



**Figure S1 Sequencing coverage and SNP distribution.** (A) Sequencing coverage of 3,756 fully genotyped rice F<sub>2</sub> individuals. (B) Distribution of 1,300,156 SNPs identified from parental genomes (grey) and 404,643 high quality SNPs identified from 3,756 F<sub>2</sub> individuals by using GBS method (cyan). The SNP density was calculated with a window size of 50 kb. The red cross on each chromosome indicates the centromere.