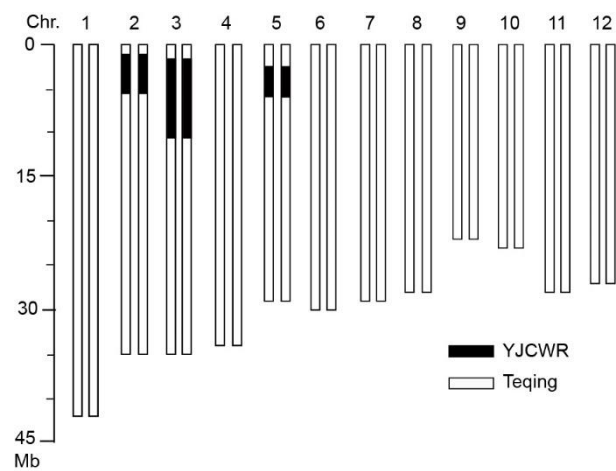
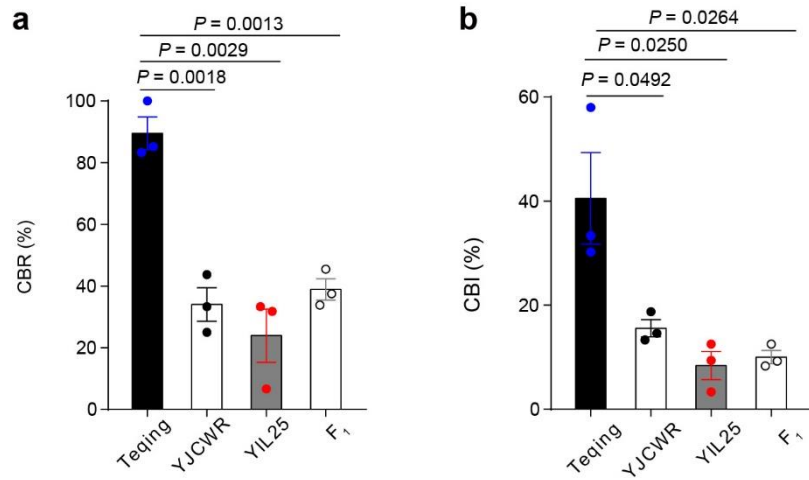


**A common wild rice-derived *BOC1* allele reduces callus
browning in *indica* rice transformation**

Zhang *et al.*



Supplementary Fig. 1. Graphic depiction of genotype of the introgression line YIL25. The black boxes represent the chromosome segments of YJCWR. The white boxes represent the Teqing genetic background.



Supplementary Fig. 2. Phenotypic comparison of various calli subcultured for 21 days. (a, b) Comparison of the CBR and CBI of Teqing, YJCWR, YIL25, and F_1 progeny derived from a cross between Teqing and YIL25. Values are means $\pm$ SE ($n = 3$ biologically independent samples). Two-tailed Student's t -tests were performed to determine significant differences. Source data are provided as a Source Data file.

Teqing AAAAAGTCCCCTAACCGTAGGATGATCAGATGGTCAACGGCGATGGCAAAGGTACGCGTTTGGTTTACCACGCGCTTCGTG 79
 YIL25 AAAAAGTCCCCTAACCGTAGGATGATCAGATGGTCAACGGCGATGGCAAAGGTACGCGTTTGGTTTACCACGCGCTTCGTG 80

Teqing CGGCGGTGGGCGGTGGGCGCCACCTGGAAGTCTAATTATTACTAGACCGAGAAATAAACAACTTGCTTCACAAGAACAT 159
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Teqing TTAGGAAACAATTTTTTGGTTTATATAATTAACCAAACCTCATACAATCAAATGTGTATGCATGAAATTTGAAATGTAAACCG 622
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Teqing TTTTTTAGACCAATTTTCTTATATTAATTAATTTATTATAGAGGAGAAATATTTTTTCTTTTTTAAAGGGAAGGAGCAC 702
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Teqing TATTCCTTCCGTTCAAGTAAGTAGTAGTCCAGACCAAAAAAGAAATAAAAAACAACCTGGCGCAAGTAAAACAGGTTCCG 782
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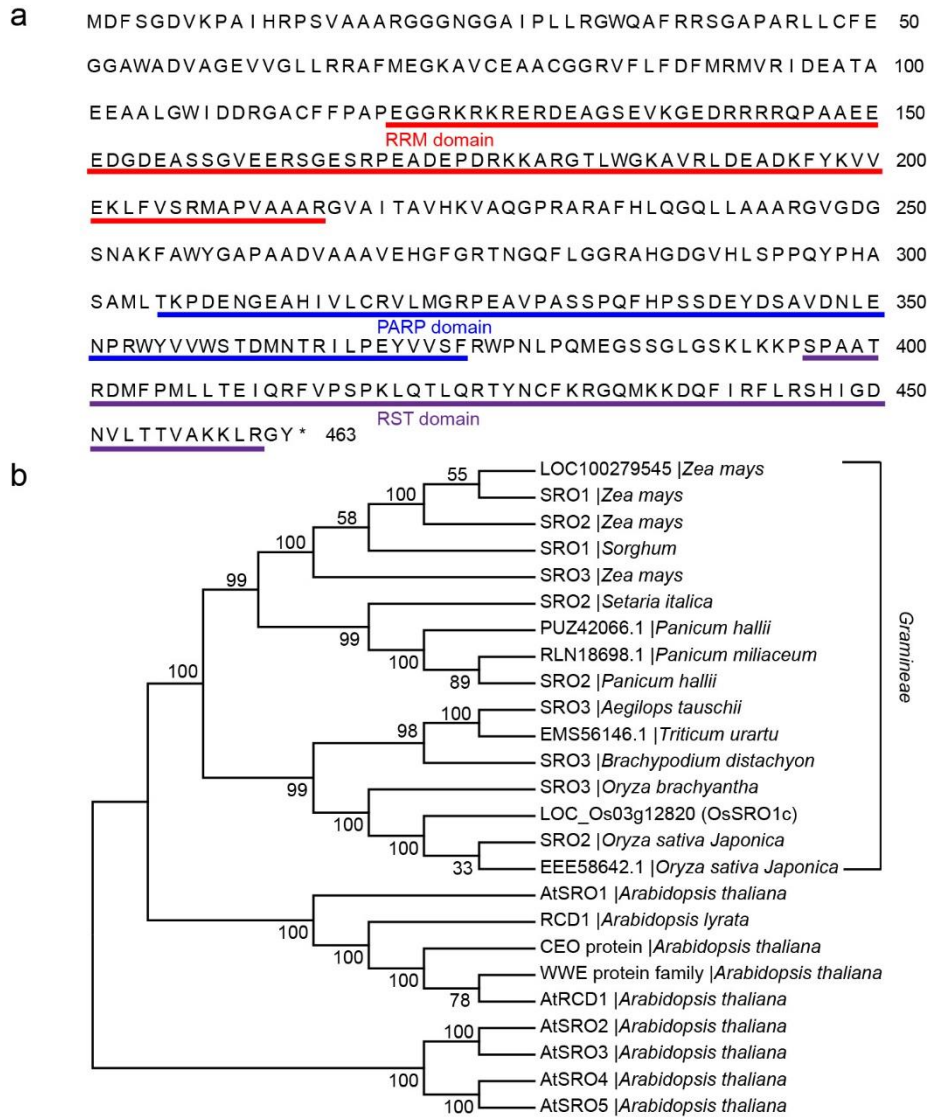
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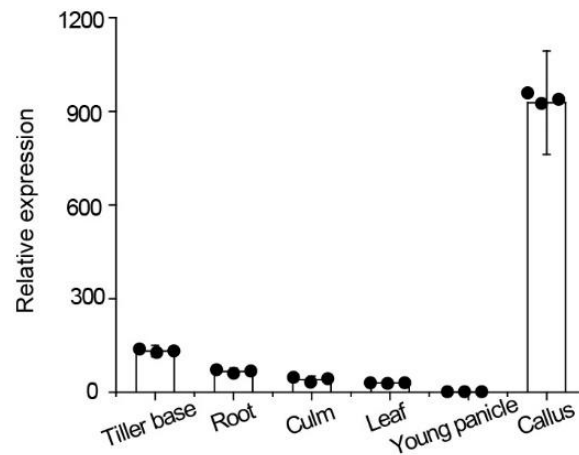
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YIL25	GTCTAACTCTTCACTATACGCAATAATTAGCACGTA	AAAAATGTTGATTTGTACCGCACTGCTATGGTTTTAATATGATCA	3920
Teqing	TGCCGACTTTATTCTGTAGTAATATGCTGCCGACTTTATTCTGTAGT	AGAACAGAATCATCTACCTGTCAATATTCTGTG	3661
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Teqing	CAAAGCGAATTCAGCTCAGCATAACGGCGTTATAACTTTAAGCGAAGCTGAAGT	CCTGAAAAATCCAATGACATAAAATTTT	3741
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Teqing	CTTTTTGTTTCAGAGAGGACAGATGAAGAAGGACCAAGTTCATCCGGTTCTTGCGCTCCCACATCGGCGACAATGTGTTGA		3821
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Teqing	CCACCGTGGCCAAGAACTCCGAGGGTACTAGT	gcaaggTgcaaaattTgtctccactccgtggctgaattcgactaaactc	3901
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Teqing	tttccccgTTTT		4233
YIL25	tttccccgTTTT		4572

Supplementary Fig. 3. Comparison of *BOC1* sequences between Teqing and YIL25.

The 337 bp deletion in the promoter region is underlined purple. The translation initiation site (ATG) and stop codon (TAG) are highlighted. The SNP variations between Teqing and YIL25 are marked by red rectangles. The 1 bp deletion is marked with a red triangle. The 5'-UTR is underlined in rose red. The four exons of the nucleotide sequences are underlined in red. The lowercase letters indicate the 3'-UTR.



Supplementary Fig. 4. Conserved domains (a) and phylogenetic analysis (b) of BOC1 protein. The RRM domain, poly (ADP-ribose) polymerase catalytic domain (PARP), and RCD1-SRO-TAF4 (RST) domain are underlined in red, blue, and purple, respectively. The neighbor-joining tree was constructed using MEGA 7 software.



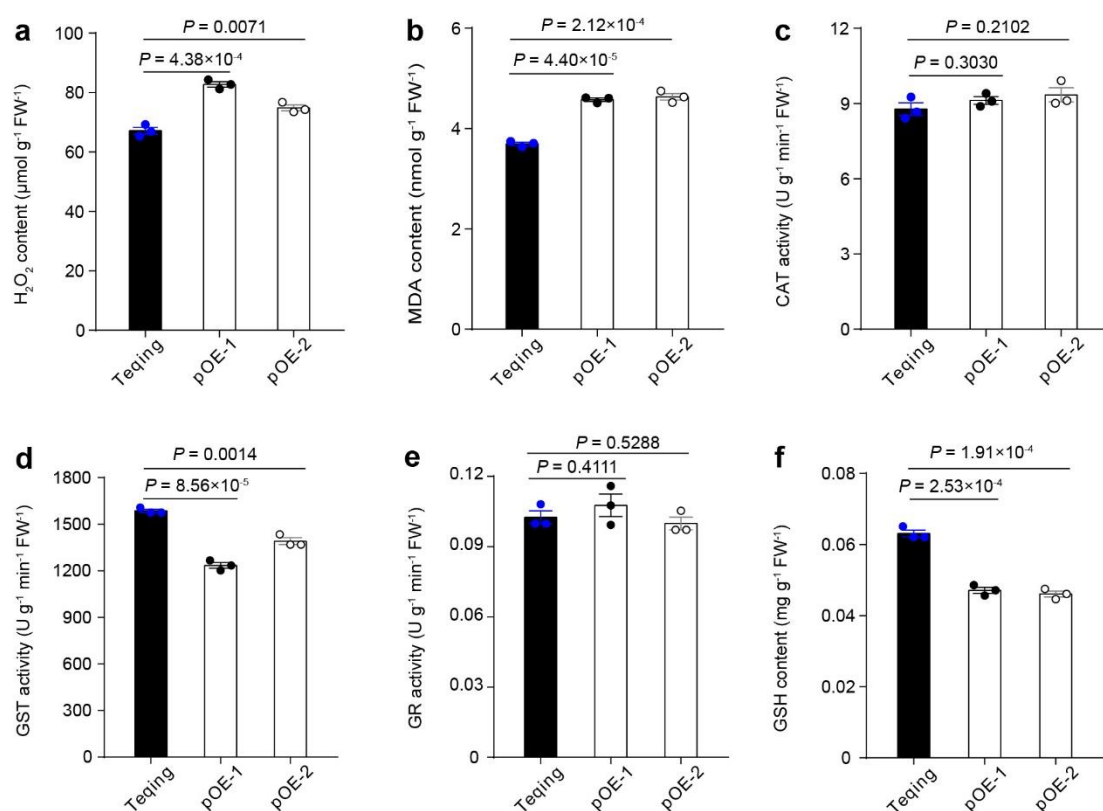
Supplementary Fig. 5. The expression pattern of *BOC1* in different organs of YIL25. Expression analysis of *BOC1* in the tiller base, root, culm, leaf, and young panicle and callus subcultured for 21 days. Data are means, with bars showing SE, $n = 3$ biological replicates. Source data are provided as a Source Data file.

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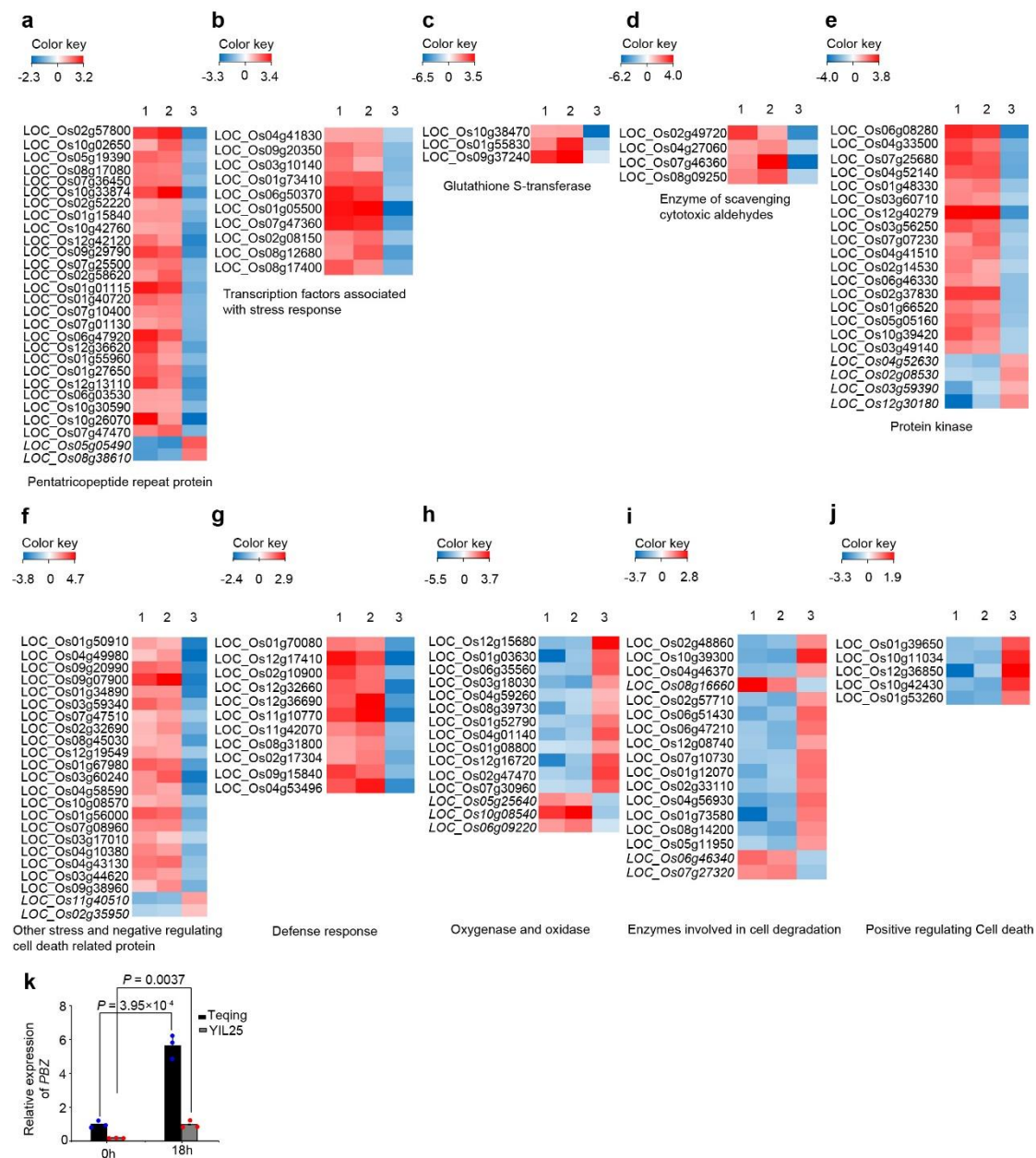
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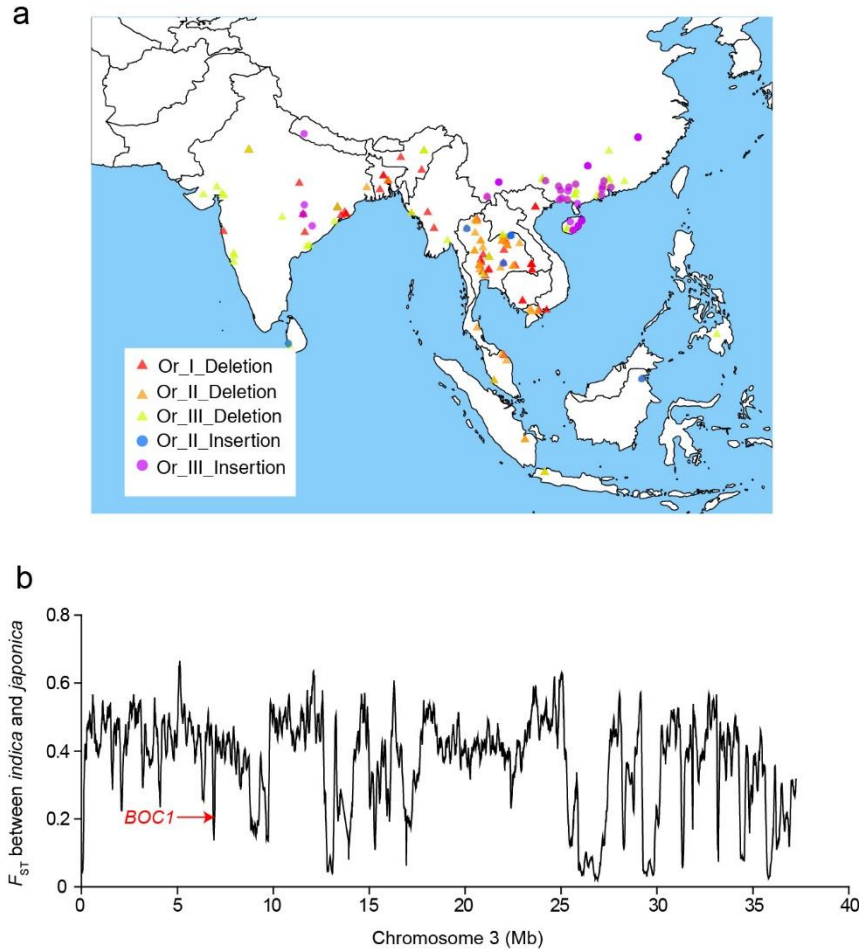
Supplementary Fig. 6. The *cis*-acting regulatory DNA elements in the 337 bp insertion associated with plant stress responses. The DOF TFBS (DOF COREZM), MYC TFBS (MYCCONSENSUSAT), ACGT TFBS (ACGTATERD1), and MYB TFBS (MYB1AT) are underlined in red, blue, brown, and purple, respectively.



Supplementary Fig. 7. Physiological and biochemical oxidative stress indices of calli subcultured for 21 days in *BOC1* overexpression transgenic plants. (a) H_2O_2 contents in Teting and two positive overexpression transgenic plants. (b) MDA contents. (c), (d) and (e) Assay of the antioxidant enzyme activities. CAT, catalase. GST, glutathione S-transferase. GR, glutathione reductase. (f) Antioxidant GSH contents. All values are presented as means $\pm$ SE ($n = 3$ biologically independent samples). P values were analyzed by two-tailed Student's t -test. Source data are provided as a Source Data file.



Supplementary Fig. 8. Differentially expressed genes in YIL25 vs Teqing, pCPL vs Teqing, and pOE vs Teqing via RNA-seq analysis. (a-j) 1 represents YIL25 vs Teqing. 2 represents pCPL vs Teqing. 3 represents pOE vs Teqing. (k) The relative expressions of *PBZ* by treated the callus of subculture 7d with 0.5% H₂O₂ treatment for 18h. *PBZ* represents *LOC_Os12g36850*. All values in (k) are presented as means ± SE (*n* = 3 biological replicates). *P* values were analyzed by two-tailed Student's *t*-test. Source data underlying Supplementary Figure 8k are provided as a Source Data file.



Supplementary Fig. 9. The 226 accessions of *Oryza rufipogon* classification with and without the 337 bp and the fixation index (F_{ST}) on chromosome 3 between the *indica* and *japonica* subspecies. The triangle represents the 337 bp deletion and the circle represents the 337 bp insertion. Or_I_Deletion, Or_II_Deletion, and Or_III_Deletion, represents the accessions of *Oryza rufipogon* without this 337 bp in group I, II, III, respectively. Or_II_Insertion and Or_III_Insertion represents the accessions of *Oryza rufipogon* with this insertion in group II and III, respectively. (a) was drawn by maps 3.3.0, an R package with GPL-2 license. Source data are provided as a Source Data.

Supplementary Table 1. QTL analysis using 198 F₂ individuals.

Phenotype	Locus	LOD ^a	PV ^b (%)	Add ^c	Dom ^d
Callus browning index	RM3131-RM3766	6.43	14	-5.33	-3.17

QTL was detected by single-point analysis and interval mapping. ^a: Logarithm of odds; ^b: The phenotypic variance explained by the QTL; ^c: Additive effects, negative value means YJCWR carried alleles decreasing CBI trait values. ^d: Dominant effect