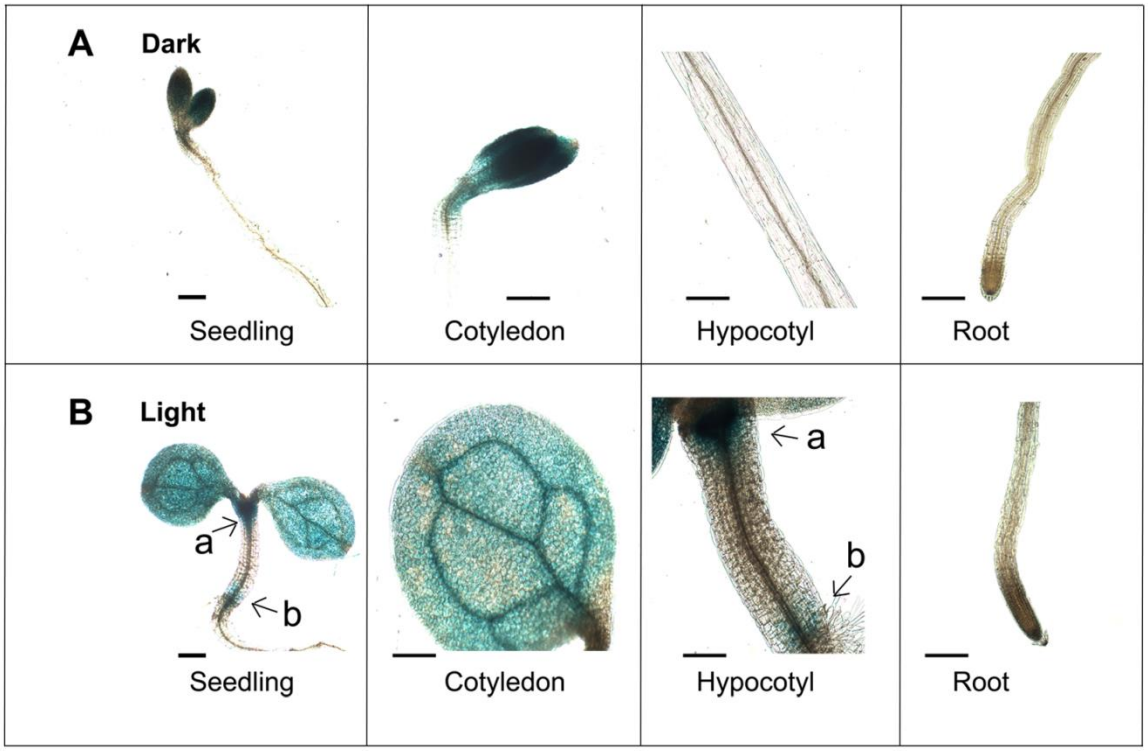
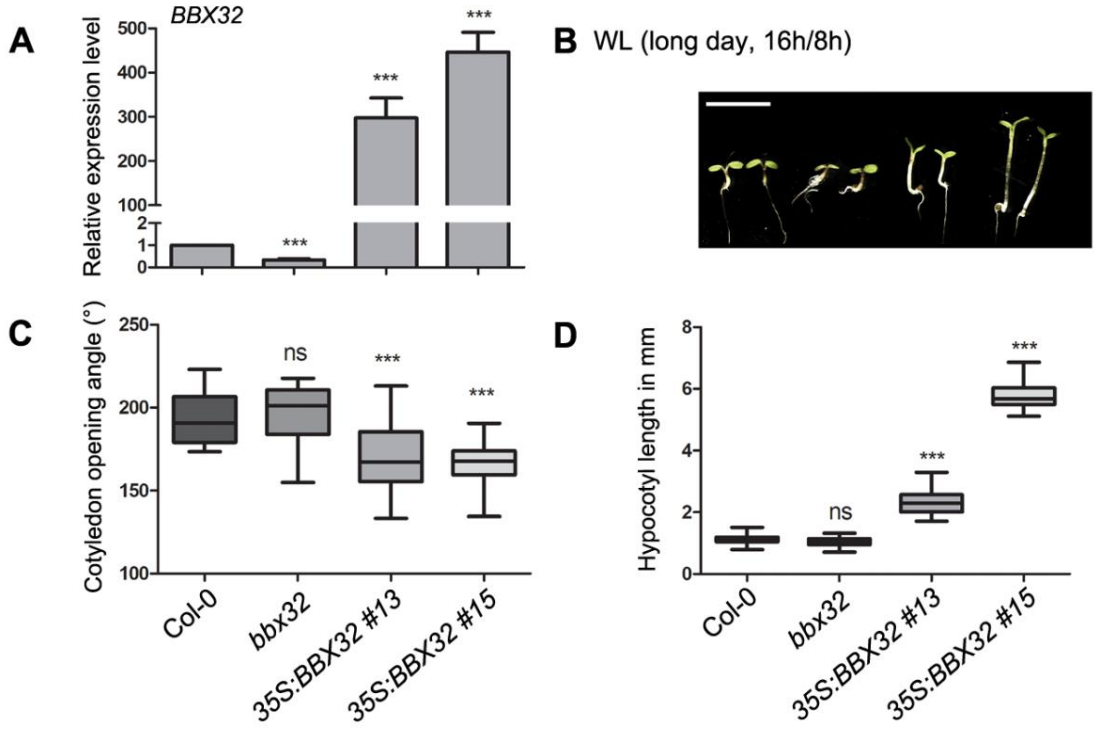


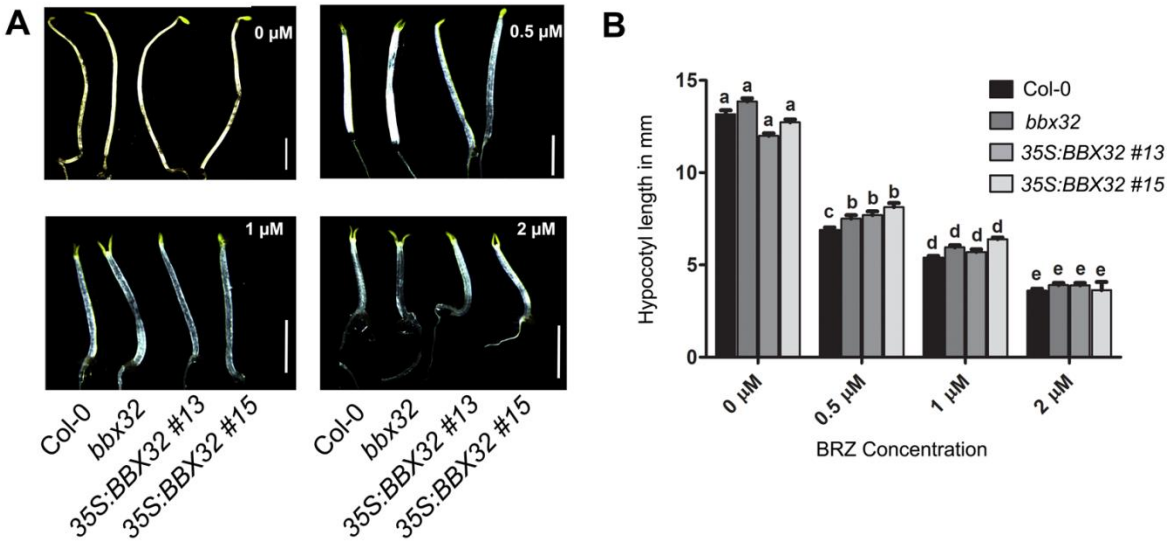

**Supplemental Figure S1. Spatial expression pattern of *BBX32* in 5-day old dark and light-grown seedlings**

**A and B**, Tissue-specific GUS expression pattern observed in 5-day old *ProBBX32:GUS* seedlings grown in dark **(A)** and in white light (WL) **(B)** at 80 µmol $m^{-2}$ $s^{-1}$ fluence (long day, 16h/8h)**.** The seedlings were treated with X-Gluc, the substrate for GUS, and the staining was observed. **a** and **b** in **B** indicate Shoot Apical Meristem (SAM) and root-hypocotyl junction respectively. The scale bar indicates 200 µm.



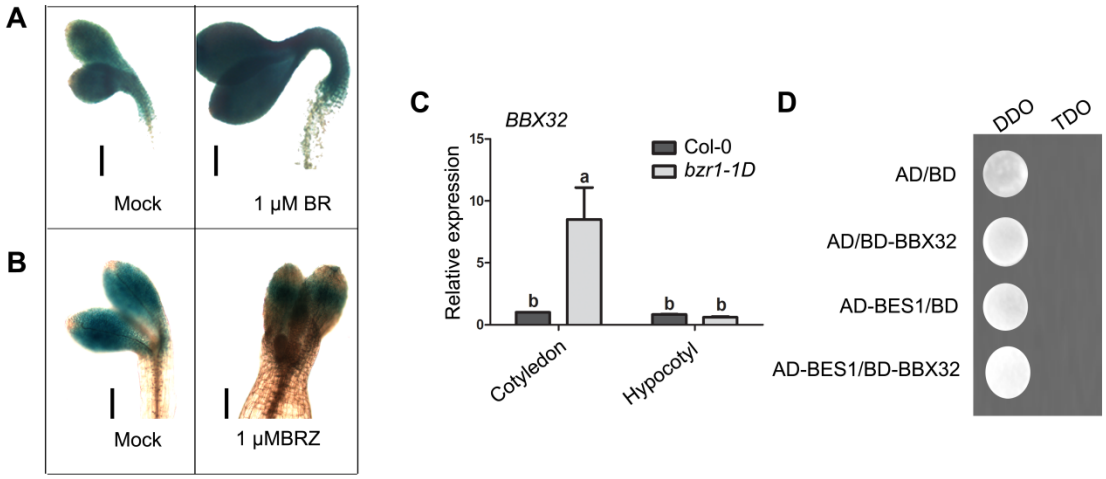

**Supplemental Figure S2. Relative expression levels and cotyledon and hypocotyl phenotypes of loss-of- and gain-of-function mutants of *BBX32***

**A**, RT-qPCR data showing relative expression levels of *BBX32* in *bbx32* and overexpressor lines *35S:BBX32 #13* and *35S:BBX32 #15* grown for 4 days in cycling white light (WL) (16h/8h). n=2, *UBQ10* was used for normalization. **B**, Representative images of seedlings of Col-0, *bbx32*, *35S:BBX32 #13* and *35S:BBX32 #15* grown in 80 µmol $m^{-2}$ $s^{-1}$ cycling WL (16h/8h) for 4 days. Scale bar = 5 mm. Representative seedling images of each genotype were spliced together to prepare the composite image for comparison purpose. **C** and **D**, Graphical representation of cotyledon opening angle **(C)** and hypocotyl lengths **(D)** of the indicated genotypes corresponding to **B**. The data represent mean of three biological replicates each with ~20 seedlings, n=3. **(A, C and D)** Error bars indicate SEM. Asterisks represent statistically significant difference (***, $P < 0.001$) as determined by one-way ANOVA followed by Dunnett's test; ns, non-significant. In the box plots **C** and **D**, centre line denotes median; box limits denote upper and lower quartiles; whiskers denote 1.5x interquartile range; points denote outliers in panels.



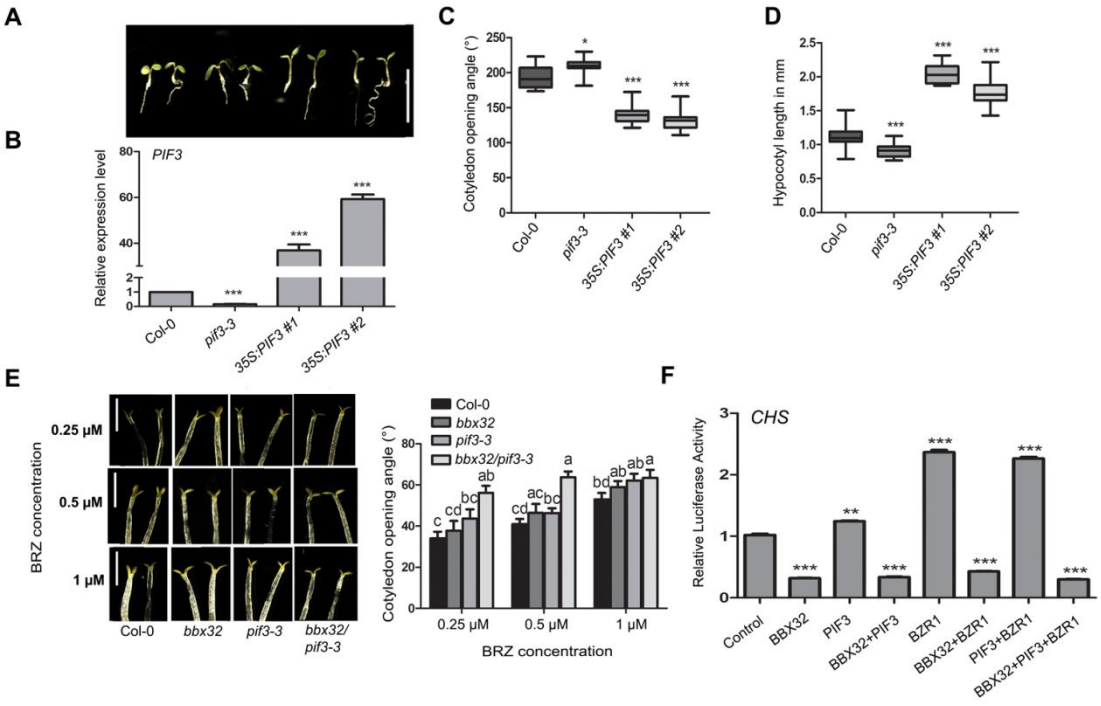

**Supplemental Figure S3. The hypocotyl elongation phenotype of *35S:BBX32* is suppressed by BRZ application in a dose-dependent manner**

**A,** Representative images of Col-0, *bbx32, 35S:BBX32 #13, 35S:BBX32 #15* treated with brassinazole (BRZ). The seedlings were grown on MS plates containing different concentrations (0.5 µM, 1 µM, 2 µM) of BRZ in dark for 7 days. The plate without BRZ was used as control. The scale bar represents 2.5 mm. Representative seedling images of each genotype were spliced together to prepare the composite image for comparison purpose. **B,** Graphical representation of average hypocotyl length (mm) of indicated genotypes at various concentrations of BRZ (0.5 µM, 1 µM, 2 µM) in dark. The data represents mean of 30 seedlings. Error bar=SEM. Significance was assessed by two-way ANOVA followed by Tukey's *post hoc* test, Letters denote statistical groups ($P<0.05$).




**Supplemental Figure S4. BR regulates *BBX32* expression, and BBX32 does not interact with BES1**

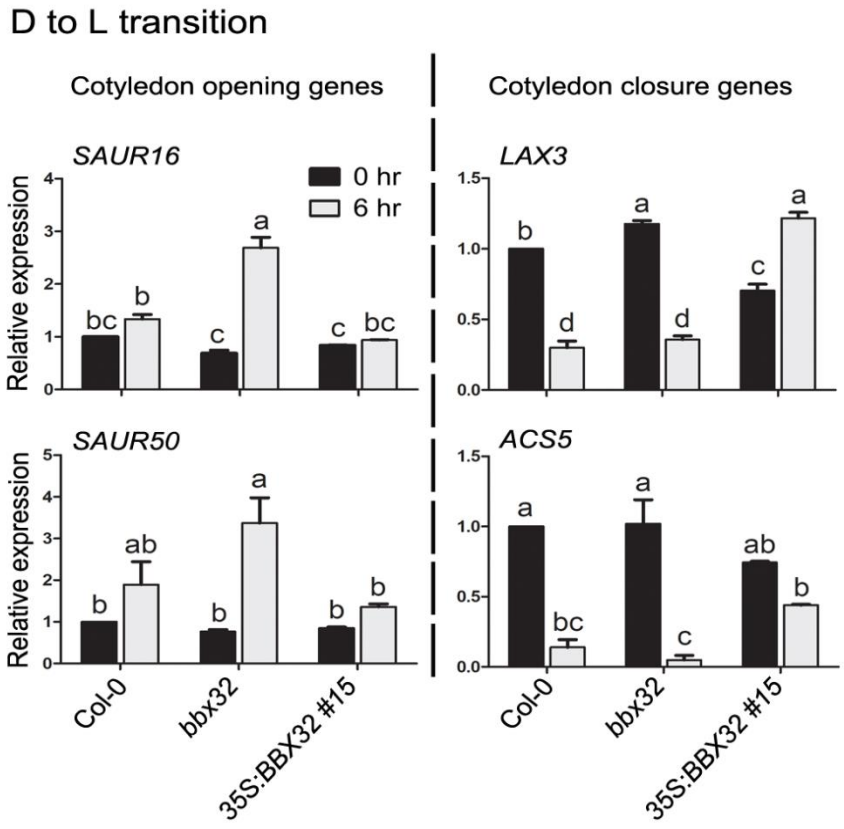
**A and B,** Representative GUS stained seedling images showing *BBX32* expression in brassinosteroids (BR) **(A)** and brassinazole (BRZ) **(B)** treated conditions in dark. **A,** The *ProBBX32:GUS* seedlings were grown in dark for 5 days with or without BR (1 µM) in the medium. The scale bar represents 200 µm. **B,** The seedlings were grown in dark for 5 days with or without BRZ (1 µM). The scale bar measures 200 µm. The mock used as control in both **A** and **B** was ethanol. **C,** Relative expression of *BBX32* in cotyledons and hypocotyls of *bzr1-1D* compared to Col-0. n=2, *UBQ10* was used for normalization. Error bar = SEM, two-way ANOVA and Tukey's *post hoc* test was performed to assess the significance, Letters denote the different statistical groups ($P<0.01$). **D,** Yeast two hybrid assay showing the interaction between BBX32 and BES1. AD and BD represents GAL4 activation domain and binding domain respectively. BBX32 fused with BD and BES1 fused with AD were tested for their interaction. DDO (double-dropout) denotes the lack of leucine and tryptophan in the medium. TDO (triple-dropout) denotes the lack of histidine additionally.




**Supplemental Figure S5. Relative expression level, cotyledon, and hypocotyl phenotypes of loss-of- and gain-of-function mutants of *PIF3* and interactions of BBX32 with PIF3 and its role in affecting transcriptional activation potential**

**A**, Representative images of Col-0, *pif3-3, 35S:PIF3 #1* and *35S:PIF3 #2* seedlings grown for 4 days in 80 µmol $m^{-2}$ $s^{-1}$ cycling white light (WL, long day, 16h/8h). Scale bar = 5 mm. **B,** RT-qPCR data showing relative expression levels of *PIF3* in *pif3-3, 35S:PIF3 #1* and *35S:PIF3 #2* grown for 4 days in cycling WL (16h/8h) compared to Col-0. n=2. *UBQ10* was used for normalization. **C and D,** Graphical representation of cotyledon opening angle **(C)** and hypocotyl lengths **(D)** of the Col-0, *pif3-3, 35S:PIF3 #1* and *35S:PIF3 #2* grown for 4 days in cycling WL (16h/8h), n=3, Error bar denotes SEM. Asterisks indicate statistically significant differences (***, P < 0.001, *, P<0.05) calculated by one-way ANOVA and Dunnett's test; ns, non-significant. In the box plots **C** and **D**, centre line denotes median; box limits denote upper and lower quartiles; whiskers denote 1.5x interquartile range; points denote outliers in panels. **E,** Representative images demonstrating the effect of different concentrations of BRZ on cotyledon opening response of 7 days old, dark-grown Col-0, *bbx32*, *pif3*-3, *bbx32pif3-3* seedlings and their corresponding cotyledon opening angles. Scale bar = 2.5 mm. The data is the mean of 30 seedlings. Error bar represents SEM, Two-way ANOVA followed by Tukey's *post hoc* test was performed to determine the statistical groups indicated by letters ( P<0.05). In **A** and **E**, Representative seedling images of each genotype were spliced together to prepare the composite image for comparison purpose. **F,**

Luciferase assay showing the effect of BBX32, PIF3, and BZR1 on the *CHS* promoter. The genes of the indicated proteins cloned in *35S* vectors and *CHS* promoter cloned in luciferase vector were co-transfected into the *Arabidopsis* protoplasts. The relative luciferase activity was measured after 16h incubation, n=2. Error bar represents SEM. One-way ANOVA followed by Dunnett's test was performed to determine the statistical significance indicated by asterisks (***, P<0.0001, **, P<0.001).




**Supplemental Figure S6. Transcriptional regulation of genes involved in opening and closing of cotyledons by BBX32 during Dark to Light transition.**

RT-qPCR data showing relative expression levels of *SAUR16*, *SAUR50*, *LAX3* and *ACS5* in isolated cotyledons of Col-0, *bbx32* and *35S:BBX32 #15* seedlings grown in dark for 3 days and moved to white light (80 µmol $m^{-2}$ $s^{-1}$) for 6 hr. n=2, Error bar = SEM. *UBQ10* was used for normalization. Letters denote the statistically different groups determined by two-way ANOVA followed by Tukey's *post hoc* test (P<0.01).

**Supplemental Table S1. List of Primers used in the study**

| Primers | Sequence (5' to3') |
|---|---|
| BBX32 SALK_059534 LP | AACTCCACCGCTCTTTCTCTC |
| BBX32 SALK_059534 RP | TTGGATTACCATTATTCCGTTTC |
| BBX32 attB1 | GGGGACAAGTTTGTACAAAAAAGCAGGCTGGATGGTGAGCTTTTGCGAGC |
| BBX32 attB2 | GGGGACCACTTTGTACAAGAAAGCTGGGTGTCAAACGTTGTCGTTTTCAG |
| BZR1 attB1 | GGGGACAAGTTTGTACAAAAAAGCAGGCTGGATGACTTCGGATGGAGCTACG |
| BZR1 attB2 | GGGGACCACTTTGTACAAGAAAGCTGGGTGTCAACCACGAGCCTTCCCATT |
| BES1 attB1 | GGGGACAAGTTTGTACAAAAAAGCAGGCTGGATGAAAAGATTCTTCTATAAT |
| BES1 attB2 | GGGGACCACTTTGTACAAGAAAGCTGGGTGTCAACTATGAGCTTTACCATT |
| PIF1attB1 | GGGGACAAGTTTGTACAAAAAAGCAGGCTGGATGCATCATTTTGTCCCT |
| PIF1 attB2 | GGGGACCACTTTGTACAAGAAAGCTGGGTGTTAACCTGTTGTGTGGT |
| PIF3 attB1 | GGGGACAAGTTTGTACAAAAAAGCAGGCTGGATGCCTCTGTTTGAGCTTT |
| PIF3 attB2 | GGGGACCACTTTGTACAAGAAAGCTGGGTGTCACGACGATCCACAAAACT |
| PIF4 attB1 | GGGGACAAGTTTGTACAAAAAAGCAGGCTGGATGGAACACCAAGGTTGG |
| PIF4 attB2 | GGGGACCACTTTGTACAAGAAAGCTGGGTGCTAGTGGTCCAAACGAGAA |
| PIF5 attB1 | GGGGACAAGTTTGTACAAAAAAGCAGGCTGGATGGAACAAGTGTTTGCTG |
| PIF5 attB2 | GGGGACCACTTTGTACAAGAAAGCTGGGTGTCAGCCTATTTTACCCATA |
| LB1.3 | ATTTTGCCGATTTCGGAAC |
| 35SEnd pro | CGCAAGACCCTTCCTCTAT |
| BBX32pro attB1 | GGGGACAAGTTTGTACAAAAAAGCAGGCTGGACTGGCTGGGGAGAATTATT |
| BBX32pro attB2 | GGGGACCACTTTGTACAAGAAAGCTGGGTGTGAGTCGATCTCTCTGATC |
| BBX32 qFP | GAGCTTTTGCGAGCTTTGTGG |
| BBX32 qRP | GGGCAGATGACACGCCGGAA |
| PIF3 qFP | CTGAAAGGAGACGGCGTGATAG |
| PIF3 qRP | CAGATAGTAACCAGACGCCATTGAC |
| UBQ10 qFP | GGCCTTGTATAATCCCTGATGAATAAG |
| UBQ10 qRP | AAAGAGATAACAGGAACGGAAACATAGT |
| WAG2 qFP | GCCGTTTCACCGCGACGGA |
| WAG2 qRP | GCGTTTGCGACTCGCGTAG |
| LAX3 qFP | CATCCCCGCATTGGCTCATA |
| LAX3 qRP | AACCCGAACCCAACTACGAA |
| ACS5 qFP | CGGGTTGGTTTAGGGTTTGTT |
| ACS5 qRP | CCCAGTTAGAGACTGTCTTCT |
| SAUR14 qFP | GATTCTCCGACAAGCCAAACT |
| SAUR14 qRP | TCTTGAAATGAAGGCTGGTCC |
| SAUR16 qFP | TGCTACGACGAGGAAGGTCT |
| SAUR16 qRP | ACCTTGTACGCTTTTCGCCT |
| SAUR50 qFP | CACTTCCCTGTCTATGTCGGA |
| SAUR50 qRP | TCTTCCTCGGCTCGTTGTAA |
| BBX32 CDS BamH1 FP | CGCGGATCCATGGTGAGCTTTTGCGAGC |
| BBX32 CDS ECoRI RP | CCGGAATTCTCAAACGTTGTCGTTTTCAG |
| BZR1 CDS BamHI FP | CGCGGATCCCGCGGATCCATGACTTCGGATGGAGCTACG |
| BZR1 CDS ECoRI RP | CCGGAATTCCCGGAATTCTCAACCACGAGCCTTCCCATT |
| PIF3 CDS BamHI FP | CGCGGATCCCGCGGATCCATGCCTCTGTTTGAGCTTTTC |
| PIF3 CDS ECoRI RP | CCGGAATTCCCGGAATTCTCACGACGATCCACAAAACTG |
| CHSpro KpnI FP | CGGGGTACCGGGATGTTAATATGGGCCAG |
| CHSpro PstI RP | AACTGCAGTATAGTATACACCAACTTGGGTT |

**Gateway sequence (attB1 or attB2) / Restriction sites (5' to 3') are indicated in red colour.**