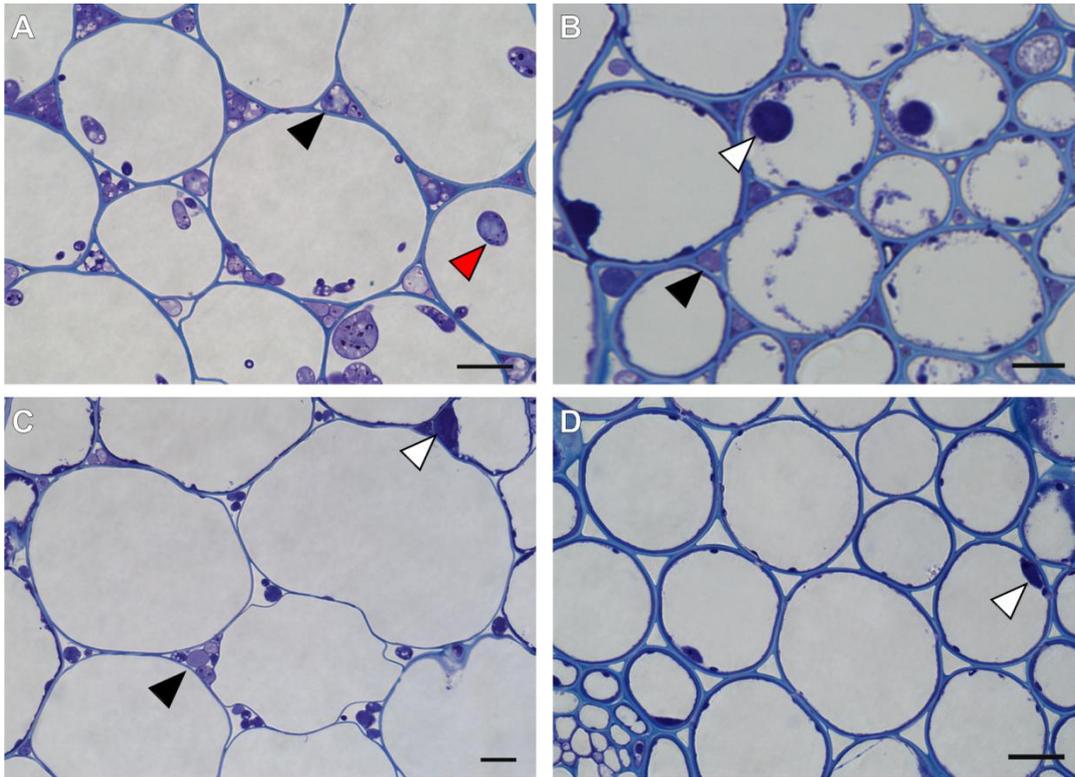


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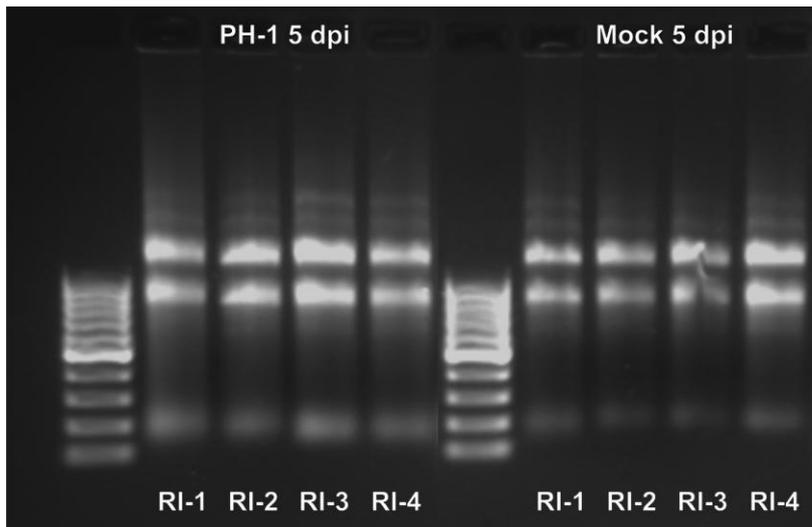
485 **Supplementary Figure 1** Confirmation that X-gluc specifically stains the hyphae of  
486 constitutive GUS expressing strain. All images in this figure are of the lemma from the  
487 inoculated floret at 2 dpi, which was stained with X-gluc prior to fixation. All images are of  
488 sequential transverse 3  $\mu$ m LR white sections; panels (A) and (B) are stained with 0.1 %  
489 TBO, pH 9, while panels (C) and (D) are not. White arrow = host nuclei, white arrowhead =  
490 intercellular fungal hyphae. Bar = 15  $\mu$ m.



491

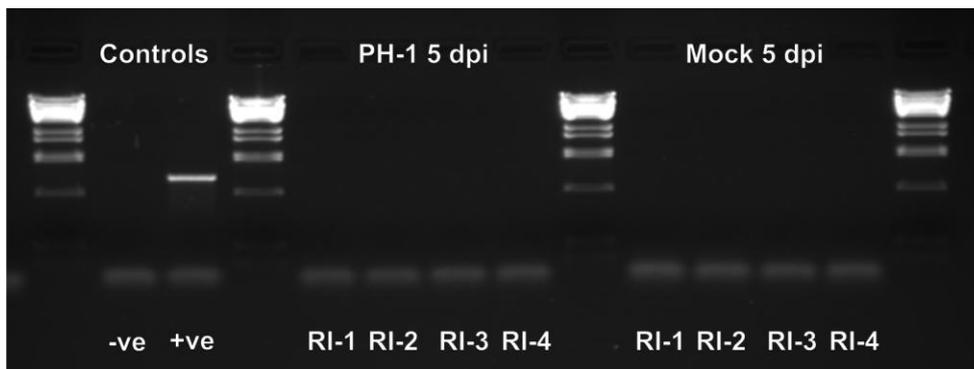
492 **Supplementary Figure 2** The identification of fungal infection in the first three rachis  
493 internodes at 5 dpi. Images of transverse 1 µm LR white sections of cortical cells within  
494 various rachis internodes stained with 0.1% TBO pH 9. The first (A), second (B), third (C)  
495 and fourth (D) rachis internode below the point of inoculation at 5 dpi. Generic legend: black  
496 arrowhead = intercellular hyphae, red arrowhead = intracellular hyphae, white arrowhead =  
497 host nuclei. Bar = 15 µm.

498



499

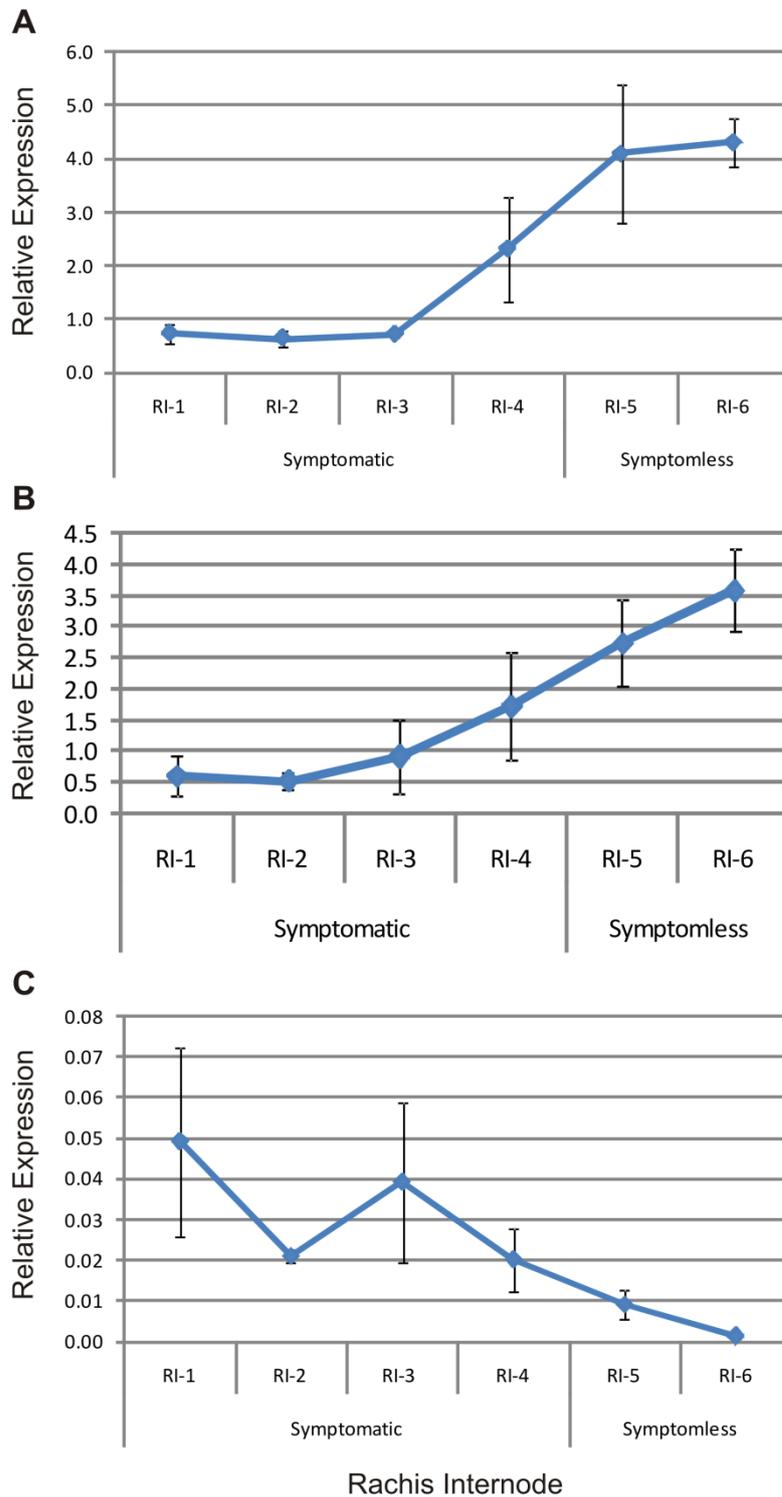
500 **Supplementary Figure 3** The extracted RNA from the rachis internodes of the PH-1 infected  
501 and the water-only control (Mock) at 5 dpi. One  $\mu\text{g}$  of total RNA was separated on a 1 %  
502 agarose gel alongside a 100 bp DNA ladder (Generuler, Fermentas). Legend: RI-1 to RI-4 =  
503 the sequential rachis internodes below the inoculated spikelet.



504

505 **Supplementary Figure 4** The extracted RNA from the rachis internodes of the PH-1 infected  
506 and the water-only control (Mock) at 5 dpi is free of genomic DNA (gDNA) contamination.  
507 Intergenic primers that only amplify gDNA were used. The presence of an amplicon (902 bp)  
508 on the 1 % agarose gel, separated alongside a lambda\_DNA\_BstE II ladder, represents the  
509 presence of gDNA. Legend: RI-1 to RI-4 = the sequential rachis internodes below the  
510 inoculated spikelet, -ve = the non template negative control, +ve = the gDNA positive  
511 control.

512



513

514 **Supplementary Figure 5** Fungal *TRI4* (A) and *TRI5* (B) gene expression in the infected  
 515 rachis internodes in which *F. graminearum* was detected at 7 dpi. Relative expression was  
 516 measured by RT-qPCR and values normalised for fungal biomass relative to the expression  
 517 of *F. graminearum*  $\gamma$ -actin and  $\beta$ -tubulin (C). Biological error is represented by one standard  
 518 deviation from the mean.

519 **Supplementary Table 1** Fungal genes selected for expression analysis by RT-qPCR, their  
 520 FGSG locus ID, BROAD (www.broadinstitute.org) / MIPS (www.mips.helmholtz-  
 521 muenchen.de) function and their primer sequence.

Fungal gene	FGSG locus ID	Broad / MIPS function	Primer sequence (5'-3')	
			Sense	Antisense
<i>FgActin</i>	07335.3	Actin / Probable Actin	ATGGTGCTCACTCACGTTGT CC	CAGTGGTGGAGAAGGTGT AACC
<i>FgTubulin</i>	09530.3	Tubulin beta chain / Beta-tubulin	TCAACATGGTGCCCTTCC	TTGGGGTCGAACATCTGC
<i>FgTri4</i>	03535.3	Trichodiene oxygenase / Trichodiene oxygenase [cytochrome P450]	AGACTACTTCAAGGACAC TGGCC	GGTAAGGGAGATTCTCTA GGGTAGC
<i>FgTri5</i>	03537.3	Trichodiene synthase [sesquiterpene cyclase] / Trichodiene synthase	GATGAGCGGAAGCATTTC C	CGCTCATCGTCTCGAATTCC
<i>FgTri6</i>	03536.3	Hypothetical protein similar to regulatory protein / Trichothecene biosynthesis positive transcription factor (TRI6)	TGTCGCTACTCAGAATGC C	CCCTGCTAAAGACCCTCA
<i>FgTri9</i>	03539.3	Conserved hypothetical protein / Hypothetical protein	TATCCACTCAAACACTCA CCCC	TGGTAGCGCATAAAGCAG C
<i>FgTri14</i>	03543.3	Hypothetical protein similar to TRI14 / Putative trichothecene biosynthesis gene	CTGATAAGCTTGAACCAC CTCG	TTGATCACAACGGGAGTT CC

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