

Transcriptome and genome sequencing elucidates the molecular basis for the high yield and good quality of the hybrid rice variety Chuanyou6203

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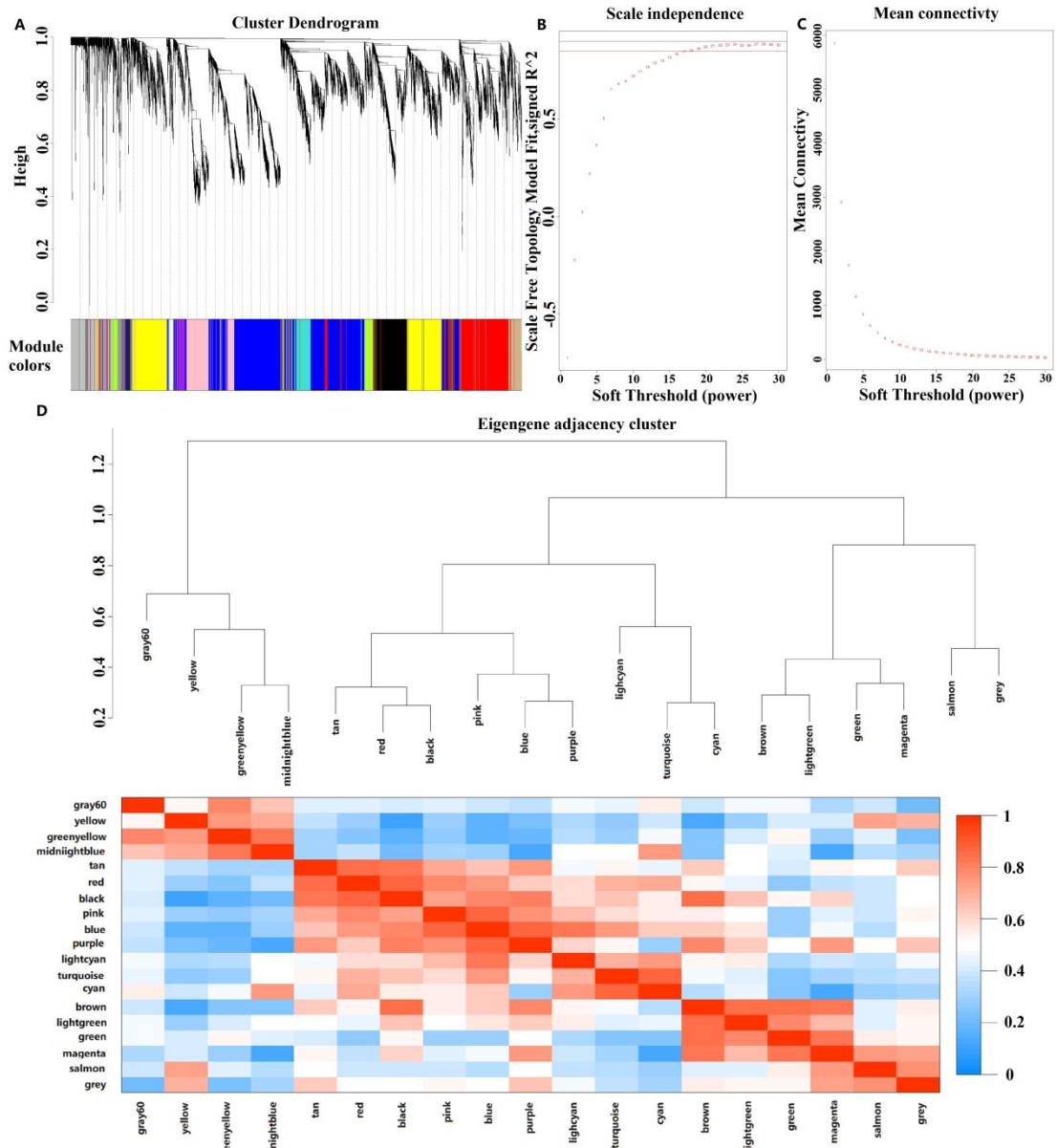


Figure S3 Weighted gene coexpression network analysis (WGCNA) of the DEGs among Chuanyou6203, Chenghui3203 and Chuan106B. A: Hierarchical cluster analysis of all DEGs models based on expression data. B and C: Selecting β , balancing the topology criterion and mean connectivity. D: Cluster and heatmap of meta-modules adjacency by eigengene.