

Exploring sunflower responses to Sclerotinia Head Rot at early stages of infection using RNA-seq analysis

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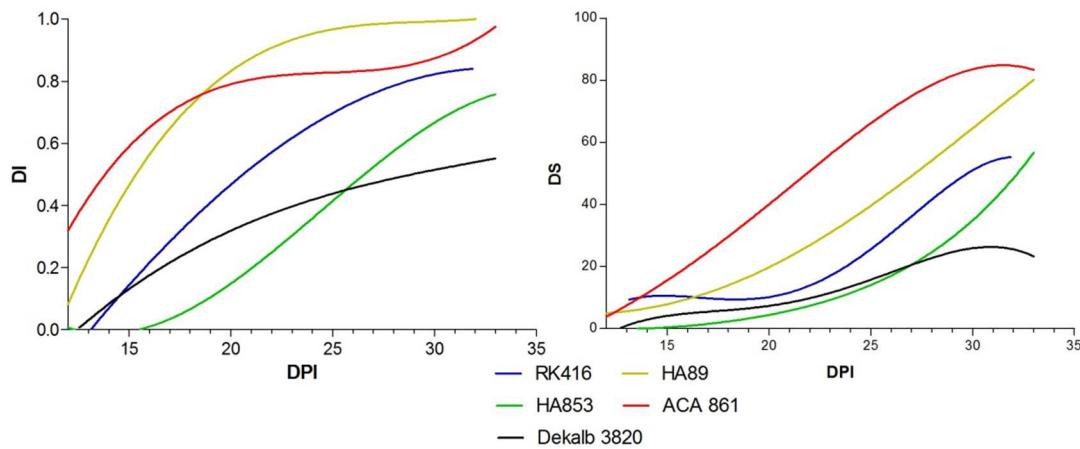
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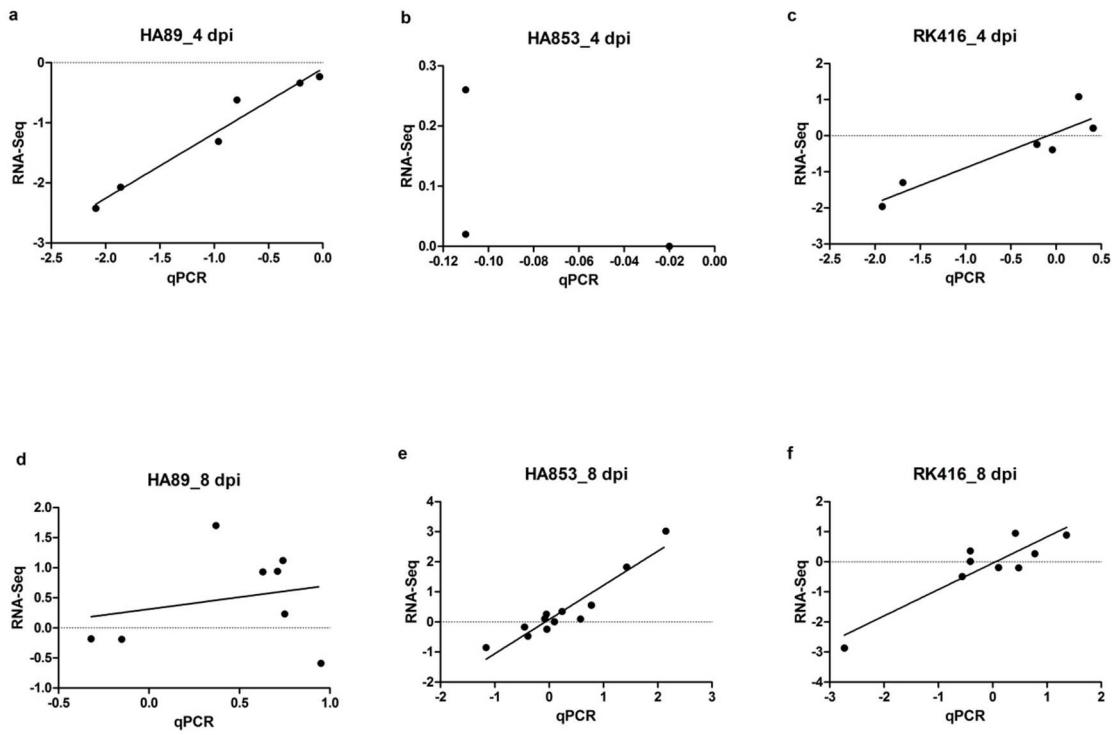
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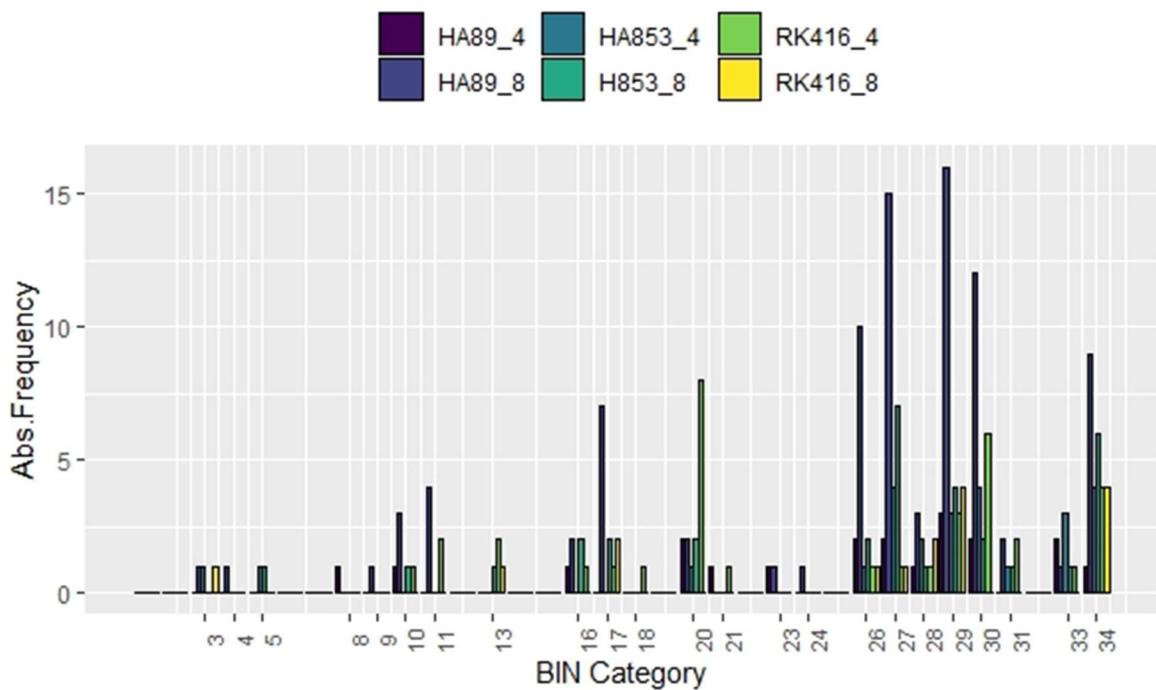
Supplementary Figures



Supplementary Figure S1. Smoothed curves of progression of disease incidence (DI; left panel) and disease severity (DS; right panel) over time.



Supplementary Figure S2. Correlation of gene expression ratios between RNA-Seq and qPCR data. A, B, C: HA89, HA853 and RK416 at 4 dpi, respectively. D, E, F: HA89, HA853 and RK416 at 8 dpi, respectively.



Supplementary Figure S3. Classification of DEGs of the different IL-time point combinations in MapMan categories. Numbers correspond to MapMan categories: 3: minor CHO metabolism; 4: glycolysis; 5: fermentation; 8: TCA / org transformation; 9: mitochondrial electron transport / ATP synthesis; 10: cell wall; 11: lipid metabolism; 13: amino acid metabolism; 16: secondary metabolism; 17: hormone metabolism; 18: Co-factor and vitamine metabolism; 20: stress; 21: redox; 23: nucleotide metabolism; 24: Biodegradation of Xenobiotics; 26: misc; 27: RNA; 28: DNA; 29: protein; 30: signalling; 31: cell; 33: development; 34: transport.