

## SUPPLEMENTS

**Supplemental Table 1.** Detailed classifications of 125 *OsWAKs* identified from the genome sequence of rice (*Oryza sativa* L.) ssp. *japonica* cv. Nipponbare and their accession numbers in TIGR/Genbank.

**Supplemental Table 2.** Detailed annotations of the 125 *OsWAKs*.

**Supplemental Table 3.** List of 38 *OsWAKs* having FL-cDNA sequence(s) and 11 *OsWAKs* with matching EST sequence(s) and the rice tissues from which FL-cDNA and EST sequences were derived.

**Supplemental Table 4.** Ratios of nonsynonymous vs. synonymous substitution rates of EGF-Ca<sup>++</sup> domain regions among 15 *OsWAKs*.

**Supplemental Data 1.** Genomic DNA sequences and predicted post-processing sequences/FL-cDNA sequences of the 125 *OsWAKs*.

**Supplemental Data 2.** Predicted protein sequences of the 125 *OsWAKs*.

**Supplemental Data 3.** Predicted (partial) protein sequences of ten *HvWAKs*.