

Table 1 Statistics of sequencing results and assembly quality

Sample	Raw reads	Clean reads	Mapped reads	Q20 (%)	Q30 (%)	GC ratio (%)
CK_R1	95 526 440	94 503 192(98.92%)	73 978 672(78.28%)	98.03	94.15	55.07
CK_R2	112 641 578	111 657 556(99.12%)	87 645 516(78.49%)	98.25	94.68	54.99
CK_R3	93 920 530	92 897 382(98.91%)	73 277 788(78.88%)	97.95	93.96	55.53
DS_R1	101 177 730	100 225 230(99.06%)	79 774 972(79.60%)	98.24	94.67	55.3
DS_R2	107 347 758	106 078 308(98.82%)	85 581 080(80.68%)	98.23	94.65	55.2
DS_R3	96 107 226	95 073 146(98.92%)	75 449 022(79.36%)	98.24	94.69	55.06
DS_Si_R1	118 341 778	116 769 034(98.67%)	90 023 782(77.10%)	98.15	94.46	55.11
DS_Si_R2	91 907 108	90 918 648(98.92%)	69 986 866(76.98%)	98	94.03	55.55
DS_Si_R3	98 975 896	97 677 626(98.69%)	74 624 146(76.40%)	98.12	94.37	55.62
total	915 946 044	905 800 122	710 341 844	-	-	-