Report

	final.contigs
# contigs (>= 1000 bp)	739
# contigs (>= 5000 bp)	100
# contigs (>= 10000 bp)	10
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2220607
Total length (>= 5000 bp)	698930
Total length (>= 10000 bp)	110319
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1102
Largest contig	13220
Total length	2469467
Reference length	4857432
GC (%)	52.11
Reference GC (%)	52.22
N50	3252
NG50	540
N75	1924
L50	235
LG50	1024
L75	479
# misassemblies	3
# misassembled contigs	2
Misassembled contigs length	8223
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	50.004
Duplication ratio	1.017
# N's per 100 kbp	0.00
# mismatches per 100 kbp	379.47
# indels per 100 kbp	0.04
Largest alignment	13220
NA50	3249
NGA50	539
NA75	1924
LA50	236
LGA50	1025
LA75	479
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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	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	8223
# local misassemblies	2
# mismatches	9217
# 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).

















