## Report

	final.contigs
# contigs (>= 1000 bp)	1770
# contigs (>= 5000 bp)	100
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4261016
Total length (>= 5000 bp)	624614
Total length (>= 10000 bp)	20616
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2566
Largest contig	10576
Total length	4842741
Reference length	4857432
GC (%)	52.19
Reference GC (%)	52.22
N50	2505
NG50	2499
N75	1473
NG75	1460
L50	628
LG50	631
L75	1253
LG75	1261
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	95.924
Duplication ratio	1.039
# N's per 100 kbp	0.00
# mismatches per 100 kbp	48.03
# indels per 100 kbp	0.00
Largest alignment	10576
NA50	2505
NGA50	2499
NA75	1473
NGA75	1460
LA50	628
LGA50	631
LA75	1253
LGA75	1261

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	2238
# indels	0
# short indels	0
# long indels	0
Indels length	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).

## 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).















