

1 **SUPPLEMENTS**

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

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

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

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

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

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

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

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