

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	2661
# contigs ( $\geq 1000$ bp)	1858
Total length ( $\geq 0$ bp)	5214493
Total length ( $\geq 1000$ bp)	4630592
# contigs	2661
Largest contig	10567
Total length	5214493
Reference length	5478683
GC (%)	50.28
Reference GC (%)	50.49
N50	2617
NG50	2502
N75	1540
NG75	1400
L50	633
LG50	684
L75	1282
LG75	1416
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	7696
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	91.828
Duplication ratio	1.036
# N's per 100 kbp	0.00
# mismatches per 100 kbp	37.19
# indels per 100 kbp	0.10
Largest alignment	10567
NA50	2616
NGA50	2500
NA75	1540
NGA75	1400
LA50	634
LGA50	685
LA75	1283
LGA75	1417

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).

## Misassemblies report

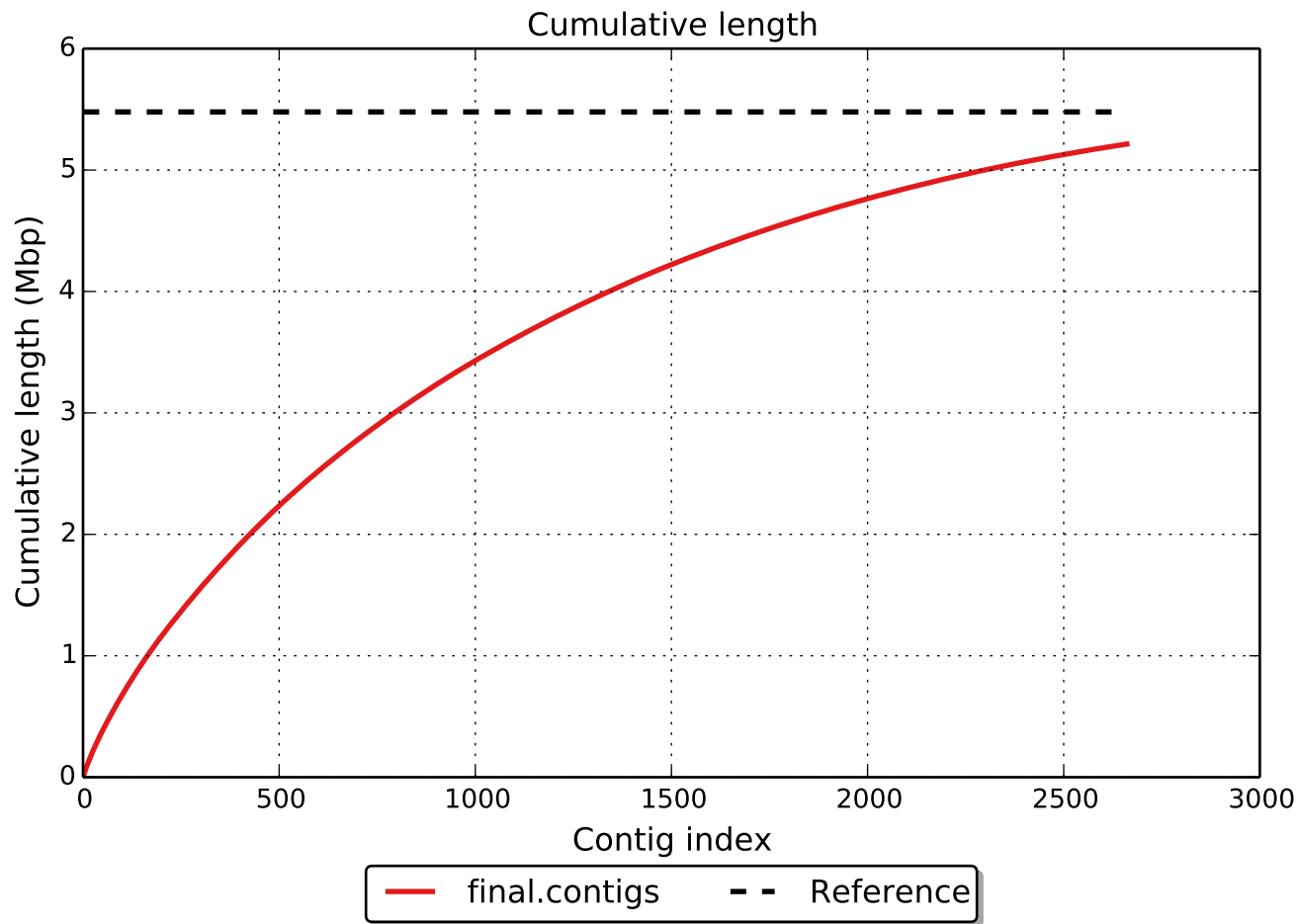
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	7696
# local misassemblies	1
# mismatches	1871
# indels	5
# short indels	3
# long indels	2
Indels length	33

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

	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

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GC content

