Supplementary Material

The following data are available in the online version of this article.

Supplemental Figure S1. Distribution of rice F-box proteins in different subfamilies.

Supplemental Figure S2. Phylogenetic relationship among the rice F-box proteins. The unrooted tree was generated using ClustalX program by neighbor-joining method. Bootstrap values from 1,000 replicates are indicated at each node. This is the larger version of the Figure 3.

Supplemental Figure S3. Phylogenetic relationship of rice and *Arabidopsis* F-box proteins containing LRR domains (**A**), kelch repeats (**B**) and tubby domain (**C**) at their C-terminus. The unrooted tree was generated using ClustalX program by neighbor-joining method. Bootstrap values from 1,000 replicates are indicated at each node. Rice and *Arabidopsis* proteins are indicated in different colors.

Supplemental Figure S4. Organ-specific expression of F-box protein encoding genes based on the microarray analysis from an earlier study (Ma et al., 2005). (A) Number of genes expressed in various organs (mentioned below each bar) is given. (B) Number of genes with organ-specific (mentioned below each bar) expression.

Supplemental Figure S5. Hierarchial clustering display of all the 617 F-box protein encoding genes represented on Affymetrix rice genome array in various rice organs and developmental stages (mentioned at the top of each lane). The average log signal values were used for clustering. The color scale (representing log signal values) is shown at the bottom.

Supplemental Figure S6. Real-time PCR analysis of representative F-box protein encoding genes differentially expressed in various tissues/developmental stages and stress treatments.

Supplemental Table S1. F-box proteins with known function in plants.

Supplemental Table S2. F-box protein encoding genes in rice. Detailed genomic information including length of ORF, protein length, number of introns within ORF and genomic locus (chromosomal location, BAC/PAC name) is provided for each F-box protein gene.

Supplemental Table S3. Putative motifs predicted in F-box proteins of FBX subfamily by MEME with an e-value less than e-100.

Supplemental Table S4. F-box protein encoding genes present on duplicated chromosomal segments of rice.

Supplemental Table S5. Availability of FL-cDNA, EST and/or peptide sequence(s) corresponding to rice F-box protein encoding genes.

Supplemental Table S6. MPSS data showing variable tissue-specific abundance of rice F-box protein encoding genes.

Supplemental Table S7. Rice F-box protein encoding genes with tissue-specific expression as revealed from MPSS data.

Supplemental Table S8. Average log signal values of 617 F-box protein encoding genes from three biological replicates of each sample.

Supplemental Table S9. F-box protein encoding genes differentially expressed under different light conditions.

Supplemental Table S10. Average log signal values of 43 F-box protein encoding genes differentially expressed under various stress conditions.

Supplemental Table S11. Primer sequences used for real-time PCR analysis.