



S1 Fig. RT-qPCR validations of microarray data across 6, 18 and 24 hours of *P. cinnamomi* infected and SA and MeJA induced samples.

Fold change expression is shown for RT-qPCR data (blue diamonds) vs. fold change data of microarray data (red squares) for *PR4* (A1-A3), *JAZ3* (B1-B3), *PRI* (C1-C3), *PAL* (D1-D3) and *$\alpha 1$ tubulin* (E1-E3). *P. cinnamomi* infected samples (A1, B1, C1, D1 and E1), SA induced samples (A2, B2, C2, D2 and E2) and MeJA induced samples (A3, B3, C3, D3 and E3). Error bars indicate the SEM for three biological replicates. The Y-axis represents relative fold change and the X-axis represents the time points after treatment.