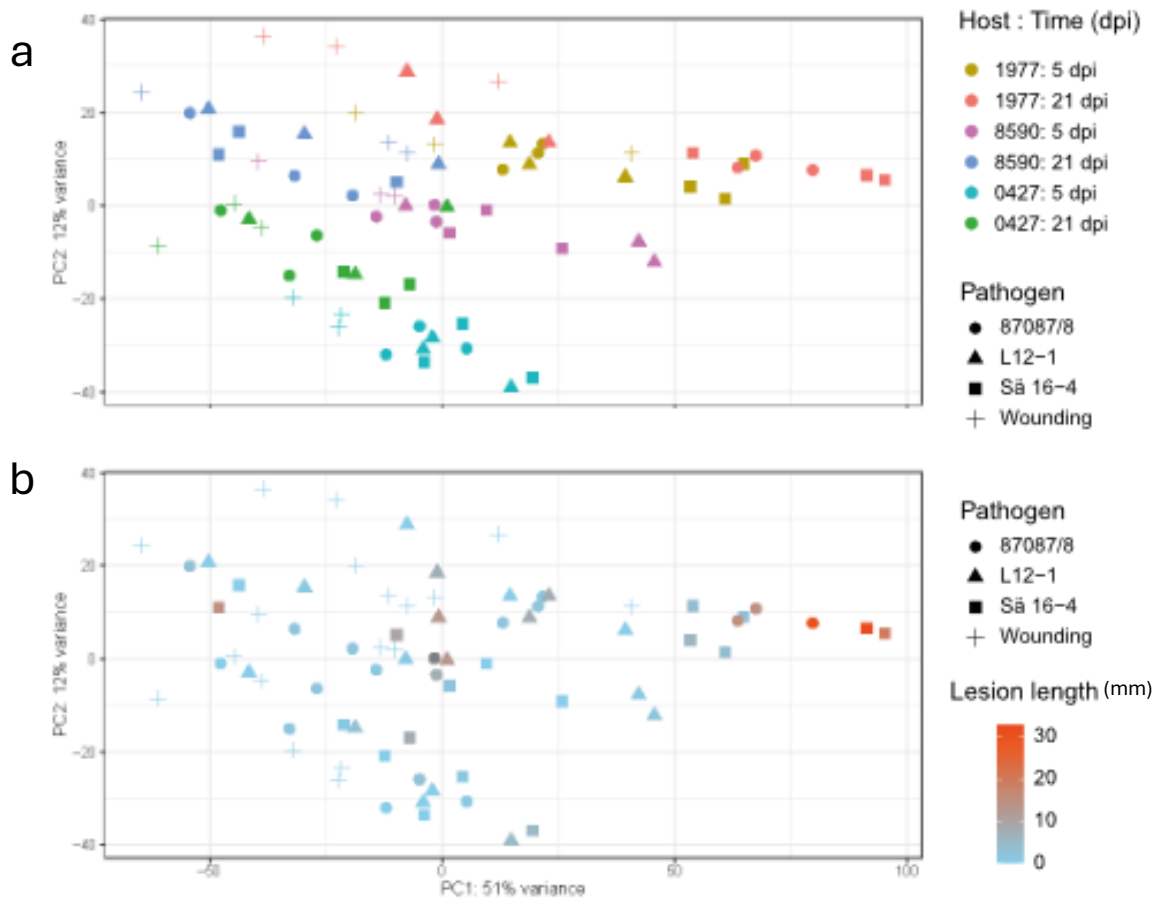
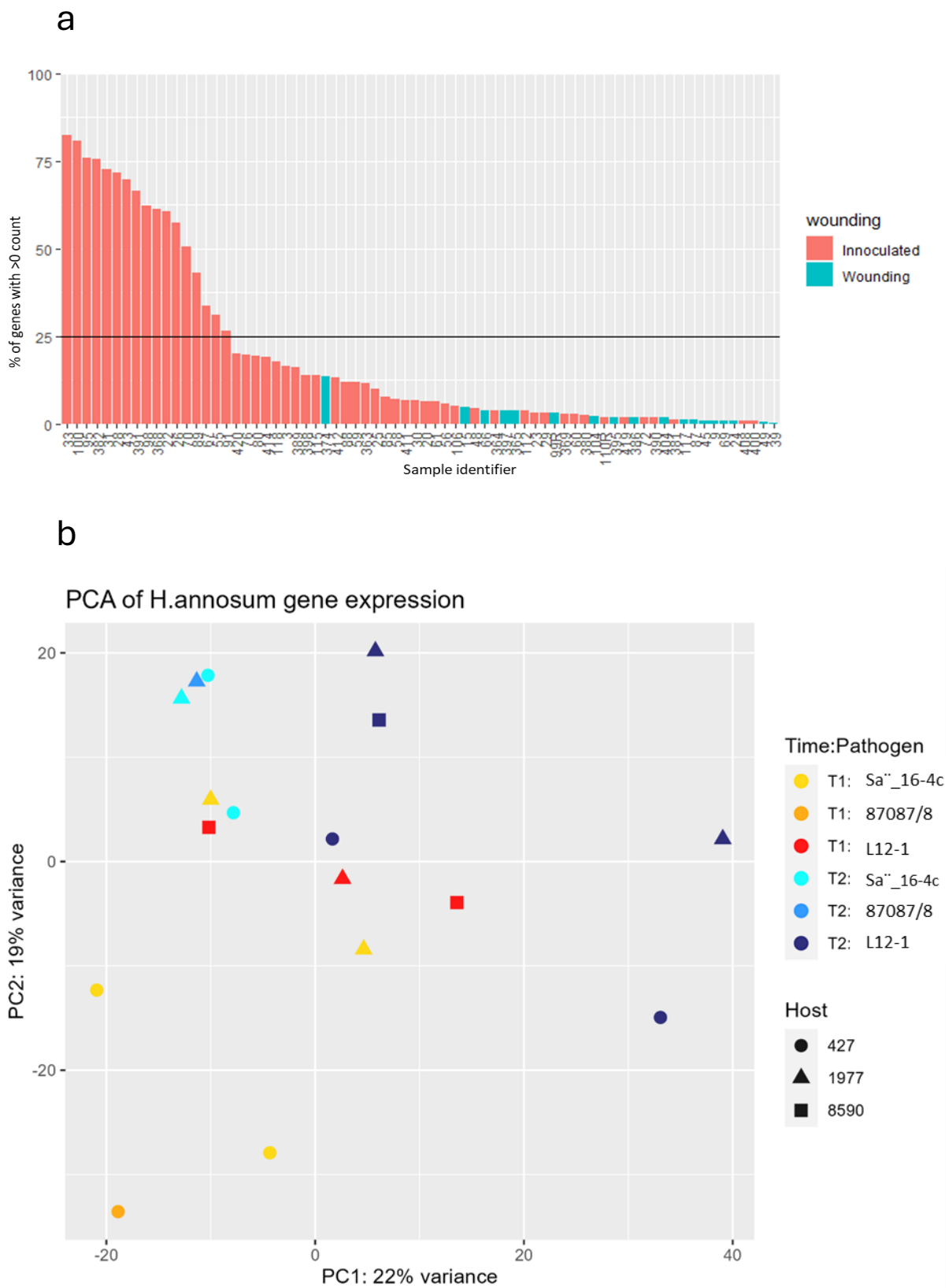
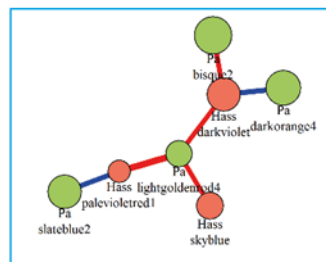
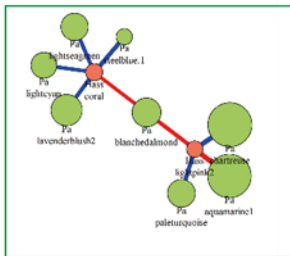
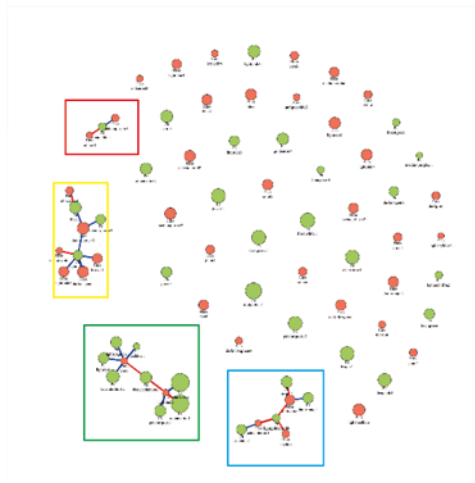
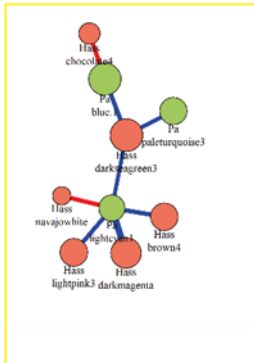
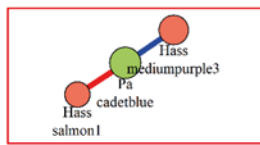




Supplementary file Figure 1. PCA of the gene counts mapped to the Norway spruce gene models, coloured by treatment and time point (a), and the measured lesion length in the phloem of each sample (b).



Supplementary Figure 2. Results of filtering for low coverage of the *Heterobasidion annosum* genome in the samples (a) the threshold line indicates the criterion that 75% of the genes in the *H. annosum* genome had zero counts the sample after the mapping. Samples in blue are from the wounding treatment and samples in red from the inoculation treatment. PCA of the 17 remaining samples indicating some separation between timepoints and an uneven representation of the isolates (Chi-square =5.323, df= 2 P=0.07).



Supplementary file Figure J