Supplemental Table 1: Summary and Quality Control Items of Samples for RNA-sequencing

Sample	Clean reads	Clean bases	GC content (%)	≥Q30 percentage (%)
Y1	21,324,300	6,397,290,000	58.72%	94.43%
Y2	28,070,803	8,421,240,900	58.59%	93.08%
Y3	24,245,204	7,273,561,200	59.01%	93.54%
B1	21,970,319	6,591,095,700	58.24%	92.84%
B2	26,008,340	7,802,502,000	58.41%	92.98%
B3	23,058,580	6,917,574,000	58.76%	93.14%