Report

	final.contigs
# contigs (>= 1000 bp)	1664
# contigs (>= 5000 bp)	103
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4073838
Total length (>= 5000 bp)	653279
Total length (>= 10000 bp)	23602
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2353
Largest contig	13353
Total length	4585631
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	2516
NG50	2494
N75	1535
NG75	1501
L50	580
LG50	591
L75	1155
LG75	1183
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	643
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	95.209
Duplication ratio	1.038
# N's per 100 kbp	0.00
# mismatches per 100 kbp	47.13
# indels per 100 kbp	0.07
Largest alignment	13353
NA50	2516
NGA50	2494
NA75	1535
NGA75	1501
LA50	580
LGA50	591
LA75	1155
LGA75	1183

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	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	643
# local misassemblies	2
# mismatches	2083
# indels	3
# short indels	3
# long indels	0
Indels length	3

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).















