

Supplemental figure legends

Fig. S1: **a)** Influence of BL and propiconazole (PPZ) on ZmBZR1 nuclear localization. **b)** ChiP qPCR to verify ChIP-seq results at *URL2*, *BR6ox2* and *BRI1-1* loci. **c)** Comparison of ZmBZR1 target genes with AtBZR1 target genes obtained by ChIP-chip on 4-week old light grown rosettes¹ and ChIP-seq on 5-day-old dark grown seedlings² **d)** Pearson correlation coefficients between replicates for inputs and BZR1 ChIP in B73xMo17 (rep1-3) and Mo17xB73 (rep4-6) **e)** Principal component analysis of the six replicates for ChIP and input **f)** Example of tissue dissection performed in this study. The meristem-enriched tissue employed for RNAseq and ChIPseq in this study is indicated by a red square. **g)** Western blot of YFP-tagged BZR1 detected by GFP1 antibody: No background signal was observed for control plants without the ZmBZR1-YFP construct. FT=Flow through; IP= Immunoprecipitation step.

Fig. S2: Correlation of CHG (**a**) and CHH (**b**) methylation in B73 and Mo17³ with allele-specific BZR1 binding. For each ASB, the difference in CG methylation between B73 and Mo17 in the 40bp surrounding the ASB is plotted against the allelic bias (expressed in percentage of B73 read counts). Red dots represent ASBs that display differential CG methylation between B73 and Mo17 as defined in Regulski et al. (2013): $\geq 70\%$ methylation in one genotype and $\leq 10\%$ methylation in the respective other genotype.

Fig. S3: VCAP of non-ASB SNPs: Variance explained (h^2) by the non-ASB-SNP set.

Fig. S4: Minor allele frequencies of ASBs and bgSNPs.

Table S1: List of 2743 BR responsive genes in Maize determined by RNA-seq.

Table S2: List of 17463 putative ZmBZR1 binding sites of the B73 inbred line

Table S3: List of 6371 ZmBZR1 target genes. Genes (defined as gene body plus 5 kb upstream and 1kb downstream) were considered target genes if they overlapped with a significant ZmBZR1 BS.

Table S4: List of 2097 conserved BRZ1 target genes in Maize and Arabidopsis

Table S5: List of 29902 ZmBZR1 binding sites reproducible in all 6 replicates of B73xMo17 F1 hybrids

Table S6: List of ZmBZR1 target genes in B73xMo17 hybrids. Genes with significant BZR1 binding sites from 5 kb upstream to 1 kb downstream of the TSS and TTS, respectively, were considered target genes.

Table S7: List of 8335 SNPs with significant allele-specific bias in linkage groups

Table S8: Genomic location of the 3297 lead SNPs of allele-specific BZR1 binding site (ASBs)

Table S9: List of putative ASB ZmBZR1 target genes (ASBs may overlap with multiple target genes).

Table S10: ASBs overlapping with variations in motifs and/or DNA methylation

Table S11: Overview of genomic distribution of ASBs and bgSNPs in relation to genes

1. Sun, Y. *et al.* Integration of Brassinosteroid Signal Transduction with the Transcription Network for Plant Growth Regulation in Arabidopsis. *Dev. Cell* **19**, 765–777 (2010).
2. Oh, E., Zhu, J.-Y., Ryu, H., Hwang, I. & Wang, Z.-Y. TOPLESS mediates brassinosteroid-induced transcriptional repression through interaction with BZR1. *Nat. Commun.* **5**, 4140 (2014).
3. Regulski, M. *et al.* The maize methylome influences mRNA splice sites and reveals widespread paramutation-like switches guided by small RNA. *Genome Res.* **23**, 1651–1662 (2013).