

Metabolomic differential analysis of interspecific interactions among white rot fungi *Trametes versicolor*, *Dichomitus squalens* and *Pleurotus ostreatus*

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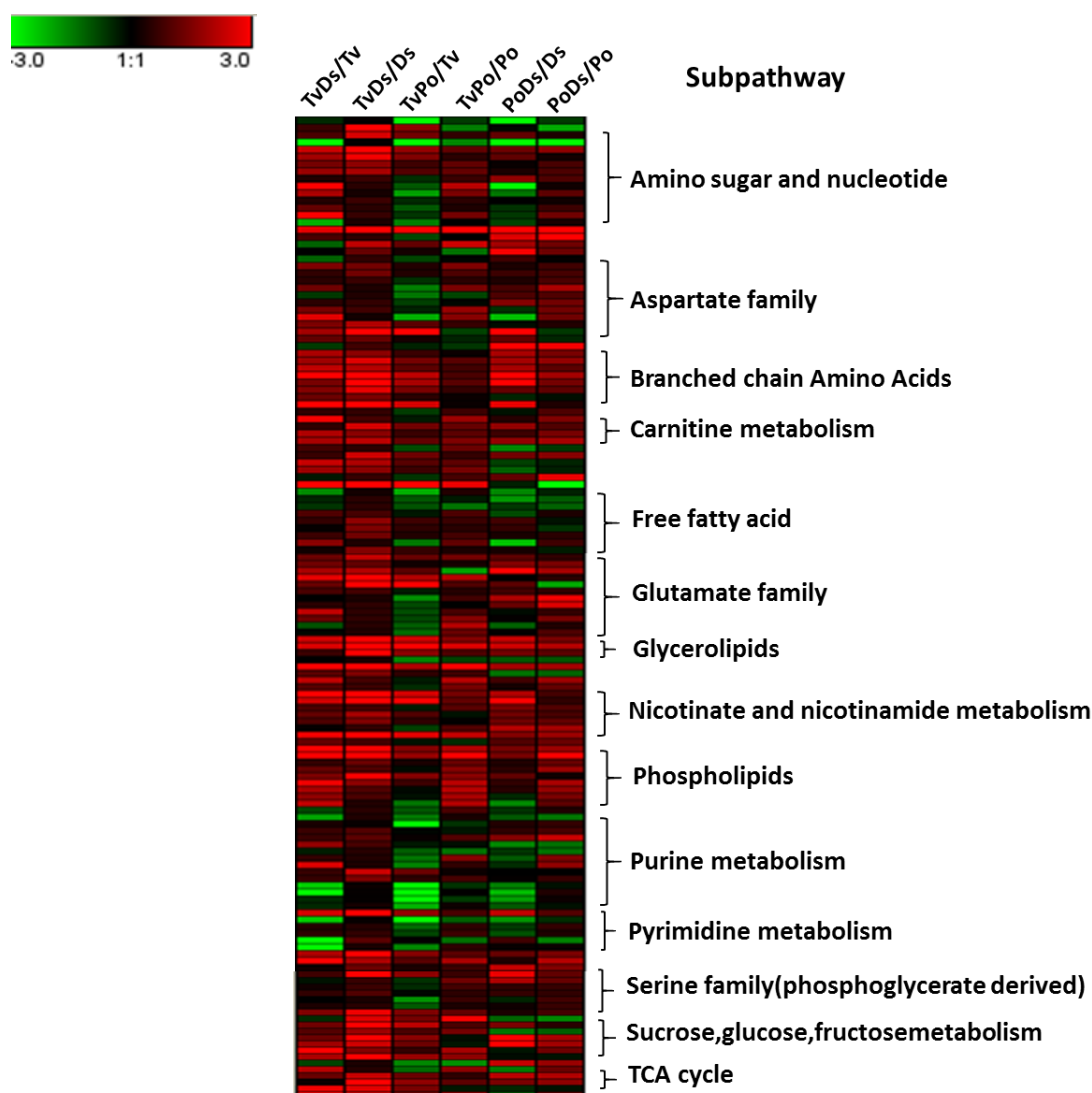
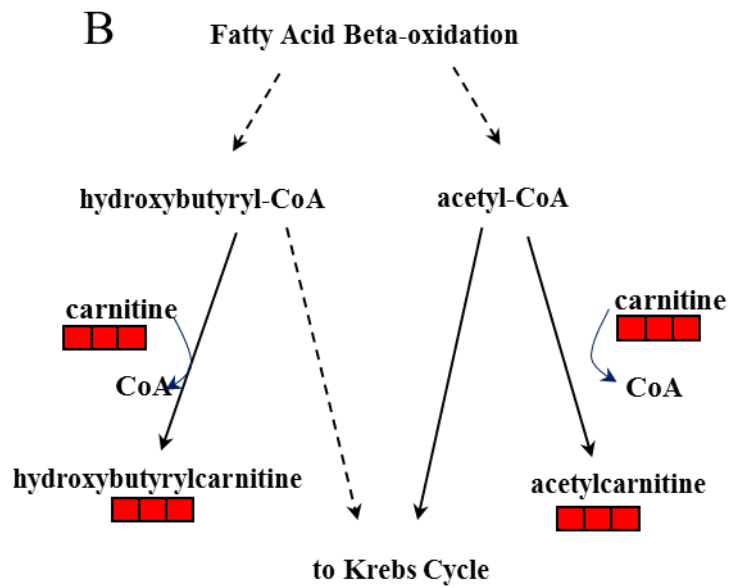
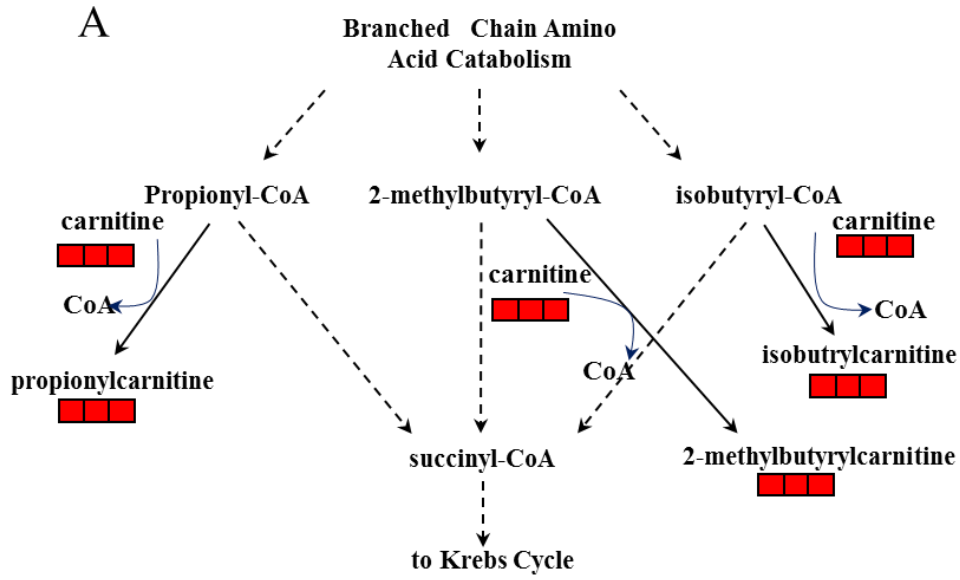


Figure S1. Heat map of fold change value of all detected metabolite contents from five biological replicates. The metabolomic data include all detected 279 metabolites. Red and green indicate increased and decreased metabolites in the interaction zones compared to both isolates. Each fold change value was calculated in log₂.

TvDs	PoDs	TvPo

- Increase in interaction zone relative to both isolates
- Decrease in interaction zone relative to both isolates
- No effect



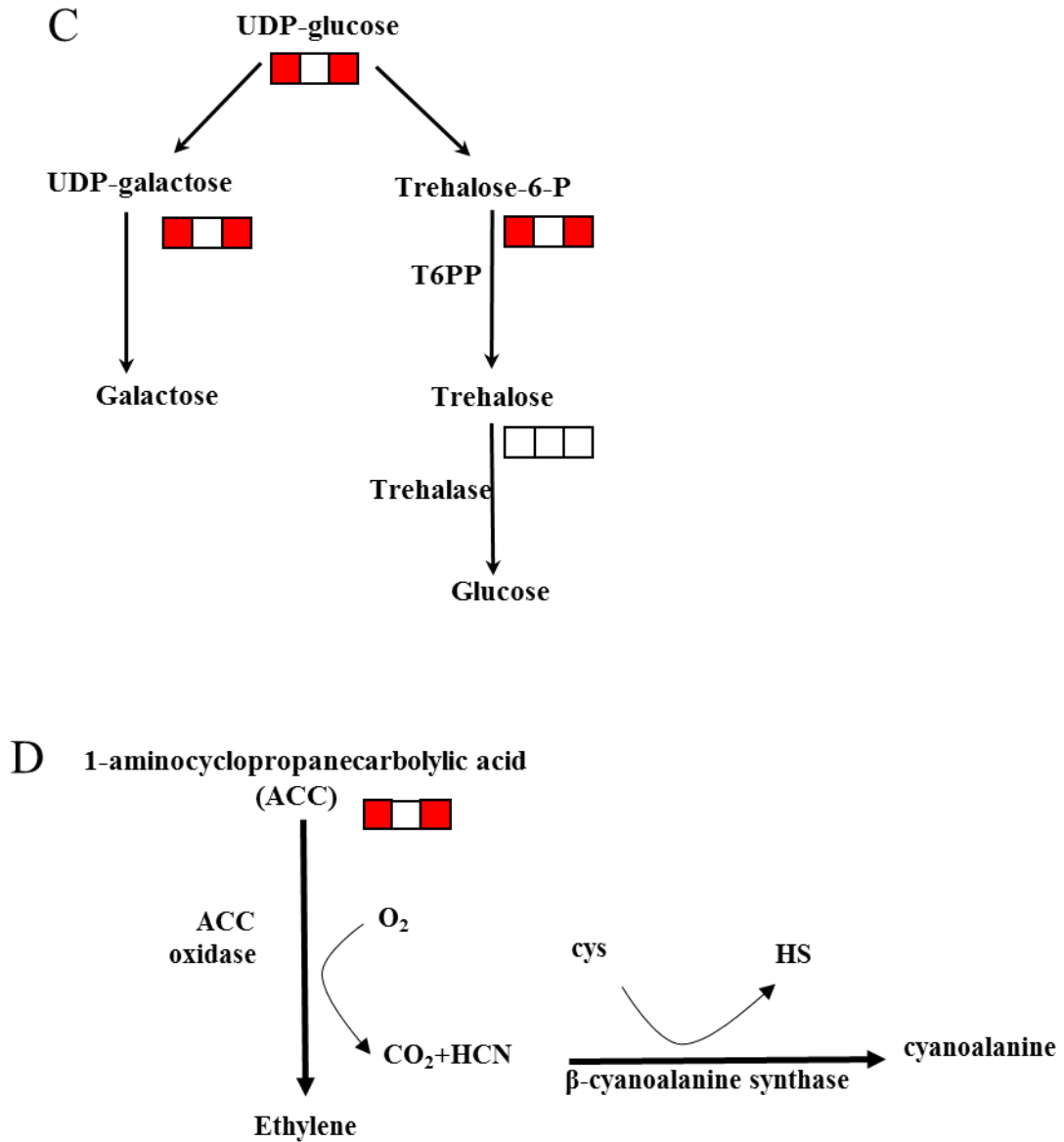


Figure S2. The significantly induced metabolic pathway in vivo. (A) Branched chain amino acids catabolic pathway; (B) Fatty acid oxidation pathway; (C) UDP-glucose catabolic pathway; (D) Ethylene synthesis pathway.