

Report

	final.contigs
# contigs (>= 0 bp)	933
# contigs (>= 1000 bp)	852
Total length (>= 0 bp)	5600965
Total length (>= 1000 bp)	5540931
# contigs	933
Largest contig	41898
Total length	5600965
Reference length	5547323
GC (%)	50.49
Reference GC (%)	50.49
N50	9449
NG50	9503
N75	5418
NG75	5525
L50	189
LG50	186
L75	387
LG75	380
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.516
Duplication ratio	1.015
# N's per 100 kbp	0.00
# mismatches per 100 kbp	25.03
# indels per 100 kbp	0.04
Largest alignment	41898
NA50	9449
NGA50	9503
NA75	5418
NGA75	5525
LA50	189
LGA50	186
LA75	387
LGA75	380

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

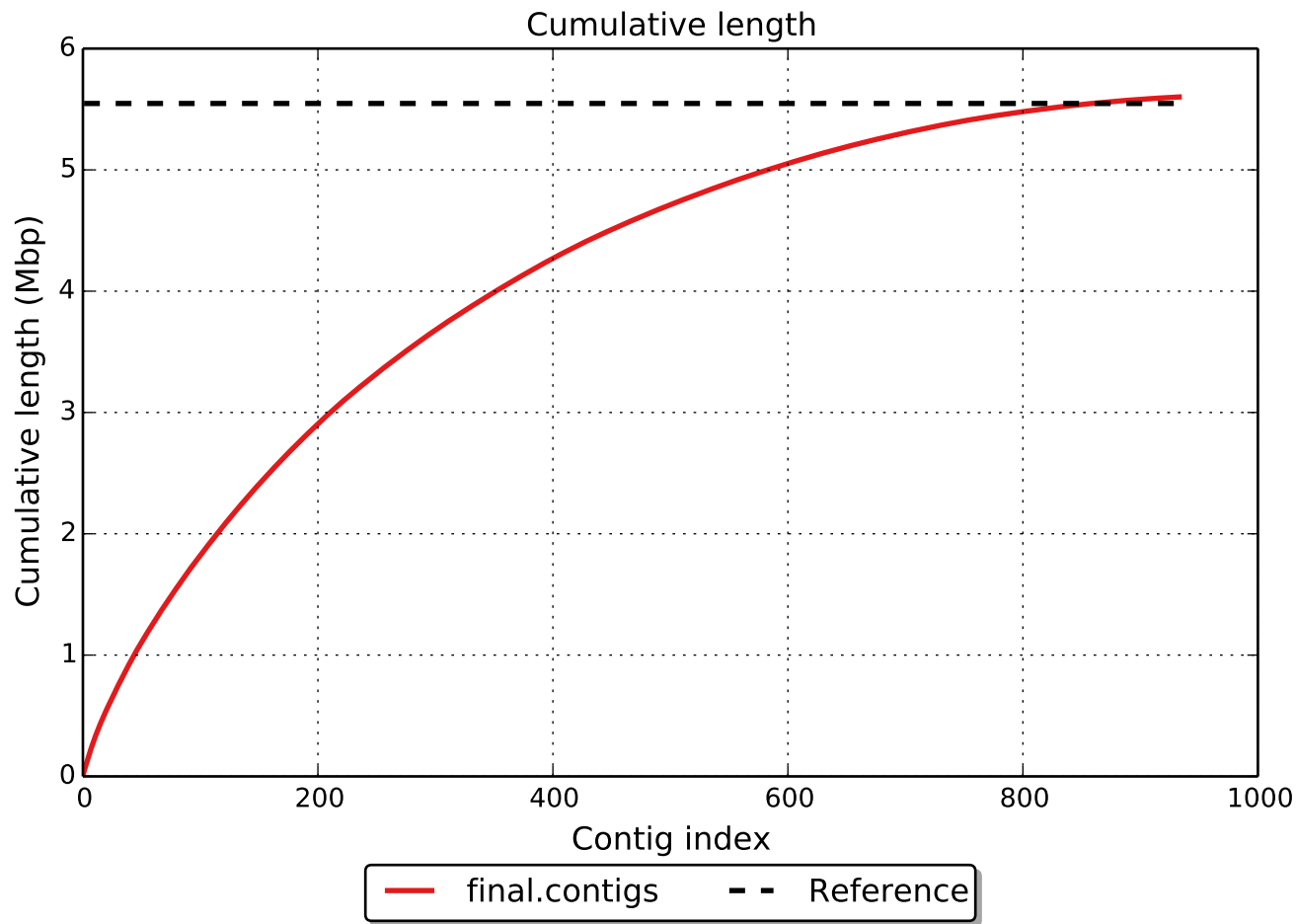
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1382
# indels	2
# short indels	2
# long indels	0
Indels length	2

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).

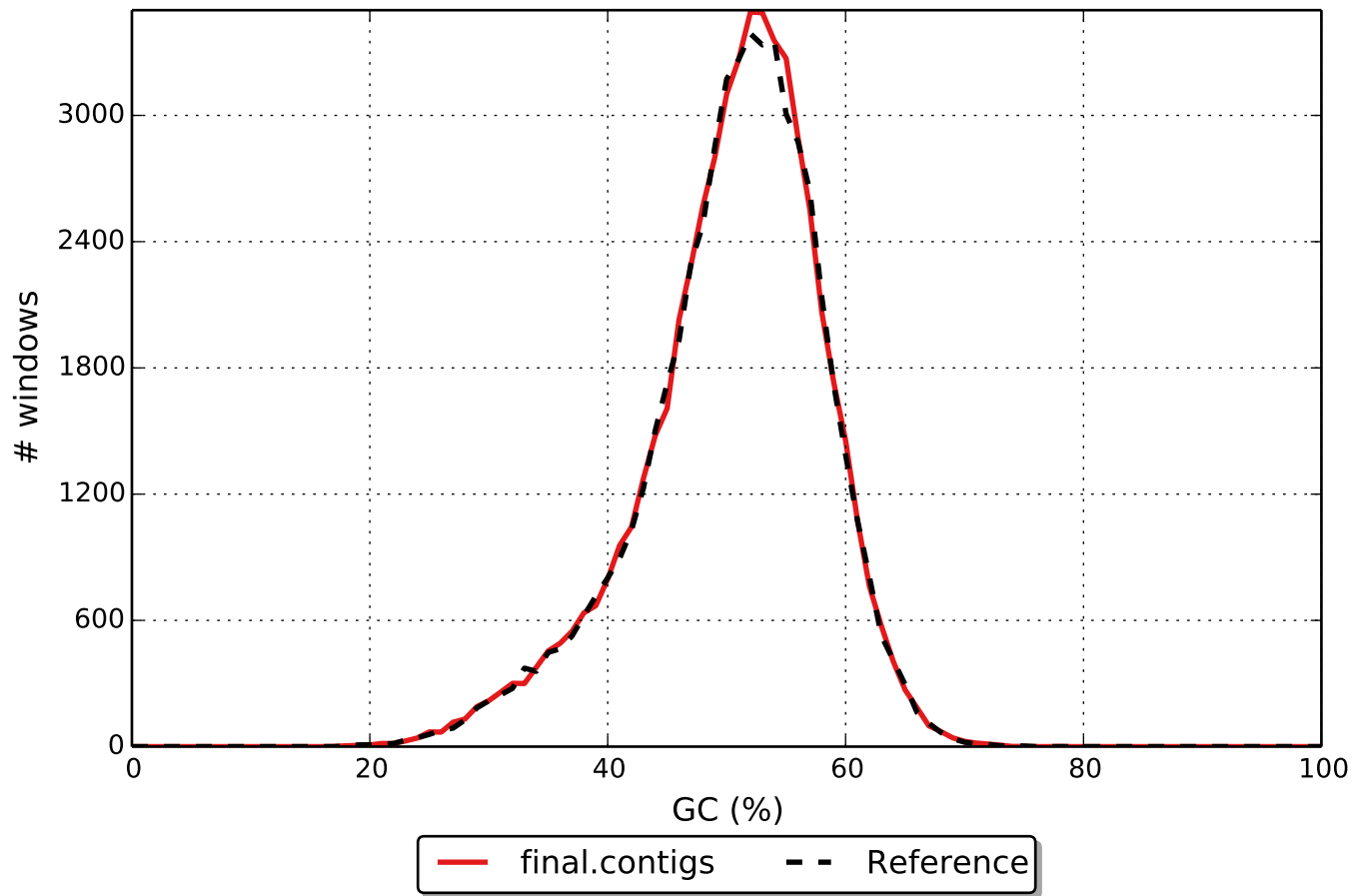
Unaligned report

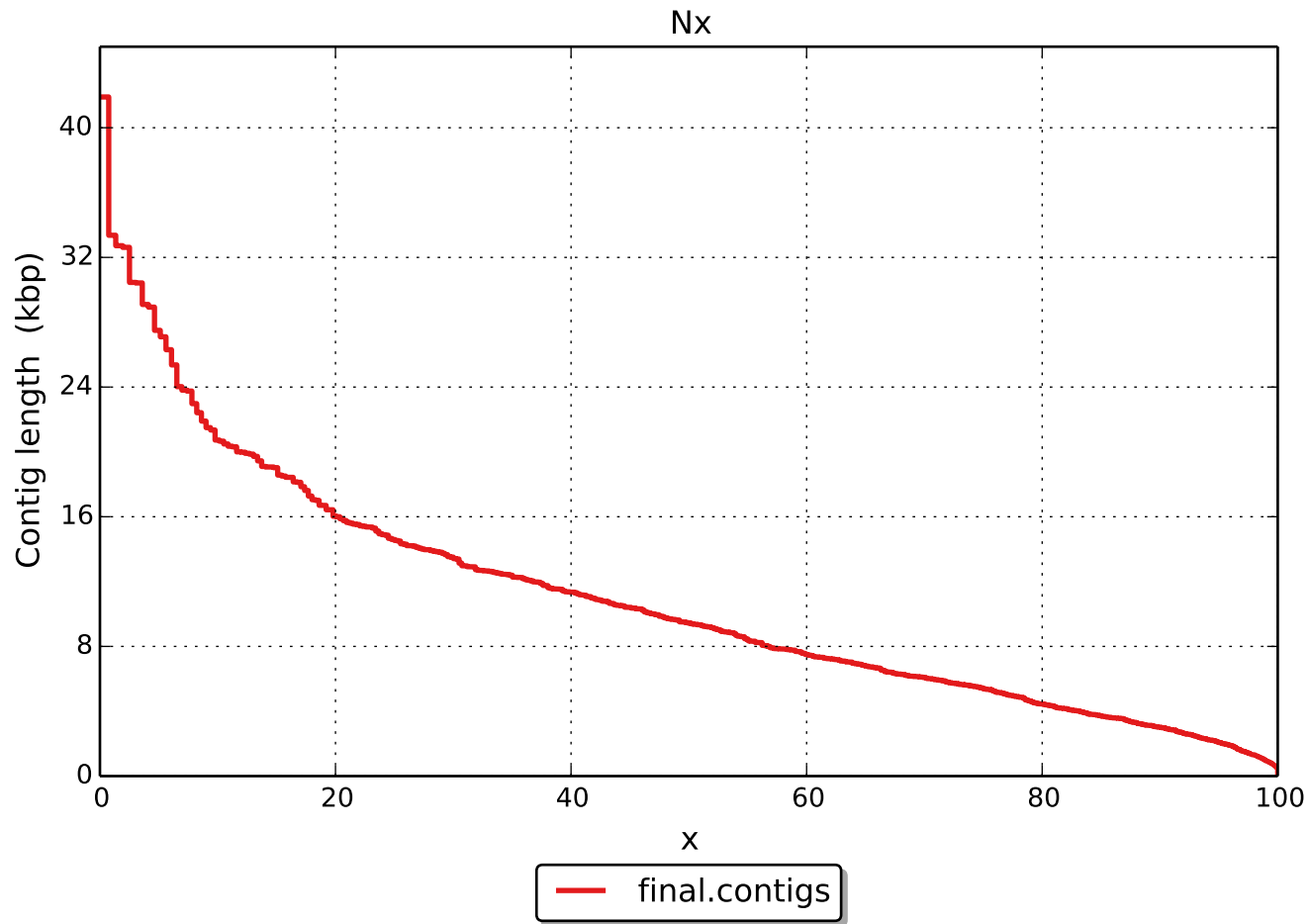
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

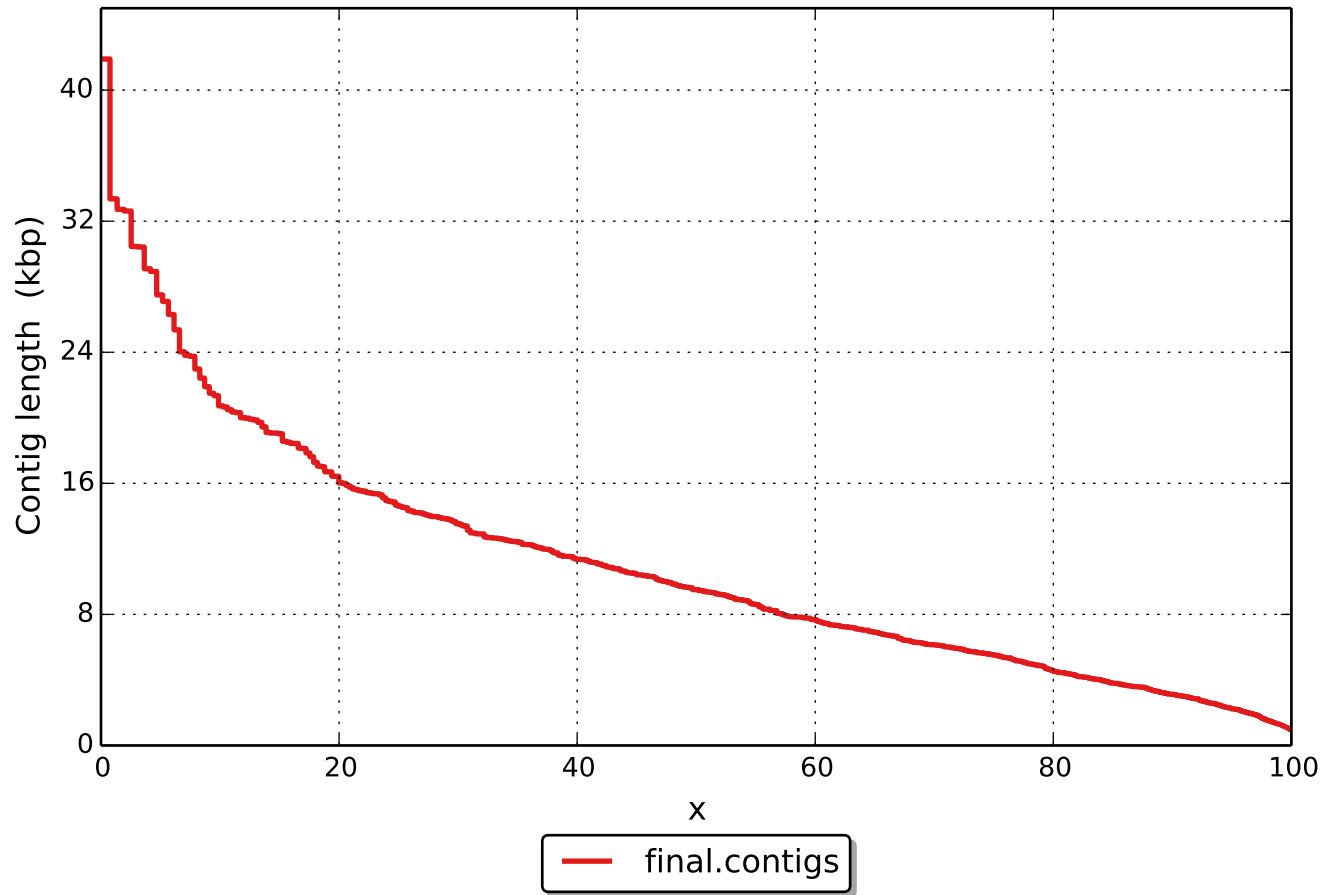


GC content



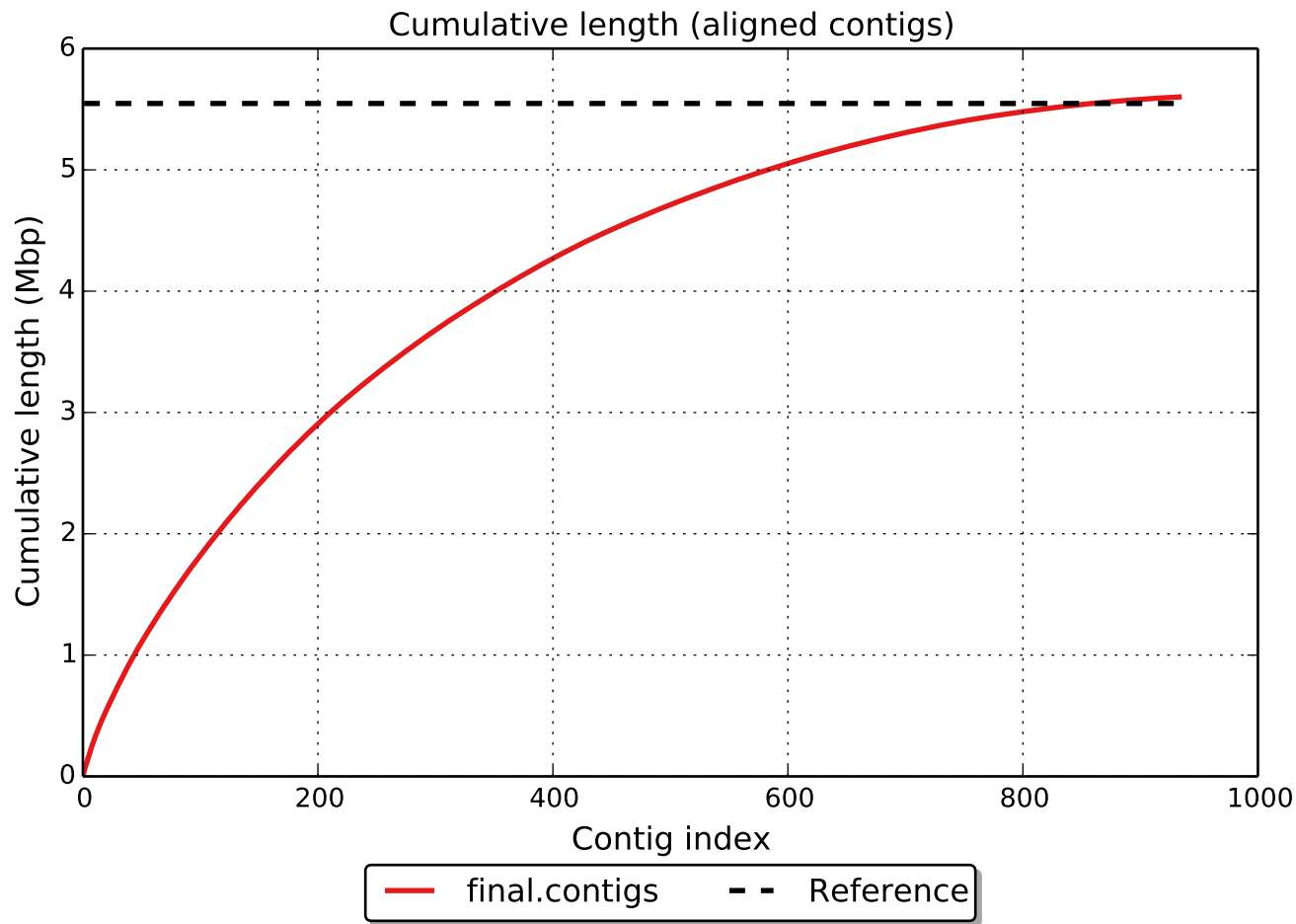


NGx

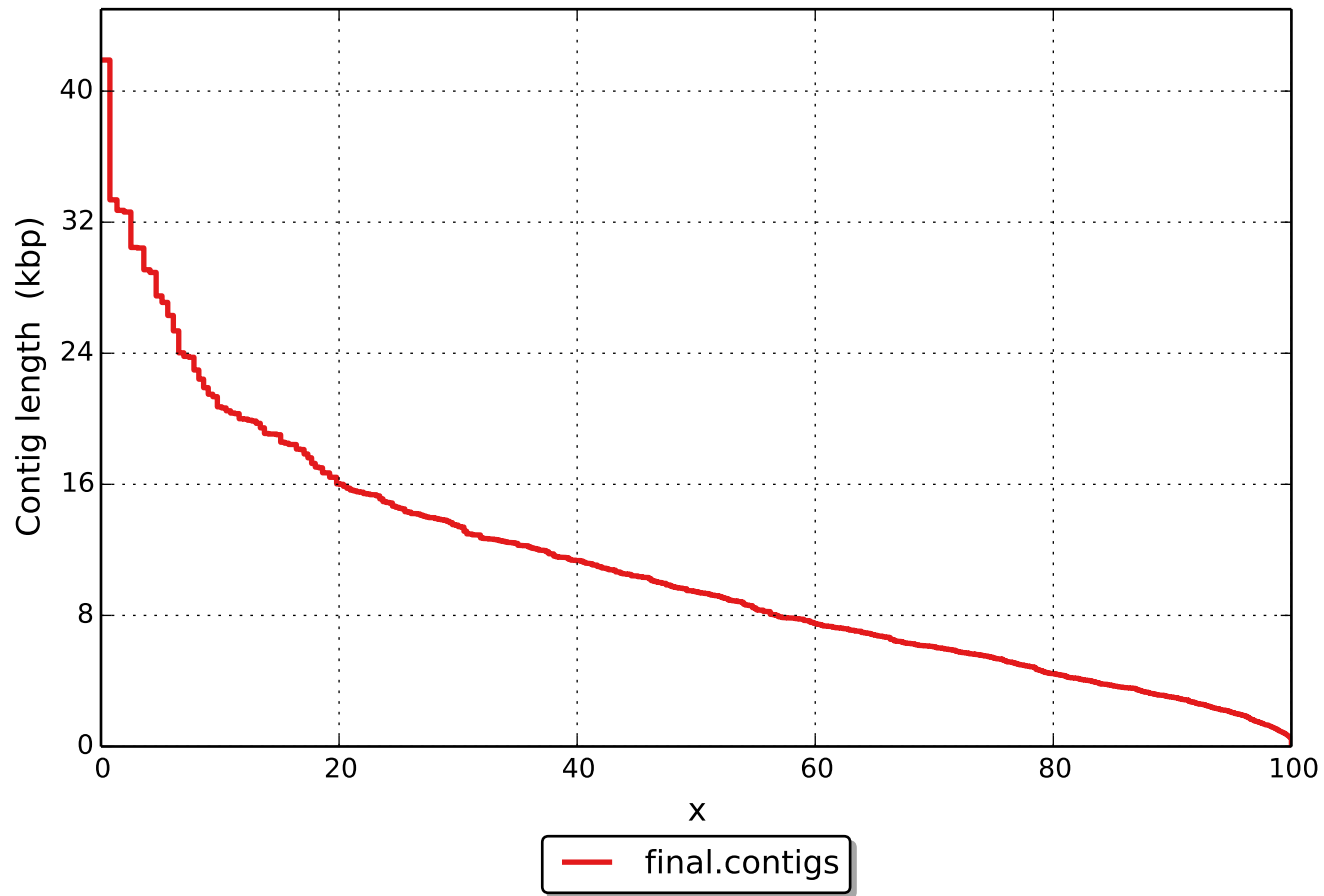


Misassemblies





NAx



NGAx

