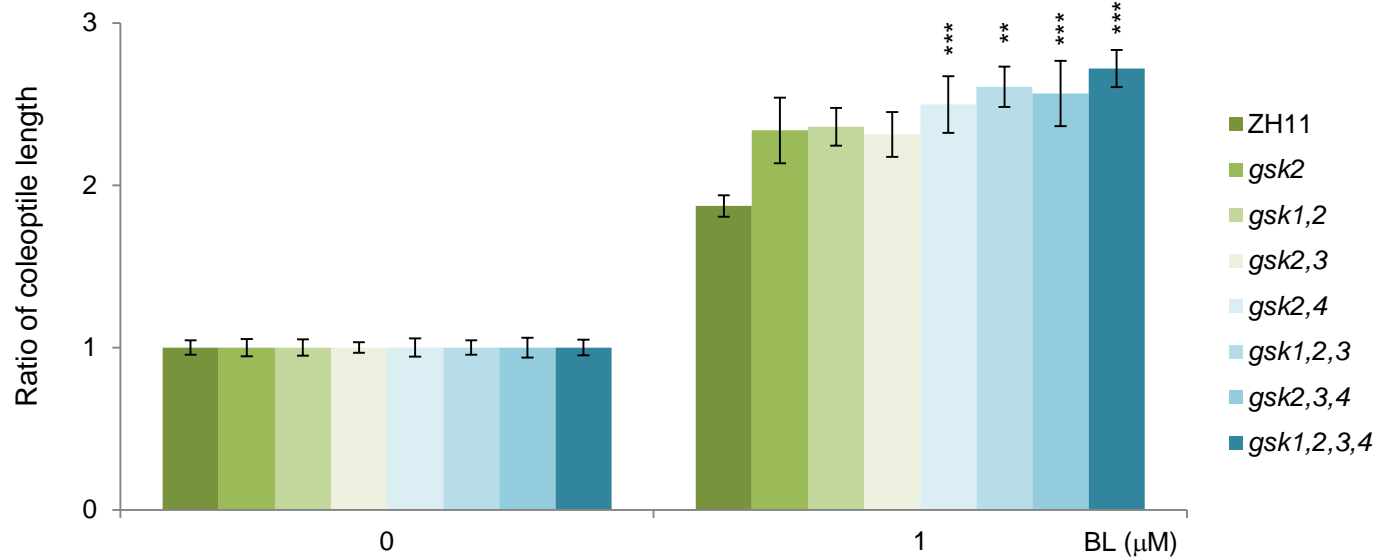
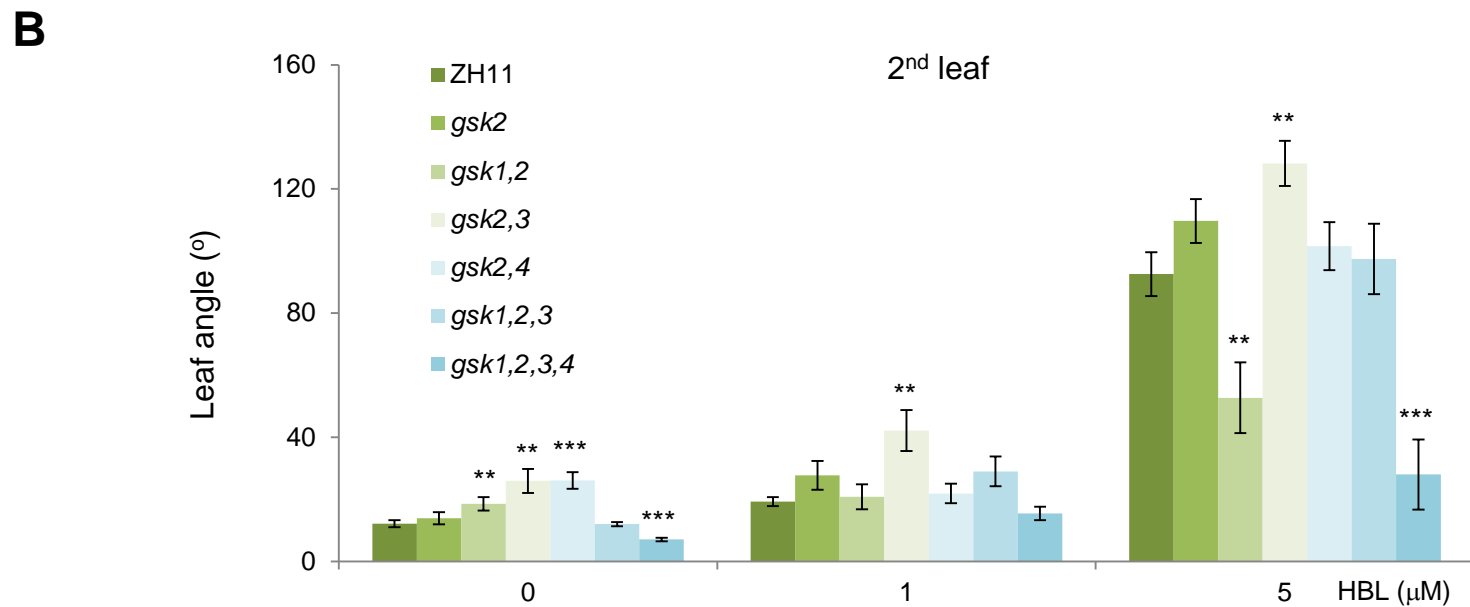
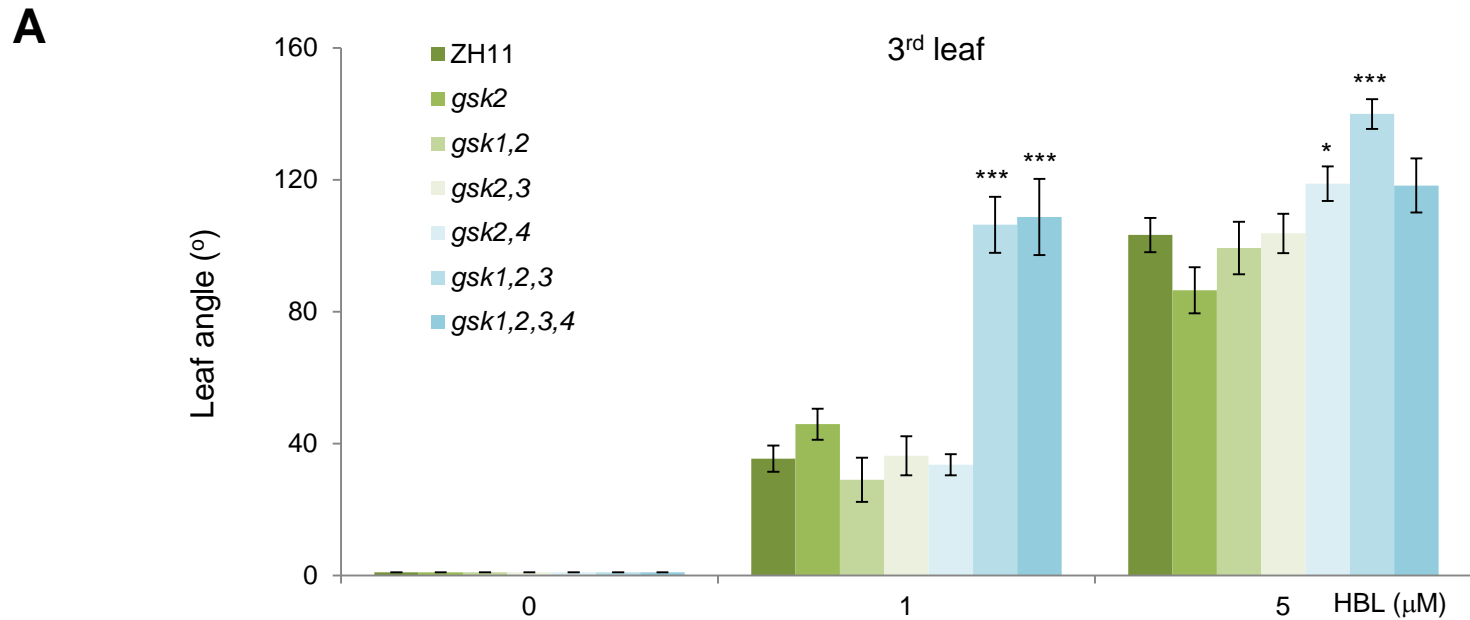


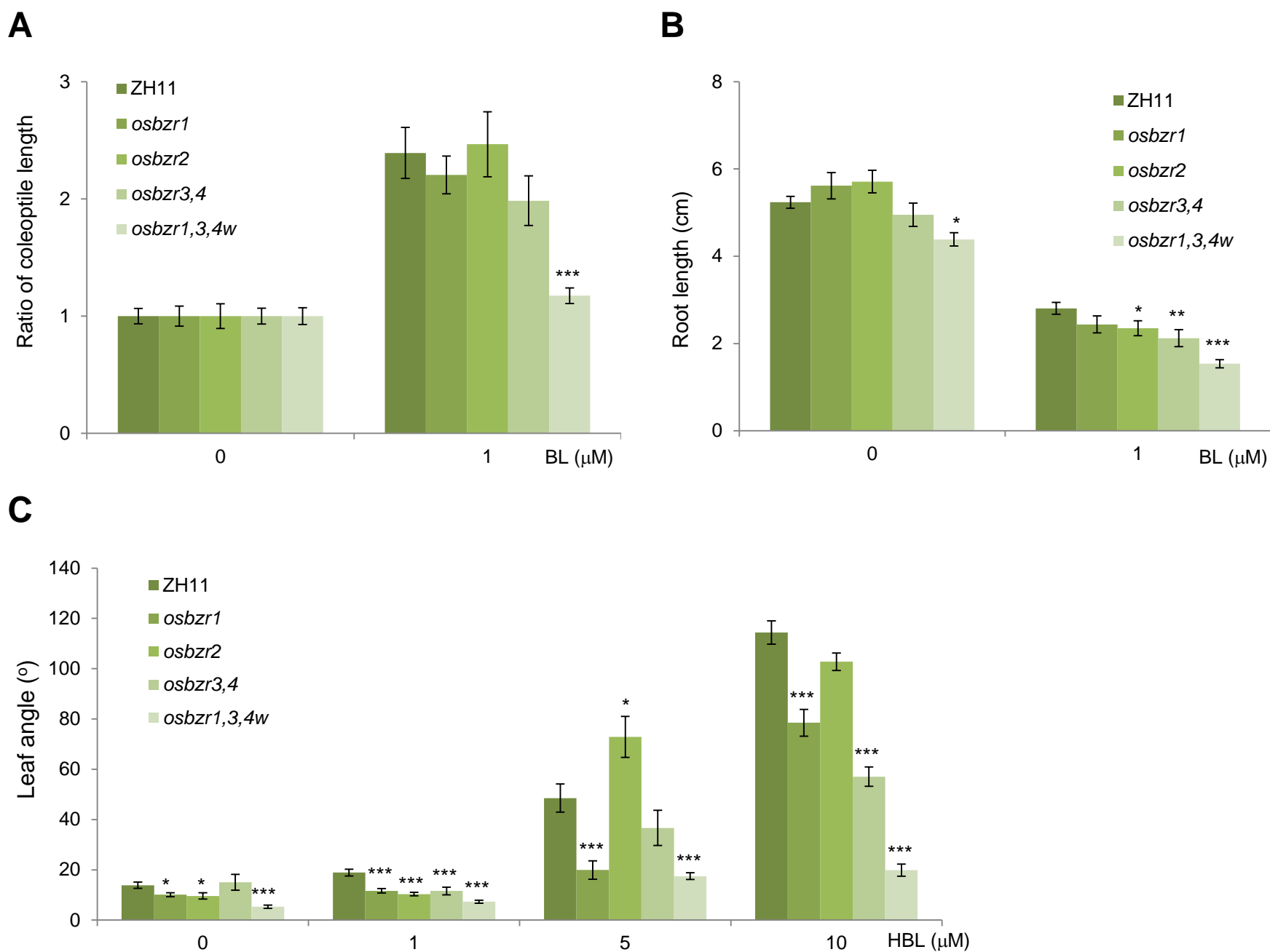
Supplemental Figure S1. Tiller number and root length of GSK-related mutants. (A) Tiller number was counted at the harvesting stage. Bars indicate SD ($n = 10$). * $P < 0.05$ generated by t -test. (B) Root length was measured after ten-day growth on agar media. Bars indicate standard error of mean values (SEM, $n = 14 - 30$). *** $P < 0.001$ generated by t -test.



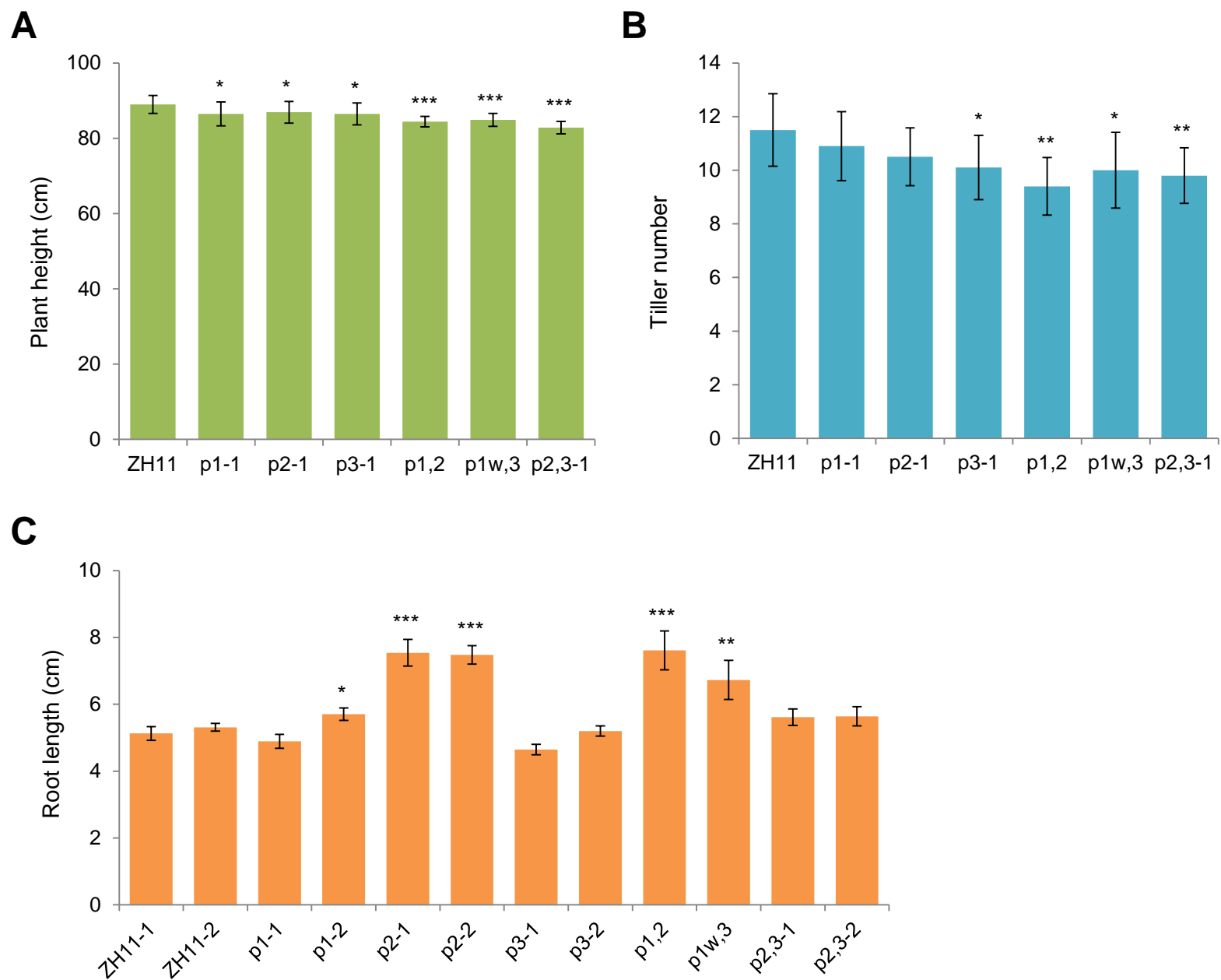
Supplemental Figure S2. BR sensitivity of GSK-related mutants evaluated by coleoptile elongation test. Coleoptile length was measured after ten-day growth on agar media with or without BL, and the ratios of BL-treated plants on those untreated were shown. Bars indicate SEM ($n = 11 - 30$). ** $P < 0.01$ and *** $P < 0.001$ generated by t -test.



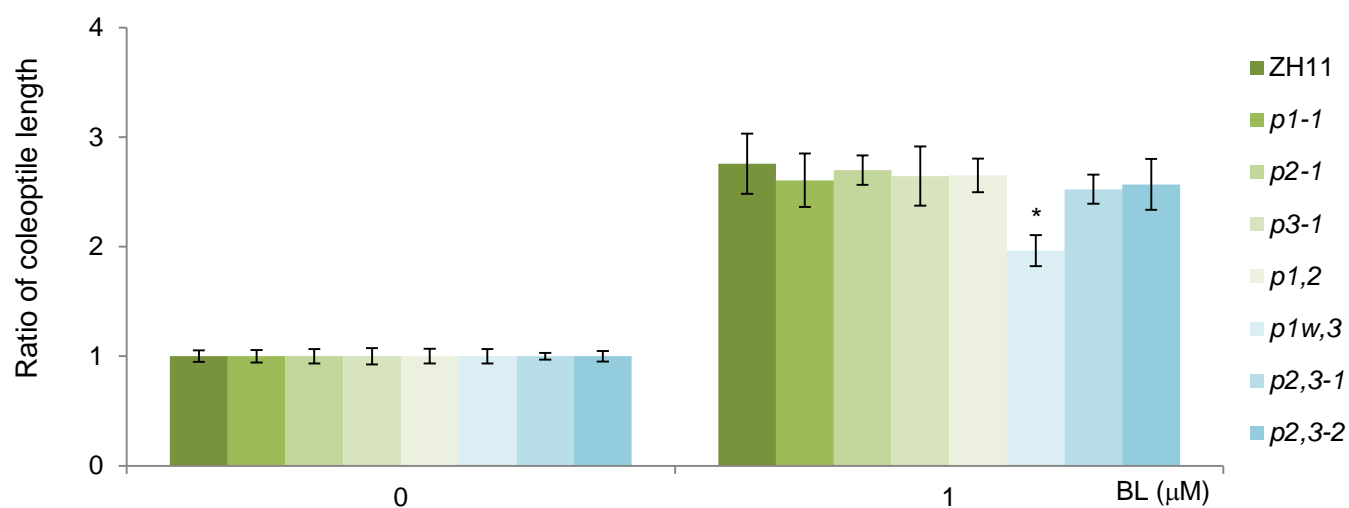
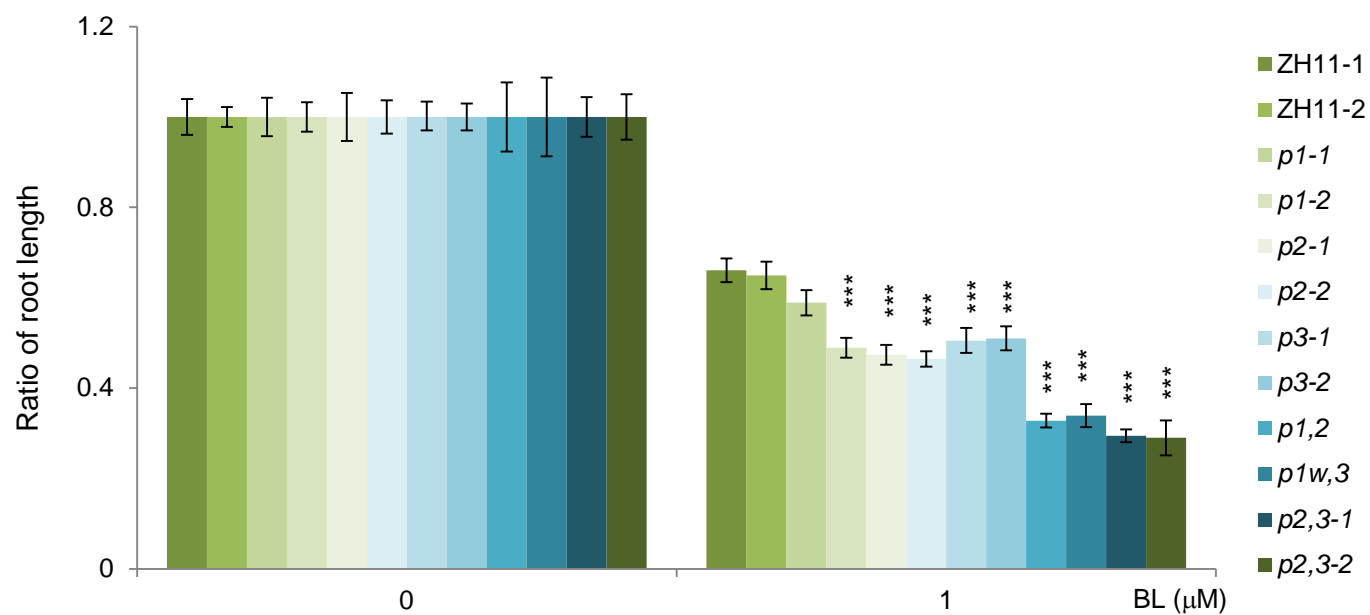
Supplemental Figure S3. BR sensitivity of GSK-related mutants evaluated by lamina bending tests of the 2nd and 3rd leaves. HBL (28-homobrassinolide) was used as BR for the analysis. HBL was applied at 3 days after germination when the 2nd leaves were emerging and leaf angles were measured after additional 4-d-growth. Note that at the time measuring the angles of the 3rd leaves, those without HBL treatment have not inclined thus were counted as zero. Bars indicate SEM ($n = 15 - 24$). * $P < 0.05$, ** $P < 0.01$ and *** $P < 0.001$ generated by t -test.



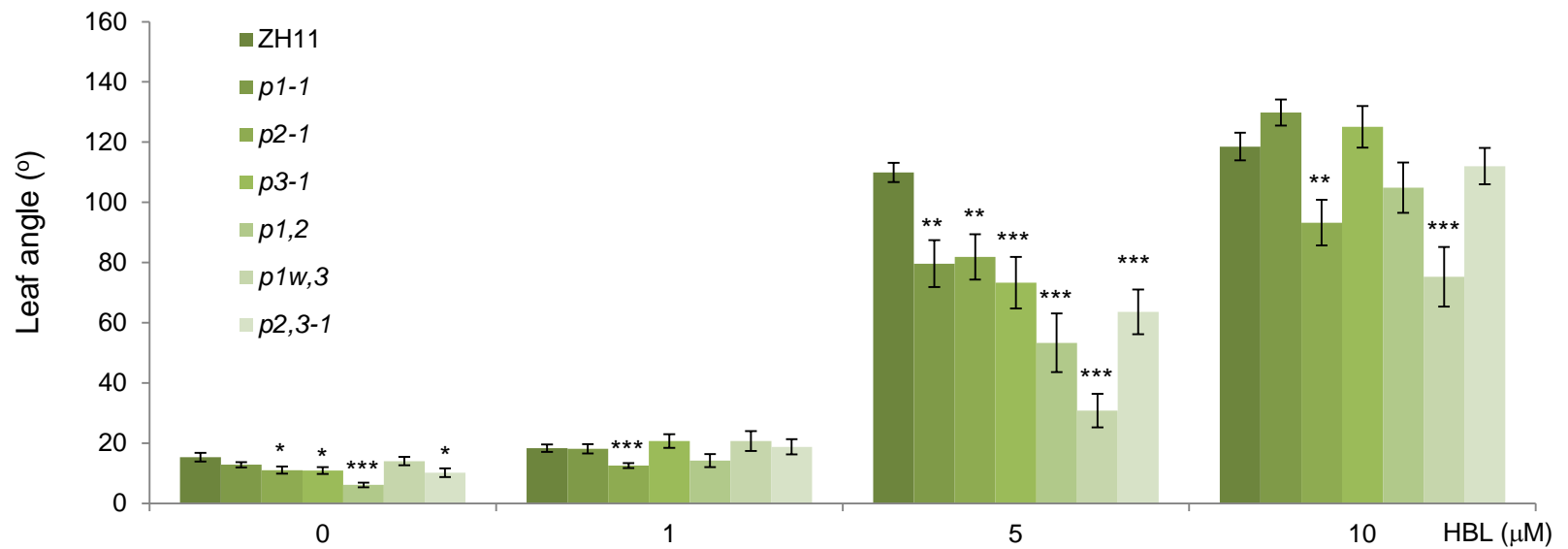
Supplemental Figure S4. BR sensitivity tests of *OsBZR*-related mutants. (A) Coleoptile length was measured after ten-day growth on agar media, and the ratios of BL-treated plants on those untreated were shown. Bars indicate SEM ($n = 8 - 21$). *** $P < 0.001$ generated by t -test. (B) Root length was measured after ten-day growth on agar media. Bars indicate SEM ($n = 8 - 25$). * $P < 0.05$, ** $P < 0.01$ and *** $P < 0.001$ generated by t -test. (C) HBL was applied at 3 days after germination when the 2nd leaves were emerging and angles (the 2nd leaves) were measured after additional 4-d-growth. Bars indicate SEM ($n = 20 - 26$). * $P < 0.05$, ** $P < 0.01$ and *** $P < 0.001$ generated by t -test.



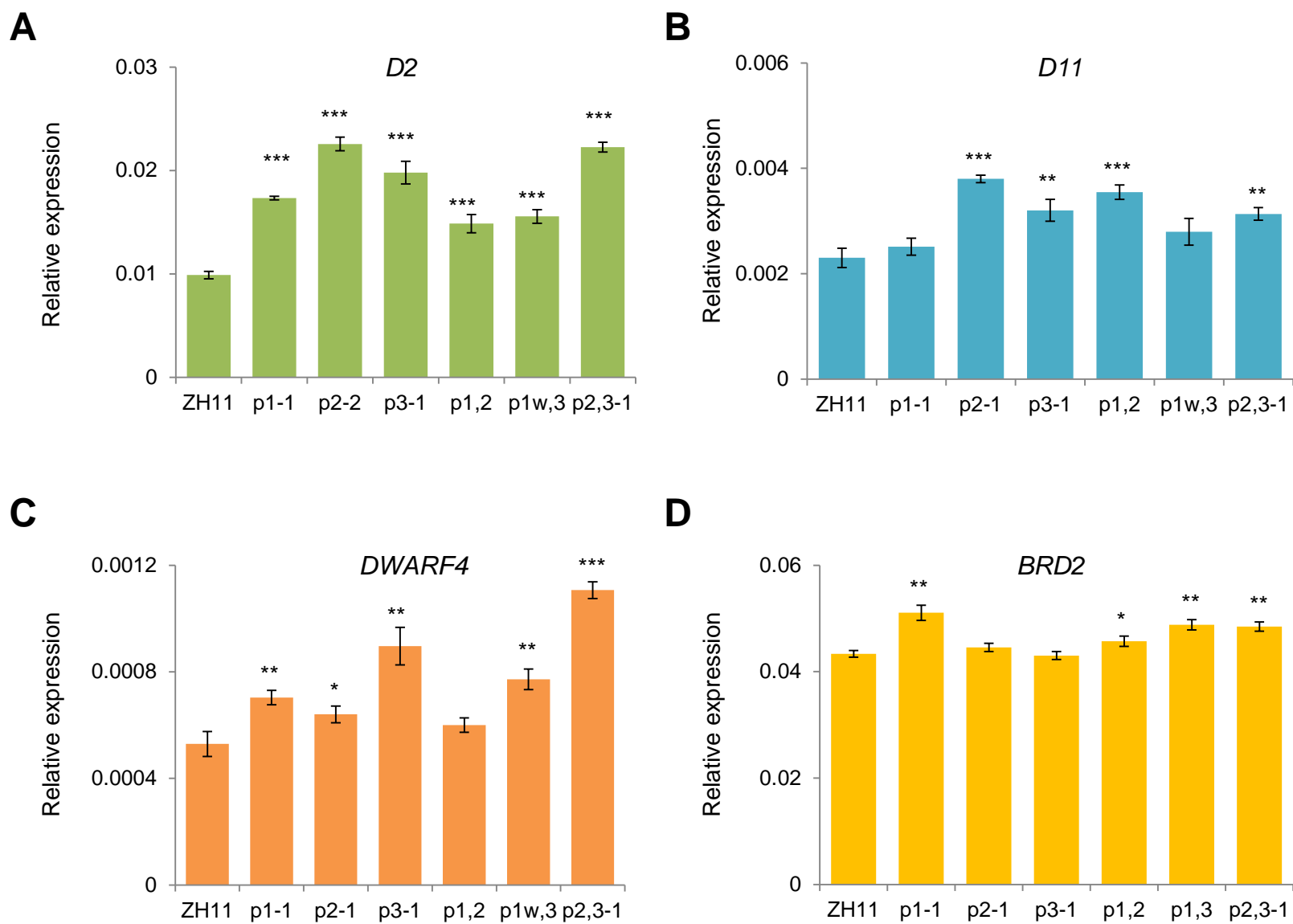
Supplemental Figure S5. Plant height, tiller number, and root length of *PPKL*-related mutants. (A) Plant height was measured at the harvesting stage. Bars indicate SD ($n = 16$). * $P < 0.05$ and *** $P < 0.001$ generated by t -test. (B) Tiller number was counted at the harvesting stage. Bars indicate SD ($n = 10$). * $P < 0.05$ and ** $P < 0.01$ generated by t -test. (C) Root length was measured after ten-day growth on agar media. A replicate of ZH11 was involved for the analysis. Bars indicate SEM ($n = 19 - 22$). * $P < 0.05$, ** $P < 0.01$ and *** $P < 0.001$ generated by t -test.

A**B**

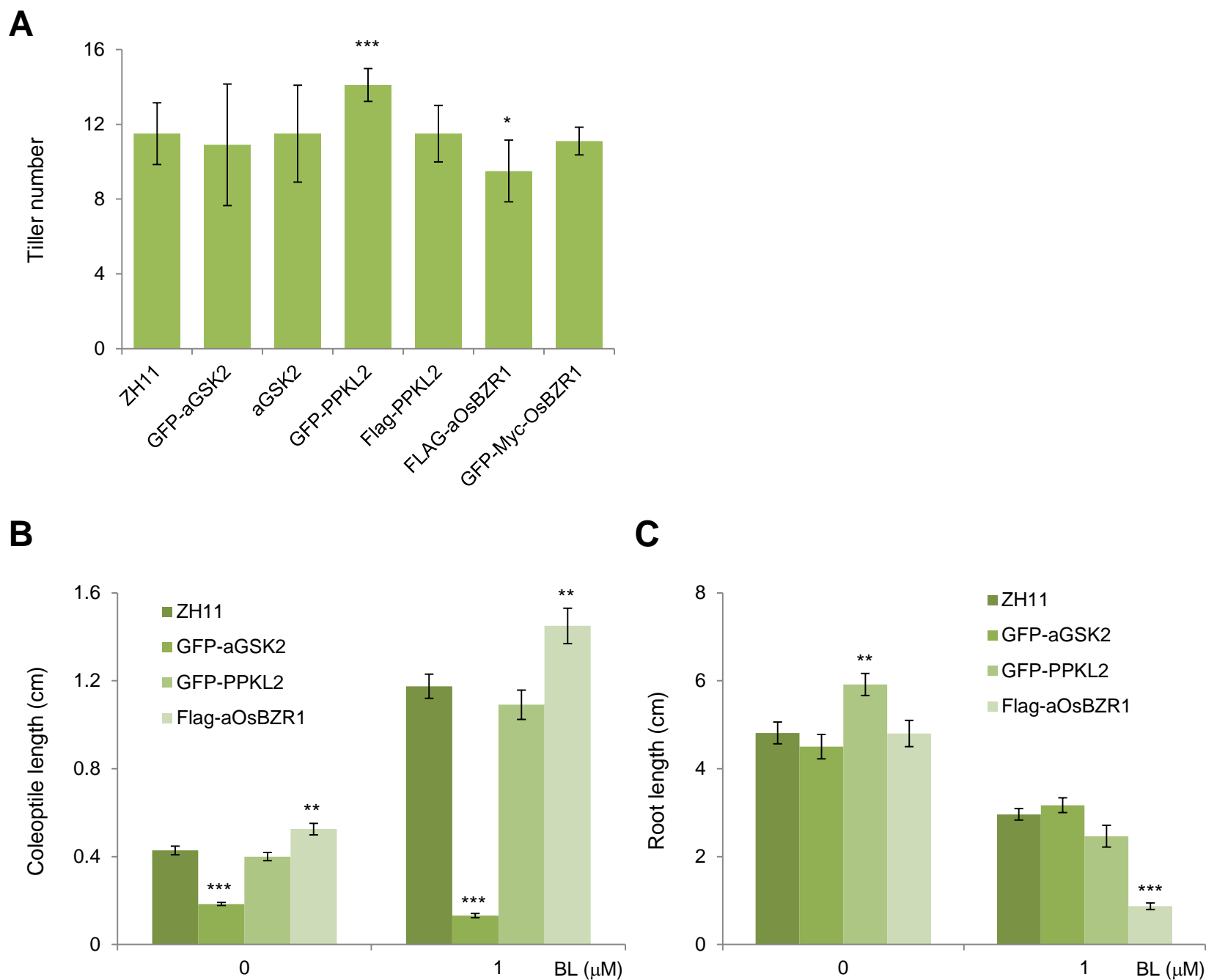
Supplemental Figure S6. BR sensitivity of *PPKL*-related mutants evaluated by coleoptile elongation test and root inhibition test. Coleoptile length and root length were measured after ten-day growth on agar media, and the ratios of BL-treated plants on those untreated were shown. Bars indicate SEM ($n = 15 - 26$). * $P < 0.05$ and *** $P < 0.001$ generated by t -test.



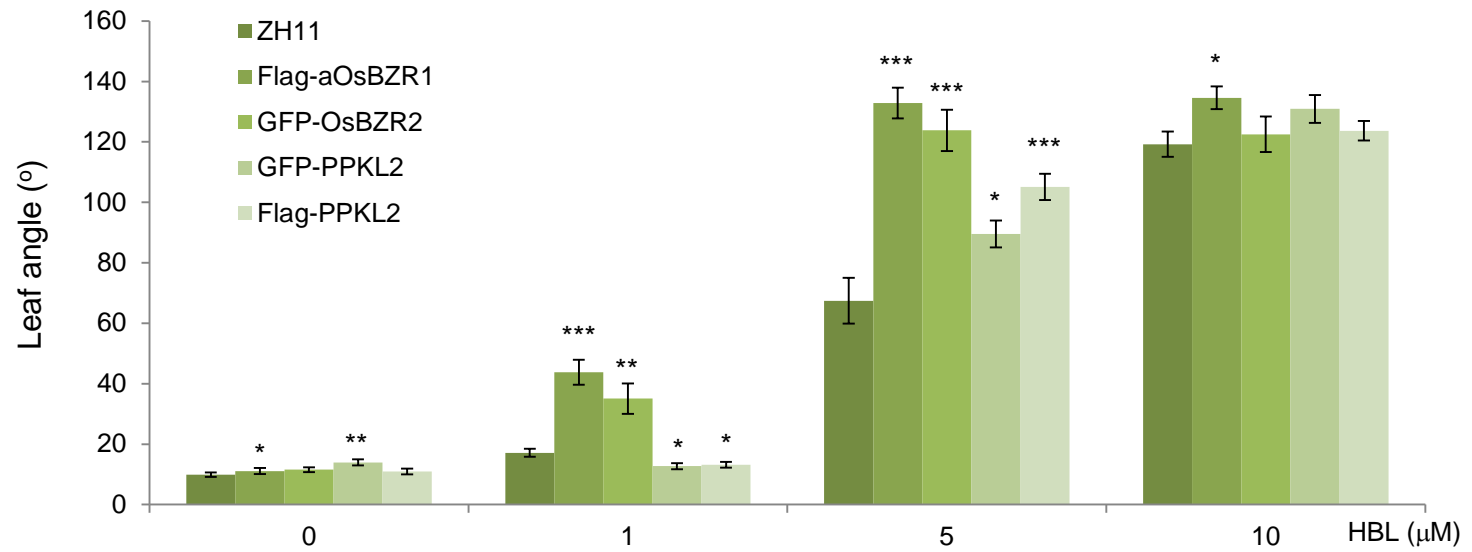
Supplemental Figure S7. BR sensitivity of *PPKL*-related mutants evaluated by lamina bending test. HBL was applied at 3 days after germination when the 2nd leaves were emerging and angles (the 2nd leaves) were measured after additional 4-d-growth. Bars indicate SEM ($n = 16 - 31$). * $P < 0.05$, ** $P < 0.01$ and *** $P < 0.001$ generated by *t*-test.



Supplemental Figure S8. Expression of BR-synthetic genes in the shoots of one-week-old seedlings of different plants. Bars indicate SD ($n = 3$). * $P < 0.05$, ** $P < 0.01$ and *** $P < 0.001$ generated by t -test.



Supplemental Figure S9. Tiller number and BR sensitivities of the representative overexpression plants. (A) Tiller number was counted at the harvesting stage. Bars indicate SD ($n = 10$). $*P < 0.05$ and $***P < 0.001$ generated by t -test. (B and C) Coleoptile length and root length were measured after ten-day growth on agar media with or without BL. Bars indicate SEM ($n = 10 - 19$). $**P < 0.01$ and $***P < 0.001$ generated by t -test.



Supplemental Figure S10. BR sensitivity of the overexpression plants evaluated by lamina bending test. HBL was applied at 3 days after germination when the 2nd leaves were emerging and angles (the 2nd leaves) were measured after additional 4-d-growth. Bars indicate SEM ($n = 16 - 31$). * $P < 0.05$, ** $P < 0.01$ and *** $P < 0.001$ generated by t -test.

Supplemental Table S1. Primer sequences for mutation identification.

Name	5' - 3' sequence
GSK1-F	GCGATTTCTCATGCGATTTT
GSK1-R	ACCAGAACCTTTGCACTTCC
GSK2-F	GGTGCTCATTTTTGGTGGTT
GSK2-R	AGGGTGGAAAAGGCCAATAC
GSK3-F	GTGGGAACTGGATCATTTGG
GSK3-R	CCCTCTTGAAAACCAGAAAGAA
GSK4-F	GGACAAAGAATGTCGCATGA
GSK4-R	AGTAGCATCCGCCACAAATC
BZR1-F:	AGAGGGAAAGCACGCTACTG
BZR1-R:	CTCGGGAAGCTCGACGAC
BZR2-F:	GCGTGATCTCTTCTCGCTTC
BZR2-R:	AATCGCCCTAGCAAAGGATT
BZR3-F:	GACTGCTCCTTCCTCCTCCT
BZR3-R:	AGCTCGAATCGAAGCAAAAA
BZR4-F:	ATGATGAACGGAGGAGGGGG
BZR4-R:	AGCGCCACAGCATCATCTCT
PPKL1-F	CTGCTGGTTTATCTGCCGAG
PPKL1-sg1-R	CAAACCTTACATGCATGGTGGC
PPKL1-sg2-F	CAAACCACCCGACGAATC
PPKL1-sg2-R	CCGTCCTCCTTCTTCTCGAT
PPKL1-sg3-F	GTACAAAATTGTTTTCGGTT
PPKL1-sg3-R	GAGGCTCACCTTGTGGAGTAA
PPKL2-sg1-F	CCTGGTTGGTTGGTTTCAGC
PPKL2-sg1-R	GACGACAACGGCGAAGTAGA
PPKL2-sg2-F	GGAGCTAGGGTTTTGGAGGT
PPKL2-sg2-R	AAGGGATGAGGAGACCTGGA
PPKL3-sg1-F	TCCTAGGGTAACCCACCACT
PPKL3-sg1-R	TTGTTGGCACAAGCATGCAA
PPKL3-sg2/3-F	GGTGTGGCGTGTCTACCTA
PPKL3-sg2/3-R	CCGTCCTCCTTCTTCTCCAT
NPT-F	CATGTGTCACGACGAGATCC
NPT-R	CGACAATCCCACTATCCTT
HPT-F	TAGGAGGGCGTGGATATGTC
HPT-R	TACACAGCCATCGGTCCAGA

Supplemental Table S2. Primer sequences for vector constructions.

Name	5' - 3' sequence (Restriction enzyme sites were indicated)
LC-PPKL2-F	GGCAGCGGCC <u>GAATTC</u> ATGGGGACGGCGGGGAAG (EcoRI)
LC-PPKL2-R	GTCGACTGCAG <u>AATTC</u> TTCATATATAAGCAAGAGAAT (EcoRI)
Flag-PPKL2-F	CGAAATCGAT <u>GGATCC</u> GATGGGGACGGCGGGGAAG (BamHI)
Flag-PPKL2-R	AGGCTACGTAG <u>GATCC</u> TTCATATATAAGCAAGAGAAT (BamHI)
LC-aGSK2-F	GGCAGCGGCC <u>GAATTC</u> ATGGACCAGCCGGCGCC (EcoRI)
LC-aGSK2-R	GTCGACTGCAG <u>AATTC</u> TTAGCTCCCAGTATTGAAGAAG (EcoRI)
LM-GSK2-F	GGGCCGCGACT <u>CTAGA</u> ATGGACCAGCCGGCGCC (XbaI)
LM-GSK2-R	AAAGCAGGACT <u>CTAGA</u> TTAGCTCCCAGTATTGAAGAAG (XbaI)
Flag-GSK2-F	CGAAATCGAT <u>GGATCC</u> GATGGACCAGCCGGCGCC (BamHI)
Flag-GSK2-R	AGGCTACGTAG <u>GATCC</u> TTAGCTCCCAGTATTGAAGAAG (BamHI)
LM-aOsBZR1-F	AAGAGGACTT <u>GAATTC</u> ATGACGTCCGGGGCGGCG (EcoRI)
LM-aOsBZR1-R	CCGGGTACCG <u>AATTC</u> CATTTTCGCGCCGACGCC (EcoRI)
Flag-aOsBZR1-F	CGAAATCGAT <u>GGATCC</u> TATGACGTCCGGGGCGG (BamHI)
Flag-aOsBZR1-R	AGGCTACGTAG <u>GATCC</u> CATTTTCGCGCCGACGCC (BamHI)
LC-OsBZR2-F	GGCAGCGGCC <u>GAATTC</u> ATGGCGACGGGAGGAGGAGG (EcoRI)
LC-OsBZR2-R	GTCGACTGCAG <u>AATTC</u> TTAAGCAGCAGCTTTGTCTAGAGCT (EcoRI)
For point mutation	
aOsBZR1-1F	ATGACGTCCGGGGCGGCGGC
aOsBZR1-1R	TCGCACTCCGGTATCGTGTCC <u>A</u> GGTGCTCGAGGCGGCGGC
aOsBZR1-2F	GCCGCCGCCTCGAGCACCT <u>T</u> GGACACGATACCGGAGTGCGA
aOsBZR1-2R	TTTCGCGCCGACGCCGAGCG

Supplemental Table S3. Primer sequences for RT-qPCR analysis.

Name	5' - 3' sequence
OsGSK1q-F	ACGGGTCACATCATCTCC
OsGSK1q-R	AGTTCCTACAACCTCGCTCC
OsGSK2q-F	CCAACCCGTGAGGAAA
OsGSK2q-R	GCGTGAAGCGAGGTCTA
OsGSK3q-F	CAGCCTCTCTTTCCTGGTGA
OsGSK3q-R	GGGATTCATGCAGCGGATTT
OsGSK4q-F	GGAGGGAAGAACGATG
OsGSK4q-R	TTGCCTGGAATACAACAC
D2q-F	AAACCGACATGGGTGAGACC
D2q-R	ACCGCAGCGTCTCTGTTATC
D11q-F	CCTAGGGGAGGACCACAAGA
D11q-R	CCAAGGTAGCTGGGCTTGAG
DWARF4q-F	GTGCTCAACTTCAGGTGGGA
DWARF4q-R	CCTAATGGGAAGGCCCTTGG
BRD2q-F	GCATTGCCGCCAAAAGTATG
BRD2q-R	TCCTGCACCTCCTTCTCAGTC
UBQq-F	GAGCCTCTGTTTCGTCAAGTA
UBQq-R	ACTCGATGGTCCATTAACC