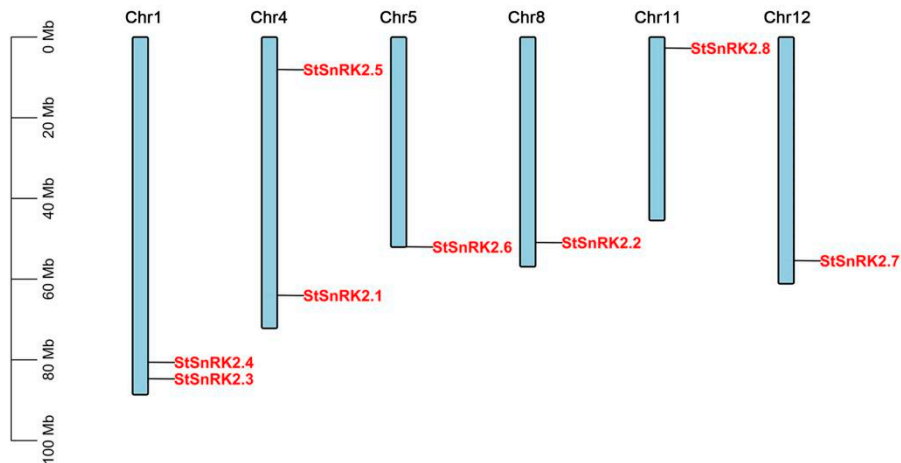
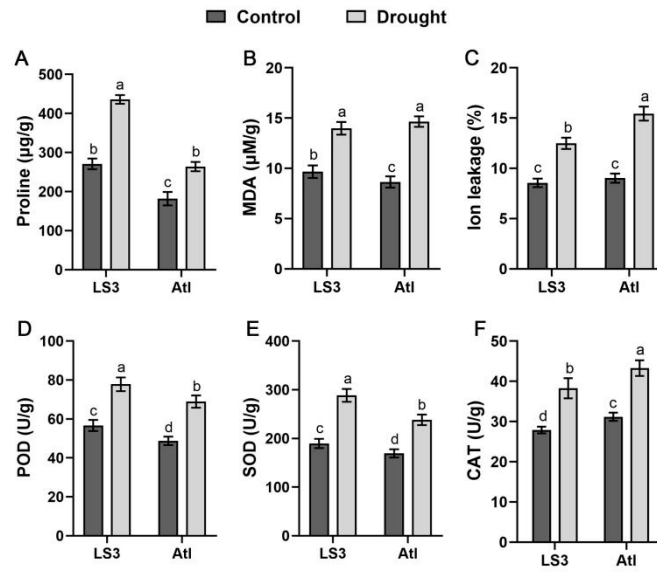


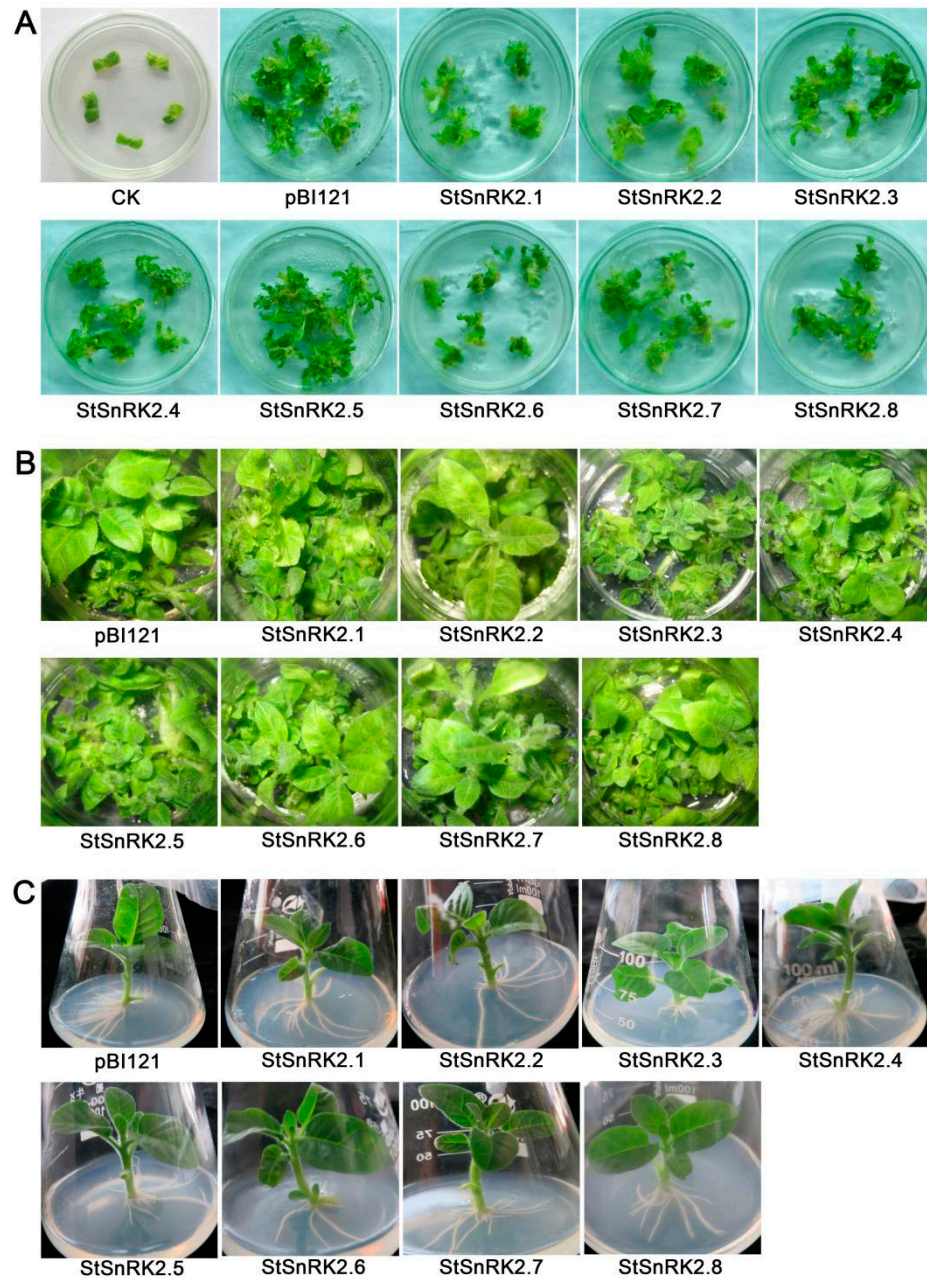
**Figure S1.** Phylogenetic relationships, conserved motifs and gene structure of the *StSnRK2* and *AtSnRK2* genes. (A) The phylogenetic tree was constructed based on the full-length sequences of SnRK2 proteins. (B) The motif compositions of *StSnRK2* and *AtSnRK2* proteins. The motifs, numbered 1-10, are displayed in different colored boxes. The protein length can be estimated using the scale at the bottom. (C) Exon-intron structures of *StSnRK2* and *AtSnRK2* genes. Green boxes indicate untranslated 5'- and 3'-regions; orange boxes indicate exons; and black lines indicate introns.



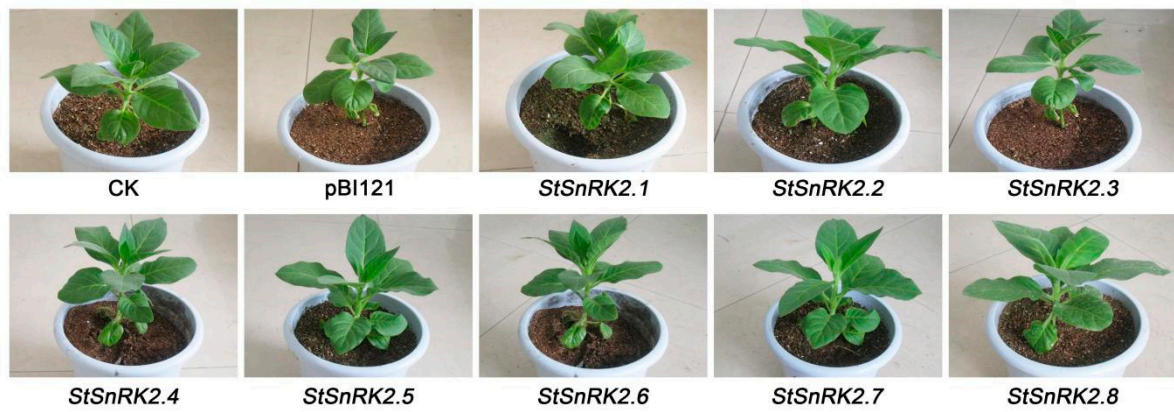
**Figure S2.** Schematic representations of the chromosomal distribution of the *StSnRK2* genes. The chromosome number is indicated to the left of each chromosome.



**Figure S3.** Determination of stress related physiological indexes in different drought-resistant potato varieties ('LS3', drought tolerance; 'Atl', drought sensitive) under water deficit condition. Data represent the means  $\pm$  SD of three replicates and different letters indicate significant difference at  $p < 0.05$ . A-F represents proline content, MDA content, ion leakage, POD activity, SOD activity, CAT activity, respectively.



**Figure S4** The screening process of *StSnRK2* transgenic tobacco. (A) Growth phenotype of *StSnRK2* transgenic callus on Kana screening medium. (B) Seedlings after differentiation of *SnRK2* transgenic callus. (C) Rooting of seedlings after differentiation of *SnRK2* transgenic callus.



**Figure S5** The growth phenotype of *StSnRK2* transgenic plants and control plants under normal conditions.