

Report

	final.contigs
# contigs (≥ 0 bp)	1092
# contigs (≥ 1000 bp)	817
Total length (≥ 0 bp)	5054891
Total length (≥ 1000 bp)	4868637
# contigs	1092
Largest contig	42944
Total length	5054891
Reference length	5478683
GC (%)	50.28
Reference GC (%)	50.49
N50	8499
NG50	7874
N75	4529
NG75	3588
L50	173
LG50	199
L75	367
LG75	446
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	91.189
Duplication ratio	1.012
# N's per 100 kbp	0.00
# mismatches per 100 kbp	521.28
# indels per 100 kbp	0.10
Largest alignment	42944
NA50	8499
NGA50	7874
NA75	4529
NGA75	3588
LA50	173
LGA50	199
LA75	367
LGA75	446

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

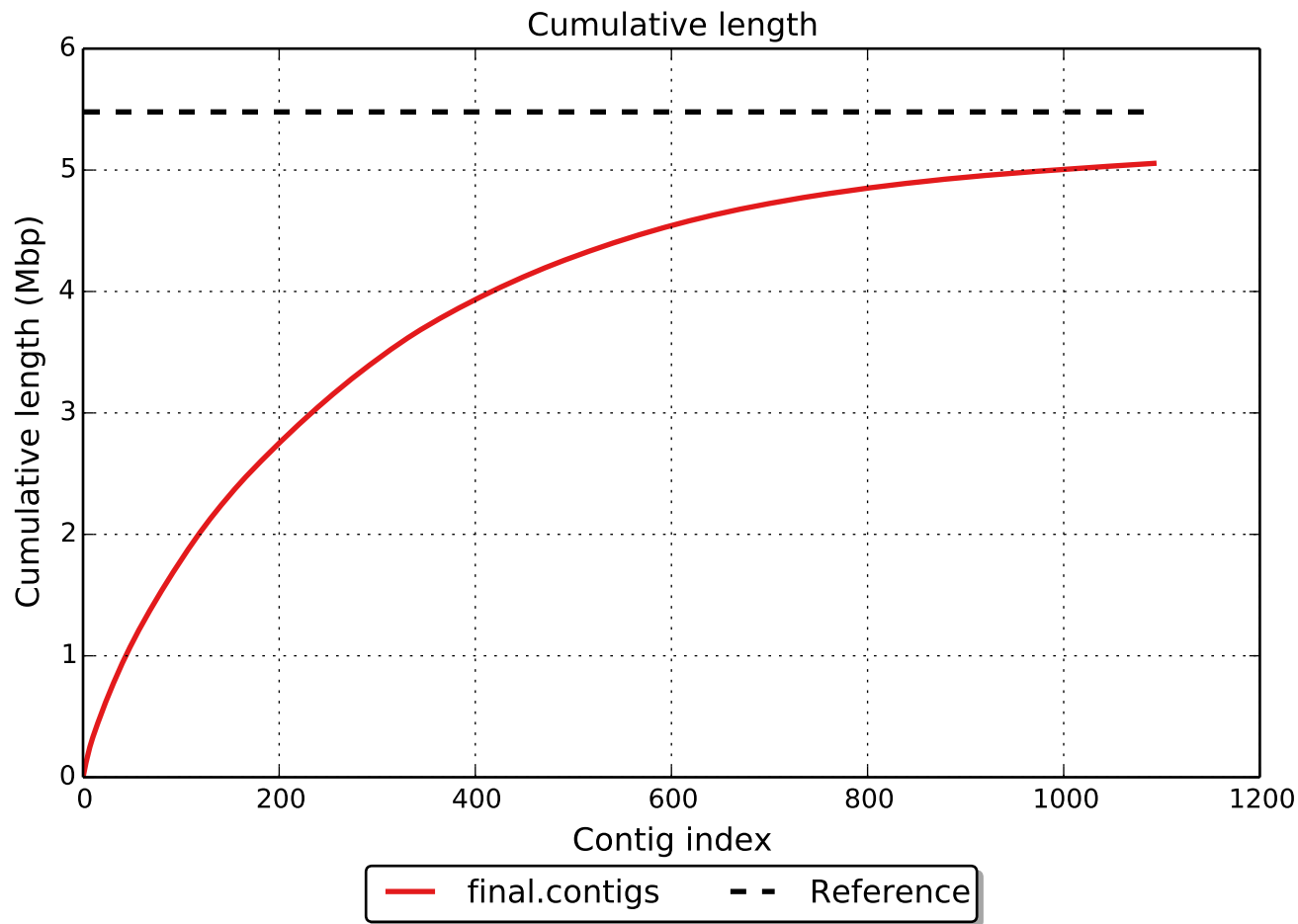
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	26043
# indels	5
# short indels	3
# long indels	2
Indels length	27

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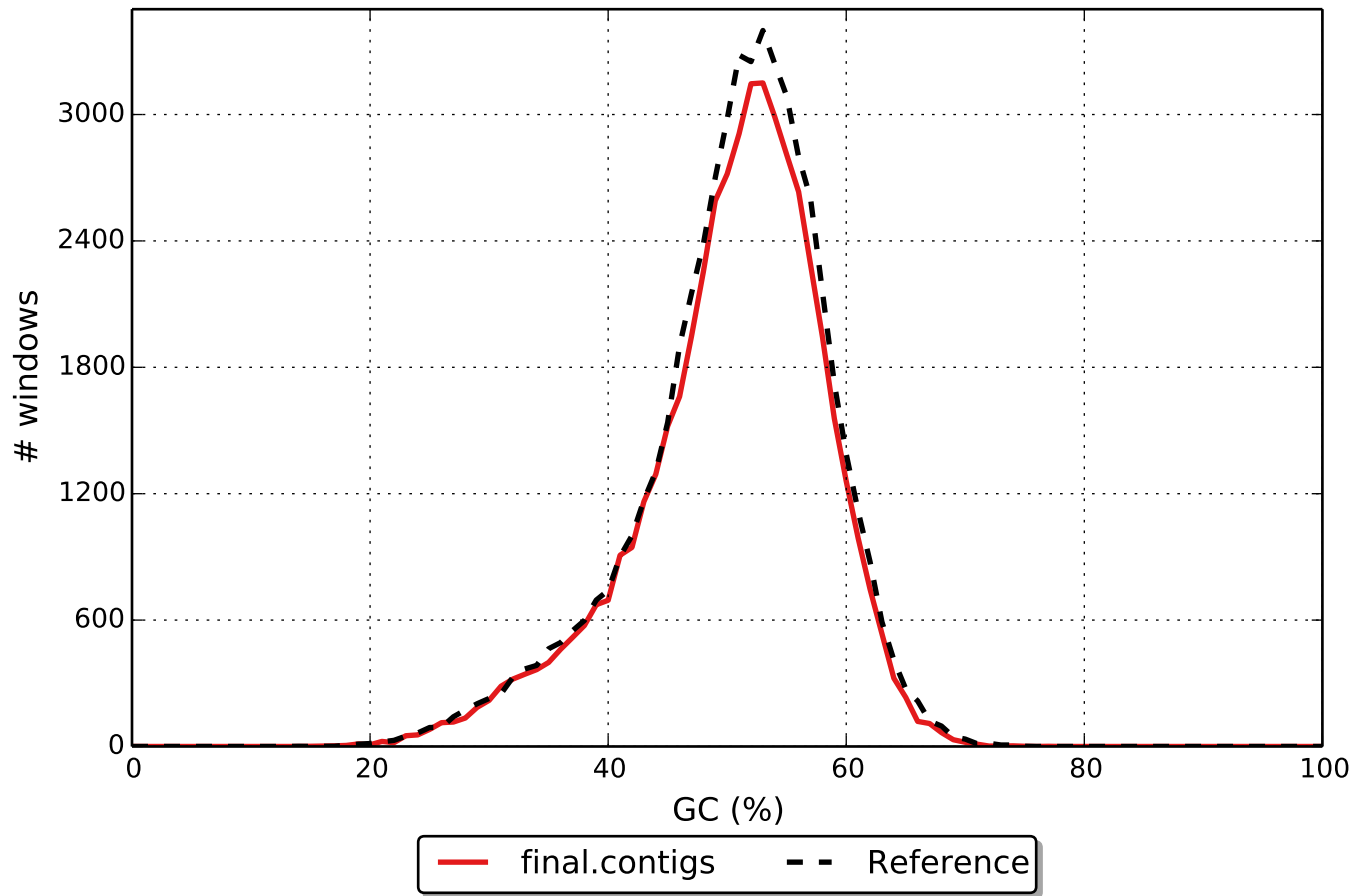
Unaligned report

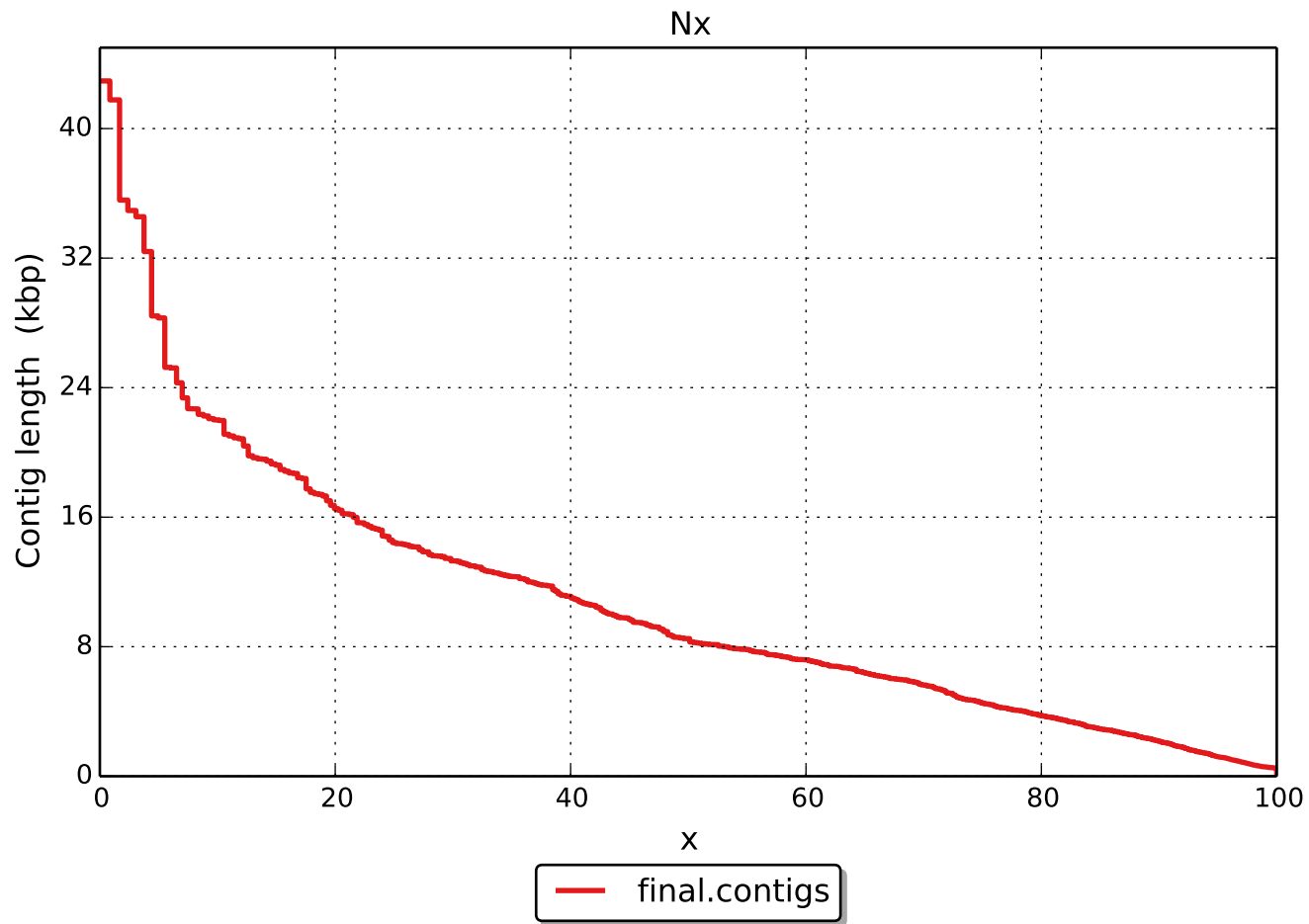
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

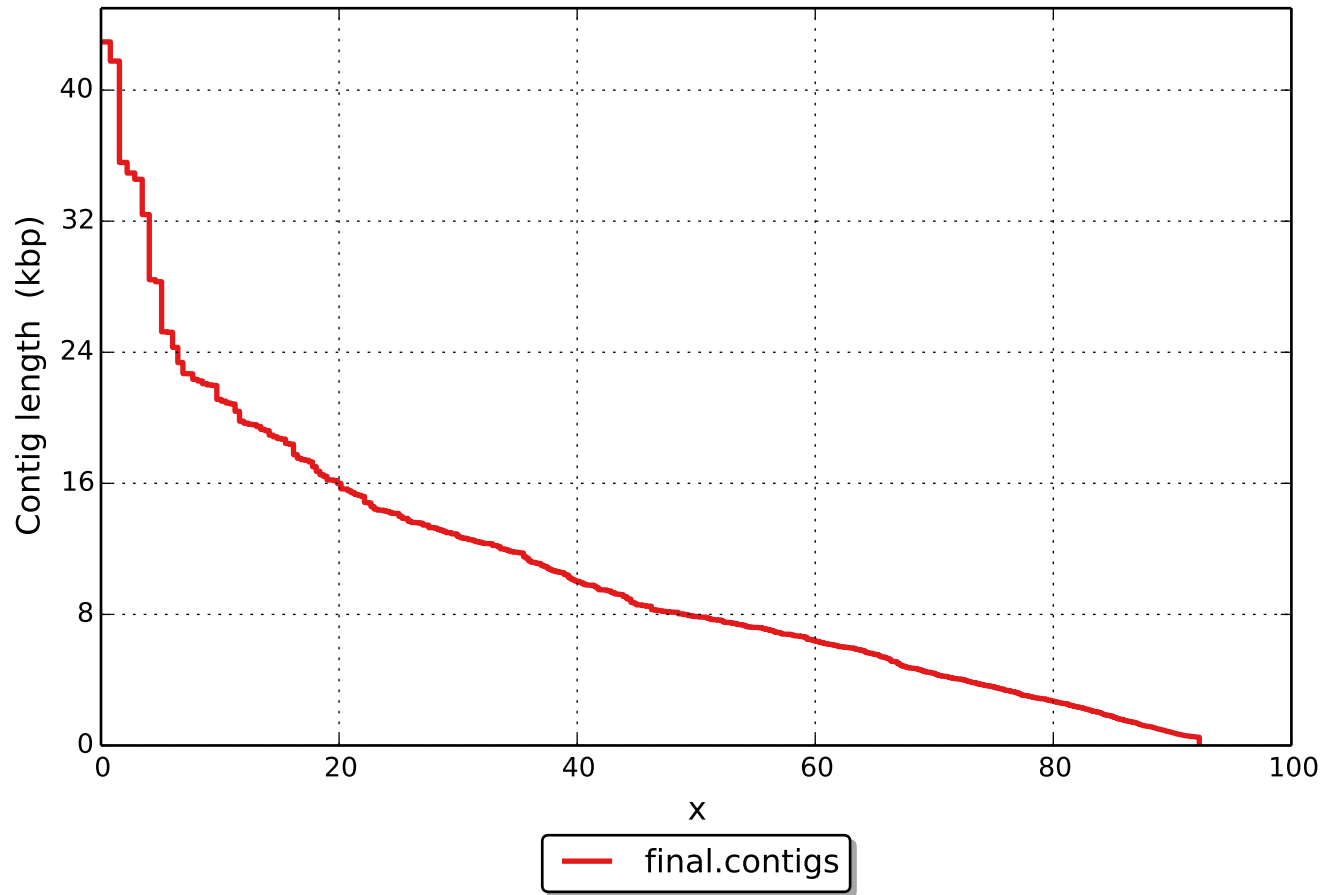


GC content



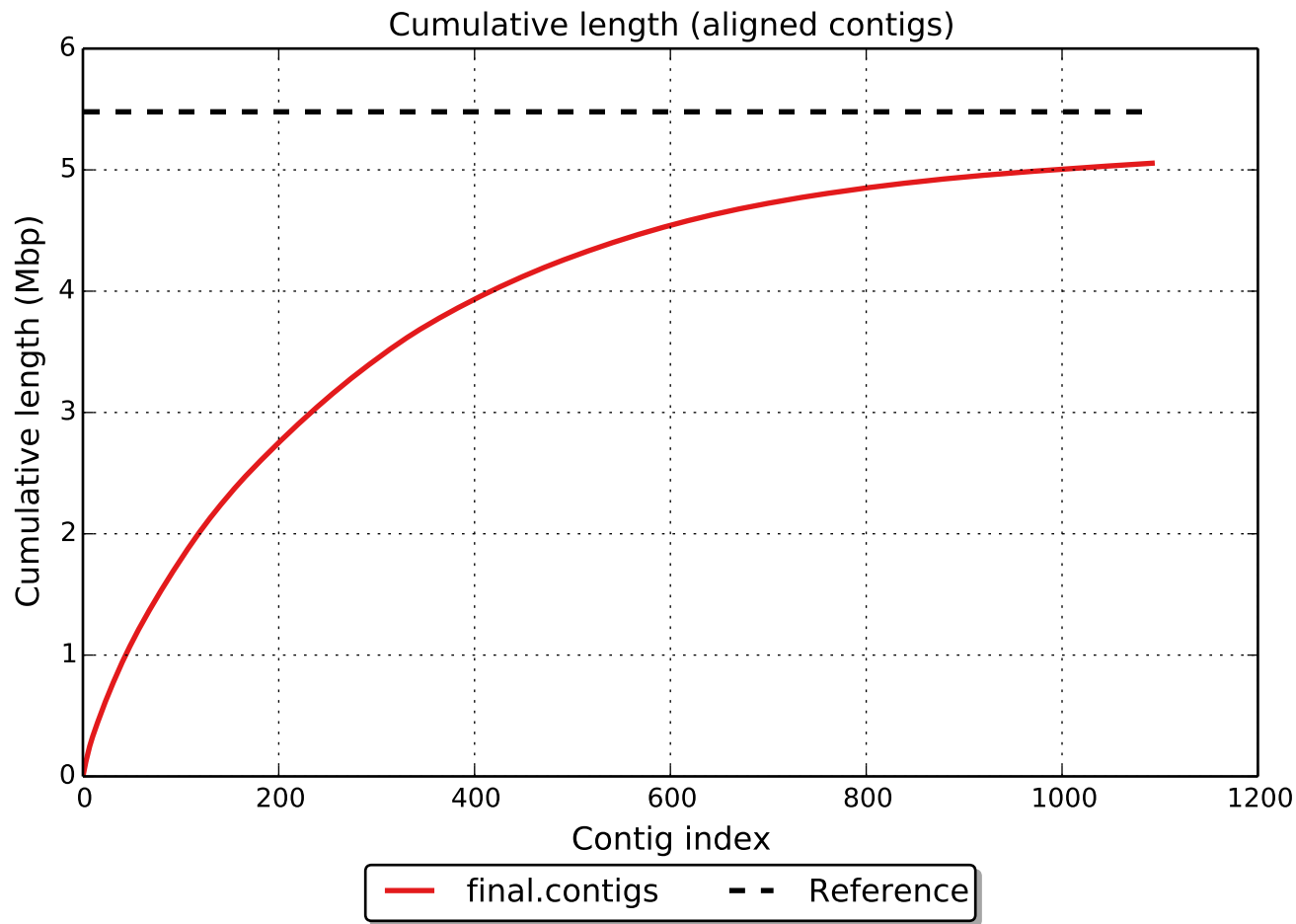


NGx

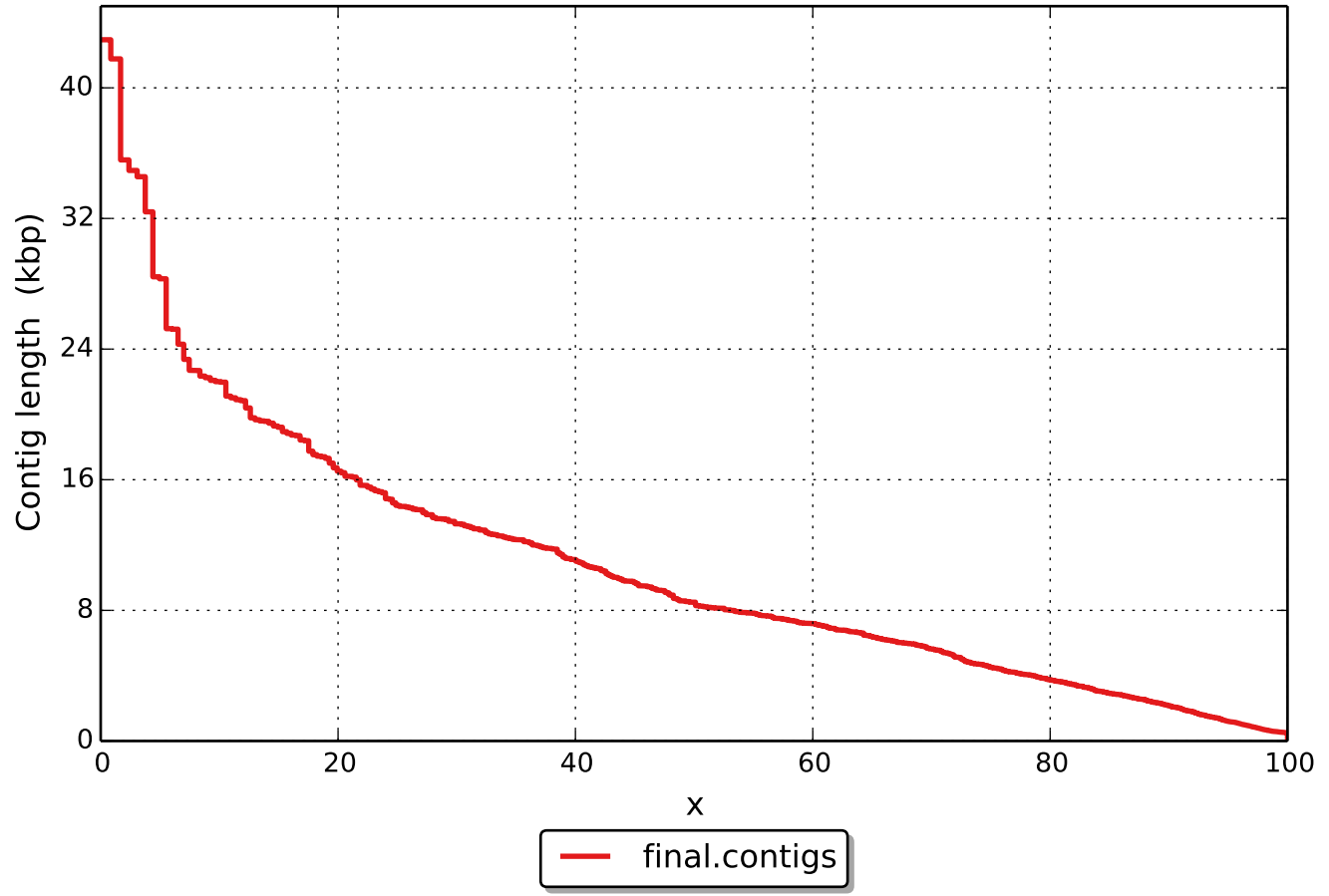


Misassemblies





NAx



NGAx

