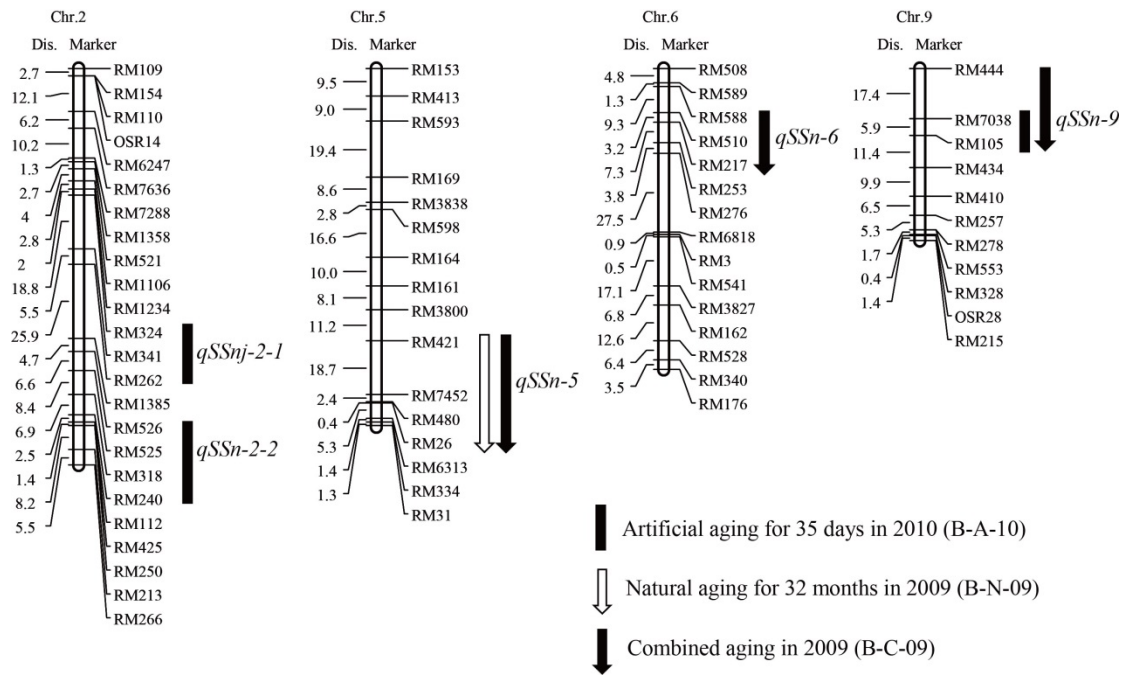


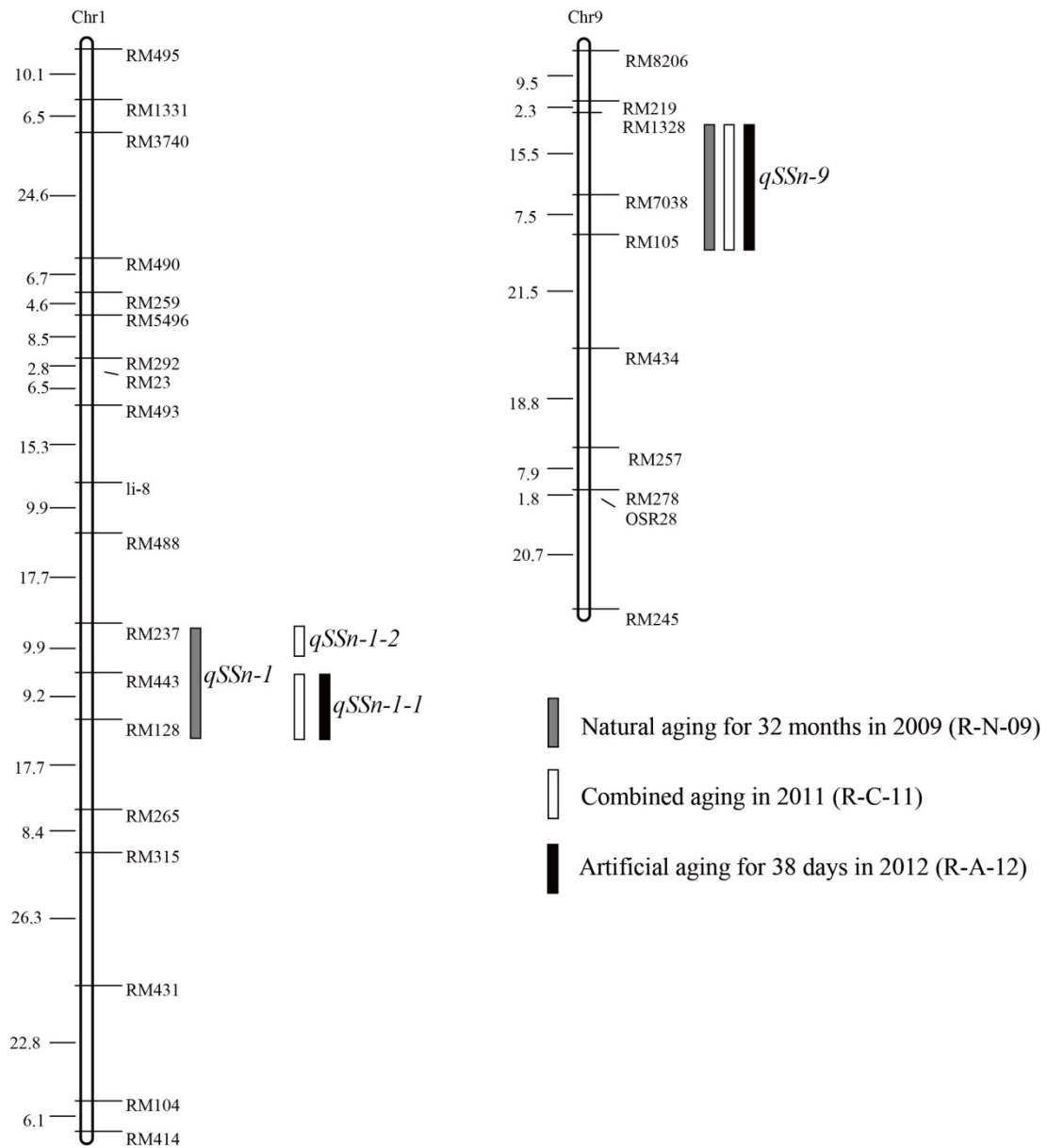
**Supplemental Fig. 1.** Graphical genotype of the near-isogenic line (NIL)

White squares indicate Nanjing35 alleles and gray squares indicate N22 alleles.

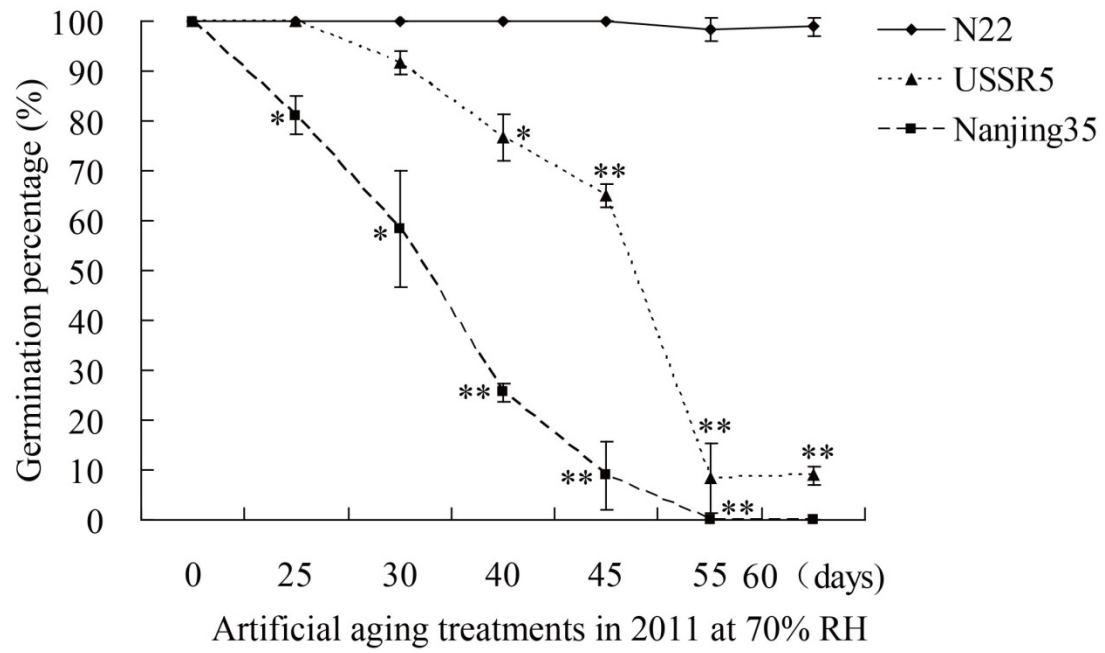
Nanjing35 was used as the recurrent parent



**Supplemental Fig. 2.** Chromosomal locations of QTL controlling seed storability in Nanjing35/N22//Nanjing35 BILs after aging treatments

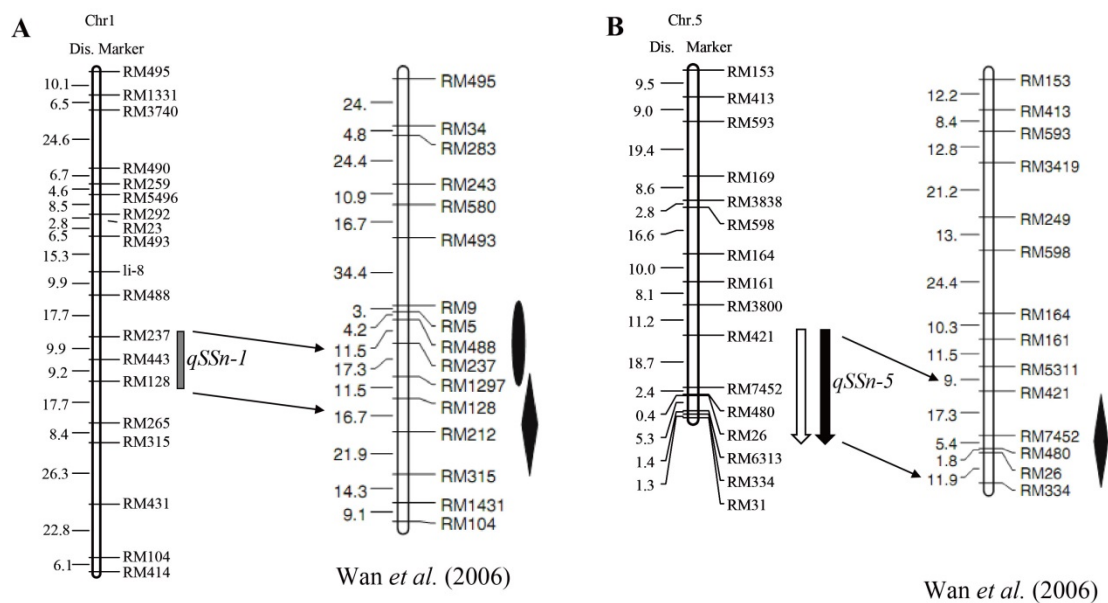


**Supplemental Fig. 3.** Chromosomal locations of QTL controlling seed storability in USSR5/N22 RILs after aging treatments



**Supplemental Fig. 4.** Response of parental accessions Nanjing35, USSR5, and N22 to artificial aging treatment for different days in 2011

Solid, short broken and long broken lines indicate GPs for N22, USSR5, and Nanjing35, respectively. Error bars indicate the standard deviations. \* and \*\* mean significant at the 0.05 and 0.01 probability level, respectively



**Supplemental Fig. 5.** Comparison between QTLs for seed storability and seed dormancy

A and B indicates Chromosome 1 and Chromosome 5, respectively

Left: QTLs for seed storability (*qSSn-1* and *qSSn-5*) detected in present study;

Right: QTLs of seed dormancy (*qSdn-1* and *qSdn-5*) reported by Wan *et al.* (2006)

Shaded rectangles indicate QTL detected in USSR5/N22 RILs after natural aging treatment; white and black arrows indicate QTL identified in Nanjing35/N22//Nanjing35 BILs after natural aging and combined aging treatments, respectively; ellipses represent QTL found in an BC<sub>1</sub> population derived from the Nanjing35/N22//Nanjing35, and diamonds represent QTL detected in the USSR5/N22 F<sub>2</sub> and USSR5/N22/USSR5 populations