Report

	contigs
# contigs (>= 0 bp)	92
# contigs (>= 1000 bp)	68
# contigs (>= 5000 bp)	51
# contigs (>= 10000 bp)	48
# contigs (>= 25000 bp)	40
# contigs (>= 50000 bp)	26
Total length (>= 0 bp)	4568967
Total length (>= 1000 bp)	4562933
Total length (>= 5000 bp)	4522694
Total length (>= 10000 bp)	4498743
Total length (>= 25000 bp)	4378623
Total length (>= 50000 bp)	3894457
# contigs	71
Largest contig	327064
Total length	4565348
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	175766
NG50	175766
N75	87064
NG75	87064
L50	10
LG50	10
L75	20
LG75	20
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.298
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5.13
# indels per 100 kbp	0.39
Largest alignment	327064
NA50	175766
NGA50	175766
NA75	87064
NGA75	87064
LA50	10
LGA50	10
LA75	20
LGA75	20

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	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	234
# indels	18
# short indels	18
# long indels	0
Indels length	25

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

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