

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: The list of 217 accessions of wild, cultivated and weedy rice species sampled in the collection.

File Name: Supplementary Data 2

Description: Genetic assignments and heterozygosity for each wild, cultivated and weedy rice accession.

File Name: Supplementary Data 3

Description: Nucleotide diversity (π) and number of raw variants (SNPs and INDELs) for each chromosome of wild, cultivated and weedy rice.

File Name: Supplementary Data 4

Description: Number and proportion of wild- and crop-specific private SNPs in Asian weedy rice strains for each chromosome.

File Name: Supplementary Data 5

Description: Number and proportion of wild- and crop-specific private SNPs in each weedy rice strain for each chromosome.

File Name: Supplementary Data 6

Description: Causative mutations of the domestication genes in the 34 Malaysian and Thai weedy accessions.

File Name: Supplementary Data 7

Description: Nucleotide diversity (π and θ) and genetic differentiation (F_{st}) of the candidate genomic regions in Malaysian weed compared to indica.

File Name: Supplementary Data 8

Description: Nucleotide diversity (π and θ) and genetic differentiation (F_{st}) of the candidate genomic regions in indica-like Thai weed compared to indica.

File Name: Supplementary Data 9

Description: Nucleotide diversity (π and θ) and genetic differentiation (F_{st}) of the candidate genomic regions in wild-like Thai weed compared to indica.

File Name: Supplementary Data 10

Description: Top 1% of the candidate genomic regions showed selective sweep in the three types of SEA weedy rice.

File Name: Supplementary Data 11

Description: Genomic regions of shared low nucleotide diversity (π) among the analyzed weedy strains.