

Report

	final.contigs
# contigs (>= 1000 bp)	95
# contigs (>= 5000 bp)	70
# contigs (>= 10000 bp)	64
# contigs (>= 25000 bp)	51
# contigs (>= 50000 bp)	31
Total length (>= 1000 bp)	4554255
Total length (>= 5000 bp)	4499164
Total length (>= 10000 bp)	4455529
Total length (>= 25000 bp)	4259867
Total length (>= 50000 bp)	3552688
# contigs	111
Largest contig	327151
Total length	4564918
Reference length	4641652
GC (℥)	50.75
Reference GC (℥)	50.79
N50	111794
NG50	111794
N75	54946
NG75	53827
L50	14
LG50	14
L75	29
LG75	30
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	12
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	98.277
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.98
# indels per 100 kbp	0.09
Largest alignment	327151
NA50	111794
NGA50	111794
NA75	54946
NGA75	53827
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	12
# mismatches	136
# indels	4
# short indels	3
# long indels	1
Indels length	89

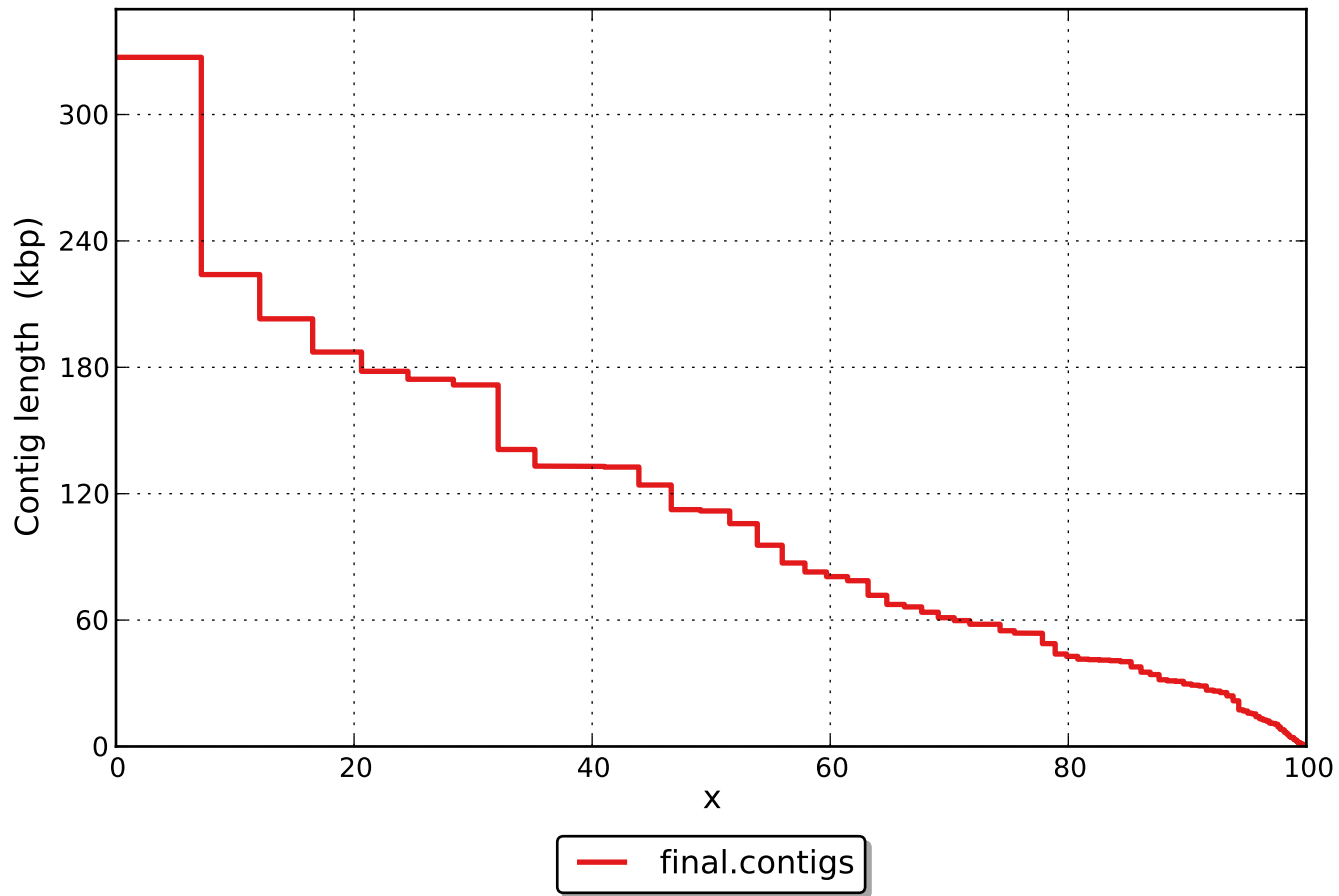
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

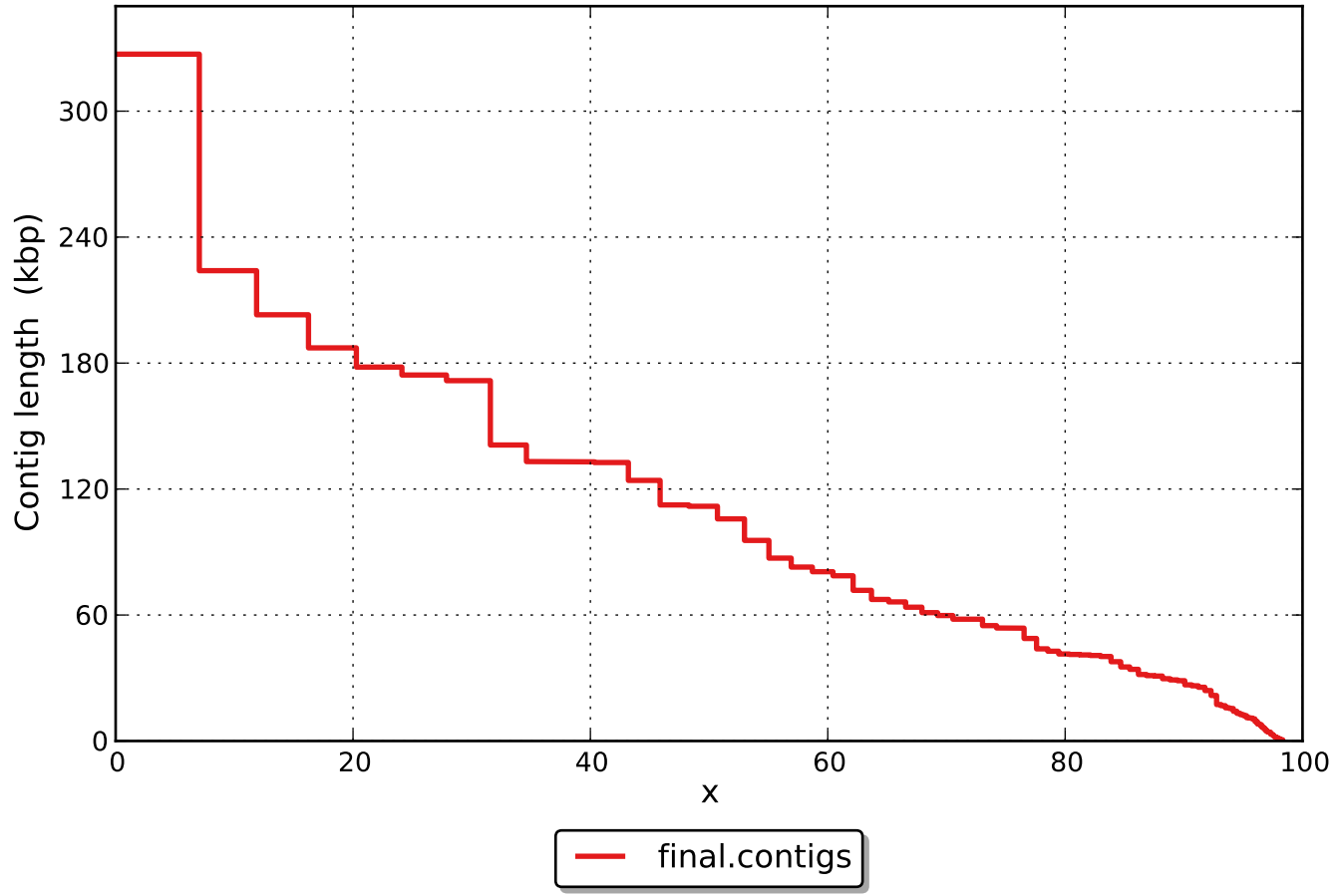
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

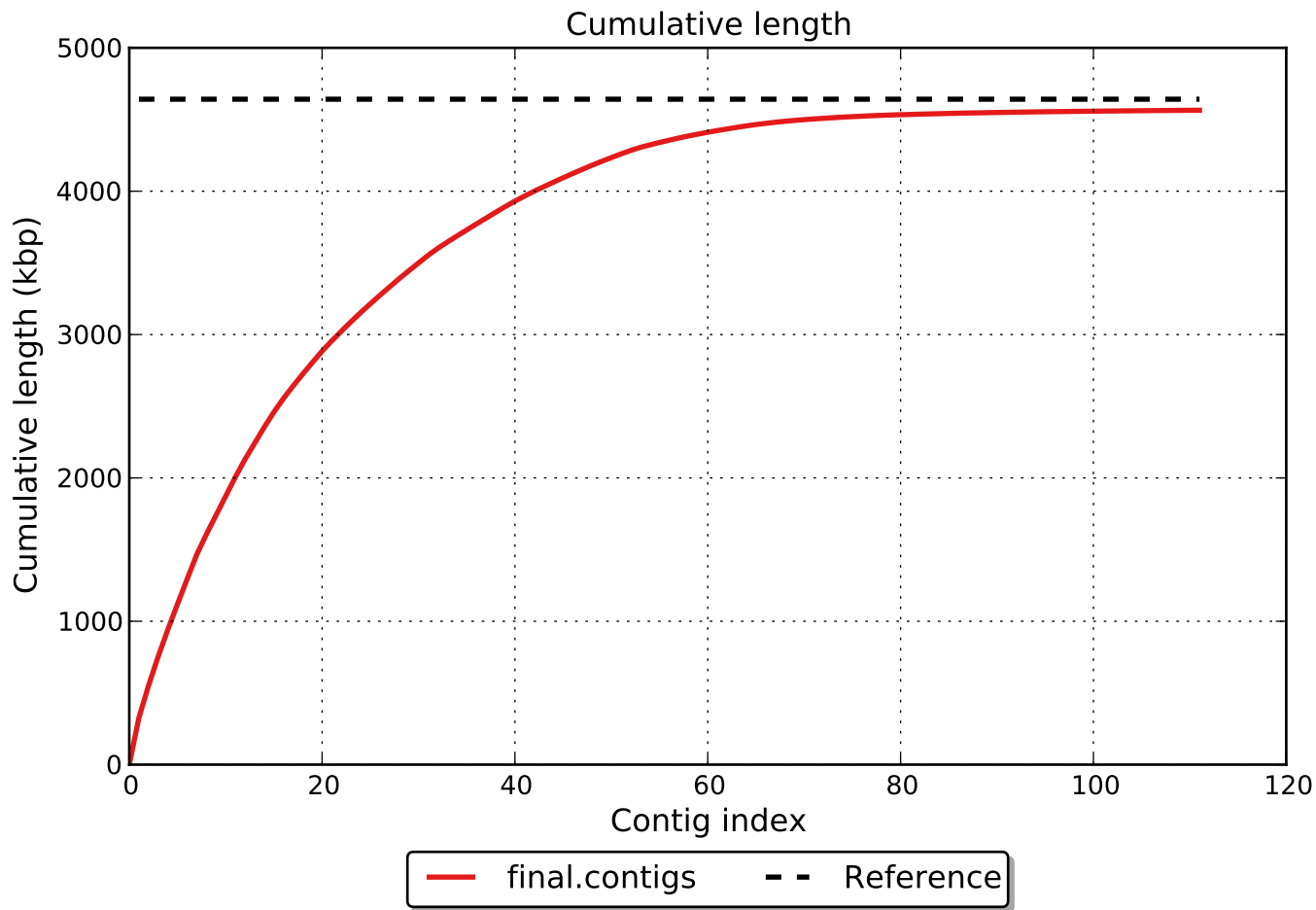
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

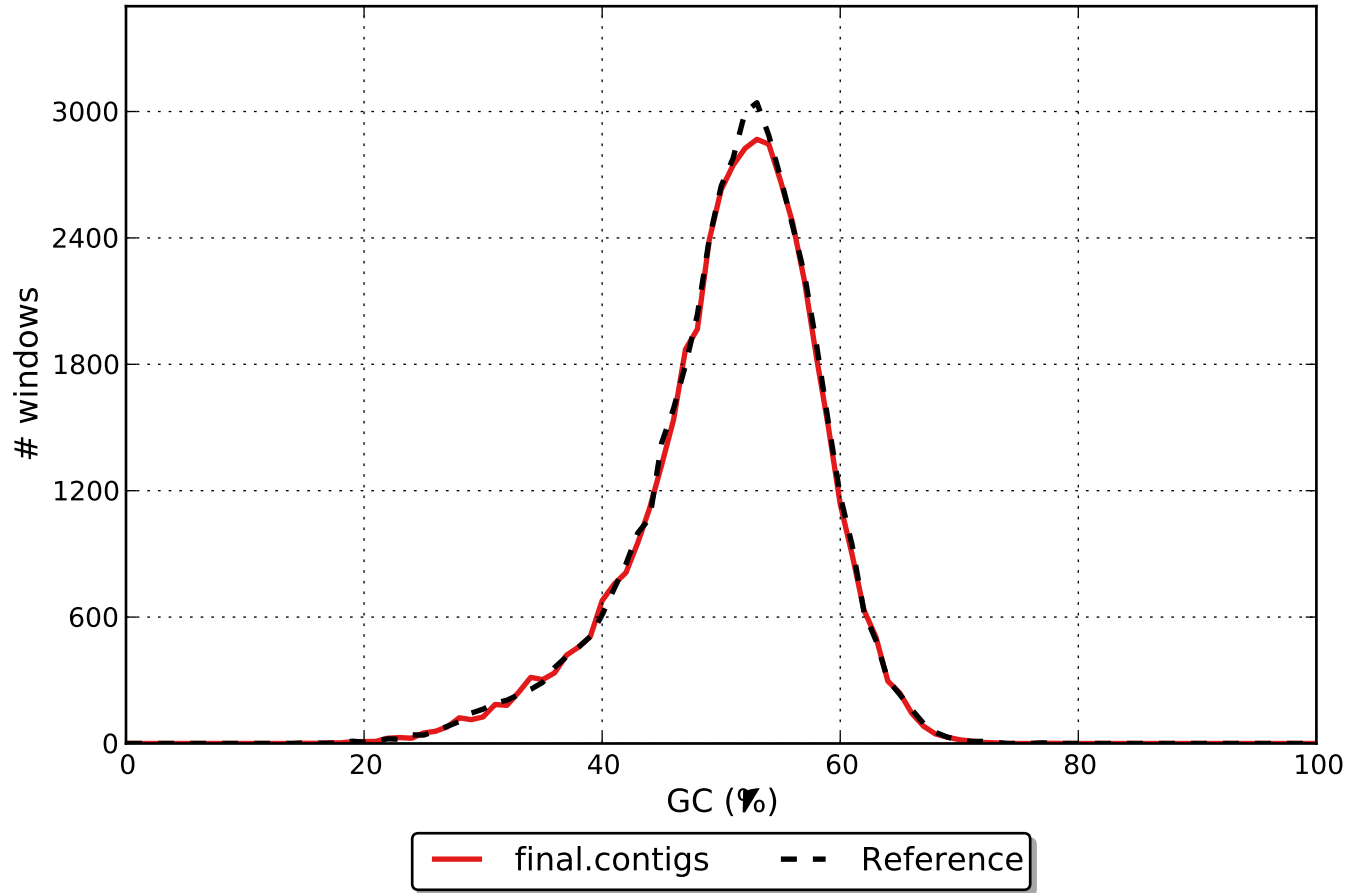


NGx





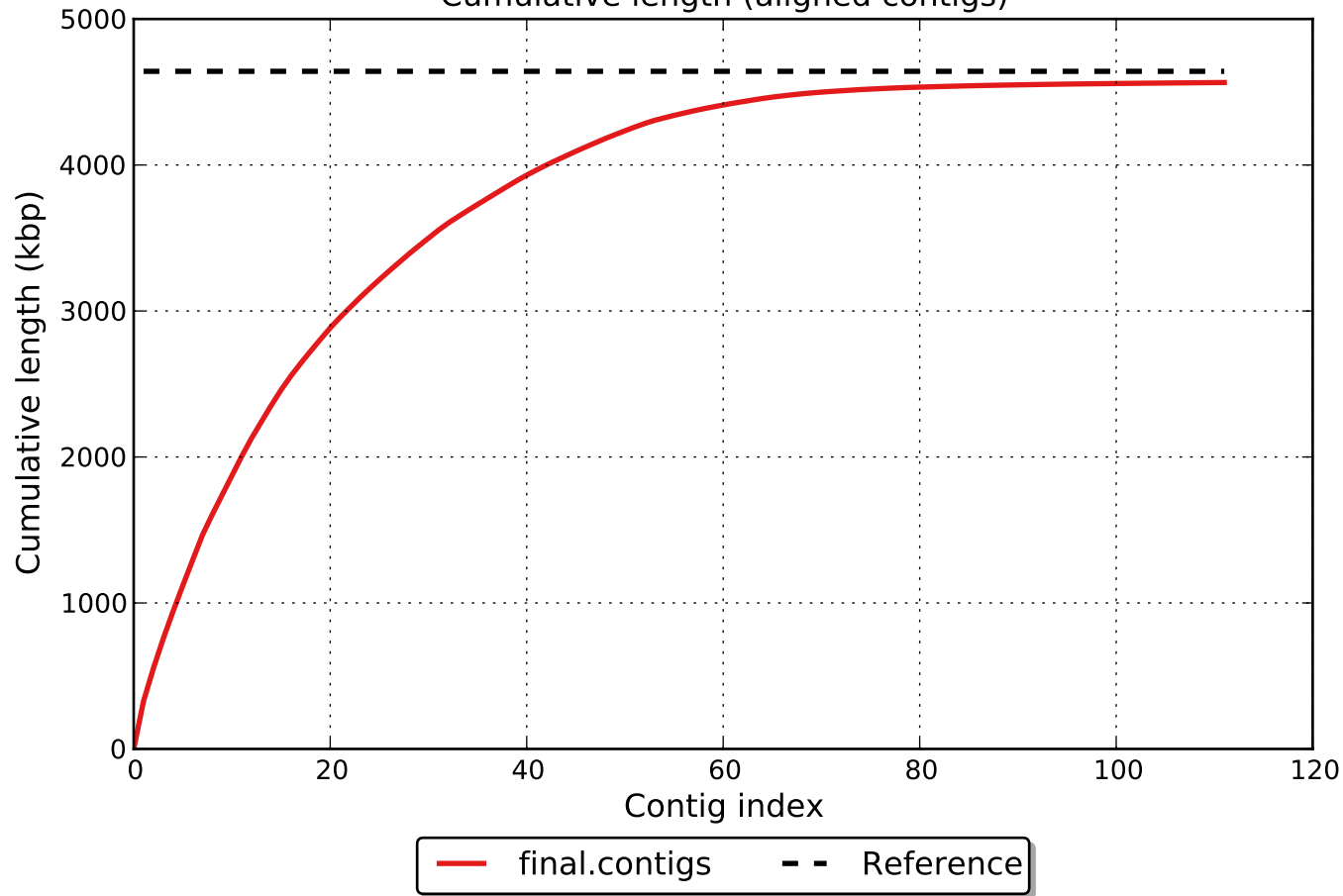
GC content



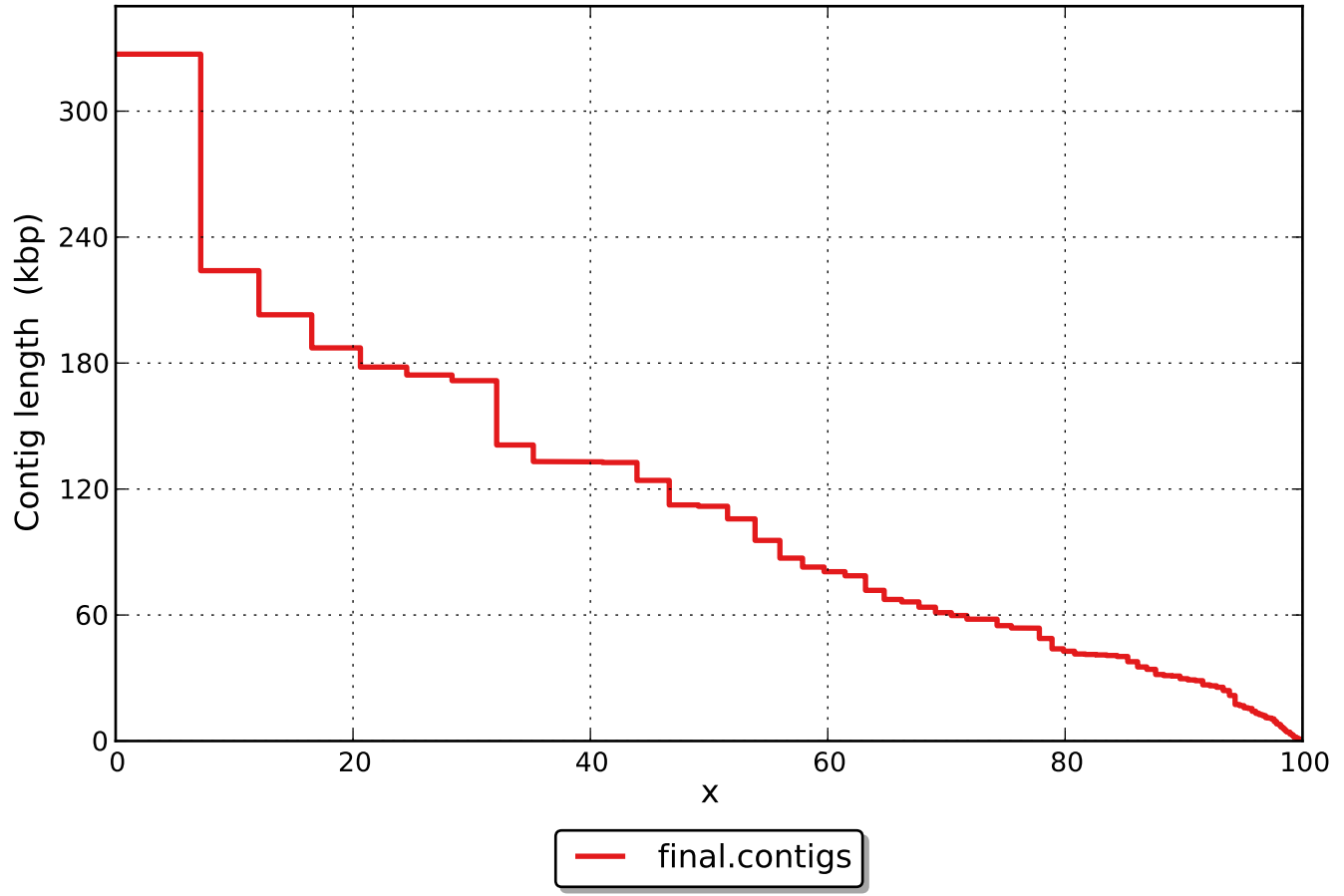
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

