Report

	conting
# contigs (>= 1000 bp)	contigs 73
# contigs (>= 1000 bp) # contigs (>= 5000 bp)	51
# contigs (>= 3000 bp) # contigs (>= 10000 bp)	47
# contigs (>= 25000 bp)	41
# contigs (>= 25000 bp) # contigs (>= 50000 bp)	29
Total length (>= 1000 bp)	4507529
Total length (>= 5000 bp)	4469855
Total length (>= 10000 bp)	4437004
Total length (>= 25000 bp)	4329343
Total length (>= 50000 bp)	3929597
# contigs	104
Largest contig	332248
Total length	4530072
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.79
N50	131793
NG50	124889
N75	82061
NG75	80259
L50	11
LG50	12
L75	22
LG75	23
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	82061
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.087
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	615.63
# indels per 100 kbp	0.82
Largest alignment	332248
NA50	131793
NGA50	124889
NA75	80259
NGA75	79547
LA50	11
LGA50	12
LA75	22
LGA75	23
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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

	contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	82061
# local misassemblies	1
# mismatches	27743
# indels	37
# short indels	37
# long indels	0
Indels length	44

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

	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).















