

Table 1 The transcriptome sequencing of 12 samples

Sample name	Raw reads	Clean reads	Clean bases	Q20 (%)	Q30 (%)	GC content (%)
YCKC_1	56 726 908	53 496 366 (94.31%)	8.02G	95.98	90.36	44.18
YCKC_2	58 005 280	54 841 974 (94.55%)	8.23G	95.86	90.13	44.25
YCKC_3	51 779 382	48 914 308 (94.47%)	7.34G	95.83	90.08	44.21
YCKB_1	56 176 868	53 026 752 (94.39%)	7.95G	96.38	91.10	44.17
YCKB_2	60 845 490	57 507 414 (94.51%)	8.63G	96.21	90.77	44.19
YCKB_3	52 947 280	49 792 940 (94.04%)	7.47G	96.21	90.76	44.62
YCGC_1	44 370 370	42 824 172 (96.52%)	6.42G	97.02	92.59	44.05
YCGC_2	51 324 278	48 314 180 (94.14%)	7.25G	95.89	90.21	44.75
YCGC_3	59 055 512	55 723 796 (94.36%)	8.36G	96.10	90.64	44.02
YCGB_1	60 497 396	57 214 740 (94.57%)	8.58G	95.82	90.04	44.21
YCGB_2	53 930 040	51 063 032 (94.68%)	7.66G	95.94	90.30	44.22
YCGB_3	52 266 686	49 474 026 (94.66%)	7.42G	95.91	90.22	44.21