Report

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	scaffolds
# contigs (>= 1000 bp)	78
# contigs (>= 5000 bp)	54
# contigs (>= 10000 bp)	49
# contigs (>= 25000 bp)	45
# contigs (>= 50000 bp)	28
Total length (>= 1000 bp)	4554363
Total length (>= 5000 bp)	4495919
Total length (>= 10000 bp)	4459233
Total length (>= 25000 bp)	4401922
Total length (>= 50000 bp)	3791601
# contigs	85
Largest contig	327052
Total length	4559054
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	132613
NG50	132613
N75	72264
NG75	67391
L50	11
LG50	11
L75	22
LG75	23
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	41750
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.159
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	61.61
# indels per 100 kbp	9.28
Largest alignment	327052
NA50	132613
NGA50	132613
NA75	72264
NGA75	67391
LA50	11
LGA50	11
LA75	22
LGA75	23

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

	scaffolds
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	41750
# local misassemblies	4
# mismatches	2807
# indels	423
# short indels	422
# long indels	1
Indels length	640

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

	scaffolds
# 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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