

Report

	final.contigs
# contigs (>= 1000 bp)	1552
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2384346
Total length (>= 5000 bp)	5476
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3902
Largest contig	5476
Total length	4069554
Reference length	4641652
GC (℥)	50.77
Reference GC (℥)	50.78
N50	1126
NG50	1018
N75	792
NG75	667
L50	1222
LG50	1490
L75	2302
LG75	2891
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	3047
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	83.811
Duplication ratio	1.046
# N's per 100 kbp	0.00
# mismatches per 100 kbp	49.20
# indels per 100 kbp	0.00
Largest alignment	5476
NA50	1126
NGA50	1018
NA75	792
NGA75	667
LA50	1223
LGA50	1490
LA75	2303
LGA75	2892

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

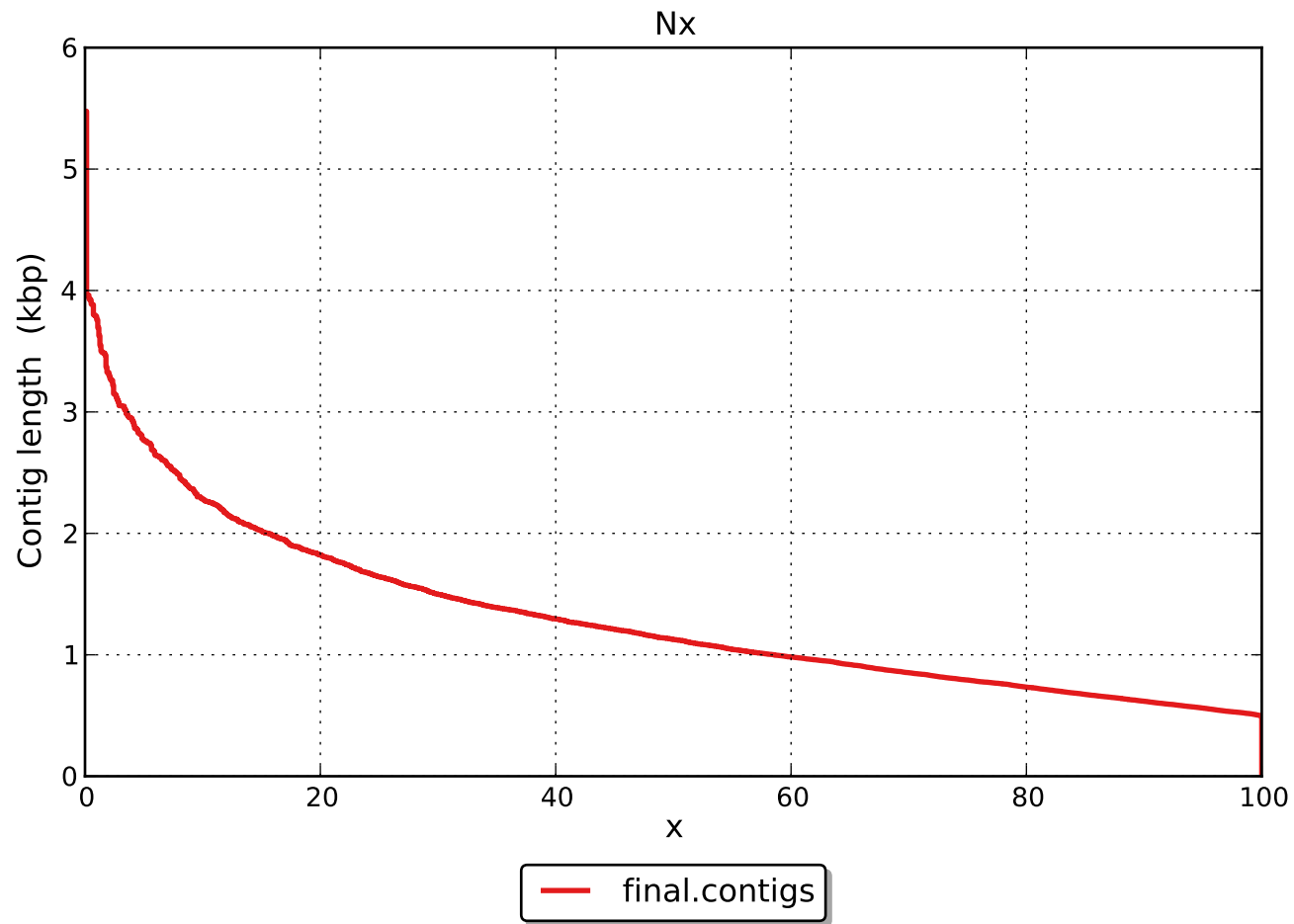
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	3047
# local misassemblies	0
# mismatches	1914
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

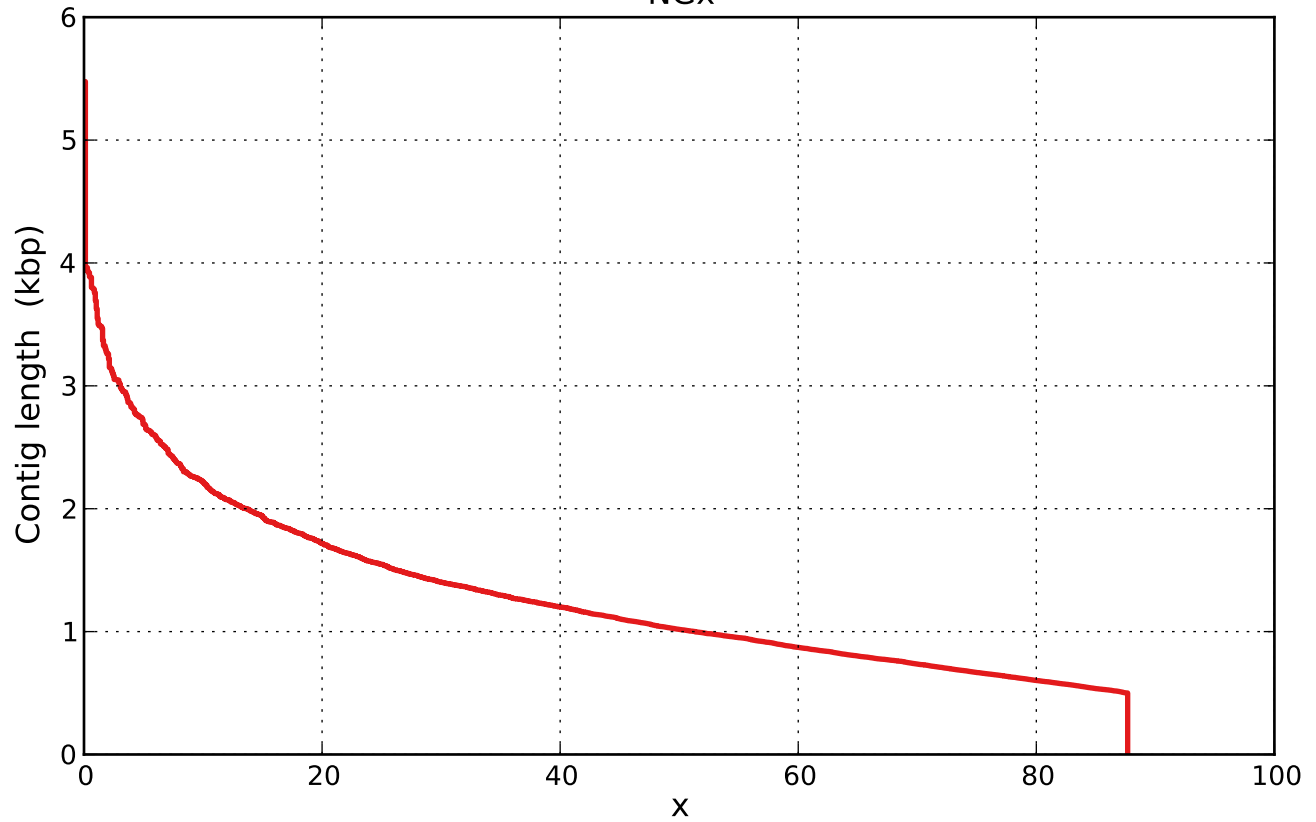
## Unaligned report

	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

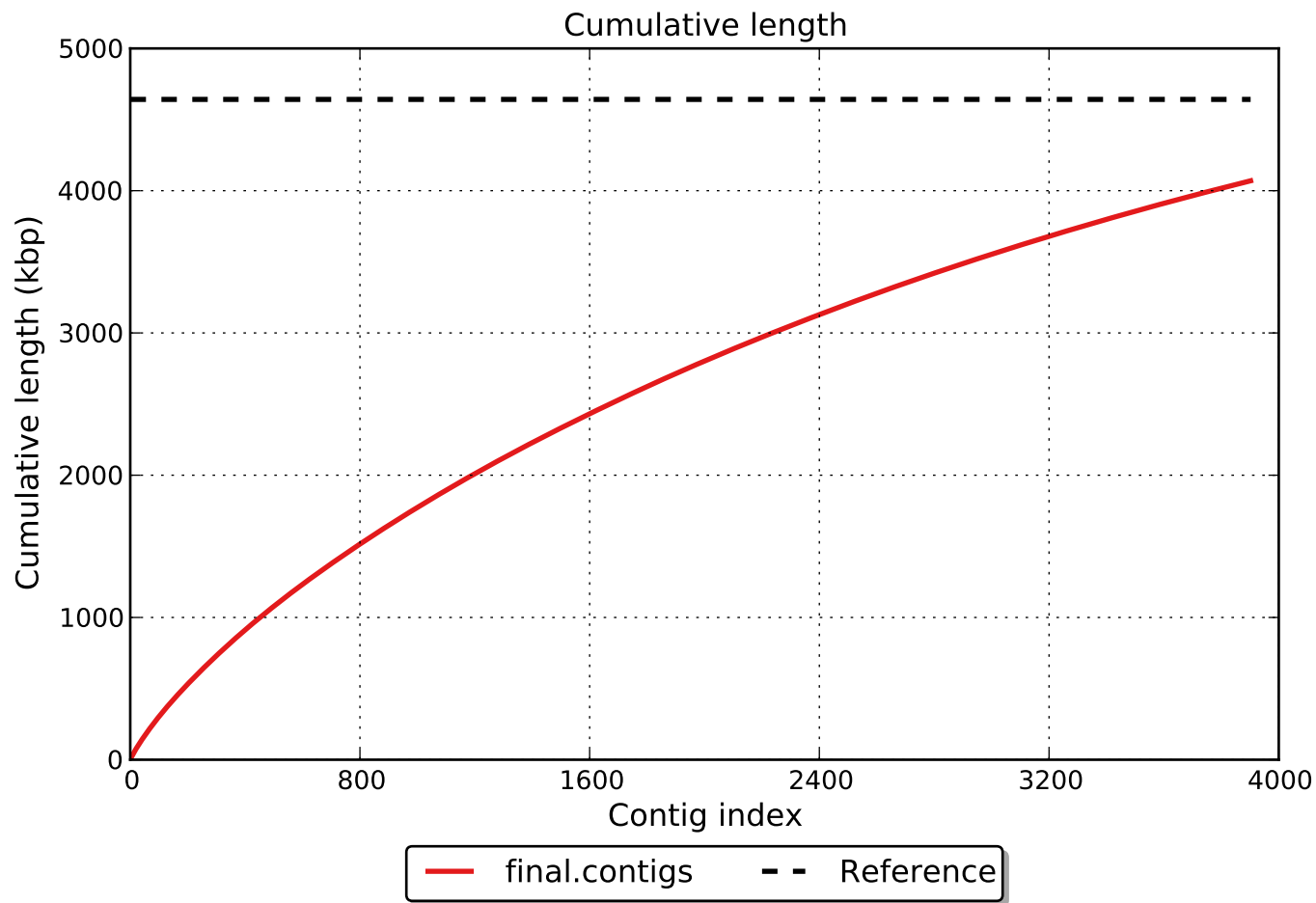
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



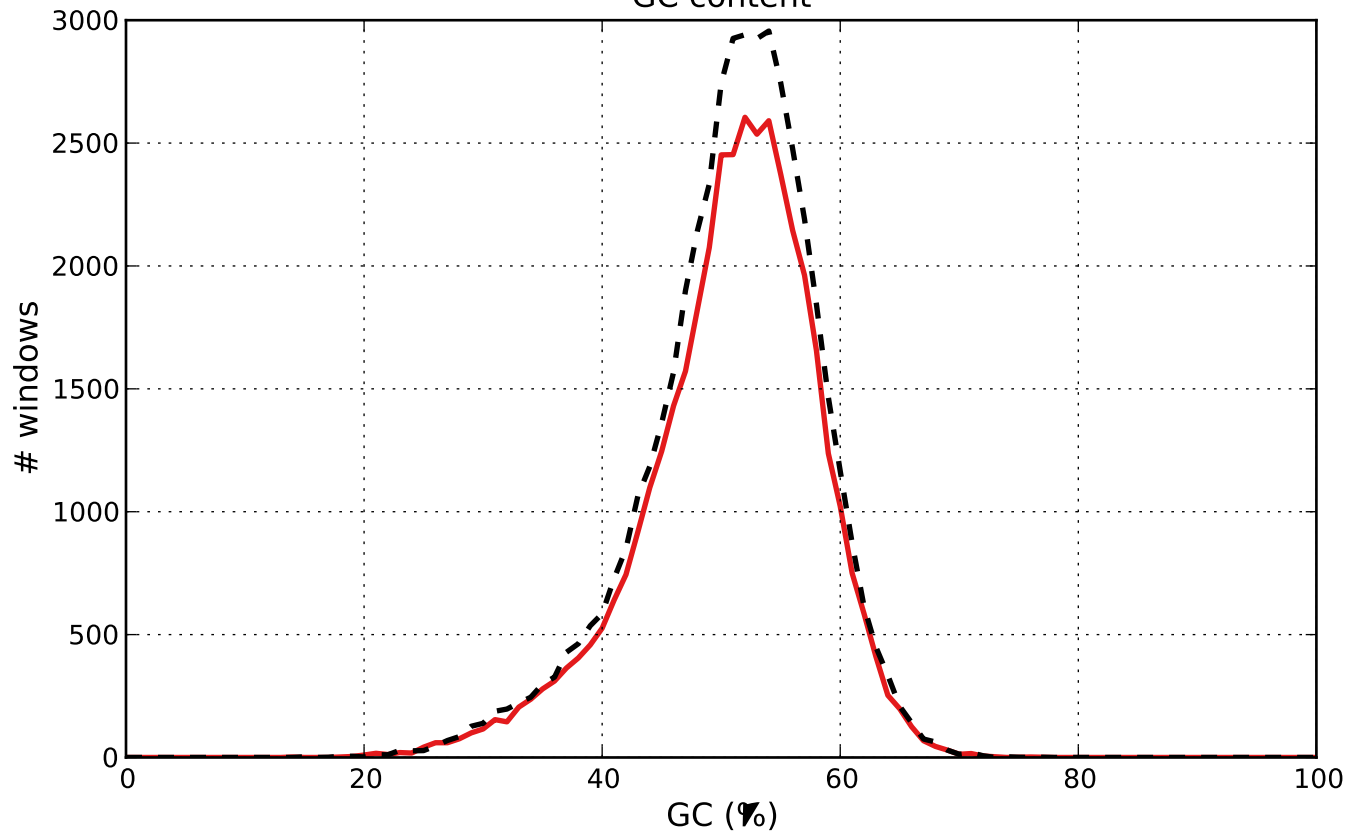
NGx



— final.contigs



GC content

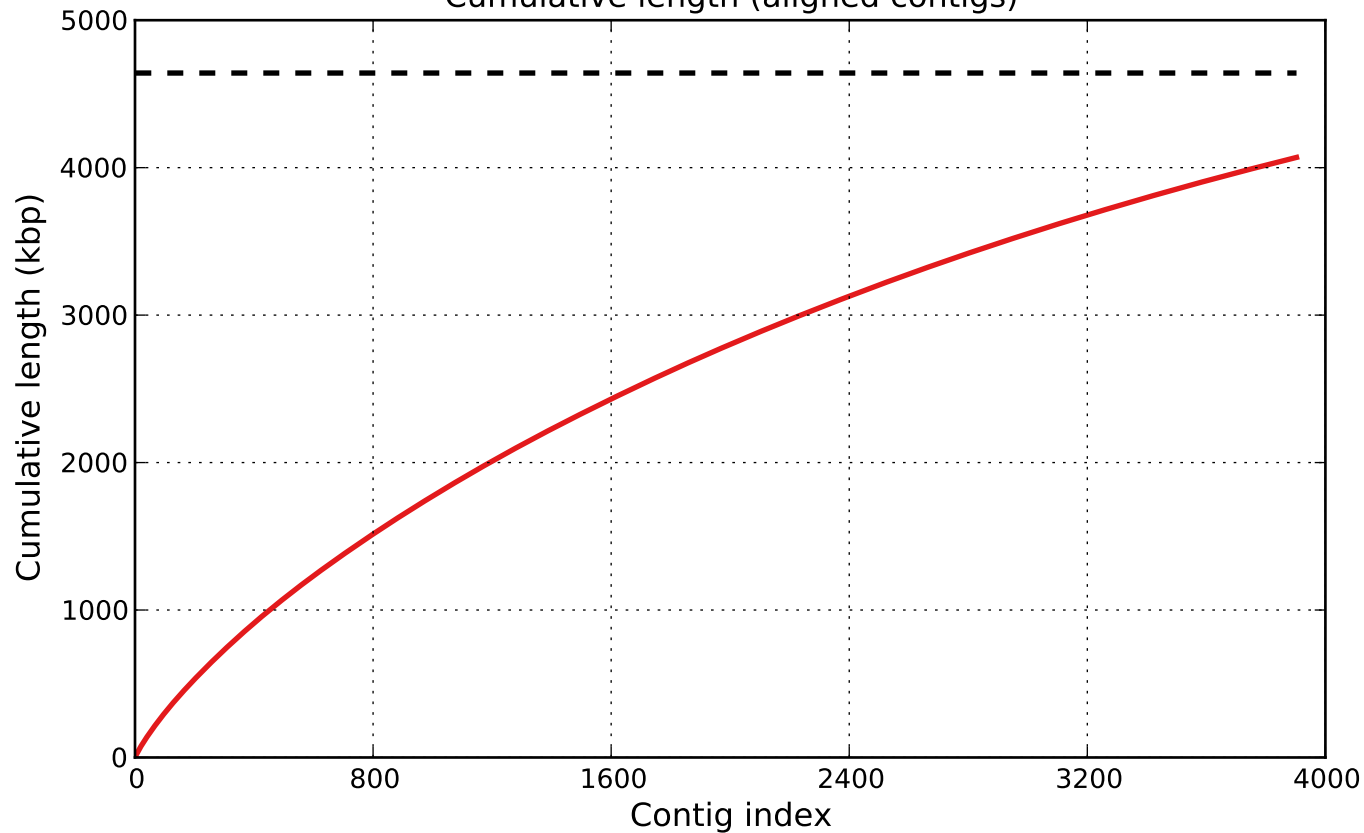


— final.contigs    - - Reference

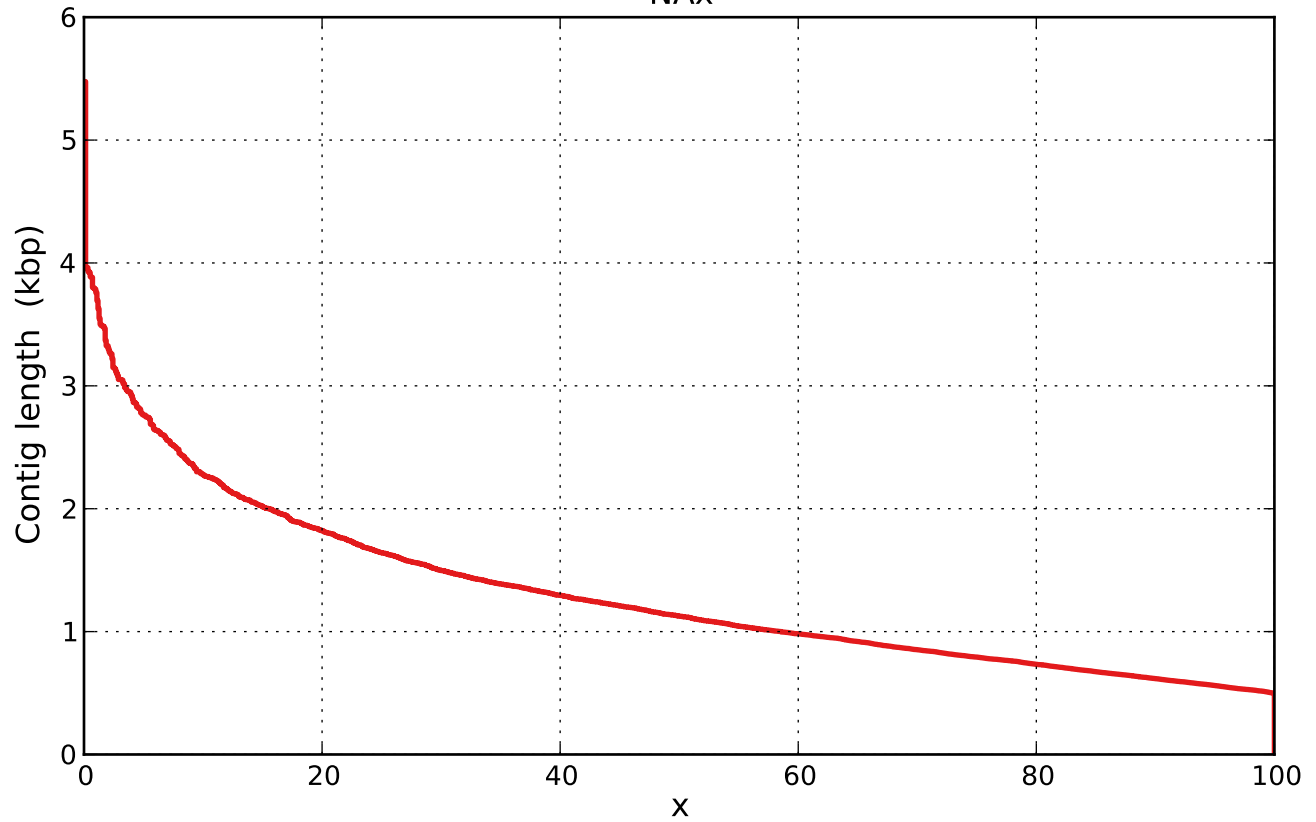




Cumulative length (aligned contigs)

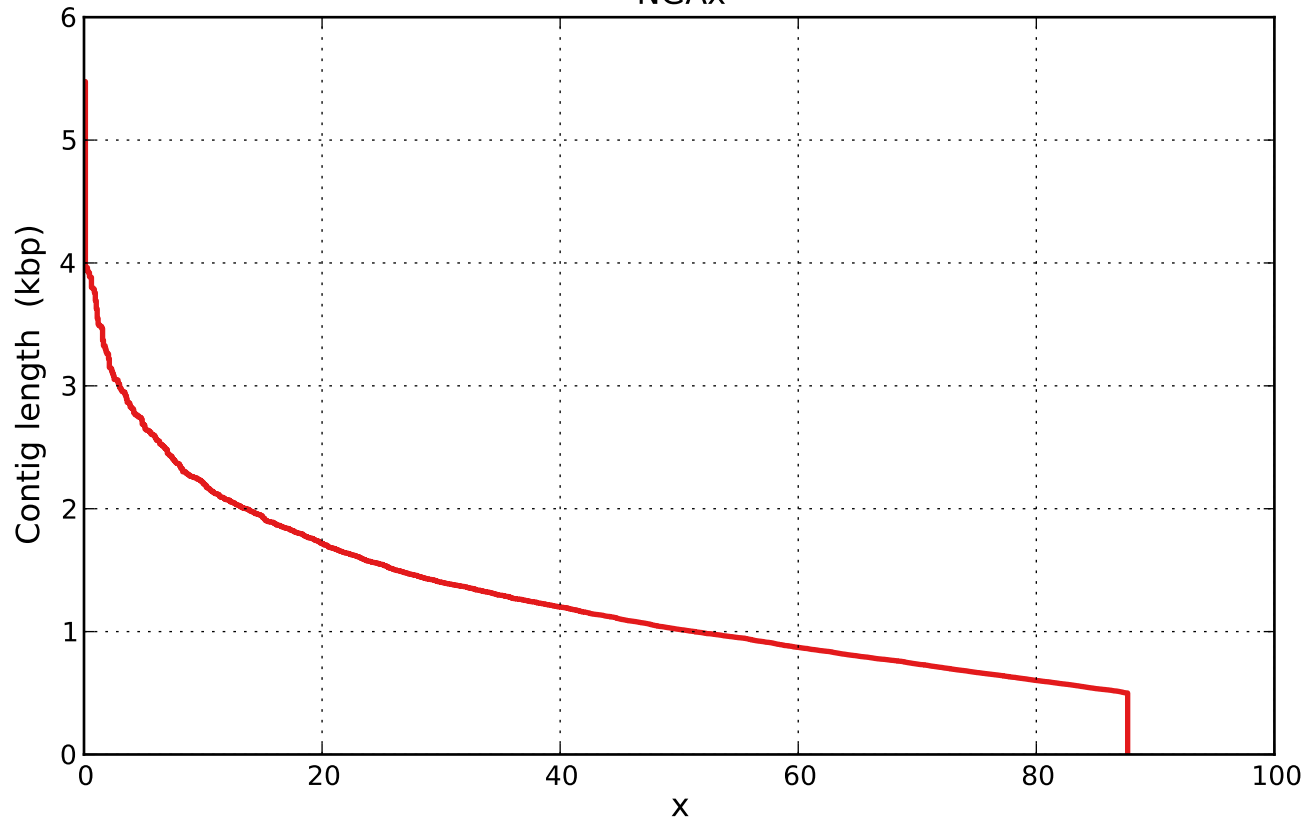


NAx



— final.contigs

NGAx



— final.contigs