

## Report

	final.contigs
# contigs (>= 0 bp)	191
# contigs (>= 1000 bp)	150
# contigs (>= 5000 bp)	120
# contigs (>= 10000 bp)	99
# contigs (>= 25000 bp)	71
# contigs (>= 50000 bp)	30
Total length (>= 0 bp)	4595312
Total length (>= 1000 bp)	4576716
Total length (>= 5000 bp)	4499202
Total length (>= 10000 bp)	4335470
Total length (>= 25000 bp)	3899554
Total length (>= 50000 bp)	2402367
# contigs	163
Largest contig	158035
Total length	4585386
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	55014
NG50	51749
N75	32592
NG75	31783
L50	28
LG50	29
L75	55
LG75	57
# misassemblies	6
# misassembled contigs	5
Misassembled contigs length	314563
# local misassemblies	8
# unaligned contigs	0 + 2 part
Unaligned length	182
Genome fraction (%)	98.435
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	33.18
# indels per 100 kbp	0.15
Largest alignment	158035
NA50	51749
NGA50	51749
NA75	32013
NGA75	31783
LA50	29
LGA50	29
LA75	56
LGA75	57

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	6
# relocations	6
# translocations	0
# inversions	0
# misassembled contigs	5
Misassembled contigs length	314563
# local misassemblies	8
# mismatches	1516
# indels	7
# short indels	7
# long indels	0
Indels length	8

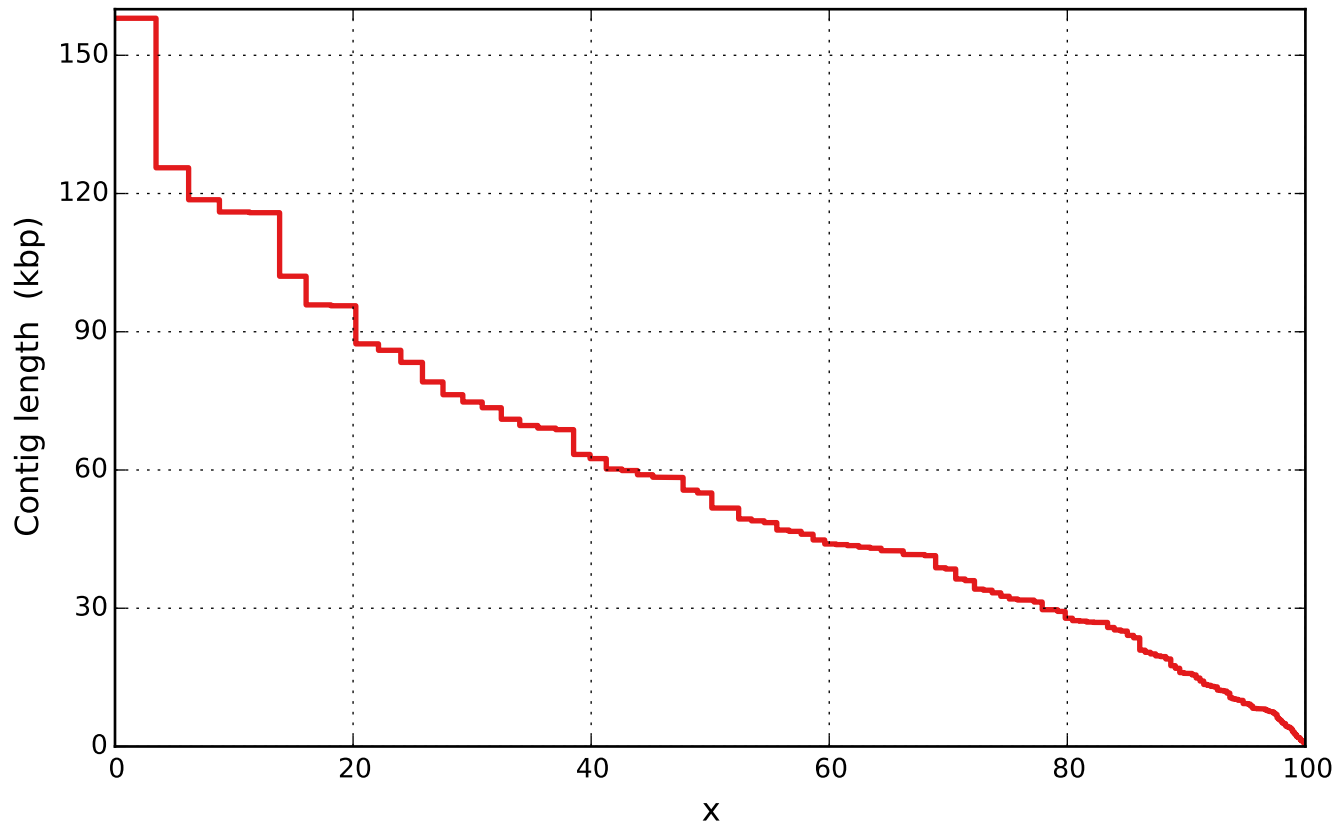
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	182
# N's	0

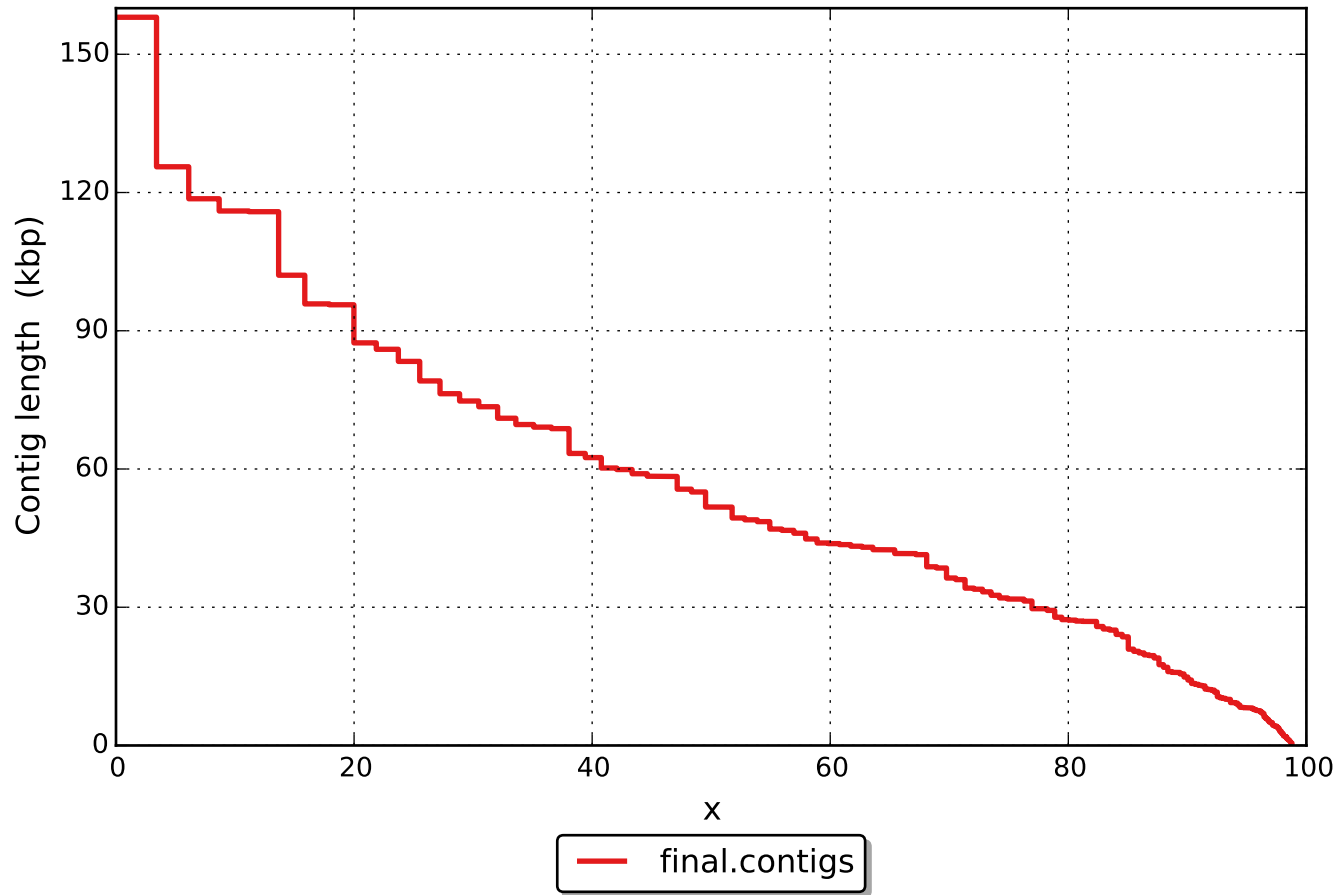
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

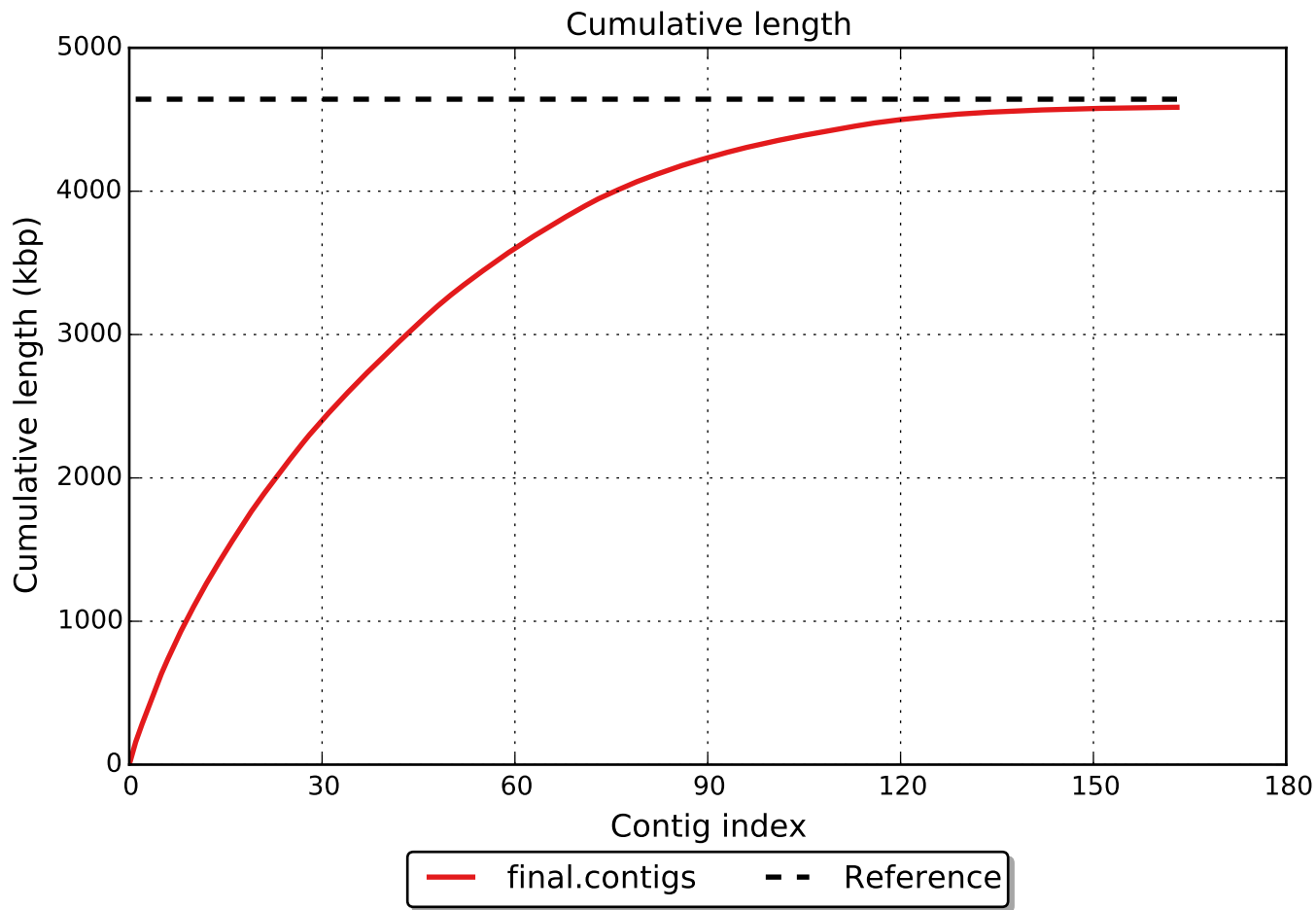
Nx



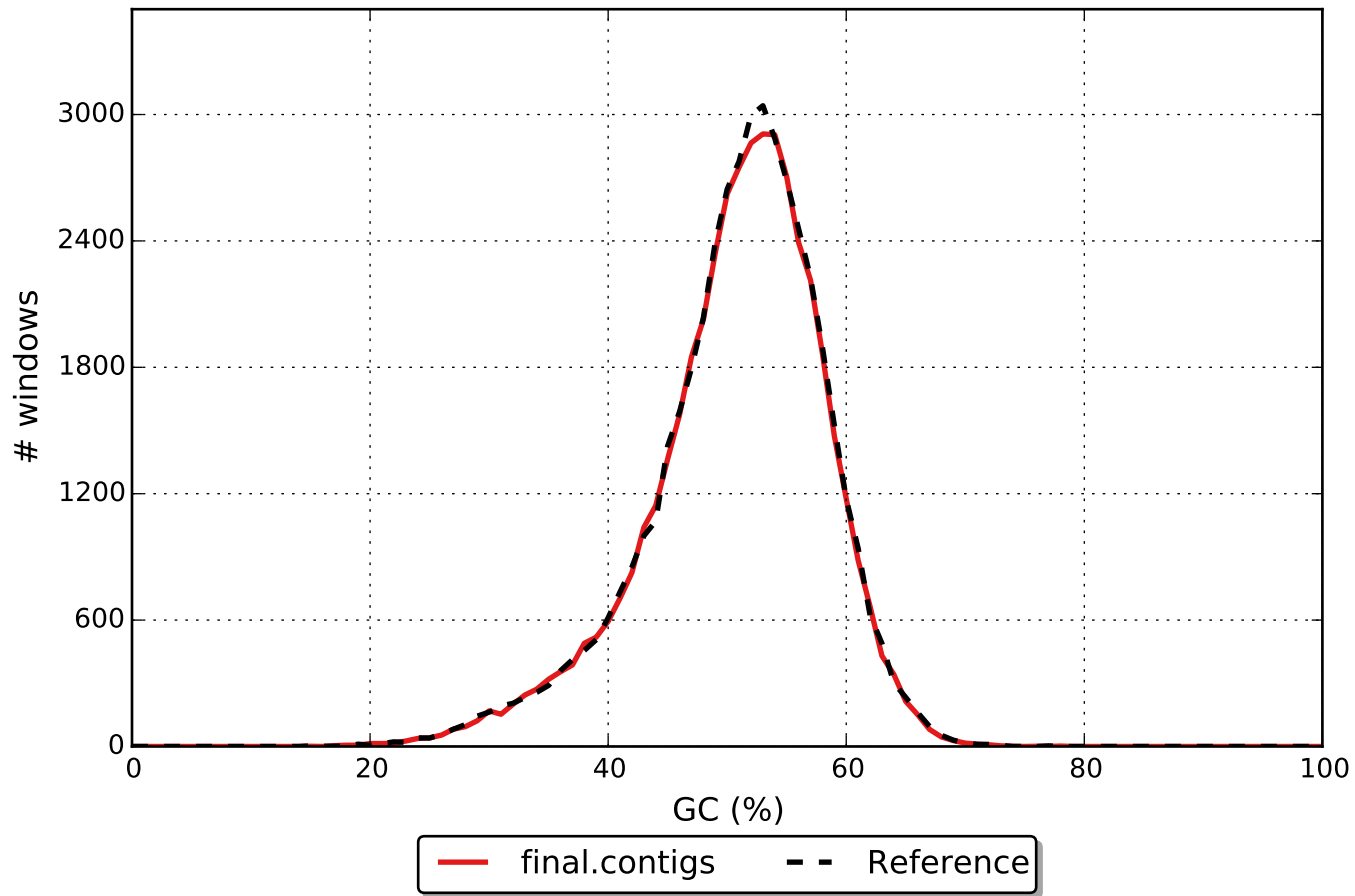
— final.contigs

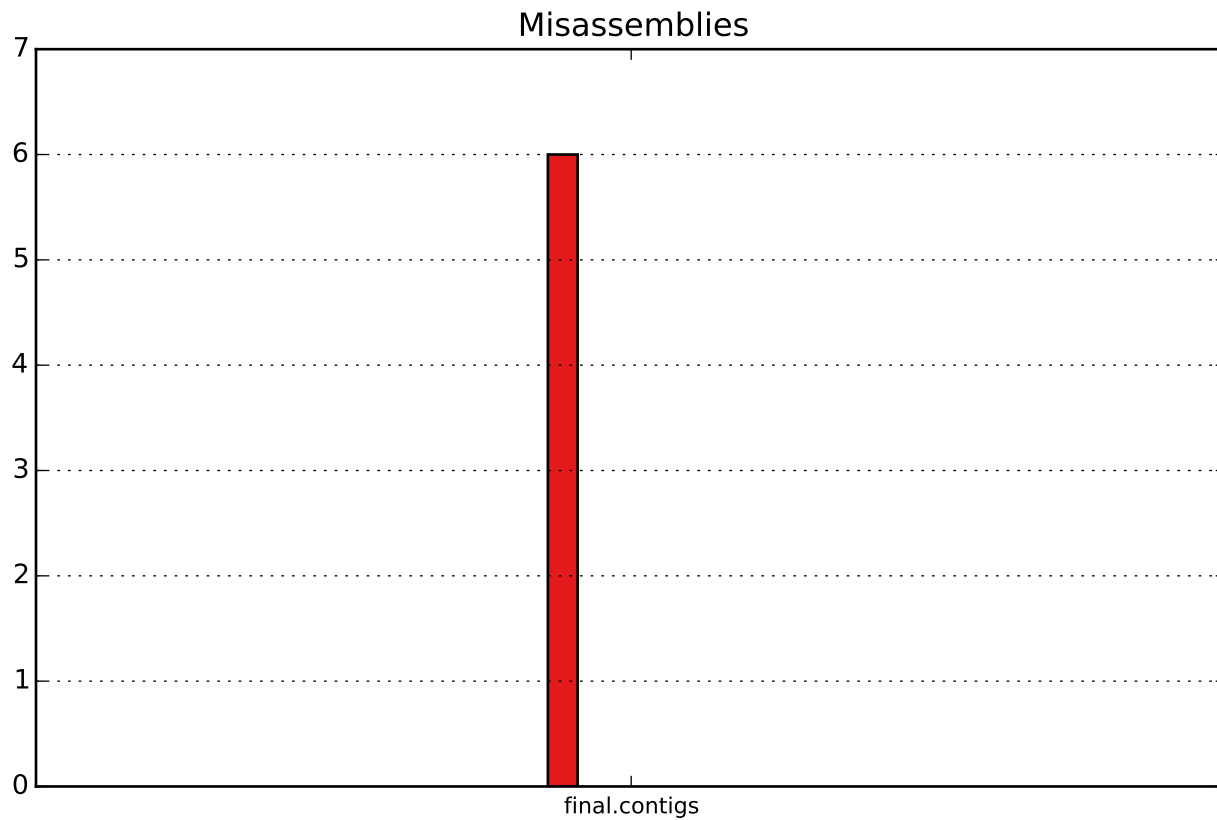
NGx





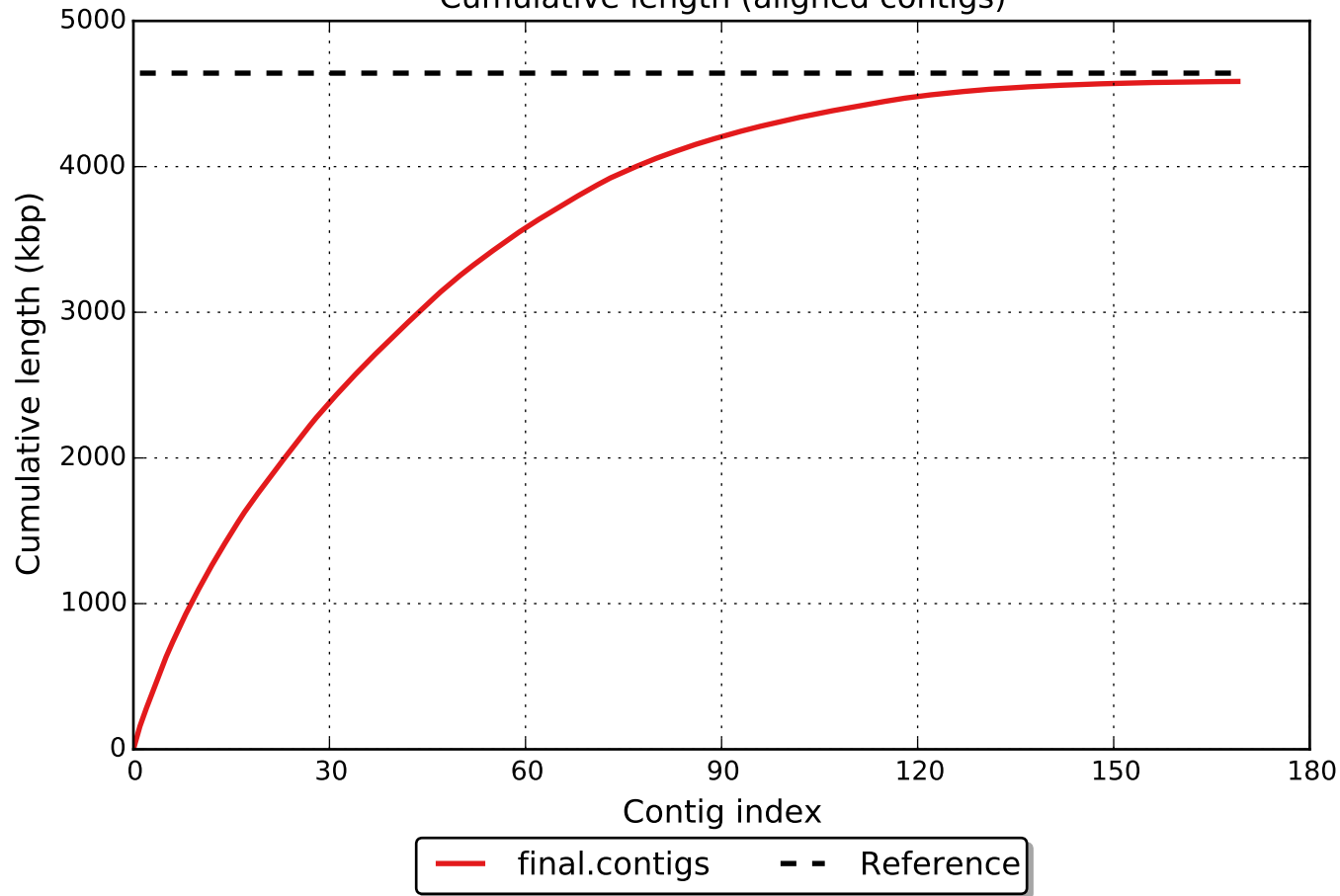
GC content



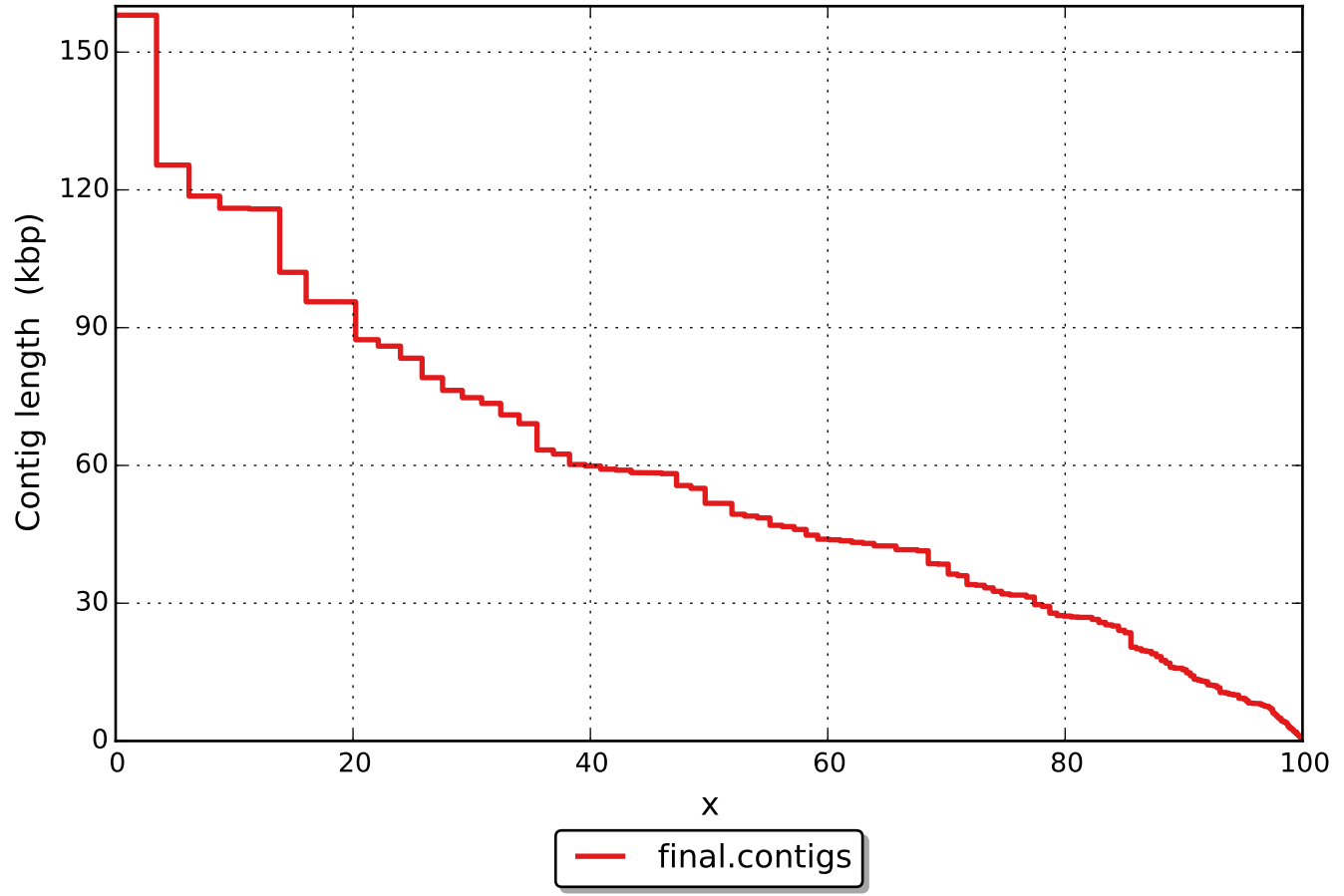




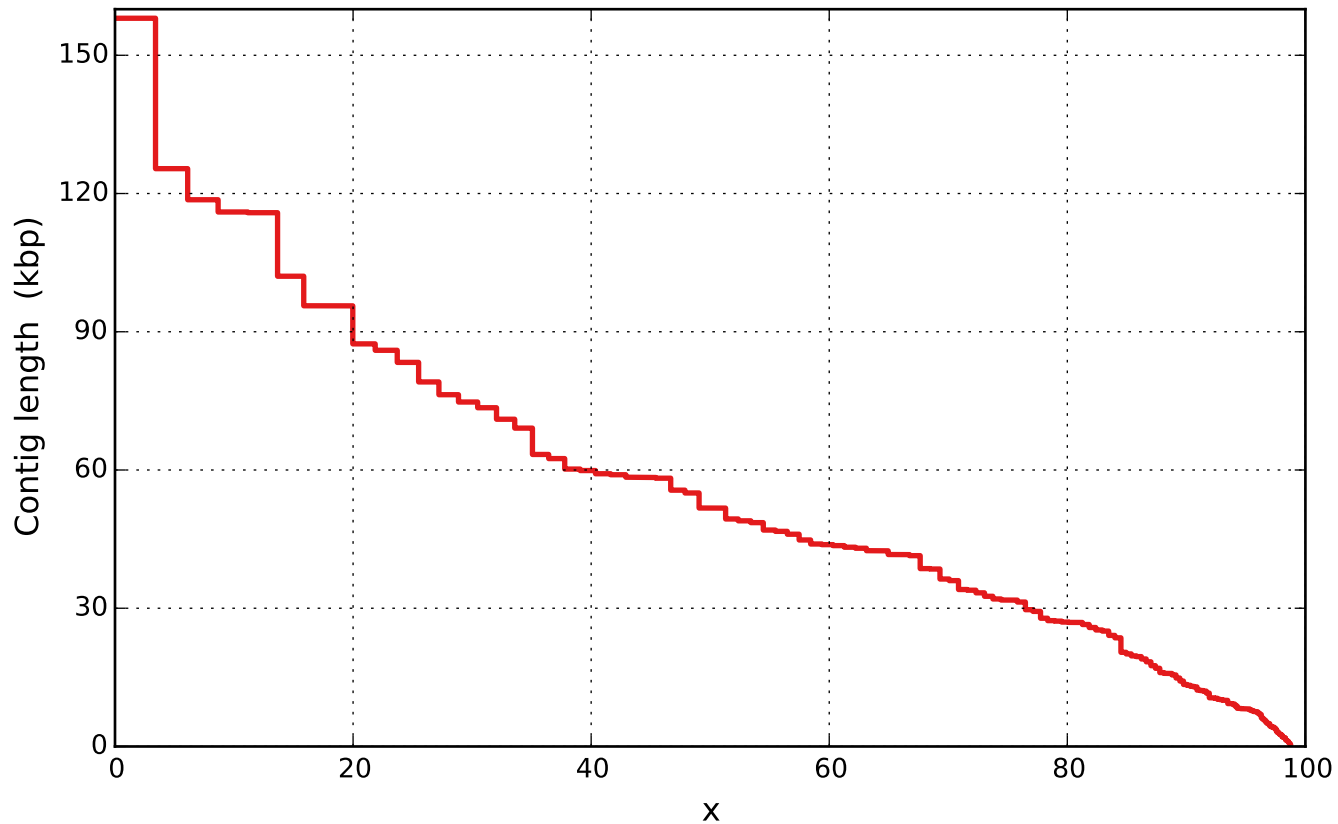
Cumulative length (aligned contigs)



NAx



NGAx



— final.contigs