

Transcriptional, hormonal and metabolic changes in susceptible grape berries under powdery mildew infection

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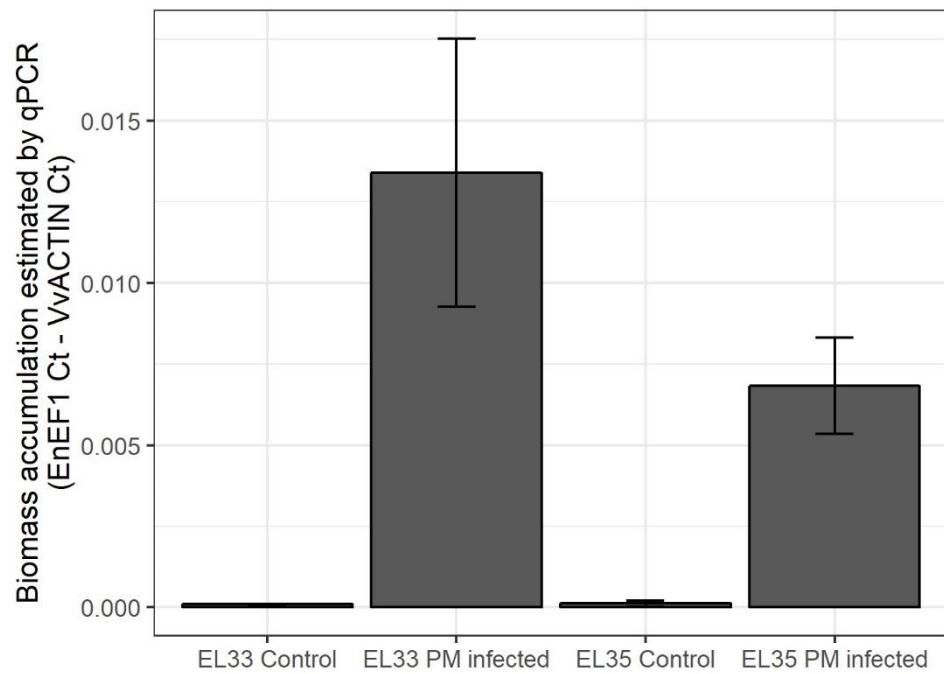
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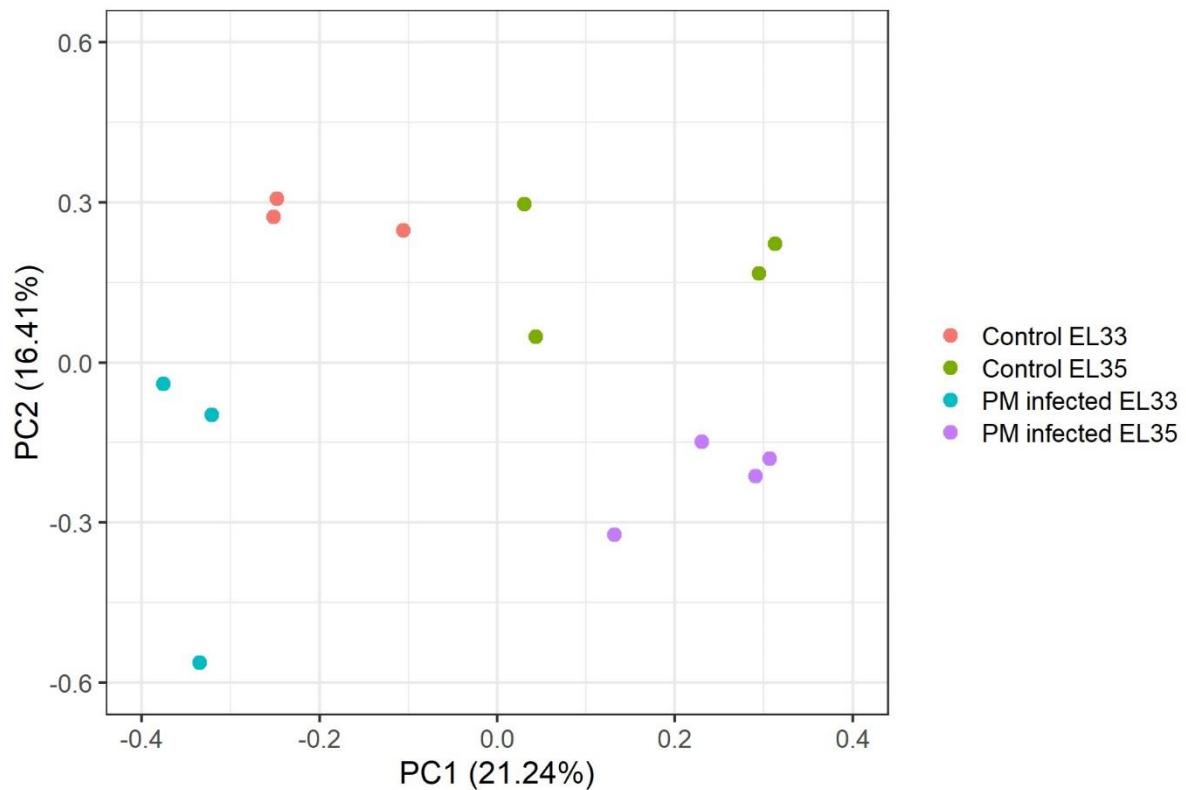
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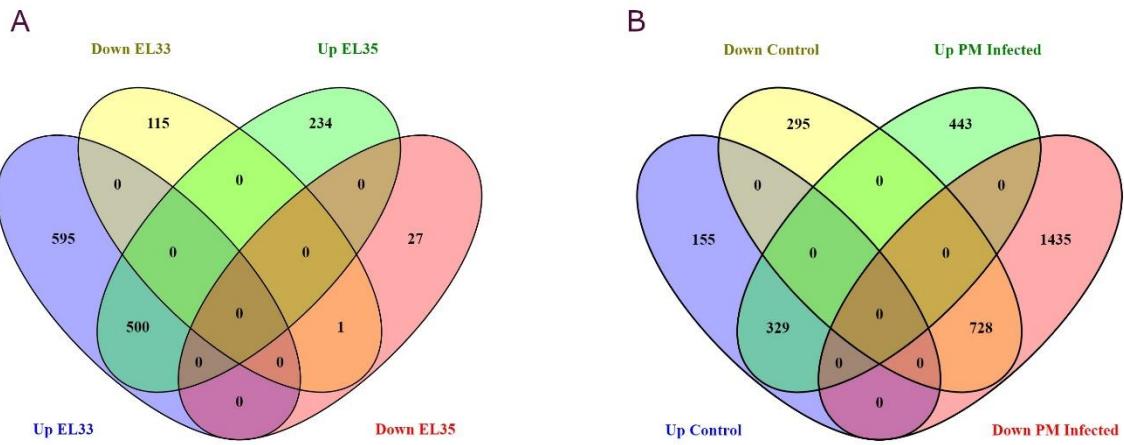
Supplementary Fig. S1 – *Erysiphe necator* biomass accumulation in powdery mildew infected and control grape berries at green and véraison stages.



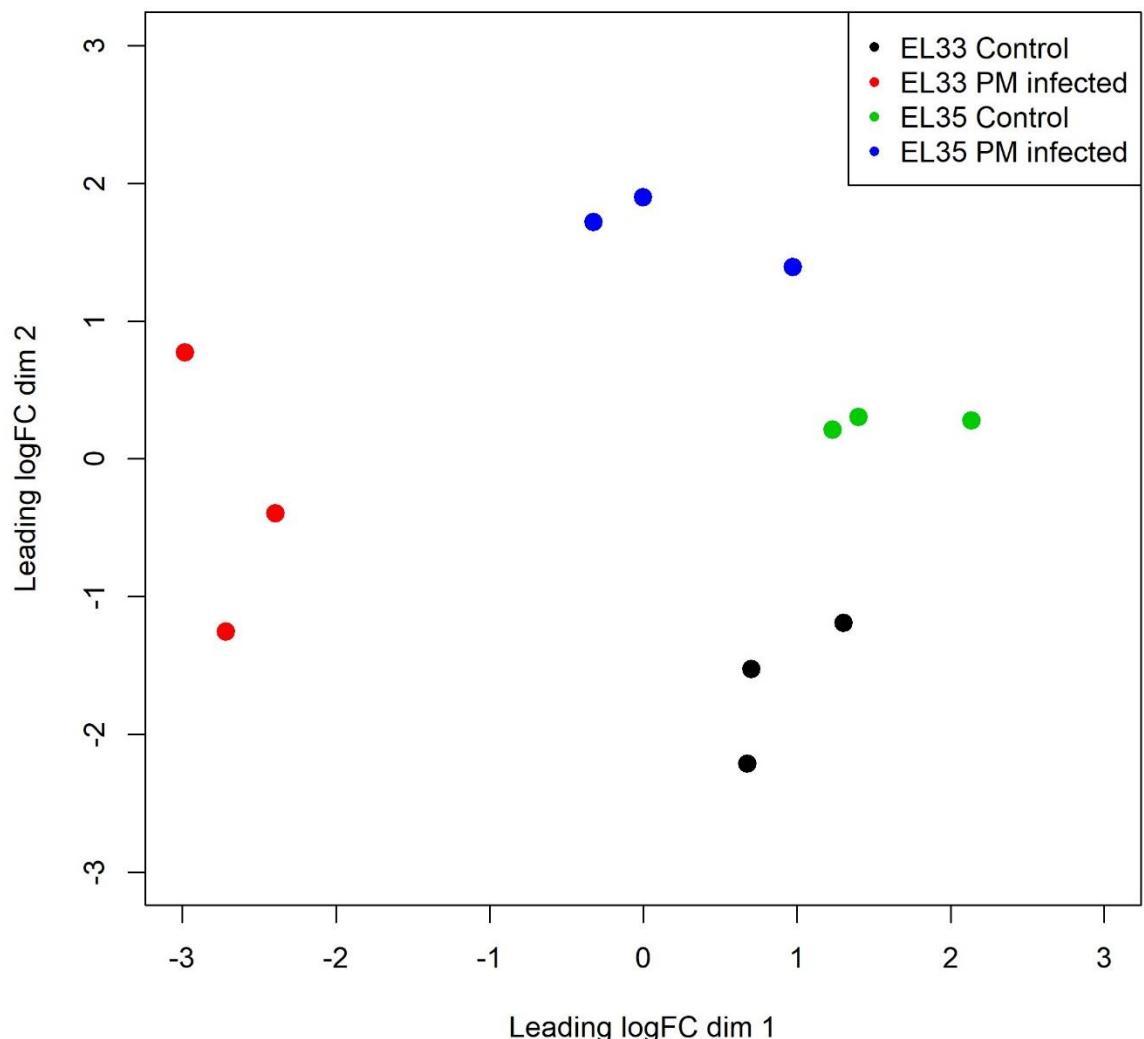
Supplementary Fig. S2 – Principal component analysis of metabolic profiles of infected and control grape berries at two ripening stages.



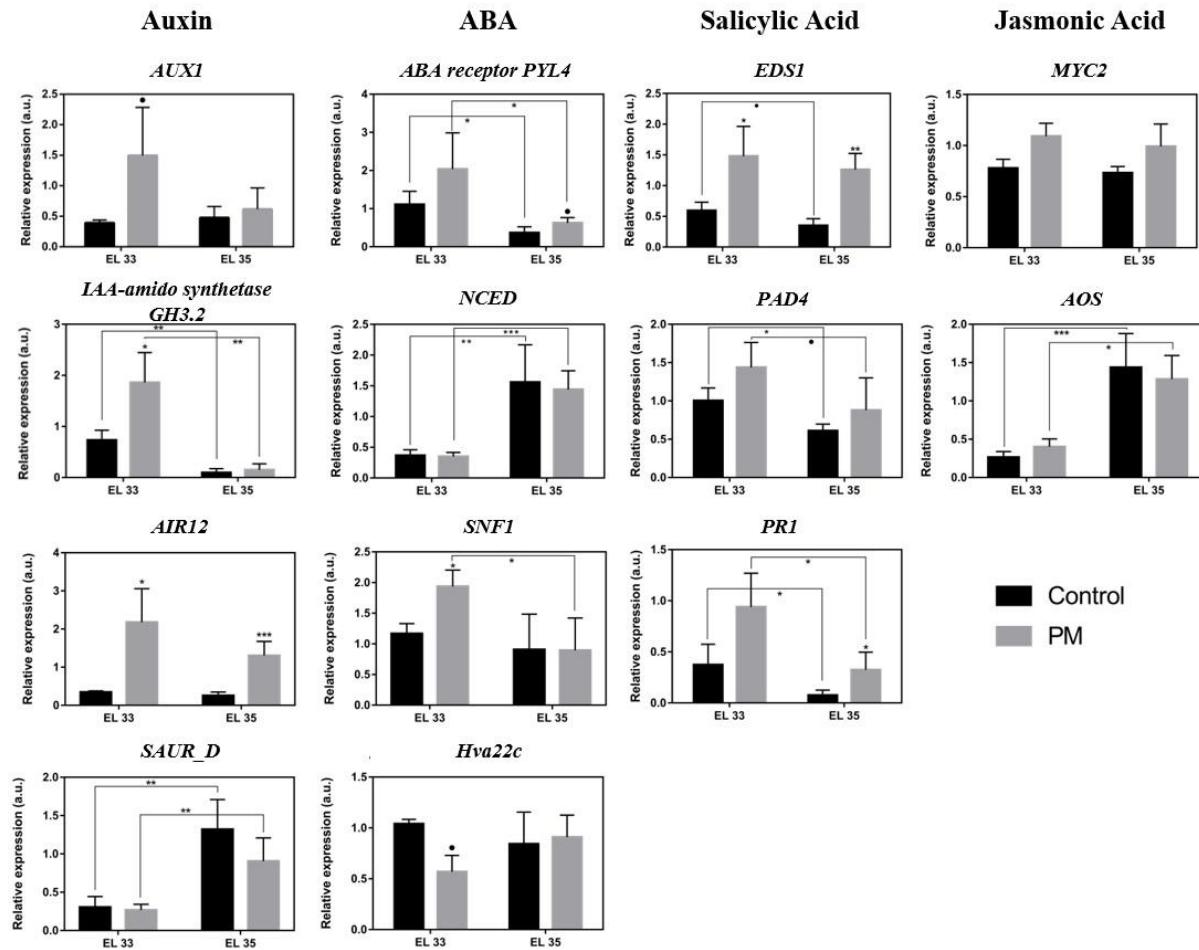
Supplementary Fig. S3 – Venn diagrams of differentially expressed genes in response to infection and ripening.



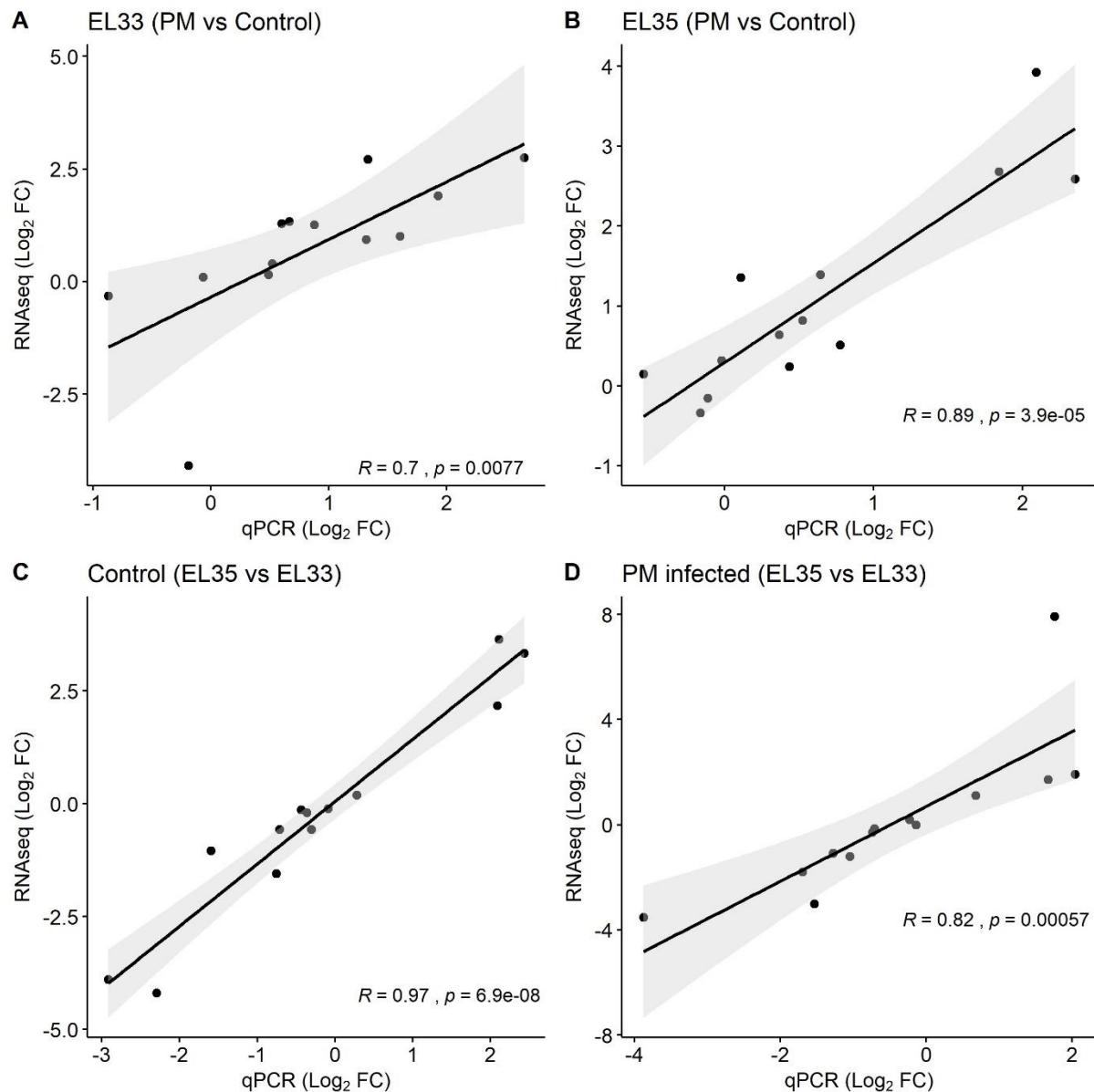
Supplementary Fig. S4 – Multidimensional scaling of RNAseq analysis of infected and control grape berries at two ripening stages.



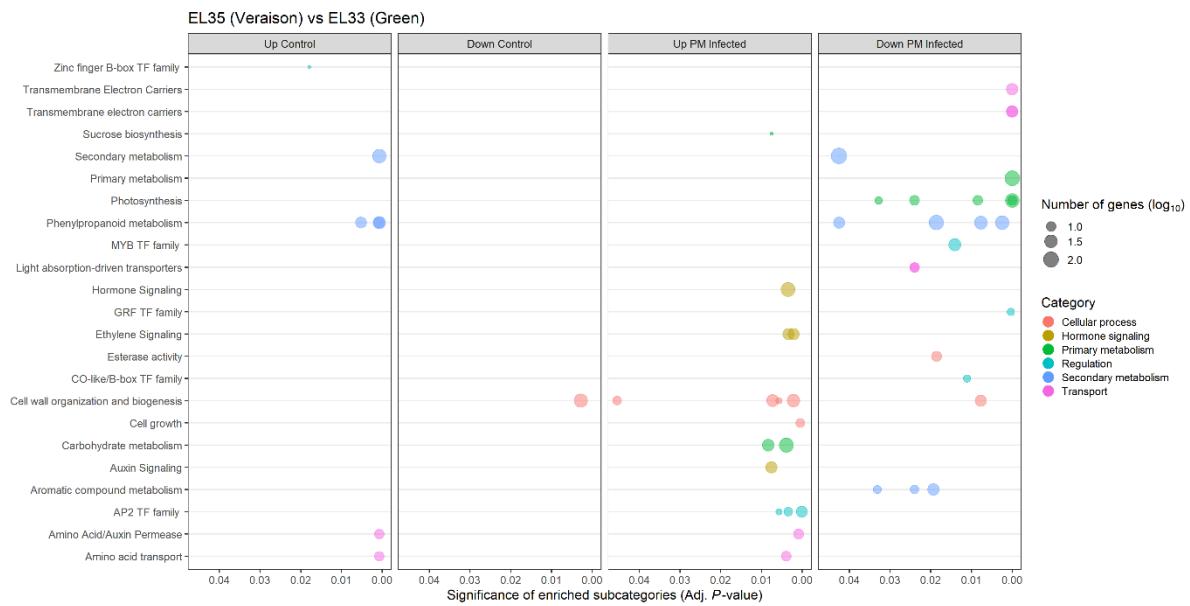
Supplementary Fig. S5 – Real-time PCR validation of gene expression.



Supplementary Fig. S6 – Pearson correlation between gene expression data obtained with real-time PCR and RNAseq data.



Supplementary Fig. S7 - Enriched functional subcategories in RNAseq data.



Supplementary Fig. S8 – Total phenolic content and phenylalanine ammonia-lyase enzyme assay.

