S2 Fig. Comparison of coding regions of *Xa23/xa23* alleles in *Oryza* species. The multiple sequence alignment was constructed using CLC Sequence Viewer 7 program. The *Xa23* in CBB23 is used as a reference. The different residues are shown in red. The consensus sequence of all the *Xa23/xa23* alleles along with percentage conservation of residue is also shown. The numbers at right side indicate the length of each sequence.