

Additional file 4. Summary statistics of the sequence assembly

Category	Number
Total clean reads	103,924,174
Total clean nucleotides (nt)	10,392,417,400
Q20 percentage	99.14%
N percentage	0.00%
GC percentage	45.7%
Total number of contigs	97,449
Average contig length (bp)	941
Total number of unigenes	83,107
Average unigene length (bp)	1,552