

Table S2. Short read coverage of *Magnaporthe oryzae* and wheat transcriptomes in Bangladeshi samples

Sample Name	No. of <i>M. oryzae</i> transcripts with FPKM > 0.5 ^{a,b}	% of <i>M. oryzae</i> transcriptome (14349 transcripts) ^b	No. of wheat transcripts with FPKM > 0.5 ^{a,c}	% of wheat transcriptome (100344 transcripts) ^c
12 (symptomatic)	9604	66.93	52245	52.07
7 (symptomatic)	2661	18.54	53850	53.67
F12 (asymptomatic)	88	0.61	54914	54.73
F7 (asymptomatic)	31	0.22	52962	52.78

^aIllumina short reads were mapped to the transcriptomes using bowtie2 (v2.1.0) and FPKM values were calculated with cufflinks (v2.1.1).

^bTranscriptome of *M. oryzae* BR32 downloaded from <http://genome.jouy.inra.fr/gemo/> was used as a reference.

^cTranscriptome of wheat downloaded from http://plants.ensembl.org/Triticum_aestivum/ was used as a reference.