Supporting Information

McNally et al. 10.1073/pnas.0900992106

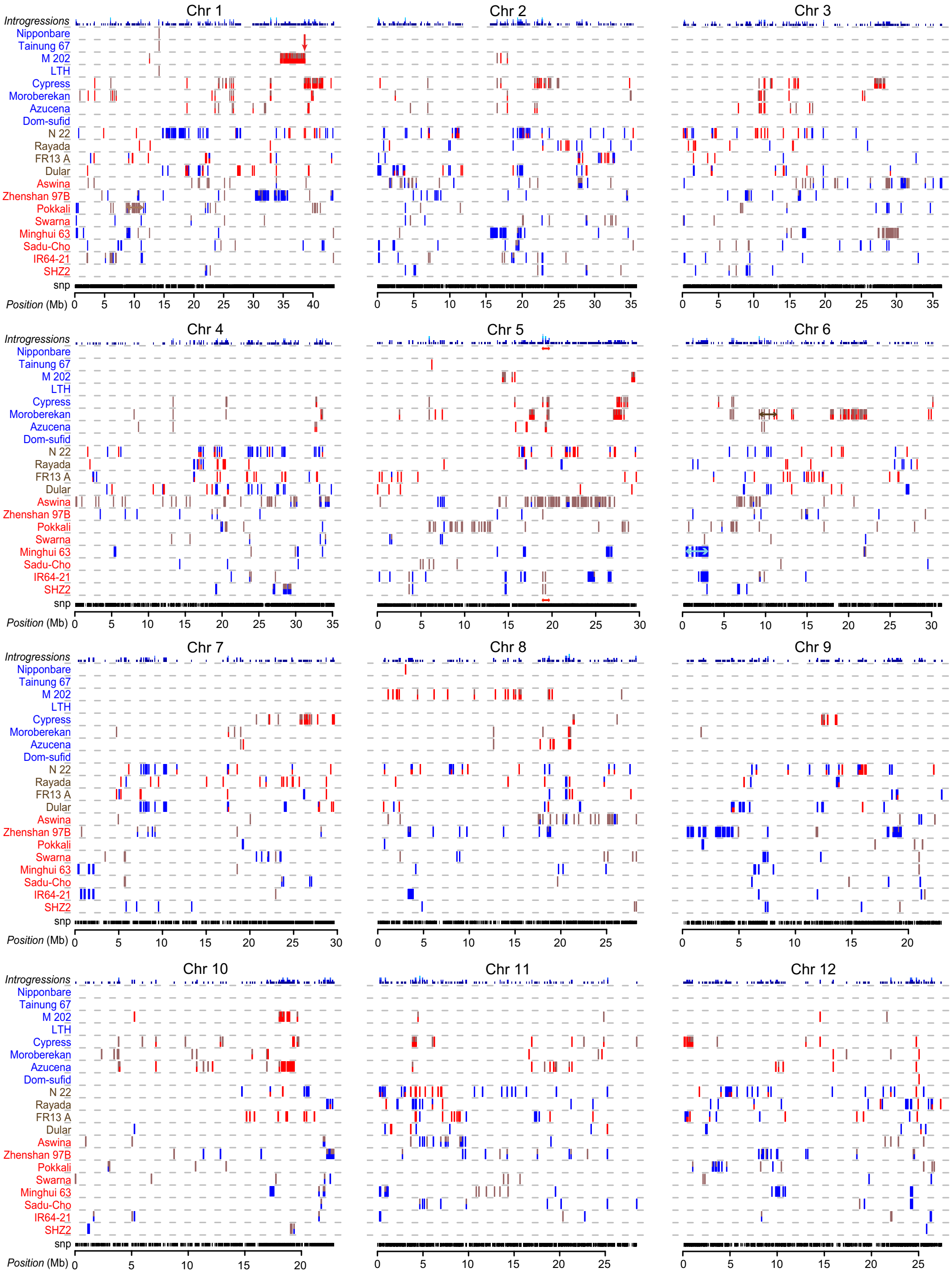

Fig. S1. Introgressed regions in all rice chromosomes. As per Fig. 3, the origin of an introgression is indicated by the color of the varietal (red from indica, blue from japonica, and brown from aus). Each vertical line corresponds to a window of 100 kb. If the source of an introgression is ambiguous, each potential donor is indicated with half of the line. Red arrow indicates *Sd1* (chromosome 1), brown bars indicate saltol (chromosome 1) and NB-ARC regions (chromosome 6), a red bar shows shared introgressions (chromosome 5), and light blue bar indicates introgressed region in Minghui 63 (chromosome 6). Chromosomes 1, 5, and 6 are included for continuity.

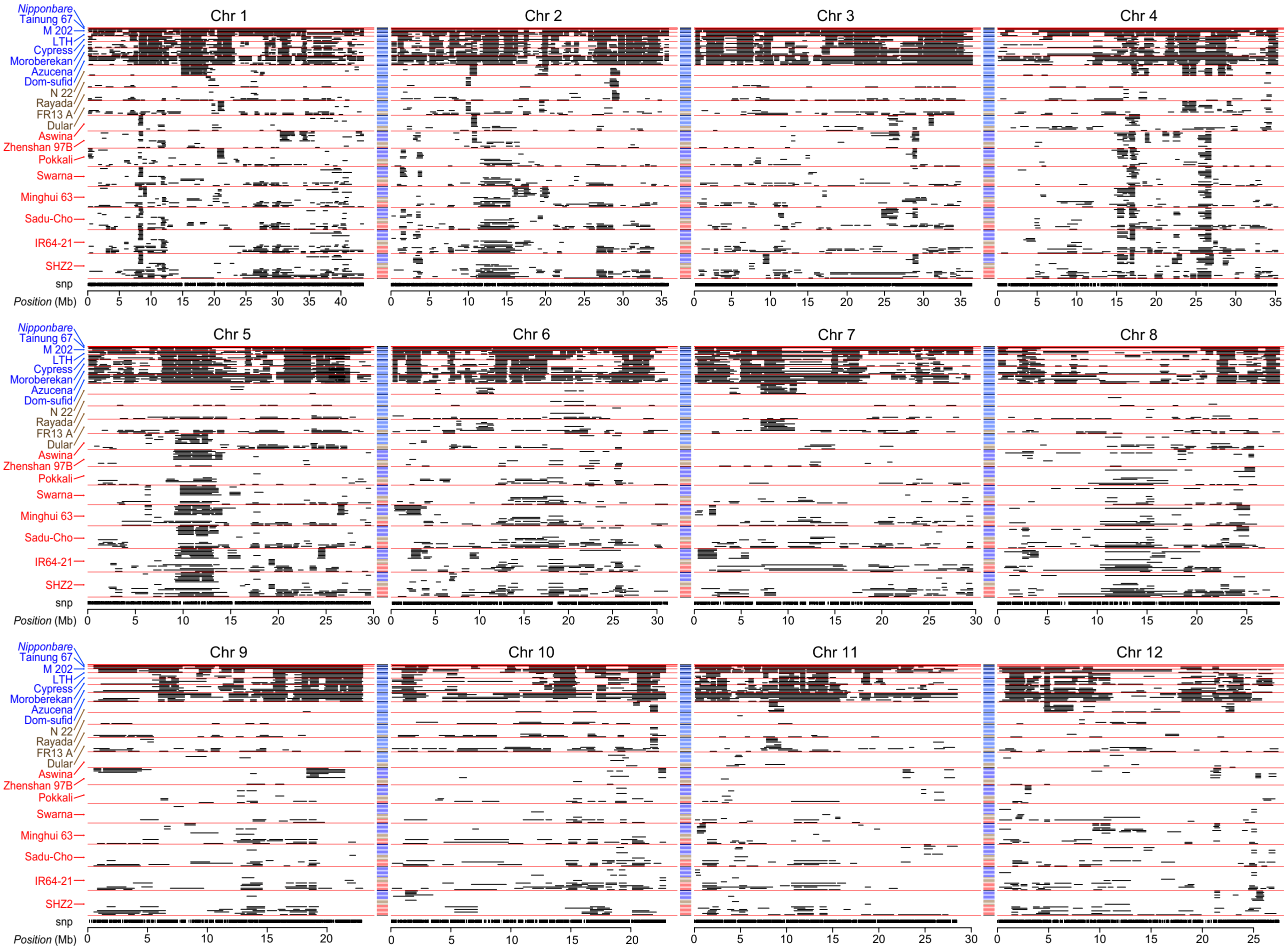

Fig. S2. Regions of extensive pairwise haplotype sharing along all rice chromosomes. SNP positions are listed as black bars in the bottom row for each chromosome. Accession pairs are sorted along the *y* axis. Each possible pairwise comparison is shown only once. For each accession, only comparisons to the accessions above it are shown. These blocks are delimited by red lines. The topmost block is the comparison between Nipponbare (italicized) and Tainung 67. Black lines indicate regions of high similarity between a pair of accessions. Adjacent chromosomes are separated by a vertical bar of lines for each pairwise comparison where the variety type of other accessions in a comparison is indicated by red (indica), brown (aus), or blue (japonica).

Other Supporting Information Files

SI Appendix (PDF)
Table S1 (PDF)
Table S2 (PDF)
Table S3 (PDF)
Table S4 (PDF)
Table S5 (PDF)
Table S6 (PDF)
Table S7 (PDF)