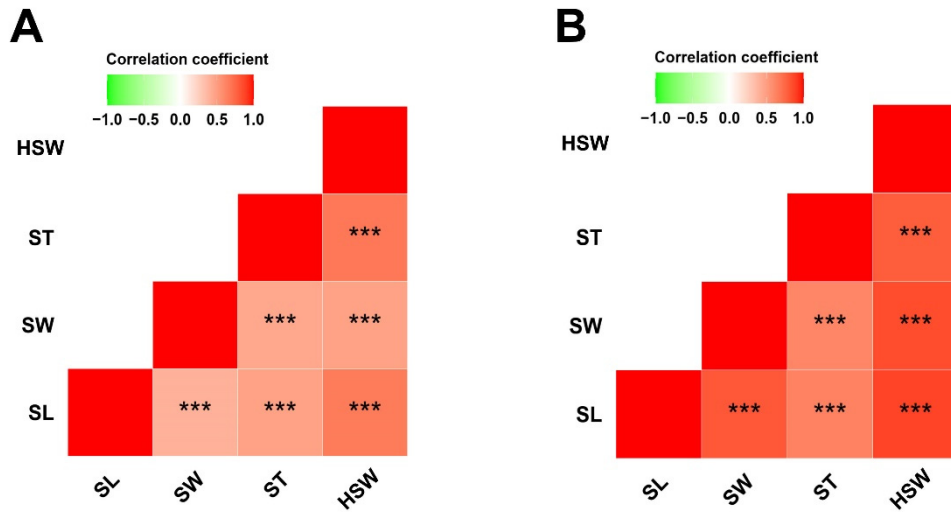
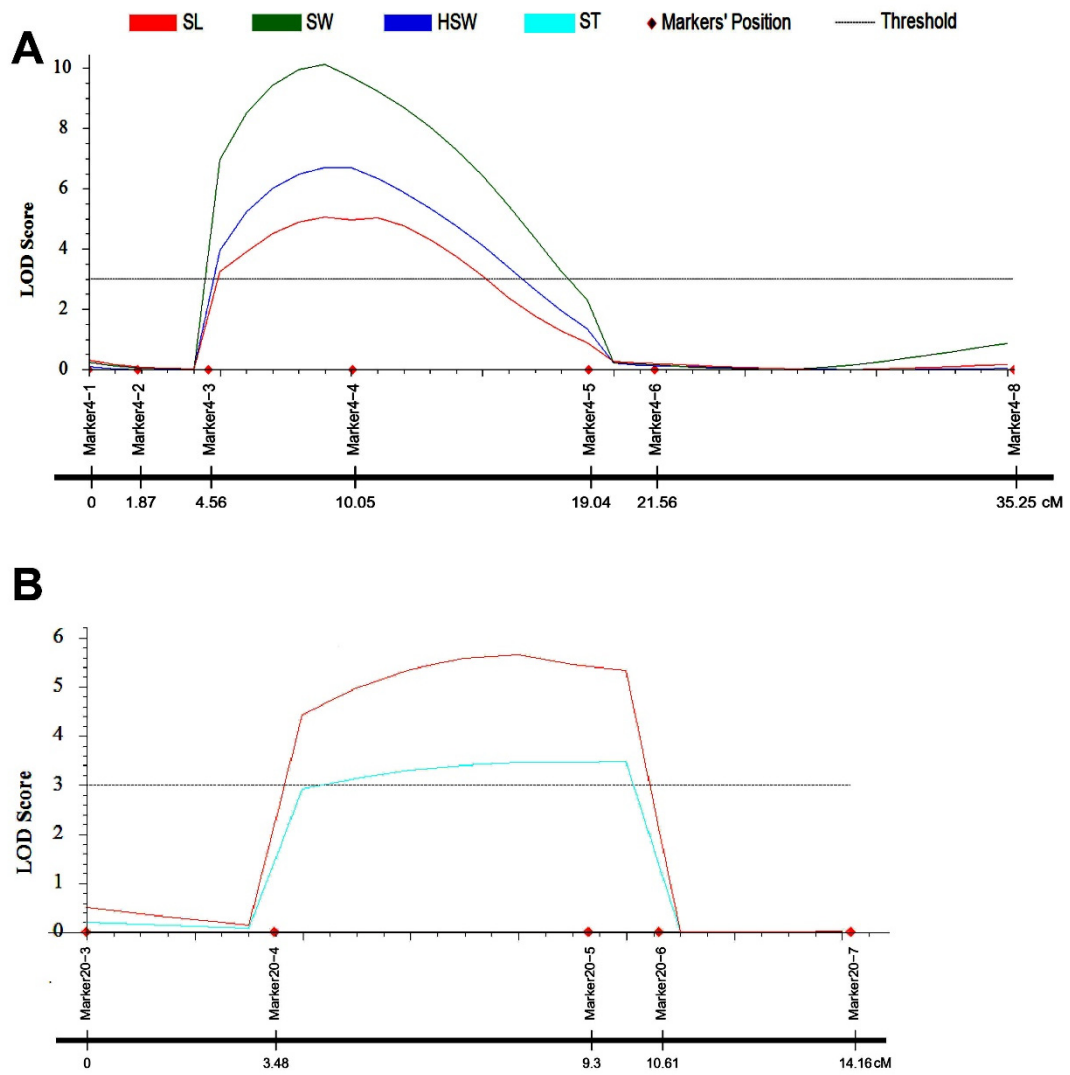


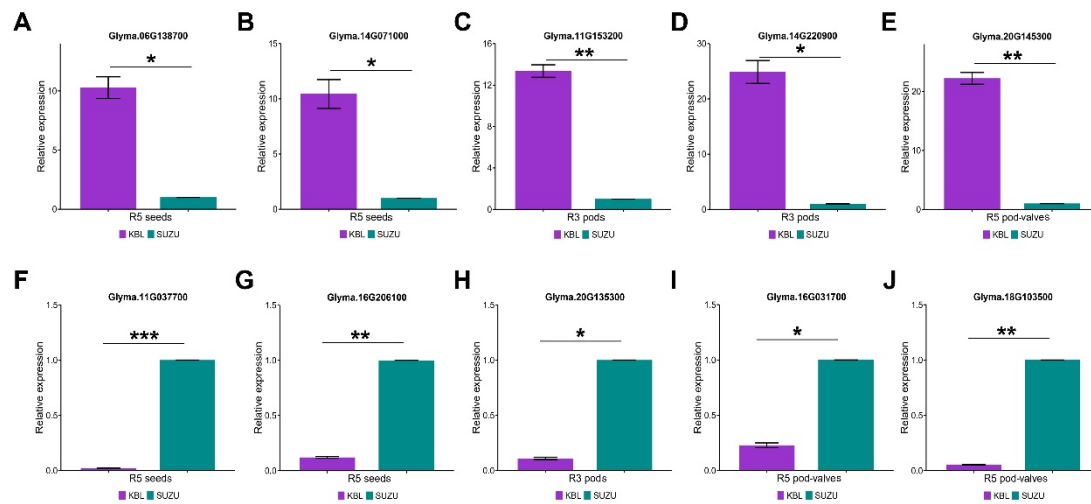
**Figure S1.** Comparison of seed size and weight traits between parental varieties. The boxplot and statistical significance between KBL and SUZU for (A) seed length, (B) seed width, (C) seed thickness, and (D) hundred-seed weight in the F<sub>4</sub> population. The boxplot and statistical significance between KBL and SUZU for (E) seed length, (F) seed width, (G) seed thickness, and (H) hundred-seed weight in the F<sub>5</sub> population. Orange boxes represent KBL and blue boxes represent SUZU. Student's *t*-test, \*\*\*  $p < 0.001$ .



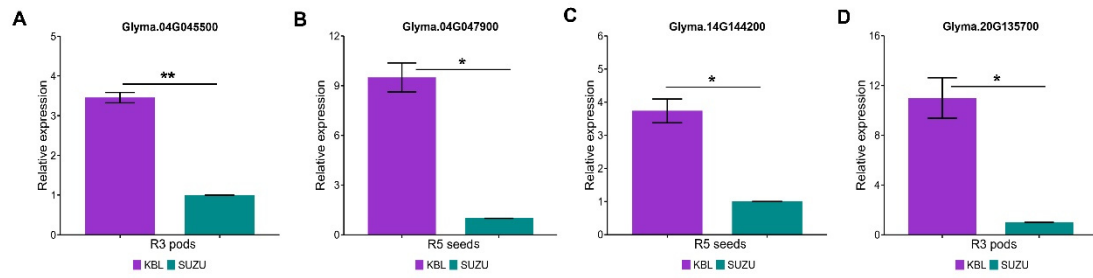
**Figure S2.** The correlation among seed length, seed width, seed thickness, and hundred-seed weight in the  $F_4$  and  $F_5$  populations. **(A)** Correlation among the four traits in the  $F_4$  population. **(B)** Correlation among the four traits in the  $F_5$  population. The Pearson correlation coefficients were shown in different colour. \*\*\*  $p < 0.001$ .



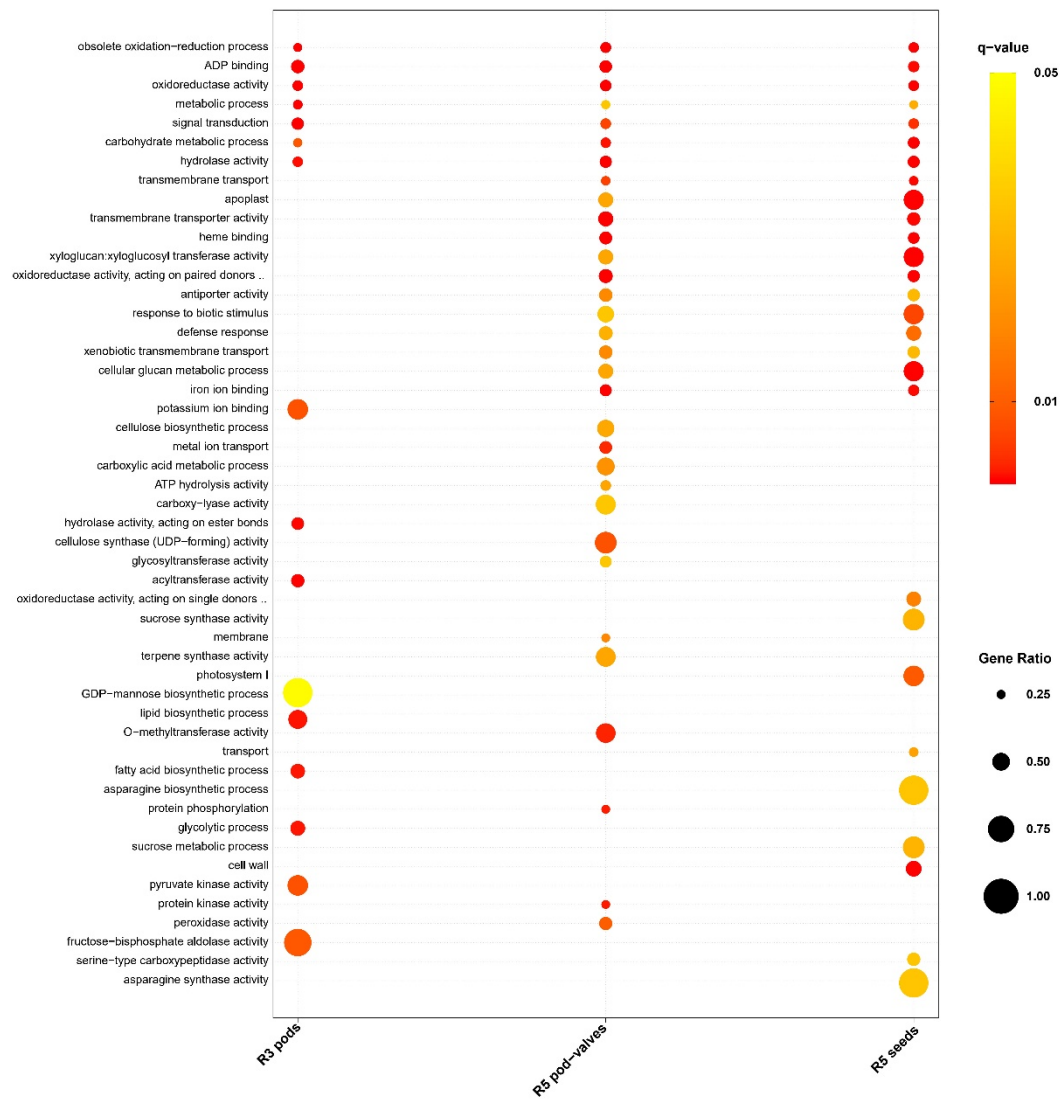
**Figure S3.** Linkage mapping of the pleiotropic *qSS4-1* and *qSS20-1* loci in  $F_4$  population. (A) QTL mapping of *qSS4-1* in the  $F_4$  population, with red curve representing seed length, bottle-green curve representing seed width, and blue curve representing hundred-seed weight. (B) QTL mapping of *qSS20-1* in the  $F_4$  population. The red and cyan curves represent seed length and seed thickness, respectively. The black dashed line denotes the LOD threshold (LOD = 3).



**Figure S4.** RT-qPCR validation of ten DEGs (A–J). Purple represents KBL, and dark-green represents SUZU. Using the SUZU as the control, the relative expression levels were calculated using the  $2^{-\Delta\Delta C_t}$  method, each sample was subjected to three biological replicates, error bars represent the standard error. Student's *t*-test, \*  $p < 0.05$ , \*\*  $p < 0.01$ , \*\*\*  $p < 0.001$ .



**Figure S5.** RT-qPCR validation of differentially expressed candidate genes in *qSS4-1*, *qSW14-1*, and *qSS20-1* (A–D). Purple represents KBL, and dark-green represents SUZU. Using the SUZU as the control, the relative expression levels were calculated using the  $2^{-\Delta\Delta C_t}$  method, each sample was subjected to three biological replicates, error bars represent the standard error. Student's *t*-test, \*  $p < 0.05$ , \*\*  $p < 0.01$ .



**Figure S6.** GO enrichment analysis of DEGs between parental varieties in three tissues. Only the significantly over-represented GO terms are shown (adjusted  $p$ -value < 0.05). The dot size and color correspond to proportions of DEGs and the  $q$ -values.