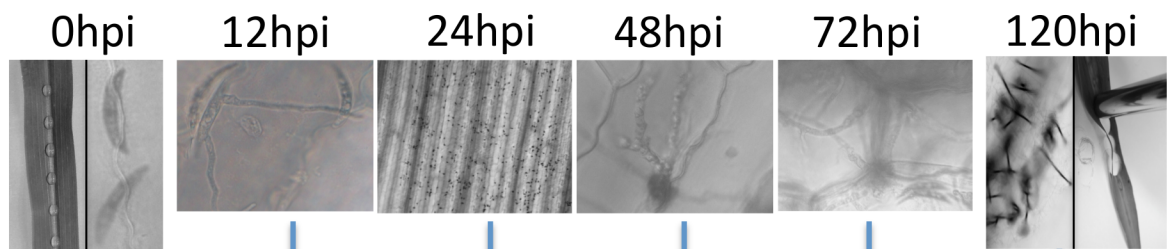


# Additional file 8



collection of infected leaf material

RNA preparation and cDNA synthesis

Illumina Sequencing (100nt paired end reads)

112 mio  
raw reads

168 mio  
raw reads

180 mio  
raw reads

231 mio  
raw reads

232 mio  
raw reads

194 mio  
raw reads

quality processing

mapping (Tophat)

2.9 mio  
mapped  
reads

2 mio  
mapped  
reads

1.8 mio  
mapped  
reads

3.5 mio  
mapped  
reads

14 mio  
mapped  
reads

36.8 mio  
mapped  
reads

merged data sets (SAMTools)  
(60 mio mapped reads)

RSeQC  
Subread

Cufflinks  
AUGUSTUS  
manual inspection

Bedtools

manual inspection

PicardTools  
SAMTools  
manual inspection

quality  
analysis

transcriptome  
re-annotation  
+  
nTAR detection

UTR annotation

AS analysis

RNA editing