

Figure S1: Minor allele frequencies (MAF) of genotyping-by-sequencing markers. (A) In raw data before filtering for missing rate and data imputation (300K SNP). (B) After filtering for missing rate and data imputation (200K SNP for the diversity panel, 90K SNP for the NAM). (C) Using 60K common high-quality shared markers between NAM and diversity panels.

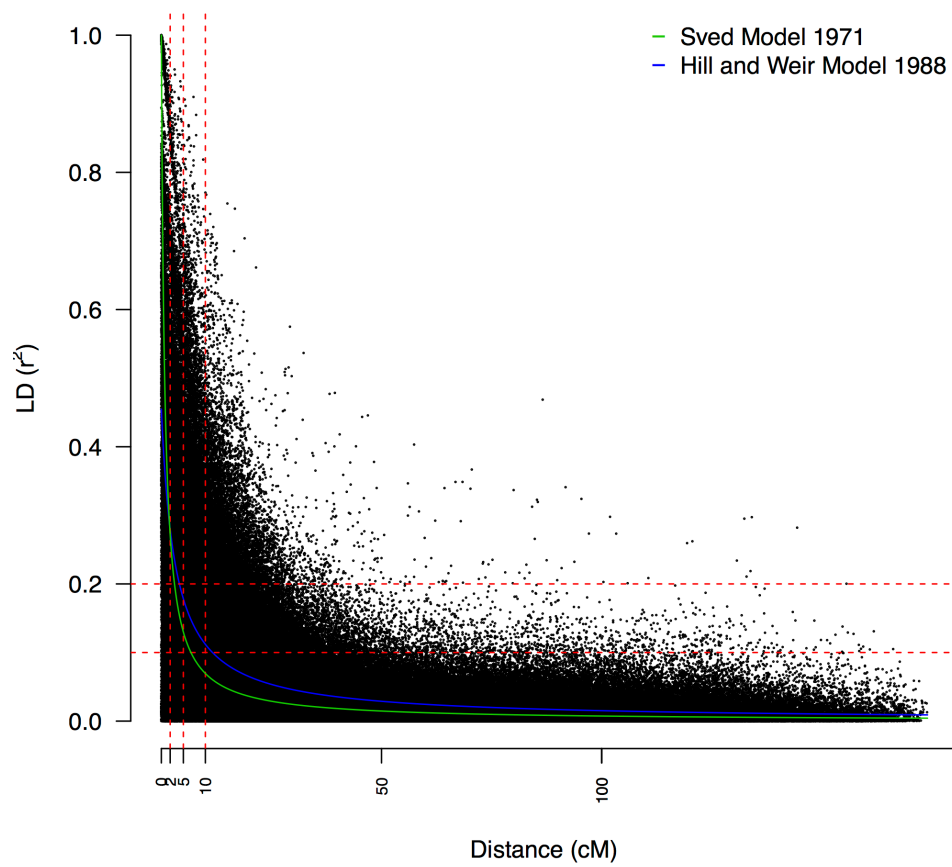


Figure S2: Linkage disequilibrium extent in the NAM population. LD (r^2) was calculated with 8349 unique loci. LD extent was modeled using non-linear model described in Sved (1971) and Hill and Weir (1988).

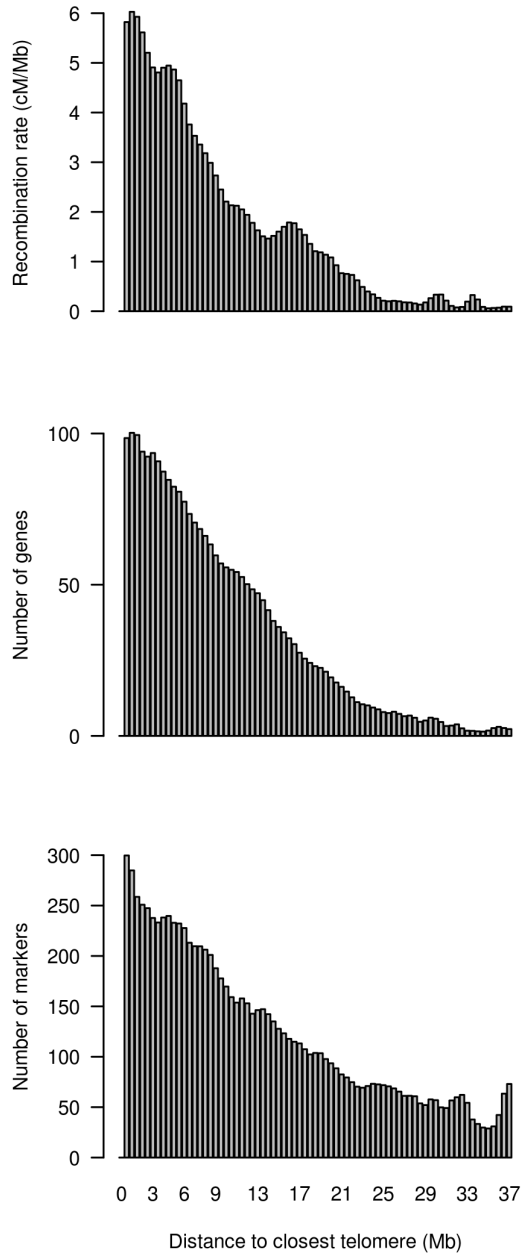


Figure S3: Recombination rates, gene and marker density versus distance from telomeres.

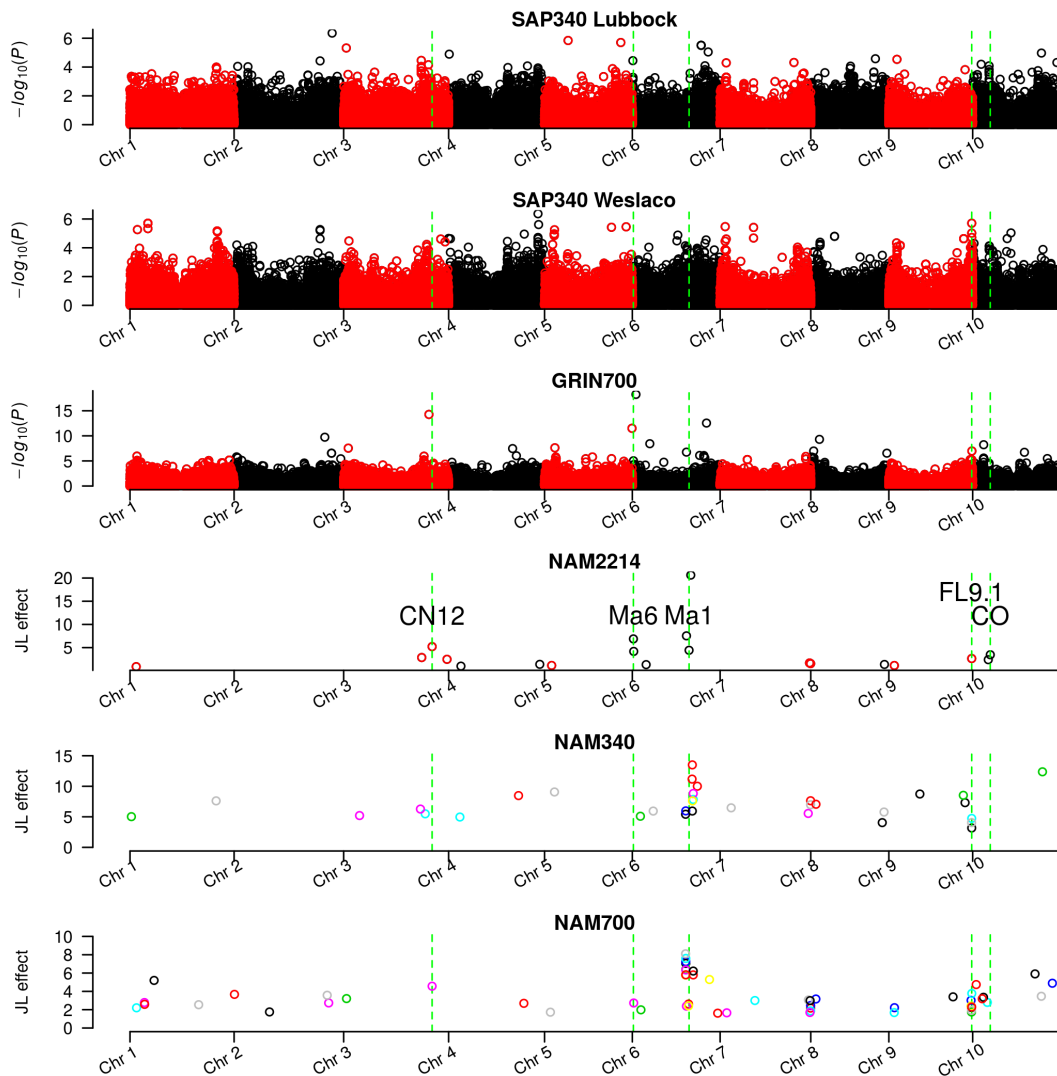


Figure S4: QTL mapping for flowering time using the diversity panels (with multi-locus mixed-models) and NAM (with joint linkage). SAP340 is a diversity panel of 340 lines, evaluated in Lubbock and Weslaco, USA. GRIN700 is a diversity panel of 700 lines evaluated in Lubbock. NAM2214 is the NAM population of 2214 RIL. NAM340 and NAM700 indicate subsets of the NAM population, including equal number of lines from each 10 families. Different colors represent results for different samples.

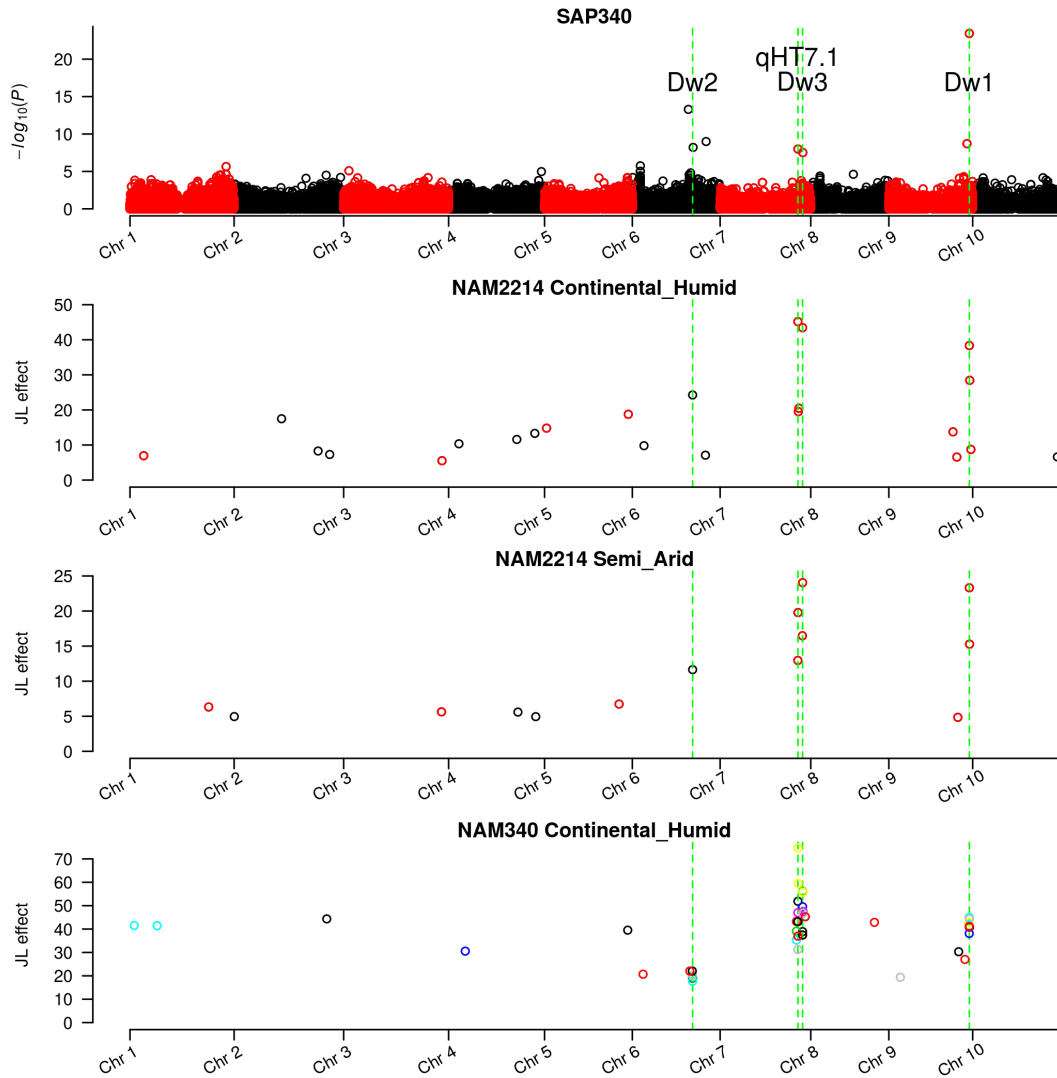


Figure S5: QTL mapping for plant height using the diversity panels (with multi-locus mixed-models) and NAM (with joint linkage). SAP340 is a diversity panel of 340 lines, evaluated in Lubbock and Weslaco, USA. GRIN700 is a diversity panel of 700 lines evaluated in Lubbock. NAM2214 is the NAM population of 2214 RIL. NAM340 and NAM700 indicate subsets of the NAM population, including equal number of lines from each 10 families. Different colors represent results for different samples.

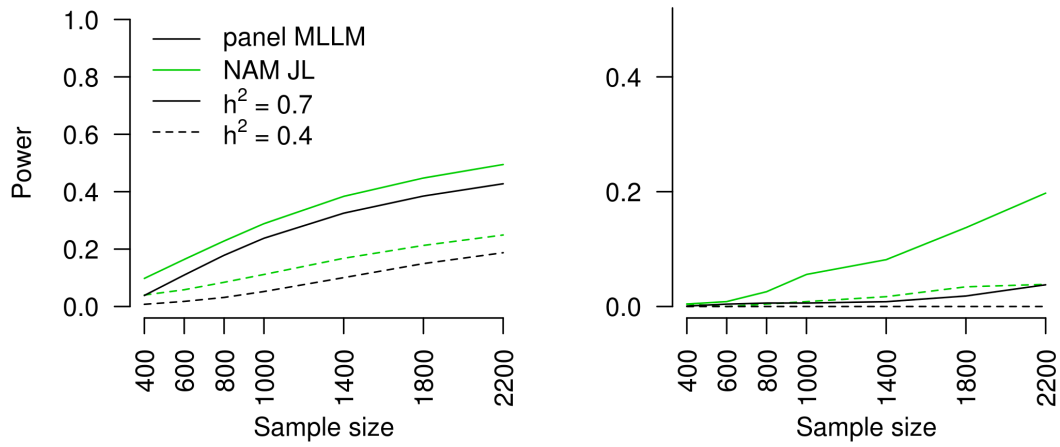


Figure S6: Power of QTL detection on chromosome 6 when under selection (A) or across the whole genome (B).

Table S1: Joint linkage QTL for flowering time and plant height

Trait ¹	SNP ²	Effect ²	Known gene (or locus)	Distance to gene (locus)
Height CH/SA	S7_55156401	45.19	(qHT7.1)	(Colocalized)
Height CH/SA	S7_58487616	43.45	Dw3	70
Height CH/SA	S9_57069231	38.36	Dw1	28
Height CH/SA	S6_42726152	24.27	(Dw2)	(Colocalized)
Height CH	S5_59380917	18.76		
Height CH	S2_33698052	17.49		
Height CH	S5_1450001	14.81		
Height CH	S9_45490823	13.75		
Height CH	S4_61088979	13.31		
Height CH	S4_48330648	11.59		
Height CH	S4_7314013	10.35		
Height CH	S6_8245968	9.80		
Height CH	S2_59585117	8.30		
Height CH	S2_67813119	7.30		
Height CH	S6_51809222	7.10		
Height CH	S1_9723354	6.95		
Height SA	S5_52851428	6.74		
Height CH	S10_60070002	6.62		
Height CH/SA	S9_48220391	6.57		
Height SA	S1_55760105	6.33		
Height SA	S4_49121762	5.60		
Height CH/SA	S3_69728543	5.53		
Height SA	S2_184254	4.96		
Flowering time	S6_41417540	20.64		
	S6_38361618	7.54		
	S6_758162	6.88	Ma6	84
	S3_62707083	5.22	SbCN12	64
	S6_40204294	4.43	Ma1	63
	S10_12485175	3.47	SbCO	199
	S3_55337873	2.87		
	S9_58743830	2.65	(SbFL9.1)	(Colocalized)
	S3_73262074	2.48		
	S7_63424491	1.67		
	S7_64151910	1.55		
	S4_64611885	1.40		
	S8_52244337	1.37		
	S6_9786706	1.33		
	S5_5055262	1.15		
	S9_3912094	1.14		
	S4_8739831	1.01		
	S1_4408231	0.89		

¹ Height QTL in continental humid (CH) or semi-arid (SA) environments or both

² Top SNP and QTL effect using the Joint-linkage model in TASSEL. If the QTL was discovered in both environments the SNP and effect size is given from the CH environment