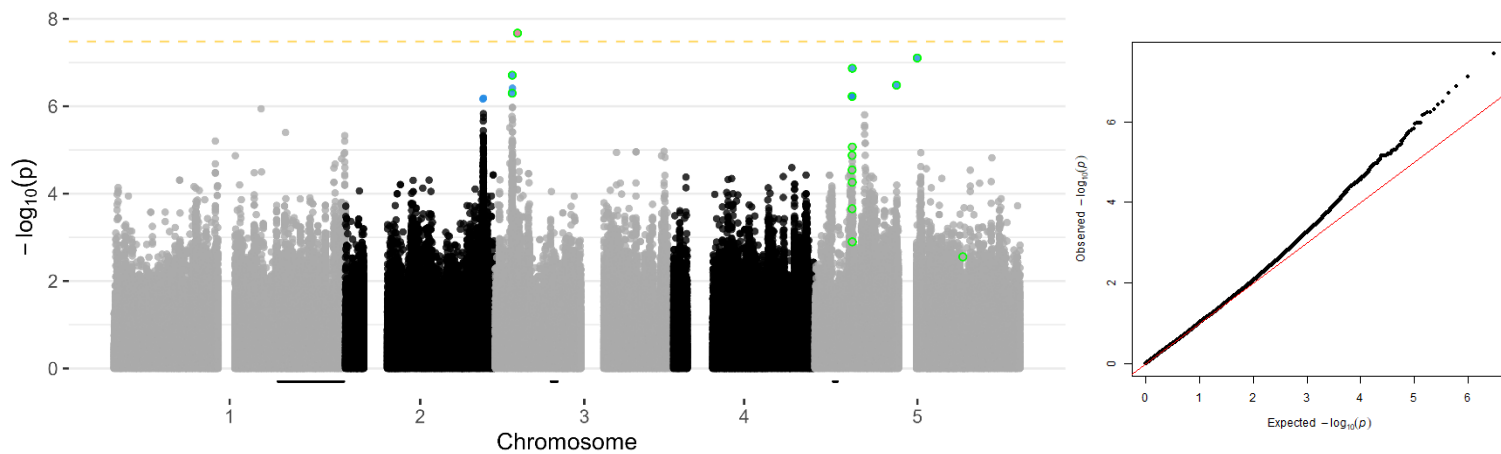
Supplemental Figure 3. PC3 and PC4 are not correlated with elevation. Genetic principal component analysis for PC3 and PC4 with all populations (A) and after excluding all BOS population individuals (B). With all populations, PC3 ($r = -0.17$, $p = 0.52$) and PC4 ($r = -0.08$, $p = 0.74$) are not correlated with elevation. Similarly, with BOS excluded neither PC3 ($r = 0.11$, $p = 0.69$) nor PC4 ($r = 0.14$, $p = 0.61$) are correlated with elevation.



Supplemental Figure 4. Additional manhattan plots for GWAS for short stamen number. (A) Manhattan plot for untransformed mean short stamen number. (B) Manhattan plot for shorts stamen number coded as a binary trait (mean short stamen number < 2 coded as cases). (C) Manhattan plot for only the subset of individuals that showed any short stamen loss (if mean short stamen number < 2, individual included in this analysis. The yellow dashed line indicates significance at $p=0.05$ after Bonferroni correction. Blue points are significant below a FDR of 0.10. Pink points are significant below a FDR of 0.05. Points with a green outline are shared between at least two GWAS below FDR 0.10 ($n = 20$). The black bars on the x axis are Bayes 95% credible intervals for short stamen number QTL identified by Royer et al. (2016).

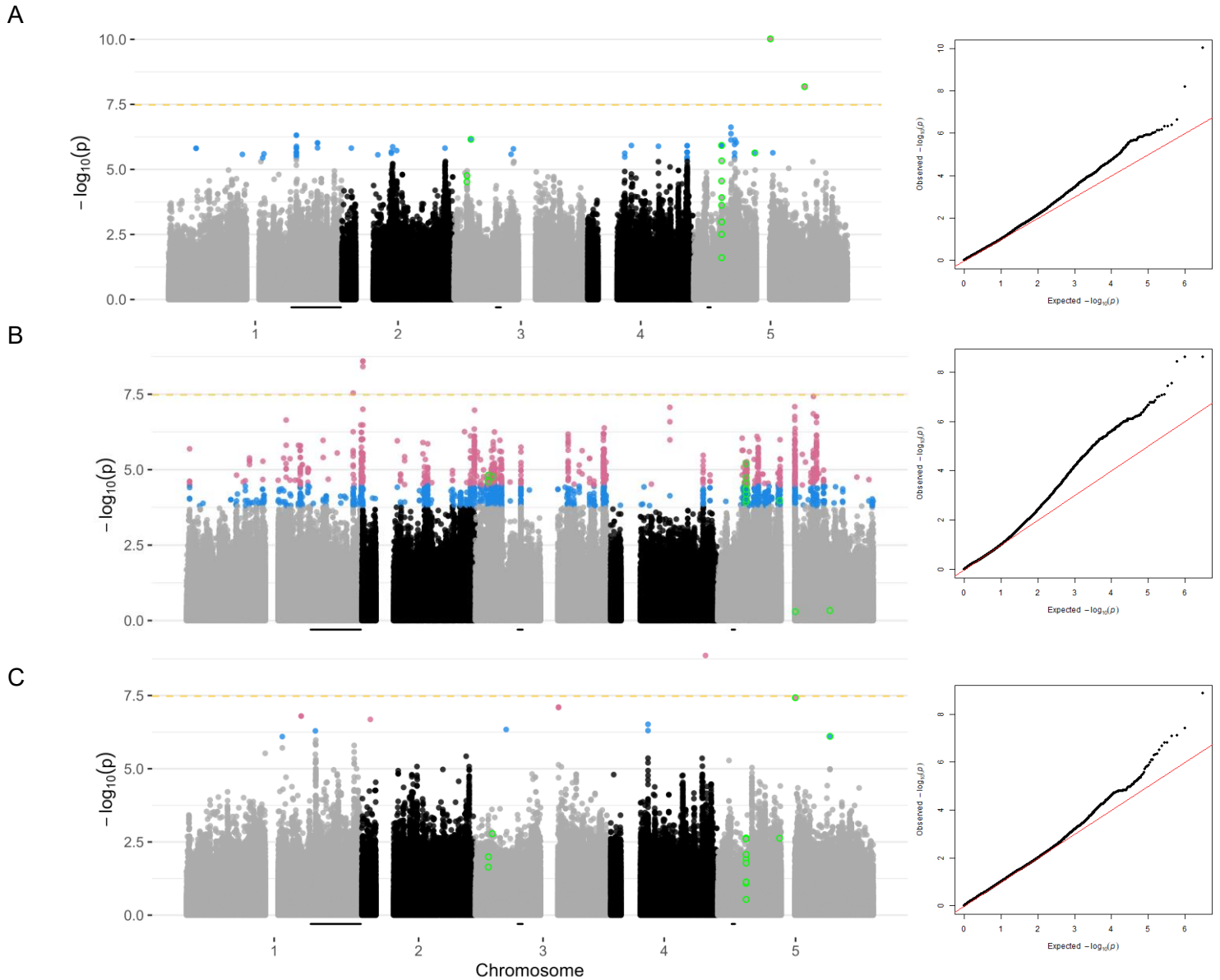


Supplemental Figure 5. Genetic Principal Component Analysis without the centromere region. Patterns of relatedness from genetic principal component analysis do not meaningfully change after excluding the centromeres whether the BOS population is included (A, B) or excluded (C, D).



Supplemental Figure 6. Manhattan plots for GWAS for short stamen number after excluding the centromere region.

Manhattan plot for arcsine transformed mean short stamen number. The yellow dashed line indicates significance at $p=0.05$ after Bonferroni correction. Blue points are significant below a FDR of 0.10. Pink points are significant below a FDR of 0.05. Points with a green outline are shared between at least two GWAS below FDR 0.10 ($n = 16$). The black bars on the x axis are Bayes 95% credible intervals for short stamen number QTL identified by Royer et al. (2016).



Supplemental Figure 7. Additional manhattan plots for GWAS for short stamen number with the centromere excluded.

(A) Manhattan plot for untransformed mean short stamen number. (B) Manhattan plot for shorts stamen number coded as a binary trait (mean short stamen number < 2 coded as cases). (C) Manhattan plot for only the subset of individuals that showed any short stamen loss (if mean short stamen number < 2, individual included in this analysis). The yellow dashed line indicates significance at $p=0.05$ after Bonferroni correction. Blue points are significant below a FDR of 0.10. Pink points are significant below a FDR of 0.05. Points with a green outline are shared between at least two GWAS below FDR 0.10 ($n = 16$). The black bars on the x axis are Bayes 95% credible intervals for short stamen number QTL identified by Royer et al. (2016).

Supplemental Tables:

Table S1. Population metadata. Population indicates the closest town to seed collection location. PopCode is a 3 letter abbreviation for each population. Elevation, latitude, and longitude data of seed collection site.

Population	PopCode	Elevation (m)	Latitude (Decimal Degree)	Longitude (Decimal Degree)
Albet	ALE	1229	42.41	1.32
Arbucies	ARU	416	41.81	2.49
Barcelona	BAR	441	41.43	2.13
Bisaurri	BIS	1444	42.49	0.53
Bossost	BOS	715	42.78	0.69
Cap de Creus	COC	519	42.32	3.16
Hortsavinya	HOR	413	41.66	2.62
Mura	MUR	836	41.67	2
Pallerols de Canto	PAL	1585	42.34	1.3
Panticosa	PAN	1706	42.76	-0.23
Pineda de Mar	PIN	177	41.66	2.66
Poblet	POB	665	41.35	1.03
Rabos	RAB	61	42.37	3.03
Santa Pellaia	SAL	332	41.93	2.92
Vilanova de Meia	VDM	991	42.03	1.03
Vielha	VIE	1605	42.63	0.76

Table S2. Sequencing Quality. For each line, total reads, the number of mapped reads, and the mapping rate from bwa are reported. The frequency of missing sites was calculated with vcftools after Base Quality Score Recalibration. Bamtools was used to report the percent of the genome with 1x and 4x coverage as well as median depth. Average quality score was extracted from vcf files with GATK. Mean, Median, and sum, where appropriate, are reported at the bottom of the table.

Line	Total Reads	Mapped Reads paired	Mapping Rate paired	Frequency Missing Sites	Percent 1X	Percent 4X	Median Depth	Average Quality (NA excluded)
ALE10	19712121	19184226	97.62	0.095284	0.93380832	0.848668447	9	26.710325
ALE12	19417011	18856422	97.48	0.0885923	0.938827568	0.89521716	10	30.779432
ALE16	3833518	3685146	96.39	0.358327	0.713647853	0.157023251	1	7.887054
ALE4	27137190	26132148	96.73	0.0779572	0.945231595	0.926439603	17	46.274956
ARB10	13753206	13249968	96.58	0.136072	0.918336322	0.728437677	6	18.480365
ARB3	21363640	20581102	96.62	0.0863734	0.94250462	0.870279153	10	30.108697
ARB6	20588486	20085288	97.8	0.101864	0.940417965	0.86537087	9	25.454609
ARB8	15833079	15240030	96.59	0.086599	0.93972272	0.861390169	9	26.609563
BAR11	7192507	6683048	93.04	0.380374	0.768546653	0.307549973	2	9.927844
BAR3	13209944	12849326	97.6	0.107214	0.933722864	0.825450573	8	23.911895
BAR4	16372218	15852820	97.17	0.081261	0.94403433	0.862889773	8	24.366533
BAR9	14955682	14190512	95.06	0.16471	0.906448036	0.66494117	5	17.04758
BIS11	8950013	8515326	95.34	0.246881	0.842364527	0.442343408	3	12.92224
BIS16	11657278	11174536	96.23	0.0878037	0.93895045	0.813676452	7	21.496708
BIS20	12101273	11628344	96.45	0.08588	0.941025012	0.811626785	7	20.769619
BIS8	13098954	12523234	95.86	0.131212	0.918908352	0.711081995	6	18.983814
BOS10	27285715	26509336	97.46	0.0757308	0.949908511	0.92948089	15	40.5501
BOS5	17913901	17379876	97.3	0.0827965	0.944301906	0.861507097	9	26.492931
BOS6	14892443	14533824	97.9	0.0875408	0.941322836	0.845040798	8	23.916785
BOS9	20317221	19721584	97.41	0.0739174	0.94939497	0.920368364	12	33.818551
COC14	19730554	19076102	96.97	0.0898506	0.941173031	0.865796868	10	28.309747
COC17	12451928	12011070	96.81	0.0851895	0.940585457	0.825846603	7	23.215236
COC19	15125859	14643166	97.19	0.0867262	0.941148308	0.874656605	9	26.718768
COC7	8533452	8025088	84.32	0.17473	0.883801574	0.5352049	4	14.979581
HOR16	20026317	19410958	97.33	0.0795994	0.945680497	0.914645713	14	39.108156
HOR4	17530713	17103746	97.89	0.0925175	0.942631583	0.881709173	10	28.726877
HOR6	19567040	18954168	97.25	0.0799675	0.946704167	0.918558619	12	34.671127
HOR7	16536756	16049354	97.36	0.101436	0.939901849	0.855900735	8	25.653929
MUR15	19893668	19235198	97	0.0966443	0.935523187	0.857908363	10	29.936208
MUR16	12603765	12159944	96.88	0.0774015	0.953907444	0.824251475	7	24.973462
MUR17	15669733	14511434	92.83	0.122035	0.922430254	0.776049139	7	21.85571
MUR20	14235087	13861624	97.75	0.100851	0.935910925	0.859243787	9	26.8259
PAL12	18863248	19341898	97.55	0.082103	0.946568051	0.900930129	10	28.776939
PAL16	3958526	3810546	96.63	0.213877	0.837400308	0.254548432	2	9.055073
PAL6	8662644	8307962	96.28	0.110427	0.921523735	0.673732957	5	17.715713
PAL7	12545857	12126038	97.03	0.0853889	0.943596279	0.846446533	7	23.099512
PAN1	13493783	13074414	97.22	0.0961753	0.93322509	0.788037511	7	22.18564

Line	Total Reads	Mapped Reads paired	Mapping Rate paired	Frequency Missing Sites	Percent 1X	Percent 4X	Median Depth	Average Quality (NA excluded)
PAN5	11454217	10947794	95.78	0.171477	0.89062912	0.557564965	4	14.332644
PAN9	14462860	13966798	96.9	0.0943379	0.939613869	0.853602381	8	25.011322
PIN3	17256729	16786270	97.61	0.0873108	0.94239514	0.886942336	10	28.245879
PIN6	12279097	11842198	96.83	0.0839895	0.943469274	0.863768506	8	24.737327
PIN7	14845446	14423300	97.5	0.0913857	0.939771193	0.855498068	8	24.938503
PIN9	19513663	18921394	97.28	0.0785065	0.944568986	0.891827492	10	30.584467
POB10	17333118	16897498	97.77	0.113248	0.93374925	0.839942669	8	24.433195
POB16	15815482	15285062	97.06	0.084191	0.945719821	0.899785275	10	30.130401
POB19	29069830	28034352	96.81	0.0788636	0.949081053	0.931900094	17	45.177738
POB7	12272121	11860176	97.01	0.0914374	0.938619091	0.803773907	7	22.173469
RAB17	20142894	19644904	97.89	0.0867714	0.942018708	0.912441866	12	34.761648
RAB20	25499341	24844970	97.76	0.083803	0.943951032	0.920764855	15	40.132486
RAB4	5574554	5372236	96.67	0.246698	0.822850644	0.373876352	3	11.745683
RAB9	17813030	17252450	97.26	0.076267	0.949048009	0.921511878	12	35.008764
SPE2	14723146	14292882	97.44	0.0907326	0.93888785	0.856997056	8	26.091352
SPE5	9009297	8542706	95.02	0.259712	0.836739117	0.482691684	3	13.762534
SPE6	21149166	20476064	97.19	0.0774476	0.948390664	0.912880539	13	36.429486
SPE7	10718970	10455162	97.92	0.10757	0.930315283	0.777761151	6	20.87309
VDM17	17074008	16566130	97.37	0.0873811	0.940959966	0.883627653	9	28.295409
VDM20	18009082	16097200	89.71	0.0839738	0.944618675	0.88943338	10	29.29148
VDM9	11975809	11616758	97.33	0.110689	0.920913962	0.728168666	6	20.901281
VIE16	14678603	14160160	96.79	0.0841149	0.941838295	0.846866663	8	24.412579
VIE3	24454713	23797668	97.58	0.0858097	0.943619342	0.890739707	11	31.334127
VIE4	15045325	14539938	96.95	0.091256	0.941023572	0.844092725	8	23.671476
VIE6	17529193	17034084	97.54	0.0823222	0.944623981	0.906702361	11	31.234305
Line	Total Reads	Mapped Reads paired	Mapping Rate paired	Frequency Missing Sites	Percent 1X	Percent 4X	Median Depth	Average Quality (NA excluded)
mean	15753452	15224790	96.58	0.113558	0.924525049	0.792506667	8.451	25.645610
median	15397796	14591552	97.115	0.088198	0.940772712	0.856448895	8	25.232966
sum	976714024	943936960						

Table S3. Model Summary Table. All models include the centromere. All flowers phenotyped (Full) or only flowers from the sequenced genotypes (Seq) denoted. Adding a quadratic elevation term increased adjusted r^2 when predicting population mean short stamen number, but a quadratic elevation term did not increase model accuracy when predicting nucleotide diversity and a quadratic nucleotide diversity term did not increase model accuracy compared to only a linear nucleotide diversity term. Residuals of model 4 are used as response variable in model 8. Residuals of model 6 are used as the response variable in model 7.

	Response Variable	Elevation estimate	Elevation p value	centered Elevation ² estimate	centered Elevation ² p value	Nucleotide Diversity estimate	Nucleotide Diversity p value	r^2	adjusted r^2	AIC score
1	Nucleotide Diversity	-1.81E-06	0.00019					0.6411	0.6155	-180.67
2	Full_PopFlwrMean	3.86E-04	0.0107					0.3819	0.3377	8.01379
3	Full_PopFlwrMean	4.82E-04	0.0041	-4.73E-07	0.137267			0.4818	0.4021	7.19102
4	Seq_PopFlwrMean					-61.5985	0.387	0.05398	-0.0359	13.4079
5	Seq_PopFlwrMean	6.47E-04	0.00882	-2.99E-07	0.34514	1.39E+02	0.16696	0.4886	0.3608	7.56529
6	Seq_PopFlwrMean	4.18E-04	0.01	-4.07E-07	0.2101			0.3964	0.3035	8.21867
7	Short Stamen Residuals					4.68E+01	0.397	0.05168	-0.0161	5.36963
8	Short Stamen Residuals	3.17E-04	0.0613	-4.54E-07	0.1955			0.2559	0.1414	10.6789

Table S4. Shared hits from short stamen number GWAS. All GWAS conducted with GEMMA. P-values are correlated with effect sizes in all GWAS. Chr, Window, and Position indicate the chromosomal position of each SNP. For each GWAS, the effect size (beta), standard error of the effect size (SE), and p-value are reported. For the arcsine transformed GWAS, effect sizes and standard errors have not been back transformed. The second page repeats the first 3 columns and reports if the SNP is in a gene, the chromosomal position of the gene, and the gene type from GBrowse with TAIR10 annotation. Notes information is from annotations within GBrowse or literature search of papers that reference each gene as reported by GBrowse, cited within the table.

Shared Short Stamen			Arcsine Transformed			Raw Phenotype			Binary: any loss?			Subset: if some loss			
Chr	Window	Position	Beta	SE	p	Beta	SE	p	Beta	SE	p	Beta	SE	p	
1	A	14262517				-0.33	0.04	1.18E-11				-0.30	0.04	1.25E-09	
3	A	2239234	0.21	0.04	3.08E-07				-0.28	0.06	2.06E-05				
	B	2253161	-0.22	0.04	1.19E-07				0.28	0.06	1.27E-05				
	C	2942726	-0.22	0.03	1.21E-08	-0.26	0.05	4.42E-07	0.25	0.05	1.64E-05				
5	A	4899729							0.23	0.06	1.64E-04				
		4899733							0.23	0.06	1.64E-04				
		4899789							0.24	0.06	9.33E-05				
		4899798	-0.26	0.05	4.66E-07	-0.33	0.06	9.49E-07	0.27	0.06	2.98E-05				
		4899803	-0.26	0.05	4.66E-07	-0.33	0.06	9.49E-07	0.27	0.06	2.98E-05				
		4899865							0.23	0.06	1.64E-04				
		4900275							0.25	0.06	5.11E-05				
		4900560							0.24	0.05	2.58E-05				
		4900628							0.23	0.06	1.72E-04				
	B	4919727							0.24	0.06	8.00E-05				
	B,C	4920179	-0.24	0.04	1.02E-07				0.32	0.06	4.96E-06				
	C	4920289								0.24	0.05	4.49E-05			
		4920304								0.24	0.05	4.49E-05			
		4920731								0.25	0.05	1.87E-05			
	D	10731997	0.20	0.03	3.11E-07	0.23	0.04	2.47E-06	-0.28	0.07	9.62E-05				
E	13458838	-0.19	0.03	4.48E-08	-0.24	0.03	4.59E-09				-0.26	0.04	4.98E-07		

Shared Short Stamen						
Chr	Window	Position	In a gene?	Gene Position	Gene Type	notes
1	A	14262517	AT1TE46795	Chr1:14262180..14263528 (+ strand)	transposable_element	in the centromere
3	A	2239234	AT3G07070.1	Chr3:2237897..2240266 (+ strand)	Protein kinase superfamily protein (PBL26, PBS1-LIKE 26)	near a GTP-binding family protein required for maintenance of inflorescence meristem identity, floral organ development, and megaspore mother cell specification
	B	2253161	AT3G07110	Chr3:2251946..2253597 (+ strand)	Ribosomal protein L13 family protein	expressed in stamen (and all other plant parts). About 40kb away from a SMAD/FHA domain-containing protein (Forkhead domain protein that is a subunit of ISWI chromatin remodeling complex. Interacts with histones and regulates the expression of genes involved in stamen filament elongation.)
	C	2942726	AT3G09580.1	Chr3:2942158..2944457 (- strand)	FAD/NAD(P)-binding oxidoreductase family protein	Expressed in stamen (and all other plant parts). Oxidoreductase located in chloroplast.
5	A	4899729	DUF1637; AT5G15120	Chr5:4898641..4900734 (+ strand)	HUP29, hypoxia response unknown protein 29, PCO1, Plant cysteine oxidase 2	involved in anaerobic respiration, cellular response to hypoxia, and peptidyl-cysteine oxidation; (Mustroph et al., 2010 Plant Physiology); Is near AT5G15110 which is expressed in pollen
		4899733				
		4899789				
		4899798				
		4899803				
		4899865				
		4900275				
		4900560				
		4900628				
	B	4919727	No	Chr5:4919548..4919824 (+ strand)	long non-coding RNA	
	B,C	4920179	No	Chr5:4919989..4919989	TE	
	C	4920289	No	Chr5:4920043..4920718 (+ strand)	long non-coding RNA	
4920304		AT5TE17795	Chr5:4920665..4921403 (+ strand)	TE		
4920731						
D	10731997	AT5G28692	Chr5:10728378..10733393 (- strand)	transposable_element_gene; locus:504955064	gypsy-like retrotransposon family	
E	13458838	No			closest thing: AT5G35200 a ENTH/ANTH/VHS superfamily protein (PICALM3) - PICALM 5 and 5b are associated with pollen tube growth (Muro et al. 2018 Commun Biol.)	