Supplementary Table S2 Assembly quality statistic.

Sample	Raw Data (bp)	Clean Data（bp）	AF_Q20（%）	AF_Q30（%）	AF_GC（%）
X6-C-1	59496686	59229912	97.09%	91.89%	54.73%
X6-C-2	36788580	36528852	96.95%	91.54%	54.24%
X6-C-3	42905856	42618852	97.11%	92.02%	54.14%
BV-C-1	41579060	41277400	97.07%	91.89%	53.23%
BV-C-2	36876828	36666530	97.26%	92.29%	53.00%
BV-C-3	37275708	36983570	97.09%	91.94%	53.18%
X6-H-1	43649604	43352570	97.27%	92.42%	50.96%
X6-H-2	48867134	48518992	97.23%	92.32%	51.09%
X6-H-3	41925552	41625514	97.28%	92.43%	51.01%
BV-H-1	38302564	38034586	97.12%	92.01%	51.92%
BV-H-2	43064792	42767318	97.24%	92.33%	52.03%
BV-H-3	39766874	39499574	97.05%	91.76%	51.99%

Note: RawData (bp): Total number of sequenced bases (unit: bp);CleanData (bp): Total number of high-quality bases after filtering (unit: bp);AF_Q20 (%): Percentage of bases with quality score ⩾ Q20 in CleanData;AF_ Q30 (%): Percentage of bases with quality score ⩾ Q30 in CleanData;AF_GC (%): GC content percentage after filtering.