

Supplementary Table S2 Evaluation of sequencing quality.

Sample	Raw reads	Raw bases	Clean reads	Clean bases	Error rate (%)	Q20 (%)	Q30 (%)	GC content (%)
0h_1	41857012	6320408812	41159018	6127429138	0.0241	98	96.12	45.75
0h_2	48803298	7369297998	47951942	7101954923	0.0238	98.12	96.41	45.64
0h_3	47604648	7188301848	46713434	6909135314	0.0243	97.83	95.97	45.63
6h_1	50359382	7604266682	49848172	7362632473	0.0237	98.15	96.47	45.52
6h_2	46272970	6987218470	45361238	6704234759	0.0257	97.27	94.86	45.65
6h_3	49776314	7516223414	49179808	7207418250	0.0237	98.17	96.53	45.67
12h_1	58844286	8885487186	57982690	8538337891	0.024	98	96.19	45.12
12h_2	54631576	8249367976	53712882	7965812117	0.0243	97.89	95.94	45.13
12h_3	58305202	8804085502	57644694	8535928001	0.0239	98.07	96.29	45.1
24h_1	50130262	7569669562	49452548	7106970413	0.0247	97.67	95.72	44.76
24h_2	45895082	6930157382	45292080	6556476864	0.0248	97.61	95.65	44.93
24h_3	51563012	7786014812	50853620	7320683759	0.0245	97.76	95.89	44.6