

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.

Table S1 Summary of resequencing data and mapping statistics on the reference genome

Sample	Clean base	Clean Num.	reads	Average depth	Q30(%)	GC(%)	Mapped(%)	Properly_ mapped(%)
C106B	5636763721	64538006		22	89.46	40.73	92.63	91.3
CH3203	26228509240	175093610		61	85.44	43.29	94.98	85.56