Report

	final.contigs
# contigs (>= 1000 bp)	1830
# contigs (>= 5000 bp)	57
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3849335
Total length (>= 5000 bp)	349017
Total length (>= 10000 bp)	14787
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2920
Largest contig	14787
Total length	4643924
Reference length	4641652
GC (%)	50.80
Reference GC (%)	50.79
N50	1973
NG50	1977
N75	1236
NG75	1237
L50	760
LG50	759
L75	1502
LG75	1500
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	95.577
Duplication ratio	1.047
# N's per 100 kbp	0.00
# mismatches per 100 kbp	62.39
# indels per 100 kbp	0.14
Largest alignment	14787
NA50	1973
NGA50	1977
NA75	1236
NGA75	1237
LA50	760
LGA50	759
LA75	1502
LGA75	1500

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	2768
# indels	6
# short indels	6
# long indels	0
Indels length	6

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).















