## Report

	final.contigs
# contigs (>= 0 bp)	8181
# contigs (>= 1000 bp)	669
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4854686
Total length (>= 1000 bp)	844482
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4354
Largest contig	2813
Total length	3335293
Reference length	4641652
GC (%)	50.69
Reference GC (%)	50.79
N50	758
NG50	643
N75	616
L50	1627
LG50	2564
L75	2851
# misassemblies	8
# misassembled contigs	8
Misassembled contigs length	9158
# local misassemblies	6
# unaligned contigs	80 + 34 part
Unaligned length	51724
Genome fraction (%)	65.402
Duplication ratio	1.082
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2493.15
# indels per 100 kbp	2.87
Largest alignment	2812
NA50	755
NGA50	639
NA75	612
LA50	1632
LGA50	2574
LA75	2863
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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	8
# relocations	7
# translocations	0
# inversions	1
# misassembled contigs	8
Misassembled contigs length	9158
# local misassemblies	6
# mismatches	75685
# indels	87
# short indels	87
# long indels	0
Indels length	87

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	80
Fully unaligned length	47444
# partially unaligned contigs	34
# with misassembly	0
# both parts are significant	0
Partially unaligned length	4280
# 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).

















