

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	14890
# contigs ( $\geq 1000$ bp)	2612
Total length ( $\geq 0$ bp)	10246649
Total length ( $\geq 1000$ bp)	3635295
# contigs	9000
Largest contig	4380
Total length	8147640
Reference length	10957366
GC (%)	50.38
Reference GC (%)	50.49
N50	939
NG50	772
N75	704
L50	3065
LG50	4716
L75	5574
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	71.018
Duplication ratio	1.047
# N's per 100 kbp	0.00
# mismatches per 100 kbp	123.69
# indels per 100 kbp	0.14
Largest alignment	4380
NA50	939
NGA50	772
NA75	704
LA50	3065
LGA50	4717
LA75	5575

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

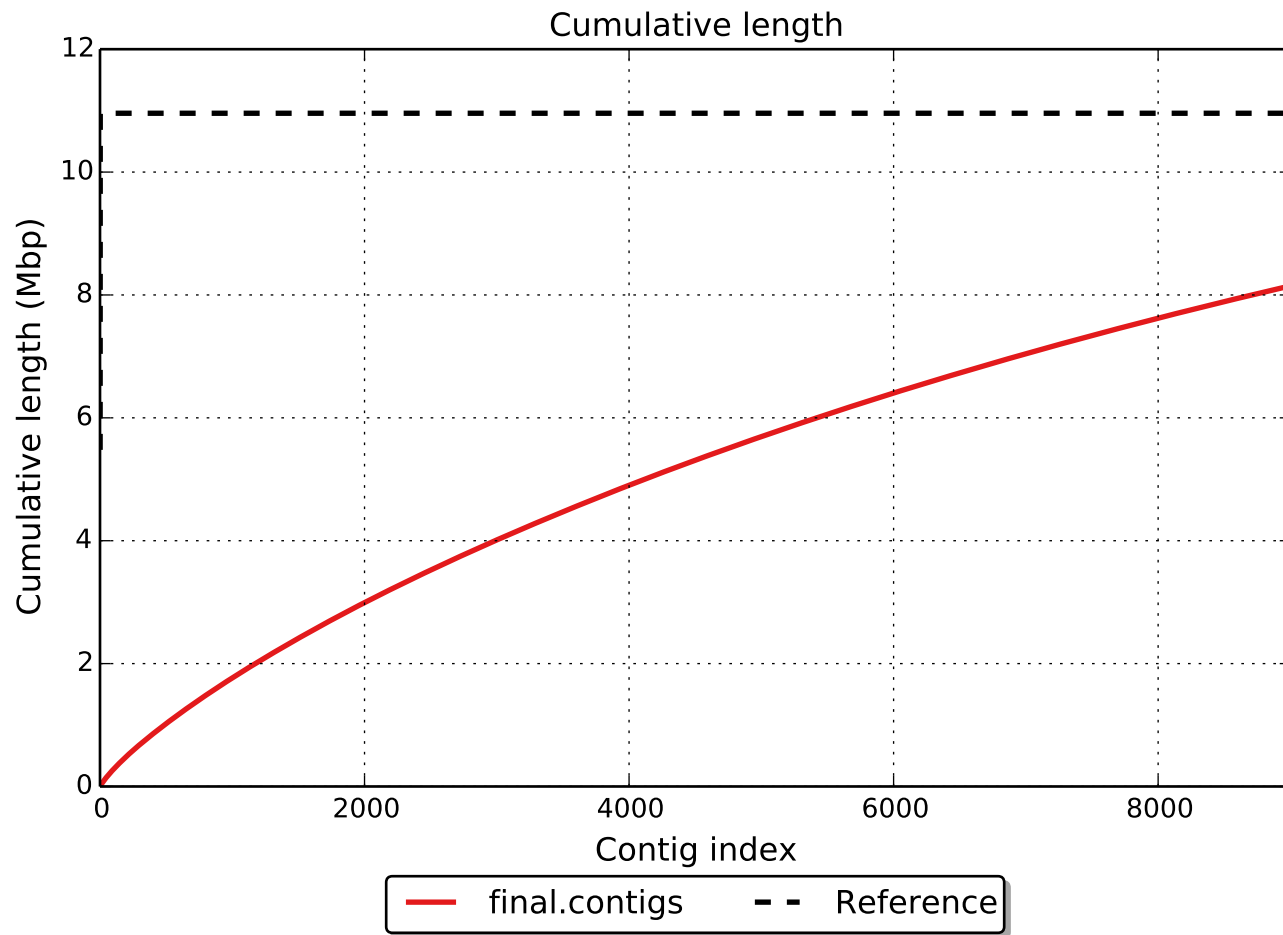
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	9625
# indels	11
# short indels	6
# long indels	5
Indels length	68

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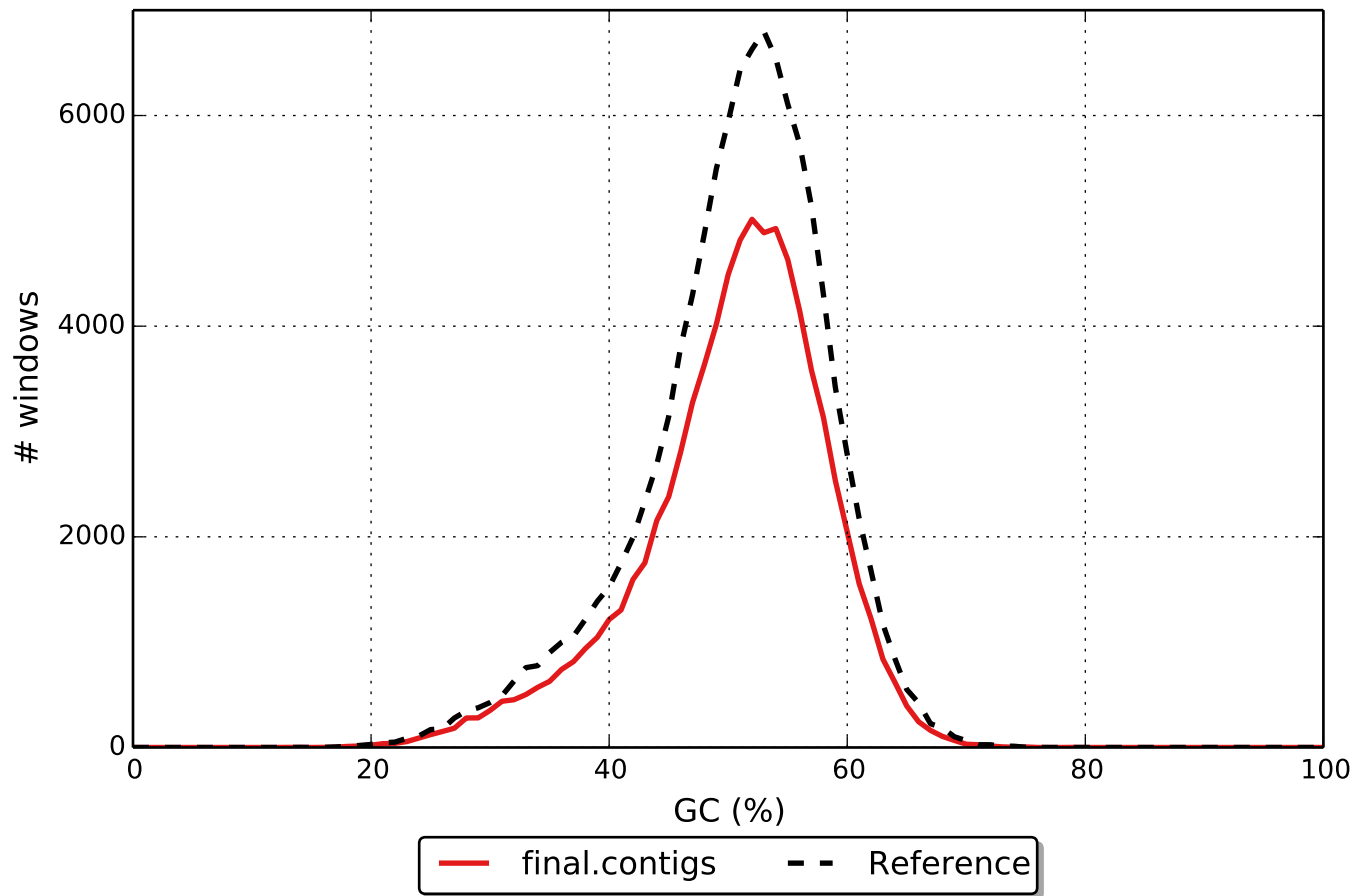
## Unaligned report

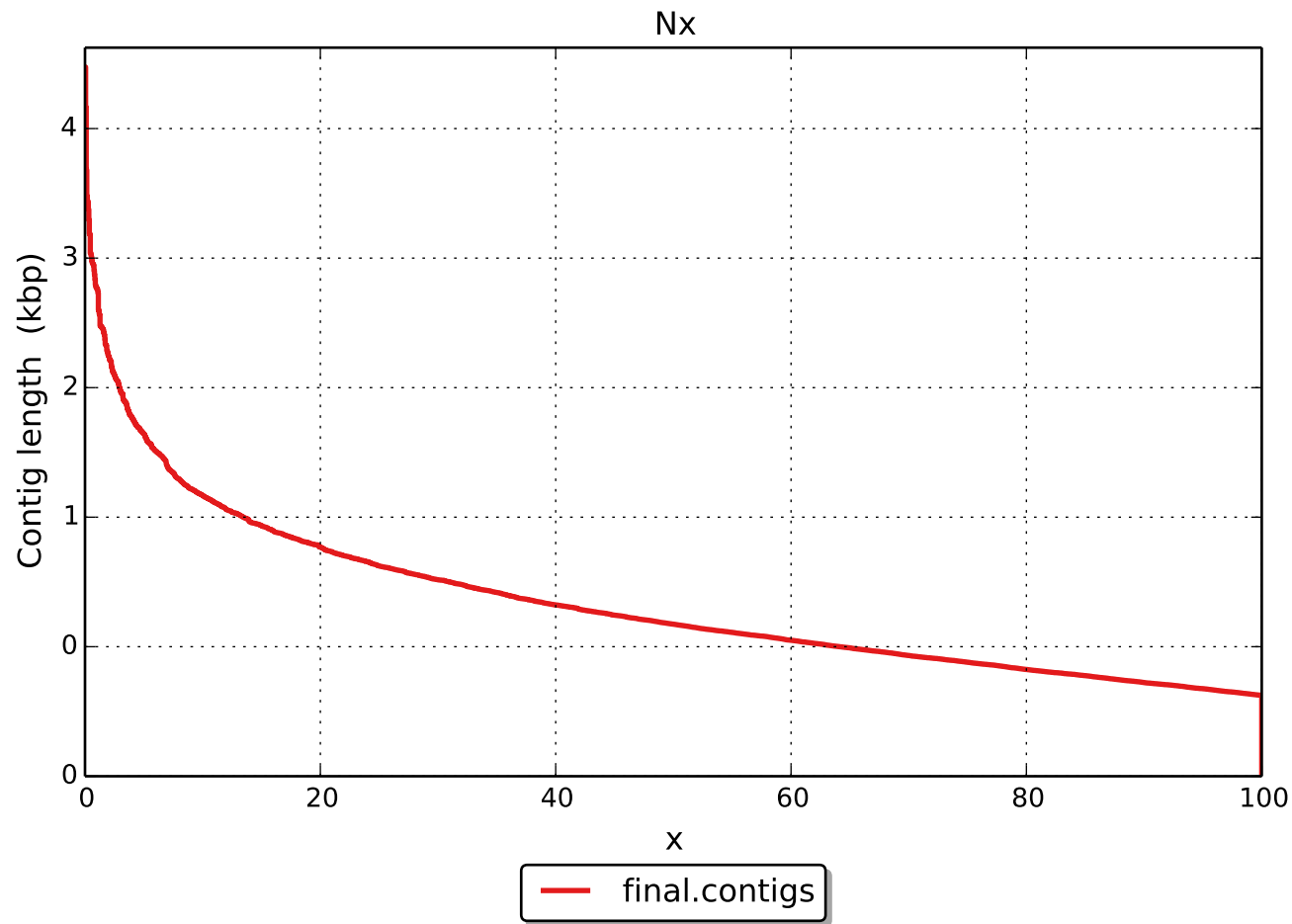
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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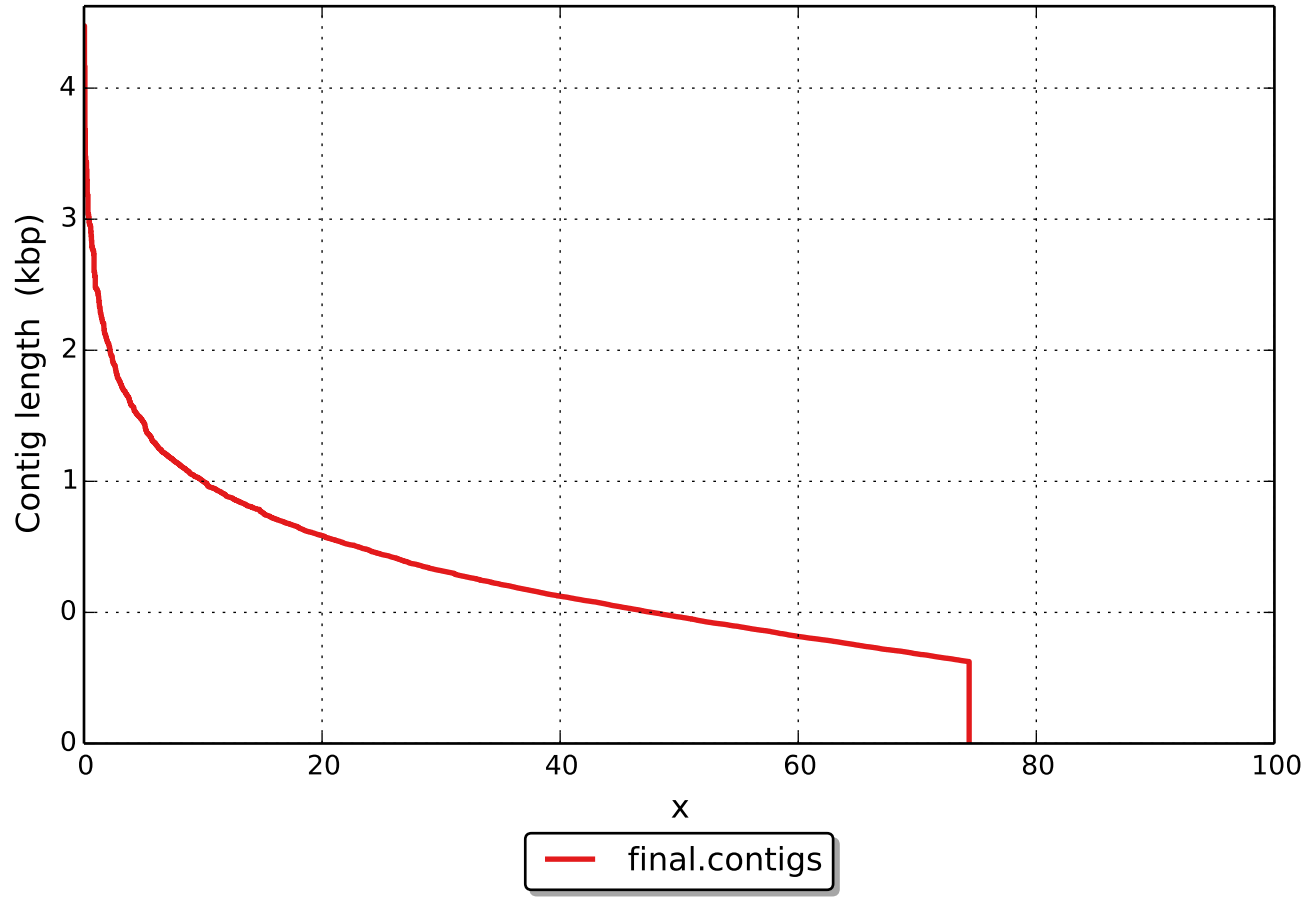


GC content





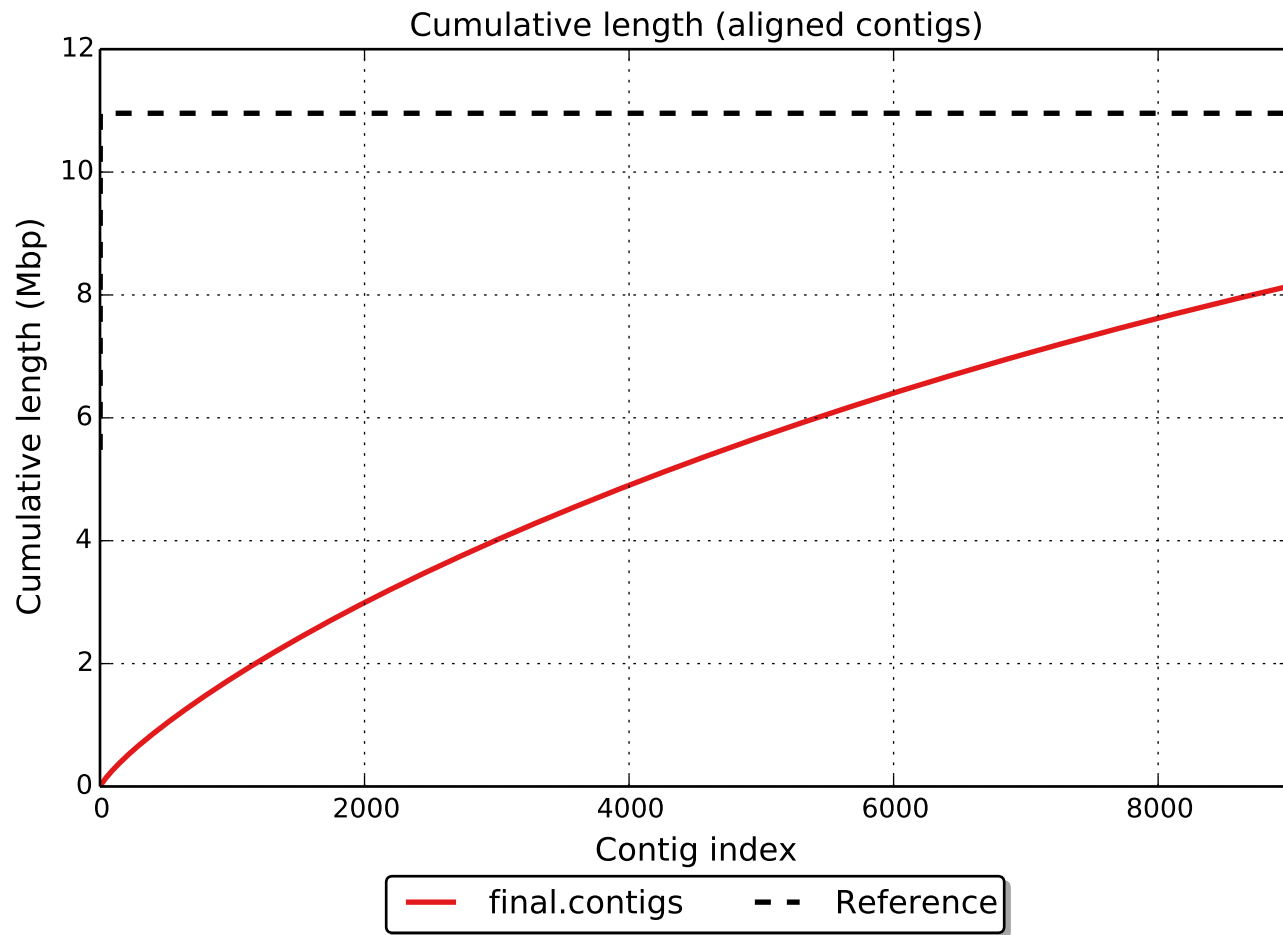
NGx



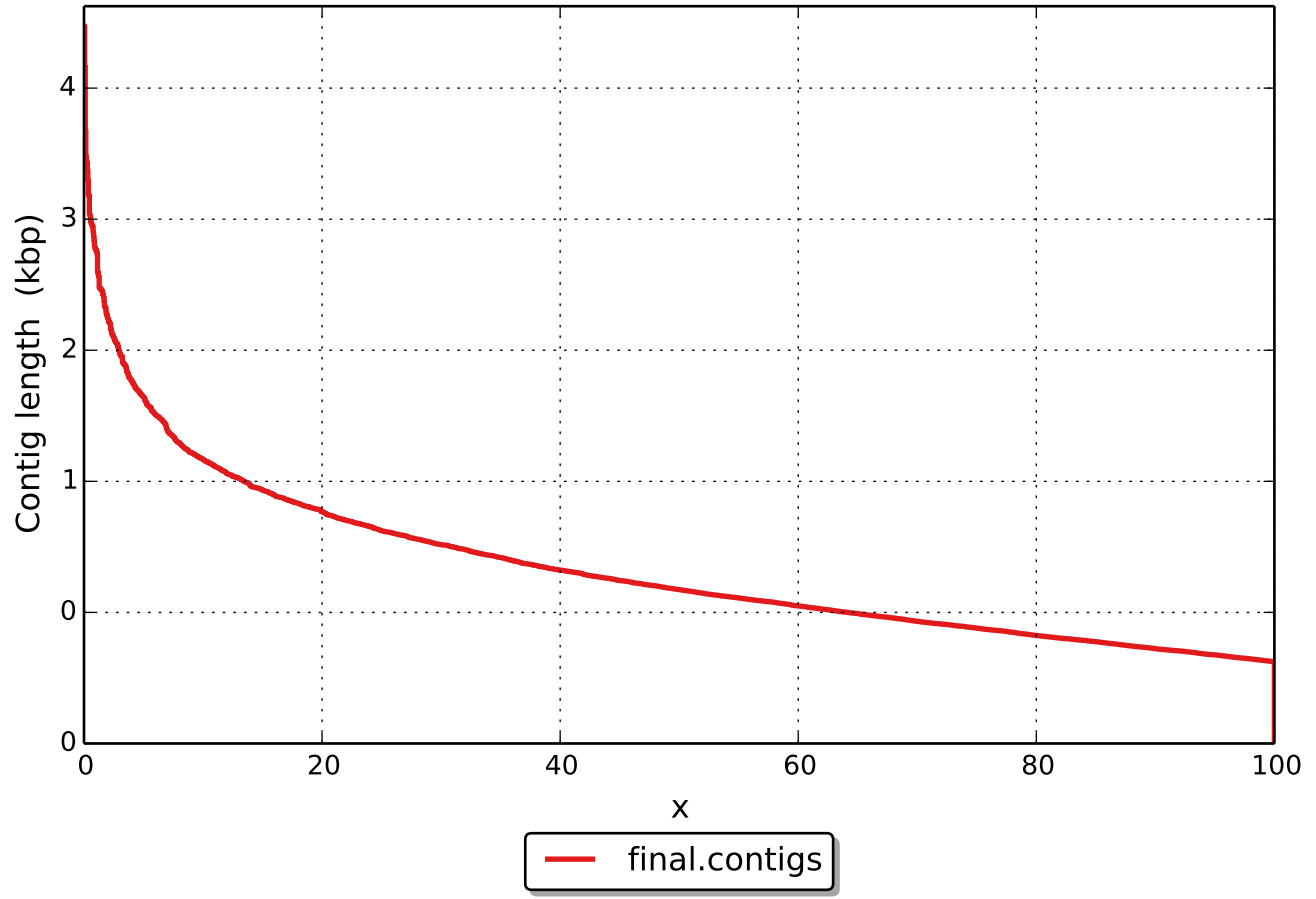
# Misassemblies







NAx



NGAx

