Report

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	final.contigs
# contigs (>= 1000 bp)	732
# contigs (>= 5000 bp)	345
# contigs (>= 10000 bp)	126
# contigs (>= 25000 bp)	10
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4605859
Total length (>= 5000 bp)	3541077
Total length (>= 10000 bp)	1995695
Total length (>= 25000 bp)	306431
Total length (>= 50000 bp)	0
# contigs	880
Largest contig	46220
Total length	4705142
Reference length	4857432
GC (%)	52.17
Reference GC (%)	52.22
N50	8411
NG50	8118
N75	5046
NG75	4678
L50	166
LG50	175
L75	343
LG75	367
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	95.385
Duplication ratio	1.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	527.70
# indels per 100 kbp	0.00
Largest alignment	46220
NA50	8411
NGA50	8118
NA75	5046
NGA75	4678
LA50	166
LGA50	175
LA75	343
LGA75	367

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

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	24450
# indels	0
# short indels	0
# long indels	0
Indels length	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).

Unaligned report

	final.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).















