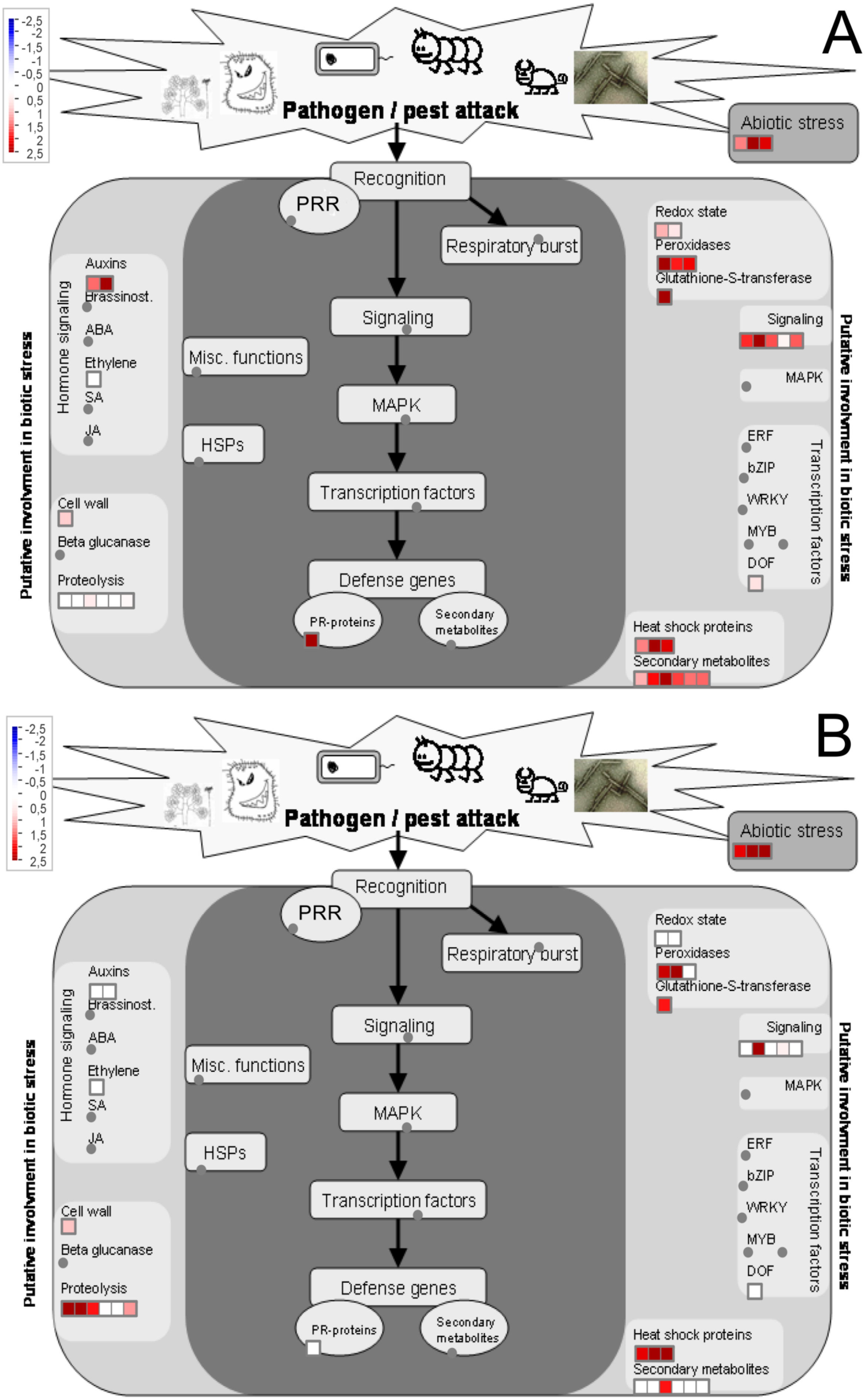
Supporting Information S2. Visualization of changes in expression during PTI response of tobacco as represented by the Biotic Stress Overview in MapMan. A) *6 hpi*. B) *48 hpi*.



Mean expression ratio of the PTI-related activated contigs from our tobacco cDNA microarray in PTI-induced vs. water treated samples was calculated based on three replicate experiments per time point and log-scaled data were visualized using the MapMan “BioticStress” pathway (http://mapman.gabipd.org).

Individual transcripts are symbolized by red or white boxes. The scale bar represents fold change and reaches to +2.5 (deep red) on the log scale, which corresponds to a 5.7 fold change in the linear scale.