

Report

	final.contigs
# contigs (>= 1000 bp)	157
# contigs (>= 5000 bp)	137
# contigs (>= 10000 bp)	114
# contigs (>= 25000 bp)	71
# contigs (>= 50000 bp)	35
Total length (>= 1000 bp)	4867173
Total length (>= 5000 bp)	4809988
Total length (>= 10000 bp)	4655025
Total length (>= 25000 bp)	3991755
Total length (>= 50000 bp)	2826197
# contigs	162
Largest contig	197199
Total length	4870605
Reference length	4857432
GC (℥)	52.23
Reference GC (℥)	52.23
N50	56927
NG50	56927
N75	27696
NG75	28009
L50	28
LG50	28
L75	59
LG75	58
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	99.989
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	197199
NA50	56927
NGA50	56927
NA75	27696
NGA75	28009
LA50	28
LGA50	28
LA75	59
LGA75	58

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	0
# mismatches	0
# indels	0
# short indels	0
# long indels	0
Indels length	0

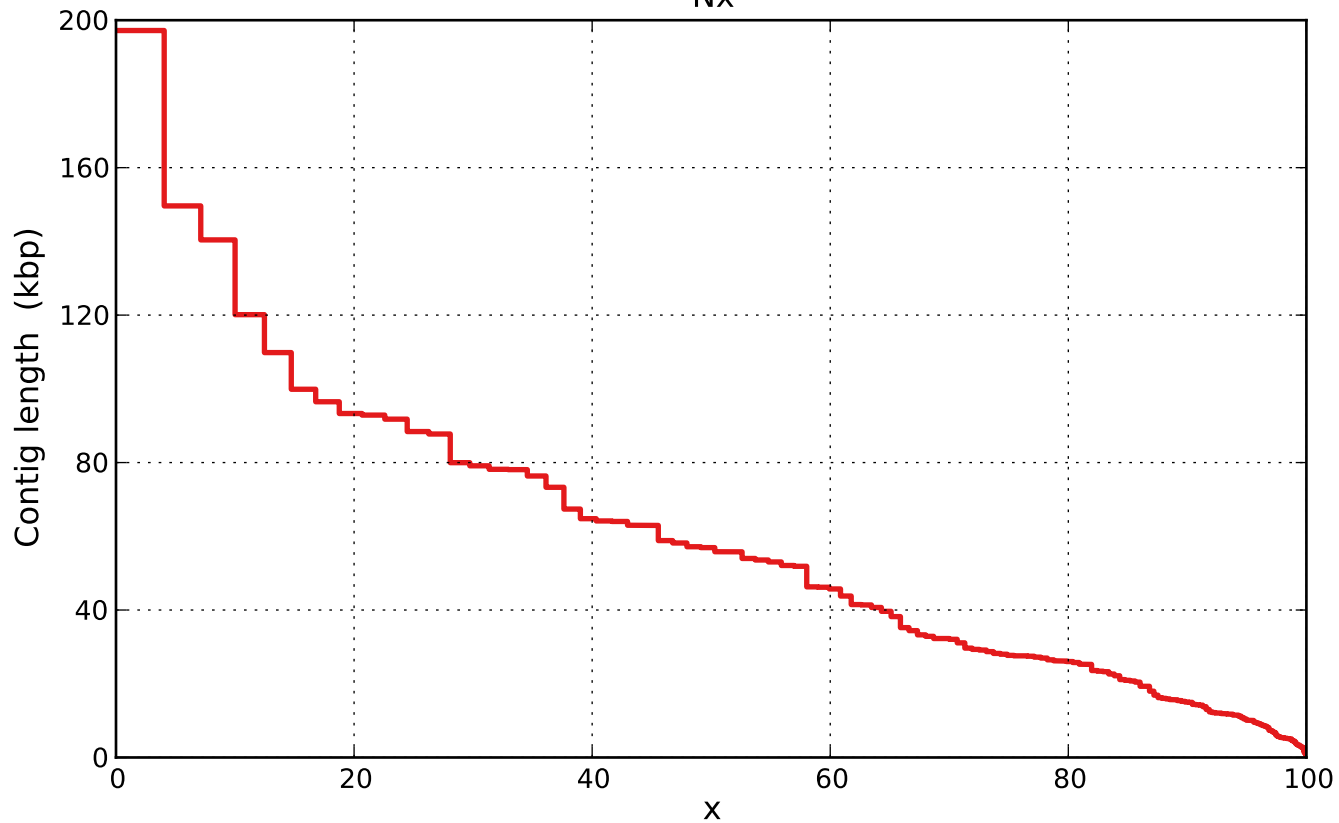
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## 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

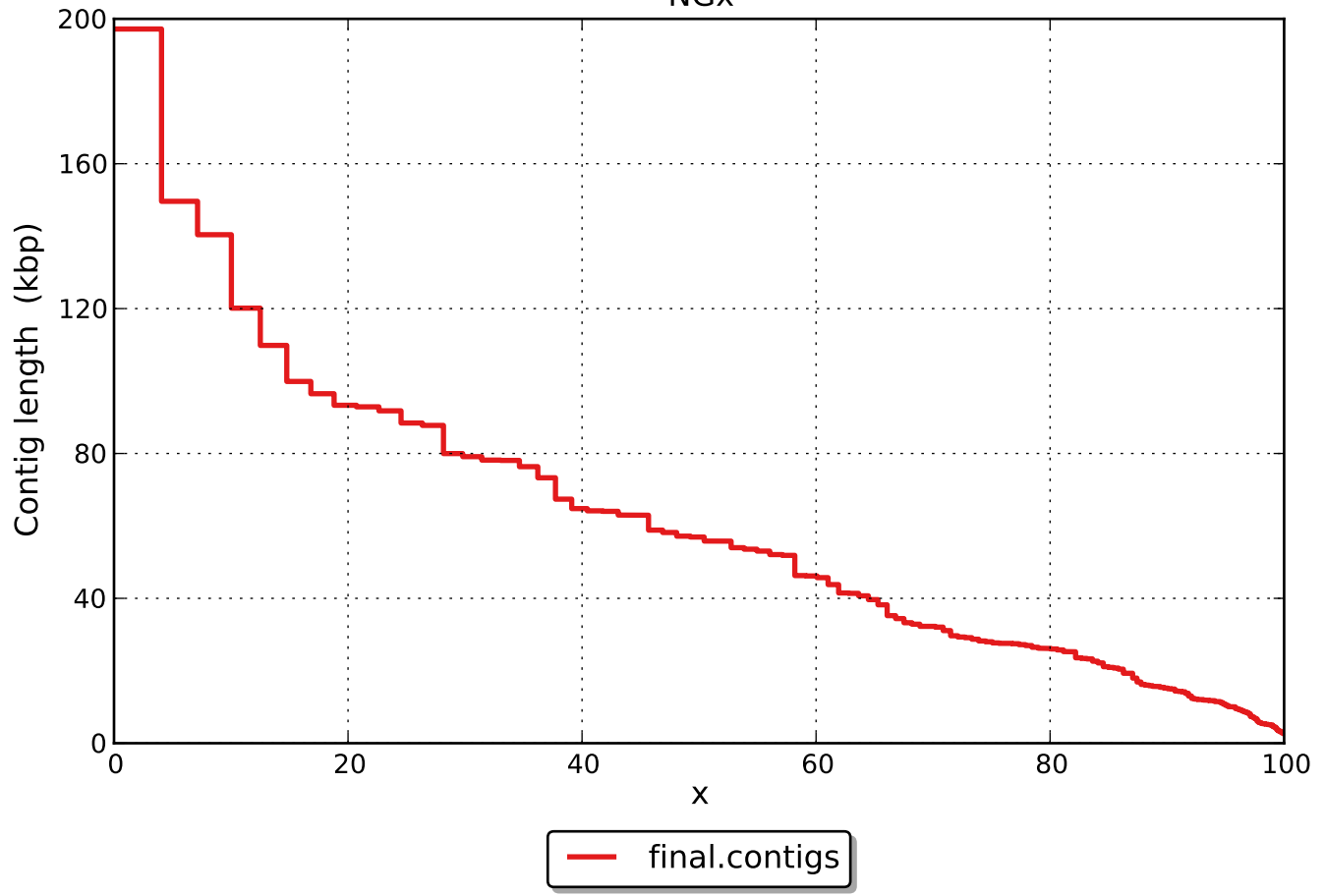
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

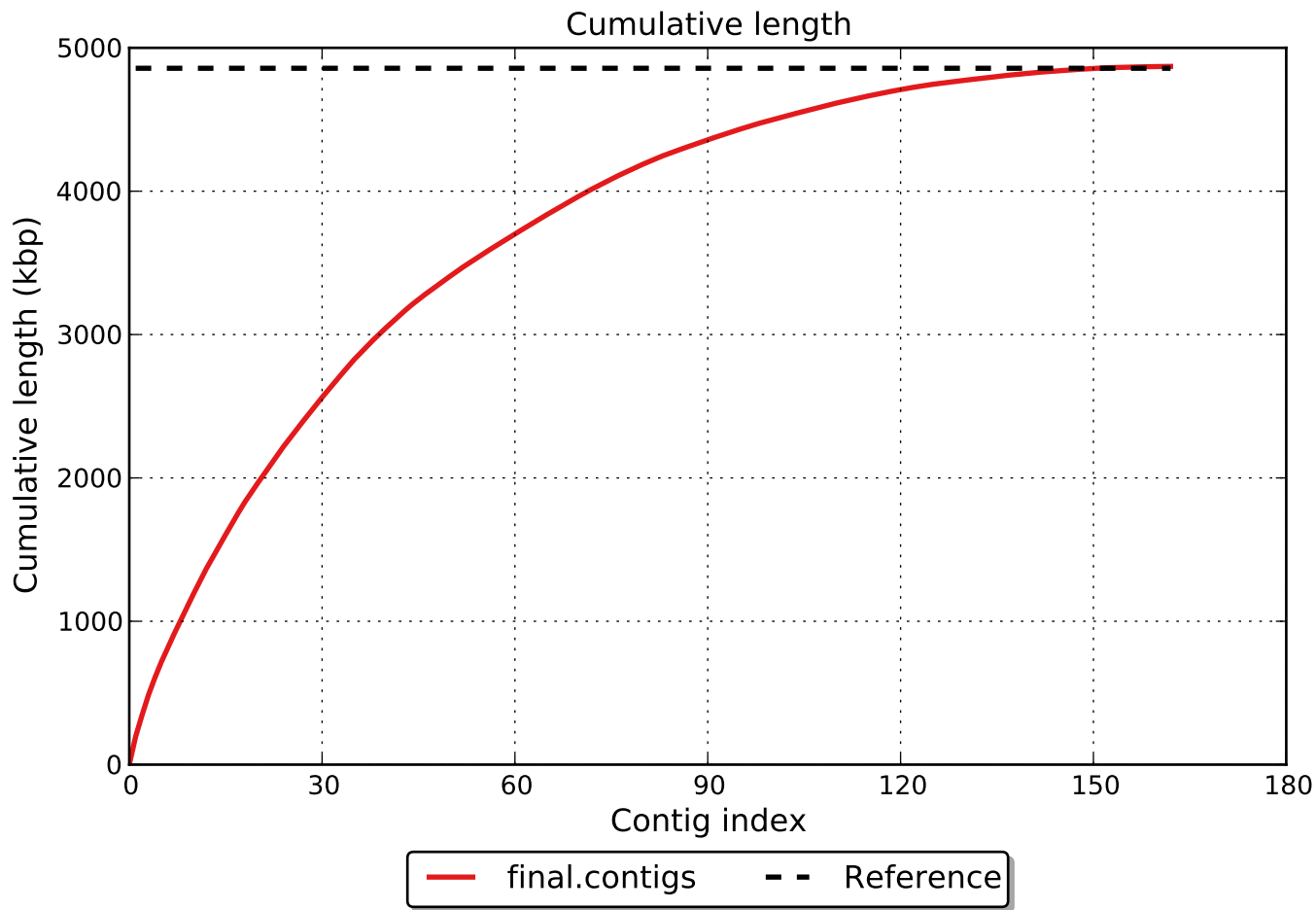
Nx



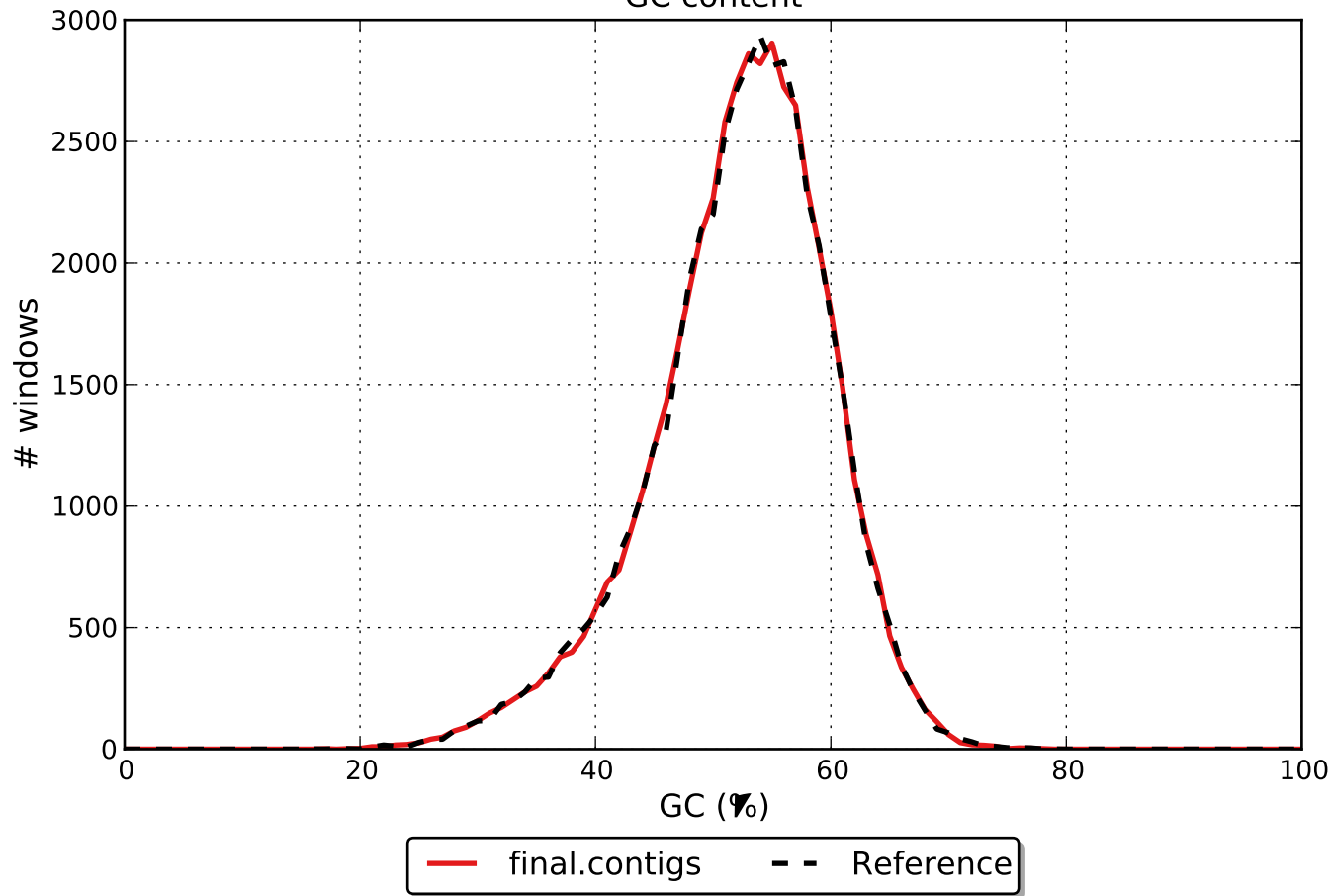
— final.contigs

NGx





GC content

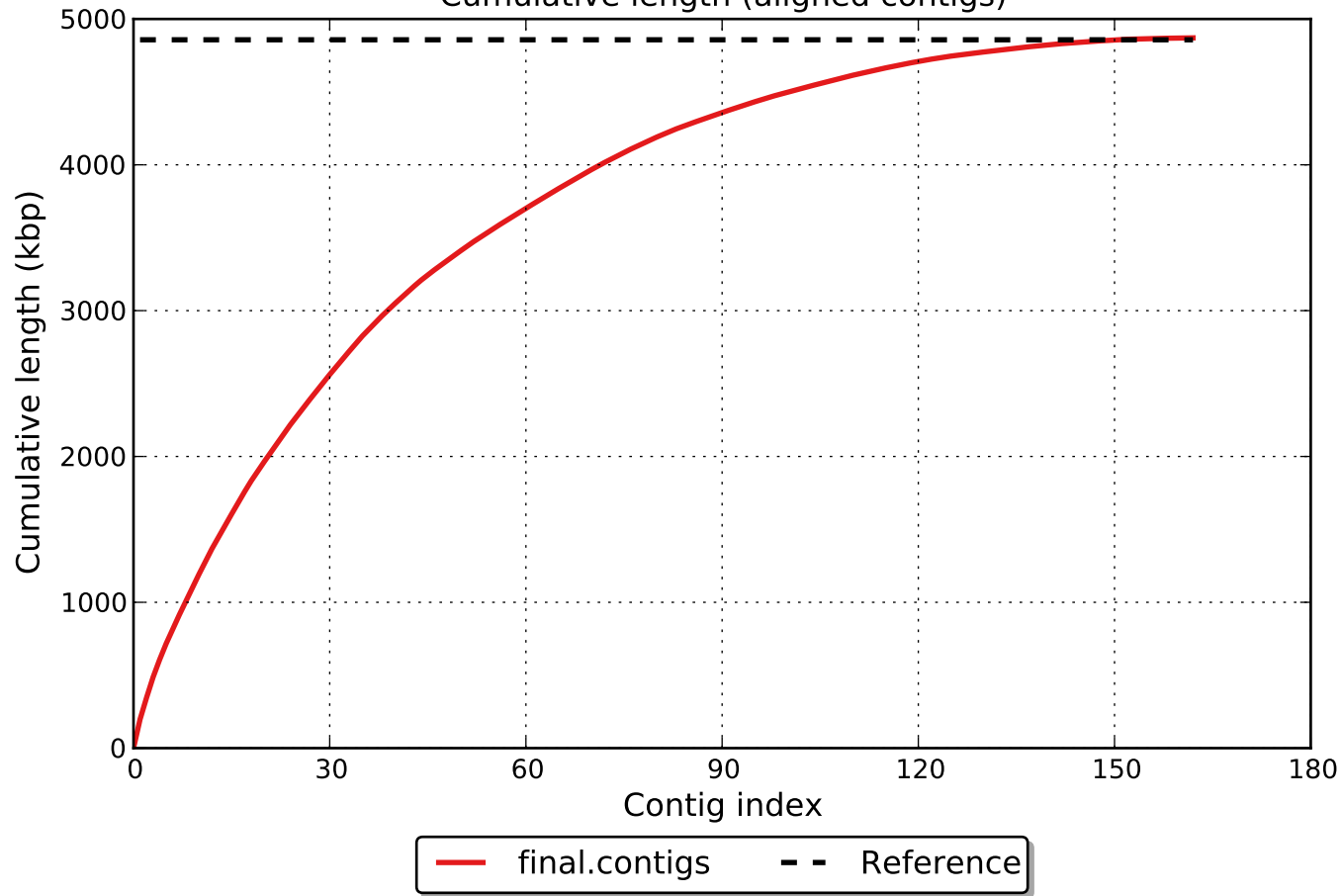


# Misassemblies

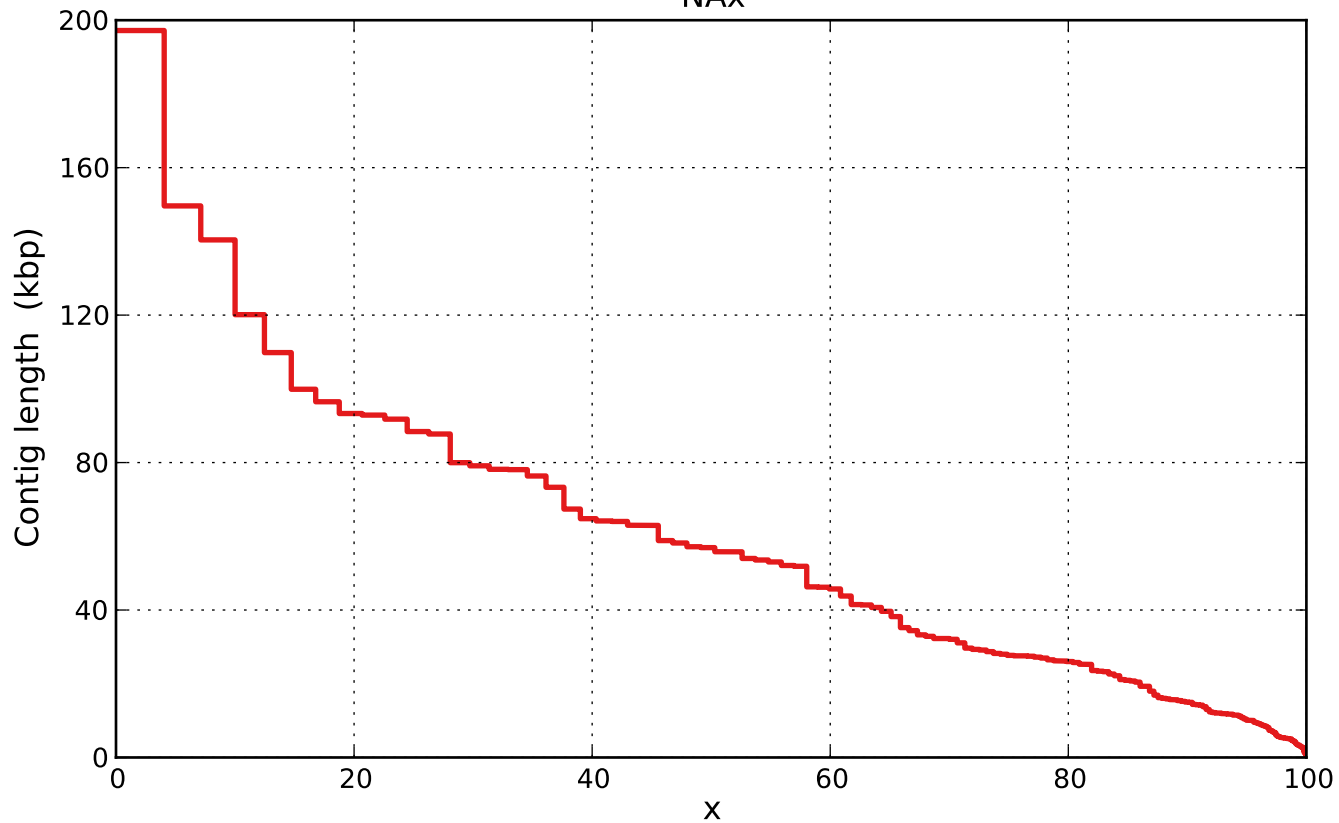




Cumulative length (aligned contigs)



NAx



— final.contigs

# NGAx

