Dual RNA-seq comparison of the pine-*Fusarium circinatum* interaction between resistant (*Pinus tecunumanii*) and susceptible (*Pinus patula*) hosts

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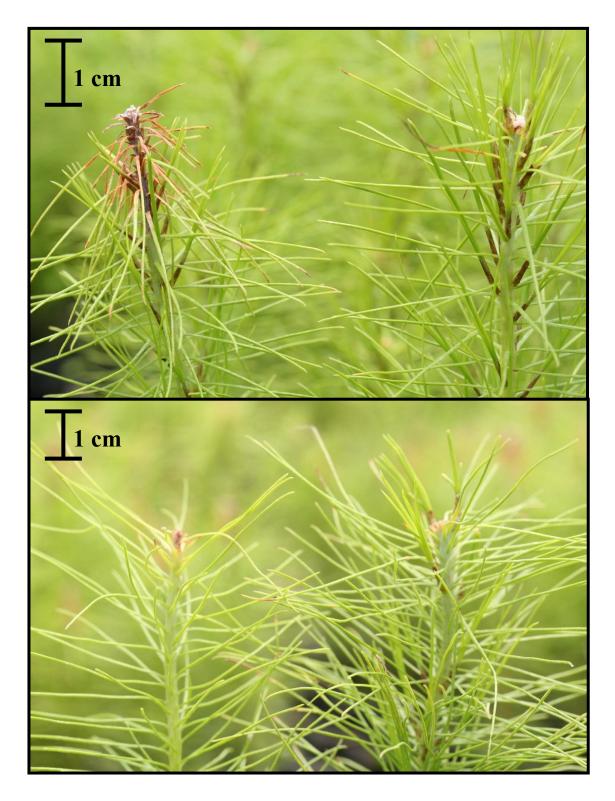


Figure S1 *Fusarium circinatum* disease symptoms on inoculated pine seedlings at 21 days post inoculation. Left – inoculated. Right – mock-inoculated. Top – *Pinus patula*. Bottom – *Pinus tecunumanii*.

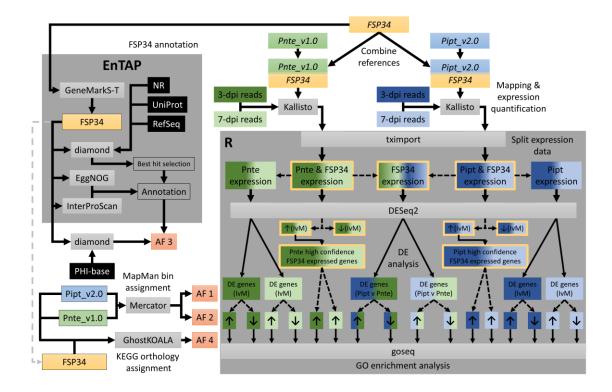


Figure S2 Bioinformatic methods flow diagram. FSP34 = *F. circinatum* proteome, Pipt_v2.0 = *P. patula* proteome, Pnte_v1.0 = *P. tecunumanii* proteome, in each case italics indicate transcriptomes. Grey boxes represent programs, orange boxes represent additional files (AF) and black boxes represent databases. Yellow represents *F. circinatum*, green represents *P. patula*, blue represent *P. tecunumanii*. In the R box dark colours represent 3-dpi and light colours represent 7-dpi. IvM = differentially expressed genes in inoculated relative to mock-inoculated samples, Pnte v Pipt = differentially expressed *F. circinatum* genes from *P. tecunumanii* data sets relative to *P. patula* data sets. Arrows refer to up- and down-regulated DE genes.

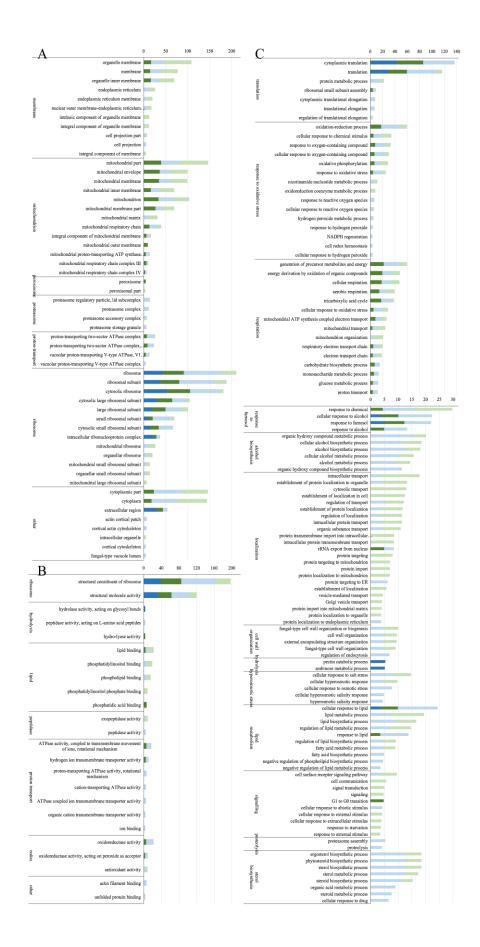


Figure S3 Gene ontology terms enriched among high confidence *in planta* expressed *F. circinatum* genes. (A) Cellular compartment, (B) Molecular Function and (C) Biological Process GO terms enriched within up-regulated data sets at 3- (dark bars) and 7- (light bars) dpi in *P. patula* (blue) and *P. tecunumanii* (green). The y-axes represent the absolute log₂(q-value) following Benjamini & Hochberg False Discovery Rate (FDR) correction.