Report

	contigs
# contigs (>= 0 bp)	124
# contigs (>= 1000 bp)	72
# contigs (>= 5000 bp)	54
# contigs (>= 10000 bp)	51
# contigs (>= 25000 bp)	42
# contigs (>= 50000 bp)	28
Total length (>= 0 bp)	4574848
Total length (>= 1000 bp)	4556333
Total length (>= 5000 bp)	4513942
Total length (>= 10000 bp)	4489842
Total length (>= 25000 bp)	4345434
Total length (>= 50000 bp)	3864735
# contigs	85
Largest contig	327173
Total length	4565850
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	133063
NG50	133045
N75	86633
NG75	86633
L50	11
LG50	12
L75	22
LG75	22
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.273
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.77
# indels per 100 kbp	0.18
Largest alignment	327173
NA50	133063
NGA50	133045
NA75	86633
NGA75	86633
LA50	11
LGA50	12
LA75	22
LGA75	22
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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	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# mismatches	172
# indels	8
# short indels	8
# long indels	0
Indels length	9

All statistics are based on contigs of size \geq 500 bp, unless otherwise noted (e.g., "# contigs (\geq 0 bp)" and "Total length (\geq 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).















