



**FDS**

**1**

**2**

**3**

**4**

**5**

**Phenotype**

**HT-V2**

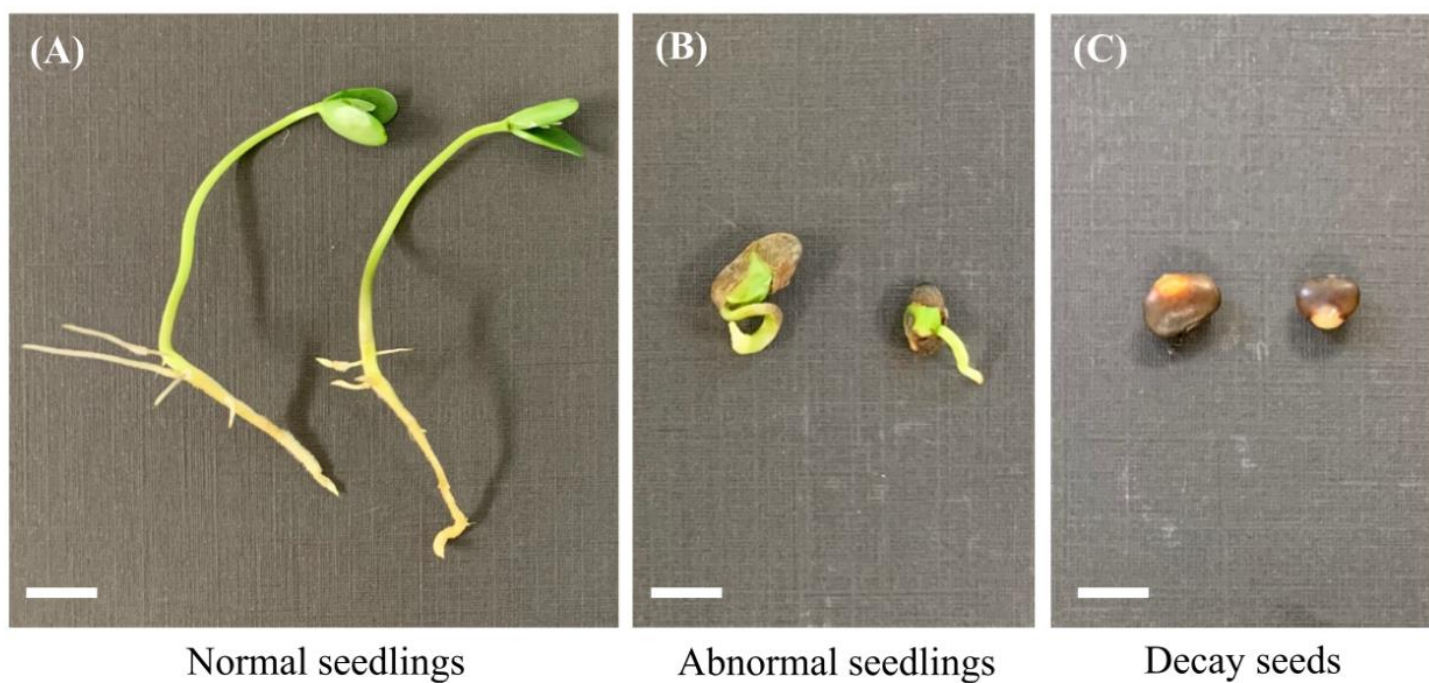
**T-V2**

**M-V2**

**S-V2**

**HS-V2**

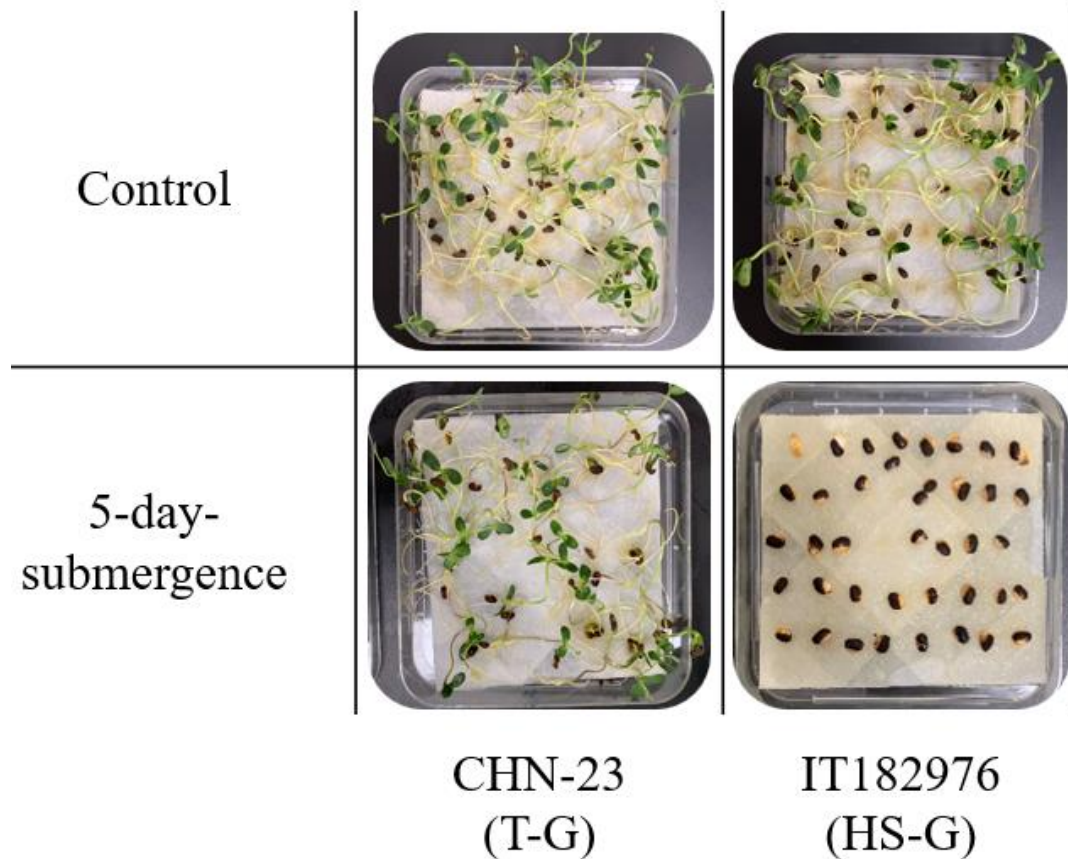
**Figure S1.** Phenotypic evaluation for foliar damage score of wild soybeans after submergence. Foliar damage score (FSD) was rated from 1 to 5. Plants were assigned into five tolerance level groups: highly tolerant (HT-V2), tolerant (T-V2), moderate (M-V2), sensitive (S-V2), and highly sensitive (HS-V2).



**Figure S2.** Different phenotypes of soybean seeds germinated under a 5-day-submergence condition. (A) Normal seedlings, (B) Abnormal seedlings, and (C) Decay seeds. White bars indicate 1 cm.

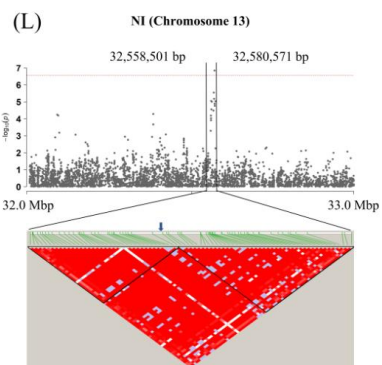
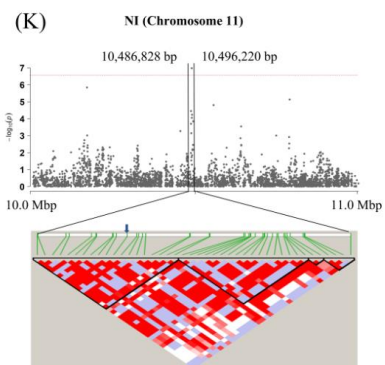
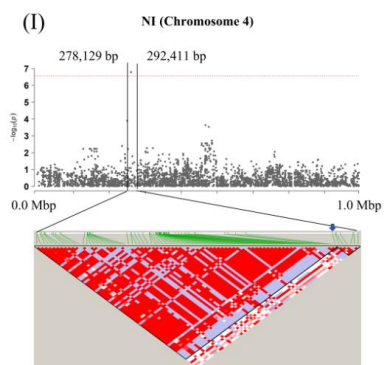
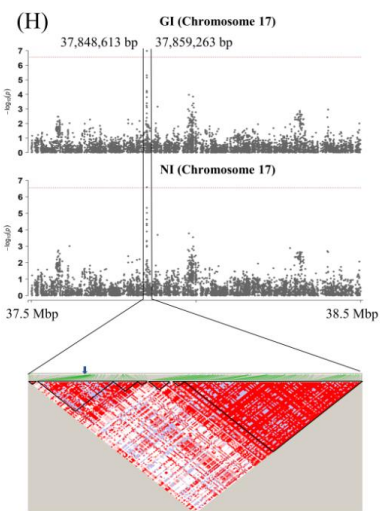
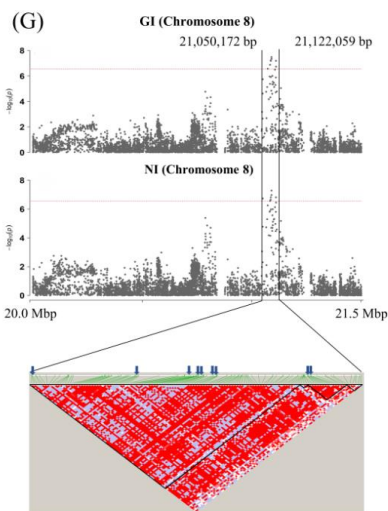
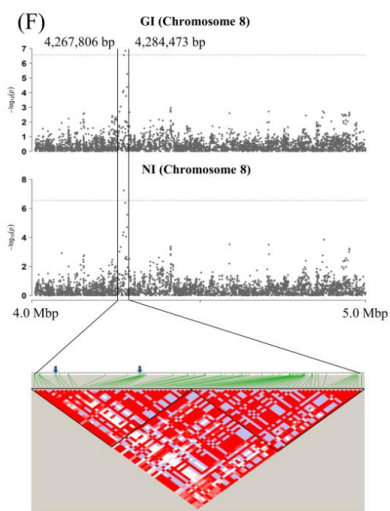
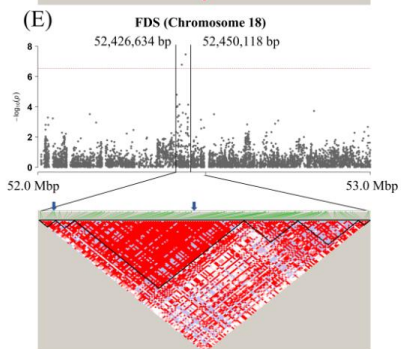
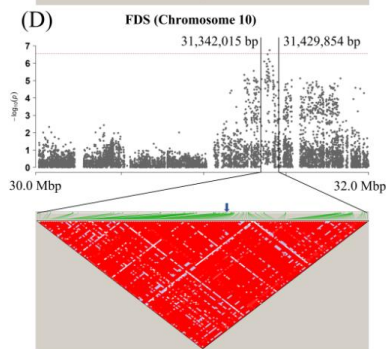
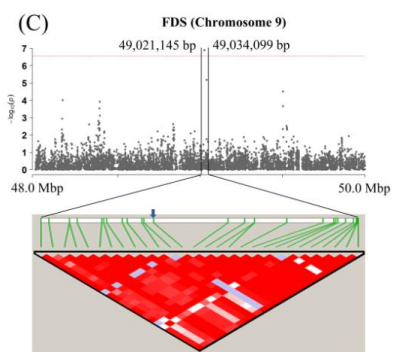
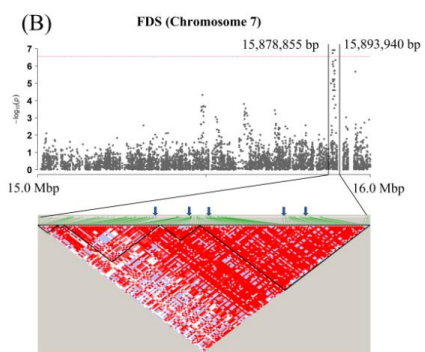
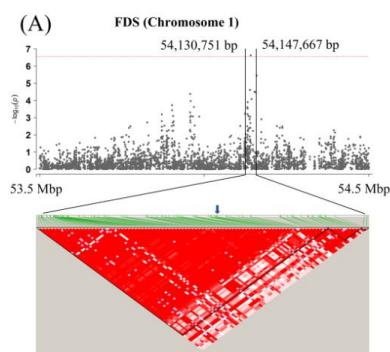


**Figure S3.** Phenotype of selected wild soybean plants under a 5-day-submergence following 2 days of drainage at the early vegetative stage. YWS294 and YWS1022 were highly tolerant (HT-V2), CHN23 was tolerant (T-V2), CHN25 was moderate (M-V2), YWS525 and IT182976 were highly sensitive (HS-V2).



**Figure S4.** Phenotype of accessions with high and low germination and normal seedling index after submergence. CHN23 was tolerant (T-G), and IT182976 was highly sensitive (HS-G).





**Figure S5.** Manhattan plot and linkage disequilibrium (LD) heatmap surrounding the significant SNPs. (A) Manhattan plot for foliar damage score (FDS) on chromosome 1. (B) Manhattan plot for FDS on chromosome 7. (C) Manhattan plot for FDS on chromosome 9. (D) Manhattan plot for FDS on chromosome 10. (E) Manhattan plot for FDS on chromosome 18. (F, G) Manhattan plot for germination index (GI) and normal seedling index (NI) on chromosome 8. (H) Manhattan plot for GI and NI on chromosome 17. (I) Manhattan plot for NI on chromosome 4. (K) Manhattan plot for NI on chromosome 11. (L) Manhattan plot for NI on chromosome 13. For the Manhattan plot, the red line indicates the Bonferroni significant threshold. For the LD heat map, the blue arrows represent the position of significant SNP in the LD block. The regions indicated by solid lines were used to determine putative candidate genes.