

Table S3 Summary of the sequencing and de novo assembly

Samples	raw_reads	clean_reads	Total mapped	clean_bases	error_rate	Q20
S4-1	55799260	55216442	46977288	8282466300	0.365	97
S4-2	52581942	51933798	43959566	7790069700	0.345	97.195
S4-3	64718080	64270062	54187442	9640509300	0.345	97.195
S7-1	59889128	59443644	51038882	8916546600	0.355	97.1
S7-2	61166972	60444520	51740942	9066678000	0.335	97.285
S7-3	58975466	58328988	49660617	8749348200	0.345	97.18
Z4-1	58275958	57771286	48838904	8665692900	0.365	96.975
Z4-2	58295876	57658526	48628565	8648778900	0.36	97.03
Z4-3	55297900	54401188	45260740	8160178200	0.33	97.415
Z7-1	51008880	50406664	43170287	7560999600	0.43	96.24
Z7-2	48025548	47570326	40555926	7135548900	0.365	96.97
<u>Z7-3</u>	49785996	48144990	40494280	7221748500	0.35	97.12

y		
Q30		GC (%)
	91.955	44.215
	92.375	44.21
	92.425	44.55
	92.195	44.61
	92.57	44.285
	92.39	44.1
	91.9	44.215
	92.03	44.16
	92.85	44.14
	90.12	44.08
	91.95	44.185
	92.28	43.905