Report

	final.contigs
# contigs (>= 1000 bp)	1376
# contigs (>= 5000 bp)	258
# contigs (>= 10000 bp)	29
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4644869
Total length (>= 5000 bp)	1912919
Total length (>= 10000 bp)	355340
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1715
Largest contig	15687
Total length	4890022
Reference length	4857432
GC (%)	52.22
Reference GC (%)	52.22
N50	3991
NG50	4001
N75	2391
NG75	2417
L50	378
LG50	374
L75	773
LG75	763
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.712
Duplication ratio	1.030
# N's per 100 kbp	0.00
# mismatches per 100 kbp	33.96
# indels per 100 kbp	0.02
Largest alignment	15687
NA50	3991
NGA50	4001
NA75	2391
NGA75	2417
LA50	378
LGA50	374
LA75	773
LGA75	763

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	1
# mismatches	1612
# indels	1
# short indels	1
# long indels	0
Indels length	1

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).















