

Report

	final.contigs
# contigs (>= 1000 bp)	95
# contigs (>= 5000 bp)	70
# contigs (>= 10000 bp)	64
# contigs (>= 25000 bp)	52
# contigs (>= 50000 bp)	33
Total length (>= 1000 bp)	4554504
Total length (>= 5000 bp)	4497649
Total length (>= 10000 bp)	4453778
Total length (>= 25000 bp)	4280978
Total length (>= 50000 bp)	3616607
# contigs	105
Largest contig	327049
Total length	4561016
Reference length	4641652
GC (℥)	50.74
Reference GC (℥)	50.79
N50	97563
NG50	95534
N75	56868
NG75	54945
L50	14
LG50	15
L75	30
LG75	31
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	13
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	98.209
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	59.23
# indels per 100 kbp	9.10
Largest alignment	327049
NA50	97563
NGA50	95534
NA75	56868
NGA75	54945
LA50	14
LGA50	15
LA75	30
LGA75	31

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	13
# mismatches	2700
# indels	415
# short indels	414
# long indels	1
Indels length	689

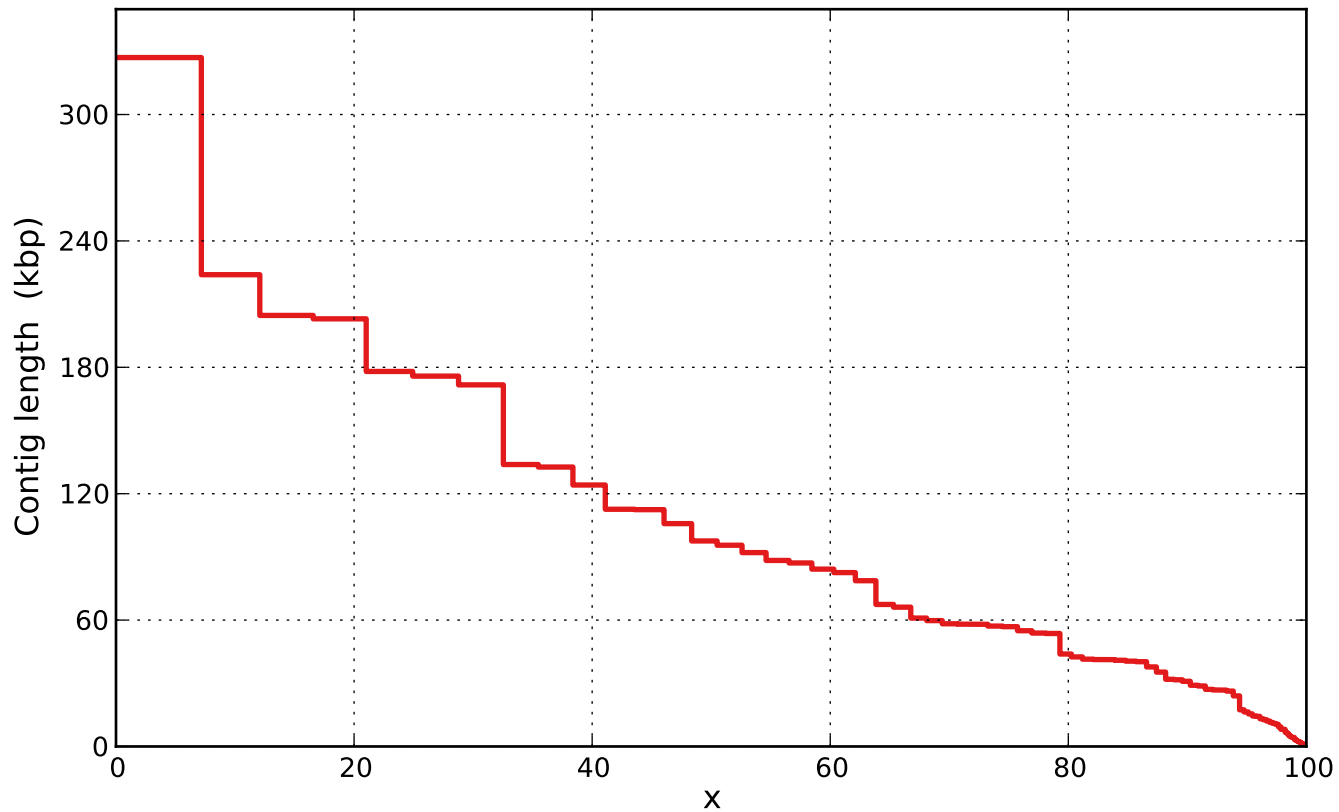
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

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

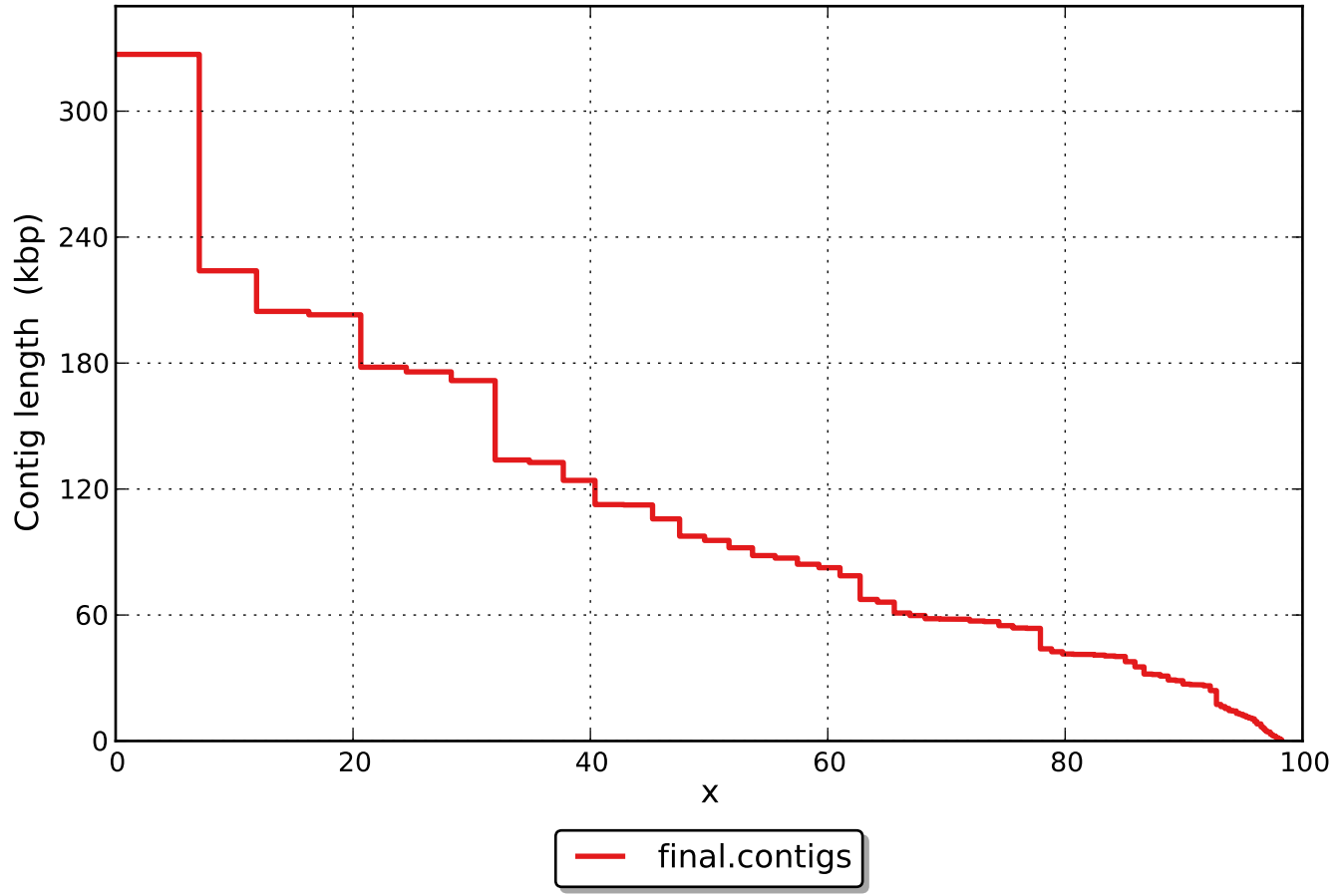
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

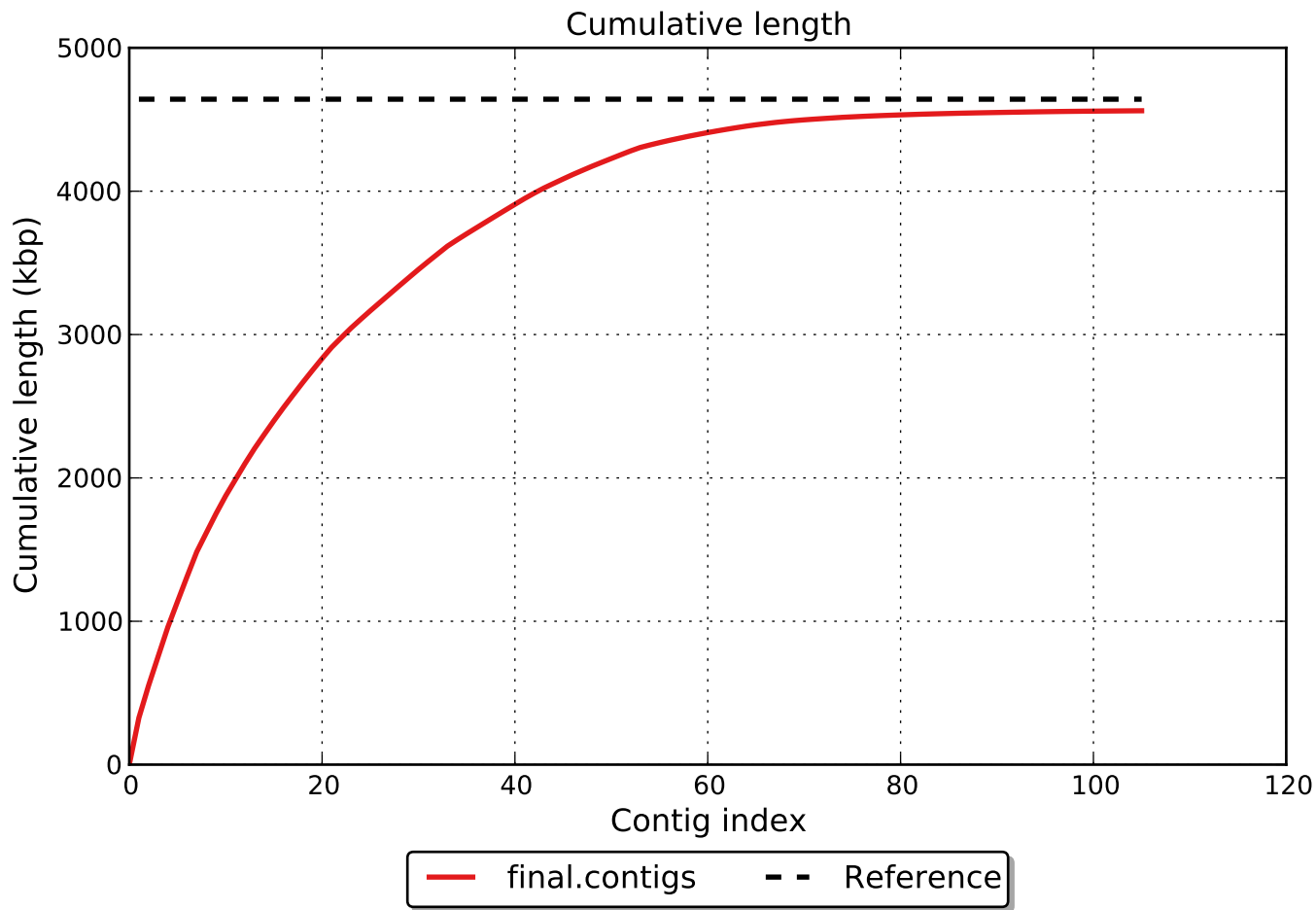
Nx



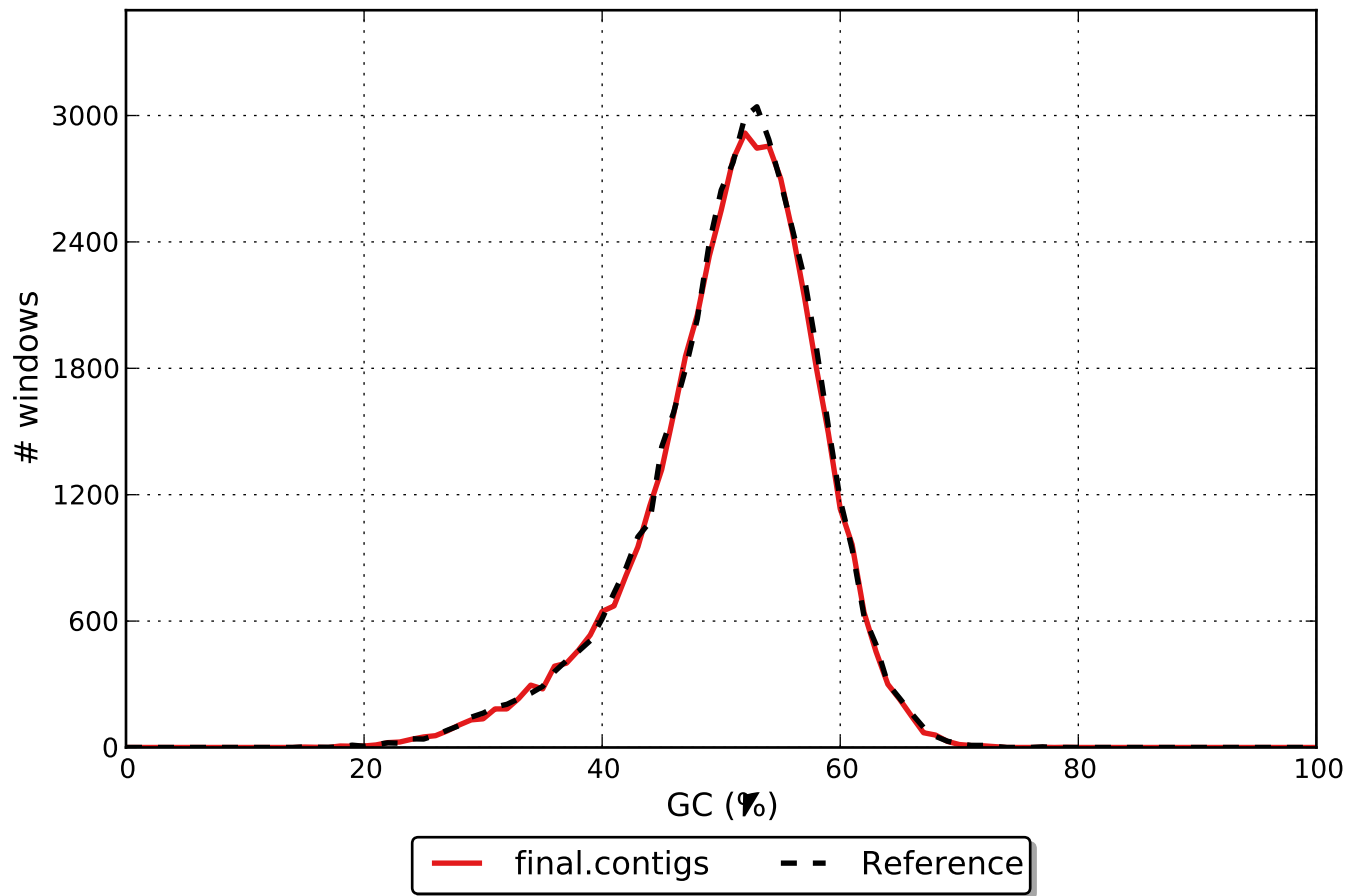
— final.contigs

NGx





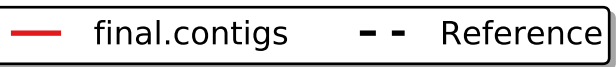
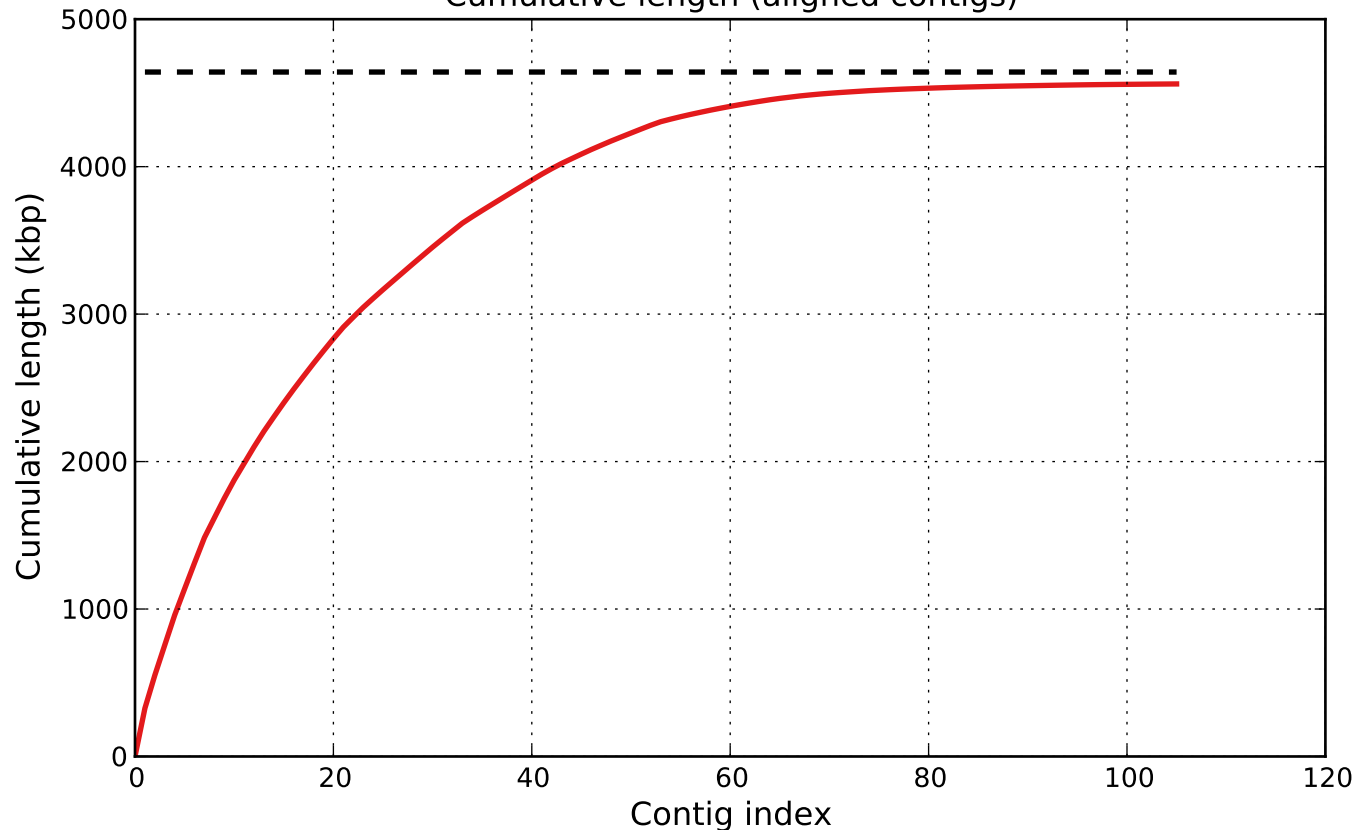
GC content



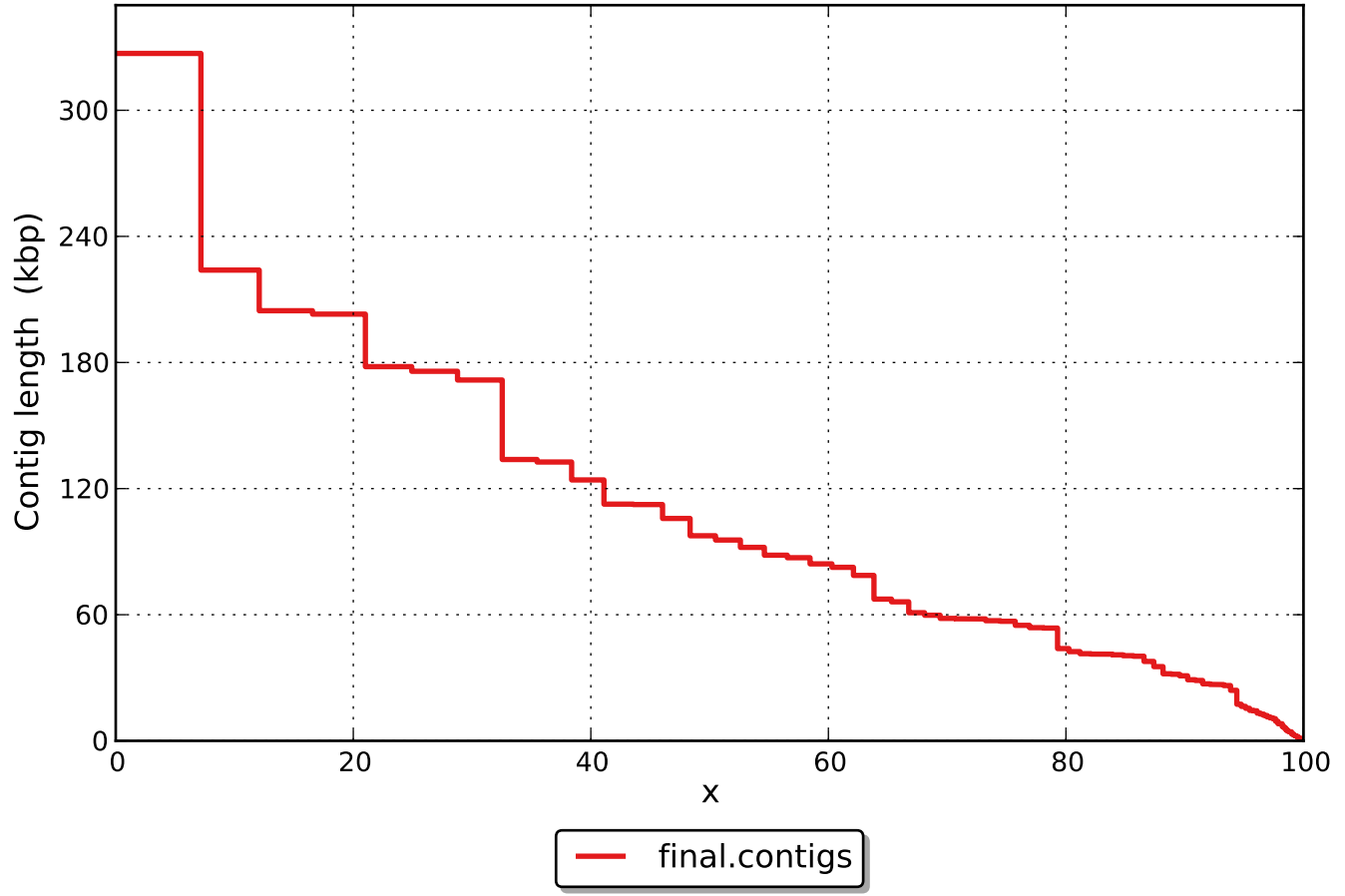
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

