

Applied Microbiology and Biotechnology

Supplemental Figures

Transcriptome changes of fission yeast cells exposed to fumonisin B1 or co-cultured with *Fusarium verticillioides*

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Fig. S1 *S. pombe*–*F. verticillioides* co-cultures were prepared (a). The cultures were incubated without shaking, at 25°C, for 2 days (*: *F. verticillioides* cells floated on the surface of the liquid, **: *S. pombe* cells settled on the bottom of the flask). Controls: *F. verticillioides* (b), and *S. pombe* monocultures (c)

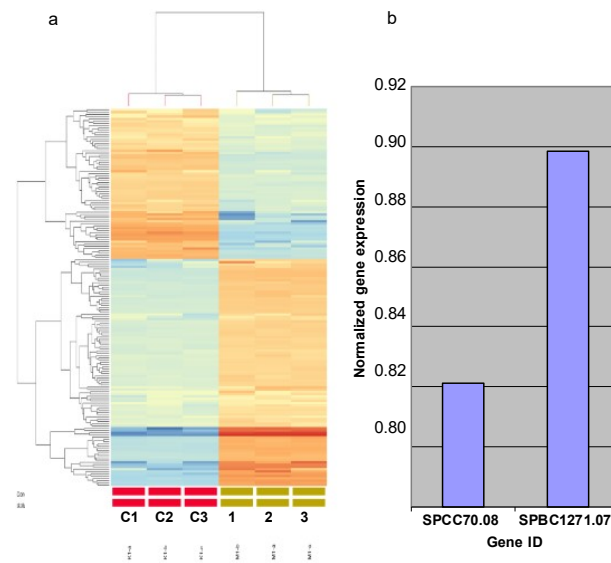


Fig. S2 RNA sequencing of the *S. pombe* cells treated with 0.5 ppm FB1. Heatmap of genes with statistically significantly altered mRNA levels (a); C1, C2, C3: control, 1, 2, 3: FB1-treated samples. Blue color: down-regulated genes, reddish color: up-regulated genes. RT-PCR analysis of randomly selected down-regulated genes confirmed the results of RNA sequencing, as their normalized gene expression was below 1 (b)

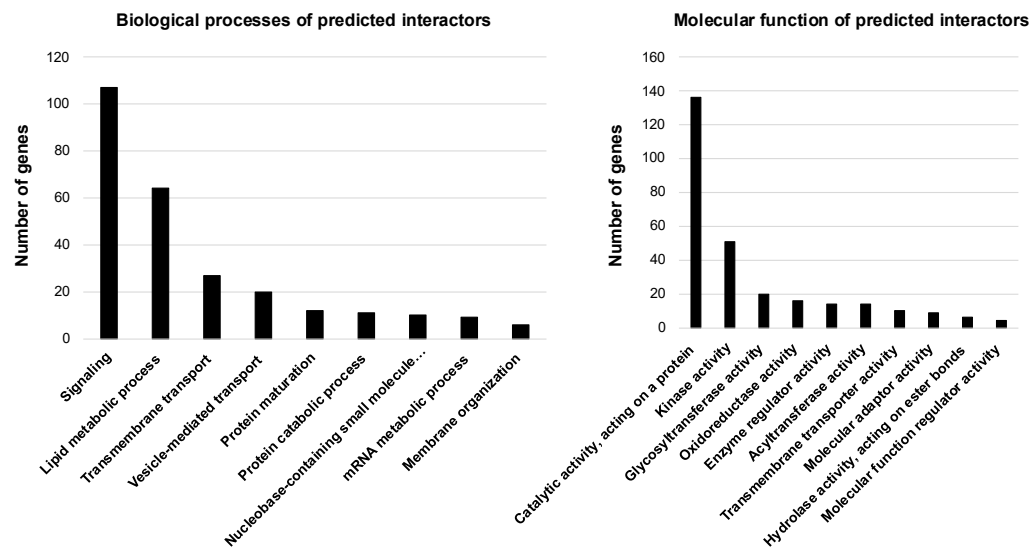


Fig. S3 Biological processes and molecular functions of the predicted interactors of the differentially expressed *S. pombe*-specific genes after FUM treatment. Bioinformatics analysis suggests that most interactor proteins may have a "signal transduction" and "catalytic activity" function

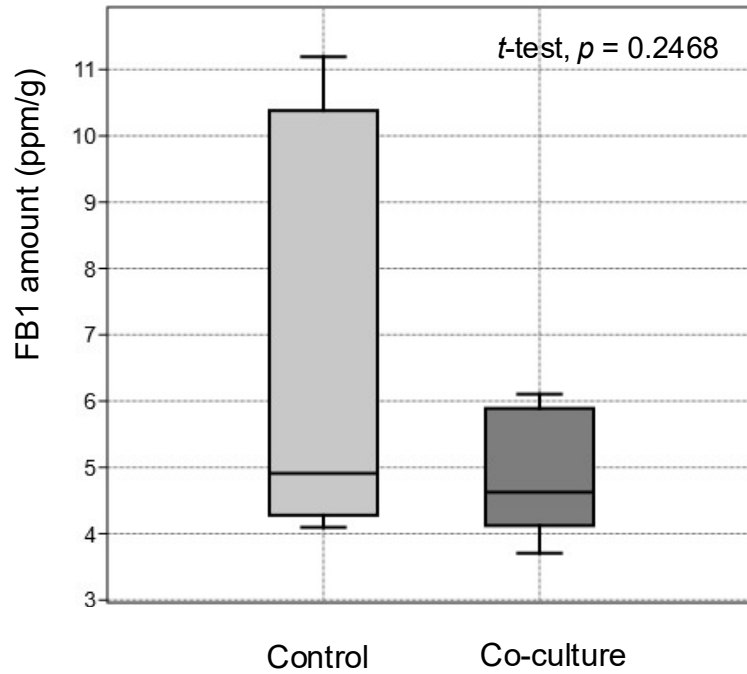


Fig. S4 Fumonisin production of *F. verticillioides* was reduced when co-cultured with *S. pombe* (PDA, pH 4.0, room temperature, 6 days); however, it was not significant. Control: *F. verticillioides* monoculture, Co-culture: *F. verticillioides* and *S. pombe* were grown on the same Petri dishes (n = 5)

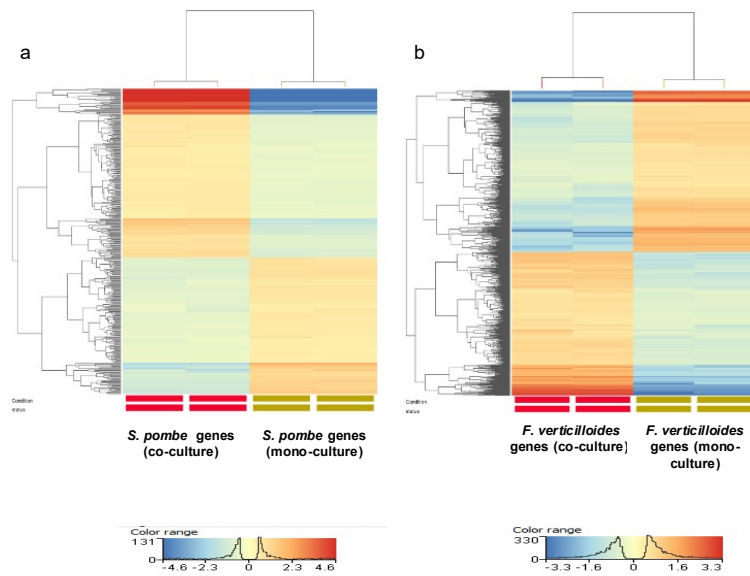


Fig. S5 *S. pombe*–*F. verticillioides* co-cultures were prepared and transcriptional profile analyses were performed from the yeast and *Fusarium* cells. Heatmap of the significantly expressed *S. pombe* (a) and *F. verticillioides* (b) genes. Blue color: down-regulated genes, reddish color: up-regulated genes