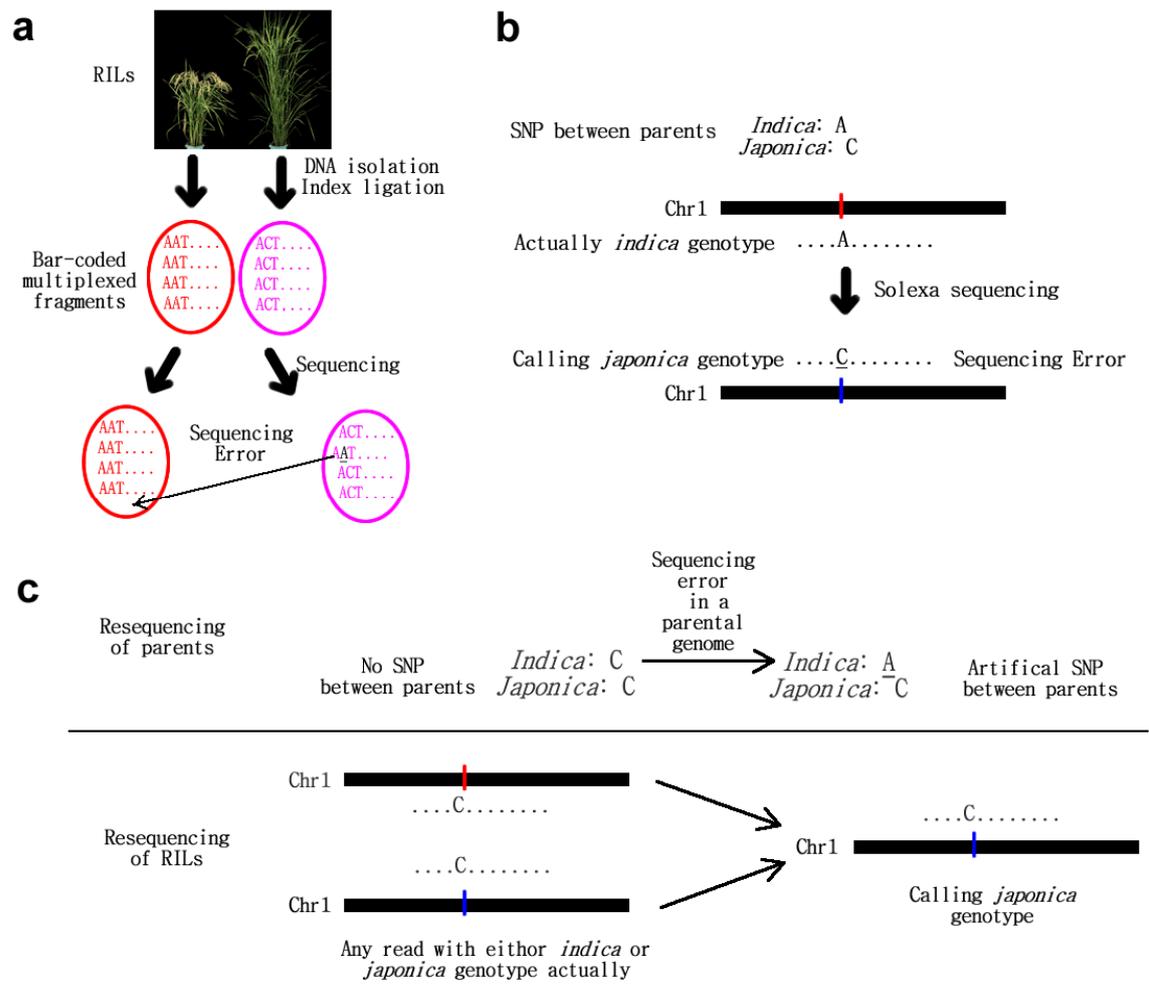Supplementary figures, tables and software:
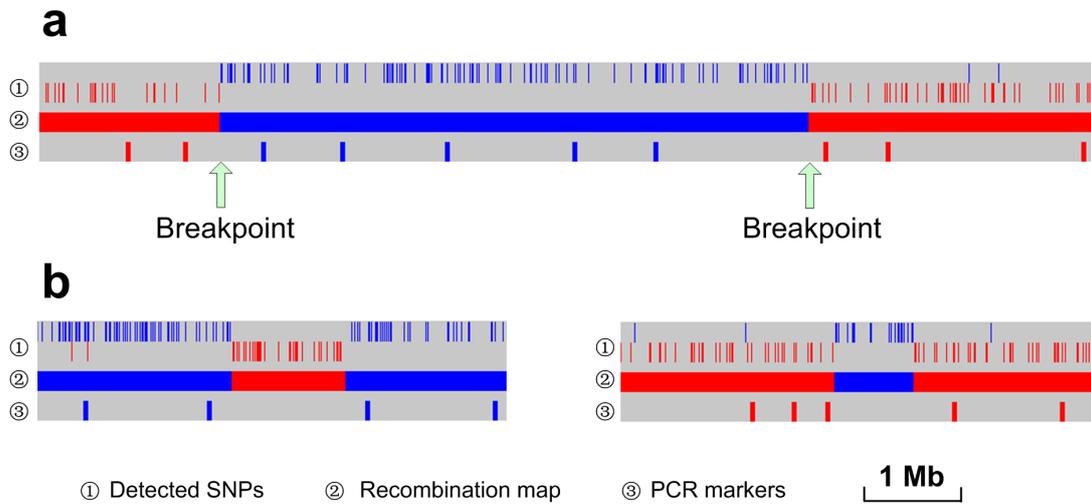

Supplementary Figure 1   Three sources of sequence errors contributing to
SNP errors.

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.

a

RILs

DNA isolation
Index ligation

Bar-coded
multiplexed
fragments

AAT....
AAT....
AAT....
AAT....

ACT....
ACT....
ACT....
ACT....

Sequencing

AAT....
AAT....
AAT....
AAT...

Sequencing
Error

ACT....
AAT....
ACT....
ACT....

b

SNP between parents   *Indica*: A
                         Japonica: C

Chr1

Actually *indica* genotype   ....A........

Solexa sequencing

Calling *japonica* genotype ....C........   Sequencing Error

Chr1

c

Resequencing
of parents

No SNP
between parents

Indica: C
Japonica: C

Sequencing
error
in a
parental
genome

Indica: A
Japonica: C

Artifical SNP
between parents

Chr1

....C........

Resequencing
of RILs

....C........

Chr1

Chr1

....C........

Calling *japonica*
genotype

Any read with eithor *indica* or
japonica genotype actually

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.

a

Breakpoint   Breakpoint

b

① Detected SNPs   ② Recombination map   ③ PCR markers   **1 Mb**

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.
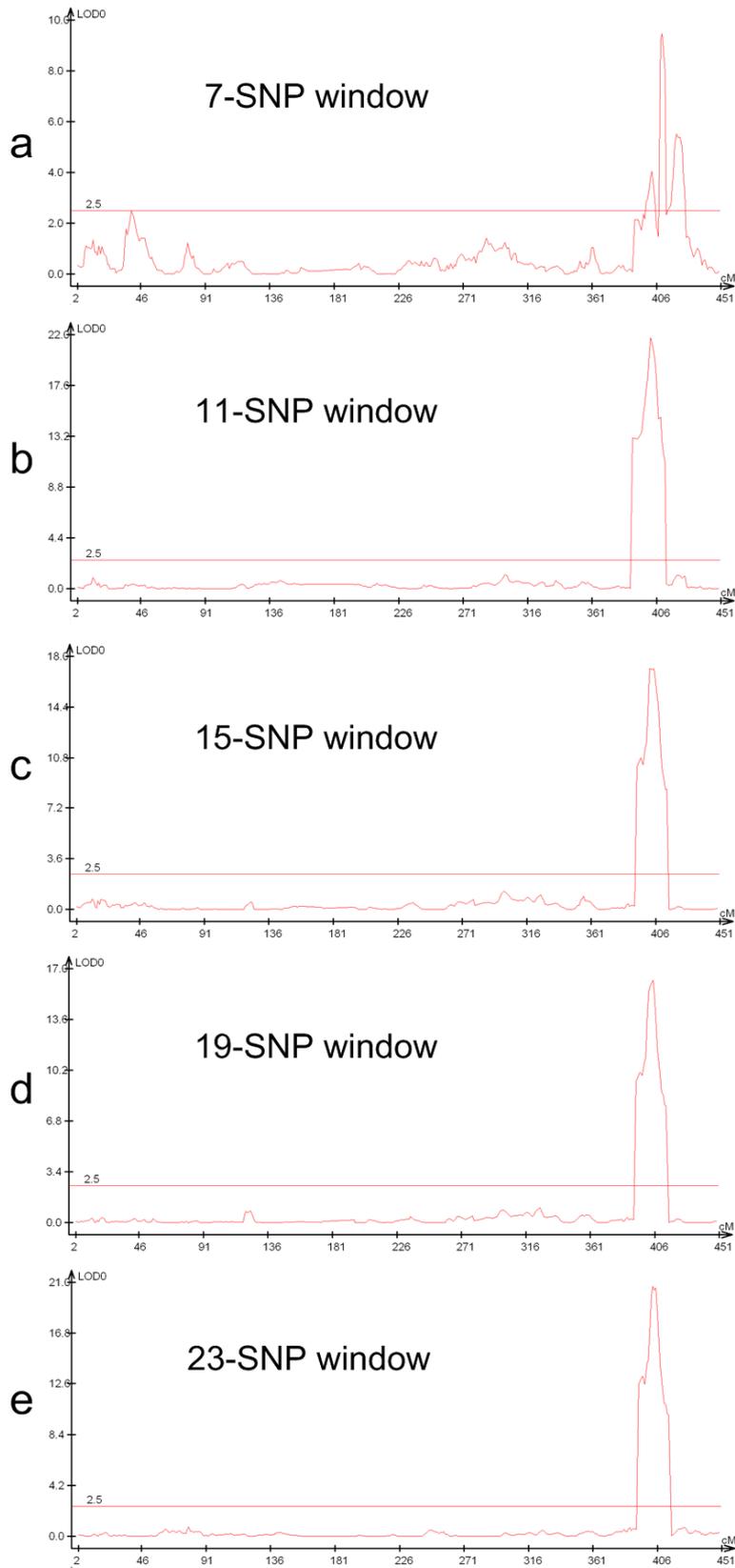
Supplementary Figure 3 Plant height QTL detected on chromosome 1 when using different window sizes. Tested window sizes in the number of SNPs include: (**a**) 7. (**b**) 11. (**c**) 15. (**d**) 19. (**e**) 23.