Table S1 Statistics of sequence comparison results between sample sequencing data and reference genome.

Sample	Raw reads	Clean reads	Q20 (%)	Q30 (%)	GC content (%)	Total reads	Reads mapped	Unique mapped
F1-1	76478376	74659540	99.09	97.25	49.88	74659540	67653220 (90.62%)	65479889 (87.70%)
F1-2	67165410	66187354	99.26	97.67	48.91	66187354	60971524 (92.12%)	58964580 (89.09%)
F1-3	54593804	53780736	99.23	97.57	49.48	53780736	49526320 (92.09%)	47939308 (89.14%)
F2-1	63361764	62556102	99.25	97.57	50.6	62556102	55788409 (89.18%)	54106483 (86.49%)
F2-2	54776788	54038894	97.96	93.73	50.45	54038894	47964415 (88.76%)	46526585 (86.10%)
F2-3	59613506	58873930	99.26	97.61	50.49	58873930	52621896 (89.38%)	51097999 (86.79%)