

Supporting Information

Morris et al. 10.1073/pnas.1215985110

SI Results and Discussion

Genome Scan and GWAS on Plant Height. Because *dw3* mutants are known to show increased upper stem elongation, we additionally mapped *dw3* based on associations with flag leaf to apex distance (flag-to-apex). In this case, the top association peak is found near the *dw3* locus (114 kb from peak; $P < 10^{-7}$). The strongest association peak for plant height traits (Fig. S4) is a narrow peak on chromosome 9 around 57.2 Mb, which colocalizes with previously described plant height locus *dw1/SbHt9.1* (1). The top association for plant height is 29 kb from a GA2-oxidase, a catabolic enzyme in the gibberellin pathway, which has been proposed as the gene underlying the plant height QTL *SbHt9.1/Dw1* (2). Overexpression of GA2ox in rice leads to semidwarf phenotypes (3).

The second most significant peak maps to chromosome 6 between 39.7 Mb and 42.6 Mb near the classical dwarfing locus *Dw2* (4, 5). *Dw2* has been mapped adjacent to *Ma1* on chromosome 6 (6), to a region of ~100 kb around 42.2 Mb, but the gene underlying this QTL has not been cloned. The association peak for total plant height and preflag leaf height maps to a histone deacetylase (*Sb06g015420*), which is homologous to well-studied global transcriptional regulators in plants (*hda*) (7, 8). In maize and *Arabidopsis*, down-regulation of closely related histone deacetylases (*hda101* and *AiHD1*, respectively) results in reduced plant height and a variety of changes in inflorescence architecture (7, 8). In rice, overexpression of *OsHDAC1* increases plant height (9), whereas the knockdown of many genes in the *OsHDAC* gene family lead to semidwarf phenotypes (10). Therefore, we propose that *dw2* phenotype is a result of loss of function in a sorghum histone deacetylase.

The fourth classical dwarfing locus in sorghum, *dw4*, has not been genetically mapped but is known to be unlinked to the other dwarfing loci (11). Based on the location of the next most significant peak in the height GWAS and heterozygosity scan, a potential physical position of the *Dw4* locus is at ~6.6 Mbp on chromosome 6 (Fig. 3B and Fig. S4). Note, because of the simultaneous intro-

gression of maturity and dwarfing alleles in conversion lines, it may not be possible to distinguish between them using genome-wide scans, and additional loci may have been involved.

Origin of Dwarfing Alleles. Did the mutations that underlie classical dwarfing alleles arise de novo in the early US grain sorghums, as is suggested in classical breeding literature (12), or were they recruited from standing variation present in African or Asian landraces? The haplotypes associated with dwarfism at *dw1/SbHT9.1*, *dw2*, and *dw3* are widely distributed among African and Asian landraces (Fig. 3), but these haplotypes could represent ancestral haplotypes on which new dwarfing mutations occurred. The classical literature, however, confirms that dwarfing alleles were already present in African landraces at the time that dwarf alleles were being adopted in US grain sorghums. For instance, dwarf durra varieties collected near Khartoum, Sudan, c. 1920 carry the *dw4* allele (*Gahan dura*) or both *dw1* and *dw4* (*hegari*) (11).

GWAS on Inflorescence Branch Length. CMLM GWAS on inflorescence branch length identified candidate genes homologous from several known regulators of inflorescence development or cell elongation (Table S2). These genes include LEUNIG (13), Theus1 (14), Short panicle1 (15), Lost meristems3 (16), Dwarf in light2 (17), Dwarf8 (18), Teosinte branched1 (19), GIGANTEA (20), Clavata1 (21), Bearded ear1 (22), Indeterminate1 (23), Gibberillin dependent dwarf1 (24), and Aberrant panicle organization1 (25). Compared with plant height components, mapping of inflorescence branch length QTL depended more on methods for controlling population structure (Fig. S4). The top association peak for branch length (whether population structure is controlled) is a SNP found in another ID1 homolog (Table S2). The minor allele at this SNP is restricted to the three broomcorn varieties in the panel, which display the most extreme branch length phenotypes, with inflorescence branches more than 0.5 m in length or >8 SDs above the species-wide mean.

1. Brown PJ, Rooney WL, Franks C, Kresovich S (2008) Efficient mapping of plant height quantitative trait loci in a sorghum association population with introgressed dwarfing genes. *Genetics* 180(1):629–637.
2. Wang Y-H, Bible P, Loganathanaraj R, Upadhyaya H (2011) Identification of SSR markers associated with height using pool-based genome-wide association mapping in sorghum. *Mol Breed* 30(11):281–292.
3. Huang J, et al. (2010) Activation of gibberellin 2-oxidase 6 decreases active gibberellin levels and creates a dominant semi-dwarf phenotype in rice (*Oryza sativa* L.). *J Genet Genomics* 37(1):23–36.
4. Quinby JR, Karper RE (1945) The inheritance of three genes that influence time of floral initiation and maturity date in milo. *Agron J* 37(5):916–936.
5. Lin YR, Schertz KF, Paterson AH (1995) Comparative analysis of QTLs affecting plant height and maturity across the Poaceae, in reference to an interspecific sorghum population. *Genetics* 141(1):391–411.
6. Klein RR, et al. (2008) The effect of tropical sorghum conversion and inbred development on genome diversity as revealed by high-resolution genotyping. *Crop Sci* 48(S1):S12–S26.
7. Tian L, Chen ZJ (2001) Blocking histone deacetylation in *Arabidopsis* induces pleiotropic effects on plant gene regulation and development. *Proc Natl Acad Sci USA* 98(1):200–205.
8. Rossi V, et al. (2007) Maize histone deacetylase *hda101* is involved in plant development, gene transcription, and sequence-specific modulation of histone modification of genes and repeats. *Plant Cell* 19(4):1145–1162.
9. Jang I-C, et al. (2003) Structure and expression of the rice class-I type histone deacetylase genes *OsHDAC1-3*: *OsHDAC1* overexpression in transgenic plants leads to increased growth rate and altered architecture. *Plant J* 33(3):531–541.
10. Hu Y, et al. (2009) Rice histone deacetylase genes display specific expression patterns and developmental functions. *Biochem Biophys Res Commun* 388(2):266–271.
11. Quinby JR, Karper RE (1954) Inheritance of height in sorghum. *Agron J* 46(5):211–216.
12. Quinby JR (1975) The genetics of sorghum improvement. *J Hered* 66(2):56–62.
13. Conner J, Liu Z (2000) LEUNIG, a putative transcriptional corepressor that regulates AGAMOUS expression during flower development. *Proc Natl Acad Sci USA* 97(23):12902–12907.
14. Cheung AY, Wu H-M (2011) THESEUS 1, FERONIA and relatives: A family of cell wall-sensing receptor kinases? *Curr Opin Plant Biol* 14(6):632–641.
15. Li S, et al. (2009) Short panicle1 encodes a putative PTR family transporter and determines rice panicle size. *Plant J* 58(4):592–605.
16. Schulze S, Schäfer BN, Parizotto EA, Voinnet O, Theres K (2010) LOST MERISTEMS genes regulate cell differentiation of central zone descendants in *Arabidopsis* shoot meristems. *Plant J* 64(4):668–678.
17. Takase T, Nakazawa M, Ishikawa A, Manabe K, Matsui M (2003) DFL2, a new member of the *Arabidopsis* GH3 gene family, is involved in red light-specific hypocotyl elongation. *Plant Cell Physiol* 44(10):1071–1080.
18. Hirsch S, Oldroyd GED (2009) GRAS-domain transcription factors that regulate plant development. *Plant Signal Behav* 4(8):698–700.
19. Choi M-S, et al. (2012) Teosinte Branched 1 modulates tillering in rice plants. *Plant Cell Rep* 31(1):57–65.
20. Fowler S, et al. (1999) GIGANTEA: a circadian clock-controlled gene that regulates photoperiodic flowering in *Arabidopsis* and encodes a protein with several possible membrane-spanning domains. *The EMBO Journal* 18(17):4679–4688.
21. Bortiri E, Hake S (2007) Flowering and determinacy in maize. *J Exp Bot* 58(5):909–916.
22. Thompson BE, et al. (2009) Bearded-ear encodes a MADS box transcription factor critical for maize floral development. *Plant Cell* 21(9):2578–2590.
23. Colasanti J, Yuan Z, Sundaresan V (1998) The indeterminate gene encodes a zinc finger protein and regulates a leaf-generated signal required for the transition to flowering in maize. *Cell* 93(4):593–603.
24. Li J, et al. (2011) Mutation of rice BC12/GDD1, which encodes a kinesin-like protein that binds to a GA biosynthesis gene promoter, leads to dwarfism with impaired cell elongation. *Plant Cell* 23(2):628–640.
25. Ikeda K, Nagasawa N, Nagato Y (2005) ABERRANT PANICLE ORGANIZATION 1 temporally regulates meristem identity in rice. *Dev Biol* 282(2):349–360.

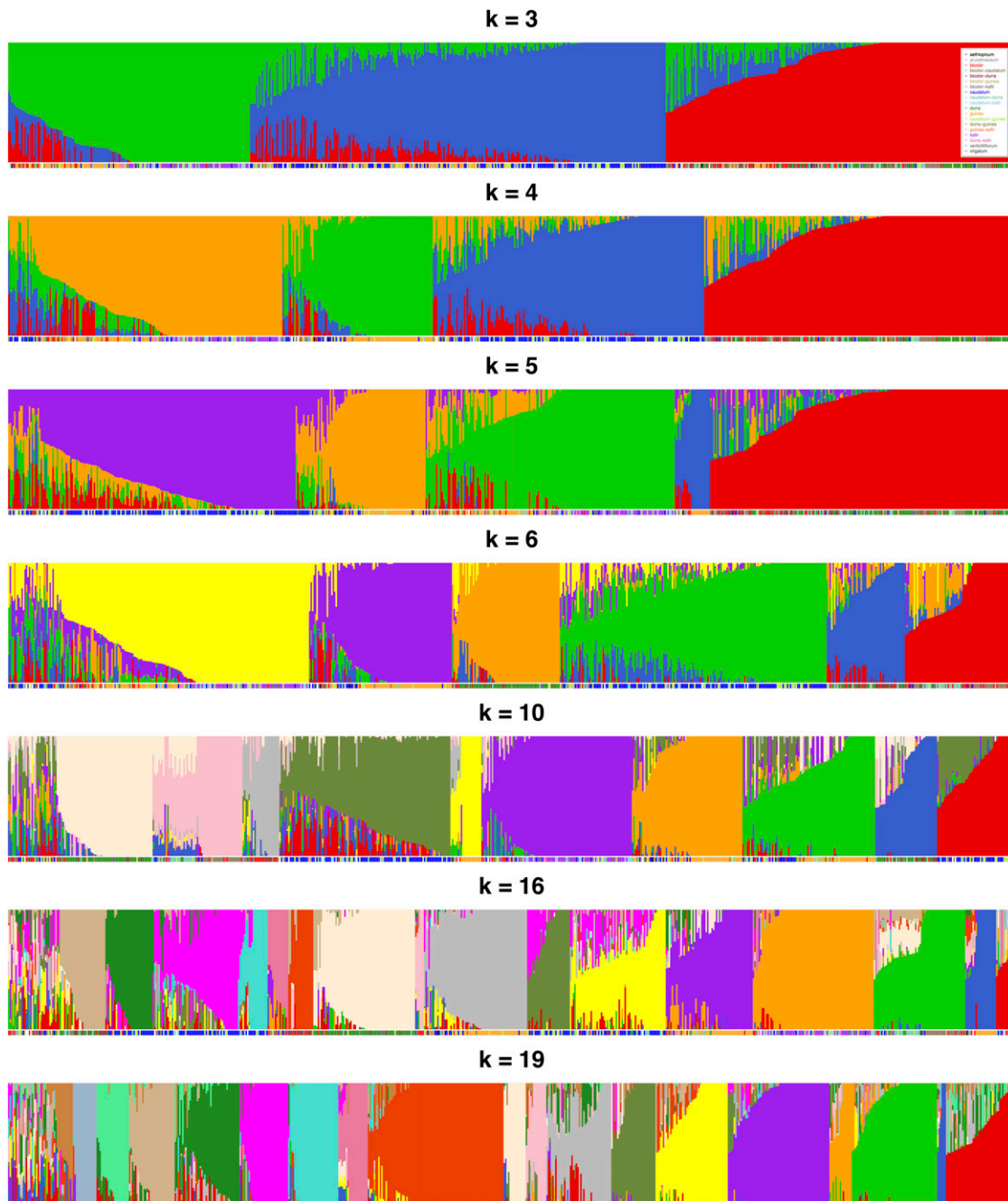


Fig. S2. Bayesian hierarchical clustering of sorghum accessions based on 265,000 SNPs. Posterior probability of membership (Q) in each population at various values of K . Color-coding of Q -value bar plots (upper section) is arbitrary, whereas color-coding for rug plots (lower section) indicates morphological type as given in the legend. For clarity, only African and Asian source-identified accessions are displayed. The lowest cross-validation error was observed at $K = 16$.

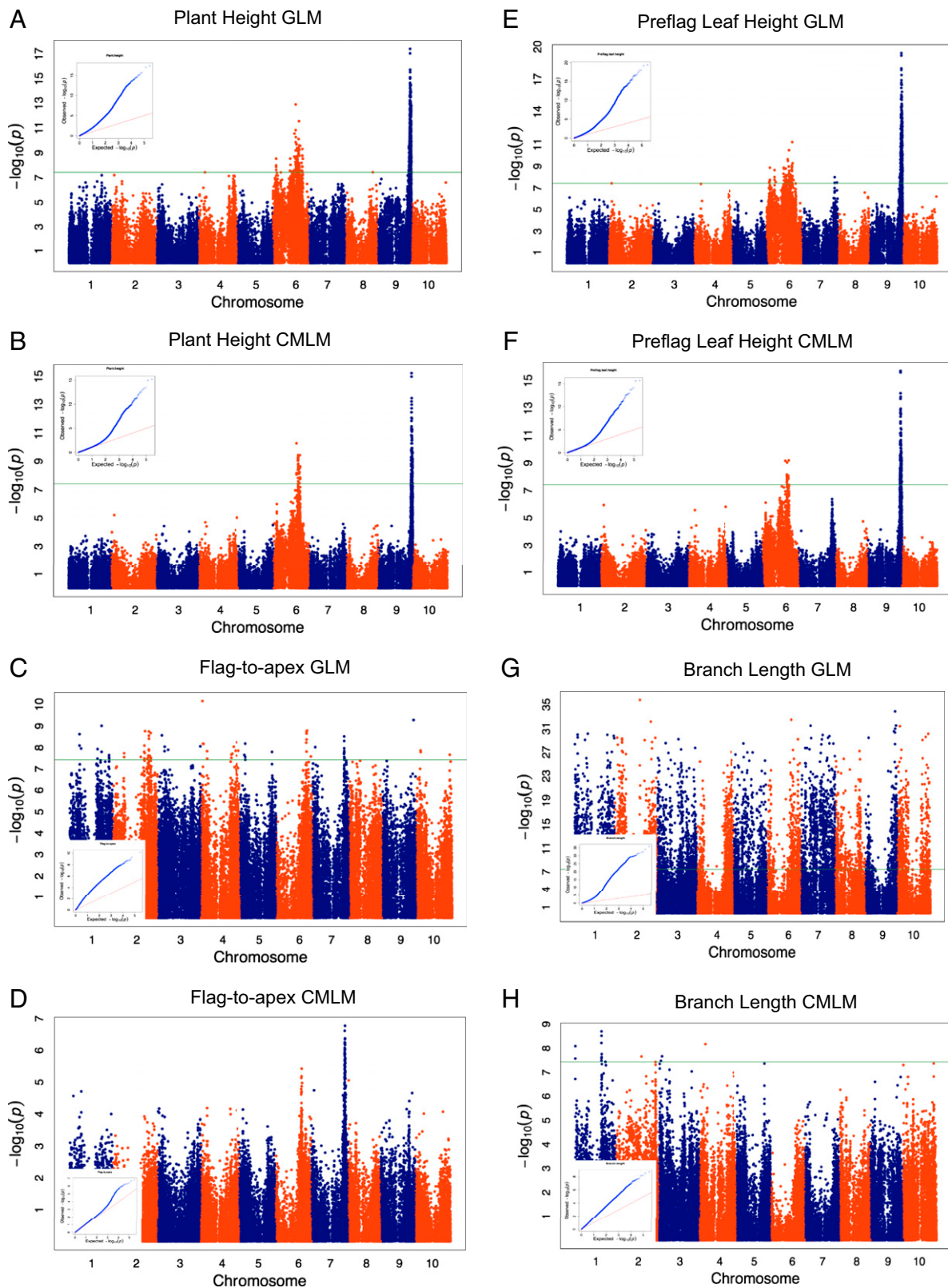


Fig. S4. Genome-wide association studies for plant height components and inflorescence branch length. Manhattan plots and quantile-quantile plots for GLM and CMLM GWAS with Bonferroni significance threshold of 0.05 [$-\log_{10}(p) \sim 7$] noted with the horizontal line for plant height (A and B), flag-to-apex distance (E and F), preflag leaf height (C and D), and inflorescence branch length (G and H).

Table S2. SNPs with significant association to inflorescence branch length

Chromosome	Position	<i>P</i>	Minor allele frequency	Effect size	Candidate gene	Distance to peak SNP	Description (Putative function)	Ref(s).
1	206,185	8.35e-09	0.07	0.04	Sb01g000300	40 kb	LEUNIG transcriptional repressor (Floral organ identity)	1
1	47,634,163	2.03e-09	0.11	0.04	Sb01g027530	30 kb, nearest	Receptor-like kinase, homolog of Theseus1 (Cell elongation)	2
1	48,244,999	1.30e-07	0.09	0.03	Sb01g027730	In gene	PTR transporter, homolog of Short panicle1 (Branch elongation)	3
1	51,696,651	1.13e-07	0.08	0.03	Sb01g029650	27 kb	GRAS transcription factor, orthologous to Lost meristems3 (Shoot determinancy)	4
1	54,759,786	3.73e-08	0.13	0.03	Sb01g032020	8 kb	IAA synthase, homologous to Dwarf in light2 (Cell elongation)	5
1	55,738,033	5.17e-08	0.07	0.03	Sb01g032800	3 kb, nearest	GRAS transcription factor similar to Dwarf8 (Cell elongation)	6
2	46,367,440	2.24e-08	0.01	0.03	Sb02g019110	In gene	C2H2 transcription factor, homolog of Indeterminate1 (Inflorescence determinancy)	7
2	55,006,467	1.49e-07	0.07	0.03				
2	71,878,020	3.79e-08	0.22	0.03	Sb02g037550	47 kb	C2H2 transcription factor, homolog of Indeterminate1 (Inflorescence determinancy)	7
3	1,776,750	7.12e-08	0.13	0.03	Sb03g001940	3 kb, nearest	TCP transcription factor, homolog of Teosinte branched1 (Cell elongation)	8
3	3,903,938	3.40e-08	0.02	0.03	Sb03g003650	15 kb	Ortholog of GIGANTEA (Flower development)	9
3	5,815,653	2.20e-08	0.14	0.03	Sb03g005740	In gene	Serine-threonine kinase, homolog of Clavata1 (Inflorescence determinancy)	10
3	19,383,642	7.95e-08	0.12	0.03				
3	59,676,964	9.40e-08	0.39	0.03				
4	10,182,131	6.87e-09	0.15	0.04				
4	61,683,384	1.05e-07	0.10	0.03	Sb04g031750	1 kb, nearest	MADS transcription factor, ortholog of Bearded ear1 (Inflorescence architecture)	11
4	62,154,189	1.48e-07	0.04	0.03	Sb04g032140	In gene	C2H2 transcription factor, homolog of Indeterminate1 (Inflorescence determinancy)	7
5	51,442,603	4.45e-08	0.10	0.03	Sb05g020940	7 kb, nearest	Kinesin-like protein, homolog of Gibberellin dependent dwarf1 (Inflorescence length)	12
9	55,320,240	1.60e-07	0.01	0.03				
10	760,293	5.05e-08	0.03	0.03				
10	9,137,944	1.58e-07	0.13	0.03				
10	56,004,421	4.41e-08	0.07	0.03	Sb10g026580	In gene	F-box protein, ortholog of Aberrant panicle organization1 (Inflorescence architecture)	13

Chr., chromosome.

- Conner J, Liu Z (2000) LEUNIG, a putative transcriptional corepressor that regulates AGAMOUS expression during flower development. *Proc Natl Acad Sci USA* 97(23):12902–12907.
- Cheung AY, Wu H-M (2011) THESEUS 1, FERONIA and relatives: A family of cell wall-sensing receptor kinases? *Curr Opin Plant Biol* 14(6):632–641.
- Li S, et al. (2009) Short panicle1 encodes a putative PTR family transporter and determines rice panicle size. *Plant J* 58(4):592–605.
- Schulze S, Schäfer BN, Parizotto EA, Voinnet O, Theres K (2010) LOST MERISTEMS genes regulate cell differentiation of central zone descendants in Arabidopsis shoot meristems. *Plant J* 64(4):668–678.
- Takase T, Nakazawa M, Ishikawa A, Manabe K, Matsui M (2003) DFL2, a new member of the Arabidopsis GH3 gene family, is involved in red light-specific hypocotyl elongation. *Plant Cell Physiol* 44(10):1071–1080.
- Hirsch S, Oldroyd GED (2009) GRAS-domain transcription factors that regulate plant development. *Plant Signal Behav* 4(8):698–700.
- Colasanti J, Yuan Z, Sundaresan V (1998) The indeterminate gene encodes a zinc finger protein and regulates a leaf-generated signal required for the transition to flowering in maize. *Cell* 93(4):593–603.
- Choi M-S, et al. (2012) Teosinte Branched 1 modulates tillering in rice plants. *Plant Cell Rep* 31(1):57–65.
- Thompson BE, et al. (2009) GIGANTEA: a circadian clock-controlled gene that regulates photoperiodic flowering in Arabidopsis and encodes a protein with several possible membrane-spanning domains. *The EMBO Journal* 18(17):4679–4688.
- Bortiri E, Hake S (2007) Flowering and determinacy in maize. *J Exp Bot* 58(5):909–916.
- Thompson BE, et al. (2009) Bearded-ear encodes a MADS box transcription factor critical for maize floral development. *Plant Cell* 21(9):2578–2590.
- Li J, et al. (2011) Mutation of rice BC12/GDD1, which encodes a kinesin-like protein that binds to a GA biosynthesis gene promoter, leads to dwarfism with impaired cell elongation. *Plant Cell* 23(2):628–640.
- Ikeda K, Nagasawa N, Nagato Y (2005) ABERRANT PANICLE ORGANIZATION 1 temporally regulates meristem identity in rice. *Dev Biol* 282(2):349–360.

Other Supporting Information Files

[Dataset S1 \(XLSX\)](#)

[Dataset S2 \(XLSX\)](#)

[Dataset S3 \(PDF\)](#)