Comparative transcriptome profiling and co-expression network analysis uncover the key genes associated with early-stage resistance to *Aspergillus flavus* in maize

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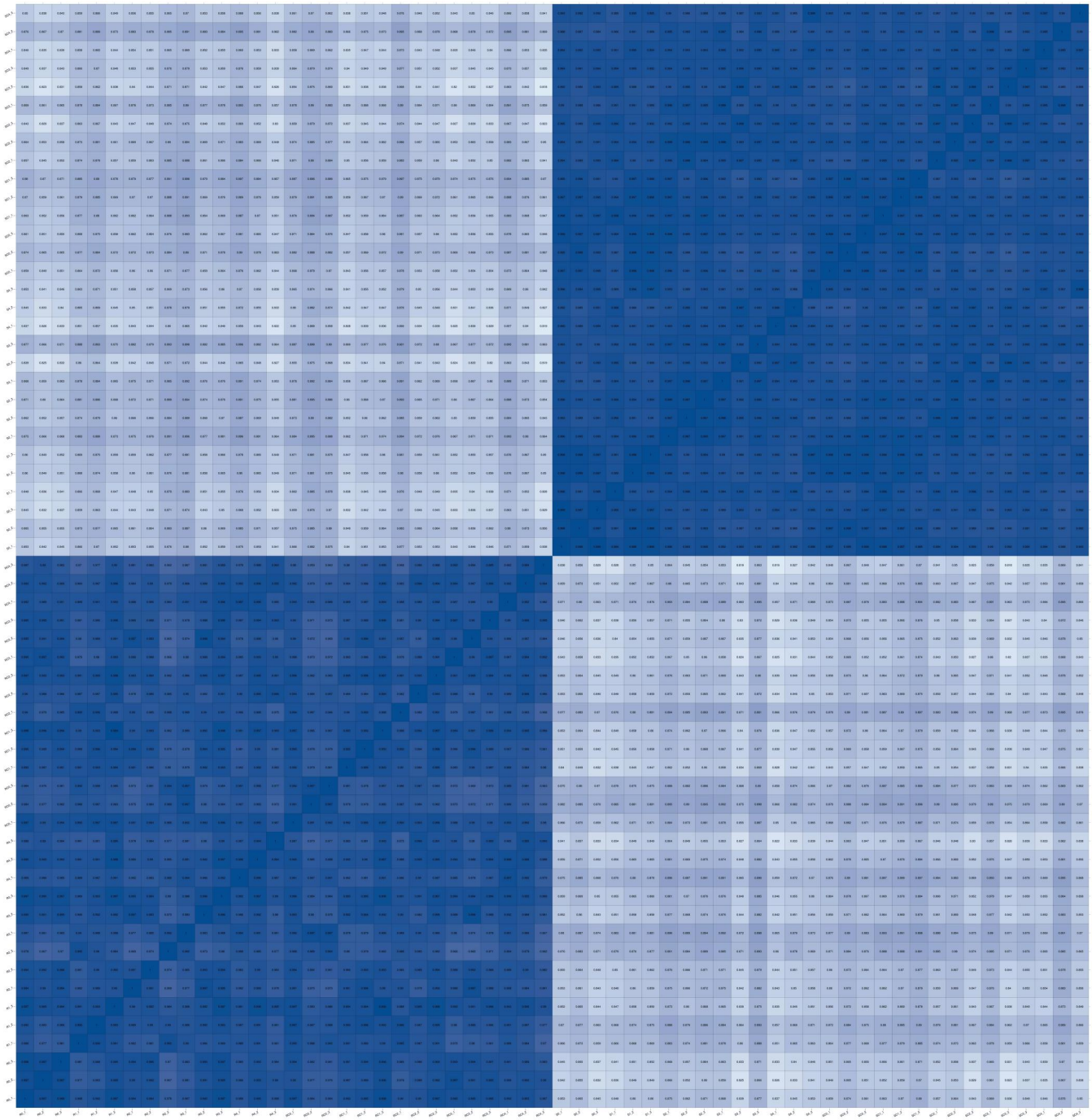

Figure S1. Pair-wise Pearson's correlation coefficients of the sequencing data of 60 samples.

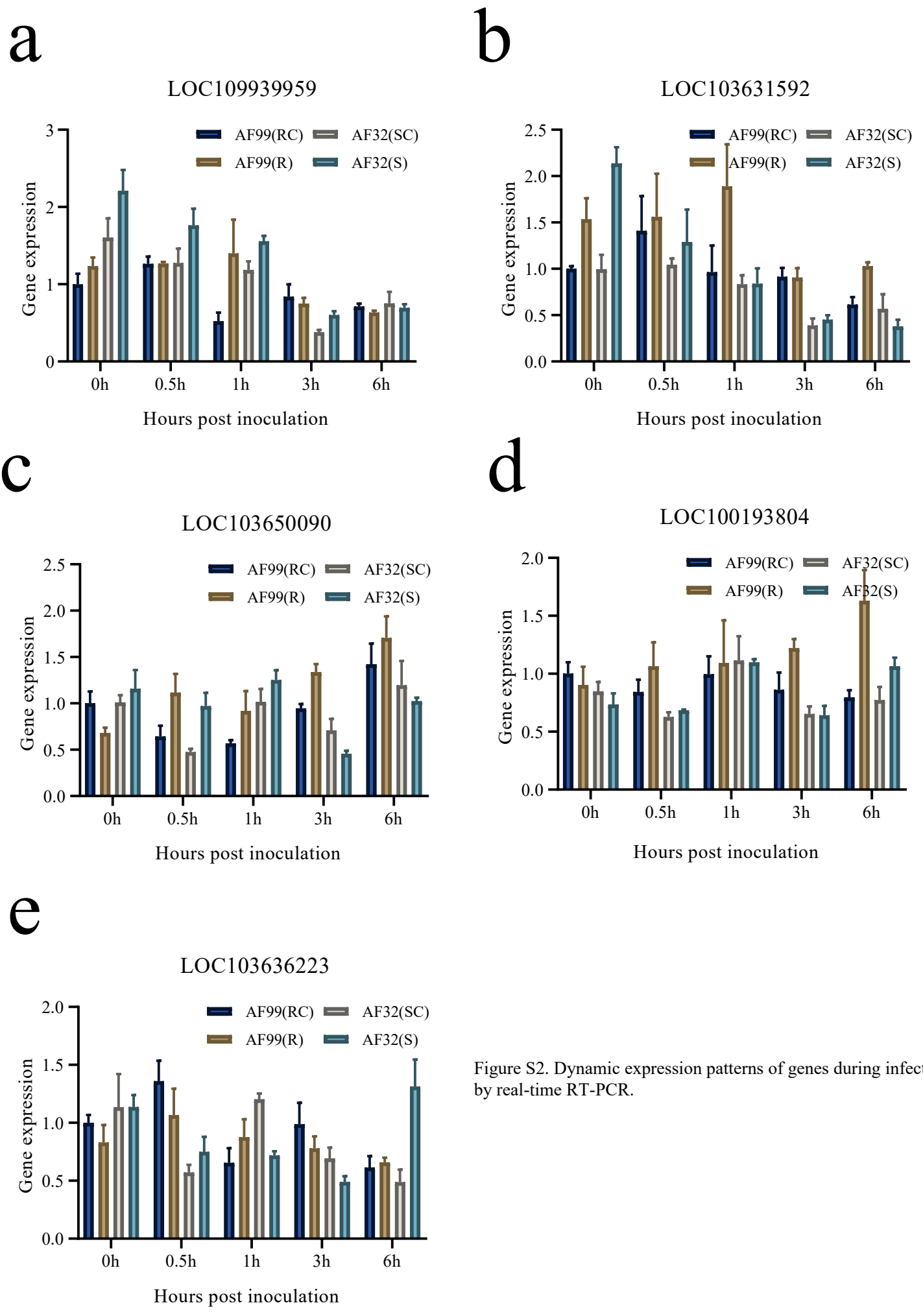

Figure S2. Dynamic expression patterns of genes during infection by real-time RT-PCR.

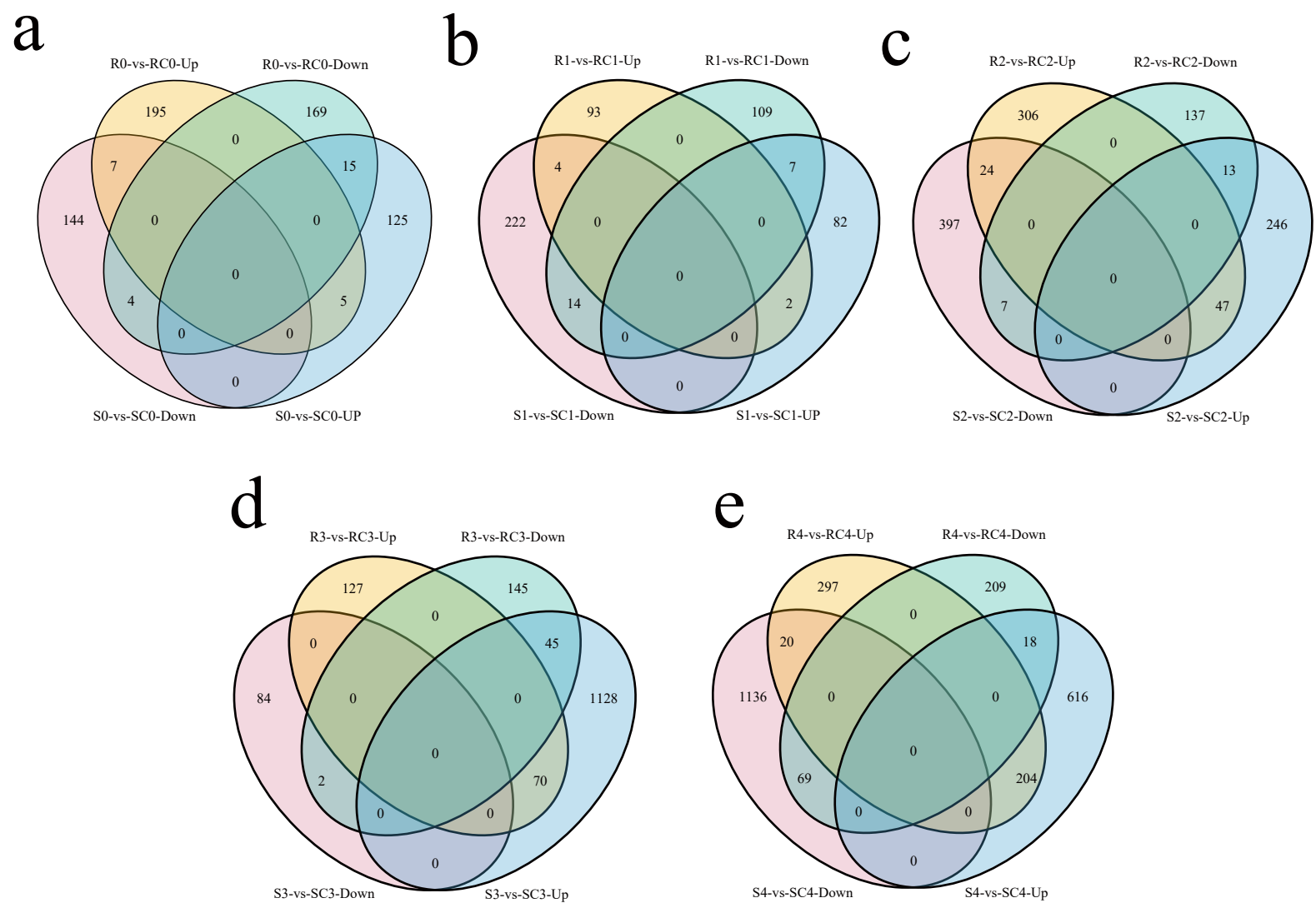

Figure S3. Venn diagrams of specific and common DEGs responding to *A. flavus* in AF99 and AF32 (infection vs. mock-treatment) at different time points (a, 0 hpi; b, 0.5 hpi; c,1.5 hpi; d, 3 hpi; e, 6 hpi).

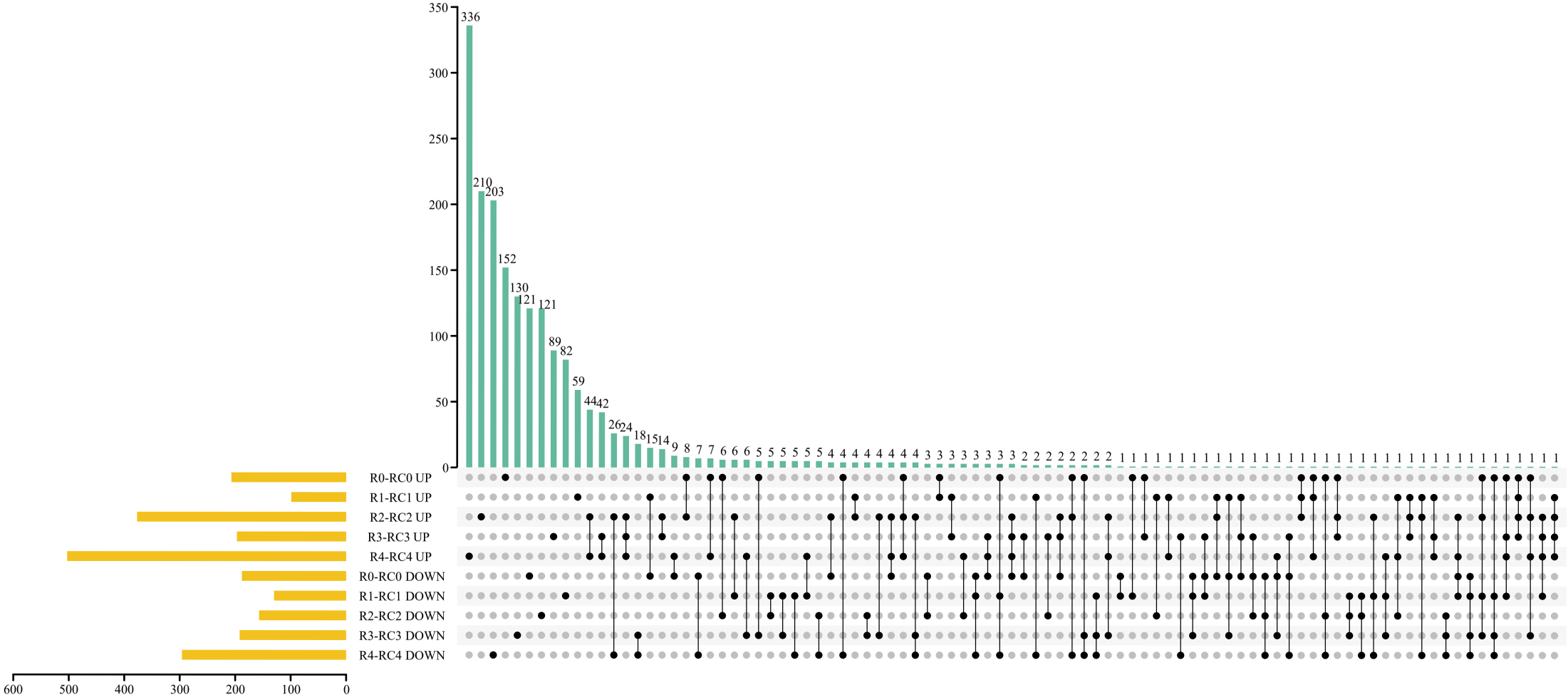

Figure S4. Venn diagram of up-regulated and down-regulated DEGs at different time points in AF99.

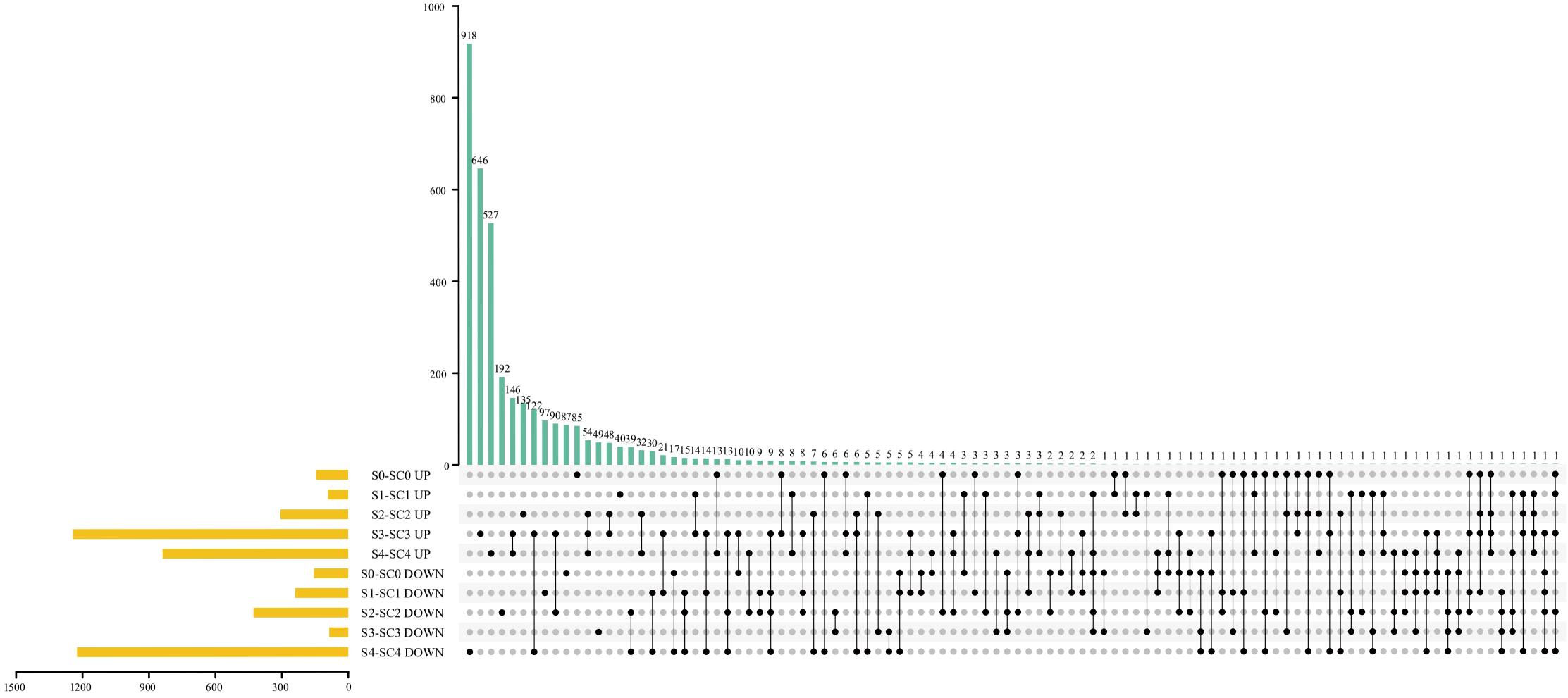

Figure S5. Venn diagram of up-regulated and down-regulated DEGs at different time points in AF32.

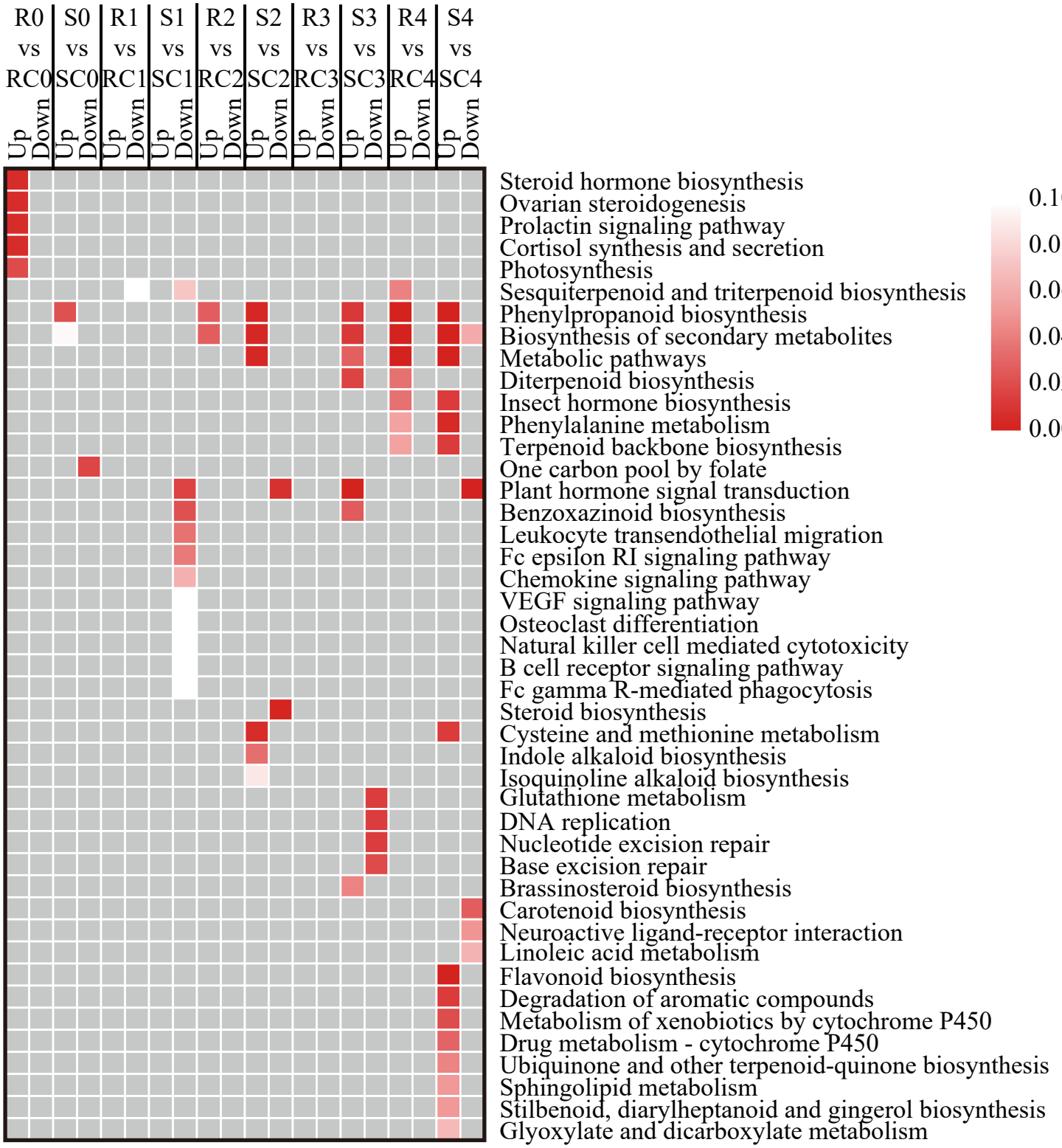

Figure S6. KEGG pathways enriched in down- and up-regulated genes responding to *A. flavus* in AF99 and AF32 (infection vs. mock-treatment) at different time points. Color depth represents the corrected p-value.

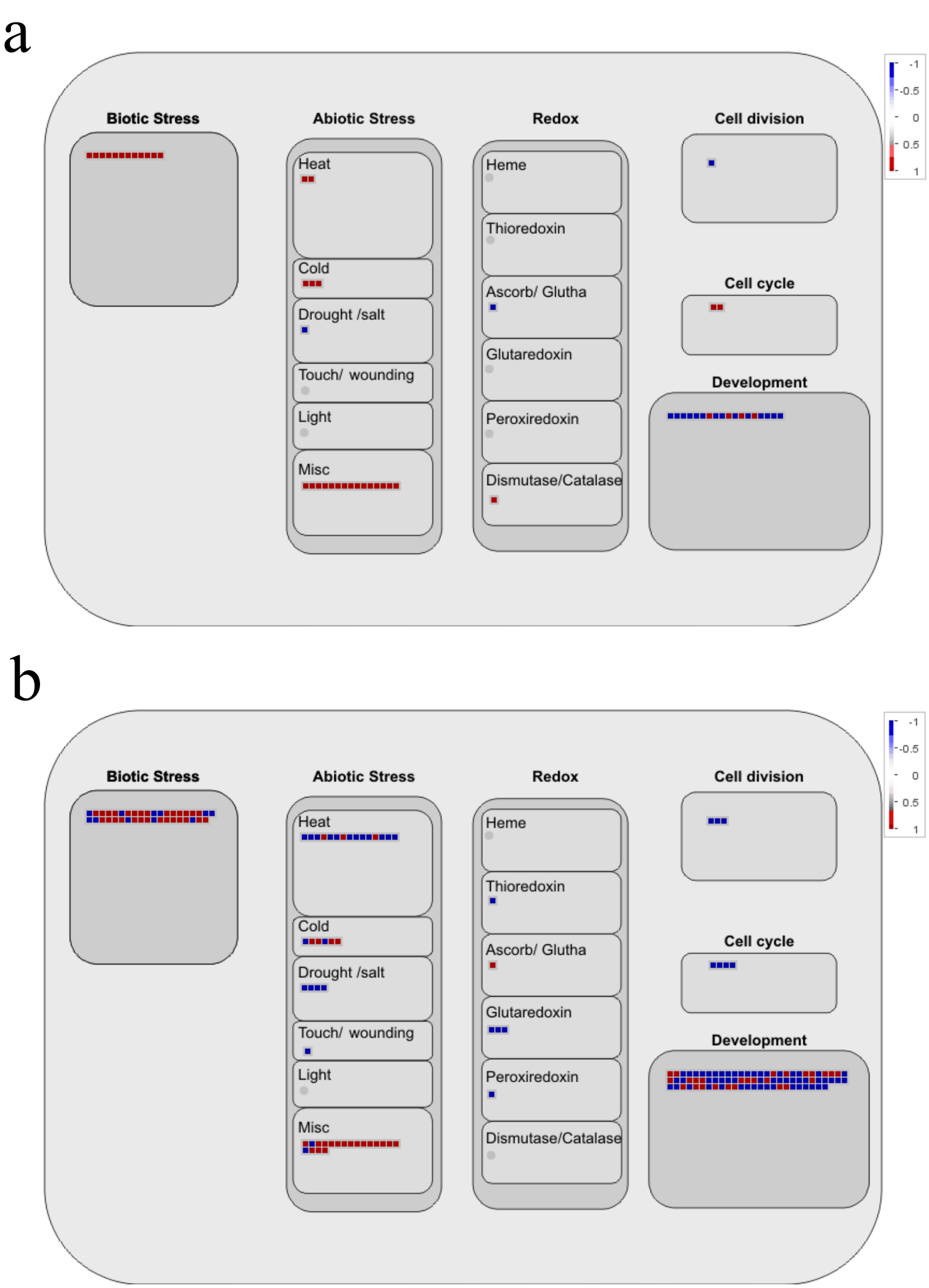

Figure S7. MapMan-based visualization of an overview of the cellular response at the T4 stage in AF99(a) and AF32(b).