

Report

	final.contigs
# contigs (>= 1000 bp)	96
# contigs (>= 5000 bp)	71
# contigs (>= 10000 bp)	64
# contigs (>= 25000 bp)	51
# contigs (>= 50000 bp)	31
Total length (>= 1000 bp)	4555229
Total length (>= 5000 bp)	4499621
Total length (>= 10000 bp)	4448450
Total length (>= 25000 bp)	4253085
Total length (>= 50000 bp)	3544631
# contigs	110
Largest contig	327142
Total length	4563914
Reference length	4641652
GC (℥)	50.75
Reference GC (℥)	50.79
N50	112683
NG50	112428
N75	54949
NG75	53788
L50	14
LG50	15
L75	29
LG75	30
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	10
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	98.273
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	59.43
# indels per 100 kbp	10.02
Largest alignment	327142
NA50	112683
NGA50	112428
NA75	54949
NGA75	53788
LA50	14
LGA50	15
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	10
# mismatches	2711
# indels	457
# short indels	452
# long indels	5
Indels length	737

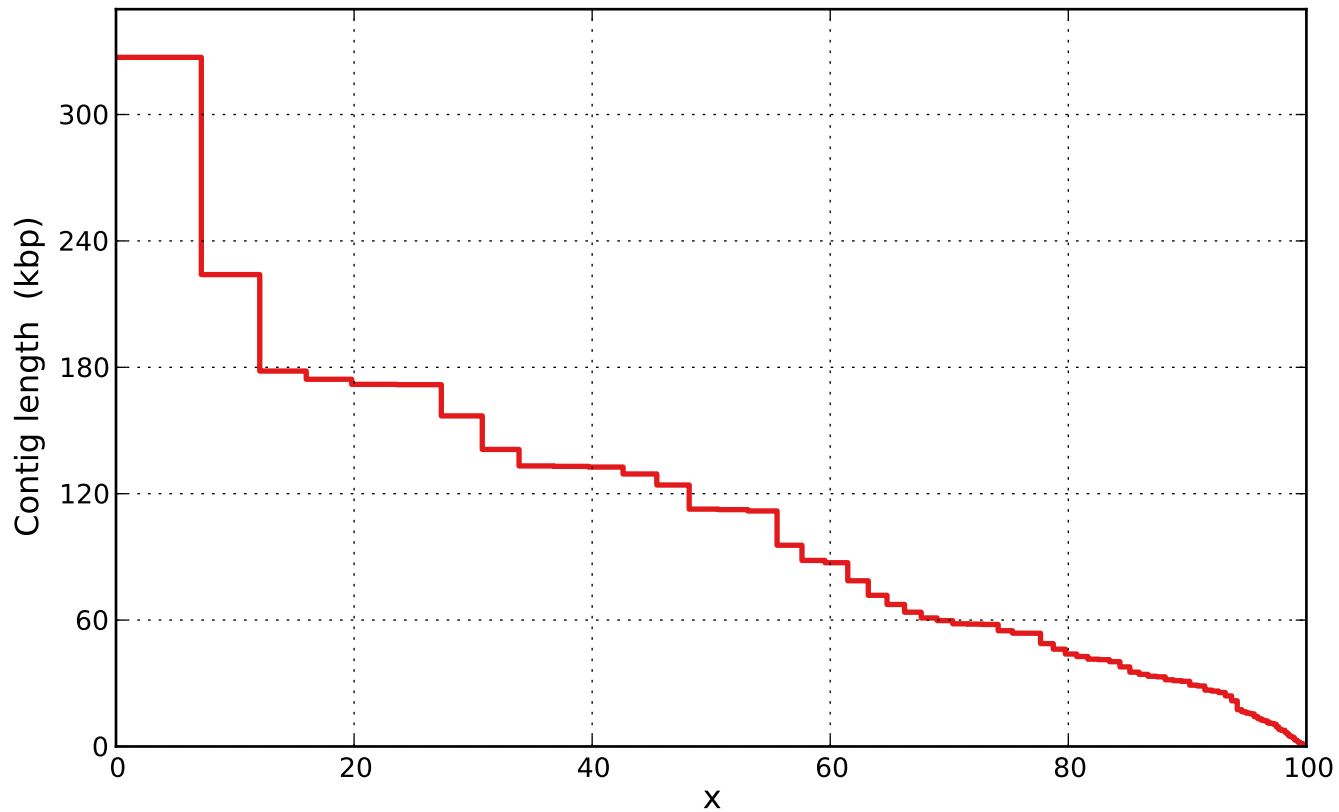
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

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

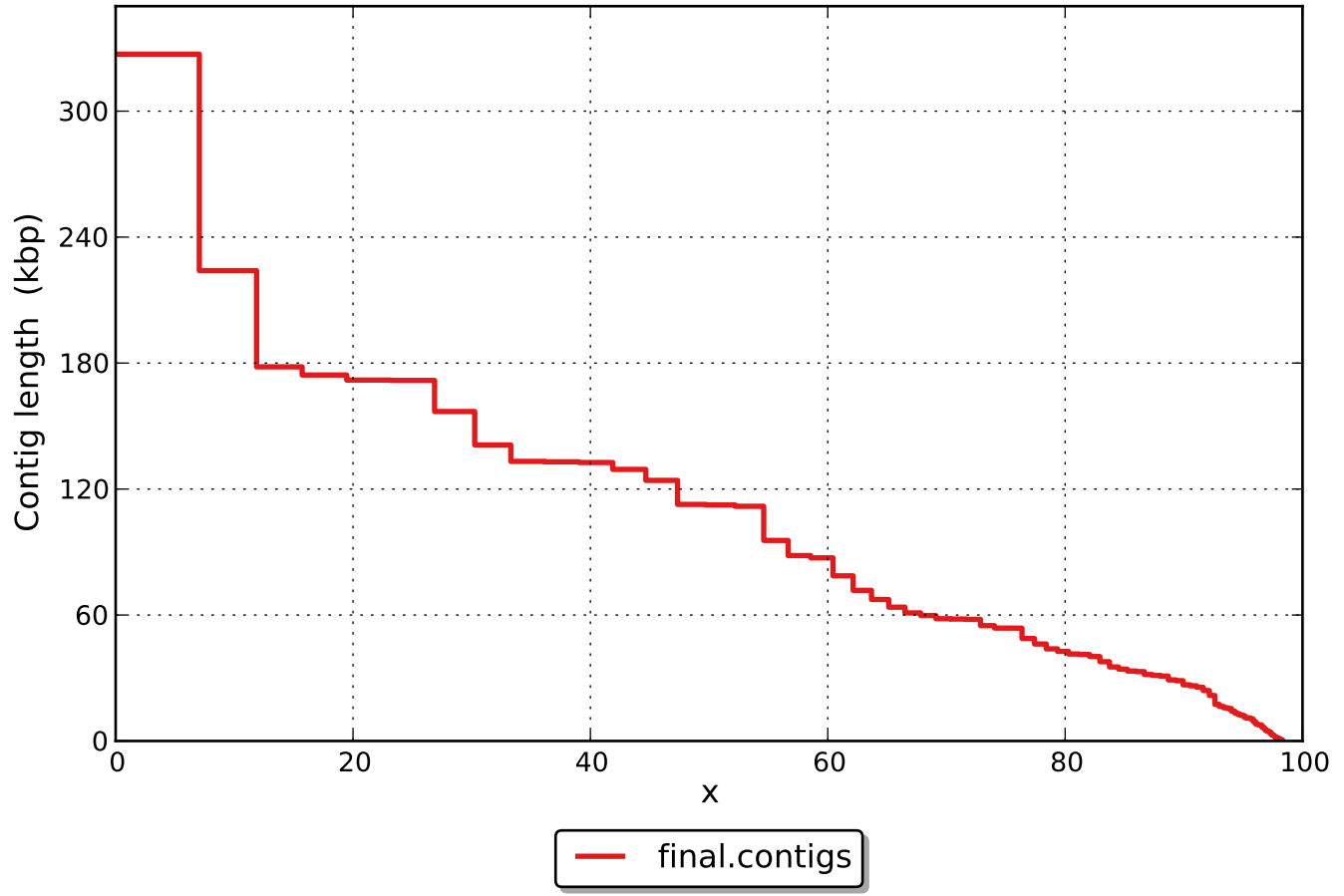
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

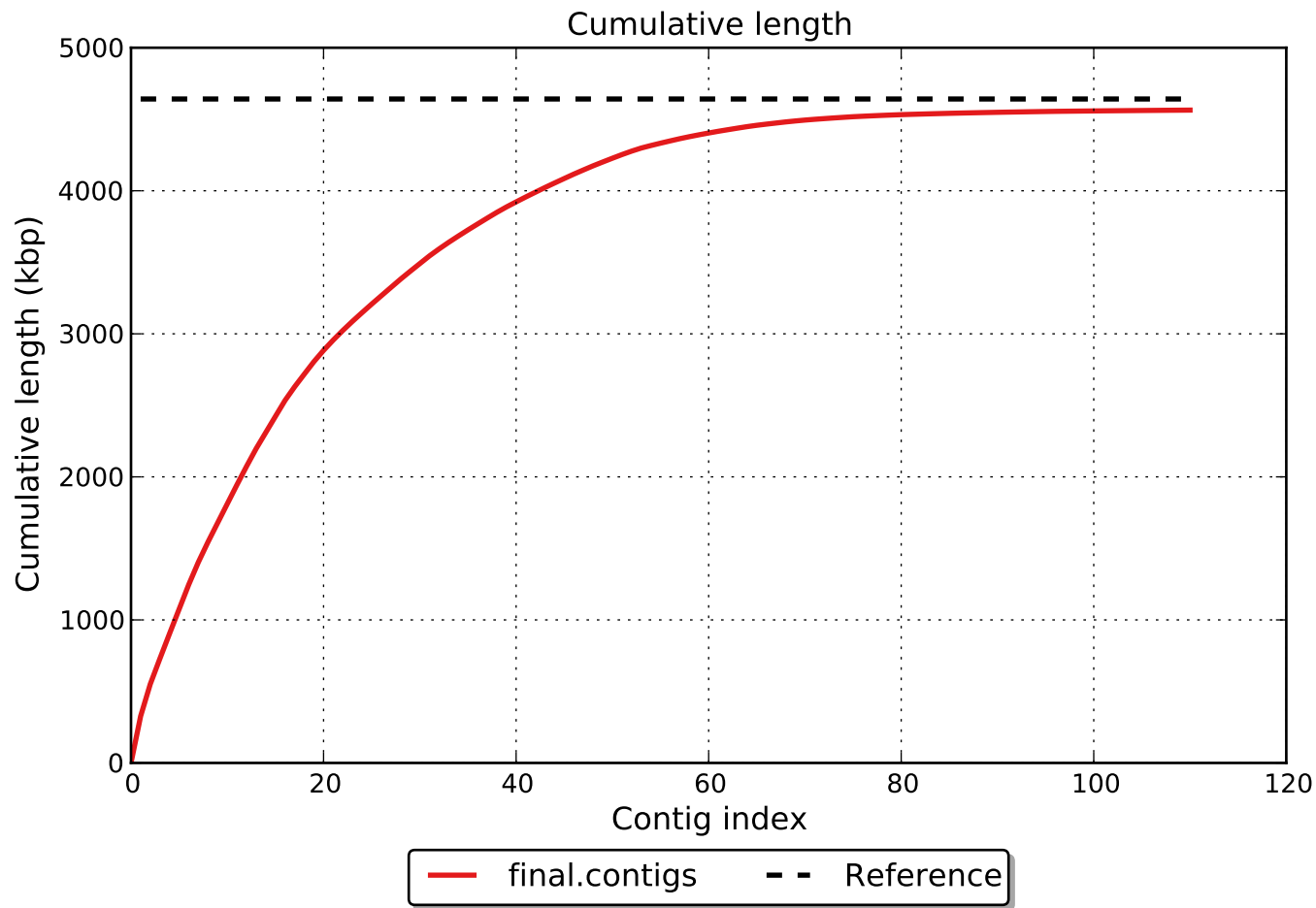
Nx



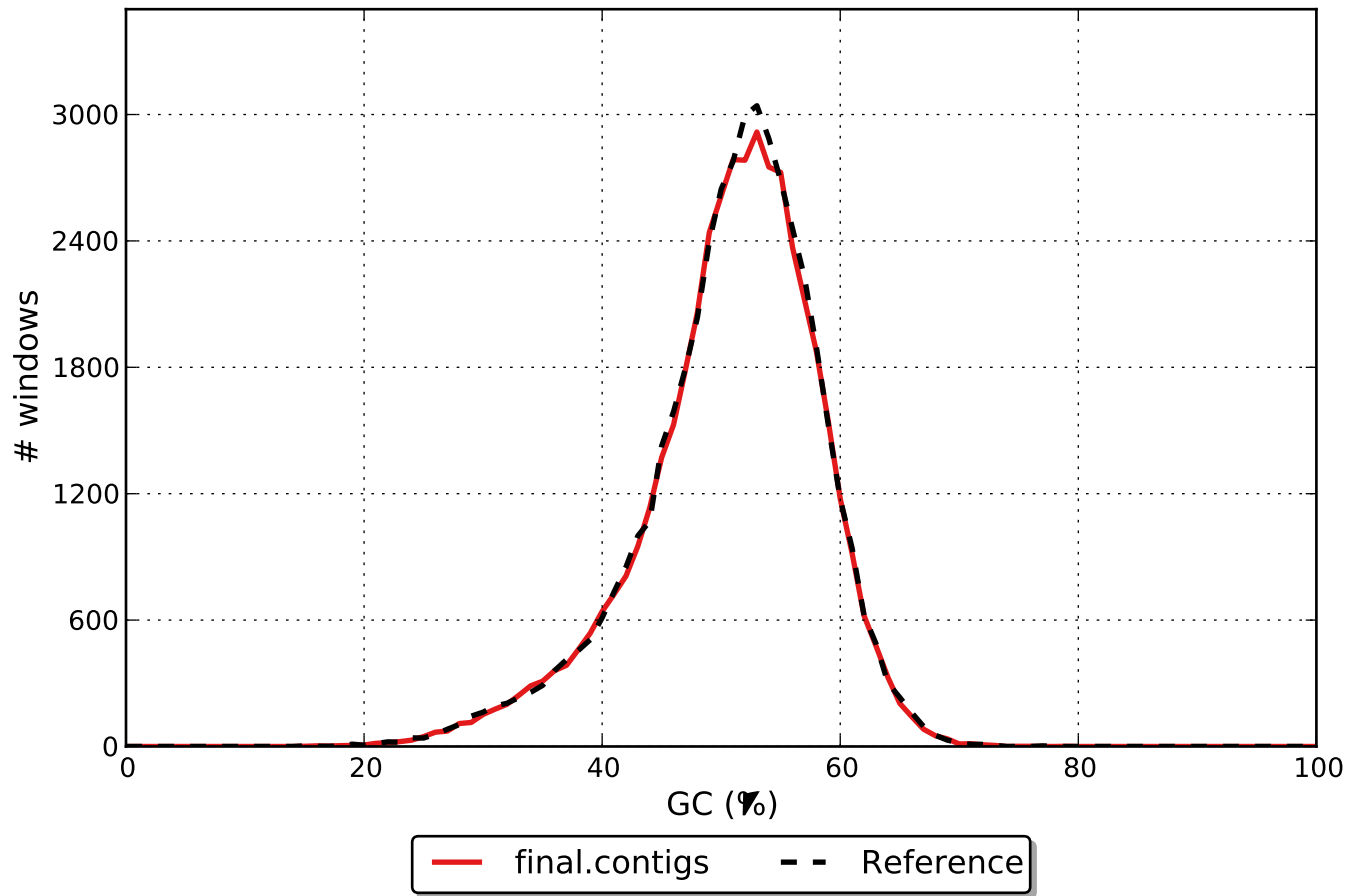
— final.contigs

NGx





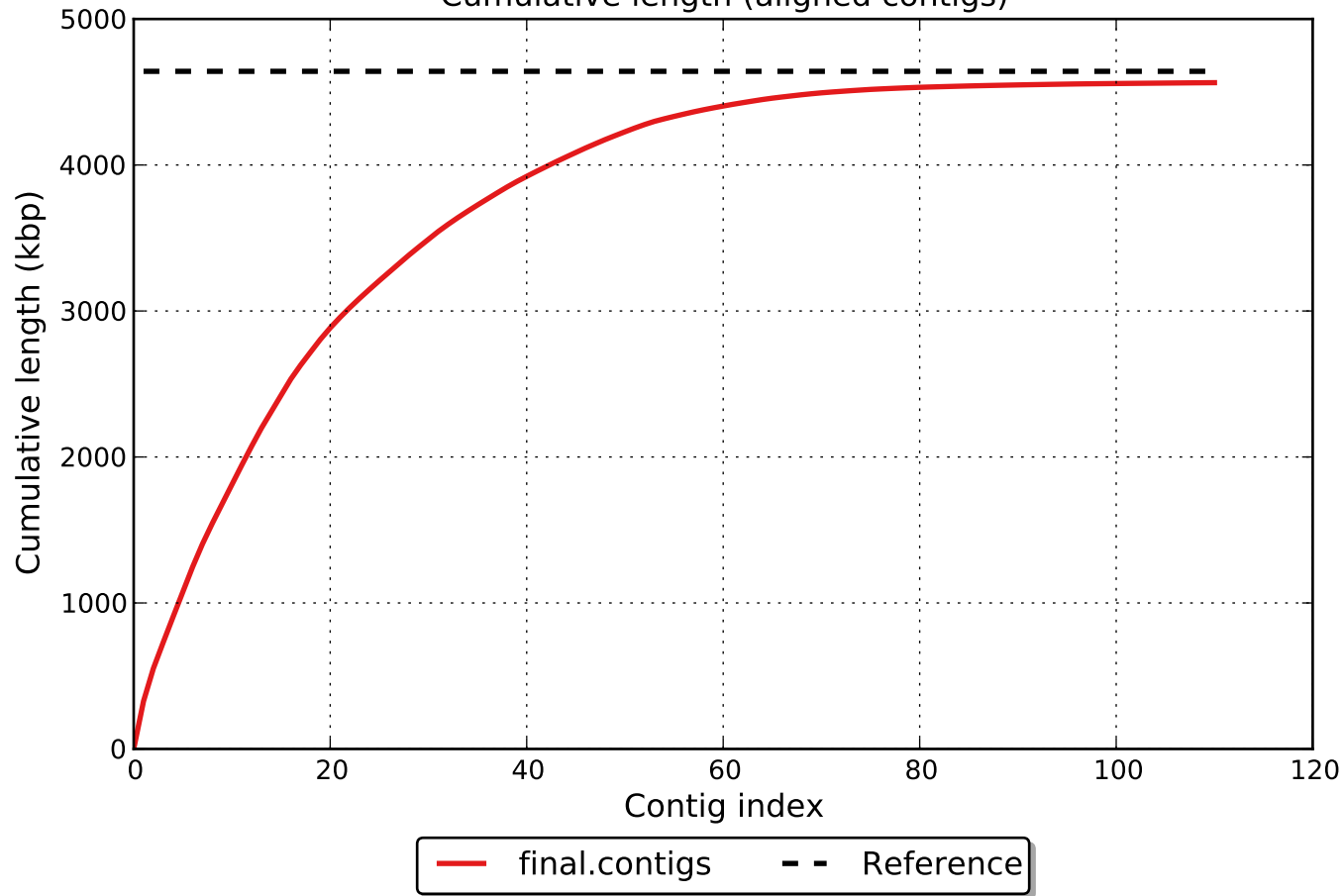
GC content



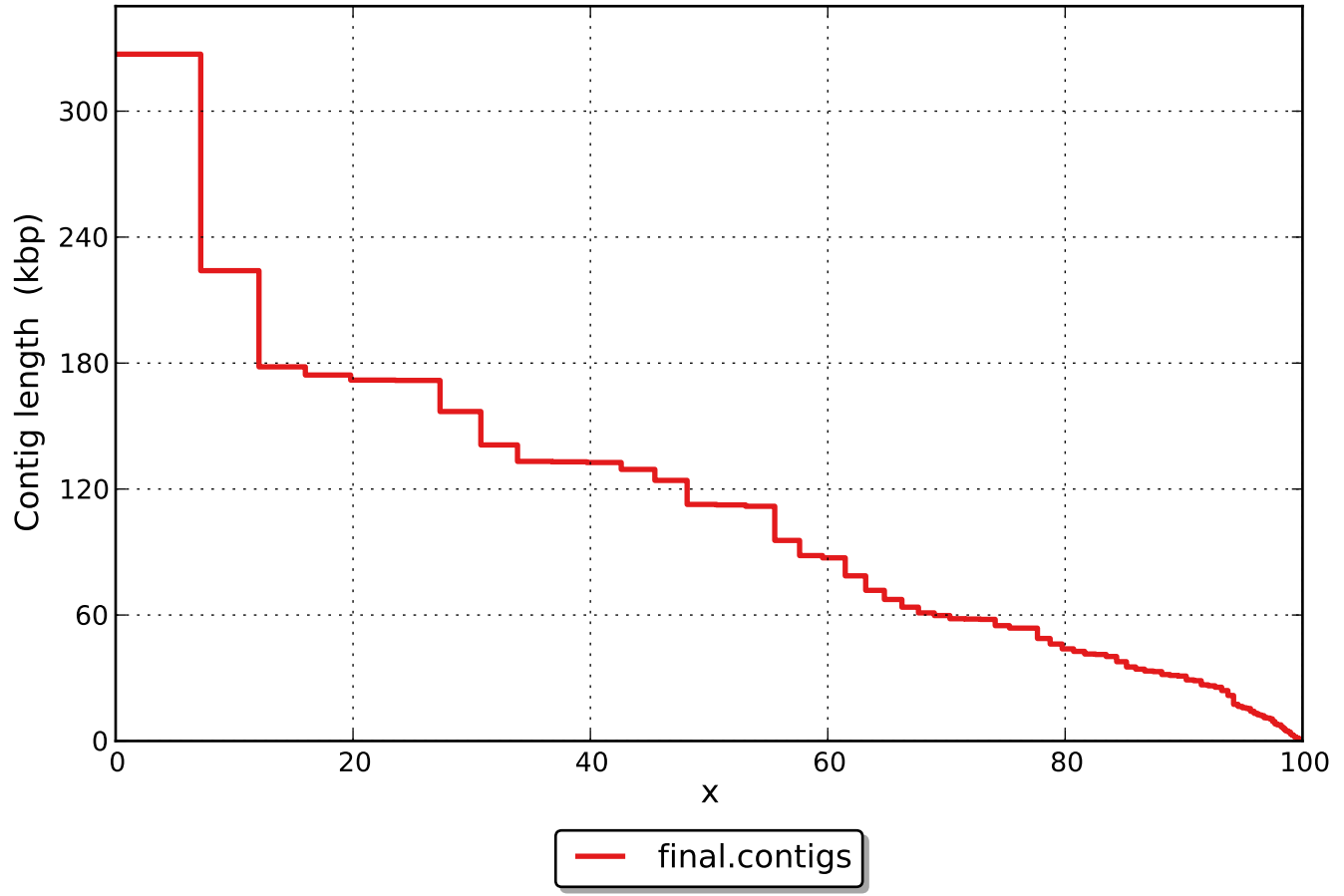
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

