## Report

	final.contigs
# contigs (>= 1000 bp)	995
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	1455896
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3688
Largest contig	3655
Total length	3312316
Reference length	4857432
GC (%)	52.21
Reference GC (%)	52.22
N50	923
NG50	687
N75	673
L50	1204
LG50	2176
L75	2258
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1221
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	64.616
Duplication ratio	1.055
# N's per 100 kbp	0.00
# mismatches per 100 kbp	251.54
# indels per 100 kbp	0.13
Largest alignment	3655
NA50	923
NGA50	687
NA75	673
LA50	1204
LGA50	2176
LA75	2258
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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	1
# relocations	0
# translocations	0
# inversions	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1221
# local misassemblies	0
# mismatches	7895
# indels	4
# short indels	4
# long indels	0
Indels length	4

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).

















