

Appendix C. The data from illumina sequencing

Sample	Raw reads	Clean reads	Clean bases (G)	Q20(%)	Q30(%)	GC(%)
ck_0 h	51,205,220	49,028,340	7.35	96.07	90.24	45.81
ck_12 h	51,288,132	49,253,470	7.39	96.43	90.97	45.55
ck_1 d	52,685,744	50,801,698	7.62	96.54	91.10	45.72
ck_4 d	50,325,308	48,194, 232	7.23	98.09	94.34	45.23
ck_7 d	55,004,614	52,175,882	7.83	96.80	92.04	45.82
T_12 h	52,571,314	49,900,796	7.36	96.39	91.36	46.07
T_1 d	51,514,080	49,038,970	7.36	96.73	92.08	46.05
T_4 d	44,104,734	42,901,134	6.44	97.09	92.65	45.63
T_7 d	51,660,600	49,654,974	7.45	96.81	92.19	45.62
Average	51,151,083	48,994,388	7.34	96.77	91.89	45.72