

Report

	final.contigs
# contigs (>= 0 bp)	2482
# contigs (>= 1000 bp)	1380
Total length (>= 0 bp)	3830247
Total length (>= 1000 bp)	3194310
# contigs	2002
Largest contig	8912
Total length	3659249
Reference length	3785550
GC (%)	32.27
Reference GC (%)	32.25
N50	2332
NG50	2262
N75	1421
NG75	1334
L50	499
LG50	527
L75	1003
LG75	1072
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	93.243
Duplication ratio	1.037
# N's per 100 kbp	0.00
# mismatches per 100 kbp	32.50
# indels per 100 kbp	0.11
Largest alignment	8912
NA50	2332
NGA50	2262
NA75	1421
NGA75	1334
LA50	499
LGA50	527
LA75	1003
LGA75	1072

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

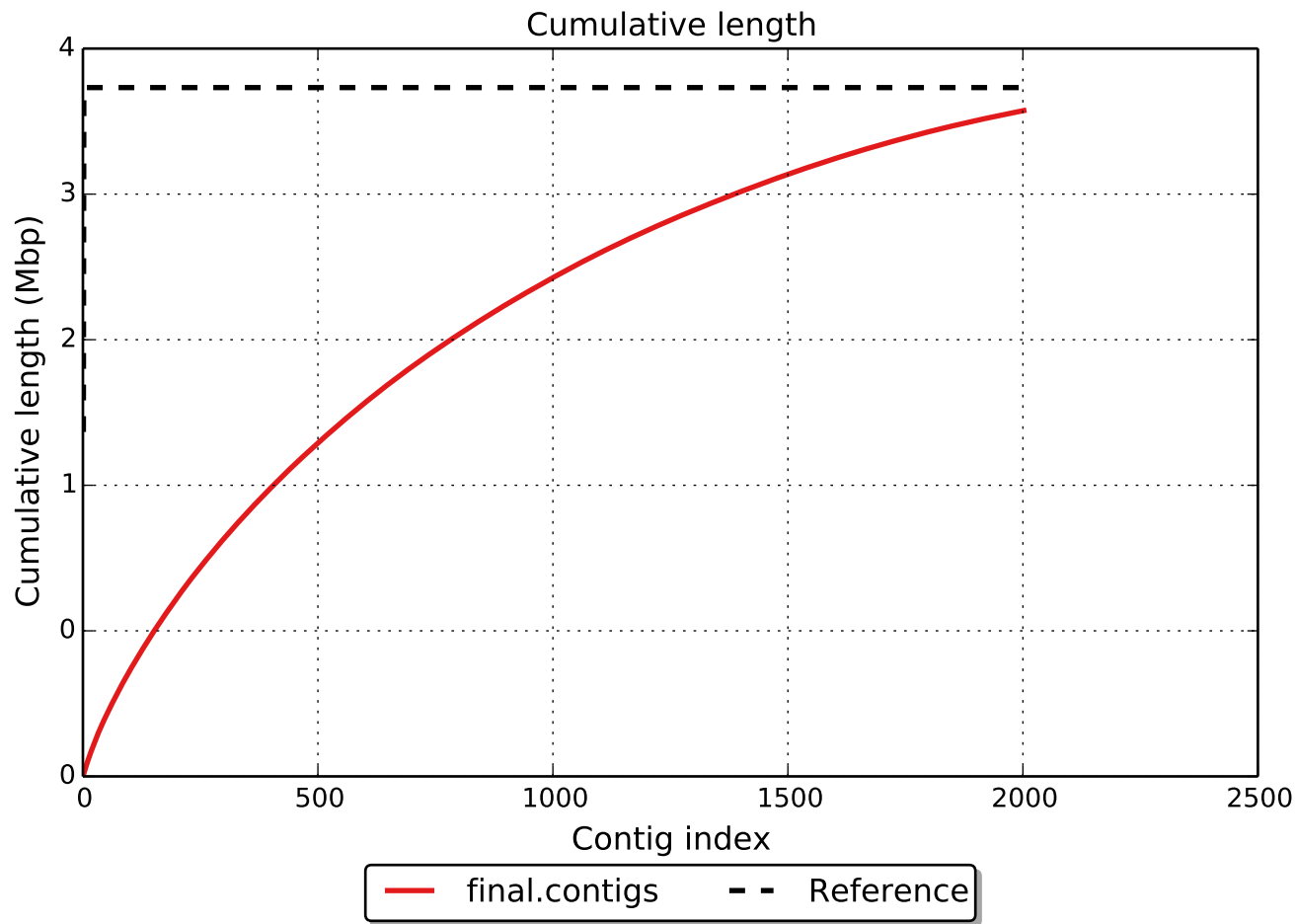
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1147
# indels	4
# short indels	4
# long indels	0
Indels length	4

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).

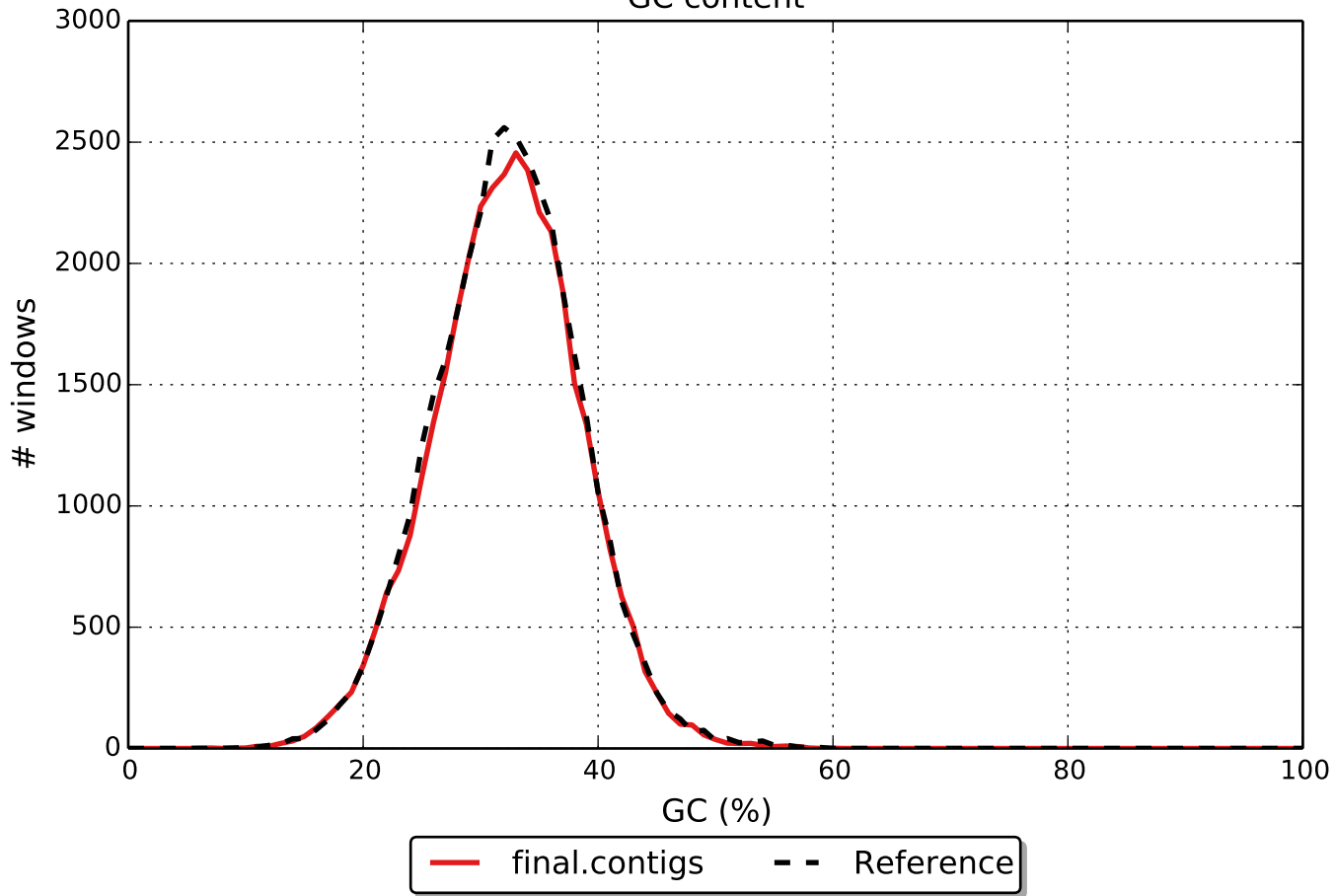
Unaligned report

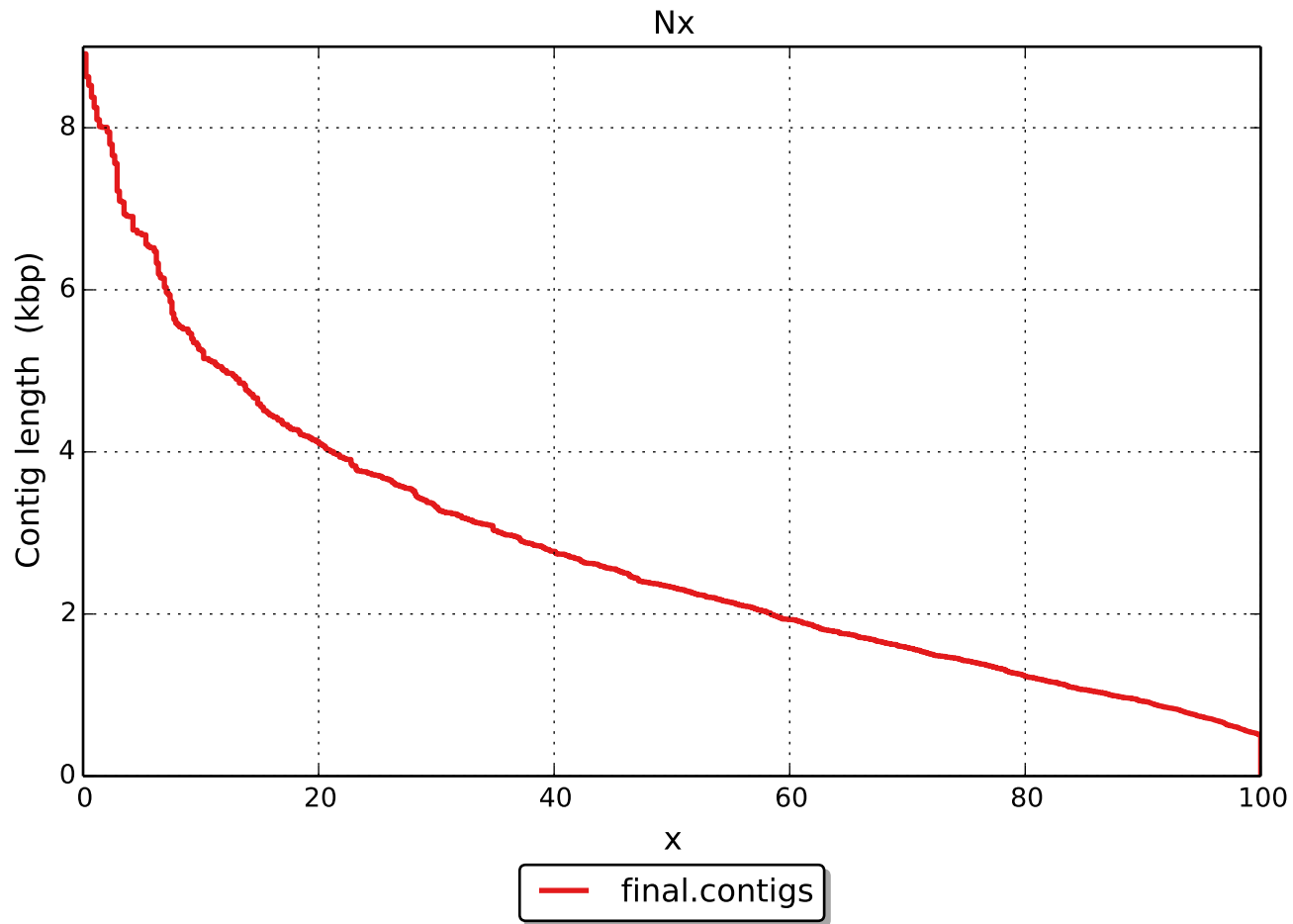
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

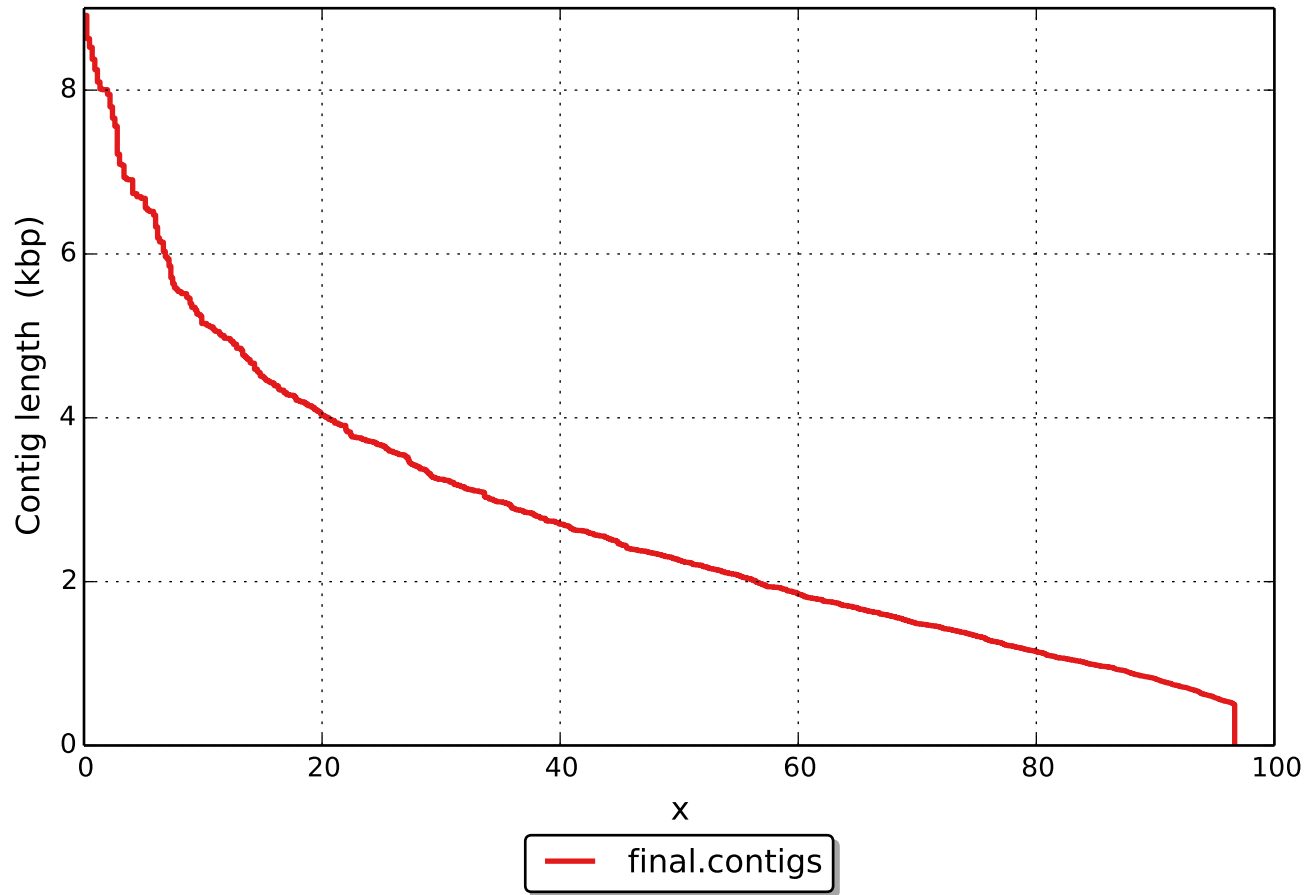


GC content



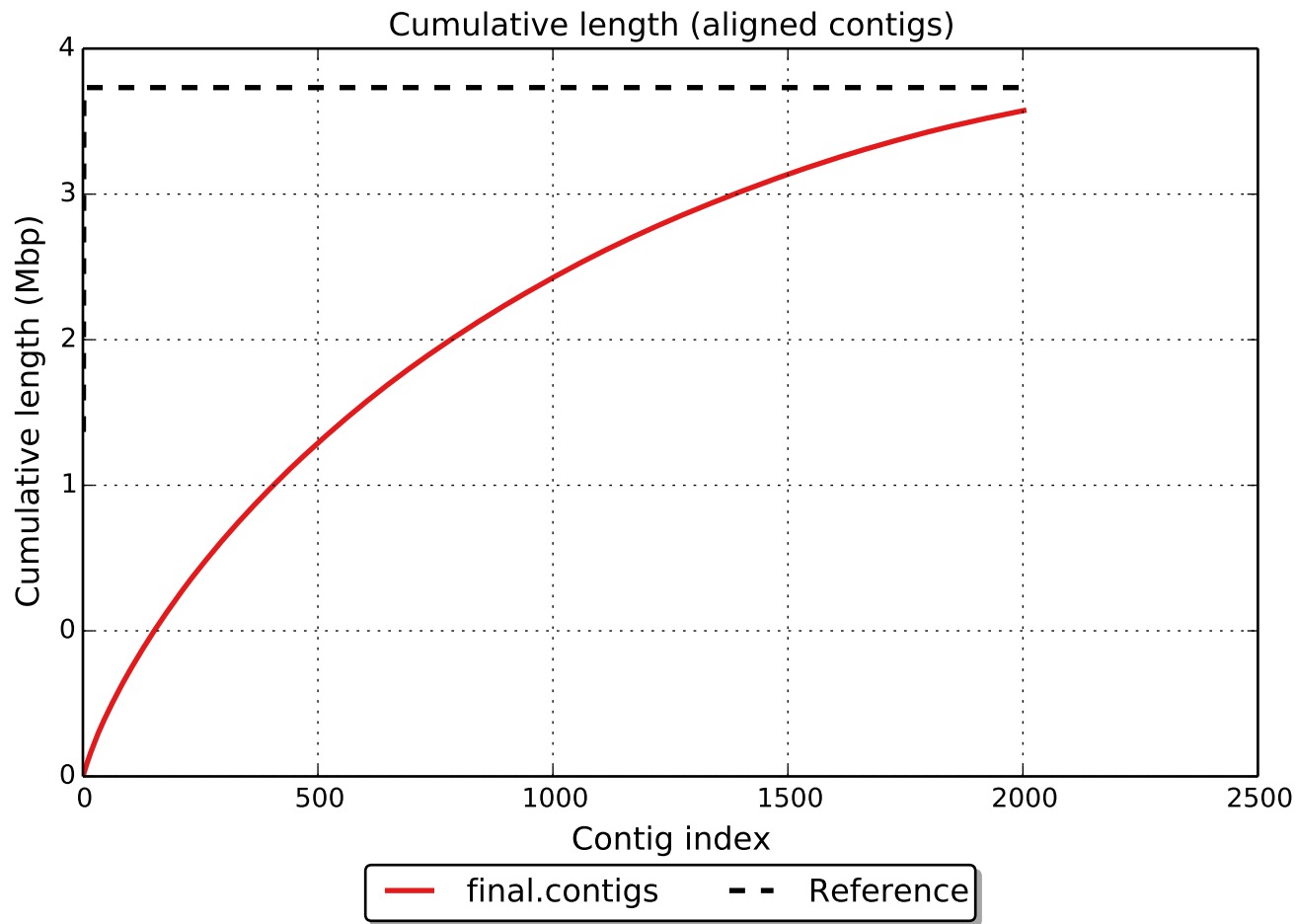


NGx

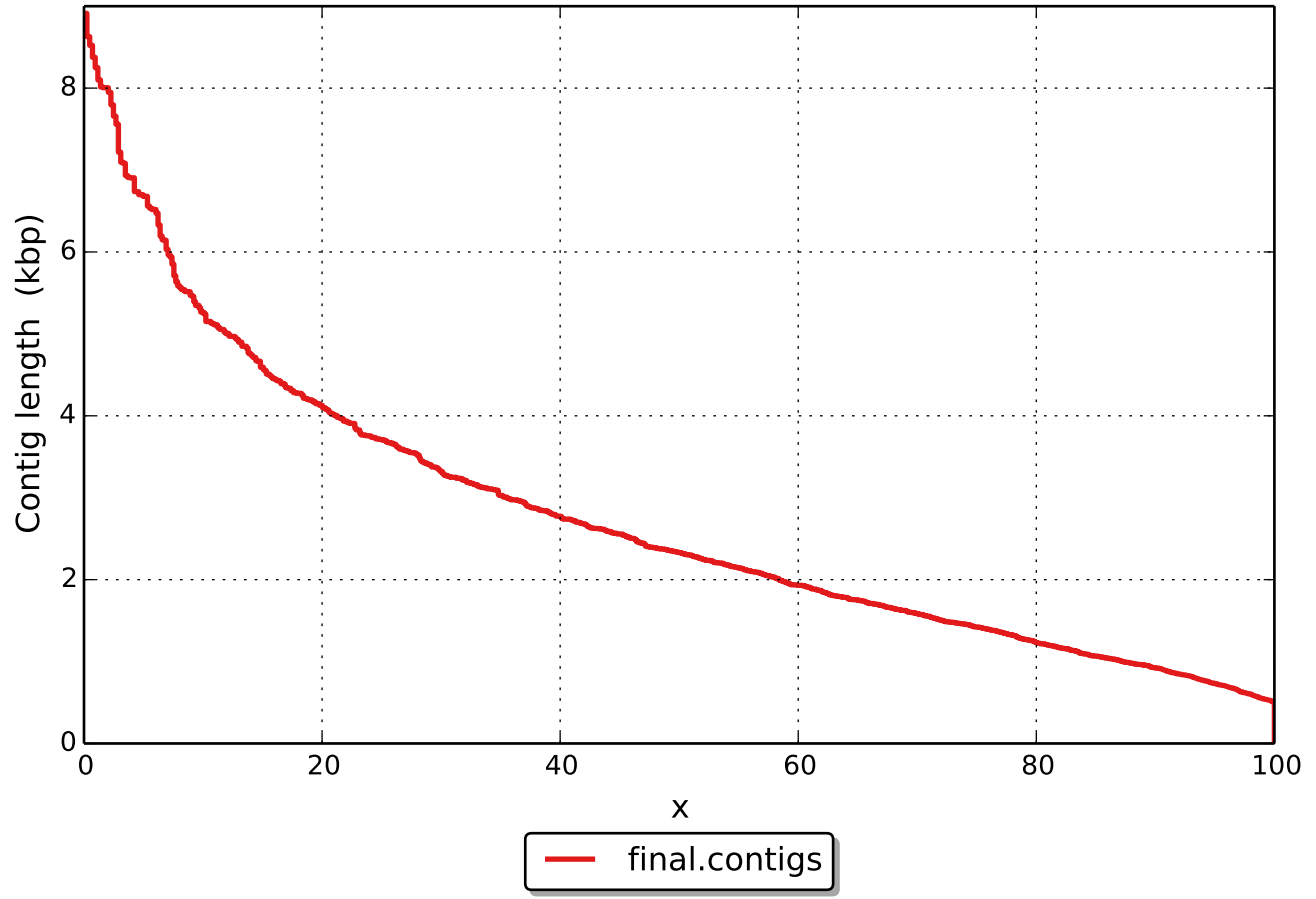


Misassemblies





NAx



NGAx

