Table S2. Summary of the sequencing statistics obtained from each sample

Sample	Raw reads	Raw bases	Clean reads	Clean bases	Q20_rate	Q30_rate	GC_content
LP01	40,025,856	6,003,878,400	40,025,838	5,795,423,030	98.247%	95.173%	46.463%
LP02	40,056,966	6,008,544,900	40,056,926	5,813,211,824	98.513%	95.766%	46.454%
LP03	40,029,802	6,004,470,300	40,029,778	5,815,512,223	98.663%	95.974%	46.441%
CK03	40,055,276	6,008,291,400	40,055,254	5,813,908,697	98.447%	95.655%	46.189%
CK01	40,003,138	6,000,470,700	40,003,064	5,829,953,353	98.391%	95.437%	46.155%
CK02	40,030,044	6,004,506,600	40,030,016	5,834,753,122	98.391%	95.490%	46.143%