

Report

	final.contigs
# contigs (≥ 0 bp)	2002
# contigs (≥ 1000 bp)	1380
Total length (≥ 0 bp)	3659249
Total length (≥ 1000 bp)	3194310
# contigs	2002
Largest contig	8912
Total length	3659249
Reference length	1892775
GC (%)	32.27
Reference GC (%)	32.25
N50	2332
NG50	3668
N75	1421
NG75	2840
L50	499
LG50	191
L75	1003
LG75	339
# misassemblies	86
# misassembled contigs	82
Misassembled contigs length	239534
# local misassemblies	0
# unaligned contigs	11 + 19 part
Unaligned length	38807
Genome fraction (%)	97.616
Duplication ratio	1.959
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1753.80
# indels per 100 kbp	1.52
Largest alignment	8522
NA50	2207
NGA50	3519
NA75	1343
NGA75	2702
LA50	523
LGA50	199
LA75	1055
LGA75	354

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

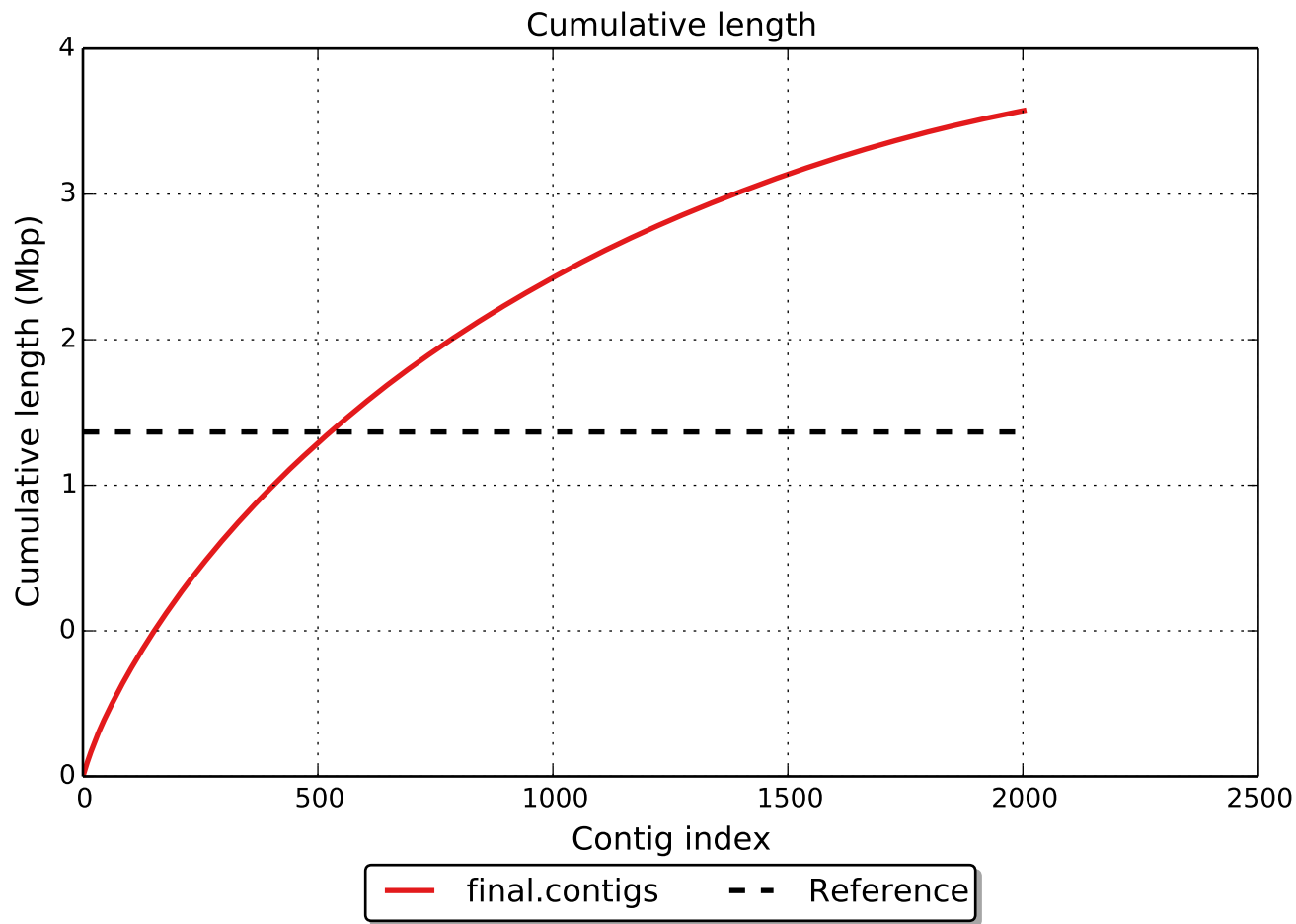
	final.contigs
# misassemblies	86
# relocations	83
# translocations	0
# inversions	3
# possibly misassembled contigs	10
# misassembled contigs	82
Misassembled contigs length	239534
# local misassemblies	0
# mismatches	32404
# indels	28
# short indels	28
# long indels	0
Indels length	28

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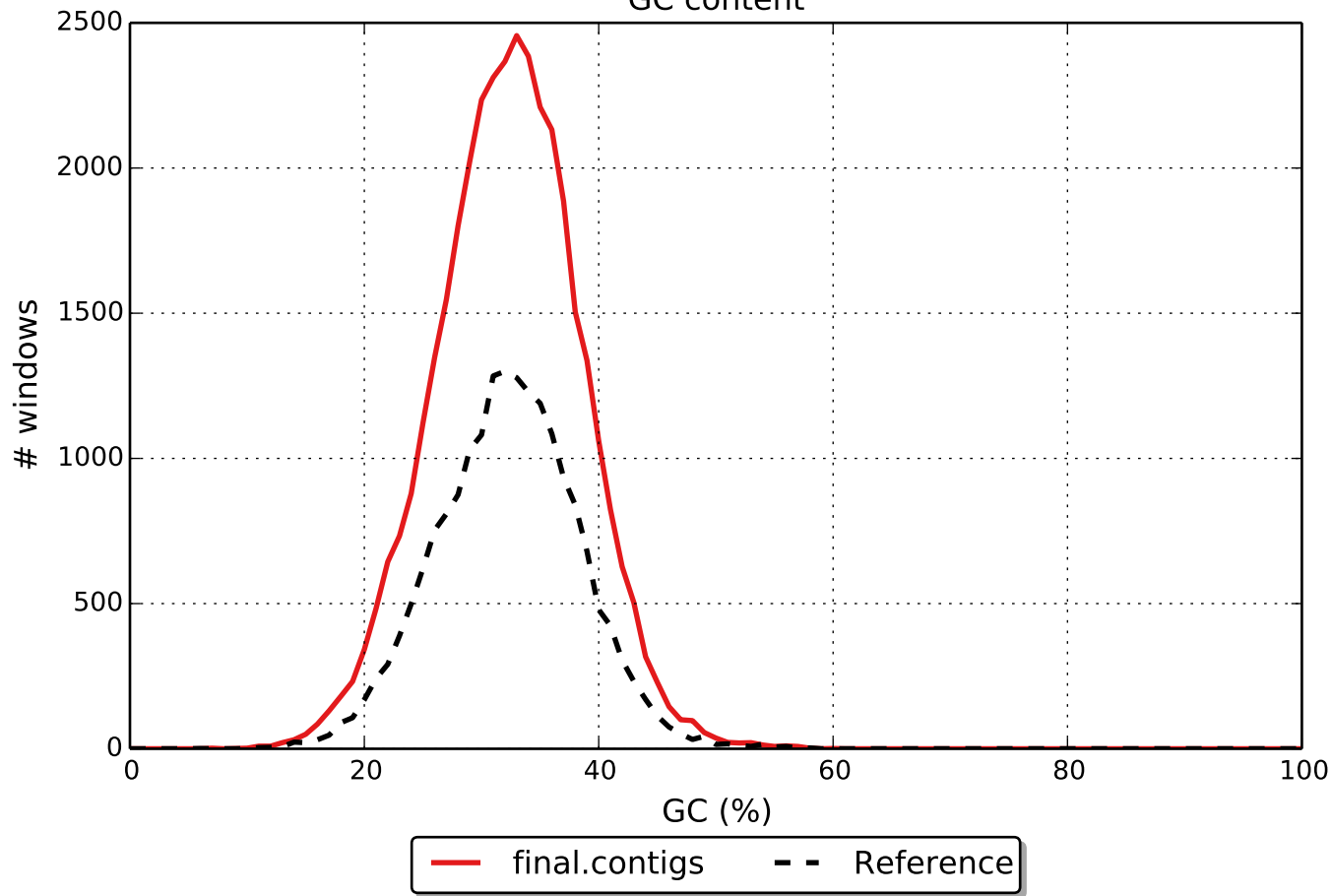
Unaligned report

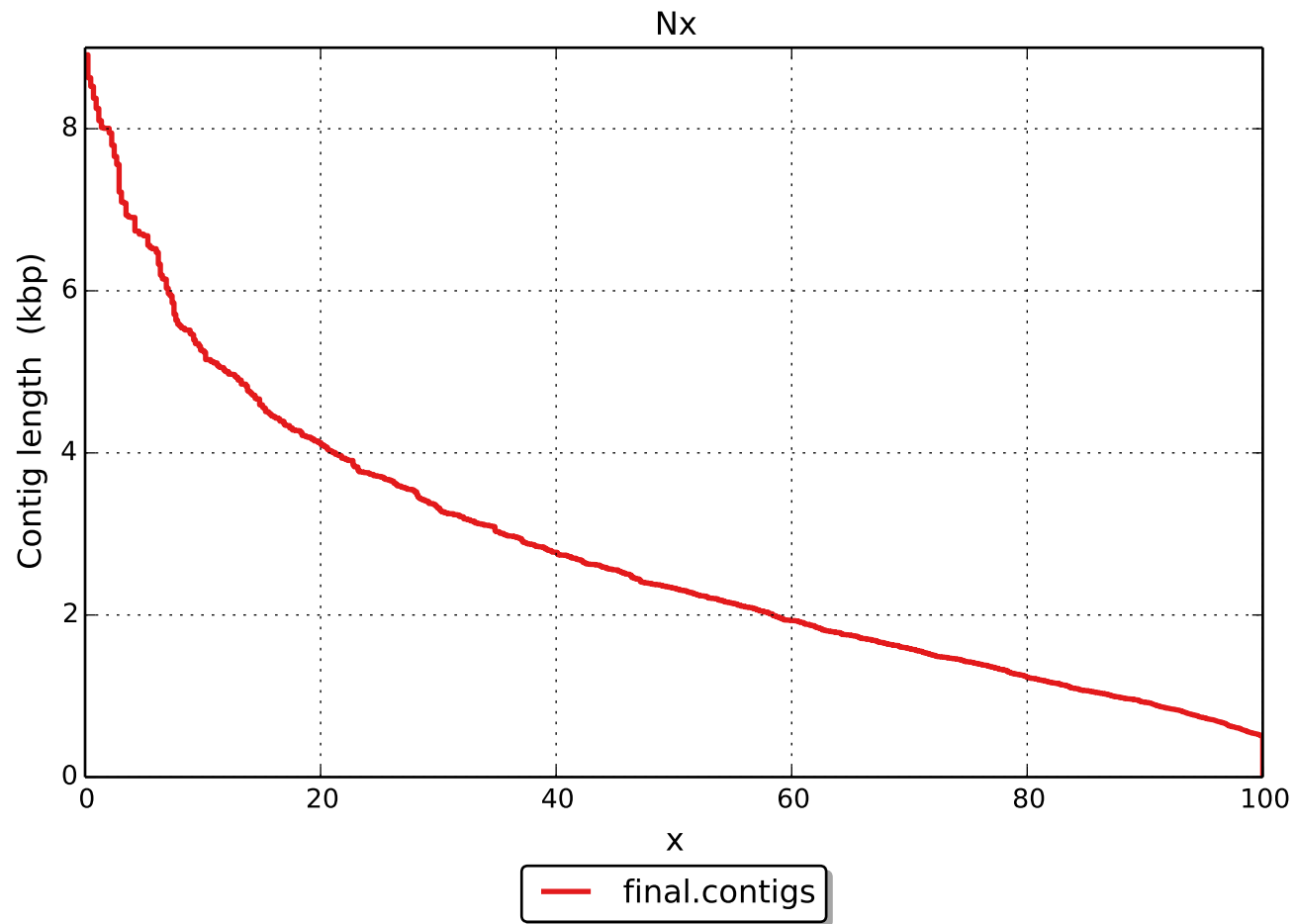
	final.contigs
# fully unaligned contigs	11
Fully unaligned length	16463
# partially unaligned contigs	19
# with misassembly	3
# both parts are significant	8
Partially unaligned length	22344
# N's	0

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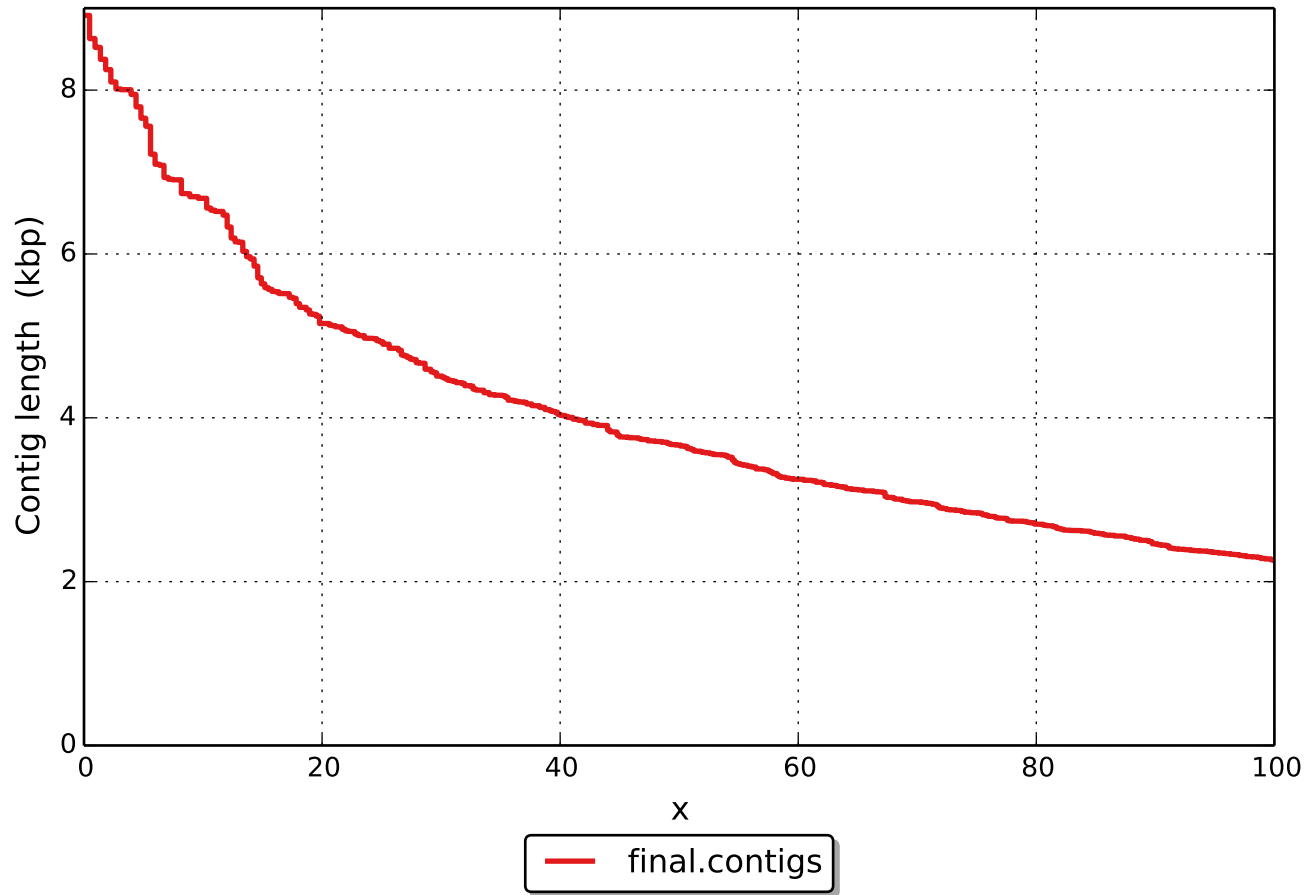


GC content

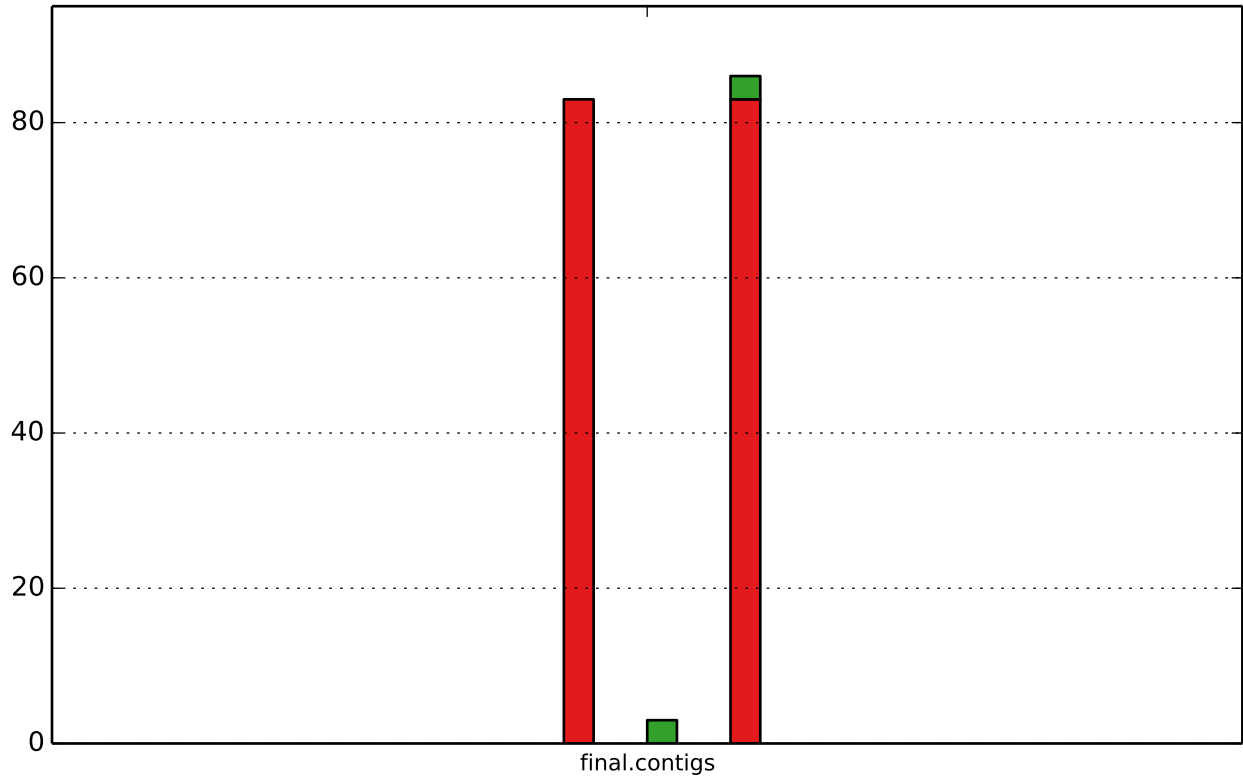


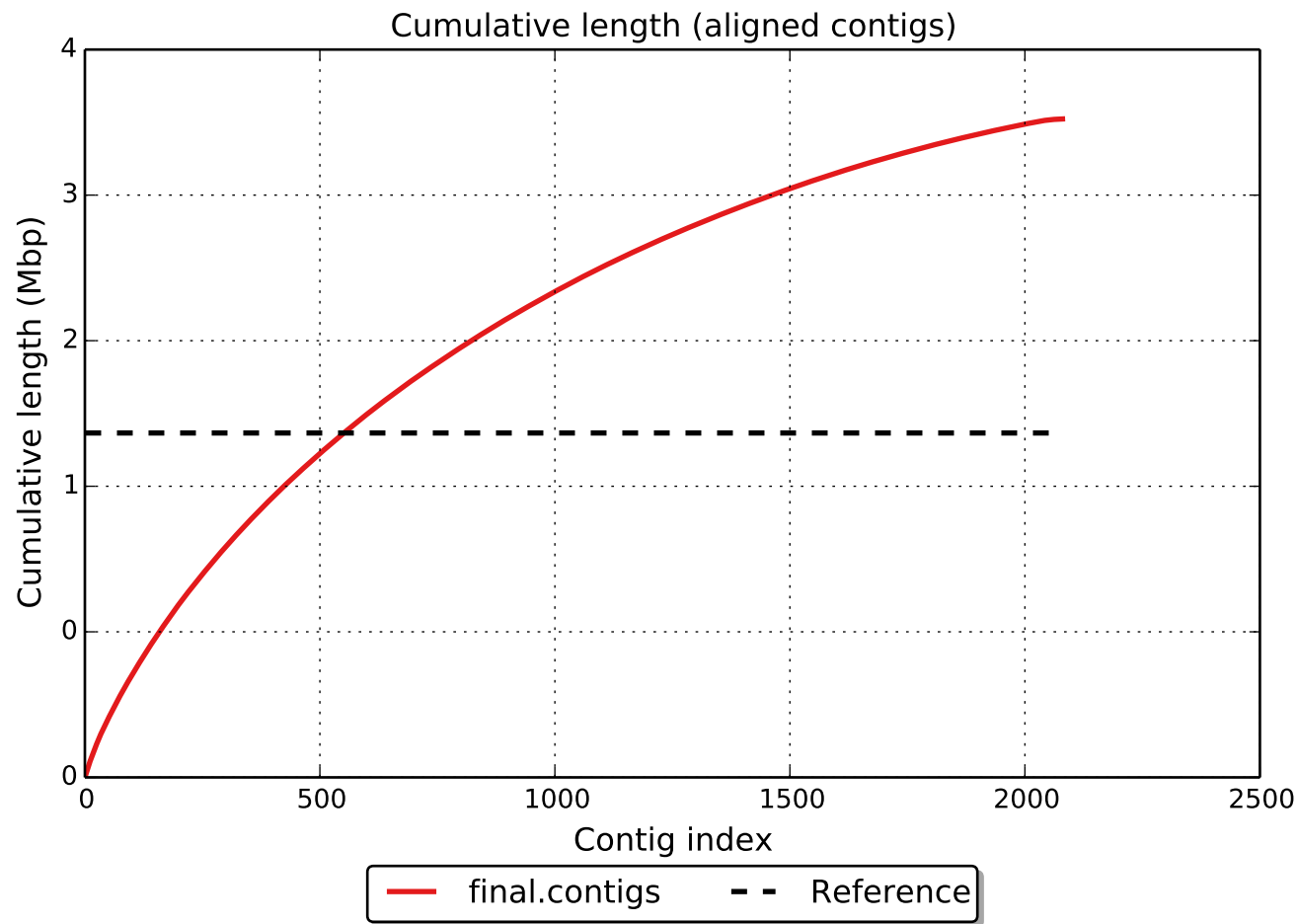


NGx

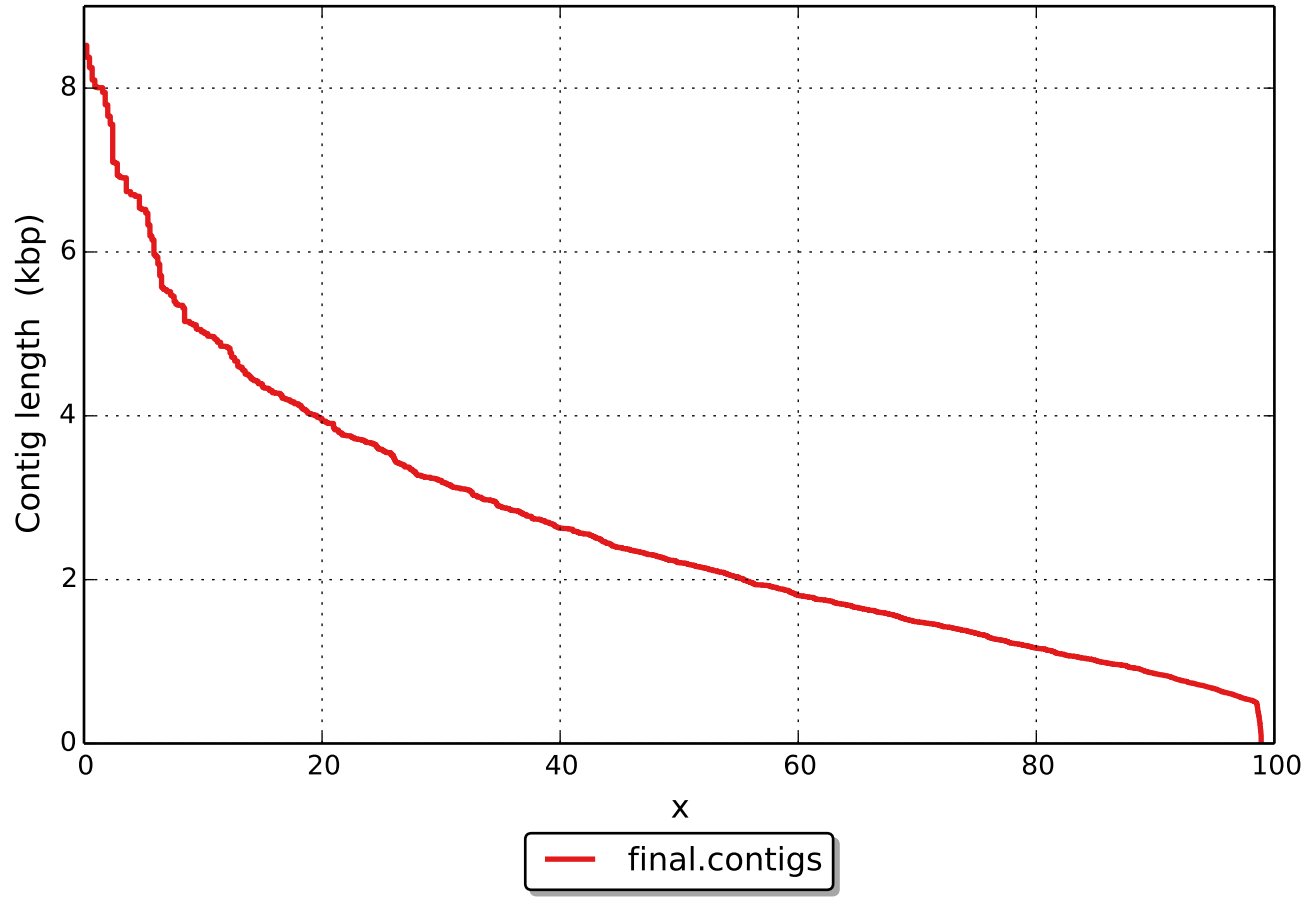


Misassemblies





NAx



NGAx

