



Figure S2 Modified sliding window approach for genotype calling, recombination breakpoint determination and bin-map construction. (A) The stacked diamonds represent SNPs along the hypothetical chromosomal region. A sliding window covering 19 SNP loci moves from left to right one SNP at a time. (B) Genotype calling and recombination breakpoint determination. The highest expected genotype probability is calculated using the reads number ratio that estimated between Minghui 63 and Zhenshan 97. The recombination breakpoints are determined by extending the homozygous blocks into the heterozygous blocks. (C) The recombination bin-map of 3,756 rice F_2 individuals sorts against the physical position of Minghui 63 genome.