R0	R1	R2	R3	R4		0.10
vs S0	vs S1	vs S2	vs S3	vs S4		0.08
u/	u/	u/	u/	ų		0.06
Up Dow	Up Dow	Up Dow	Up Dow	Up Dow		0.04
					MAPK signaling pathway - plant Photosynthesis	0.02
					Selenocompound metabolism Sulfur metabolism	0.00
					Folate biosynthesis Metabolism of xenobiotics by cytochrome P450 Drug metabolism - cytochrome P450 Leukocyte transendothelial migration Fc epsilon RI signaling pathway Ras signaling pathway Chemokine signaling pathway Fc gamma R-mediated phagocytosis Regulation of actin cytoskeleton Pancreatic secretion Focal adhesion cAMP signaling pathway Rap1 signaling pathway Phospholipase D signaling pathway Natural killer cell mediated cytotoxicity Inositol phosphate metabolism VEGF signaling pathway Sesquiterpenoid and triterpenoid biosynthesis B cell receptor signaling pathway Osteoclast differentiation Carbohydrate digestion and absorption Biosynthesis of secondary metabolites Plant hormone signal transduction Biosynthesis of antibiotics Prodigiosin biosynthesis Microbial metabolism in diverse environments	

Figure S8. KEGG analysis of the specific differentially expressed genes of fungal-inoculated kernels between AF99 and AF32.

Color depth represents the degree of significance, as shown in the scale at the right (corrected p-value).



Figure S9. Determination of soft-thresholding power ( $\beta$ ).

a: scale-free topology fit index as a function of the soft-thresholding power, the red line indicates that R2 is equal to 0.85. b: mean connectivity as a function of the soft-thresholding power.

Sample dendrogram and trait heatmap



Figure S10. The sample dendrogram and trait heatmap.

Lines: "0" for AF32 and "1" for AF99; Ino: "0" for mock and "1" for *A. flavus* inoculation; Time: "0, 0.5, 1.5, 3, 6" indicate the time after inoculation; RC0: "1" for the three biological repetitions of AF99 (mock-treated) at the T0 stage and "0" for other samples; R0: "1" for the three biological repetitions of AF99 (*A. flavus* inoculation) ) at the T0 stage and "1" for other samples; SC0:"1" for the three biological repetitions of AF32 (mock-treated) at the T0 stage and "0" for all the other samples; S0:"1" for the three biological repetitions of AF32 (mock-treated) at the T0 stage and "0" for all the other samples; S0:"1" for the three biological repetitions of AF32 (*A. flavus* inoculation) at the T0 stage and "0" for all the other samples; S0:"1" for the three biological repetitions of AF32 (*A. flavus* inoculation) at the T0 stage and "0" for all the other samples; S0:"1" for the three biological repetitions of AF32 (*A. flavus* inoculation) at the T0 stage and "0" for all the other samples; S0:"1" for the three biological repetitions of AF32 (*A. flavus* inoculation) at the T0 stage and "0" for all the other samples; S0:"1" for the three biological repetitions of AF32 (*A. flavus* inoculation) at the T0 stage and "0" for all the other samples; S0:"1" for the three biological repetitions of AF32 (*A. flavus* inoculation) at the T0 stage and "0" for all the other samples; S0:"1" for the three biological repetitions of AF32 (*A. flavus* inoculation) at the T0 stage and "0" for all the other samples; the rest are similar as "RC0", "R0", "SC0" and "S0".



Module Membership in brown module



Figure S11. Scatterplots of gene significance versus module membership for the brown/R0(a), magenta/SC1(b), pink/S1(c), black/S2(d) and brown/S3(e), with correlations and p-values indicated.





Figure S12. GO and KEGG pathway analysis of 110 hub genes identified in this study. a. GO analysis of 110 hub genes. Each circle represents an enrichment category, and the size of the circle indicates the number of genes. Detailed enrichment results are shown in Table S9. b. The top 20 associated KEGG pathways for the 110 hub genes.





4.00 3.00 2.00 1.00 0.00 -1.00 -2.00

-3.00