

Report

	final.contigs
# contigs (>= 0 bp)	150
# contigs (>= 1000 bp)	85
# contigs (>= 5000 bp)	59
# contigs (>= 10000 bp)	54
# contigs (>= 25000 bp)	46
# contigs (>= 50000 bp)	29
Total length (>= 0 bp)	4590379
Total length (>= 1000 bp)	4564936
Total length (>= 5000 bp)	4506705
Total length (>= 10000 bp)	4469919
Total length (>= 25000 bp)	4341522
Total length (>= 50000 bp)	3774932
# contigs	99
Largest contig	327235
Total length	4574787
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	132728
NG50	132728
N75	63760
NG75	63760
L50	12
LG50	12
L75	24
LG75	24
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.452
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.68
# indels per 100 kbp	0.02
Largest alignment	327235
NA50	132728
NGA50	132728
NA75	63760
NGA75	63760
LA50	12
LGA50	12
LA75	24
LGA75	24

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
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	77
# indels	1
# short indels	1
# long indels	0
Indels length	1

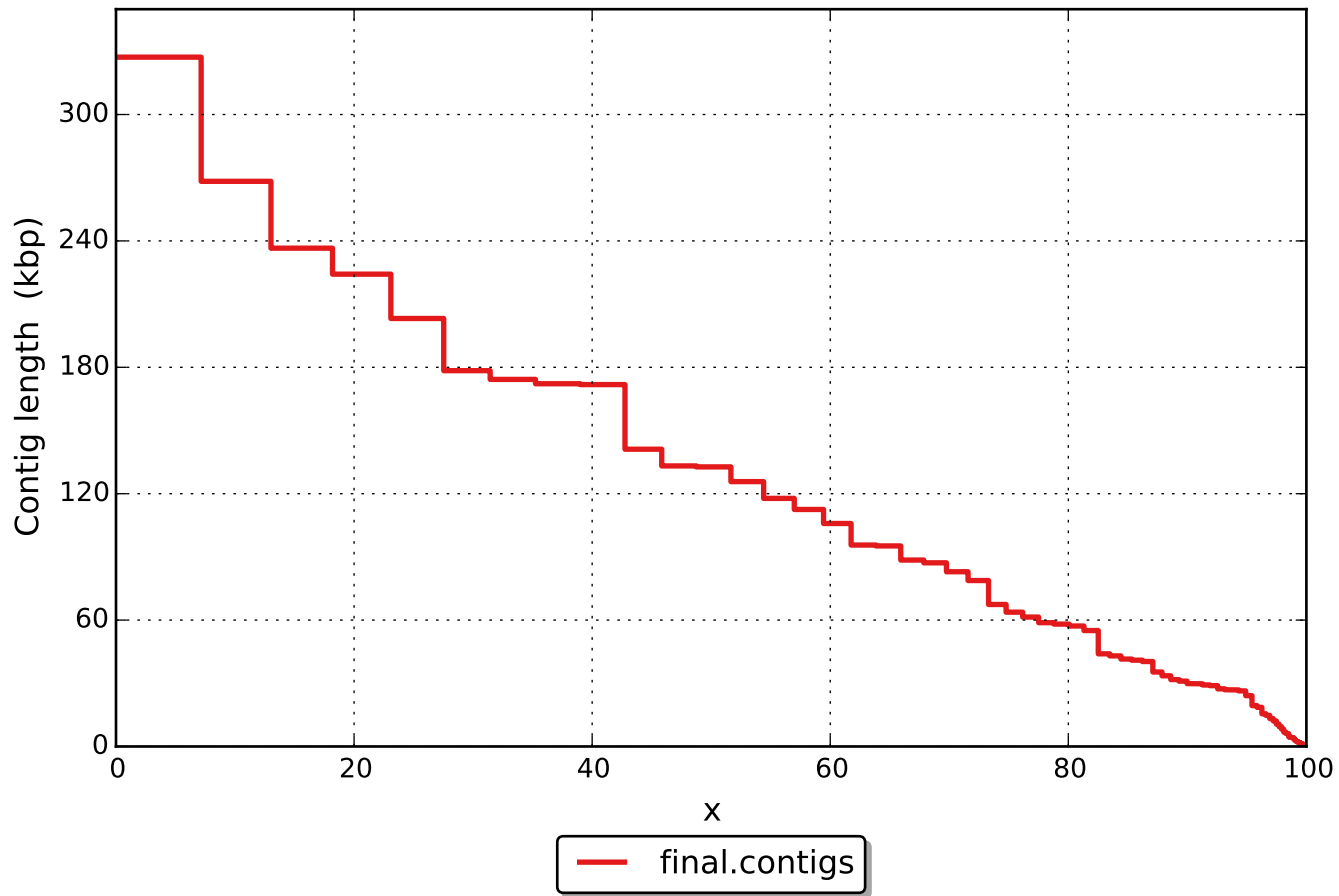
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

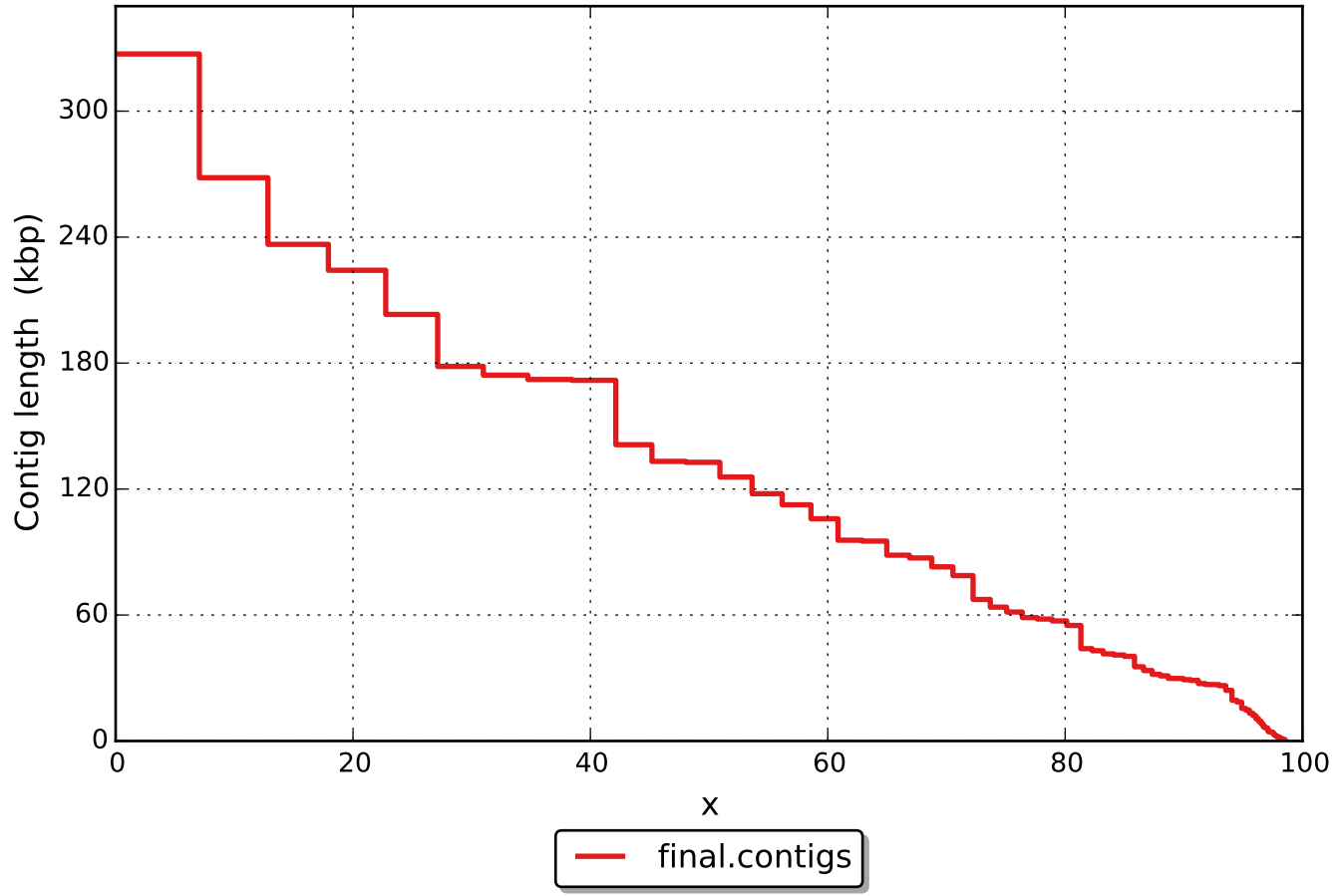
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

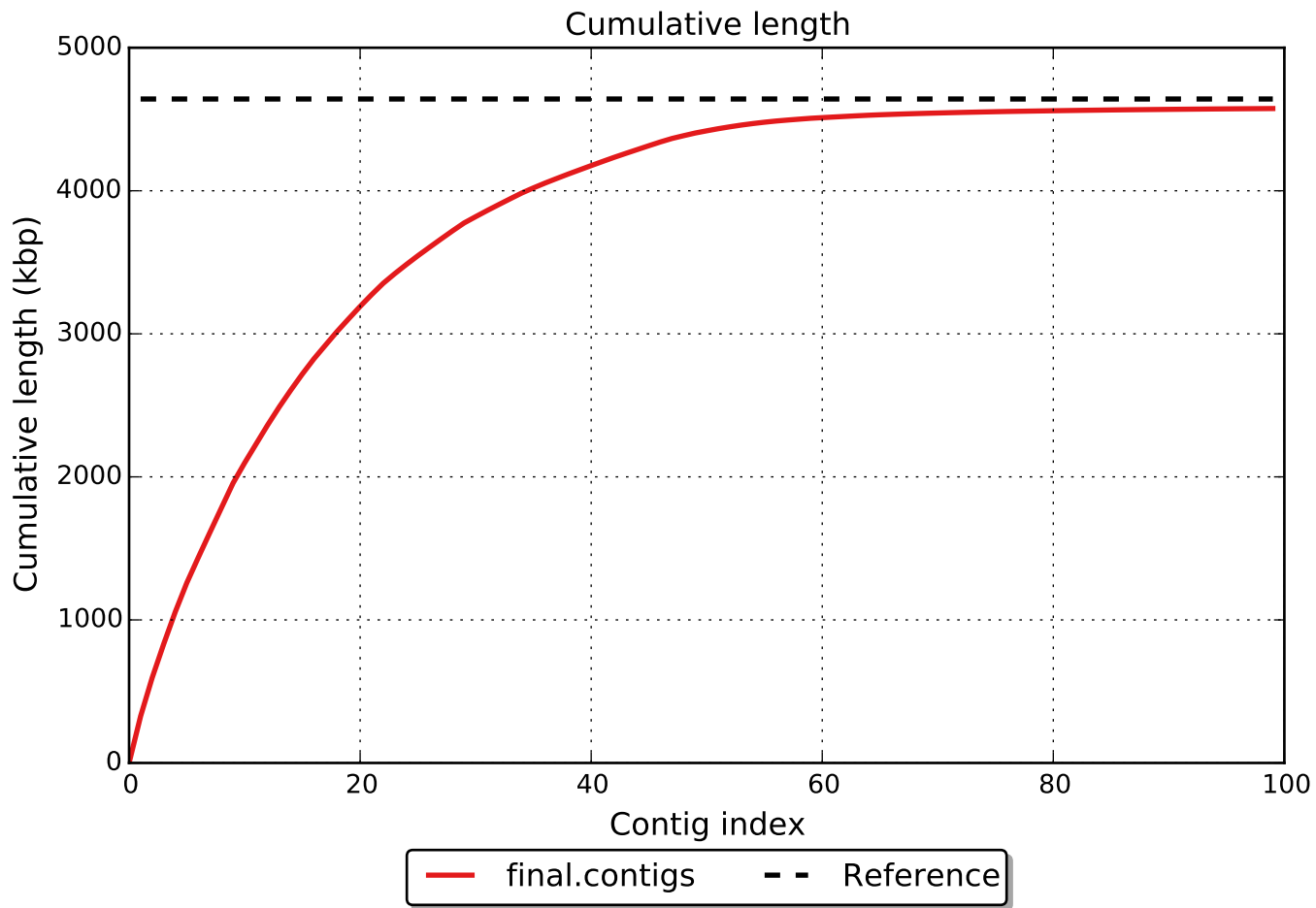
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

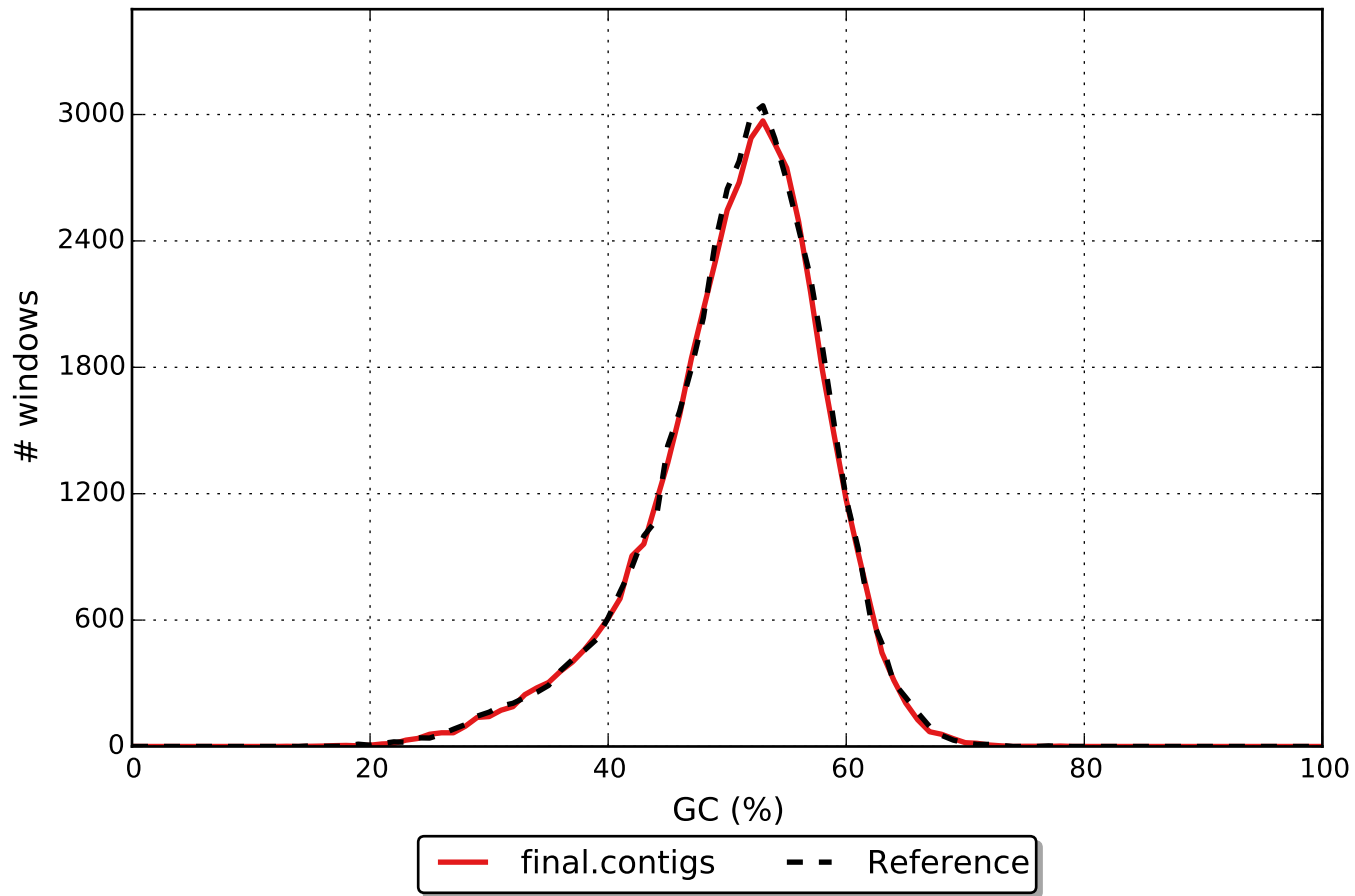


NGx





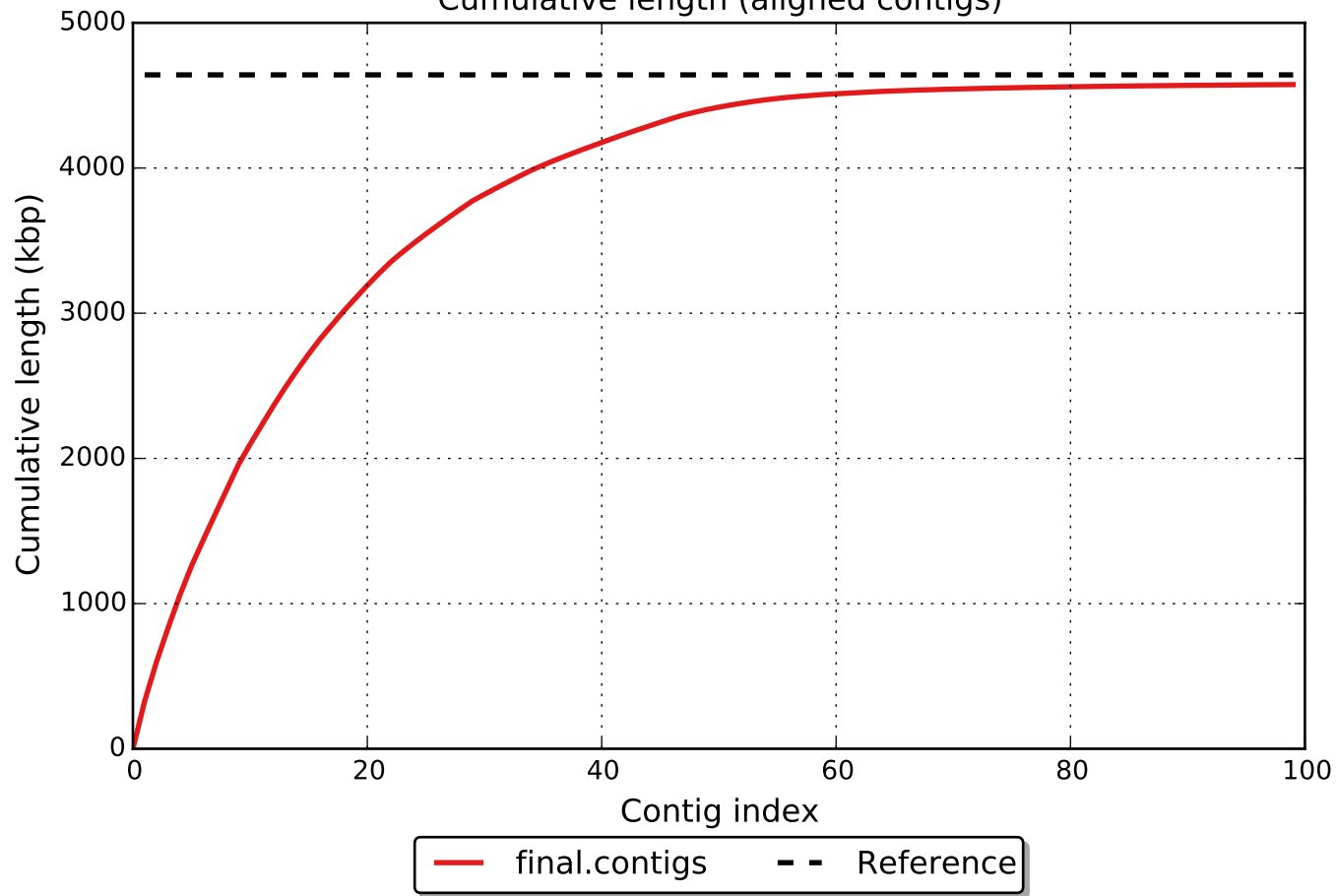
GC content



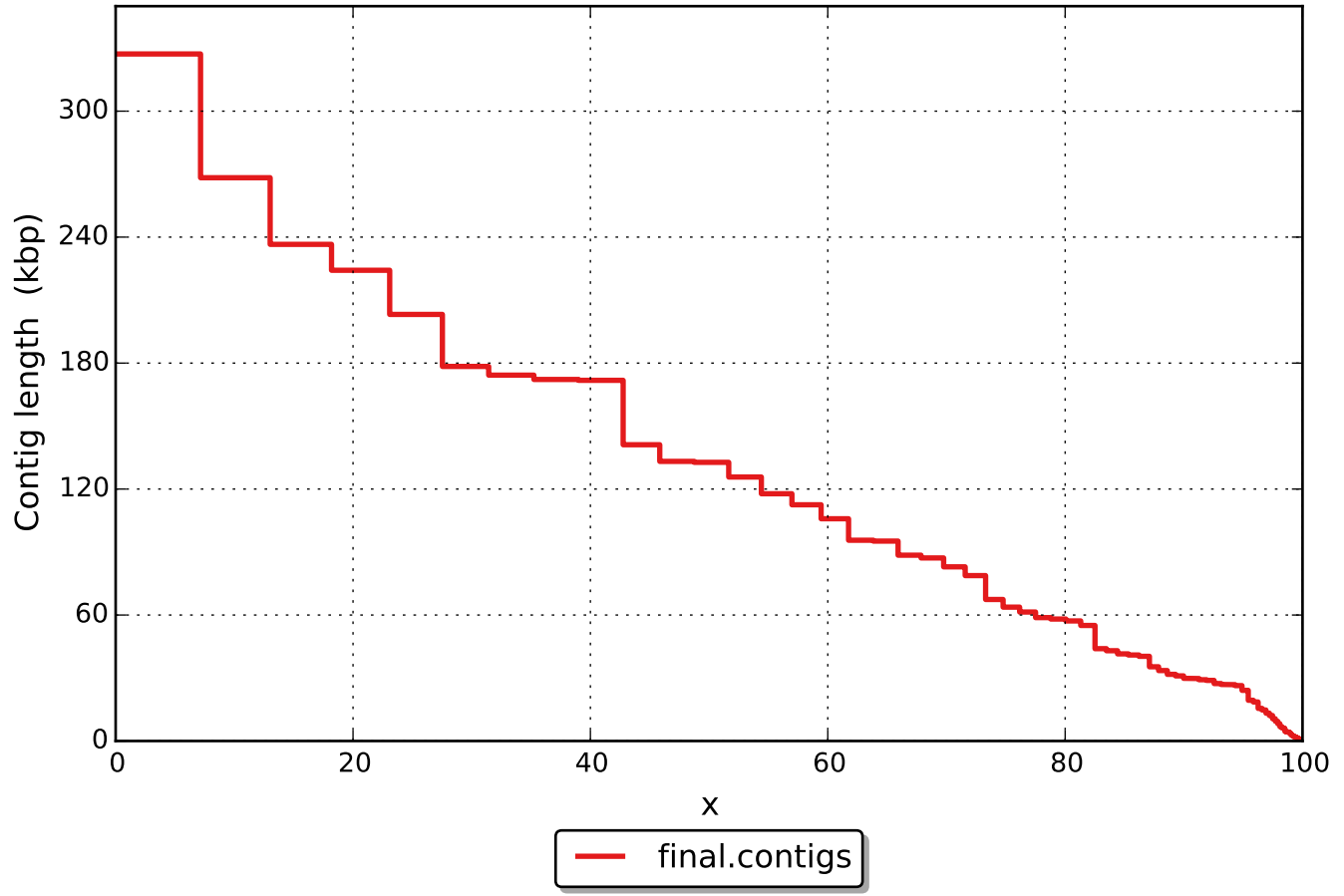
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

