

Table S1. Statistics of preprocessed raw reads.

Cultivar	Raw data(Gb)	Step1^a(Gb)	Step2^b(Gb)	Step3^c(Gb)	Step^d(Gb)
H6	14.98	14.96	12.02	10.12	10.08
SP3B	11.57	11.57	9.55	7.94	7.91
Total	26.55	26.53	21.57	18.06	17.99

^aRemoval of bacterial genome using reference mapping

^bRemoval of duplicated reads

^cQuality trimming (cut off = Q20)

^dRemoval of rRNA