



**Additional file 7: Figure S5** MapMan analysis of the secondary metabolic pathways using the differentially expressed genes derived from (a) comparison C+F vs C, and (b) comparison W+F vs W. Red arrows indicate the pathways enriched in up-regulated genes. Blue and red colors indicate down- and up-regulated genes, respectively. The colored bar in each panel shows fold changes in gene expression. The four treatments were non-inoculated cultivated rice (C), cultivated rice inoculated with *Magnaporthe oryzae* (C+F), non-inoculated wild rice (W), and wild rice inoculated with *M. oryzae* (W+F).