

Report

	final.contigs
# contigs (>= 1000 bp)	1596
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2452035
Total length (>= 5000 bp)	5476
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4043
Largest contig	5476
Total length	4204538
Reference length	4641652
GC (℥)	50.80
Reference GC (℥)	50.78
N50	1123
NG50	1039
N75	790
NG75	699
L50	1265
LG50	1468
L75	2386
LG75	2827
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	3047
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	85.913
Duplication ratio	1.054
# N's per 100 kbp	0.00
# mismatches per 100 kbp	83.13
# indels per 100 kbp	0.00
Largest alignment	5476
NA50	1123
NGA50	1039
NA75	790
NGA75	699
LA50	1266
LGA50	1469
LA75	2387
LGA75	2828

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

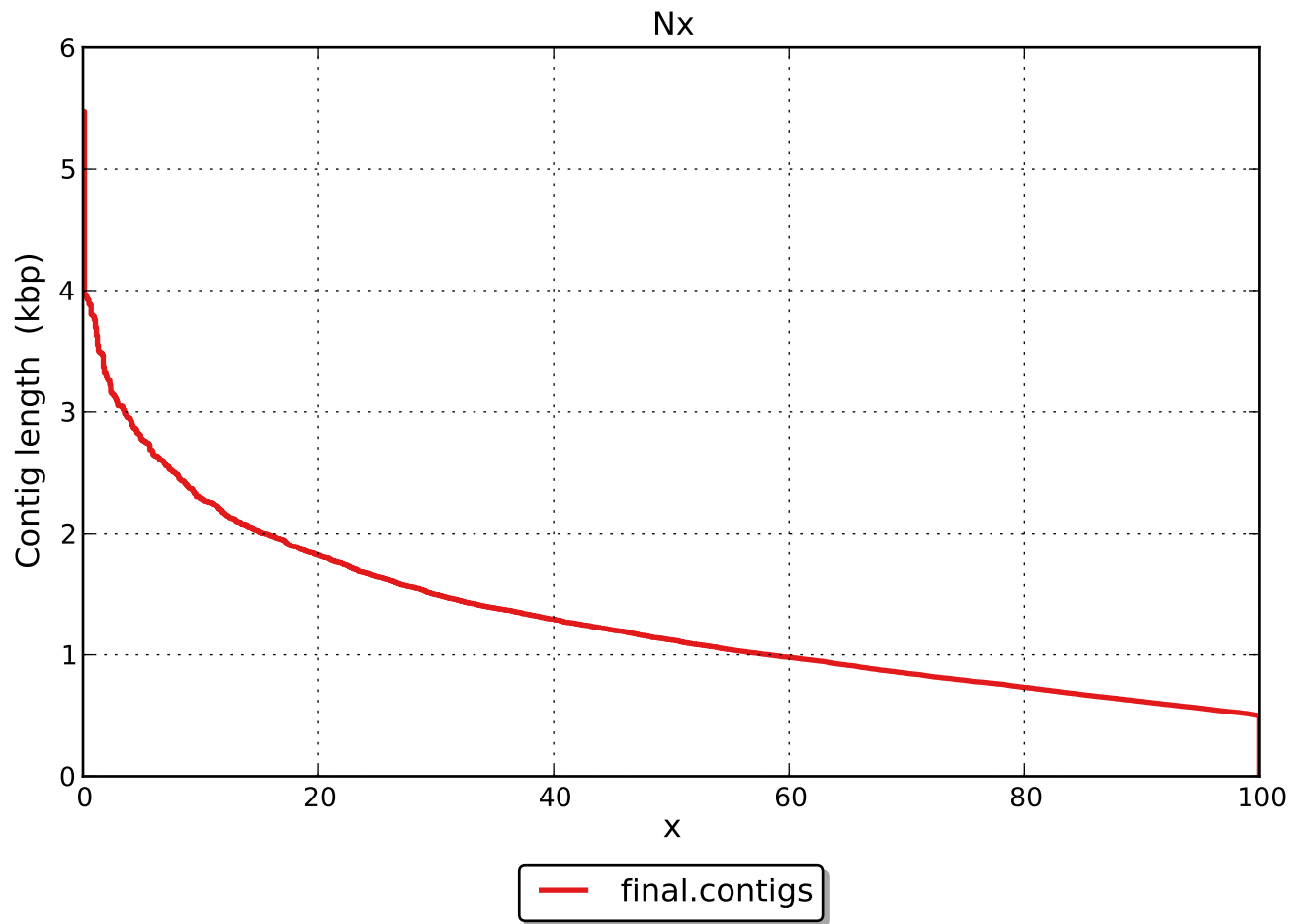
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	3047
# local misassemblies	0
# mismatches	3315
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

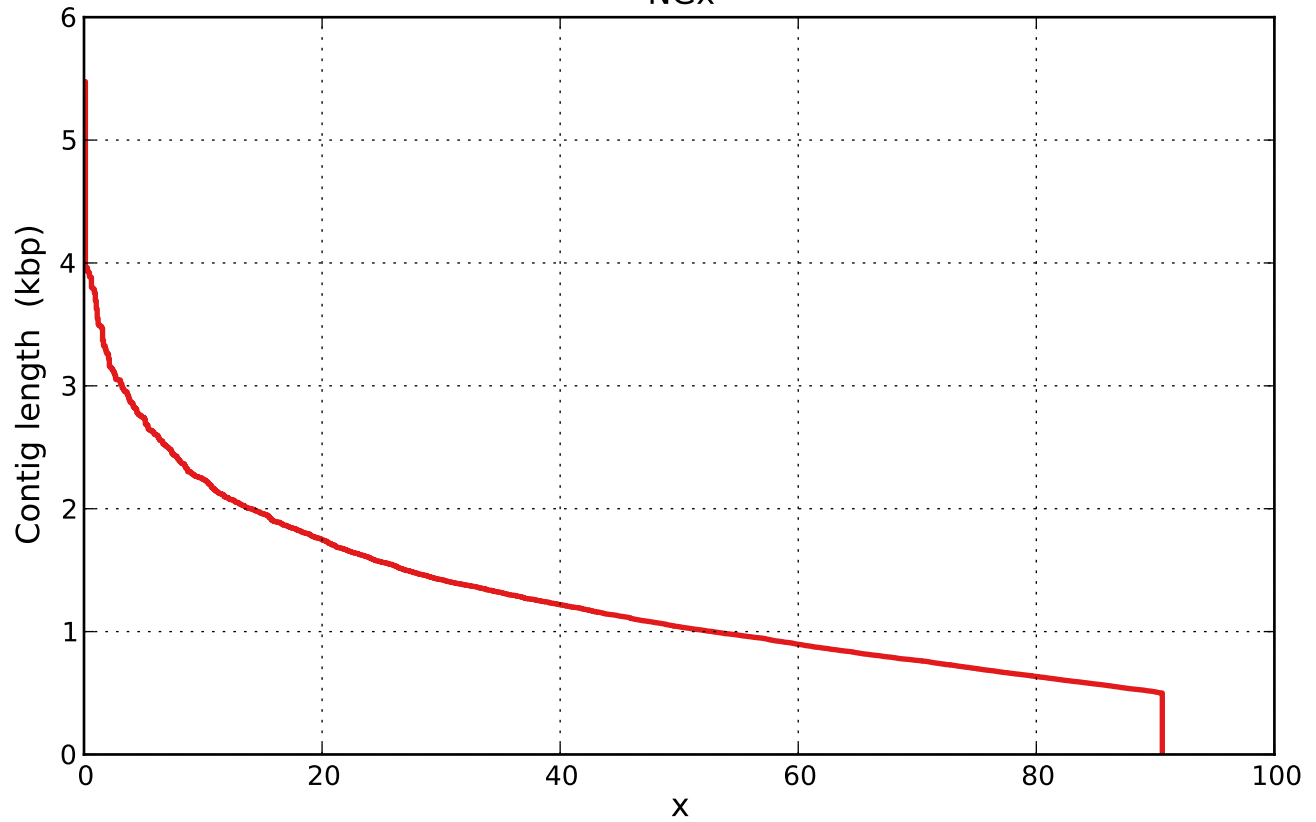
## Unaligned report

	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

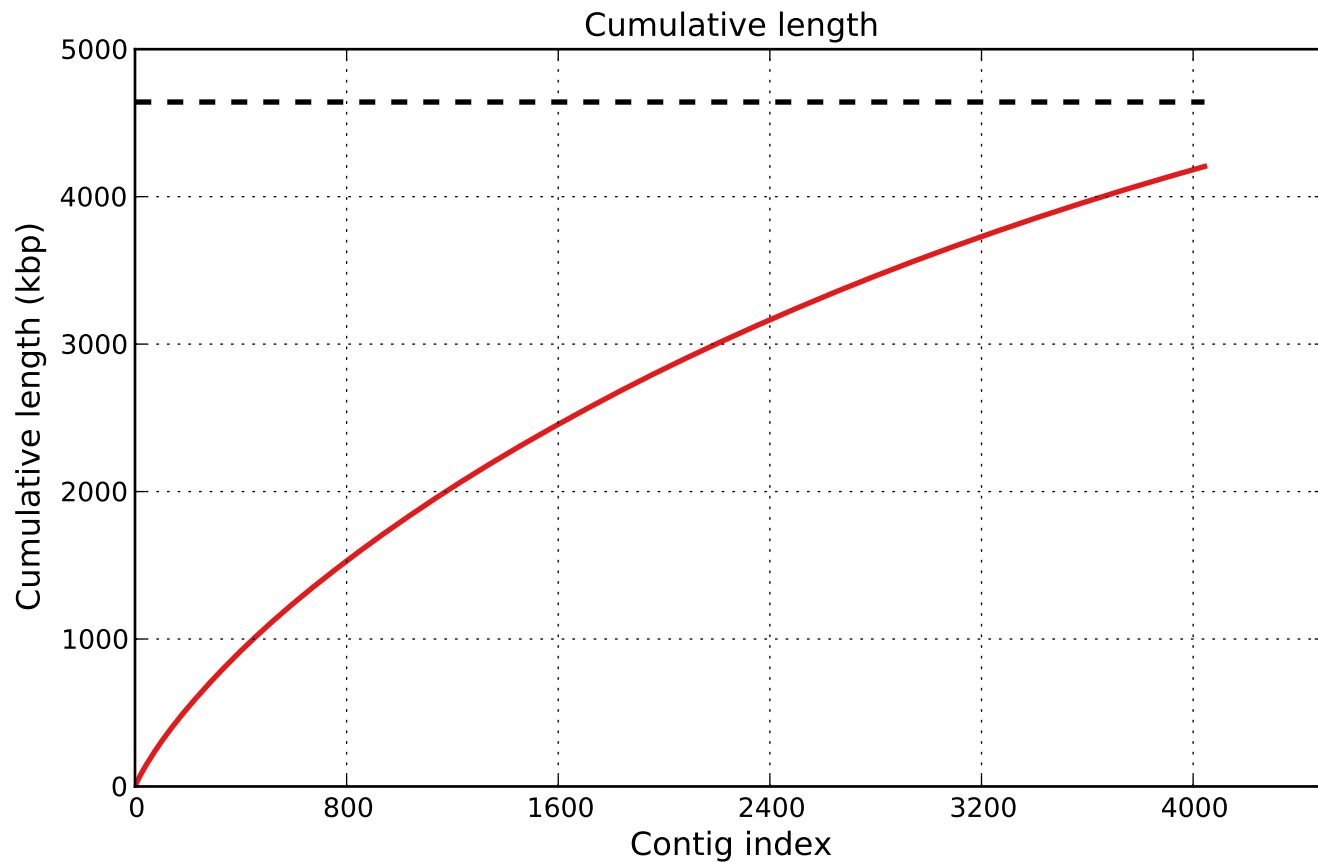
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



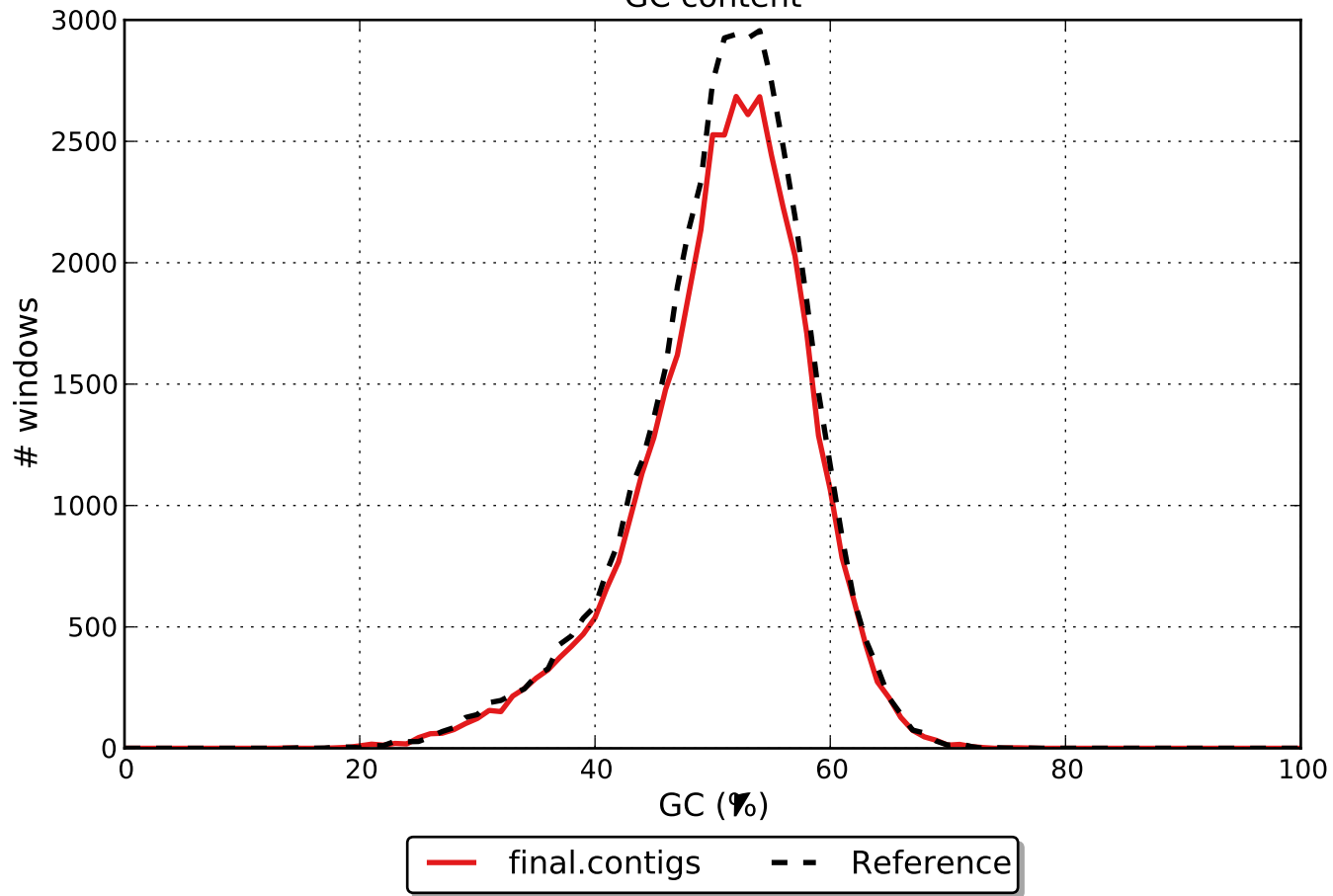
NGx



— final.contigs



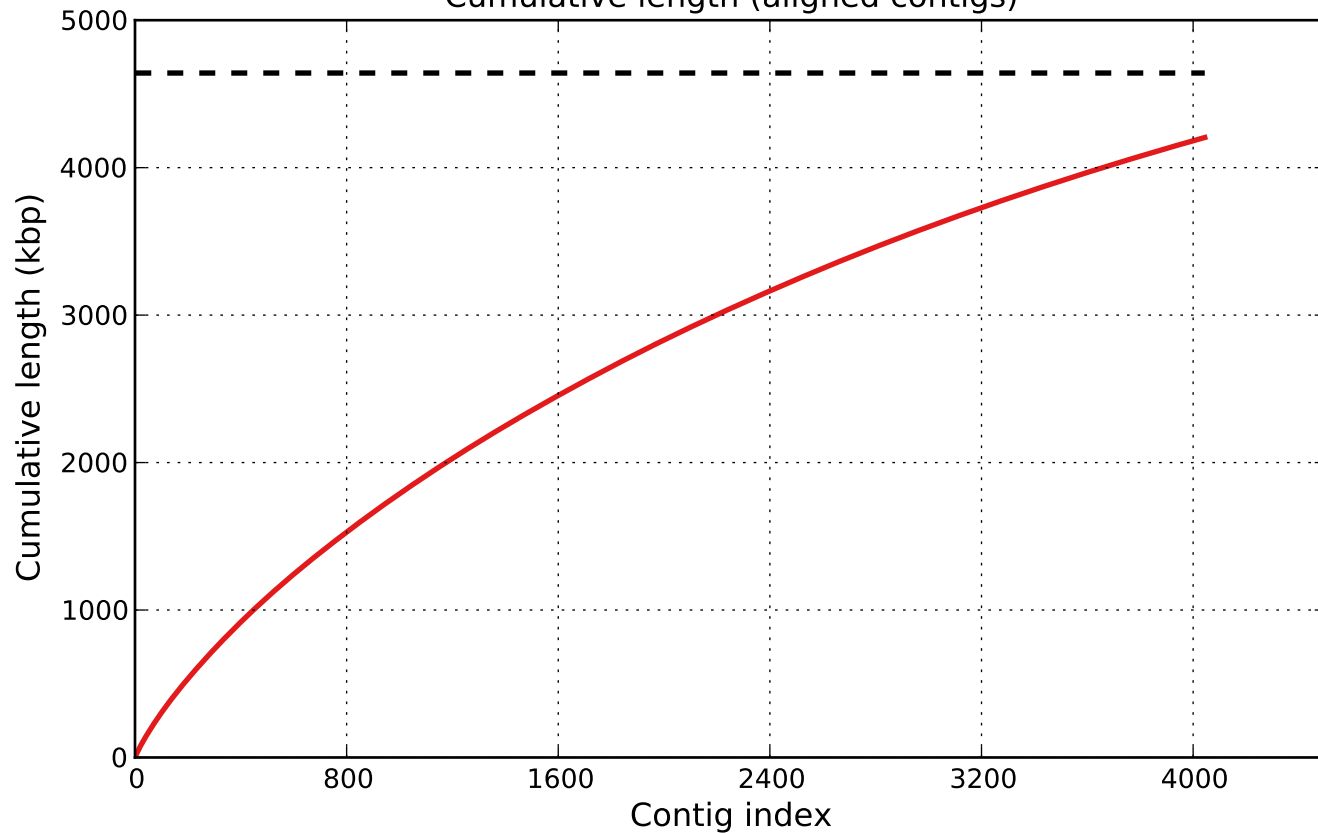
# GC content



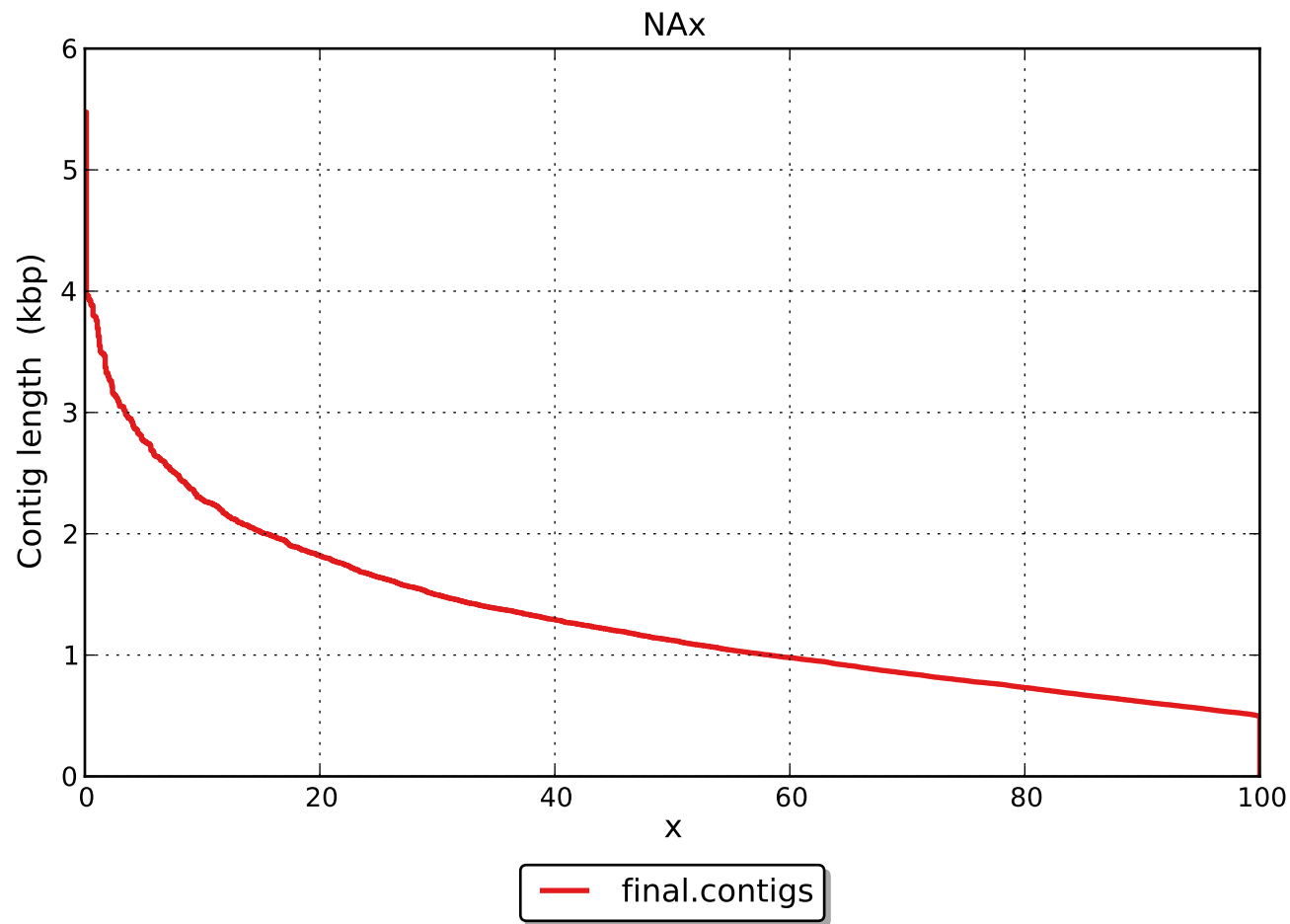




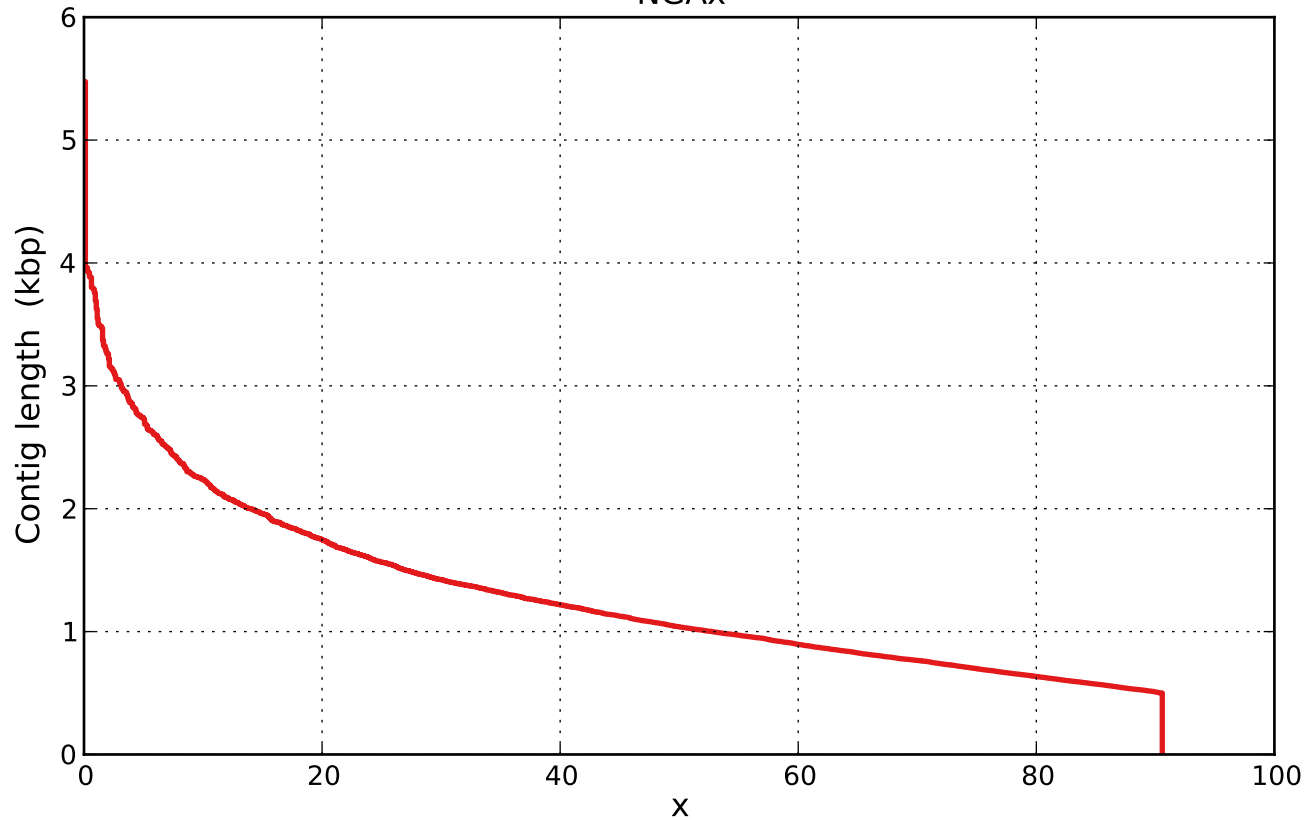
Cumulative length (aligned contigs)



— final.contigs      - - Reference



NGAx



— final.contigs