

Report

	final.contigs
# contigs (>= 0 bp)	111
# contigs (>= 1000 bp)	81
# contigs (>= 5000 bp)	61
# contigs (>= 10000 bp)	56
# contigs (>= 25000 bp)	46
# contigs (>= 50000 bp)	29
Total length (>= 0 bp)	4579320
Total length (>= 1000 bp)	4565072
Total length (>= 5000 bp)	4519775
Total length (>= 10000 bp)	4483029
Total length (>= 25000 bp)	4335521
Total length (>= 50000 bp)	3754148
# contigs	93
Largest contig	327235
Total length	4573243
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	132731
NG50	132731
N75	61429
NG75	58799
L50	12
LG50	12
L75	24
LG75	25
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.425
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.44
# indels per 100 kbp	0.42
Largest alignment	327235
NA50	132731
NGA50	132731
NA75	61429
NGA75	58799
LA50	12
LGA50	12
LA75	24
LGA75	25

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	157
# indels	19
# short indels	14
# long indels	5
Indels length	102

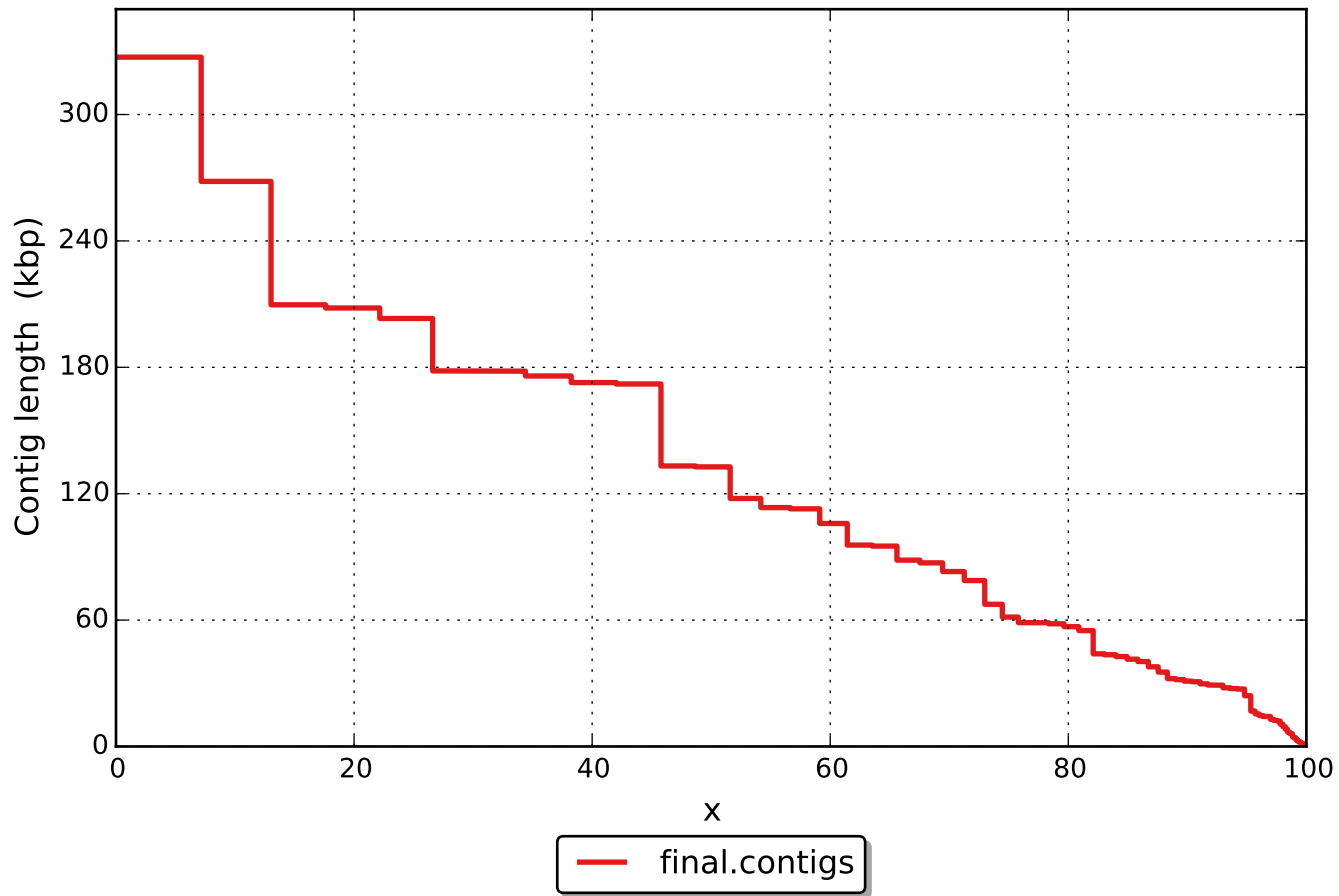
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

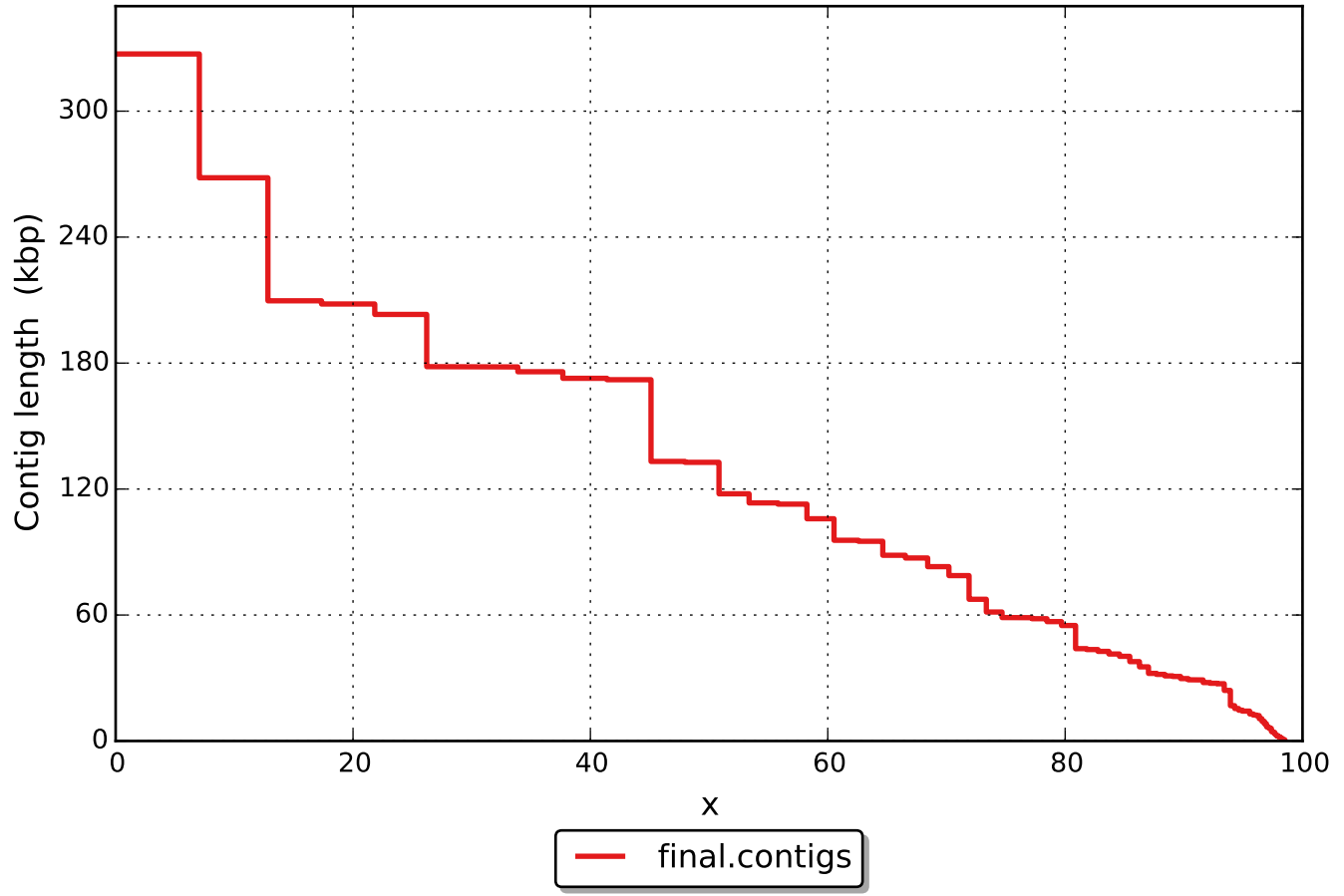
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

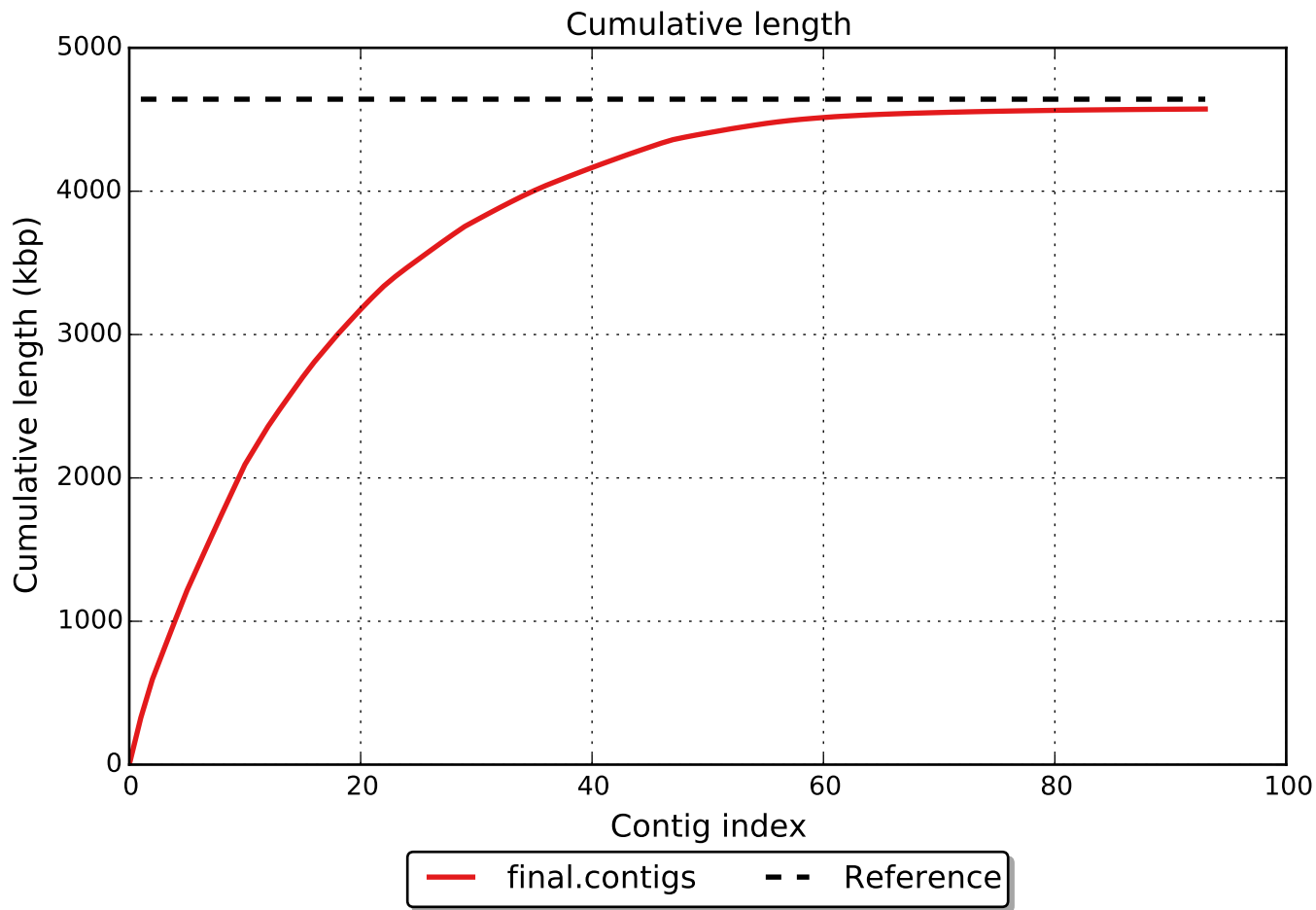
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

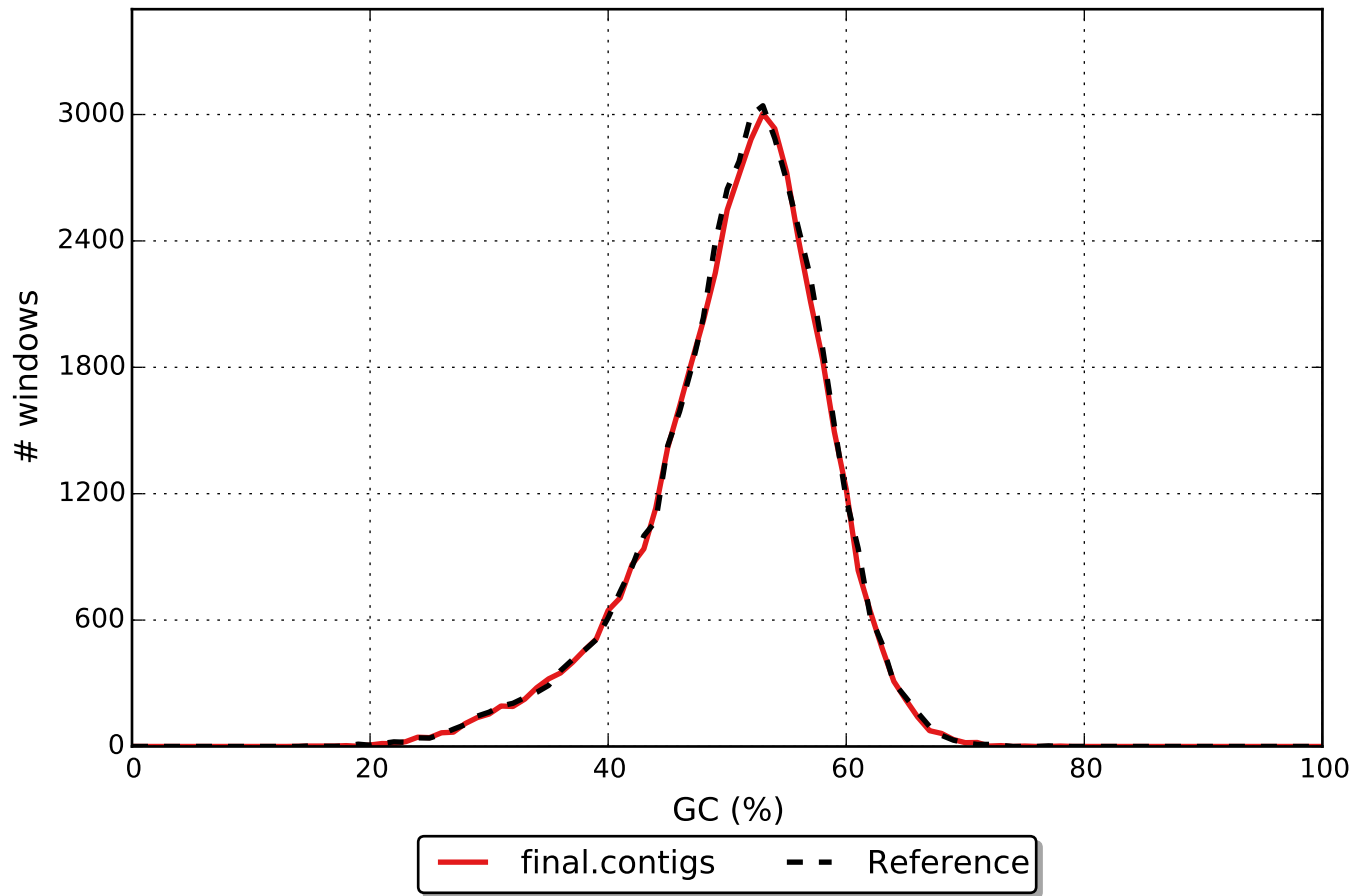


NGx





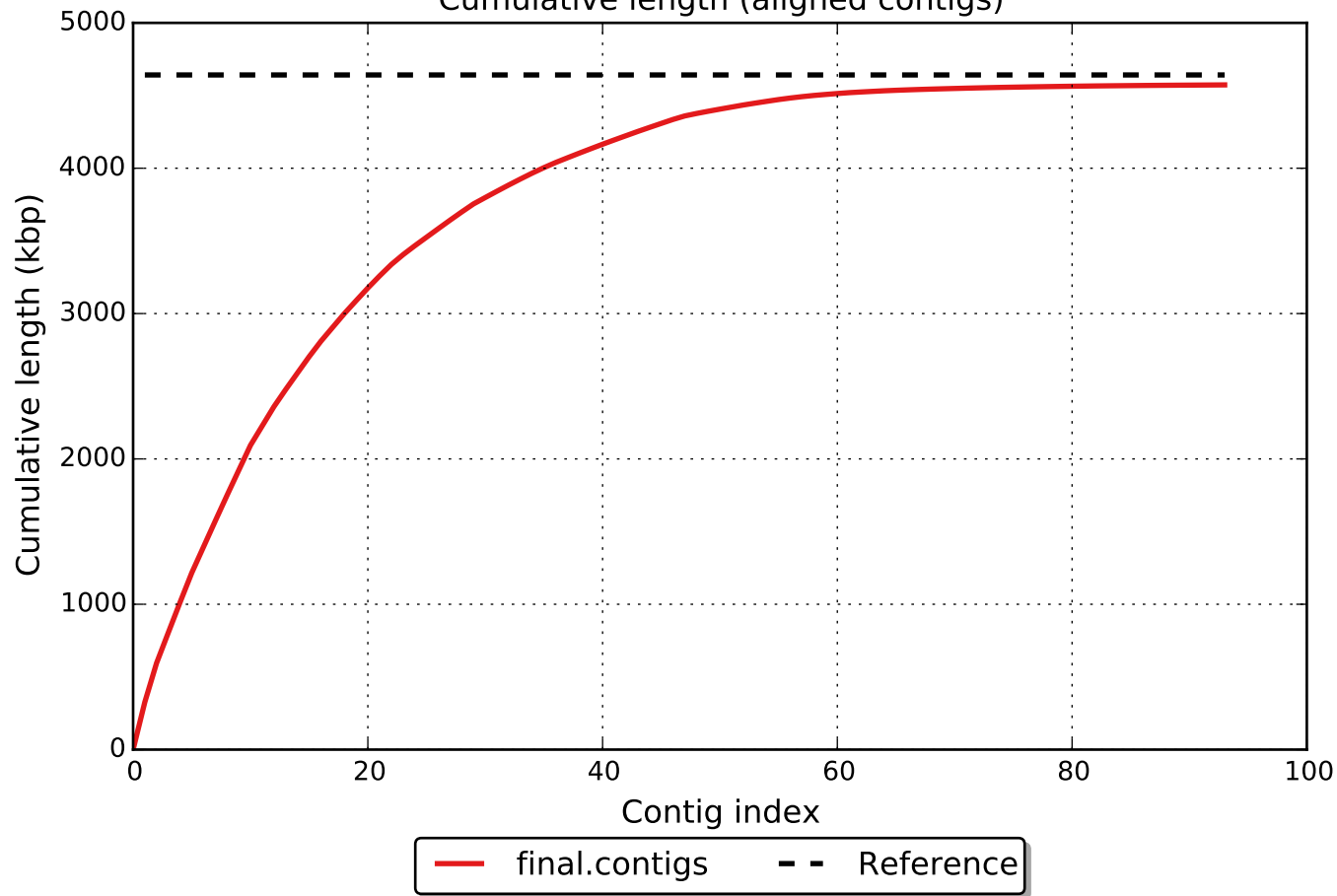
GC content



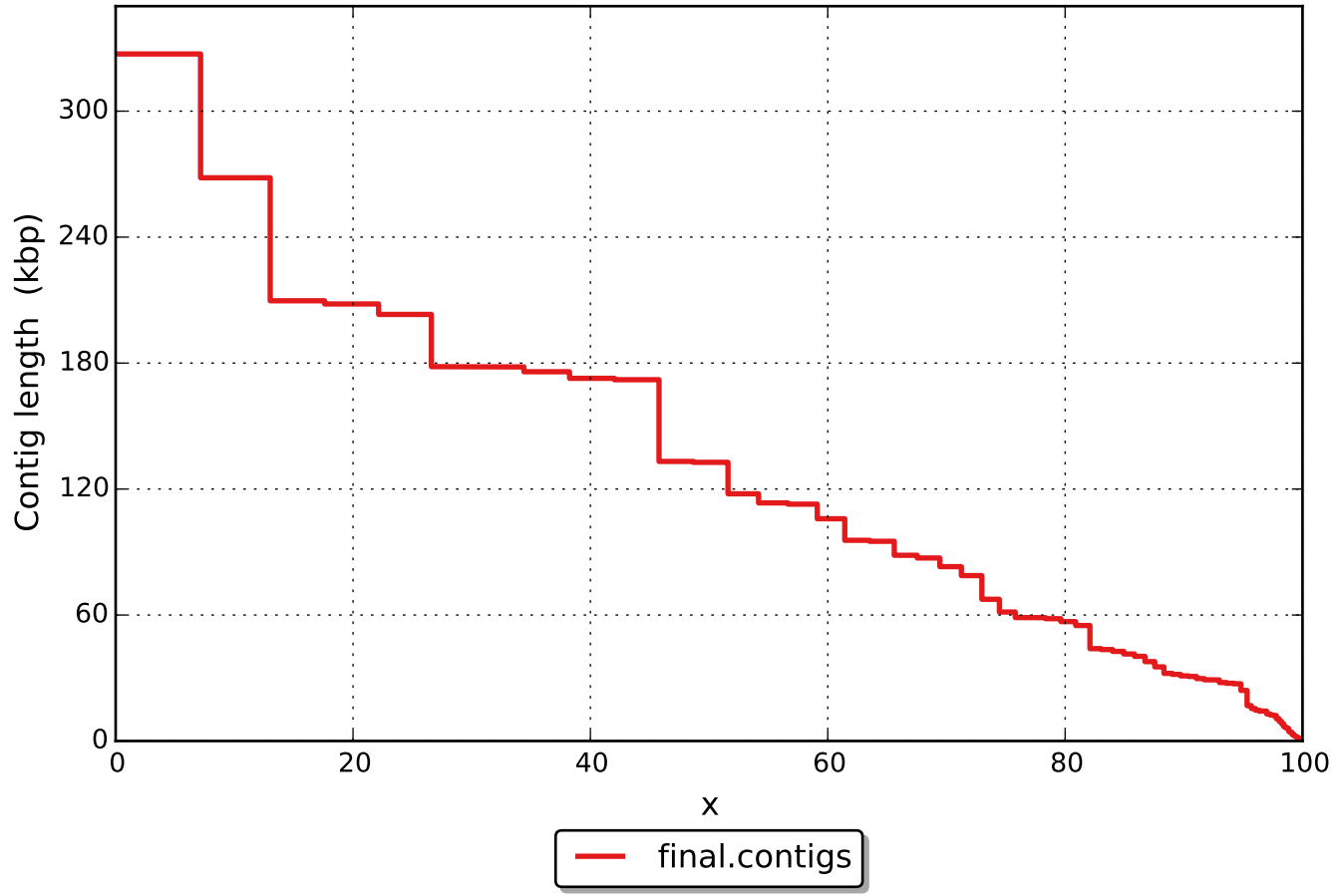
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

