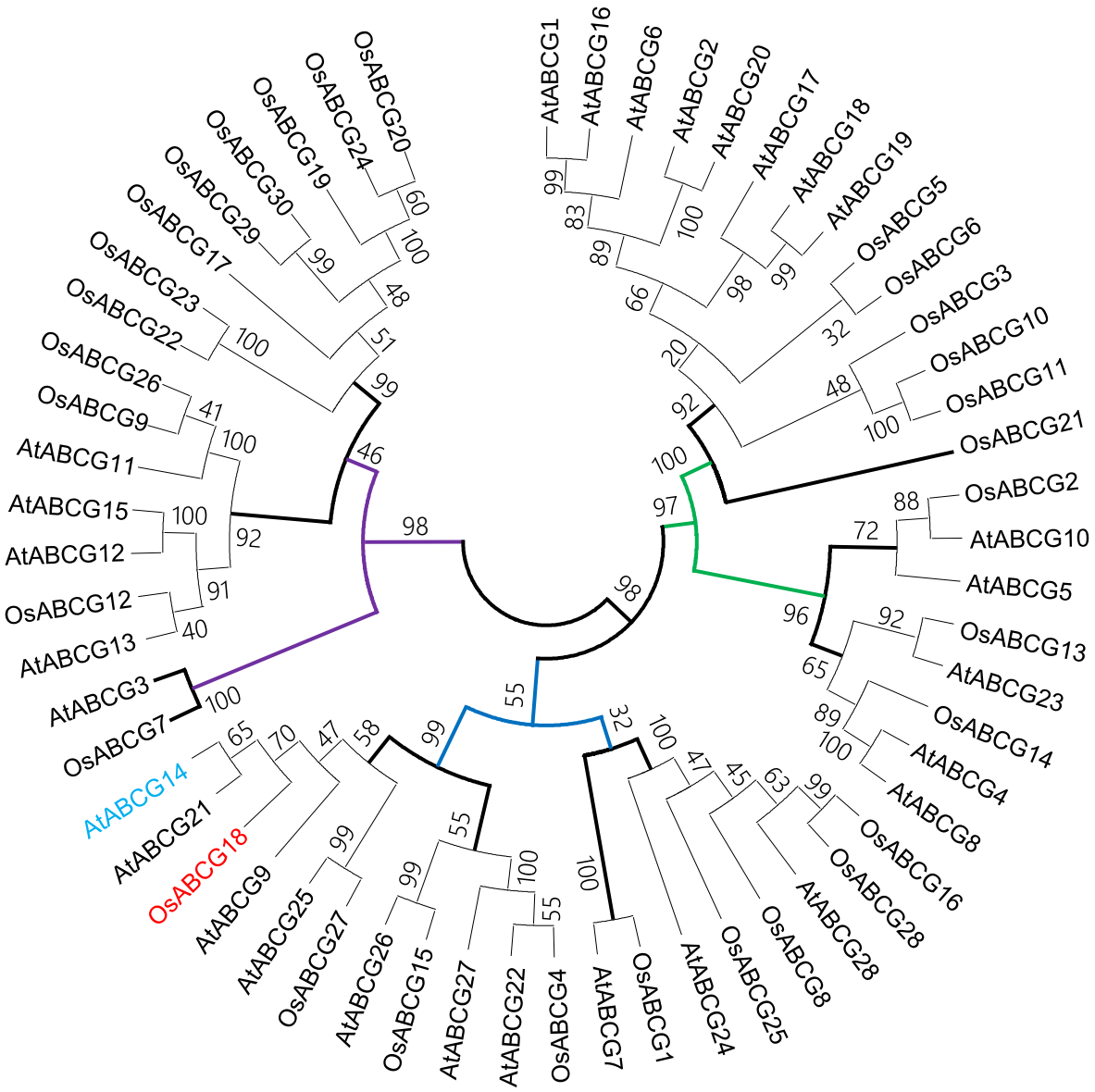


**Fig. S1 Phylogenetic relationship of the half-size ABC transporter subfamily G from rice and *Arabidopsis*.** The phylogenetic tree was constructed based on a complete protein sequence alignment of half-size ABCGs from *Arabidopsis* and rice with MEGA6 software using the neighbor-joining method. AtABCG14 and OsABCG18 are highlighted in blue and red, respectively.

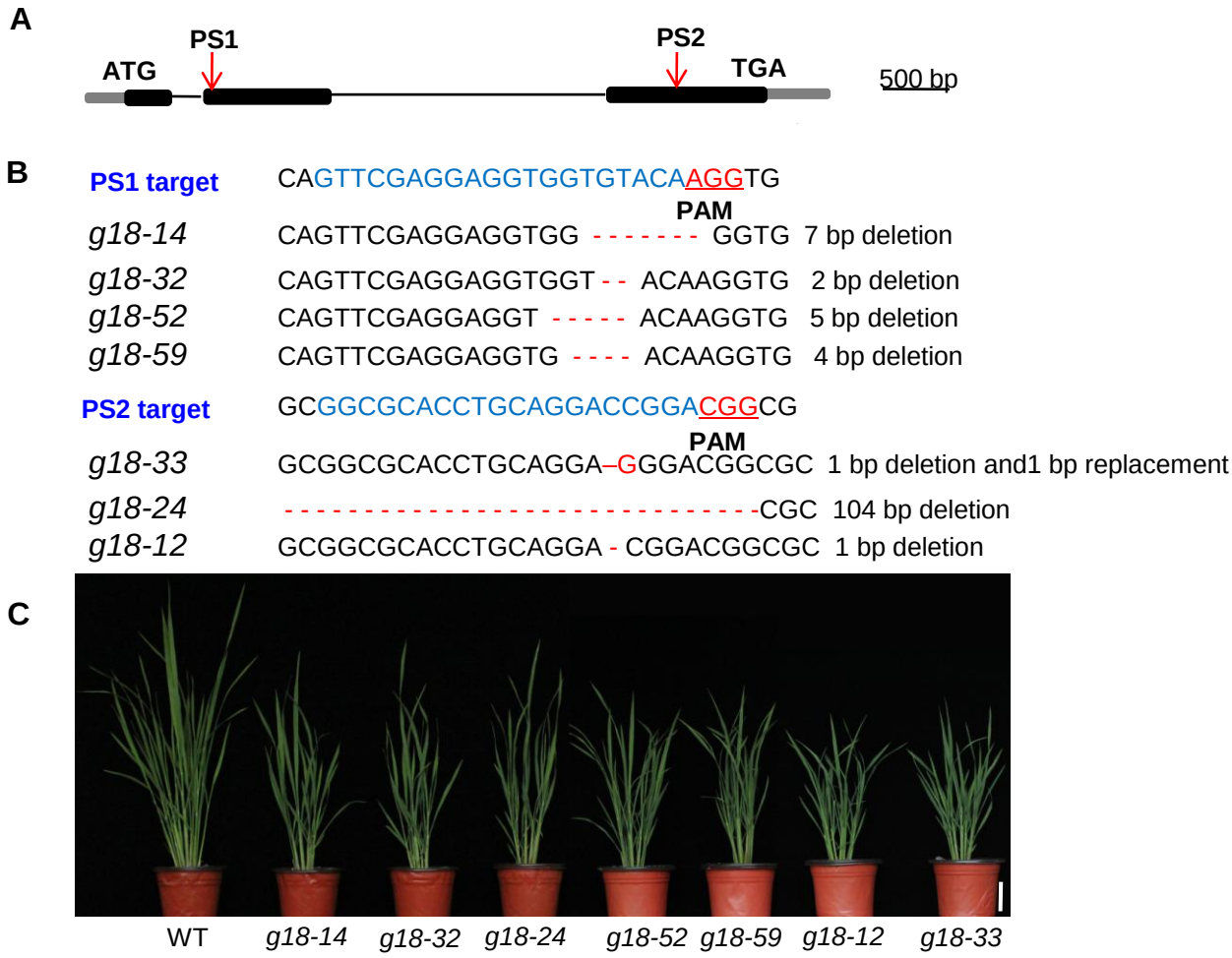


**Fig. S2 Loss-of-function mutants of *OsABCG18* generated by CRISPR/Cas9.**

(A) Schematic of the *OsABCG18* gene structure and the two target sites PS1 and PS2 for gene editing; the underlined red characters are PAM sites. (B) Detection of the targeted mutations (deletion or insertion) at the PS1 and PS2 sites in the *OsABCG18* locus based on DNA sequencing. (C) Morphological phenotypes of 55-DAG wild-type and seven independent *osabcg18* mutant rice plants in (A) and (B). The *g18-14*, *g18-32*, *g18-52* and *g18-59* mutant lines were generated by the first gRNA targeting a 305-324-bp site of the CDS close to the start codon; the *g18-33*, *g18-24* and *g18-12* mutant lines were generated by the second gRNA target in the trans-membrane domain (1598-1617 bp site of CDS). Scale bar, 10 cm.

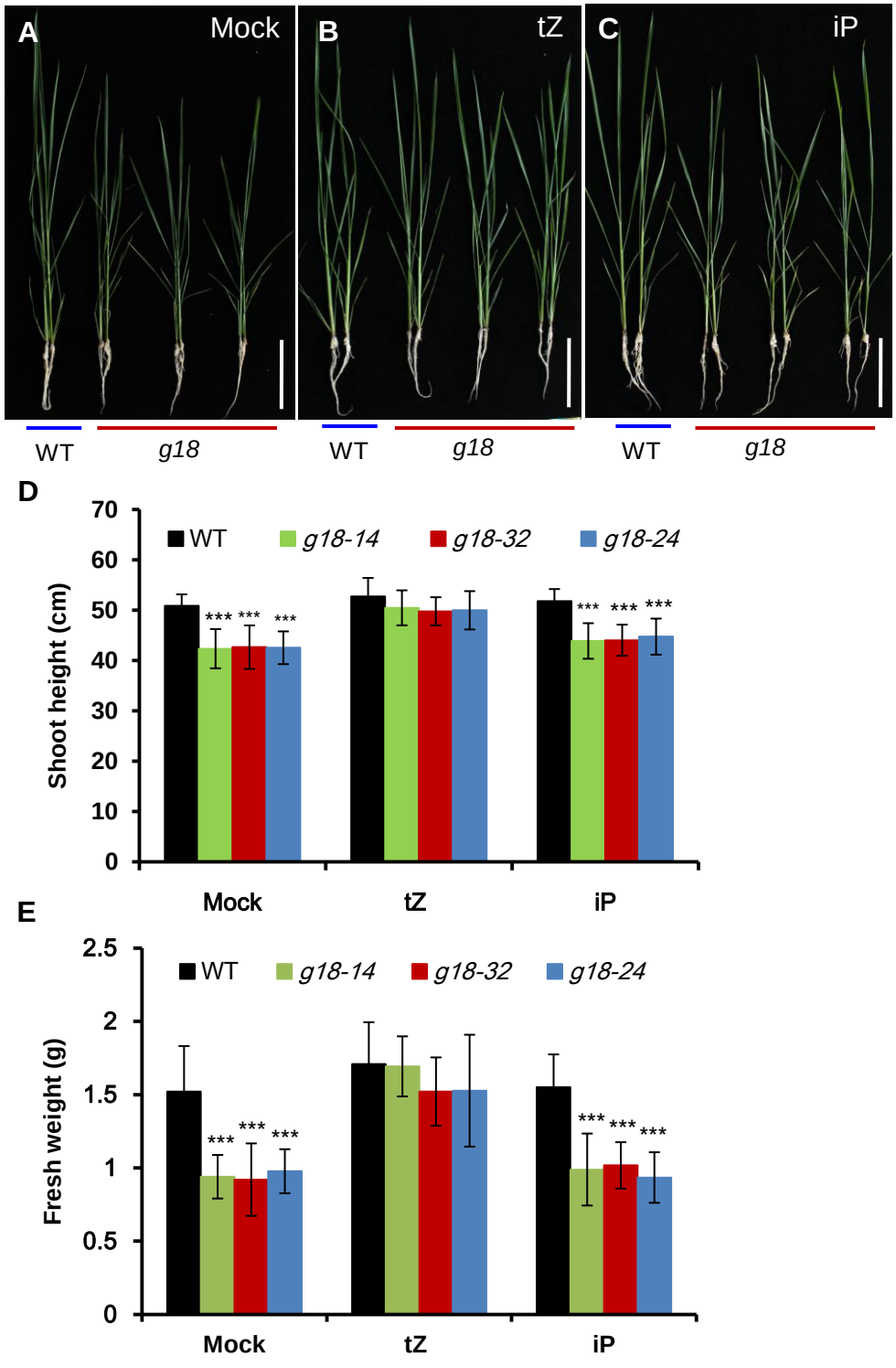


**Fig. S3 Complement of the growth defect of *osabcg18* mutant by *t*Z treatment.**

Five-week-old plants of wild type and *osabcg18* mutants treated with the mock (A), tZ (B) or iP (C) for 25 days. Quantification of plant height (d) and fresh weight (e) of wild type and *osabcg18* mutants . Data are means ± SD (n = 10). Scale bars, 10 cm; **and *** indicates $P < 0.01$ and $P < 0.001$ (Student's *t*-test).

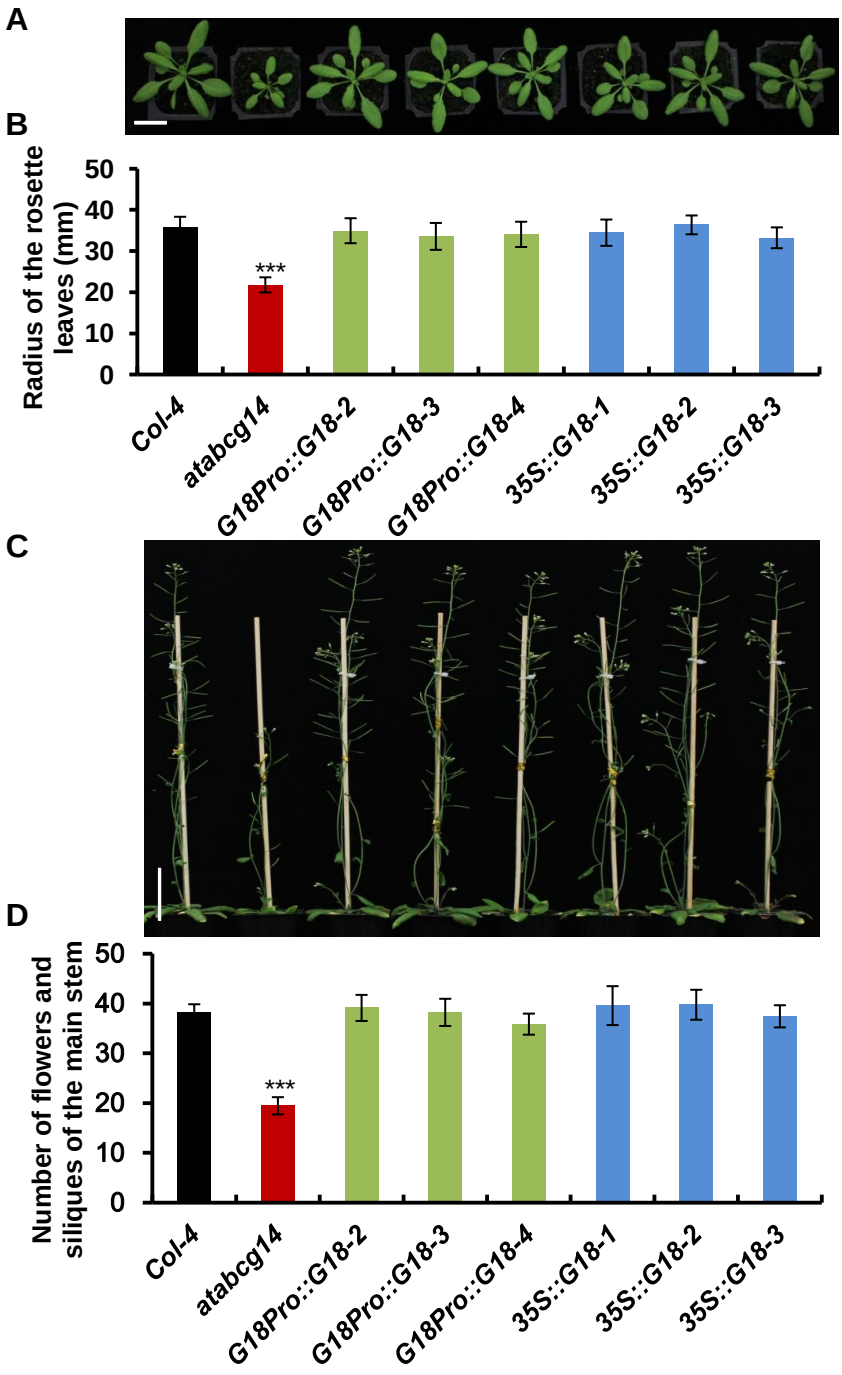


**Fig. S4 Expression of *OsABCG18* rescued the phenotype of the *atabcg14* mutant.**
(A) The 25-DAG plants of Col-4, *atabcg14* and *atabcg14* complemented by *OsABCG18* driven by the OsABCG18 promoter ($G18_{Pro}$) or the 35S promoter. The small rosette leaf phenotype of *atabcg14* was rescued to wild type by overexpression of *OsABCG18*. Scale bar, 2 cm. (B) The radius of the rosette leaves of the plants in (A). (C) The 40-DAG plants of Col-4, *atabcg14* and *atabcg14* mutants complemented by *OsABCG18* driven by the OsABCG18 promoter or the 35S promoter. The dwarf phenotype of *atabcg14* was rescued by overexpression of *OsABCG18*. Scale bar, 5 cm. (D) The numbers of siliques and flowers in the primary stem in (C). The numbers of siliques and flowers were significantly reduced in the *atabcg14*, and the phenotype was rescued to wild type by expression of *OsABCG18*. The data are means $\pm$ SD ($n \geq 10$), ***, $P < 0.001$ (Student's *t*-test).

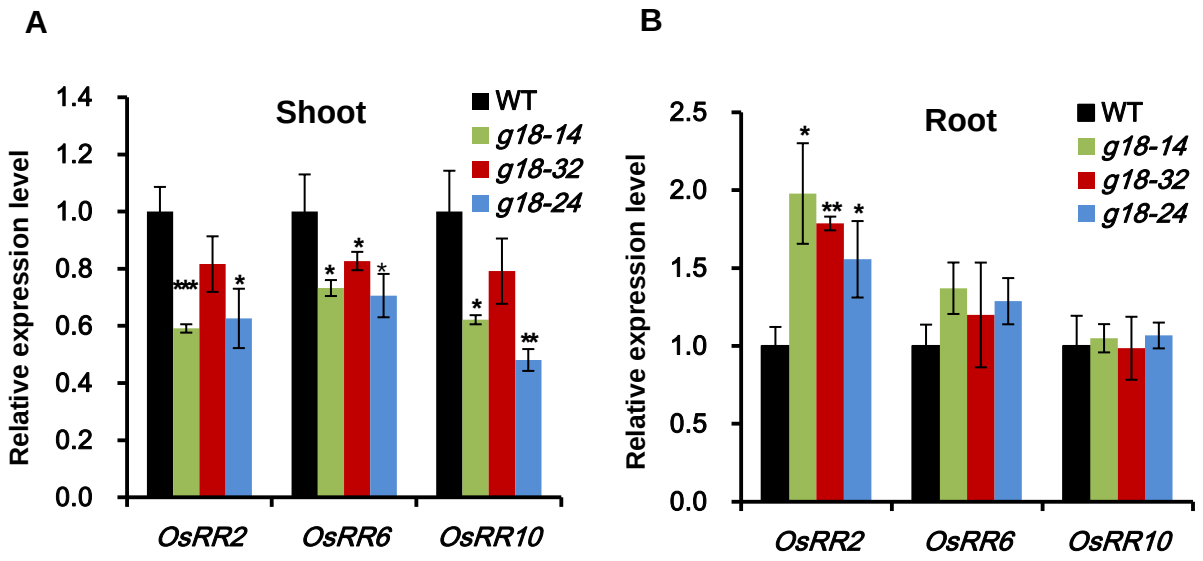


**Fig. S5 Transcriptional analysis of cytokinin-responsive genes in roots and shoots of wild type and *osabcg18* mutant lines.**

CK-responsive *OsRR2*, *OsRR6* and *OsRR10* gene expression levels were all reduced in shoots (A) but enhanced in roots (B) of the three *osabcg18* mutants lines compared with the same tissues in wild type. RNA was extracted from plants (Fig. 3E) grown in the field. Values are means ± SD (n = 3). *, $P < 0.05$,**, $P < 0.01$ and *** $P < 0.001$ (Student's *t*-test).

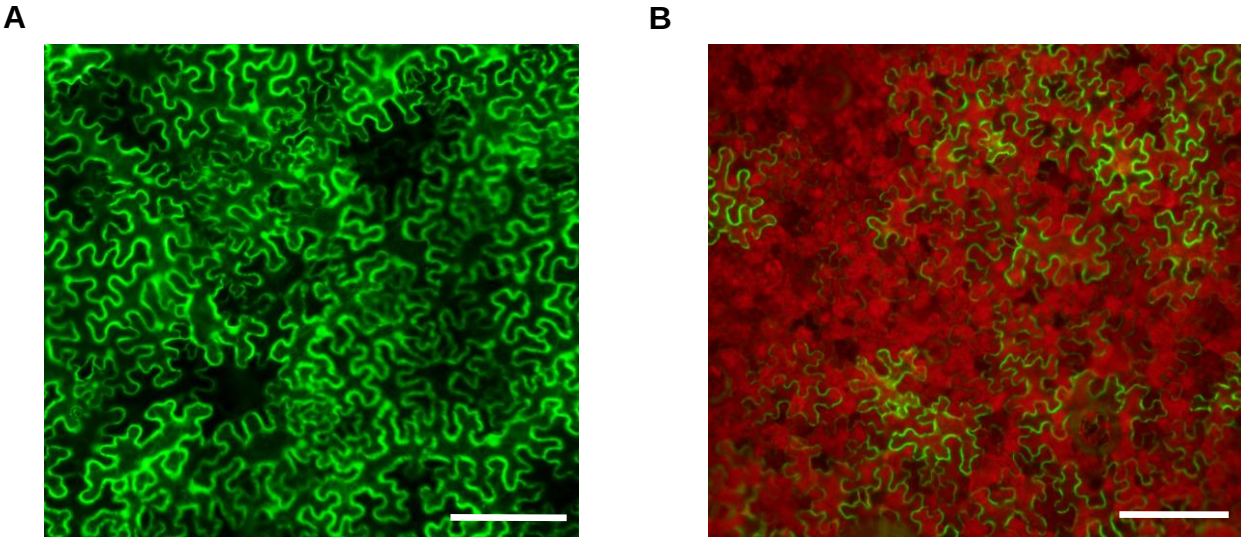


**Fig. S6 Transient expression of GFP-OsABCG18 in tobacco leaves.**

Transient expression of empty vector (A) and EGFP-ABCG18 (B) in tobacco leaves. Bar = 50 μm.

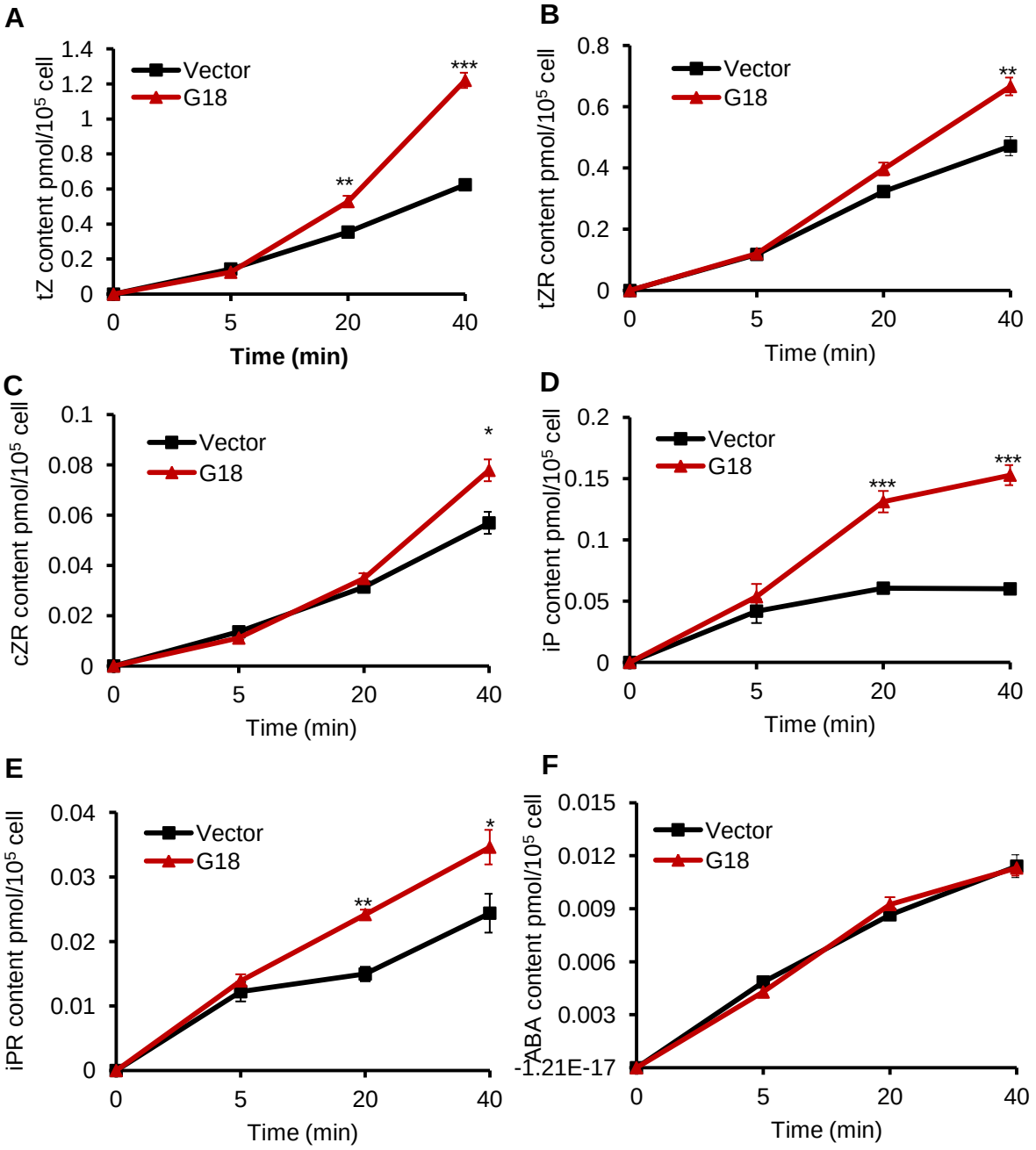


**Fig. S7 OsABCG18 mediated efflux transport of various cytokinins in tobacco protoplasts.**

(A), (B), (C), (D), (E) and (F) Quantification of exported cytokinins of tZ, tZR, DHZ, iP, iPR, cZR and ABA (negative control) from protoplast isolated from tobacco leaves transformed with OsABCG18 or empty vector at the time points of 0, 5, 20, 40 min. Data are means ± SE (n = 4). *, ** and *** indicate *P*-values of $P < 0.05$, $P < 0.01$ and $P < 0.001$ respectively, from Student's *t*-test.

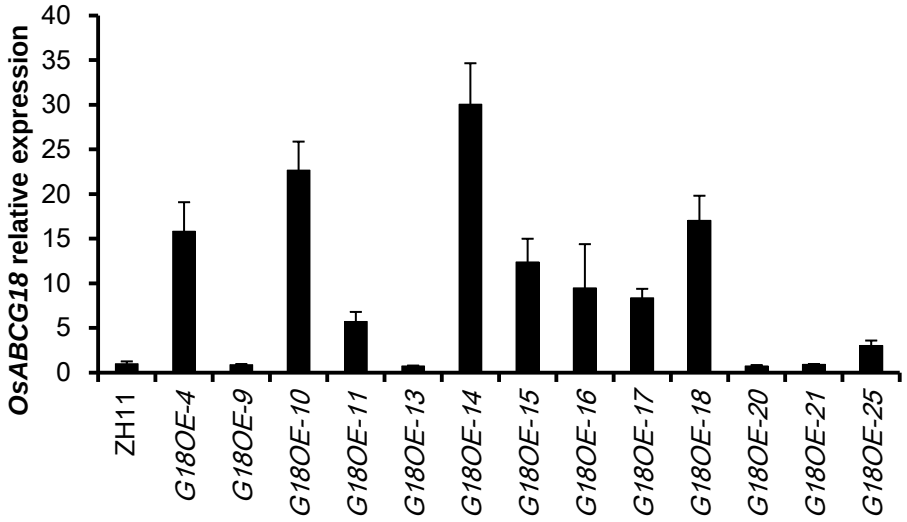


**Fig. S8 Expression of *OsABCG18* in *OsABCG18*$_{pro}$*::EGFP-OsABCG18* transgenic lines at the T2 generation.**

The 15-DAG seedlings were used for RNA extraction and qRT-PCR analysis. The ZH11 represents wild-type rice Zhonghua 11, G18OE represents *OsABCG18*$_{pro}$*::EGFP-OsABCG18* transgenic lines. The G18OE-10, G18OE-14 and G18OE-25 lines were chosen for further study.

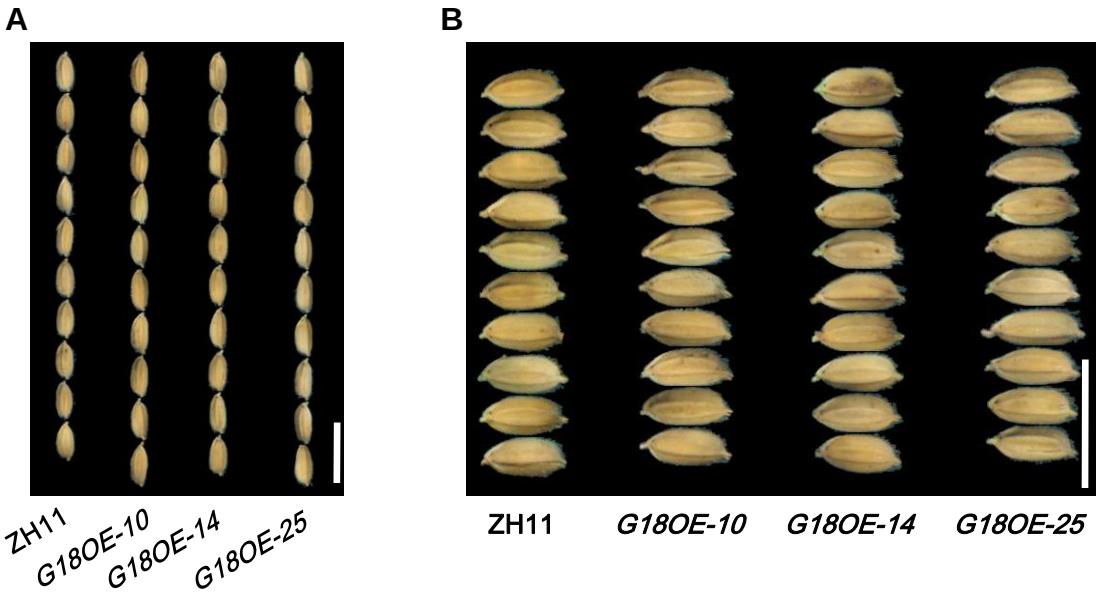


**Fig. S9 Grain size of *OsABCG18*$_{pro}$*::EGFP-OsABCG18* transgenic lines.**

The seeds used for the seed size assay are from the T3 generation. The seed length (A) and width (B) of the ZH11 and *OsABCG18*$_{pro}$*::EGFP-OsABCG18* lines G18OE-10, -14 and -25 are presented. Scale bars, 1 cm.

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