

Table 2 Sequence summary results of transcriptome in each sample

Sample	Clean-reads	Clean-bases	Clean-reads Q30	GC
CK1	50.90 M	7.14 G	93.93%	43.25%
CK2	47.05 M	6.55 G	92.38%	42.63%
T1	56.96 M	8.05 G	93.60%	43.84%
T2	55.15 M	7.75 G	94.21%	43.33%