Report

	final.contigs
# contigs (>= 1000 bp)	1322
# contigs (>= 5000 bp)	226
# contigs (>= 10000 bp)	30
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4357886
Total length (>= 5000 bp)	1676891
Total length (>= 10000 bp)	382152
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1657
Largest contig	16586
Total length	4604338
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	3914
NG50	3888
N75	2305
NG75	2268
L50	368
LG50	372
L75	750
LG75	763
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.888
Duplication ratio	1.024
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.47
# indels per 100 kbp	0.00
Largest alignment	16586
NA50	3914
NGA50	3888
NA75	2305
NGA75	2268
LA50	368
LGA50	372
LA75	750
LGA75	763
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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	66
# 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).















