

Table 1 Summary statistics of the RAD-seq

Data types	Data size
Raw base (bp)	39 377 398 500
Clean base (bp)	39 288 966 600
Effective rate (%)	99.78
Q20 (%)	96.75
Q30 (%)	91.43
GC content (%)	33.87
Clean reads	130 963 222
Removed duplication reads	77 437 310
Clean duplication rate (%)	40.87
Digestion reads	75 883 448
Digestion ratio (%)	97.99
Cluster tag number	24 848 206
Cut tag number	450 203
Cut pair reads	43 491 152
Total contig base (bp)	103 788 703
Total contig number	393 324
Average contig length (bp)	263
N50 length (bp)	111 338