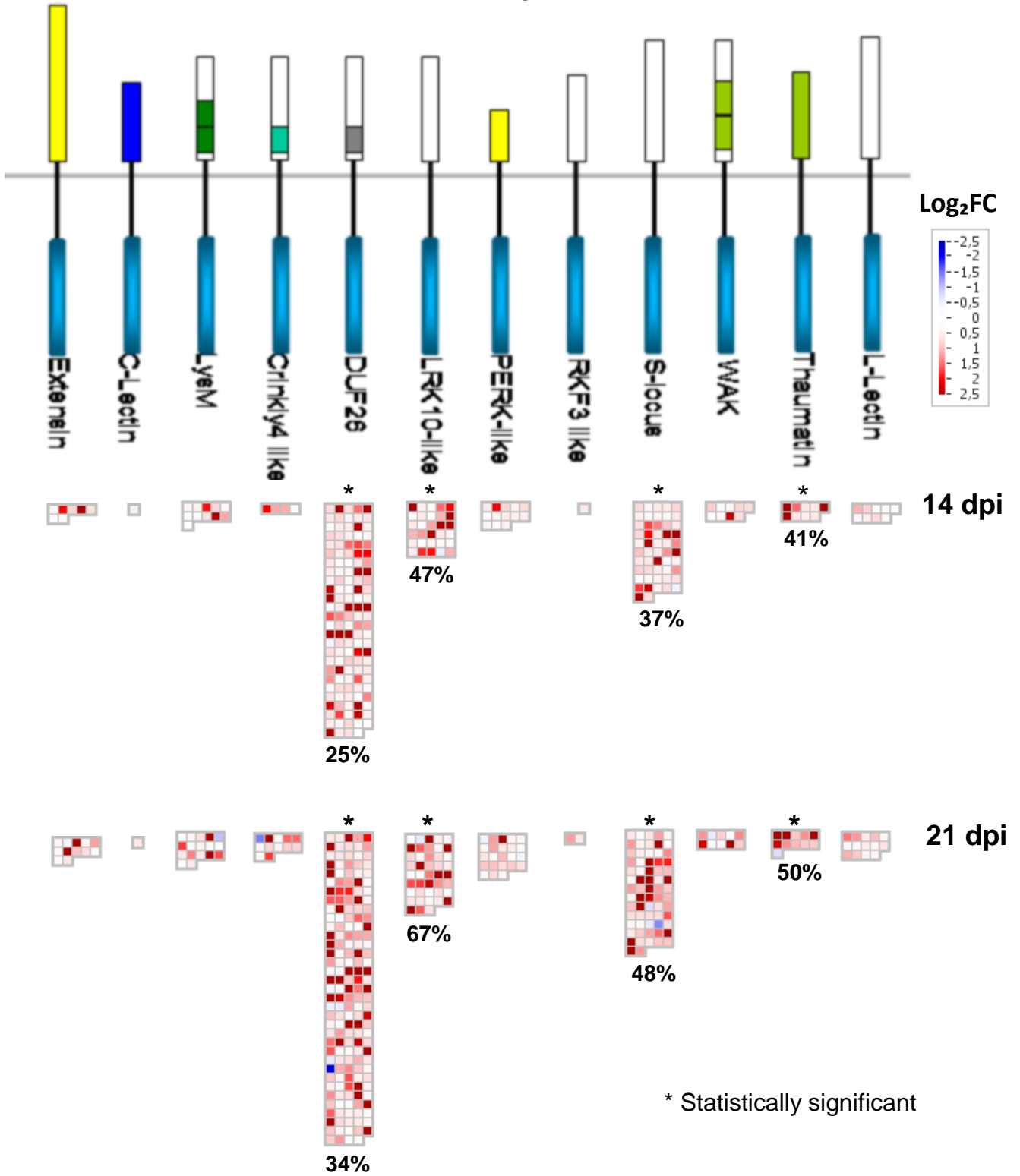
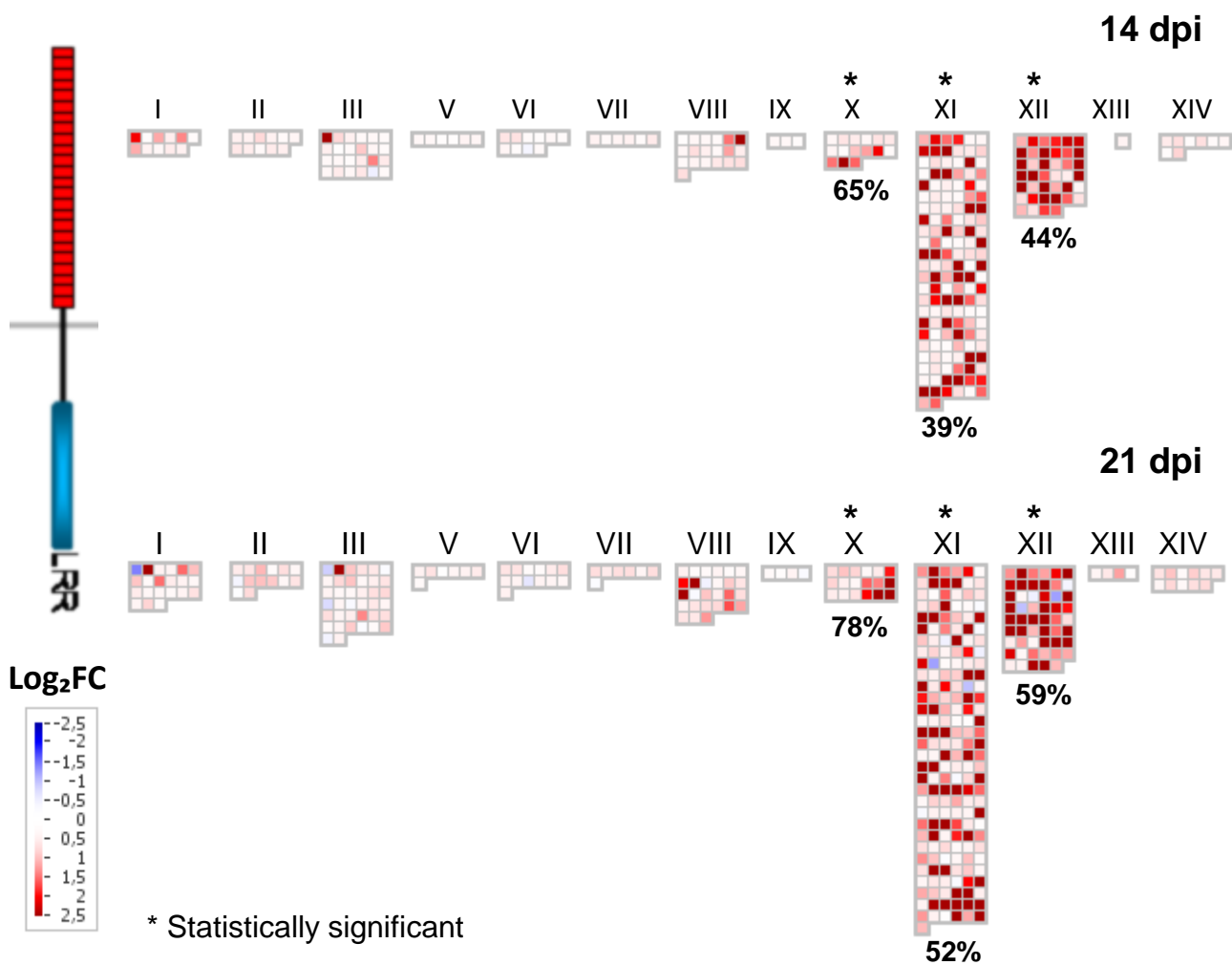


# RLKs



Additional file 4: FigS4A

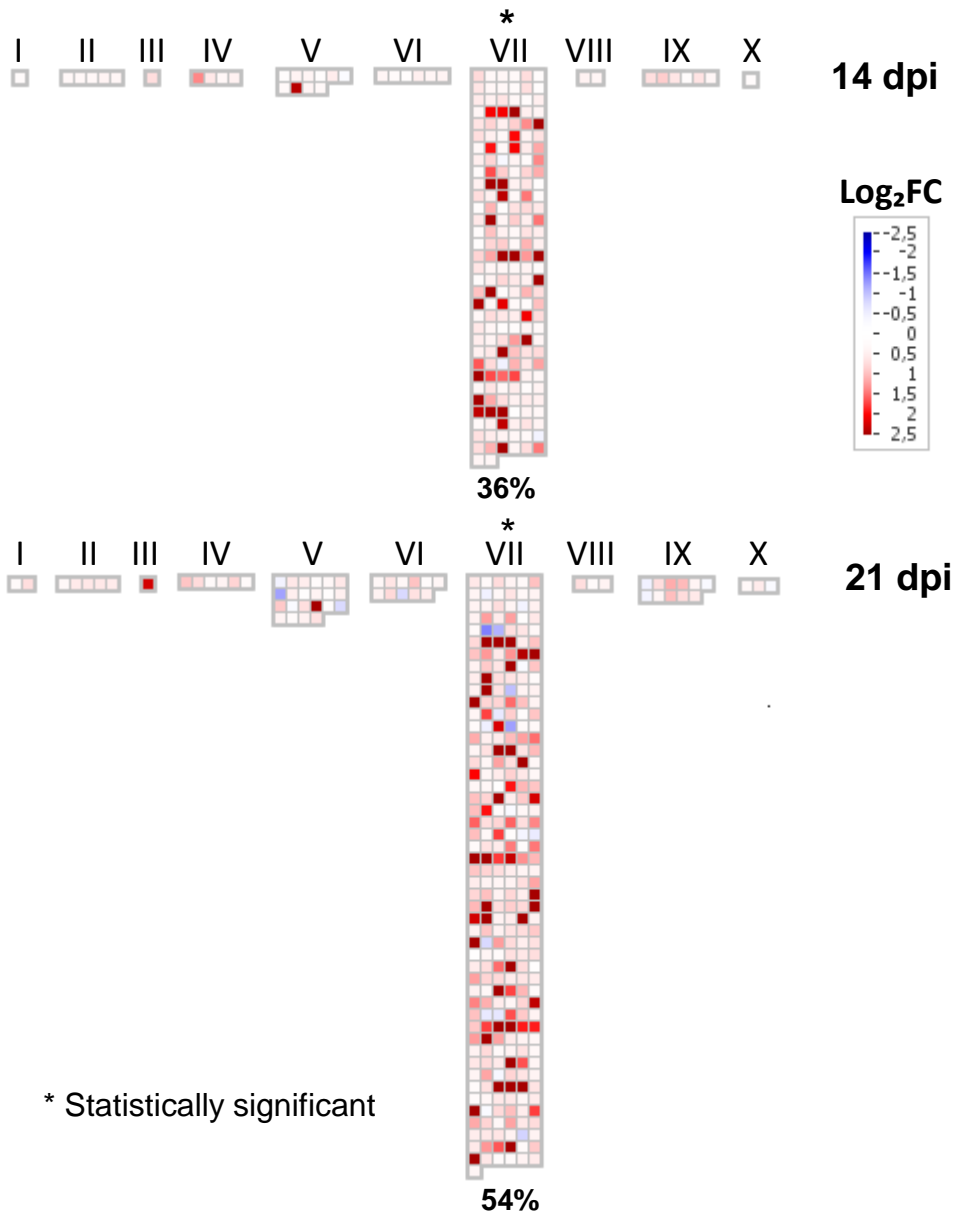
# LRR-RLKs



Additional file 4: FigS4B

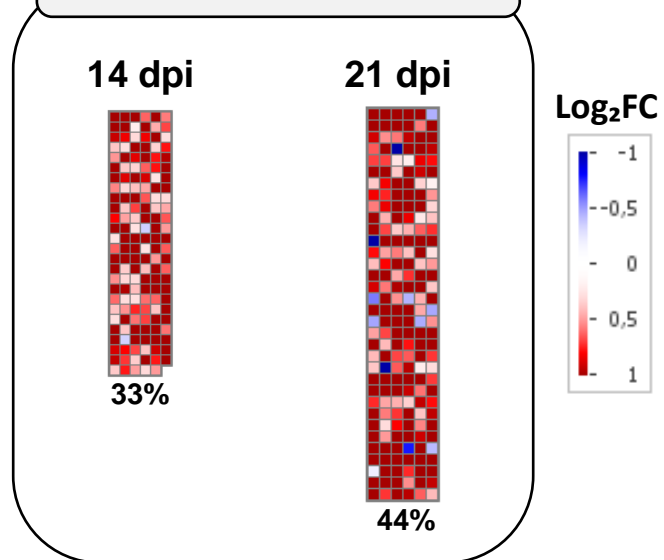
# RLCKs

## Receptor like cytoplasmatic kinases



Additional file 4: FigS4C

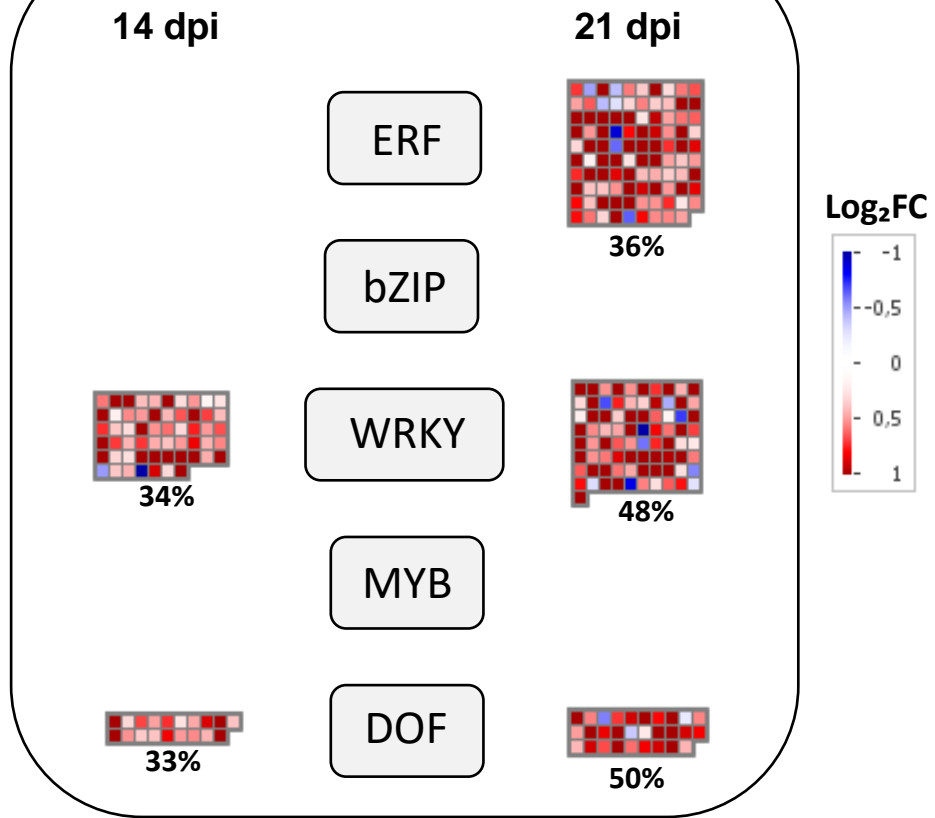
## Biotic receptors (NLRs)



*Just statistically significant categories are shown*

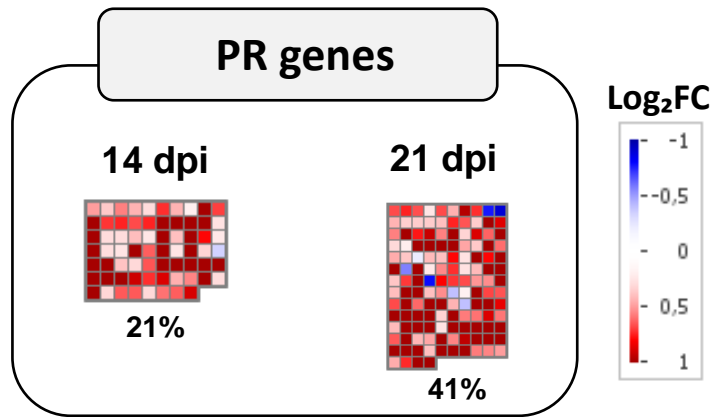
**Additional file 4: FigS4D**

## Transcription factors-Biotic stress



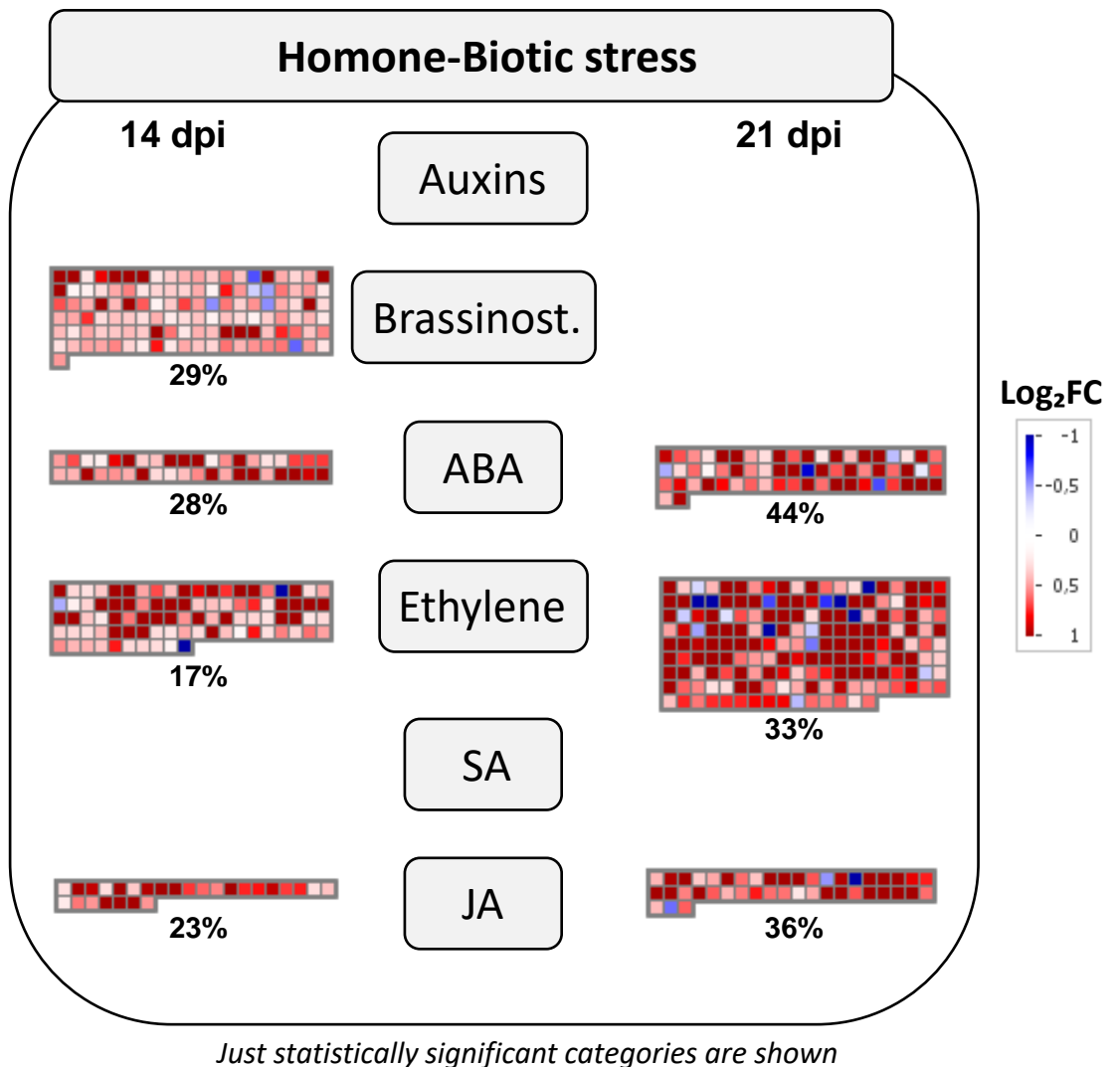
*Just statistically significant categories are shown*

**Additional file 4: FigS4E**



*Just statistically significant categories are shown*

**Additional file 4: FigS4F**



**Additional file 4: FigS4G**

**Additional file 4: Fig. S4. Immunity-related categories (MapMan ontology) enriched in upregulated genes in response to TYLCV infection at 14 and 21 dpi.** A) Receptor-like kinases (RLKs) (BIN 30.2 signaling.receptor kinases). B) Leucine rich RLKs (LRR-RLKs) (BIN 30.2 signaling.receptor kinases). Classes IV and XV from LRR-RLKs are excluded in MapMan representation. C) Receptor like cytoplasmic kinases (RLCK) (BIN 29.4.1 protein.postranslational modification.kinase). D) Biotic receptors NLR proteins (BIN 20.1.2 stress.biotic.receptors). E) Biotic stress-related transcription factors (BIN 27.3 RNA.regulation of transcription). F) Pathogenesis-related (PR) proteins proteins (BIN 20.1.7 stress.biotic.PR-proteins). G) Biotic stress-related hormones (BIN 17 hormone metabolism). Only statistically significant MapMan BINs are shown in D) E) F) and G). Statistically significant MapMan BINs are identified with a \* in A), B) and C) (Wilcoxon test and Benjamini-Hochberg correction adjusted p-values  $\leq 0.05$ ). Each square corresponds to the Log<sub>2</sub>FC of a DEG, and the color represents its upregulation (red) or downregulation (blue). The percentage of gene enrichment for each MapMan ontology term is shown.