5 dpi   **10 dpi**

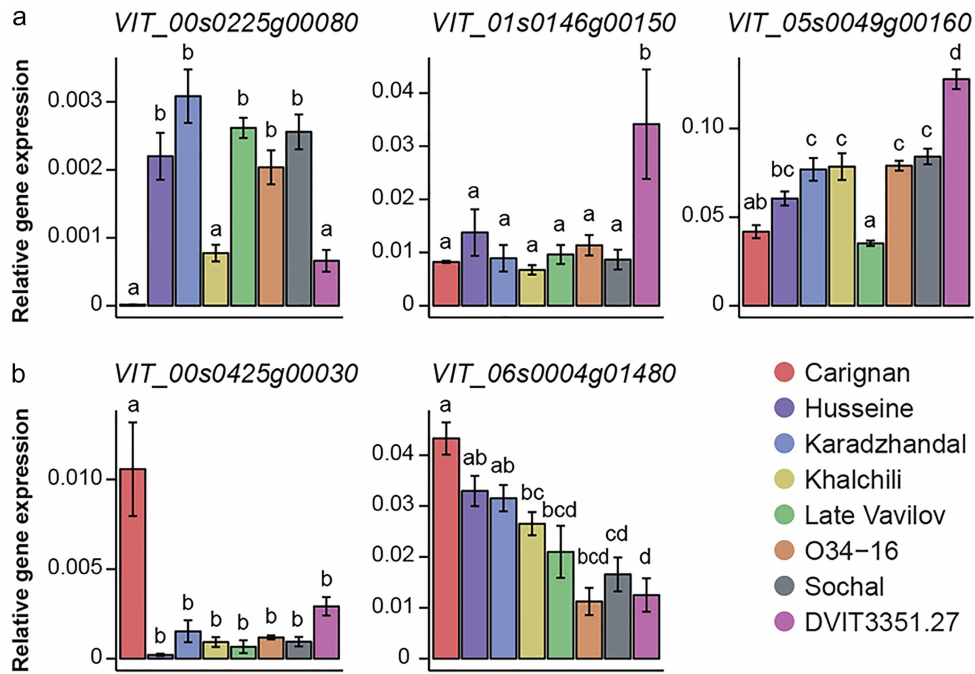**Figure S1.** Micrographs of E. necator infection at 5 and 10 dpi.

Figure S2. Constitutively differentially expressed genes measured by qRT-PCR in completely independent samples. Bar plots represent the relative mean expression of genes based on RNAseq constitutively more highly expressed in the PM-partial resistant accessions (A) or in 'Carignan' (B). Letters correspond to significant differences between accessions ($P \leqslant 0.05$; error bars indicate SD; $n = 3$ or 4). Healthy samples from a new independent set of plants were used in this analysis.
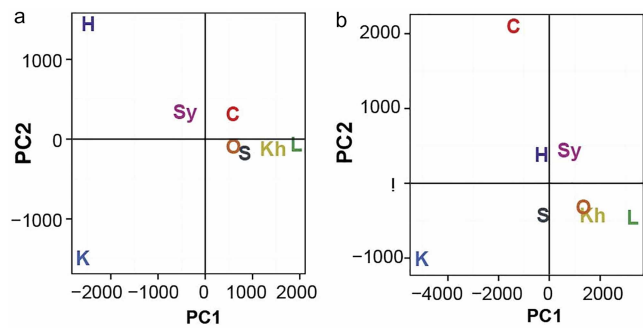
Figure S3. Graphical representation of principal coordinate analysis based on pairwise distances calculated from overlaps of differentially expressed genes between accessions at 1 (A) and 5 (B) dpi.
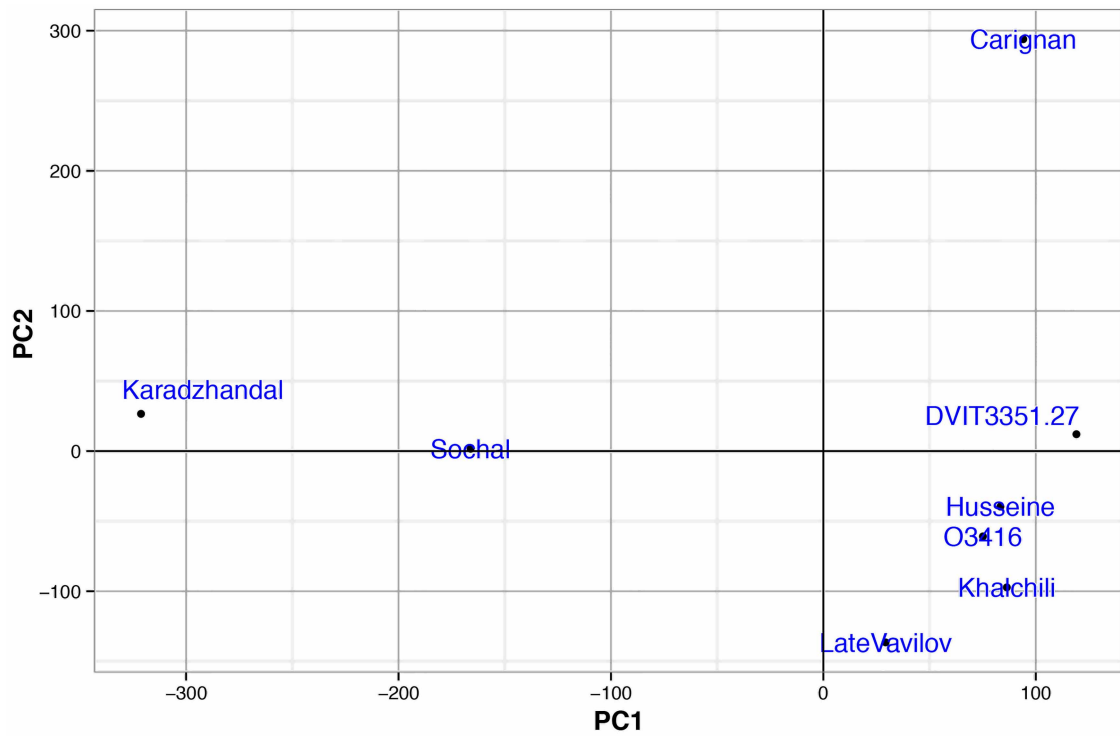
Figure S4. Graphical representation of principal coordinate analysis based on pairwise distances calculated from overlaps of GO terms found in differentially expressed genes at 5 dpi.
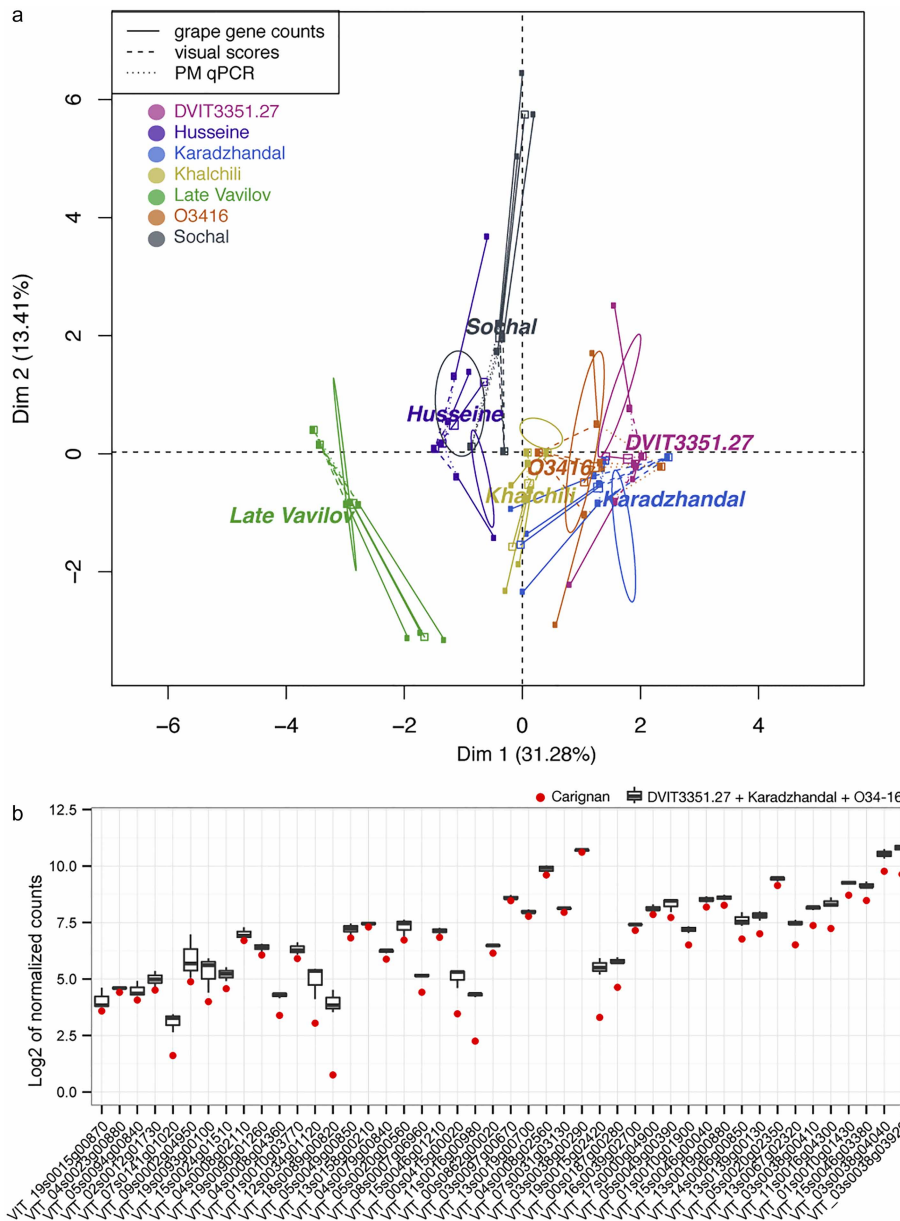
Figure S5. (A) Multiple factor analysis (MFA) of the seven PM-partially resistant genotypes using three variables: normalized counts of expressed genes, PM visual scores and *E. necator* biomass measured by qPCR (as previously reported in Figure 1). Each point represents a biological replicate for a given genotype. Ellipses define confidence areas (95%) for each genotype, while black squares represent their correspondent center of gravity. DIM, dimension. (B) Forty-six genes correlated with dimension 1 from panel A ($R \geqslant 0.7$, $P < 0.01$) with more counts than 'Carignan' in all three most phenotypically resistant accessions 'Karadzhandal' DVIT3351.27 and O34-16.