

## **Supplementary Information**

### **Efficient Biodegradation of Patulin by *Aspergillus niger* FS10 and Metabolic Response of Degrading Strain**

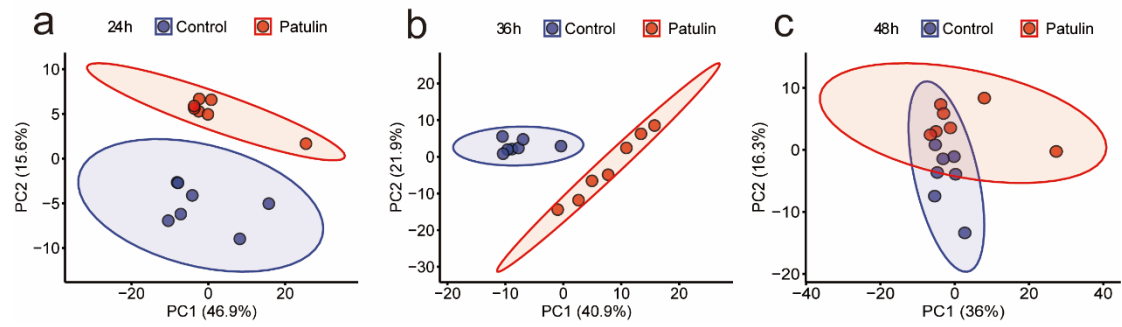
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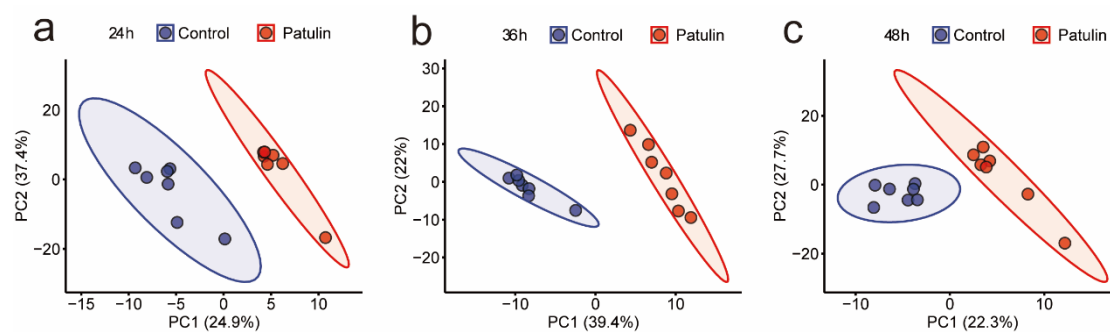
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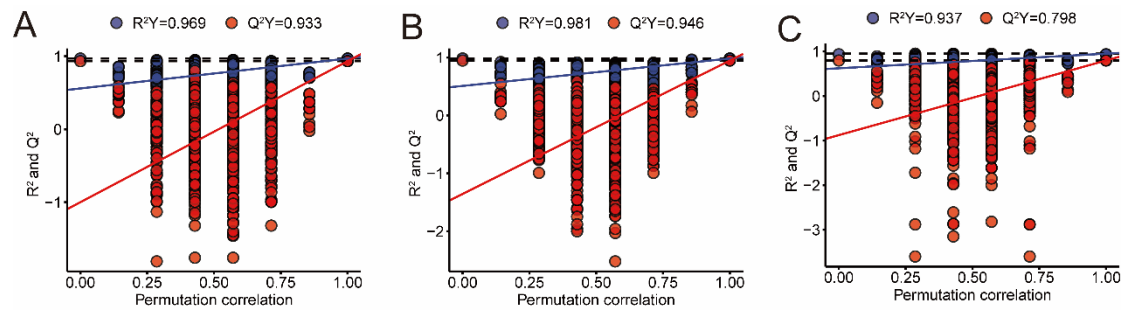
† These authors contributed equally to this work.



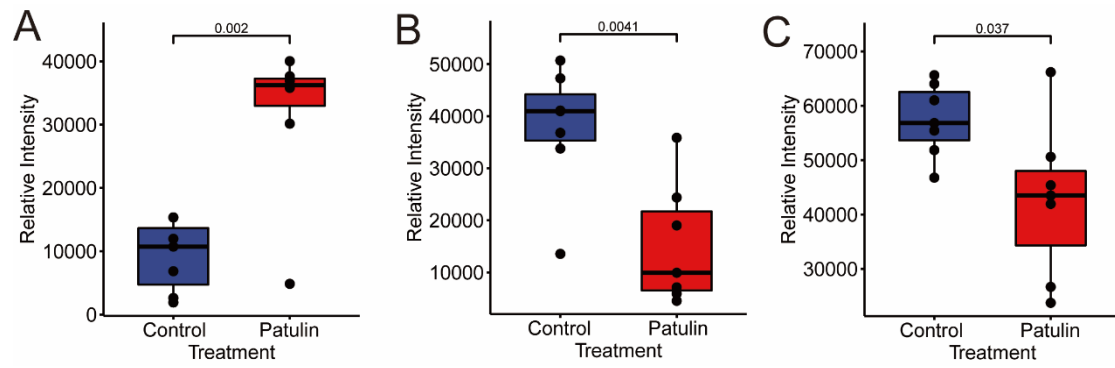
**Figure S1** PCA of control samples (blue) and patulin treatment samples (red) in different degradation time. (a) 24 h, Variance of PC<sub>1</sub> is 46.9% and variance of PC<sub>2</sub> is 15.6%. (b) 36 h, Variance of PC<sub>1</sub> is 40.9% and variance of PC<sub>2</sub> is 21.9%. (c) 48 h, Variance of PC<sub>1</sub> is 36% and variance of PC<sub>2</sub> is 16.3%. Results are expressed as means of seven replicates.



**Figure S2** Partial Least Squares Discrimination Analysis (PLS-DA) (a) 24 h. (b) 36 h. (c) 48 h. The control group (blue), the patulin treatment group (red). There was a significant separation between each group, indicating that there was a significant difference in the metabolism of *A. niger* FS10 between the control group and the patulin treatment group.



**Figure S3** Permutation test (A) 24 h,  $R^2Y=0.969$ ,  $Q^2Y=0.933$ . (B) 36 h,  $R^2Y=0.981$ ,  $Q^2Y=0.946$ . (C) 48 h,  $R^2Y=0.937$ ,  $Q^2Y=0.798$ . The scores of  $R^2Y$  and  $Q^2Y$  in each group were higher, which indicated that the prediction of the model was reliable and could be used for the analysis of differential metabolites.



**Figure S4** Boxplots of the relative concentration change of glutathione. (A) 24 h. (B) 36 h. (C) 48 h. The control group (blue), the patulin treatment group (red)