



Homozygous DNA segment from Teqing      Phenotype similar to Teqing  
 Homozygous DNA segment from YIL19      Phenotype similar to YIL19  
 Interval in chromosome where crossover took place

**Figure S2.** The genotype and phenotype of segregating population of *GN2* Progeny testing of homozygous recombinant flanking the locus of *GN2* between RM5300 and RM6312 with F<sub>2</sub> plants. The number of recombinants between adjacent markers was indicated under the linkage map. On the right were the phenotypic variances of each group from the control of Teqing and YIL19 for grain number. The black bar indicated the phenotype was similar to that of Teqing, while the white bar represented the similar phenotype as YIL19. At least ten plants from each homozygous recombinant were individual harvested and evaluated. A t-test was carried out during the comparison among the recombinant families and their parents.

Fine mapping of *GN2*. The 20 recombinants between markers R1 and R2 were redivided into six groups according to their genotype. The genotype condition between R1 and R2 were shown on the left. The open bar showed a part of the PAC clone AP005303. To the right were the phenotypic variances of each group from the control of Teqing and YIL19 for grain number of main panicle. The black bar indicated the phenotype was similar to that of Teqing, while the white bar represents the similar phenotype as YIL19. The phenotype evaluation and data analysis was the same as progeny testing.