Report

	contigs
# contigs (>= 1000 bp)	61
# contigs (>= 5000 bp)	46
# contigs (>= 10000 bp)	43
# contigs (>= 25000 bp)	38
# contigs (>= 50000 bp)	26
Total length (>= 1000 bp)	4534256
Total length (>= 5000 bp)	4500135
Total length (>= 10000 bp)	4476440
Total length (>= 25000 bp)	4389531
Total length (>= 50000 bp)	3981473
# contigs	79
Largest contig	333130
Total length	4546811
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	166049
NG50	166049
N75	94985
NG75	87829
L50	10
LG50	10
L75	19
LG75	20
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	36005
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.907
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	112.93
# indels per 100 kbp	0.40
Largest alignment	333130
NA50	166049
NGA50	166049
NA75	94985
NGA75	87829
LA50	10
LGA50	10
LA75	19
LGA75	20
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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	36005
# local misassemblies	2
# mismatches	5132
# indels	18
# short indels	18
# long indels	0
Indels length	18

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).















