Fig S6. Multiple sequence alignment of the IRE1’ C-termini.

Protein sequences of the Arabidopsis IRE1s (AtIRE1A, At2g17520; AtIRE1B, At5g24360), rice IRE1 (OsIRE1, LOC_Os07g28820), yeast IRE1 (ScIRE1, NP_011946) and human IRE1 (HsIRE1, NP_001424) were subjected to sequence alignment using CLUSTAL.2.1 with the default setting. Only the C-terminal regions beyond the transmembrane domains are shown. The protein kinase domain is shaded in grey while the endonuclease domain is shaded in yellow. Amino acids predicted to be important for the protein kinase activity or endonuclease activity are highlighted in red.