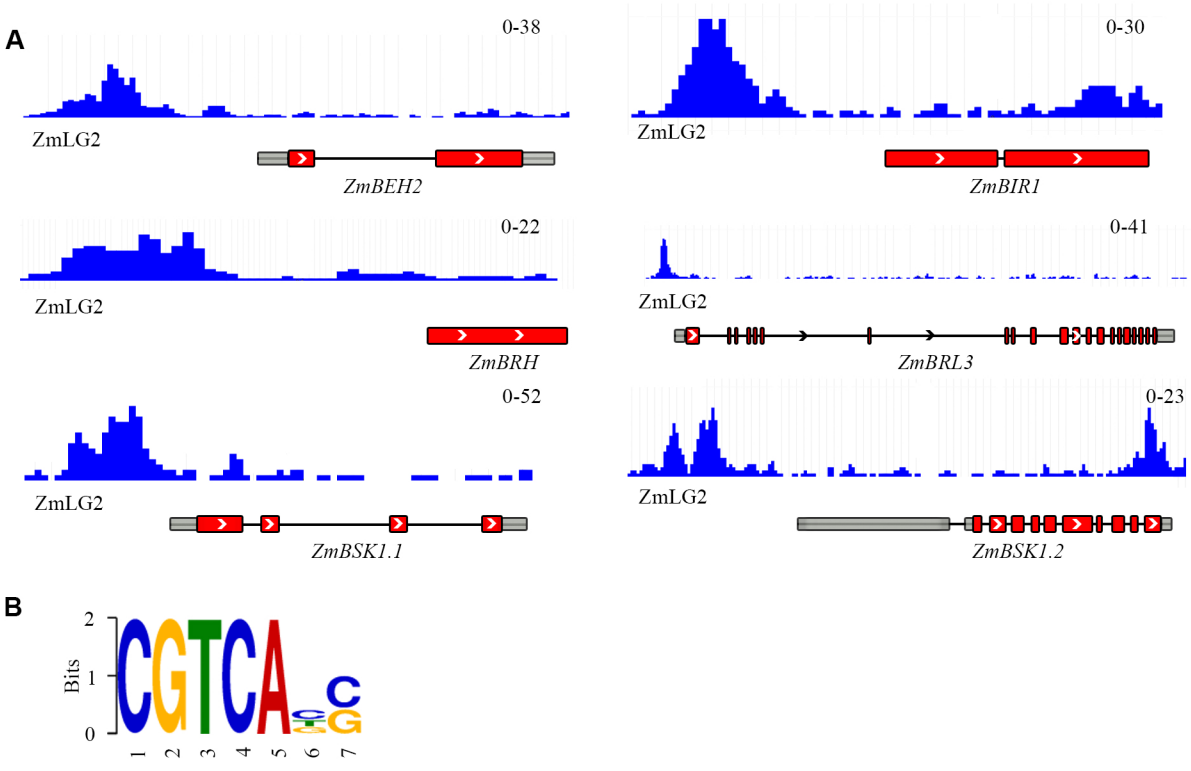
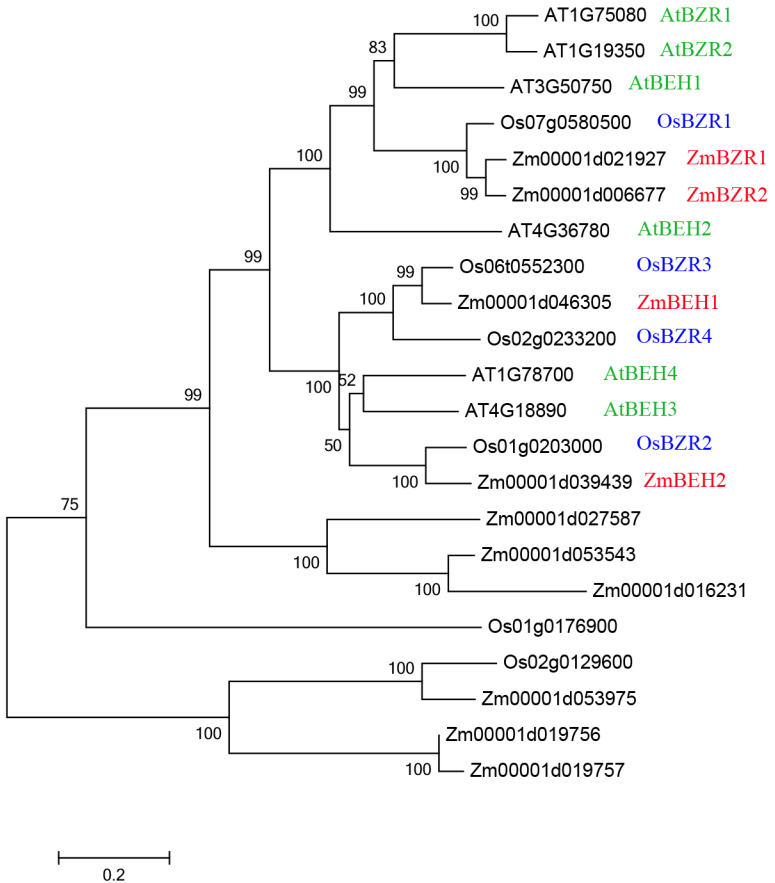
Supplemental Table S1. The list of primers used in this paper.

Name	Primer (5'-3')	Gene	Construct
BZR1-Pro-pg0800-F	ggtatcgataagcttGTGGCGGAGCGCCGTGGACGC	*ZmBZR1*	PGreen0800
BZR1-Pro-pg0800-R	tagaactagtggatccGGTCTGATGCTCAGCCAGCC	*ZmBZR1*	PGreen0800
BEH1-Pro-pg0800-F	ggtatcgataagcttTCGACTAGTGTAACGTGATGCACAC	*ZmBEH1*	PGreen0800
BEH1-Pro-pg0800-R	tagaactagtggatccCGGATCTCGCGGATCTGCTCC	*ZmBEH1*	PGreen0800
BZR1-JG4-F	gattatgcctctcccgaattcATGACGTCCGGGGCGGCGG	*ZmBZR1*	pJG4-5
BZR1-JG4-R	agaagtccaaagcttctcgagTCACTTGGCGCCGACGCCG	*ZmBZR1*	pJG4-5
BEH1-JG4-F	gattatgcctctcccgaattcATGACGAGCGGCGCCGGGGG	*ZmBEH1*	pJG4-5
BEH1-JG4-R	agaagtccaaagcttctcgagTCAGGAAGGATCTGCACGAG	*ZmBEH1*	pJG4-5
SCL28-pro-pLACZi-F	attggatcggaattcAGTACTATTCTTCTTTCATG	*ZmSCL28*	pLACZi
SCL28-pro-pLACZi-R	agatccccgggtaccTTGTCCACGTGGGATGCTG	*ZmSCL28*	pLACZi
BEH1-pro-F-pLACZi-F	attggatcggaattcCCGTTTGACCACGAAACCGC	*ZmBEH1*	pLACZi
BEH1-pro-R-pLACZi-R	agatccccgggtaccAGGGACCAGCTTTTGCAAAG	*ZmBEH1*	pLACZi
BZR1-BD-F	gcatatggccatggaggccgaattcATGACGTCCGGGGCGGCGG	*ZmBZR1*	pGBKT7
BZR1-BD-R	tatgctagttatgcggccgctgcagTCACTTGGCGCCGACGCCG	*ZmBZR1*	pGBKT7
BZR1-CLUC-F	gtcccggggcggtaccATGACGTCCGGGGCGGCGGCG	*ZmBZR1*	p1300-35S-Cluc
BZR1-CLUC-R	tccatttgttggatcccgTCACTTGGCGCCGACGCCGAGCG	*ZmBZR1*	p1300-35S-Cluc
BEH1-NLUC-F	ctcggtacccgggatccaATGACGAGCGGCGCCGGGGGA	*ZmBEH1*	p1300-35S-Nluc
BEH1-NLUC-R	acgagatctggtcgacGGAAGGATCTGCACGAGTCTT	*ZmBEH1*	p1300-35S-Nluc
UFMu-09491-F1	GAGGAAGACGCAGGCGAGGAG	*ZmSCL28*	UniformMu genotyping,UFMu-09491
TIR8.2	CGCCTCCATTTCGTCGAATCCSCTT	*ZmSCL28*	UniformMu genotyping,UFMu-09491
UFMu-09491-F2	CTCCAAGCGGGCGAGCAACC	*ZmSCL28*	UniformMu genotyping,UFMu-09491
UFMu-09491-R	CCCGCTCGTTGAGGGTGAAGT	*ZmSCL28*	UniformMu genotyping,UFMu-09491
UFMU13537/03258-F	GGCTGGCTGAGCATCAGACC	*ZmBZR1*	UniformMu genotyping,UFMu-13537,UFMU-03258
UFMU13537/03258-R	TGGCGTGGTAGGACGGCACC	*ZmBZR1*	UniformMu genotyping,UFMu-13537,UFMU-03258
UFMU-03258-F	AGCGGGAGAACAACAAGCG	*ZmBZR1*	UniformMu genotyping,UFMu-03258
TIR6	AGAGAAGCCAACGCCAWCGCCTCYATTTCGTC	*ZmBZR1*	UniformMu genotyping,UFMu-13537,UFMU-03258
UFMu-13537-R	GGCTCGGGAAGCTCGACGAC	*ZmBZR1*	UniformMu genotyping,UFMu-13537
UFMu-13557-F	CCACCACCACTCATCCCGTTTG	*ZmBEH1*	UniformMu genotyping,UFMu-13557
UFMu-13557-R	TCCCTGCGGCGGTTGTTCTC	*ZmBEH1*	UniformMu genotyping,UFMu-13557
TIR8.4	CGCCTCCATTTCGTCGAATCACCTC	*ZmBEH1*	UniformMu genotyping,UFMu-13557
lg2-PC414-F	gtcgactctagaggatccccGGGATGGTGCAAGGCGAGGAGAG	*ZmLG2*	PC414,Gateway LR
lg2-PC414-R	CGAGCTCGTCGACCTCGAGAAATCCGGCGAACTGGT	*ZmLG2*	PC414,Gateway LR
BEH1-PC414-F	acgacggccagtgccaagcttATGACGAGCGGCGCCGGGG	*ZmBEH1*	PC414,Gateway LR
BEH1-PC414-R	tatgaccatgattacgaattcGGAAGGATCTGCACGAGTC	*ZmBEH1*	PC414,Gateway LR
BZR1-EMSA-Bio–F	GGGTGTGCCAGCGTAGCACGTACCTCAGCGTCATAGGCTA	*ZmBZR1*	EMSA,3'Biotin
BZR1-EMSA-Bio–R	TAGCCTATGACGCTGAGGTACGTGCTACGCTGGCACACCC	*ZmBZR1*	EMSA,3'Biotin
BZR1-EMSA–F	GGGTGTGCCAGCGTAGCACGTACCTCAGCGTCATAGGCTA	*ZmBZR1*	EMSA
BZR1-EMSA-R	TAGCCTATGACGCTGAGGTACGTGCTACGCTGGCACACCC	*ZmBZR1*	EMSA
BEH1-EMSA-Bio–F1	ATGGGCCCCGCGCGTCAGGGAGCGACGTCG	*ZmBEH1*	EMSA,3'Biotin
BEH1-EMSA-Bio–R1	CGACGTCGCTCCCTGACGCGCGGGGCCCAT	*ZmBEH1*	EMSA,3'Biotin
BEH1-EMSA-Bio-F2	GGCGTGATGATTGCGCTCTGACGAGACGGCGGCTGTCGAGG	*ZmBEH1*	EMSA,3'Biotin
BEH1-EMSA-Bio-R2	CCTCGACAGCCGCCGTCTCGTCAGAGCGCAATCATCACGCC	*ZmBEH1*	EMSA,3'Biotin
BEH1-EMSA-Bio-F3	AGGAGTACATTCACCGTCACGCTGACGCAGATGCTTCCATC	*ZmBEH1*	EMSA,3'Biotin
BEH1-EMSA-Bio-R3	GATGGAAGCATCTGCGTCAGCGTGACGGTGAATGTACTCCT	*ZmBEH1*	EMSA,3'Biotin
BEH1-EMSA-Bio-F4	CATGGAGATAGAAGAAAACGTCATCCGAGGAGTACATTCAC	*ZmBEH1*	EMSA,3'Biotin
BEH1-EMSA-Bio-R4	GTGAATGTACTCCTCGGATGACGTTTTCTTCTATCTCCATG	*ZmBEH1*	EMSA,3'Biotin
BEH1-EMSA-F4	CATGGAGATAGAAGAAAACGTCATCCGAGGAGTACATTCAC	*ZmBEH1*	EMSA
BEH1-EMSA-R4	GTGAATGTACTCCTCGGATGACGTTTTCTTCTATCTCCATG	*ZmBEH1*	EMSA
BEH1-P4-m1-F	CATGGAGATAGAAGAAAGCGTCATCCGAGGAGTACATTCAC	*ZmBEH1*	EMSA
BEH1-P4-m1-R	GTGAATGTACTCCTCGGATGACGCTTTCTTCTATCTCCATG	*ZmBEH1*	EMSA
BEH1-P4-m2-F	CATGGAGATAGAAGAAAAAGTCATCCGAGGAGTACATTCAC	*ZmBEH1*	EMSA

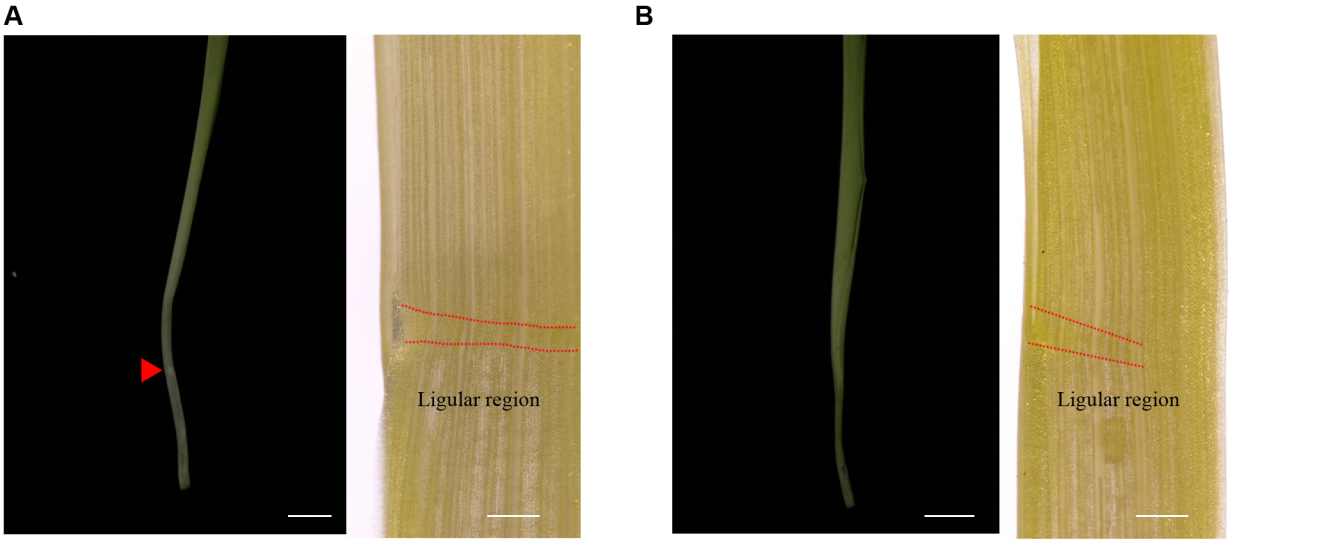
BEH1-P4-m2-R	GTGAATGTACTCCTCGGATGACTTTTTCTTCTATCTCCATG	*ZmBEH1*	EMSA
BEH1-P4-m3-F	CATGGAGATAGAAGAAAACATCATCCGAGGAGTACATTCAC	*ZmBEH1*	EMSA
BEH1-P4-m3-R	GTGAATGTACTCCTCGGATGATGTTTTCTTCTATCTCCATG	*ZmBEH1*	EMSA
BEH1-P4-m4-F	CATGGAGATAGAAGAAAACGACATCCGAGGAGTACATTCAC	*ZmBEH1*	EMSA
BEH1-P4-m4-R	GTGAATGTACTCCTCGGATGTCGTTTTCTTCTATCTCCATG	*ZmBEH1*	EMSA
BEH1-P4-m5-F	CATGGAGATAGAAGAAAACGTAATCCGAGGAGTACATTCAC	*ZmBEH1*	EMSA
BEH1-P4-m5-R	GTGAATGTACTCCTCGGATTACGTTTTCTTCTATCTCCATG	*ZmBEH1*	EMSA
BEH1-P4-m6-F	CATGGAGATAGAAGAAAACGTCGTCCGAGGAGTACATTCAC	*ZmBEH1*	EMSA
BEH1-P4-m6-R	GTGAATGTACTCCTCGGACGACGTTTTCTTCTATCTCCATG	*ZmBEH1*	EMSA
BEH1-P4-m7-F	CATGGAGATAGAAGAAAGAAAAGTCCGAGGAGTACATTCAC	*ZmBEH1*	EMSA
BEH1-P4-m7-R	GTGAATGTACTCCTCGGACTTTTCTTTCTTCTATCTCCATG	*ZmBEH1*	EMSA
BZR1-qF	ATGTGTACTACTACGTAGCGTC	*ZmBZR1*	RT-qPCR
BZR1-qR	ACAACGATTGTTCTTTCACCTG	*ZmBZR1*	RT-qPCR
BEH1-qF	CCTACGGCAACTACAACCTG	*ZmBEH1*	RT-qPCR
BEH1-qR	TTTACATCCCTTGCGGTAGG	*ZmBEH1*	RT-qPCR
SCL28-BsF	AATAATGGTCTCAGGCGcagtcacgcaggccgtttcc	*ZmSCL28*	pBUE411
SCL28-F0	GcagtcacgcaggccgtttccGTTTTAGAGCTAGAAATAGC	*ZmSCL28*	pBUE411
SCL28-R0	cggttgctcgcccgcttggaCGCTTCTTGGTGCC	*ZmSCL28*	pBUE411
SCL28-BsR	ATTATTGGTCTCTAAACcggttgctcgcccgcttgga	*ZmSCL28*	pBUE411
BZR1-BsF	AATAATGGTCTCAGGCGaaggcgctctgccgcgaggc	*ZmBZR1*	pBUE411
BZR1-F0	GaaggcgctctgccgcgaggcGTTTTAGAGCTAGAAATAGC	*ZmBZR1*	pBUE411
BEH1-BsF	AATAATGGTCTCAGGCGgcgcgagaacaaccgccgca	*ZmBEH1*	pBUE411
BEH1-F0	GgcgcgagaacaaccgccgcaGTTTTAGAGCTAGAAATAGC	*ZmBEH1*	pBUE411
BEH1-R0	gcccaagcactgcgacaacaCGCTTCTTGGTGCC	*ZmBEH1*	pBUE411
BEH1-BsR	ATTATTGGTCTCTAAACgcccaagcactgcgacaaca	*ZmBEH1*	pBUE411
SCL28-cas9-F	AAGACGAAGCCACAGAGGAGGT	*ZmSCL28*	genotyping
SCL28-cas9-R	CCCTGCAATGGATCGATGGAACC	*ZmSCL28*	genotyping
BZR1-cas9-F	GCTGAGCATCAGACCATGACGTC	*ZmBZR1*	genotyping
BZR1-cas9-R	CTGCCAAGACCAAGACCCAAGG	*ZmBZR1*	genotyping
BEH1-cas9-F	CACCAGGGTGCCCACGTGGAG	*ZmBEH1*	genotyping
BEH1-cas9-R	CCGAAACCACCAAGCACGACTACTGG	*ZmBEH1*	genotyping



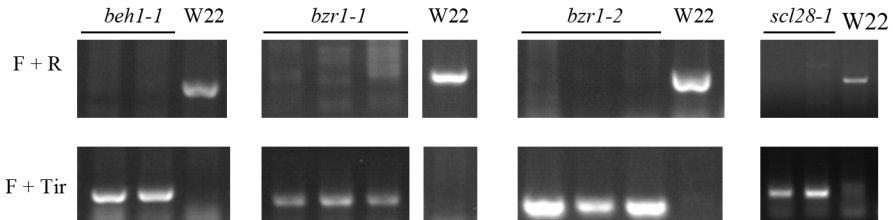
Supplemental Figure S1. ZmLG2 binds to the promoter of BR signaling related genes. A, Genome-browser viewer of ZmLG2 ChIP-Seq binding profiles for *ZmBEH1*, *ZmBEH2*, *ZmBRH*, *ZmBRL3*, *ZmBSK1.1* and *ZmBSK1.2*. B, ZmLG2 binding motif (CGTCA) was identified by the MEME-ChIP.



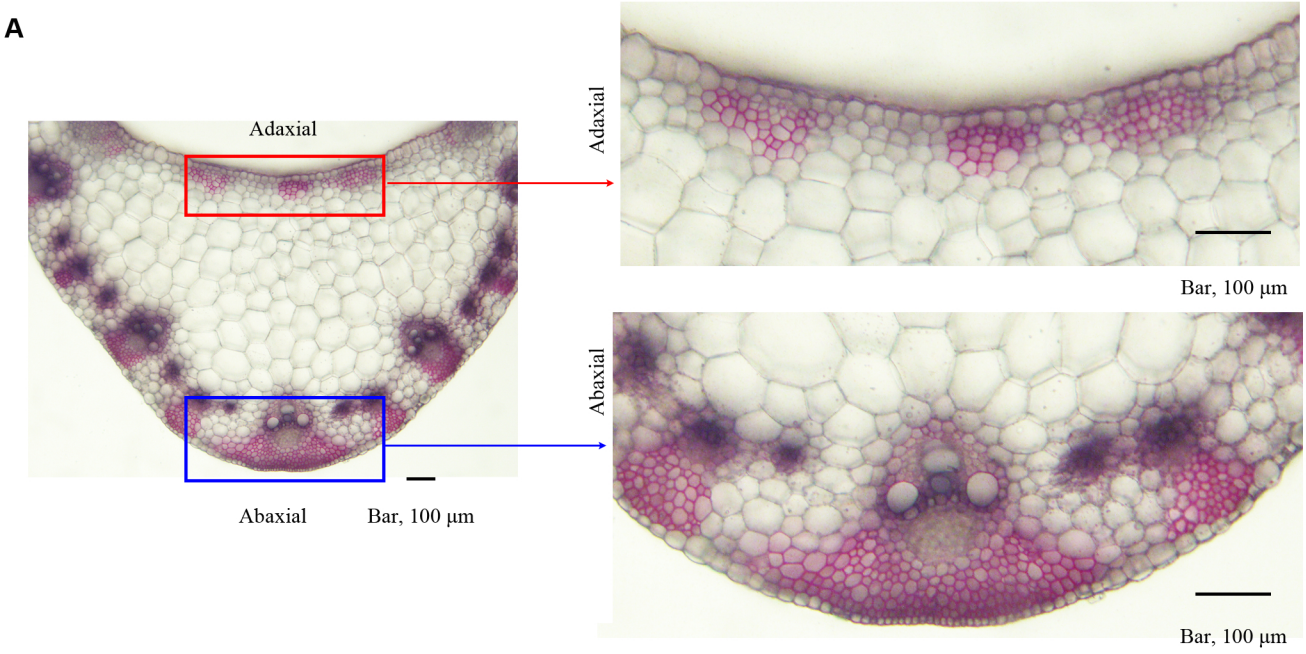
Supplemental Figure S2. Phylogenetic analysis of BZR1/BES1 family proteins in maize, rice and *Arabidopsis*. The protein sequences of BZR1/BES1 were obtained from NCBI database. ZmBZR1, ZmBZR2 and ZmBEH1 are marked with red. Bootstrap values from 1000 replicates are indicated at each node and the scale represents the branch length.



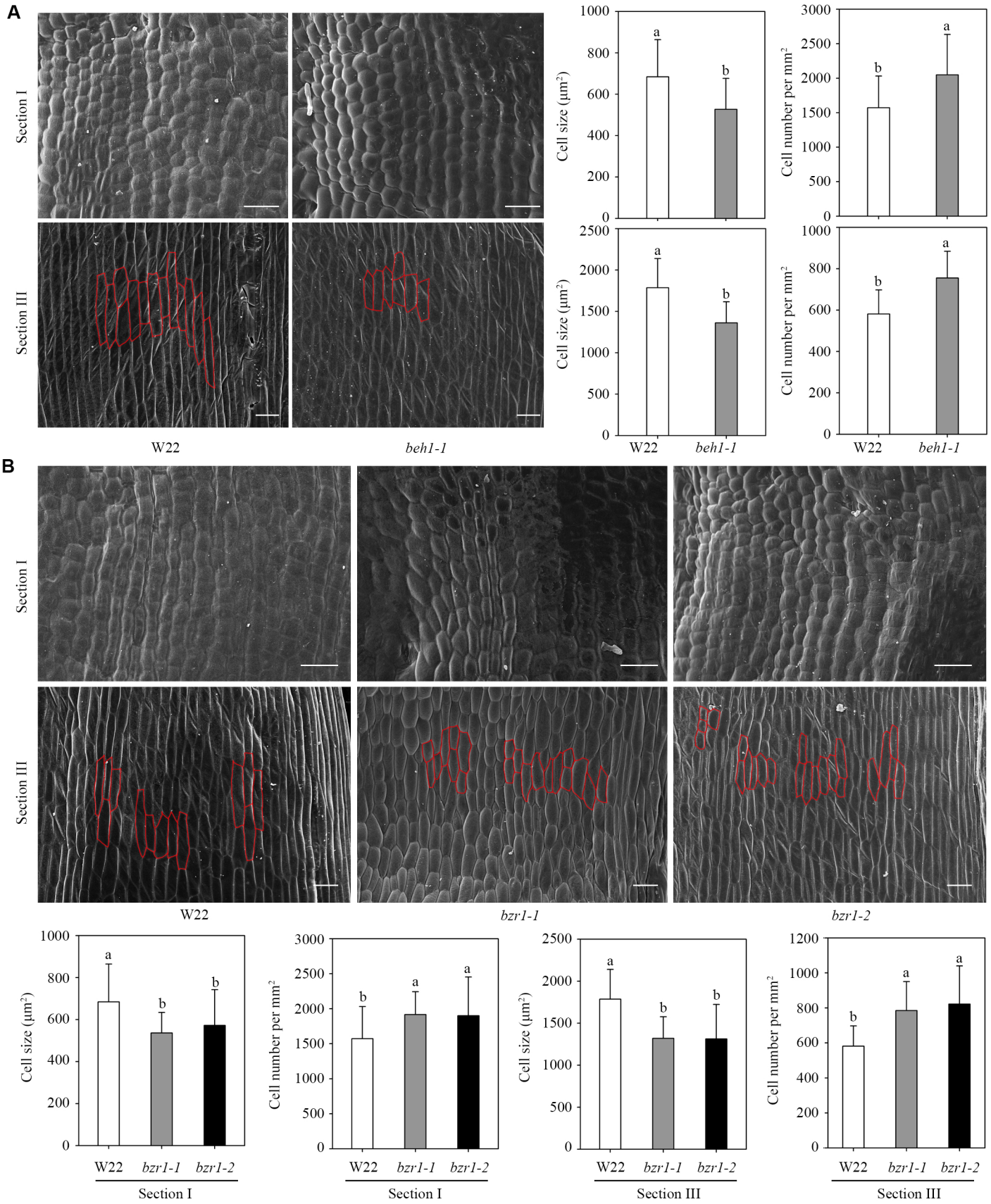
Supplemental Figure S3. Tissues from the ligular region of V3 leaves were harvested for RT-qPCR assay. A, WT seedlings. B, *lg2* seedlings. The seedlings are 18 days old. Ligular regions are marked with a red triangle. The enlarged ligular regions are marked with red dotted lines.



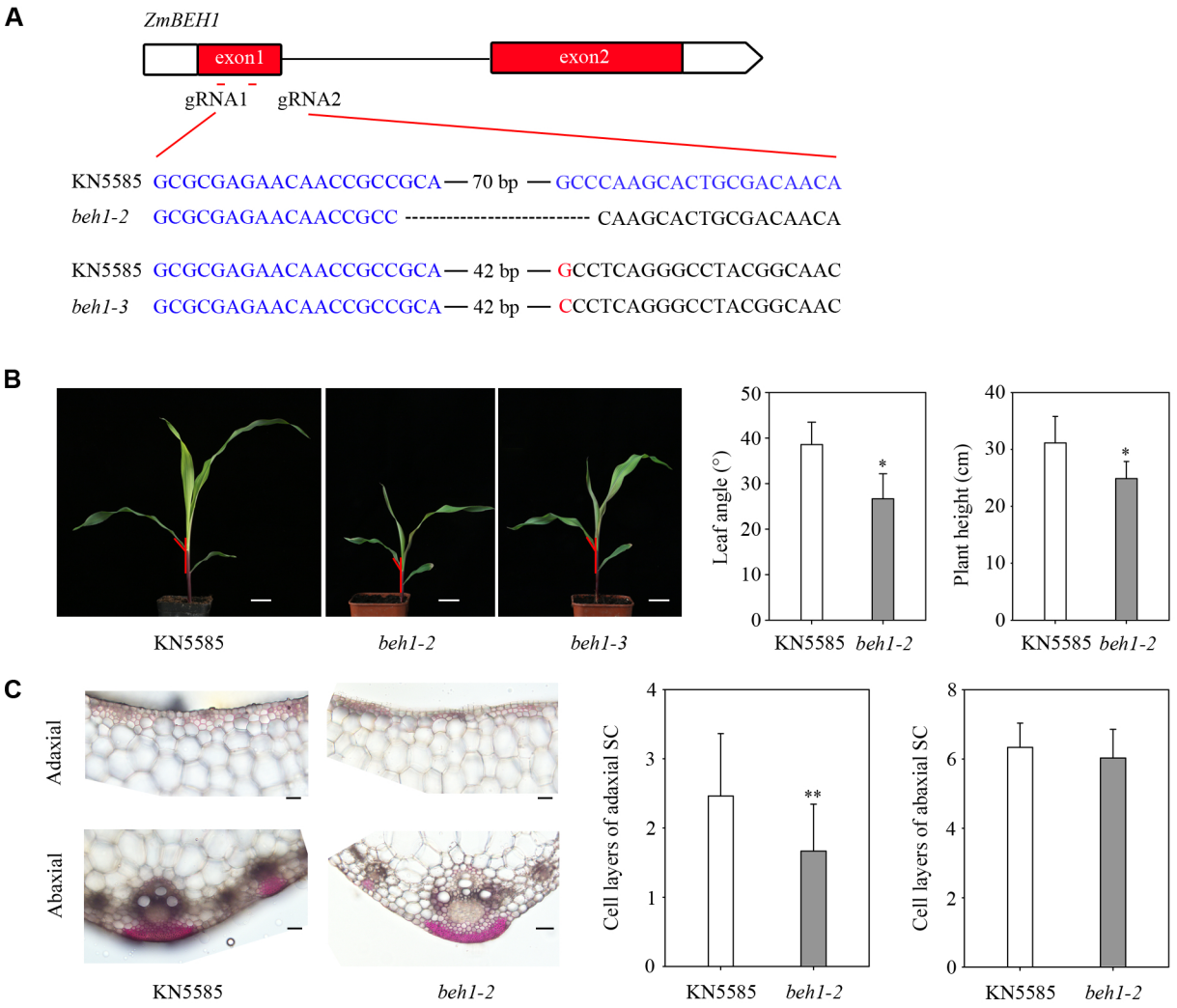
Supplemental Figure S4. PCR identification of *beh1-1*, *bzr1-1*, *bzr1-2* and *scl28-1* mutants. "F + Tir" is the primer pair used to detect the *Mu* insertion in the mutants, "F + R" is the primer pair used to detect the wild type genes of *ZmBEH1*, *ZmBZR1* and *ZmSCL28*. W22 is the wild type control.



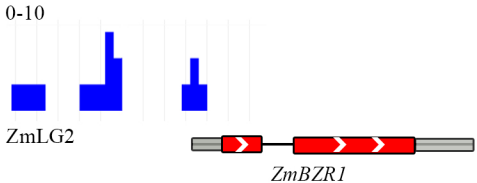
Supplemental Figure S5. Diagram of the cross-section and scanning electron microscopic observation of the auricle. A, The cross-section of auricle. The adaxial and abaxial sides of the auricle are labeled by red box and blue box, respectively. B, Diagram showing the side of auricle observed by the scanning electron microscope. The auricle is marked by red-dotted lines based on the lack of stomata. The auricles were divided into three parts (I-III), representing close to midrib, 1/2 and the margin of the auricle, respectively.



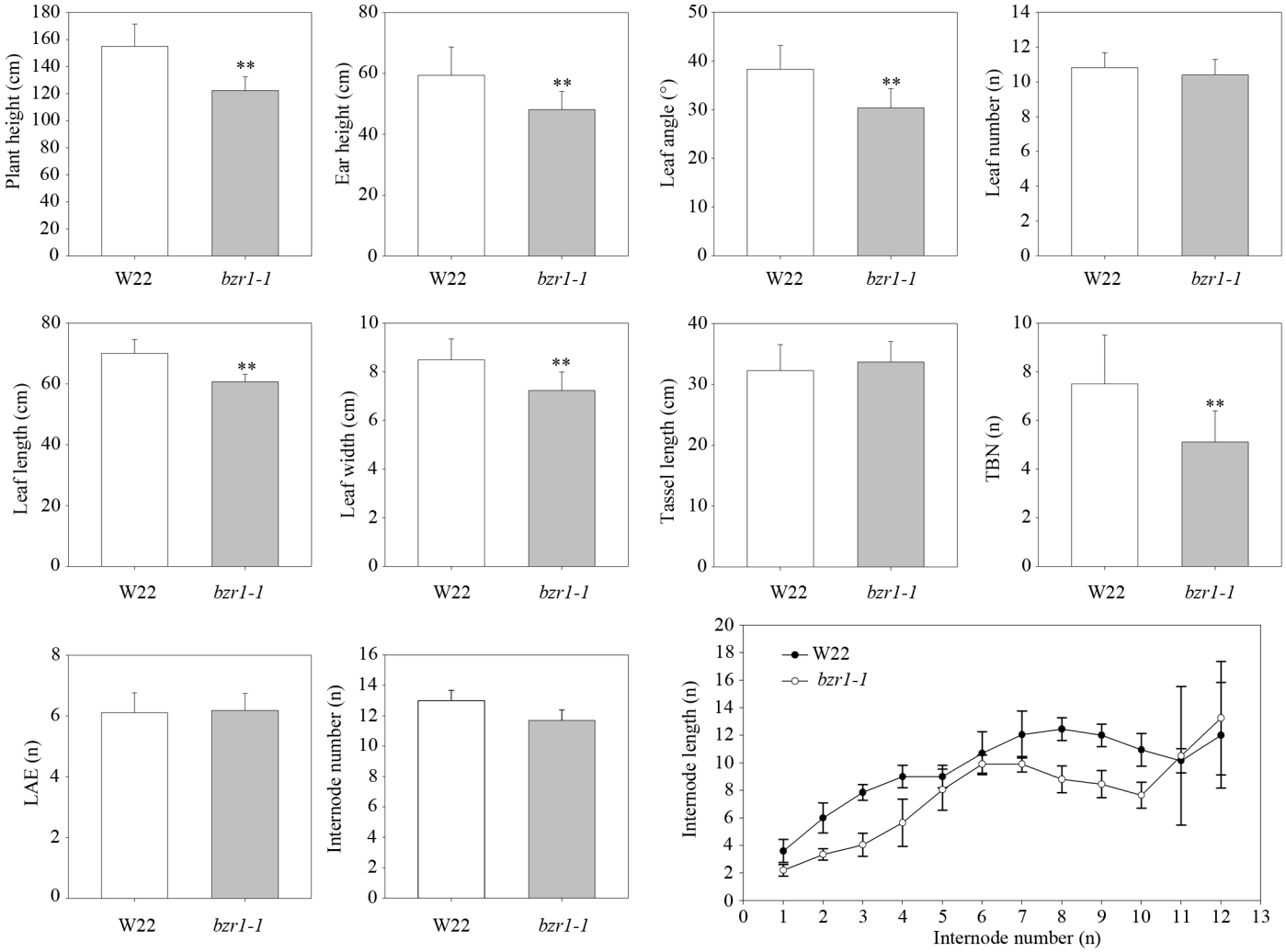
Supplemental Fig. S6. Scanning electron microscopic analysis of auricles in W22, *beh1-1*, *bzr1-1* and *bzr1-2*. A, Parts I and III of the auricle in W22 and *beh1-1*. Bar, 50 μm. B, Parts I and III of the auricle in W22, *bzr1-1* and *bzr1-2*. Parts I and III of the auricle was presented and partially cellular outline were labeled by red lines. n = 20. Bar, 50 μm. Error bars are SD. Statistical significance was determined by a two-sided t test. Different letters above the columns indicate statistically significant differences between groups.



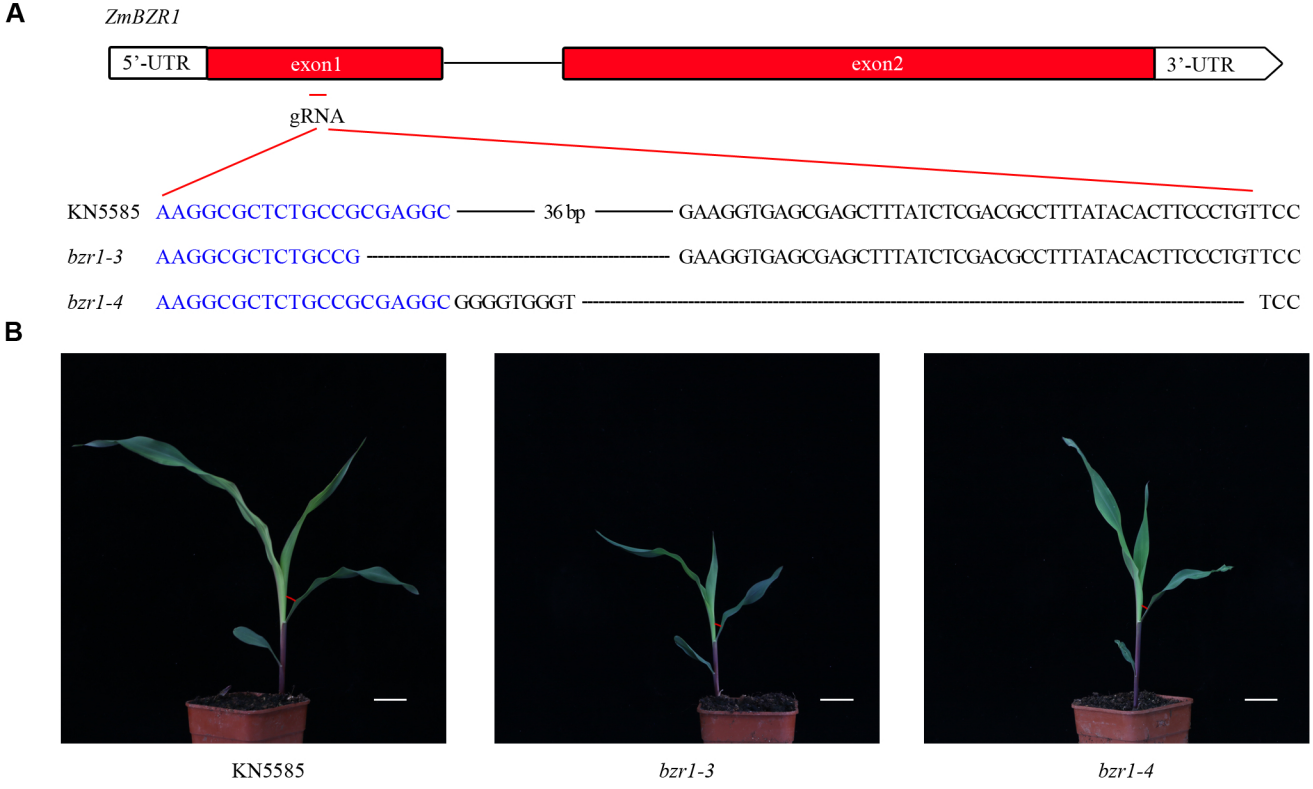
Supplemental Figure S7. Phenotypes of *beh1-2* and *beh1-3* mutants. A, CRISPR/Cas9-mediated knock-out of *ZmBEH1*. The two sgRNA target sequences within the first exon is highlighted in blue. The dashes indicate deleted nucleotides in the two isolated knock-out lines which were named *beh1-2* and *beh1-3*. KN5585 is the inbred wild type line used for maize transformation. B, Observation of plant morphology at V2 stage. Quantitative measurements of leaf angle and plant height between KN5585 and mutants. n = 10. Bar, 3 cm. C, Observation of transverse section of *beh1-2* ligule at V2 stage. The sclerenchyma cell (SC) layers stained red with safranin. Number of SC cell files at the adaxial and abaxial side were calculated from 10 replicates. The second leaf was used to detect the above phenotypes. Bar, 100 μm. Error bars are SD. *P < 0.05, **P < 0.01 (Student's t test).



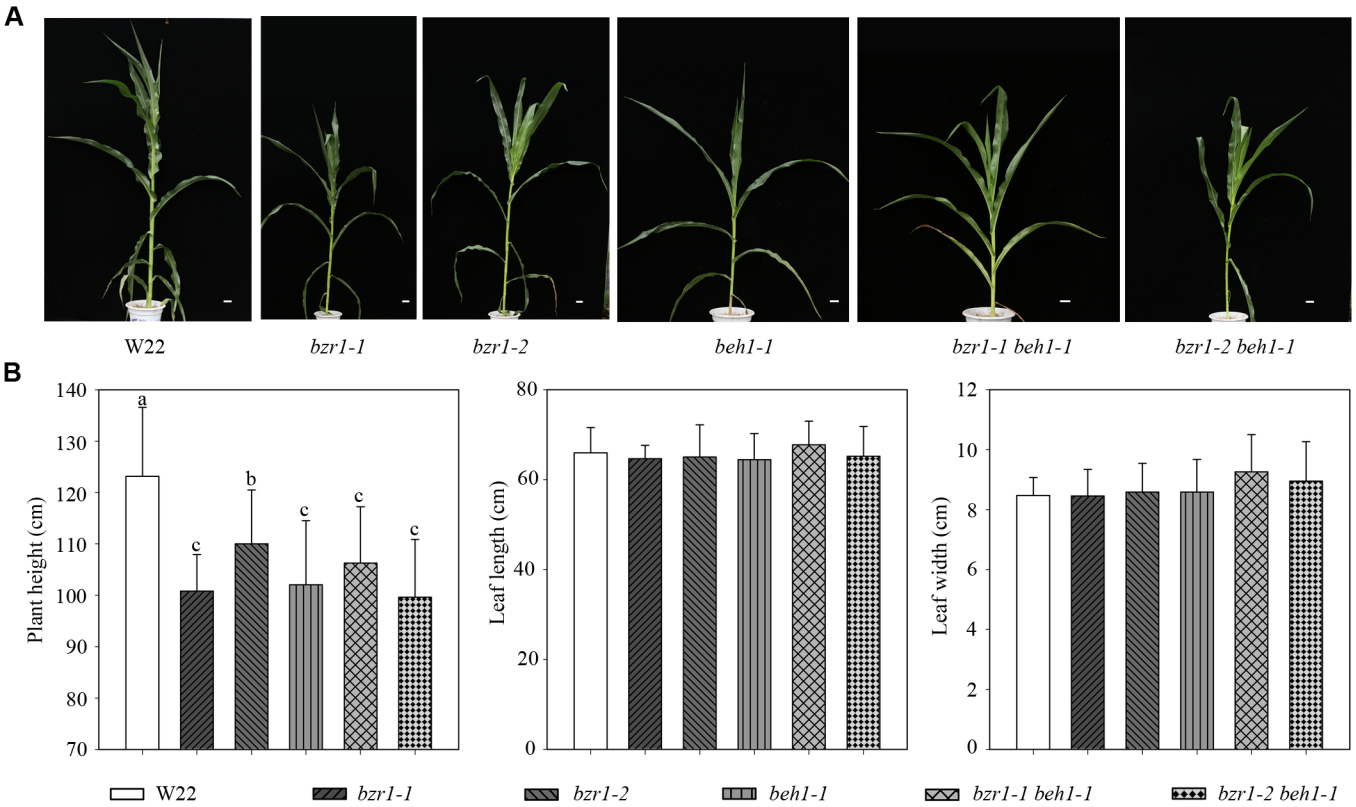
Supplemental Figure S8. ZmLG2 ChIP-Seq binding profile for *ZmBZR1*.



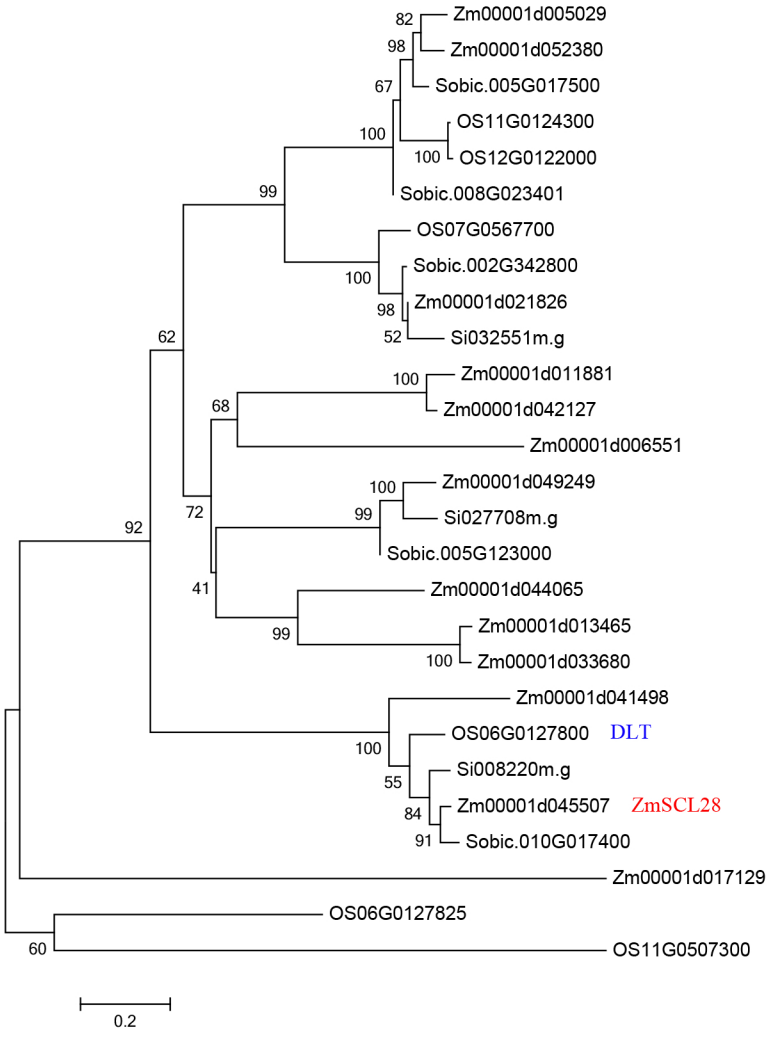
Supplemental Figure S9. Agronomic characters of the *bzr1-1* mutant. Quantitative measurements of plant height, leaf angle, ear height, leaf number, leaf length, leaf width, tassel length, tassel branch number (TBN), leaf above ear (LAE) at blister stage in a line chart. We detected leaf angle, leaf length and leaf width using the first leaf above the ear. Internode number and internode length were measured after harvesting. Error bars are SD. Numbers indicate internodes from the first to the uppermost. **P < 0.01 (Student's t test), n = 20.



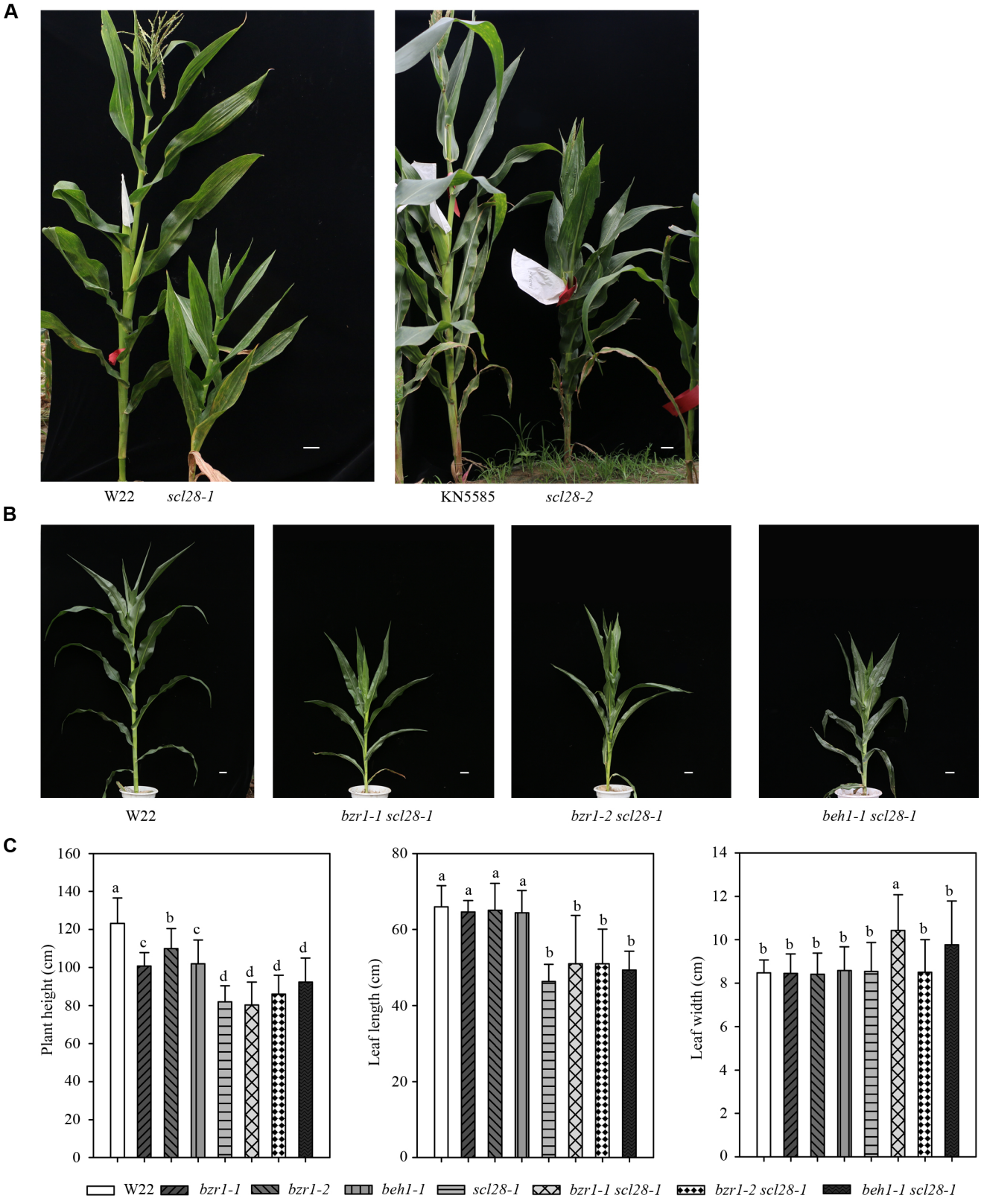
Supplemental Figure S10. Characterization of the CRISPR/Cas9-mediated knock-out mutants of *ZmBZR1*. A, CRISPR/Cas9-mediated knock-out of *ZmBZR1*. The sgRNA target sequence within the first exon is highlighted in blue. The dashes indicate deleted nucleotides in the two isolated knock-out lines which were named *bzr1-3* and *beh1-4*. B, *bzr1-3* and *beh1-4* plants displayed similar phenotypes as that of *bzr1-1* and *bzr1-2* mutants at V2 stage. Bar, 3 cm.



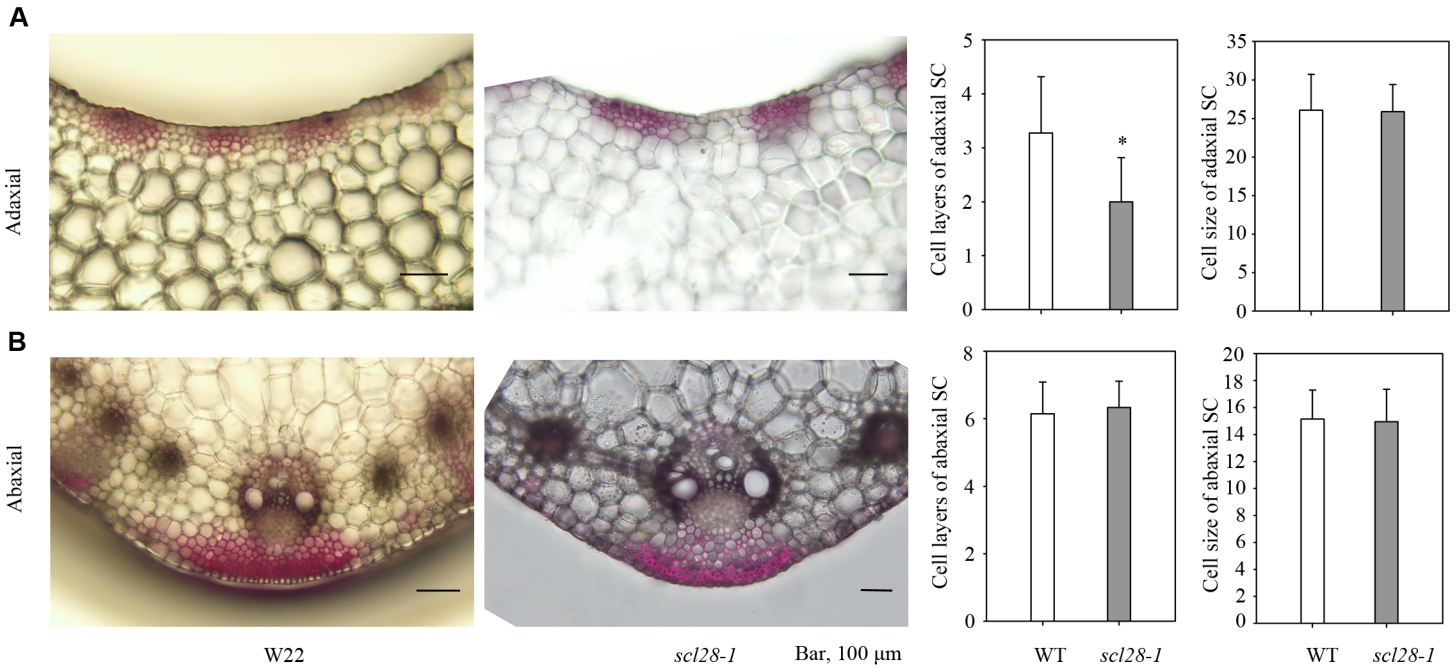
Supplemental Figure S11. Phenotypes of the single and double mutants of *bzr1-1*, *bzr1-2* and *beh1-1*. A, Gross morphology of 54-day-old WT and mutant plants. Bar, 5 cm. B, Quantitative measurements of plant height, leaf length and leaf width. We detected leaf length and leaf width using the first leaf above the ear. Error bars are SD. Different letters above the columns indicate statistically significant differences between groups (Student's t test), n = 20.



Supplemental Figure S12. Phylogenetic analysis of SCL family. Phylogenetic analysis of SCL family proteins from maize, rice, foxtail millet and sorghum. The protein sequences were obtained from NCBI database. ZmSCL28 was marked with red, DLT was marked with blue. Bootstrap values from 1000 replicates are indicated at each node and the scale represents the branch length.



Supplemental Figure S13. Phenotypes of *scl28-1*/*scl28-2* and *bzr1-1 scl28-1*, *bzr1-2 scl28-1*, *beh1-1 scl28-1* double mutant plants. A, Gross morphology of WT and *scl28-1/2* mutant plants at blister stage. Bar, 5 cm. B, Gross morphology of WT and *bzr1-1 scl28-1*, *bzr1-2 scl28-1*, *beh1-1 scl28-1* double mutant plants at V10 stage. Bar, 5 cm. C, Quantitative measurements of plant height, leaf length and leaf width, n = 20. We measured leaf angle, leaf length and leaf width using the sixth leaf. Error bars are SD. Different letters above the columns indicate statistically significant differences between groups (Student's t test).



Supplemental Figure S14. Cross-sections of the ligular region from W22 and *scl28-1* plants at the V2 stage. The sclerenchyma cell (SC) layers were stained red with safranin. The number of SC cell files and cell size on the adaxial and abaxial sides was calculated from 10 replicates. Error bars are SD. * represents $P < 0.05$ determined by Student's t-test.