

Report

	final.contigs
# contigs (>= 1000 bp)	97
# contigs (>= 5000 bp)	72
# contigs (>= 10000 bp)	66
# contigs (>= 25000 bp)	52
# contigs (>= 50000 bp)	31
Total length (>= 1000 bp)	4554509
Total length (>= 5000 bp)	4507427
Total length (>= 10000 bp)	4462528
Total length (>= 25000 bp)	4246976
Total length (>= 50000 bp)	3540315
# contigs	109
Largest contig	327146
Total length	4562531
Reference length	4641652
GC (℥)	50.75
Reference GC (℥)	50.79
N50	105738
NG50	105738
N75	54941
NG75	53828
L50	14
LG50	14
L75	29
LG75	30
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# unaligned contigs	0 + 1 part
Unaligned length	51
Genome fraction (℥)	98.245
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	57.83
# indels per 100 kbp	9.32
Largest alignment	327146
NA50	105738
NGA50	105738
NA75	54941
NGA75	53828
LA50	14
LGA50	14
LA75	29
LGA75	30

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	4
# mismatches	2637
# indels	425
# short indels	424
# long indels	1
Indels length	667

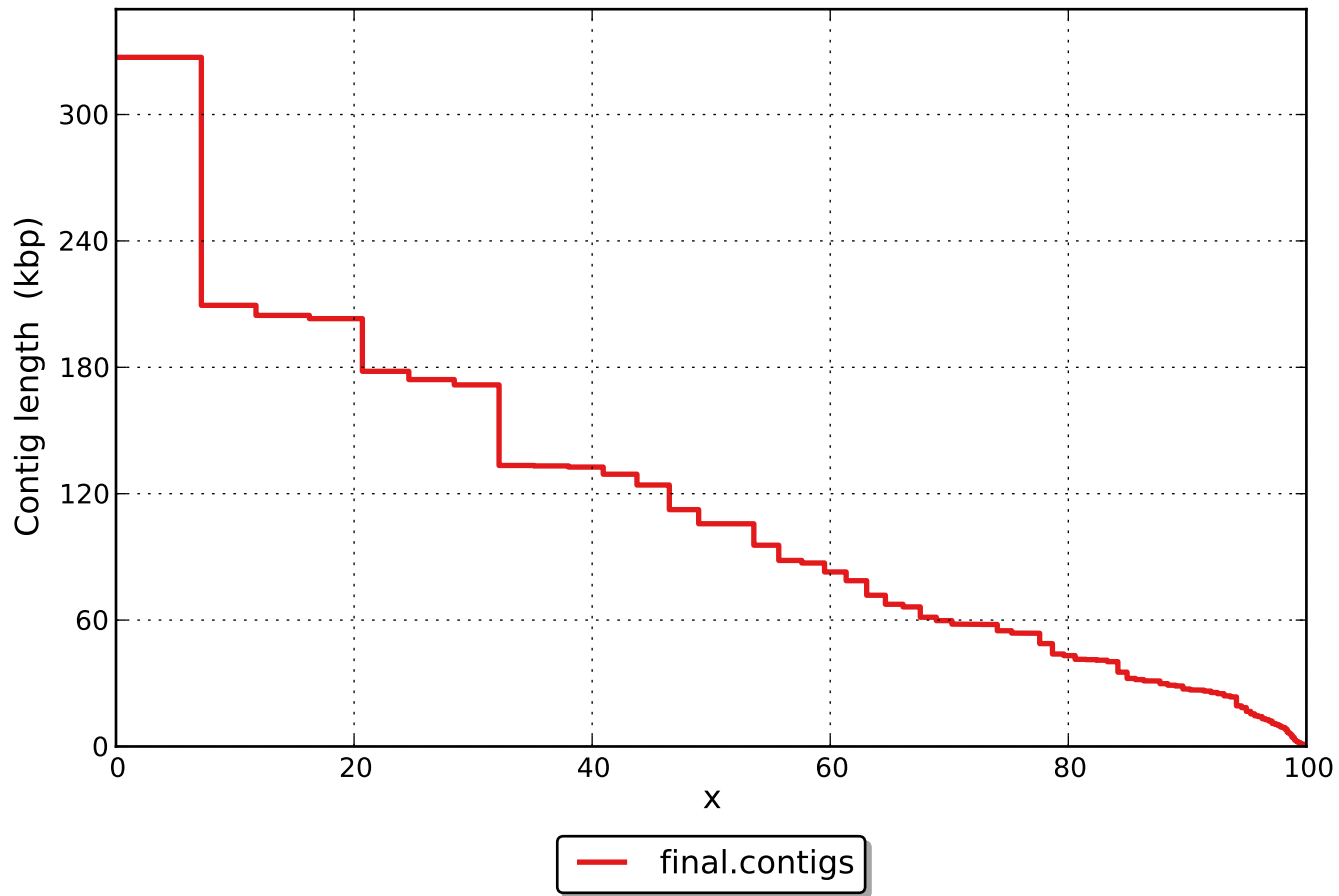
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

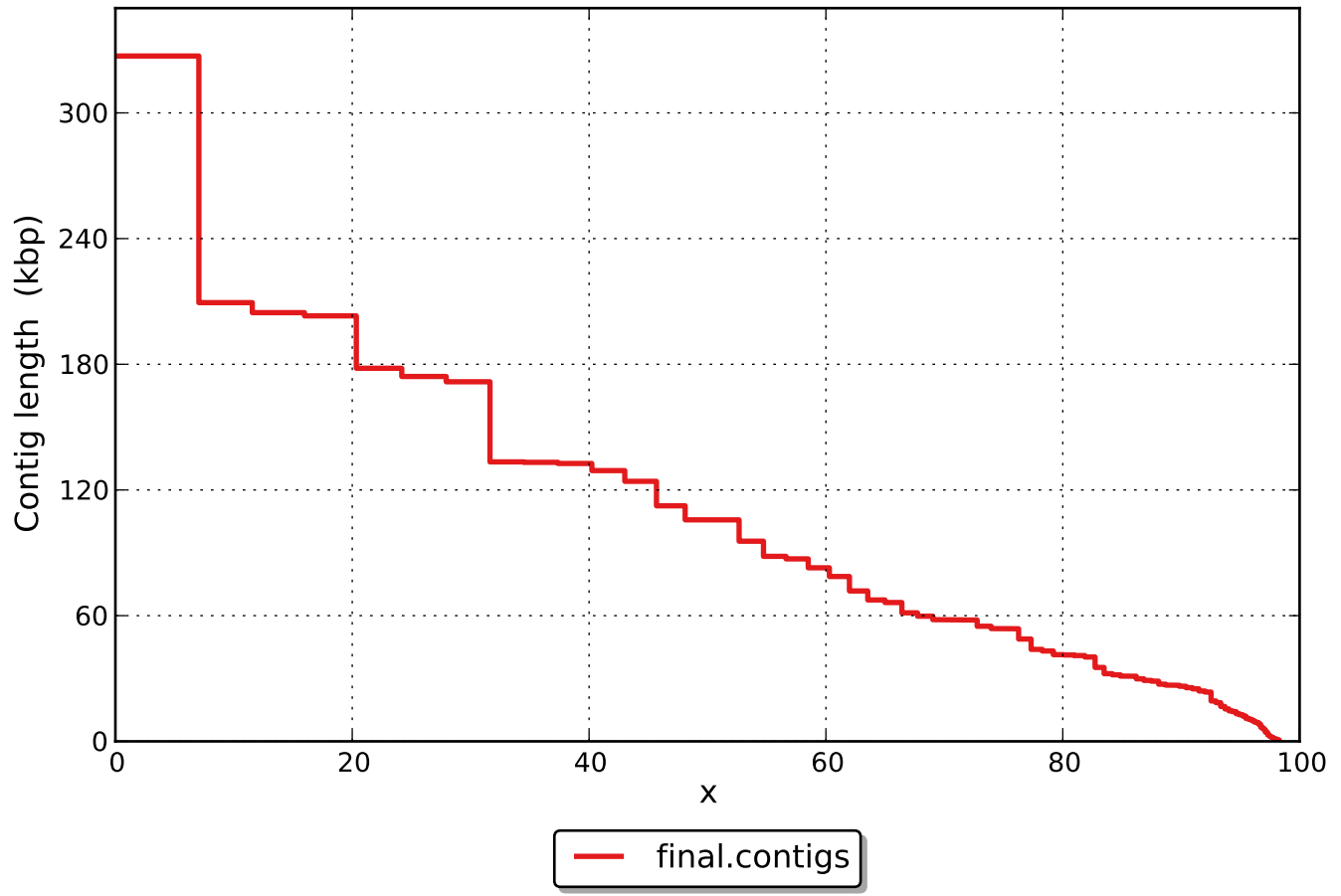
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	51
# N's	0

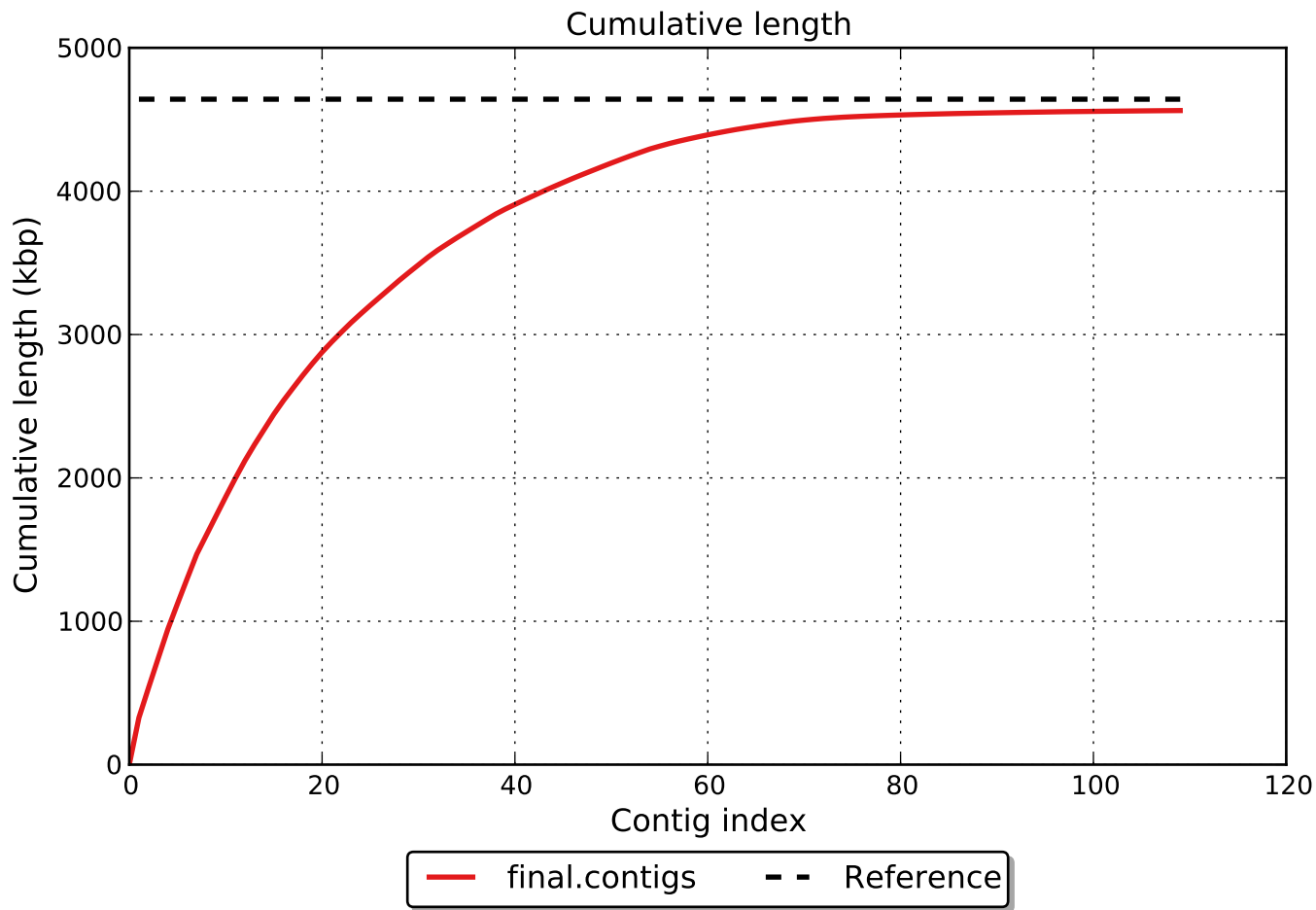
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

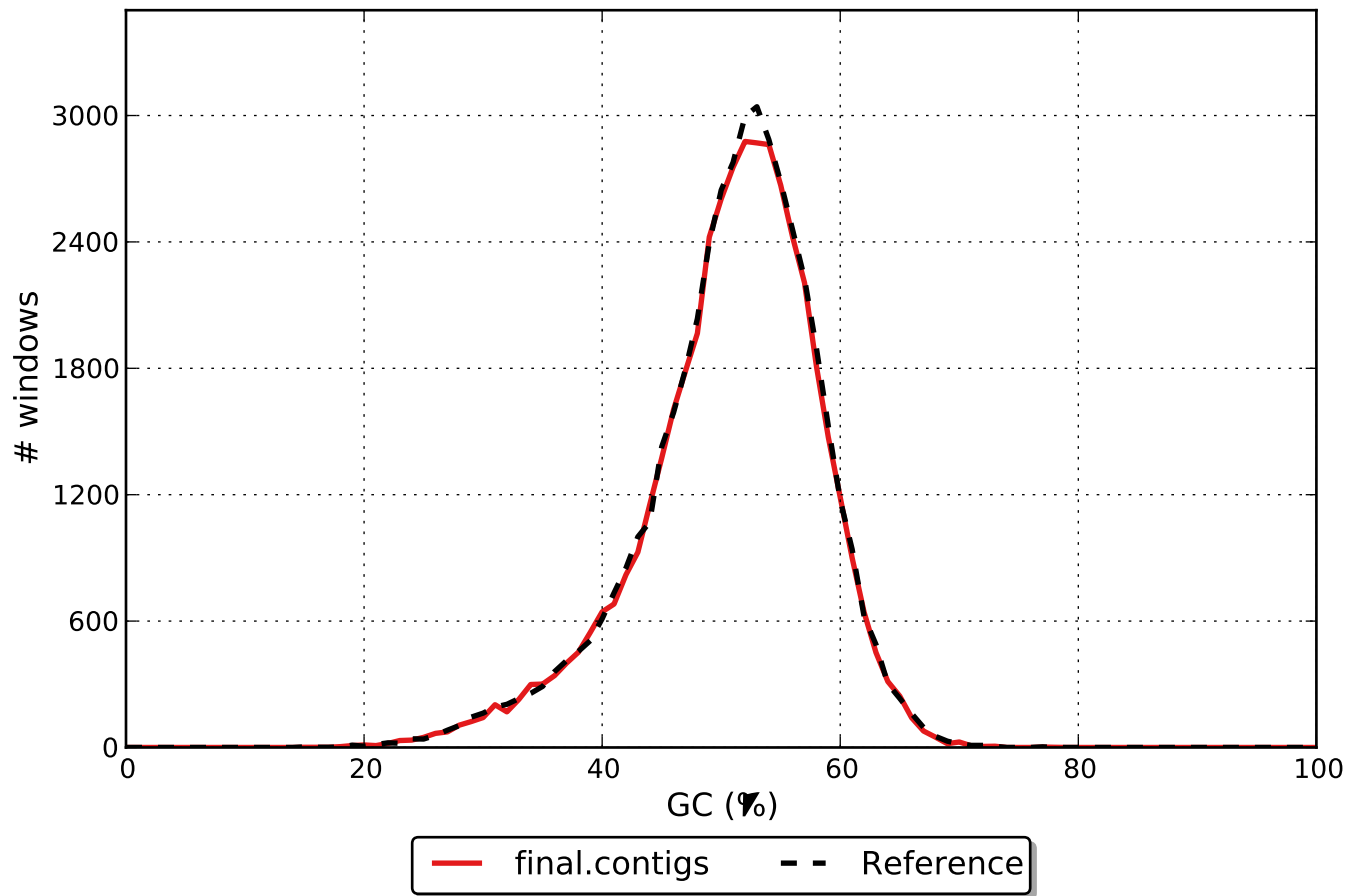


NGx





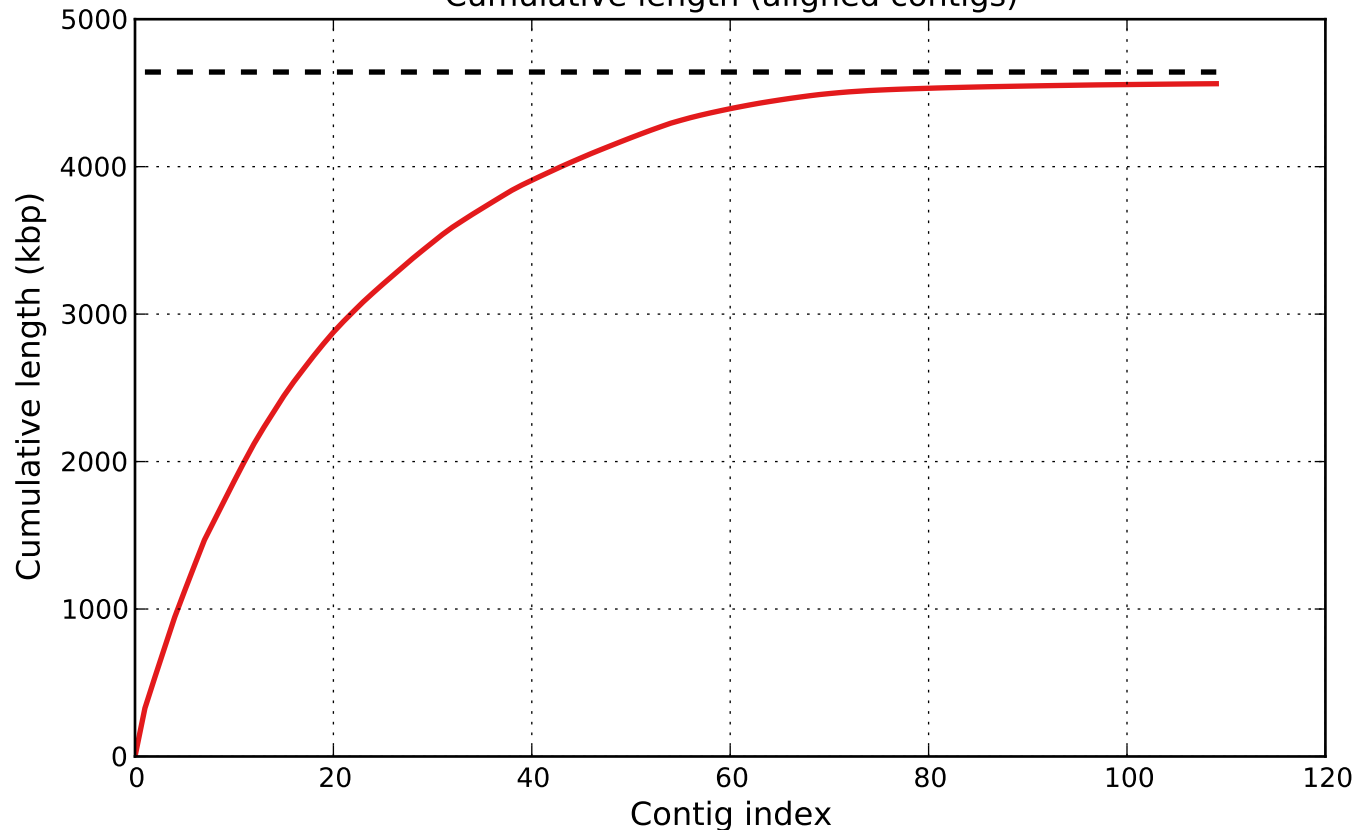
GC content



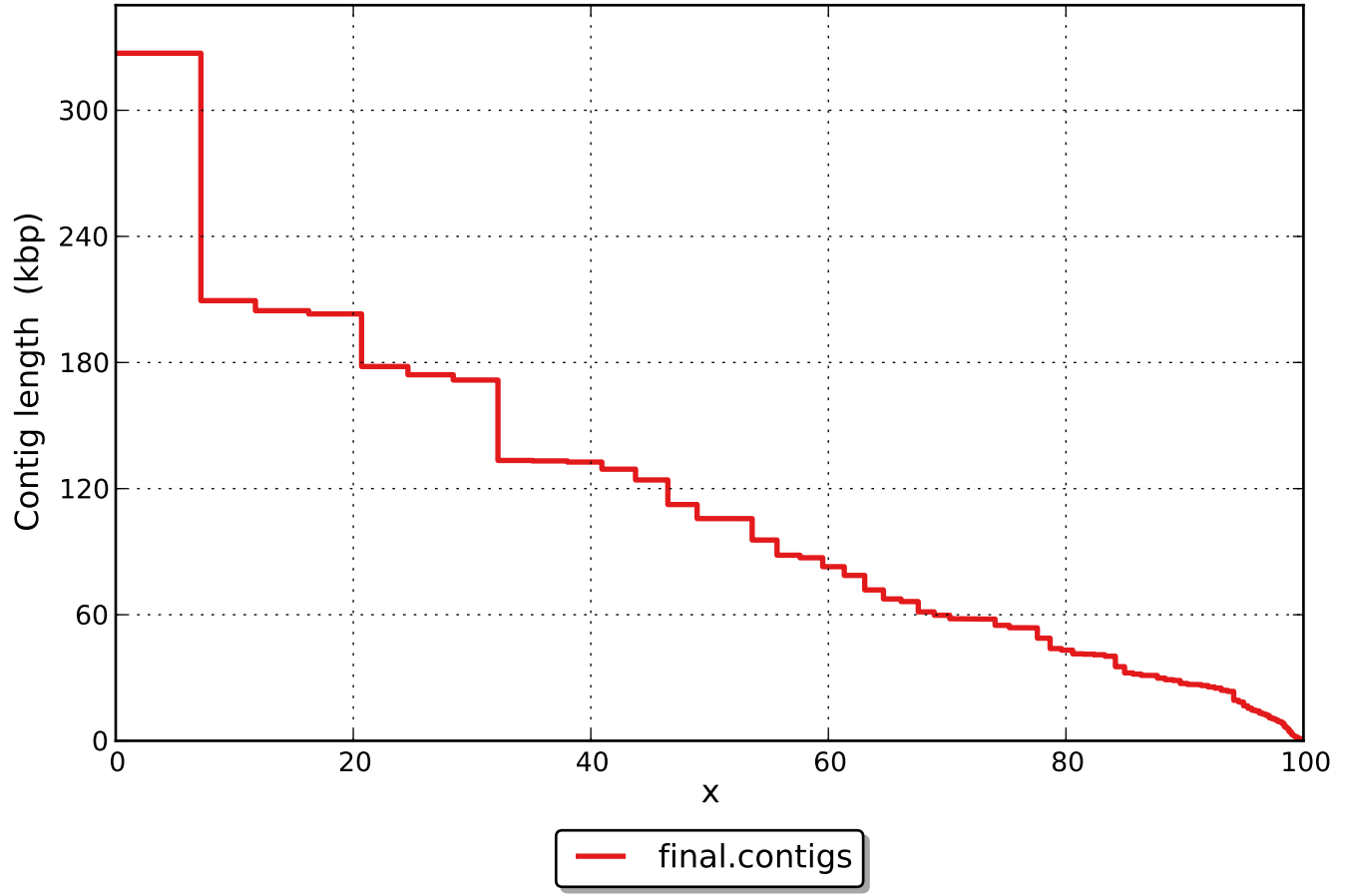
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

