

Table 1 Statics of high-through put sequencing.

Sample	Raw reads	Raw bases	Clean reads	Clean bases	Error rate (%)	Q20 (%)	Q30 (%)	GC content (%)
COLD1	46341400	6951210000	45899300	6.71E+09	0.0114	98.71	96.1	52.15
COLD2	47250524	7087578600	46795718	6.85E+09	0.0114	98.69	96.04	52.18
COLD3	41466450	6219967500	41048930	6E+09	0.0114	98.72	96.12	52.12
HEAT1	46072536	6910880400	45521712	6.65E+09	0.0117	98.58	95.74	52.24
HEAT2	44536370	6680455500	44097602	6.48E+09	0.0117	98.57	95.7	52.21
HEAT3	41589980	6238497000	41169418	6.03E+09	0.0116	98.62	95.84	52.1
NT1	62621216	9393182400	61906522	9.04E+09	0.0119	98.46	95.42	52.32
NT2	41923862	6288579300	41508494	6.05E+09	0.0117	98.58	95.74	52.25
NT3	43972542	6595881300	43520738	6.33E+09	0.0118	98.53	95.58	52.76