

Report

	final.contigs
# contigs (≥ 0 bp)	1115
# contigs (≥ 1000 bp)	828
Total length (≥ 0 bp)	5105265
Total length (≥ 1000 bp)	4913086
# contigs	1115
Largest contig	42944
Total length	5105265
Reference length	5478683
GC (%)	50.28
Reference GC (%)	50.48
N50	8293
NG50	7897
N75	4488
NG75	3645
L50	175
LG50	198
L75	373
LG75	442
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 2 part
Unaligned length	228
Genome fraction (%)	92.140
Duplication ratio	1.011
# N's per 100 kbp	0.00
# mismatches per 100 kbp	524.40
# indels per 100 kbp	0.14
Largest alignment	42944
NA50	8293
NGA50	7897
NA75	4488
NGA75	3645
LA50	175
LGA50	198
LA75	373
LGA75	442

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

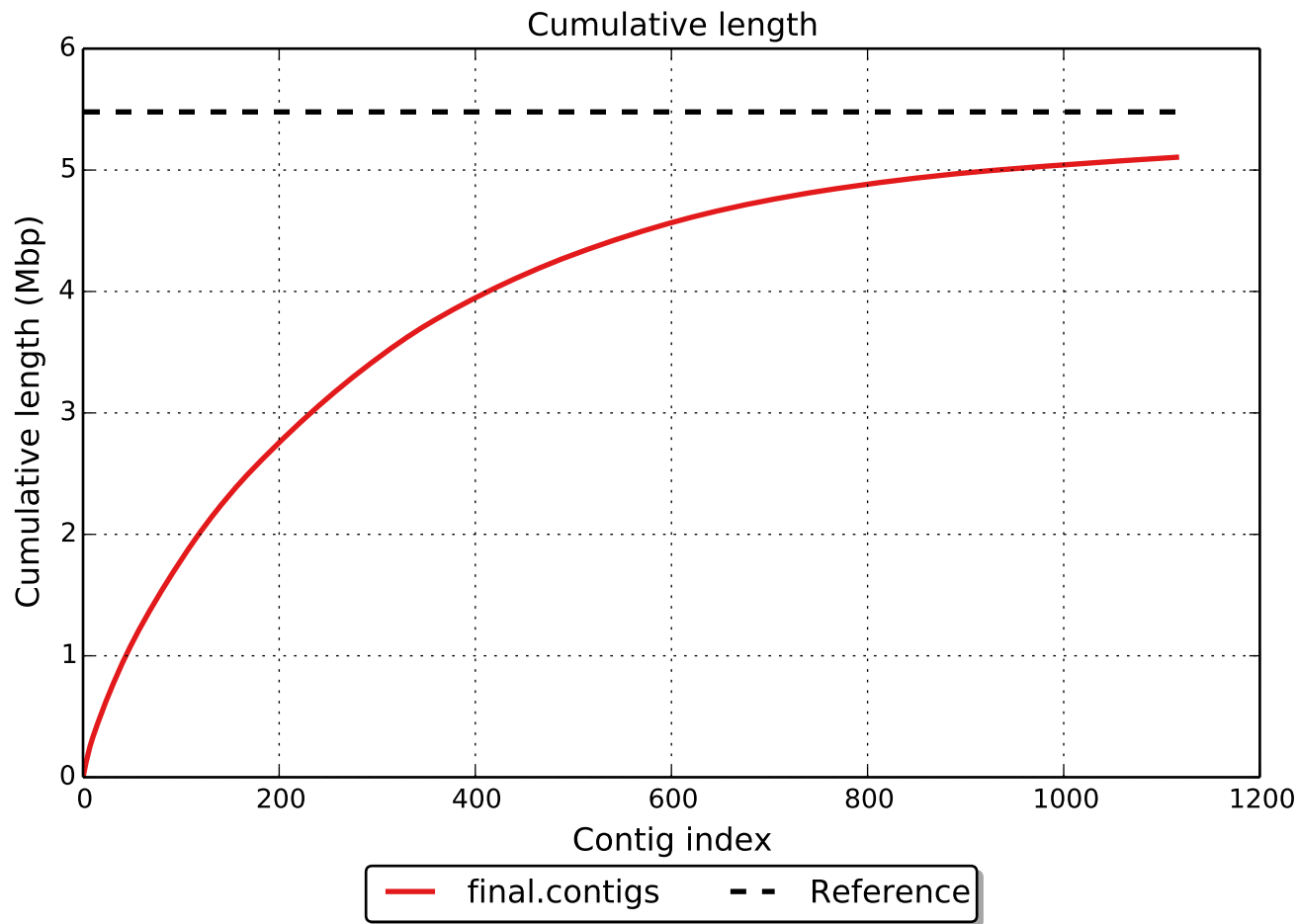
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	26472
# indels	7
# short indels	6
# long indels	1
Indels length	12

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).

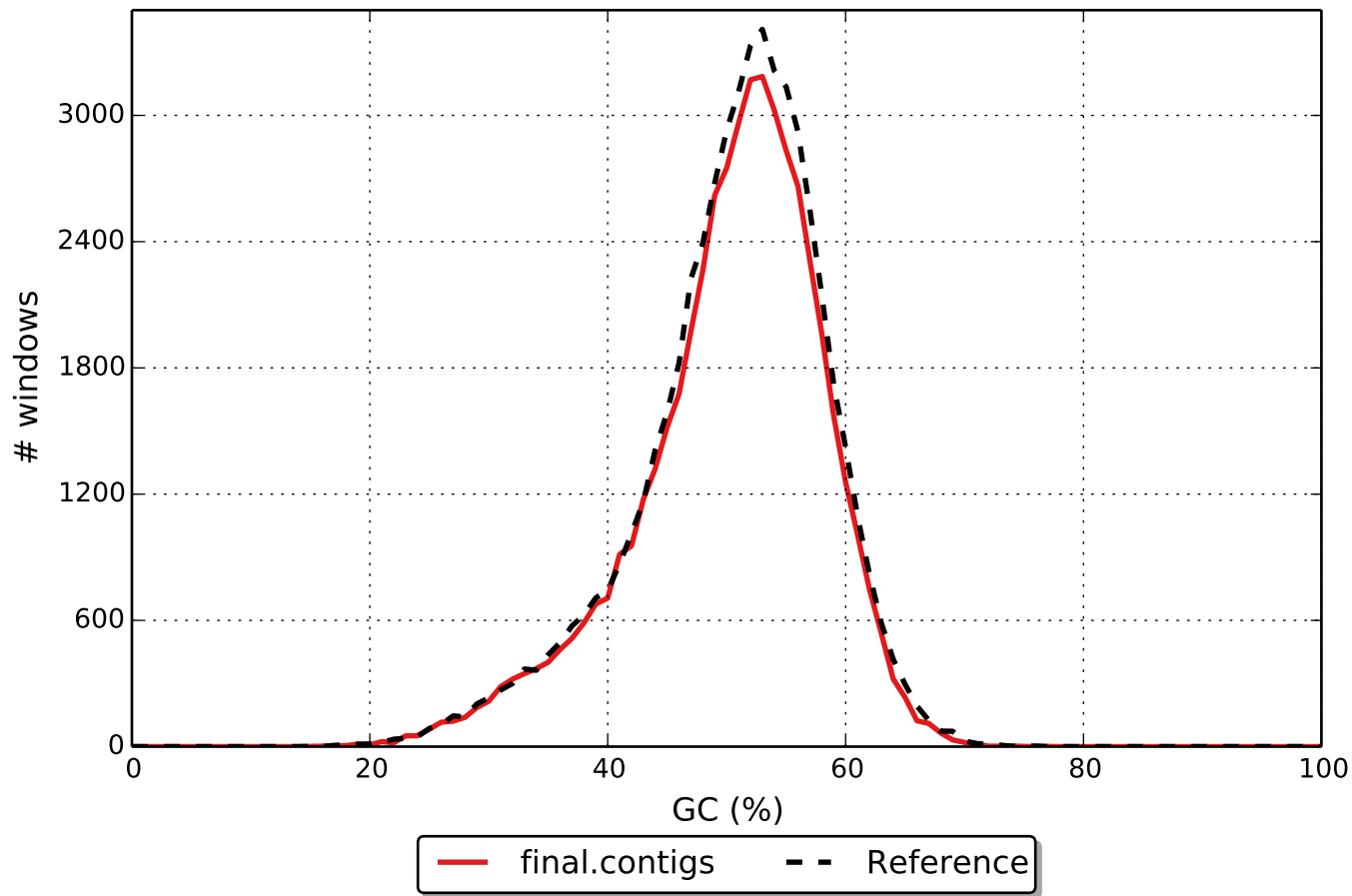
Unaligned report

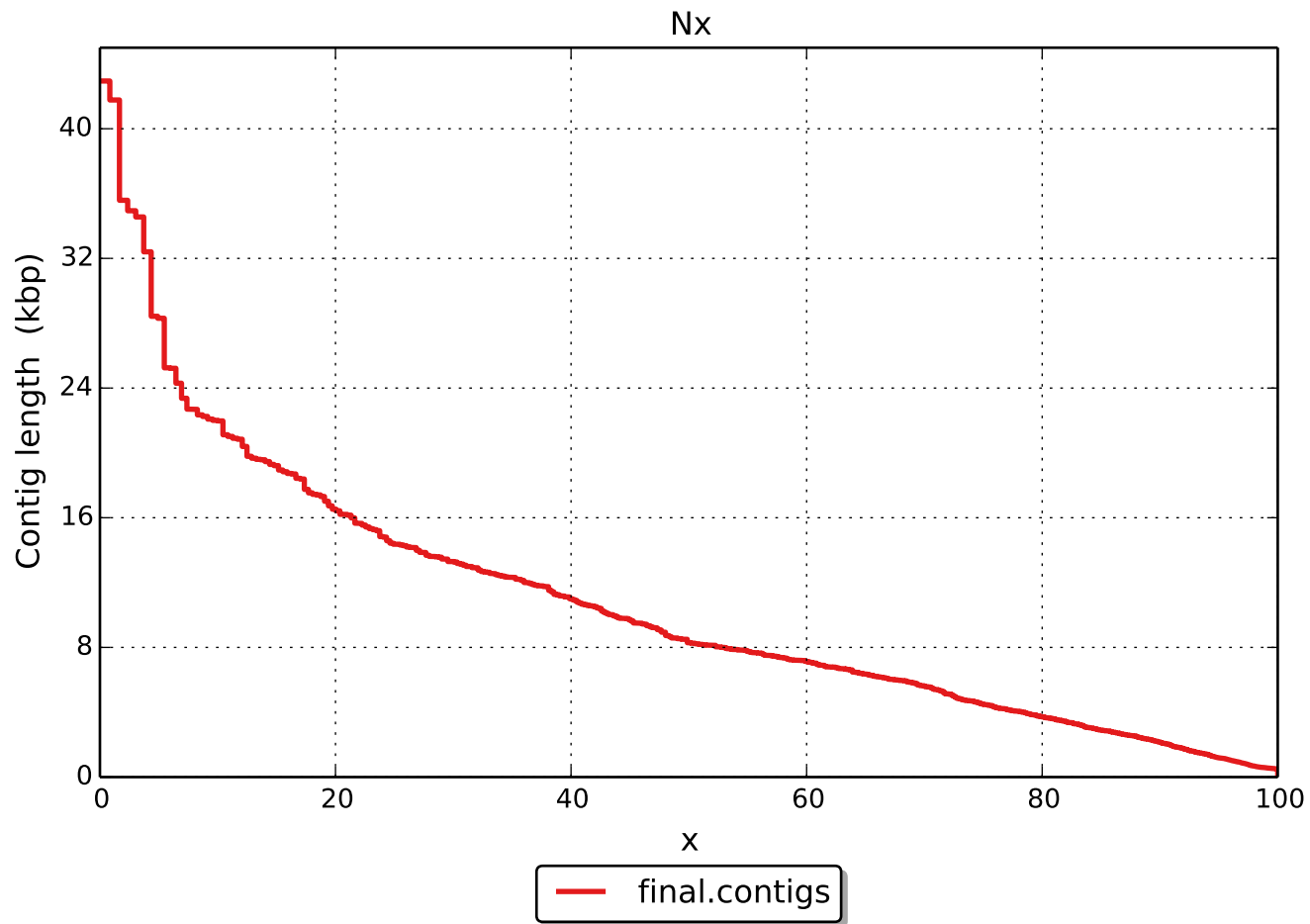
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	228
# N's	0

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).

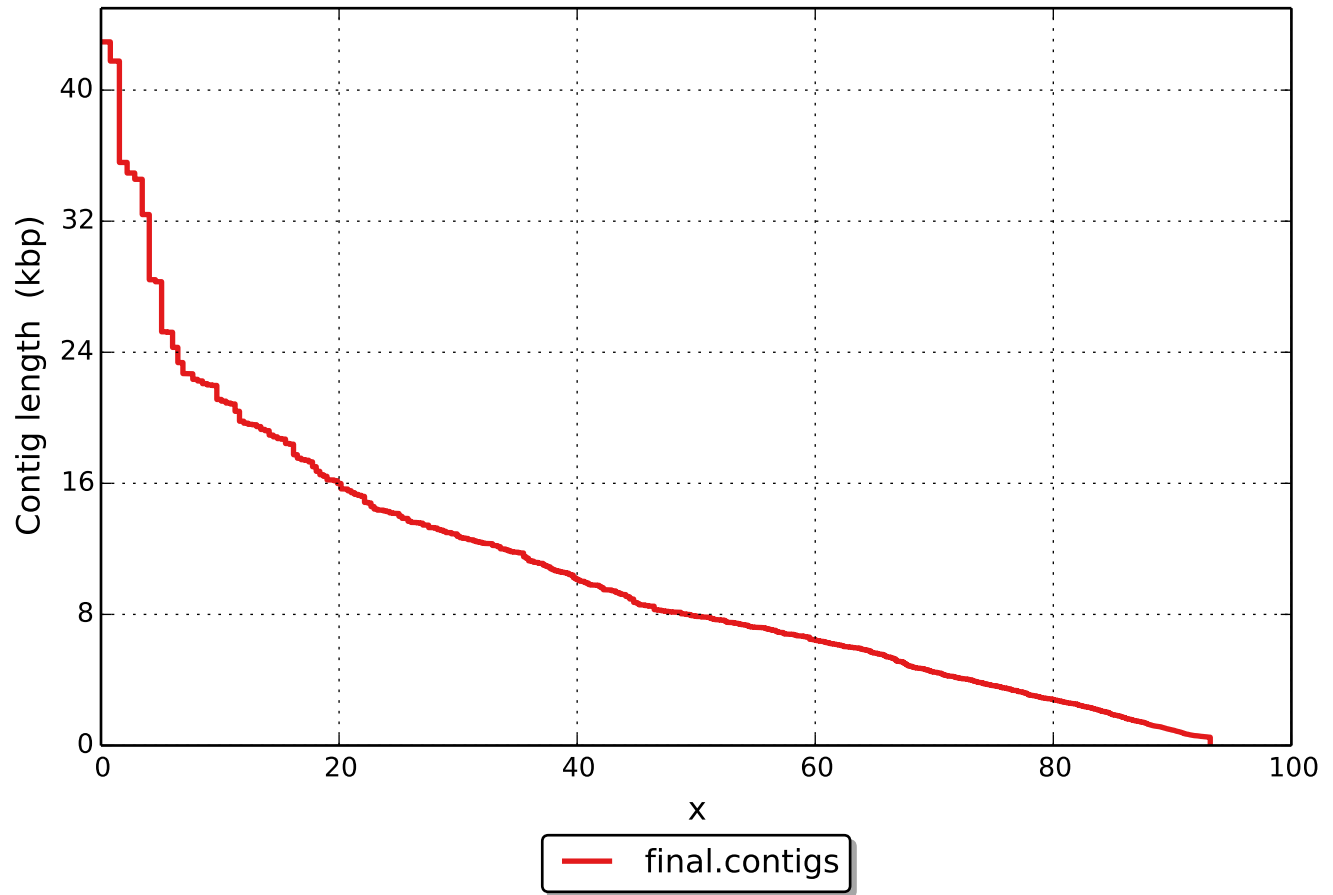


GC content



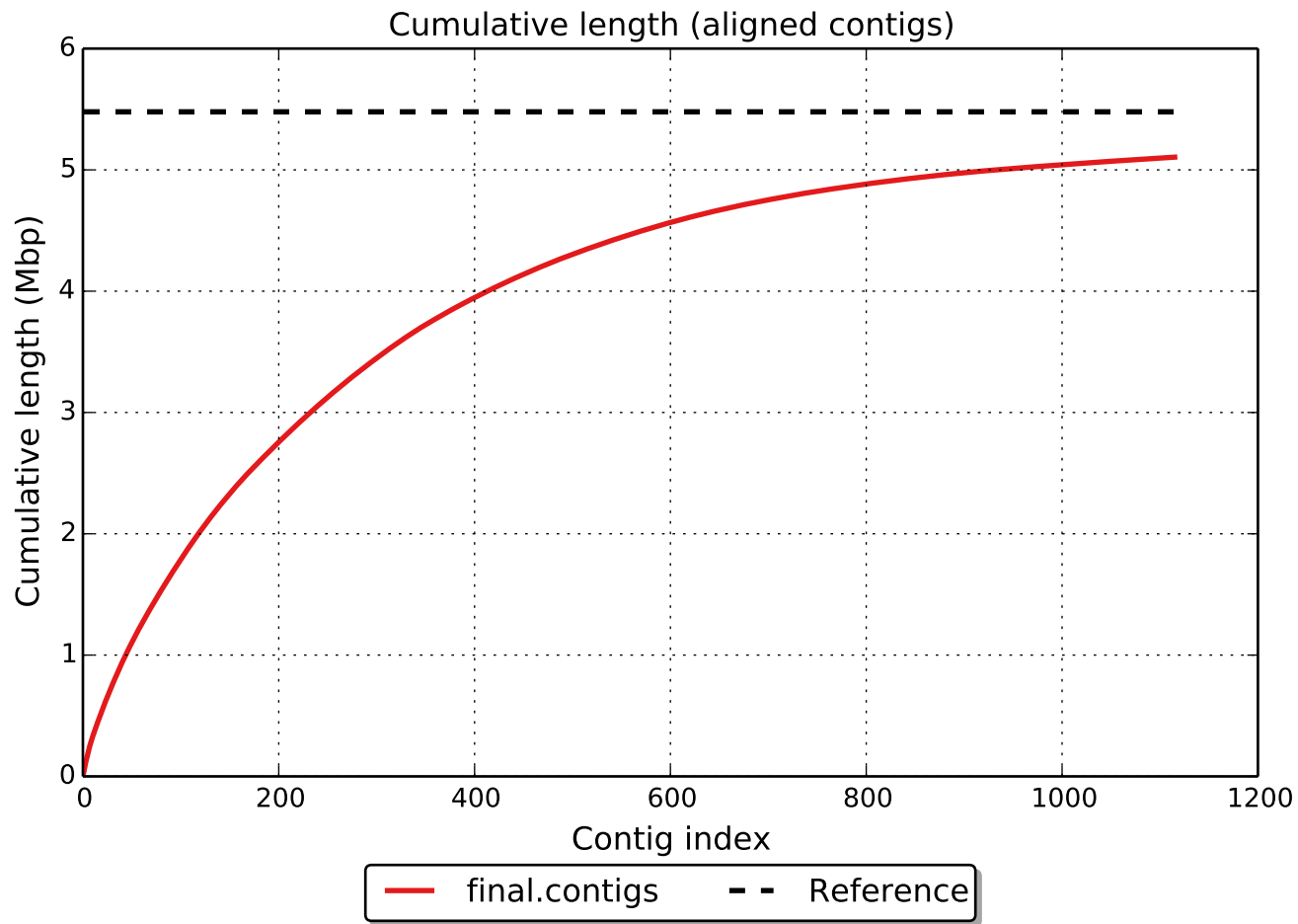


NGx

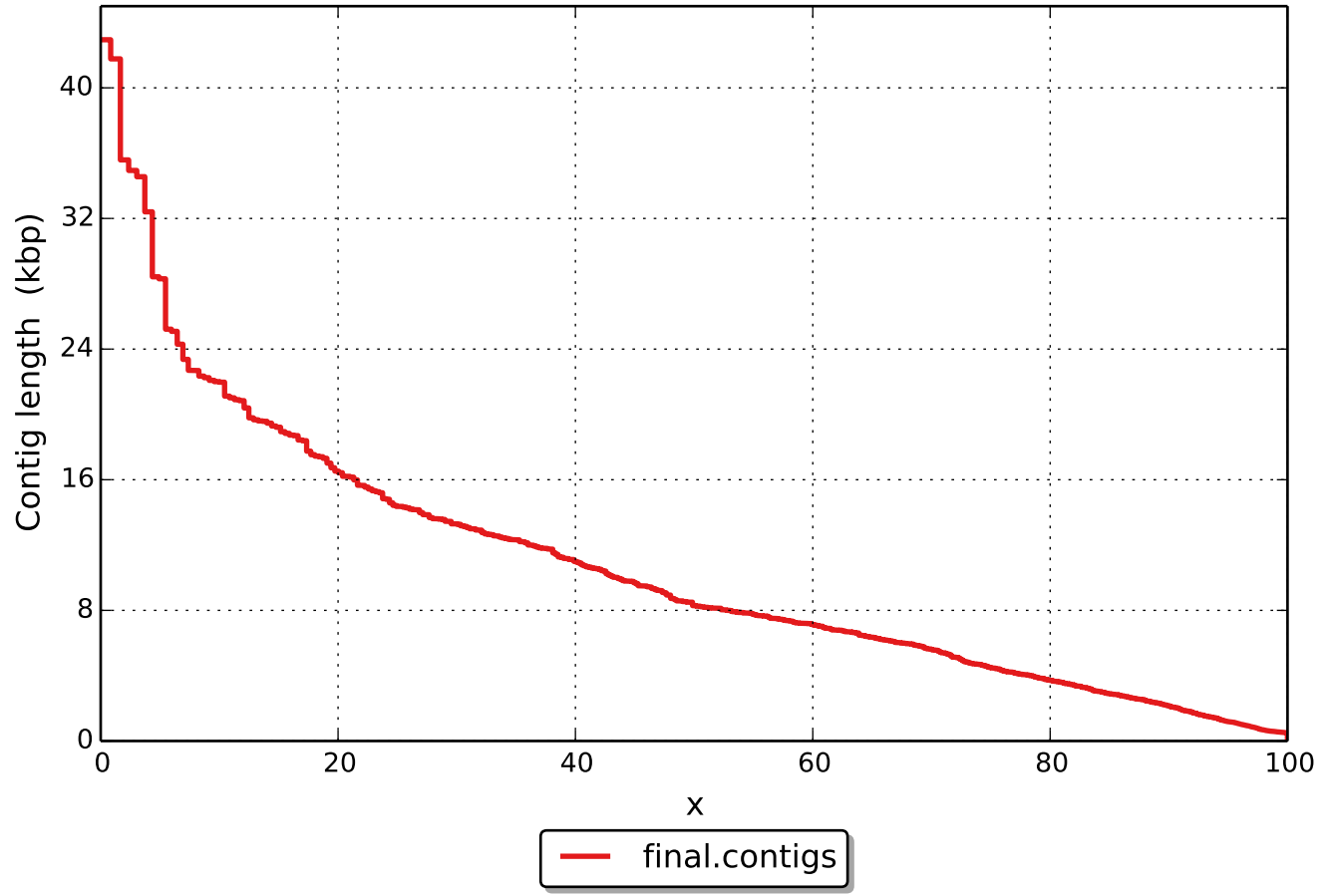


Misassemblies





NAx



NGAx

