

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	4447
# contigs ( $\geq 1000$ bp)	1967
Total length ( $\geq 0$ bp)	4998731
Total length ( $\geq 1000$ bp)	3206384
# contigs	4447
Largest contig	6941
Total length	4998731
Reference length	5478683
GC (%)	50.49
Reference GC (%)	50.49
N50	1241
NG50	1158
N75	848
NG75	748
L50	1332
LG50	1533
L75	2555
LG75	3007
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	87.357
Duplication ratio	1.044
# N's per 100 kbp	0.00
# mismatches per 100 kbp	51.21
# indels per 100 kbp	0.08
Largest alignment	6941
NA50	1241
NGA50	1158
NA75	848
NGA75	748
LA50	1332
LGA50	1533
LA75	2555
LGA75	3007

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

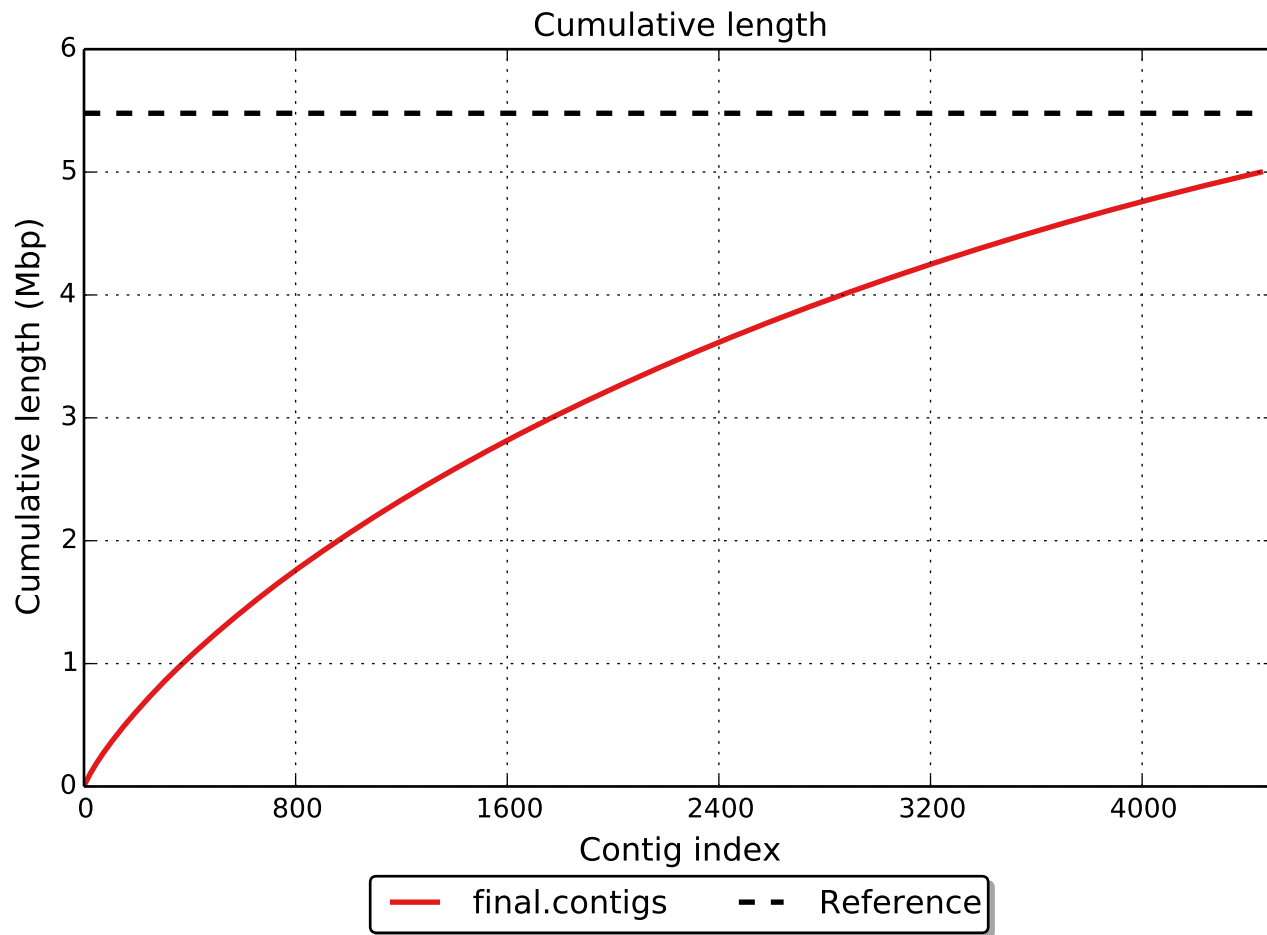
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	2451
# indels	4
# short indels	2
# long indels	2
Indels length	32

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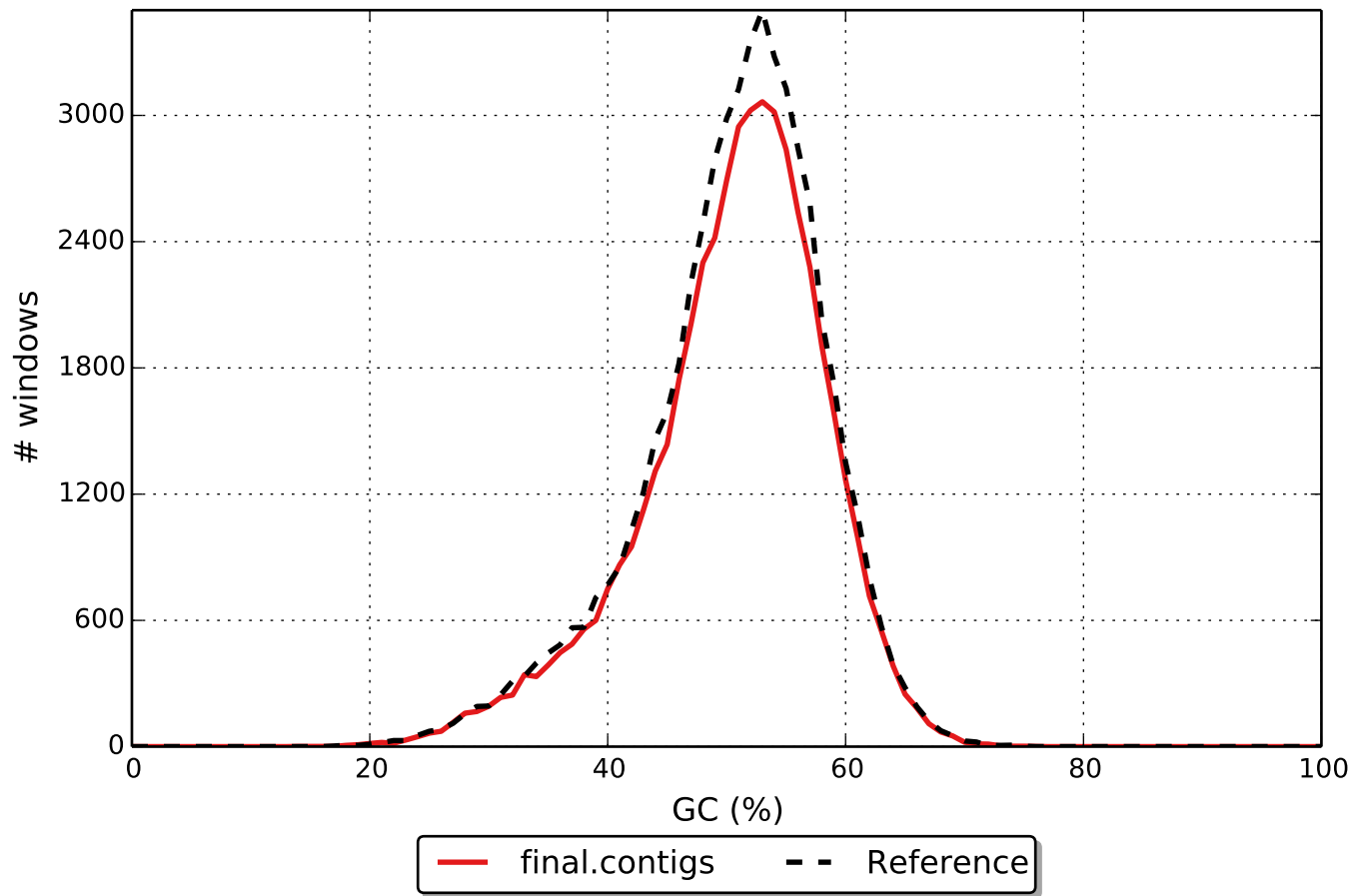
## Unaligned report

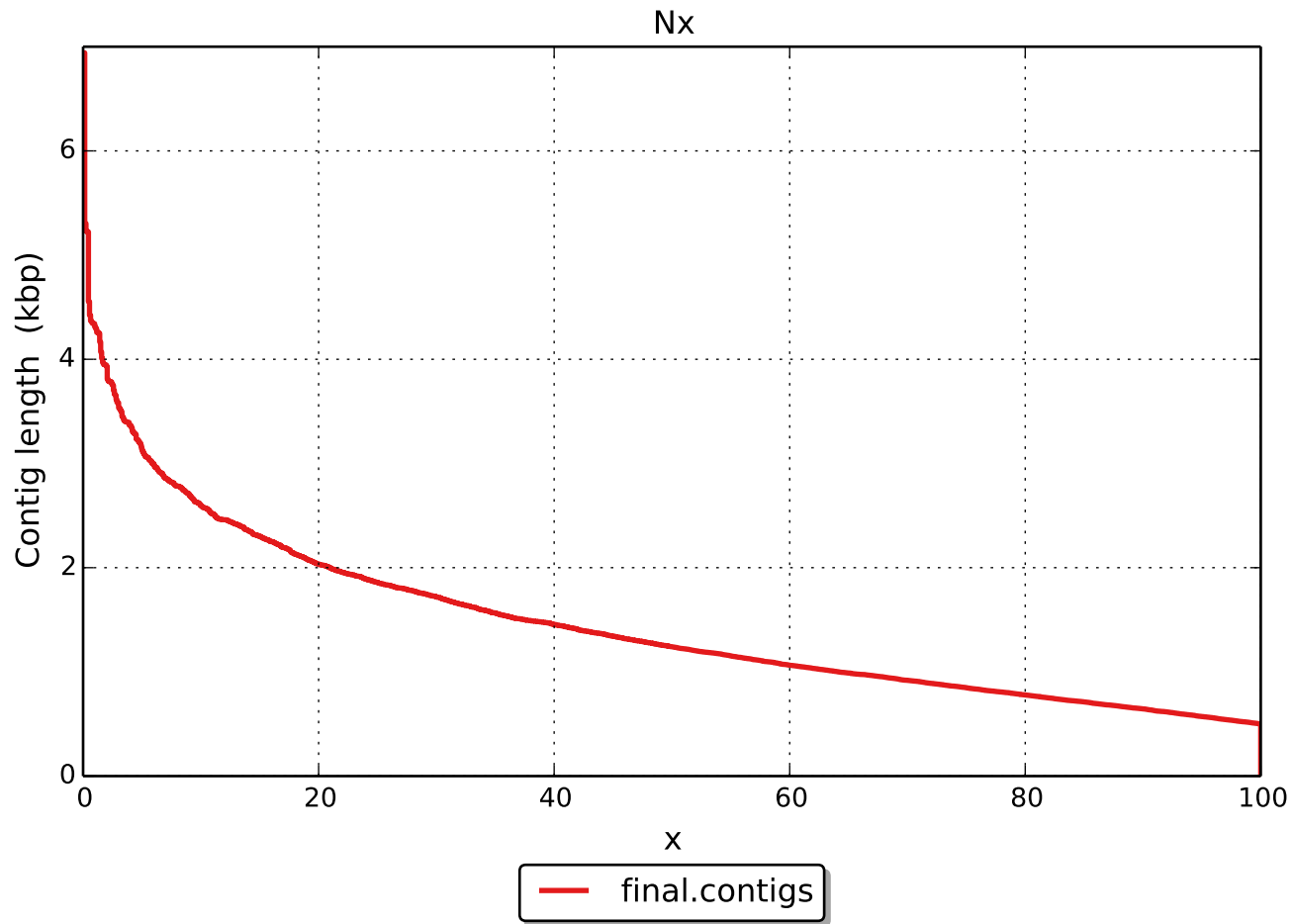
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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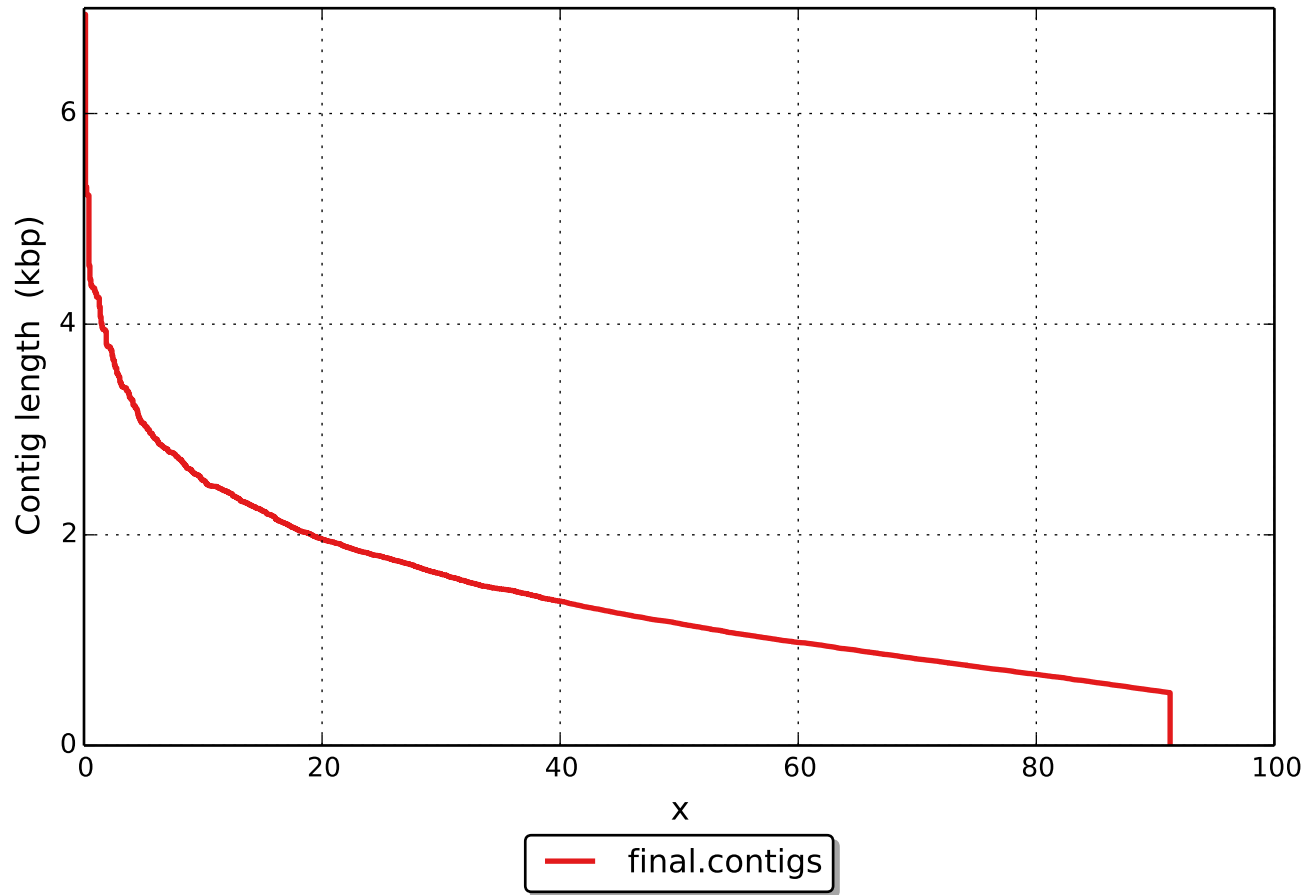


GC content





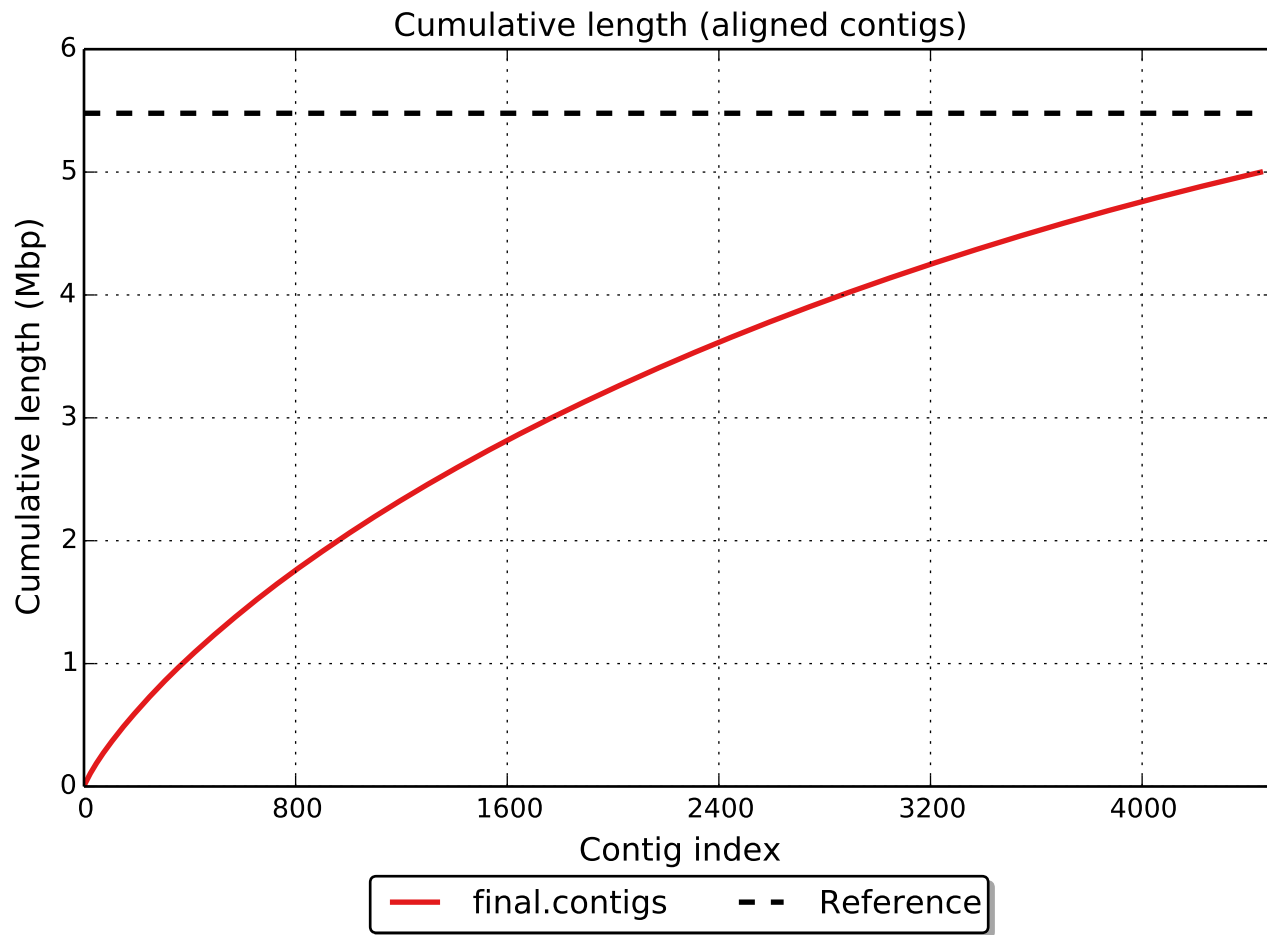
NGx



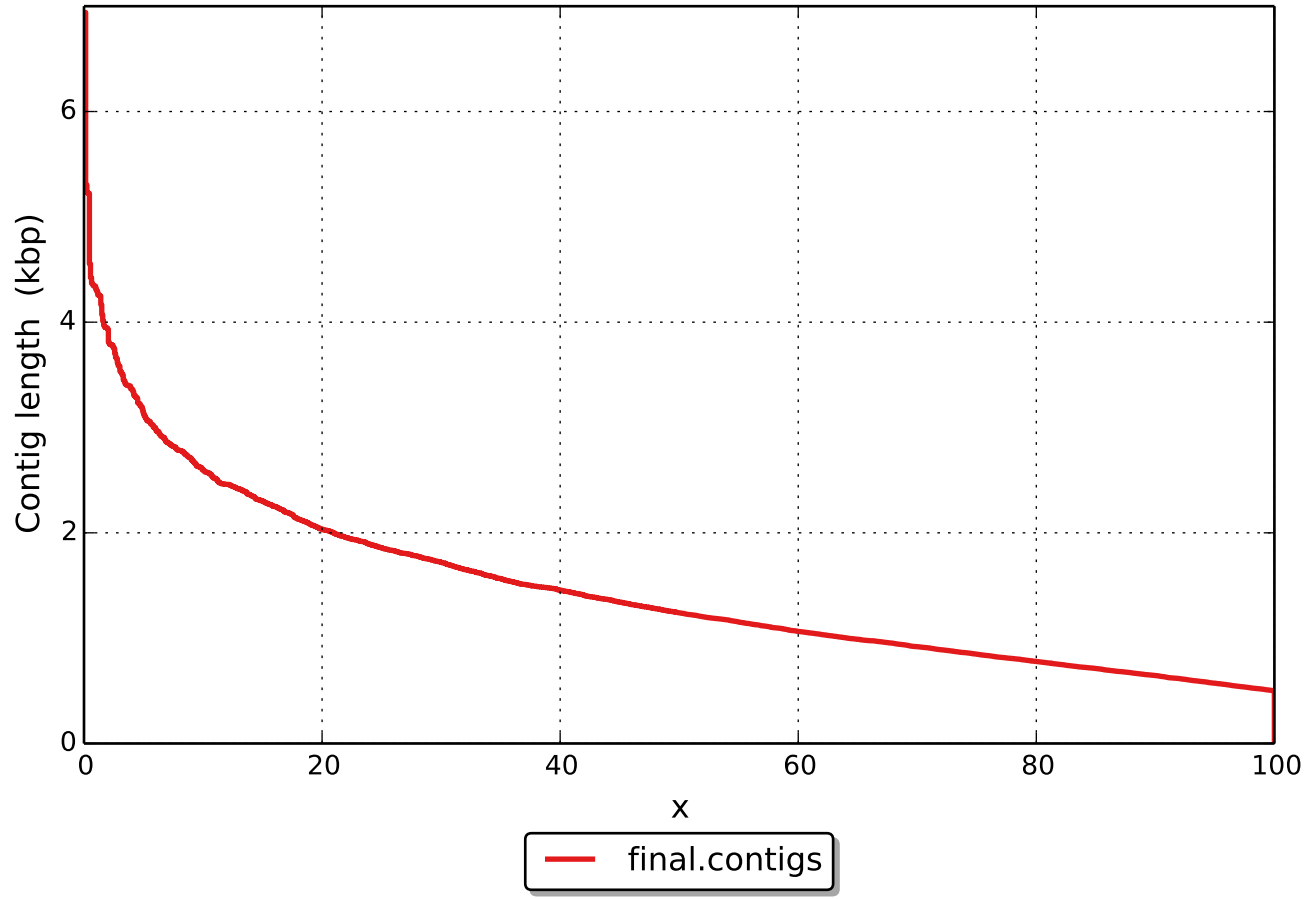
# Misassemblies







NAx



NGAx

