Report

	final.contigs
# contigs (>= 1000 bp)	512
# contigs (>= 5000 bp)	313
# contigs (>= 10000 bp)	170
# contigs (>= 25000 bp)	37
# contigs (>= 50000 bp)	2
Total length (>= 1000 bp)	4801876
Total length (>= 5000 bp)	4256908
Total length (>= 10000 bp)	3241321
Total length (>= 25000 bp)	1241452
Total length (>= 50000 bp)	115496
# contigs	566
Largest contig	60536
Total length	4841657
Reference length	4857432
GC (%)	52.21
Reference GC (%)	52.22
N50	14232
NG50	14232
N75	8247
NG75	8243
L50	102
LG50	102
L75	214
LG75	215
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	12230
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.584
Duplication ratio	1.011
# N's per 100 kbp	0.00
# mismatches per 100 kbp	14.56
# indels per 100 kbp	0.02
Largest alignment	60536
NA50	14232
NGA50	14232
NA75	8247
NGA75	8243
LA50	102
LGA50	102
LA75	214
LGA75	215

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	12230
# local misassemblies	1
# mismatches	697
# 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).















