Supplementary Materials

Hao D.C. et al. Functional and Transcriptomic Characterization of a Dye-decolorizing Fungus from *Taxus* Rhizosphere

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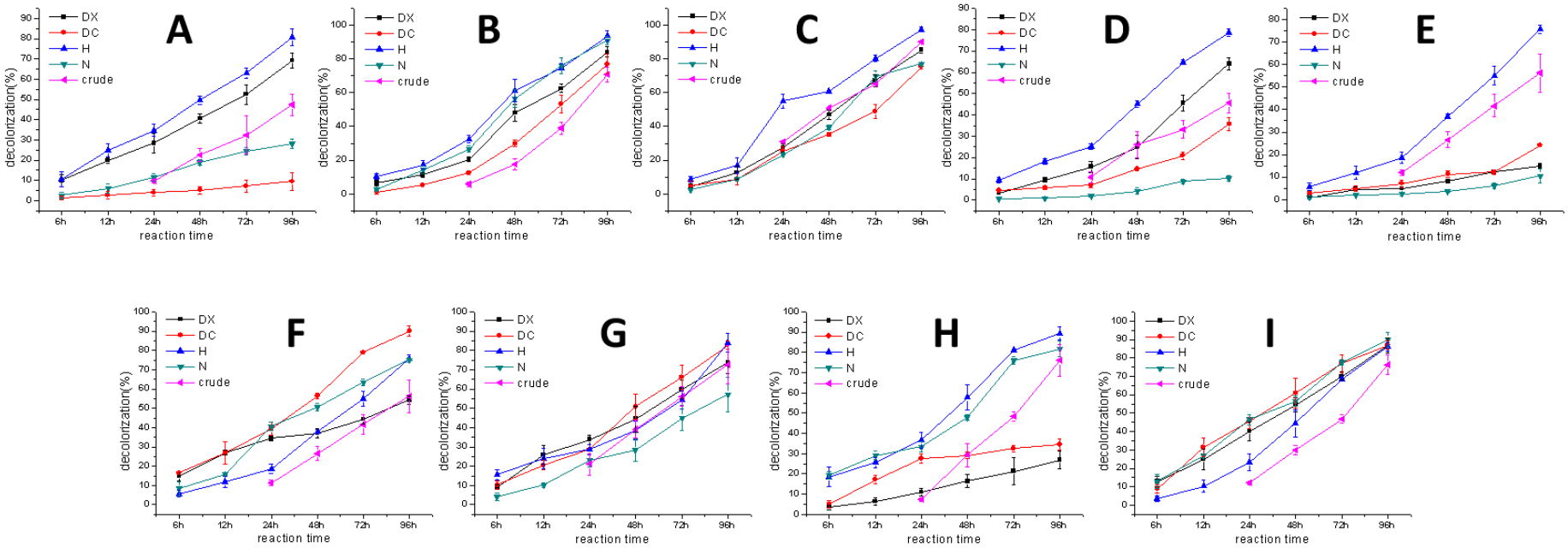

Fig. S1. Decolorization of nine reactive dyes by laccase-producing fungi isolated from *Taxus* rhizospheres: A. reactive black 5; B. RG 19; C. reactive deep blue M-2GE; D. reactive brilliant orange K-GN; E. reactive brilliant red KE-7B; F. reactive navy blue B-GD; G. reactive brilliant blue X-BR; H. reactive brilliant blue K-3R; I. reactive turquoise blue KN-G. DX, *Aspergillus*; DC, *Glomerella*; H, *M. verrucaria* strain DJTU-sh7; N, *T. stollii*; crude, crude enzyme of DJTU-sh7. Y axis represents the percentage of dye decolorization. Error bars are standard deviations (n = 3).

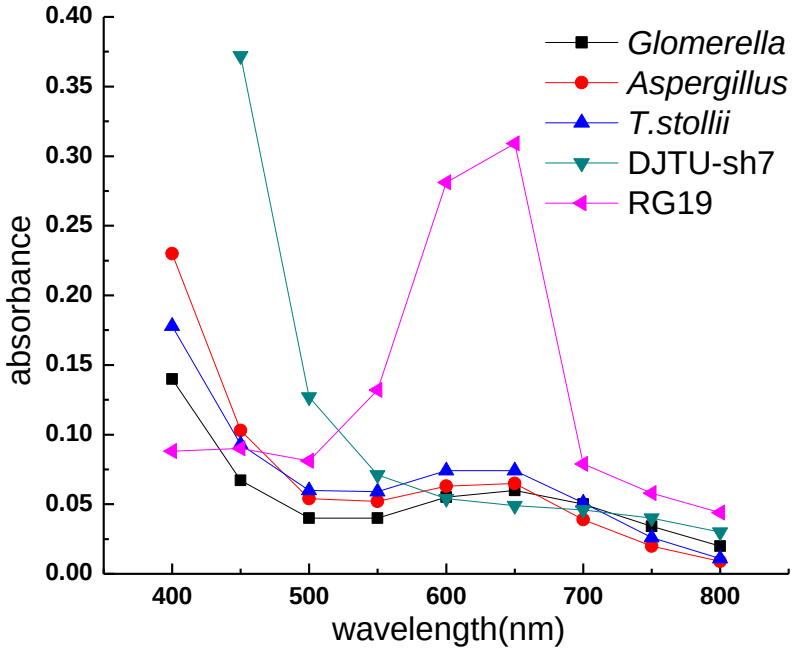

Fig. S2. UV-Vis spectrophotometric analysis of RG 19 (initially 20 mg/l) and metabolites formed by *M. verrucaria* strain DJTU-sh7 and other three fungal strains in 72h.

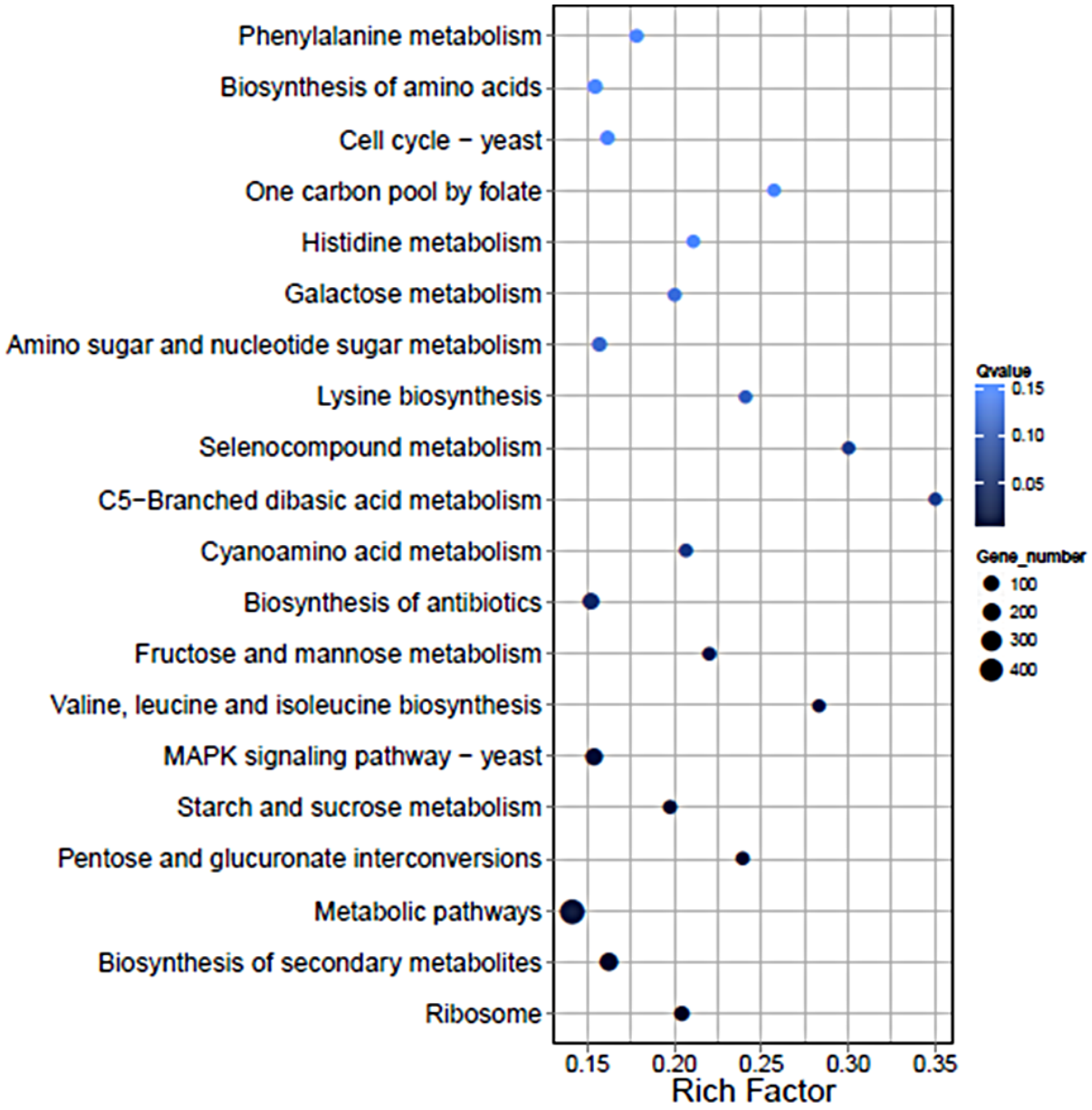

Fig. S3. Metabolic pathway enrichment analysis of DEGs. The whiter the color, the larger the *q* value; the more blue the color, the smaller the *q* value, and the more significant the enrichment. The size of the dots represents the number of DEGs (the larger the dot, the larger the DEG number). Rich factor is the quotient of no. of DEGs belonging to a pathway and no. of Unigenes belonging to the same pathway; the larger the rich factor, the more obvious the enrichment.