Characterization of a common wheat (Triticum aestivum L.)

TaSnRK2.7 gene involved in abiotic stress responses

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Supplementary materials

Fig. S1 Identification of *TaSnRK2.7* transformed *Arabidopsis* plants. (A) Determination of green fluorescence in roots of transgenic *Arabidopsis* plants. Assays were performed at the seedling stage with a laser-scanning confocal microscope. Images were taken in dark field for green fluorescence, and the root outline and combination are in bright field. (B) RT-PCR analysis of transgenic plants. M: 200-bp ladder; Lanes 1-9, p35S-*TaSnRK2.7-GFP*-NOS transformed plants; Lane 10, wild-type *Arabidopsis* (negative control); Lane 11, p35S-*GFP*-NOS transformed plant (negative control); Lane 12, p35S-*TaSnRK2.7-GFP*-NOS plasmid DNA (positive control). (C) Expression levels of *TaSnRK2.7* in transgenic *Arabidopsis* lines L1-L6. The lowest expression of *TaSnRK2.7* in L4 was regarded as standard.

Fig. S2 Morphological characterization of TaSnRK2.7 plants. (A) Comparison of seed germination and seedlings between TaSnRK2.7 transformants and controls grown on MS medium. (B) Phenotypes of mature transgenic lines and WT grown in soil (4 weeks). (C) Grain yields of TaSnRK2.7 and WT plants. The seeds of transgenic TaSnRK2.7 and WT plants cultured under well-watered conditions were harvested separately. The grain yield of each plant was measured after dehydration, and there were no significant differences. L1-L6, six individual TaSnRK2.7 transgenic lines; WT, wild type; GFP, GFP transgenic line. Values are mean \pm SE, n=10.

Fig. S1

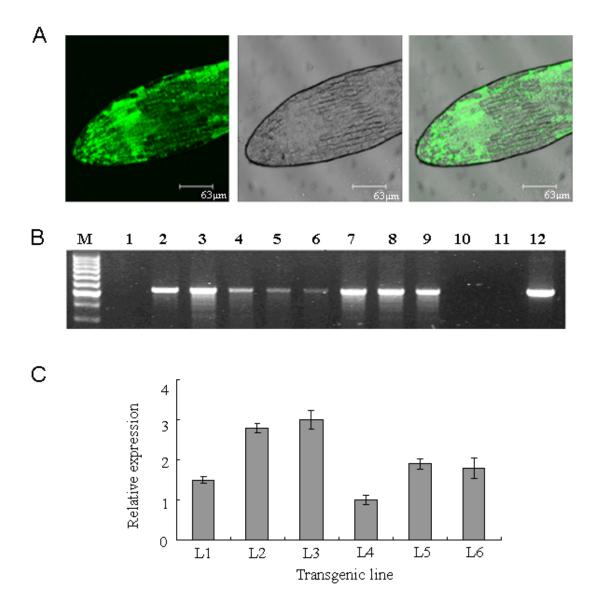


Fig. S2

