Fig S1. The distribution of 2,301 SNPs on the 12 rice chromosomes.
Fig S2. Phylogenetic tree of 412 Southeast Asian Ind3 accessions and 81 MDI landraces. The tree was generated by the neighbor-joining method using 2,301 SNPs common to both the 3K rice genome dataset and the MDI dataset.
Chr 1

Position (pb)

Chr 2

Position (pb)

Chr 3

Position (pb)

MDI landraces
MDI improved varieties
Fig S3. The π-value distribution of 99 MDI rice accessions through overall 459 chromosomal regions. The distribution is separately displayed in each of the 12 chromosomes. All π-values were calculated by the sliding window method in TASSEL v5.2.43 using the diversity tool with step and window sizes of five SNPs across 2,301 SNPs. X and Y axes indicate the nucleotide positions of SNPs in the chromosomes and π-values, respectively.
Chr 4

π-value

Position (bp)

MDI landraces
Vietnam
Cambodia
Thailand
Philippines
Laos
Indonesia
Malaysia
Myanmar
Chr 6

$\pi$-value vs Position (bp)

- MDI landraces
- Vietnam
- Cambodia
- Thailand
- Philippines
- Laos
- Indonesia
- Malaysia
- Myanmar

Position (bp)
Chr 8

π-value

Position (bp)

MDI landraces
Vietnam
Cambodia
Thailand
Philippines
Laos
Indonesia
Malaysia
Myanmar

π-value

Position (bp)
Chr 9

\[ \pi \text{-value} \]

Position (bp)

MDI landraces
Vietnam
Cambodia
Thailand
Philippines
Laos
Indonesia
Malaysia
Myanmar
Fig S4. The π-value distribution of eight subpopulations and MDI landraces through overall 459 chromosomal regions. The distribution is separately displayed in each of the 12 chromosomes. All π-values were calculated by the sliding window method in TASSEL v5.2.43 using the diversity tool with step and window sizes of five SNPs across 2,301 SNPs. In panels for each chromosome, the upper panel displays the π-value distributions for the nine subpopulations, and the lower panel shows the π-value distributions for a whole of 493 accessions from the nine subpopulations. X and Y axes indicate the nucleotide positions of SNPs in the chromosomes and π-values, respectively.
Fig S5. Genome-wide genetic diversity profiles of Ind3 accessions from individual countries and the MDI landrace population. High π-value regions (π > 0.45) are shown in reds, whereas low π-value regions (π < 0.05) are shown in blues. For clarity, only π-values from five-SNP regions encompassing more than 500 kbp are shown.