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

Juansheng Ren^{1*}, Fan Zhang^{2*}, Fangyuan Gao¹, Lihua Zeng³, Xianjun Lu¹, Xiuqin Zhao², Jianqun Lv¹, Xiangwen Su¹, Liping Liu¹, Mingli Dai¹, Jianlong Xu², Guangjun Ren^{1**}

¹Crop Research Institute, Sichuan Academy of Agricultural Sciences, Chengdu, 610066, P.R. China

²Institute of Crop Sciences, Chinese Academy of Agricultural Sciences, Beijing, 100081, P.R. China

³Sichuan Normal University, Chengdu, 610066, P.R. China

^{*}These authors contributed equally to the work

^{**}Corresponding author email: guangjun61@sina.com.

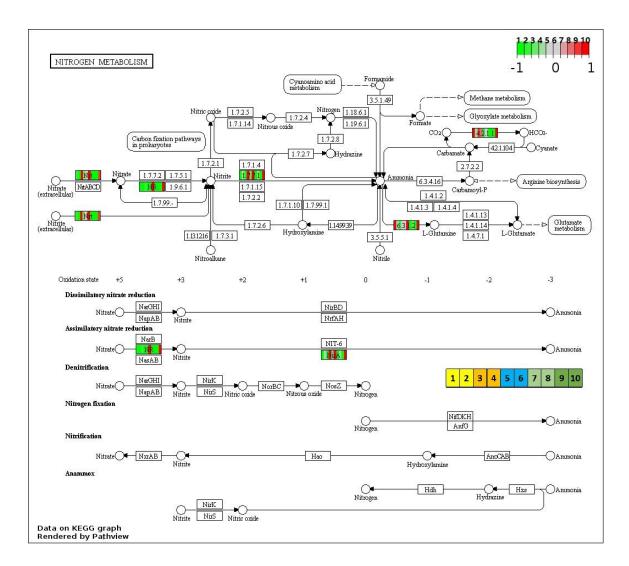


Figure S9. DEGs belonging to green-yellow and yellow modules enrich the pathway of nitrogen metabolism by PATHVIEW Wed (https://pathview.uncc.edu/). 1 and 2 represent panicle samples 7 days before heading. 3 and 4 represent panicle samples 3 days after heading. 5 and 6 represent panicle samples 15 days after heading. 7 and 8 represent sword leaf samples 7 days before heading. 9 and 10 represent sword leaf samples 3 days after heading.