

Supplemental Data

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

Supplemental Figure S1. Position and pattern of introns within the basic and hinge regions of the bZIP domains of the OsbZIP transcription factors.

Supplemental Figure S2. Alignment of basic and hinge regions of OsbZIP proteins. The OsbZIP proteins are classified into 11 groups (I-XI) according to their DNA binding specificity and amino acid sequences in basic and hinge regions.

Supplemental Figure S3. Amino acid sequence alignment of the leucine zipper region of 89 OsbZIP proteins. The OsbZIP proteins are classified into 29 sub-families (BZ1-BZ29) with similar predicted dimerization properties.

Supplemental Figure S4. Phylogenetic relationship among the OsbZIP proteins based on (a) bZIP domain (b) basic and hinge regions (c) leucine zipper defined from the first leucine.

Supplemental Figure S5. Phylogenetic relationship among the OsbZIP proteins and other known plant bZIP proteins.

Supplemental Figure S6. Organ-specific expression of *OsbZIP* genes based on the microarray analysis from an earlier study (Ma et al., 2005).

Supplemental Figure S7. Hierarchical clustering display of 85 *OsbZIP* genes represented on Affymetrix rice genome array in various rice organs and developmental stages (mentioned at the top of each lane).

Supplemental Figure S8. Real-time PCR analysis of representative *OsbZIP* genes differentially expressed in various tissues/developmental stages and stress treatments.

Supplemental Figure S9. Venn diagrams representing number of differentially regulated *OsbZIP* genes in various organs under different light conditions based on the microarray analysis from an earlier study (Jiao et al., 2005).

Supplemental Table S1. bZIP transcription factors identified in plants.

Supplemental Table S2. OsbZIP transcription factor genes. Detailed genomic information including TIGR locus IDs, gene names, ORF length, protein length, position of bZIP domain, number of introns within ORF, intron pattern within the basic and hinge regions of the bZIP domain, genomic locus (chromosomal location and BAC/PAC

accession no.) and group on the basis of DNA-binding site specificity is provided for each *OsbZIP* gene.

Supplemental Table S3. *OsbZIP* genes present on duplicated chromosomal segments of rice.

Supplemental Table S4. Additional conserved motifs in OsbZIP proteins as predicted by MEME.

Supplemental Table S5. Classification of OsbZIP proteins into sub-families with similar predicted dimerization specificity.

Supplemental Table S6. Availability of Full Length-cDNA and/or EST corresponding to *OsbZIP* genes.

Supplemental Table S7. *OsbZIP* genes expressed in at least one of the six organs or cell types.

Supplemental Table S8. Average log signal values of 85 *OsbZIP* genes from three biological replicates of each sample.

Supplemental Table S9. Relationship between expression pattern of *OsbZIP* genes and intron pattern, conserved motifs, gene duplication, predicted DNA-binding specificity and phylogenetic analysis.

Supplemental Table S10. *OsbZIP* genes differentially expressed under different light conditions.

Supplemental Table S11. Average log signal values of 37 *OsbZIP* genes differentially expressed under various abiotic stress conditions.

Supplemental Table S12. Relationship between expression pattern of *OsbZIP* genes and hetero-dimerization of OsbZIP transcription factors.

Supplemental Table S13. Primer sequences used for real-time PCR analysis.