Supplementary figures, tables and software:

**Supplementary Figure 1**  Three sources of sequence errors contributing to SNP errors.

**Supplementary Figure 2**  Comparison between sequencing and PCR-based mapping resolution.

**Supplementary Figure 3**  Plant height QTL detected on chromosome 1 when using different window sizes.

**Supplementary Table 1**  Bin map of the 150 rice RILs.

**Supplementary Table 2**  Primer sequences of PCR markers in Figure 5.

**Supplementary Source Code**  High-throughput genotyping software for short reads

Additional online information:

Pseudomolecules harboring SNPs identified between *indica* cv. 9311 and *japonica* cv. Nipponbare are posted at our lab website: http://www.ncgr.ac.cn/english/edatabase.htm.
Supplementary Figure 1 Three sources of sequence errors contributing to SNP errors. (a) RIL sequence errors occurred in the three-base indexes. (b) RIL sequence errors occurred in 33-mers. (c) Sequence errors in the genome sequences of the mapping parents.
Supplementary Figure 2 Comparison between sequencing and PCR-based mapping resolution.  (a) Resolution of recombination breakpoints in a randomly selected region of chromosome 1 of RIL #76.  The left breakpoint is mapped 19.9kb between SNPs with physical positions at 4978982 and 4998889 bp, and 0.8Mb between PCR markers with physical positions around 4635793 and 5424755 bp.  The right breakpoint is mapped 45.5 kb between SNPs with physical positions at 10925442 and 10970967 bp, and 1.7 Mb between the PCR markers with physical positions around 9390352 and 11116800 bp.  (b) Two randomly selected examples showing detected double crossovers by sequencing-based method but not by PCR-based mapping.  Left: a region on chromosome 2 of RIL #38; Right: a region on chromosome 5 of RIL #10. Names, primer sequences, and physical locations of the PCR markers are given in Supplementary table 2.  Red, indica genotype; Blue, japonica genotype.
Supplementary Figure 3 Plant height QTL detected on chromosome 1 when using different window sizes. Tested window sizes in the number of SNPs include: (a) 7. (b) 11. (c) 15. (d) 19. (e) 23.