

Report

	final.contigs
# contigs (>= 1000 bp)	349
# contigs (>= 5000 bp)	249
# contigs (>= 10000 bp)	158
# contigs (>= 25000 bp)	49
# contigs (>= 50000 bp)	12
Total length (>= 1000 bp)	4797231
Total length (>= 5000 bp)	4493113
Total length (>= 10000 bp)	3817292
Total length (>= 25000 bp)	2127001
Total length (>= 50000 bp)	818837
# contigs	382
Largest contig	102285
Total length	4820882
Reference length	4857432
GC (℥)	52.20
Reference GC (℥)	52.22
N50	21355
NG50	21273
N75	11390
NG75	11007
L50	62
LG50	63
L75	139
LG75	142
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	98.666
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.29
# indels per 100 kbp	0.00
Largest alignment	102285
NA50	21355
NGA50	21273
NA75	11390
NGA75	11007
LA50	62
LGA50	63
LA75	139
LGA75	142

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	62
# indels	0
# short indels	0
# long indels	0
Indels length	0

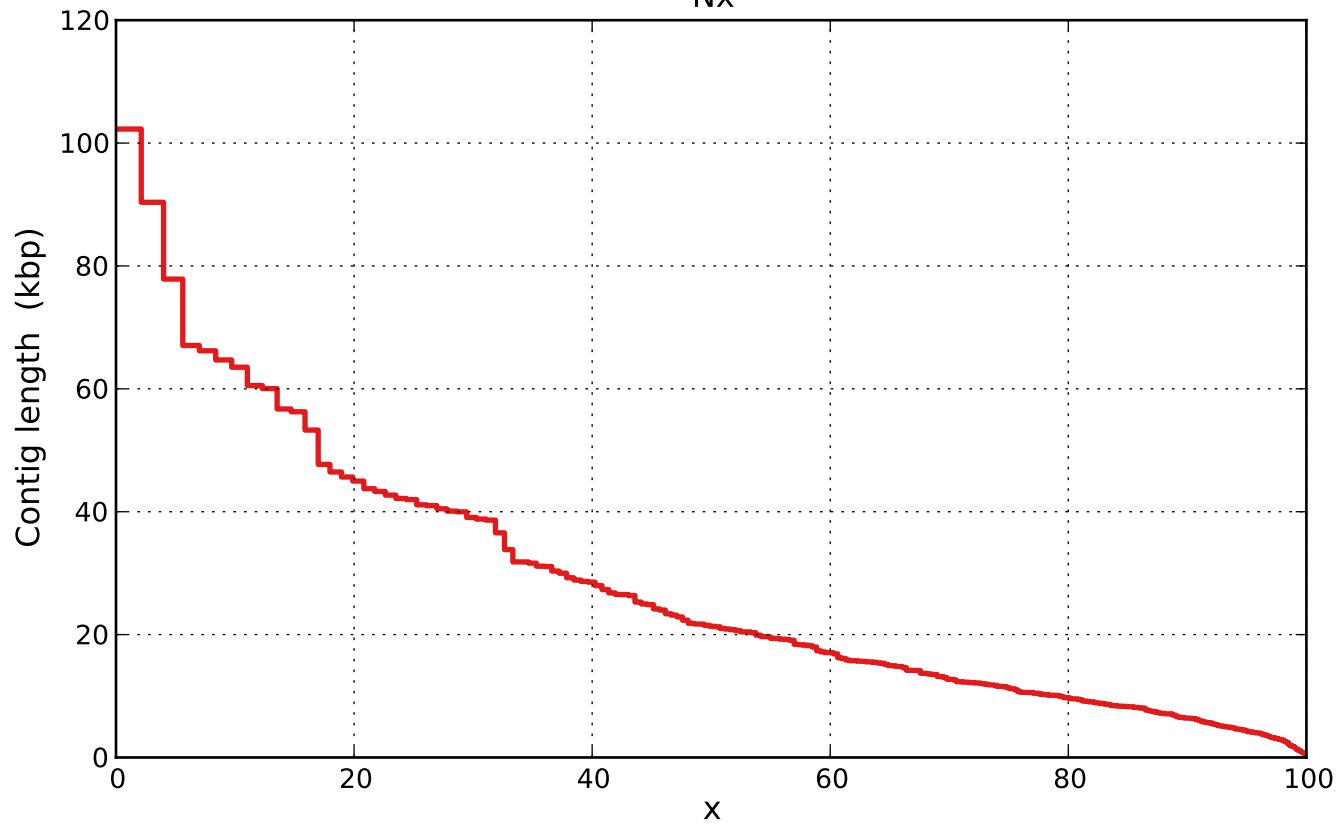
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## 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

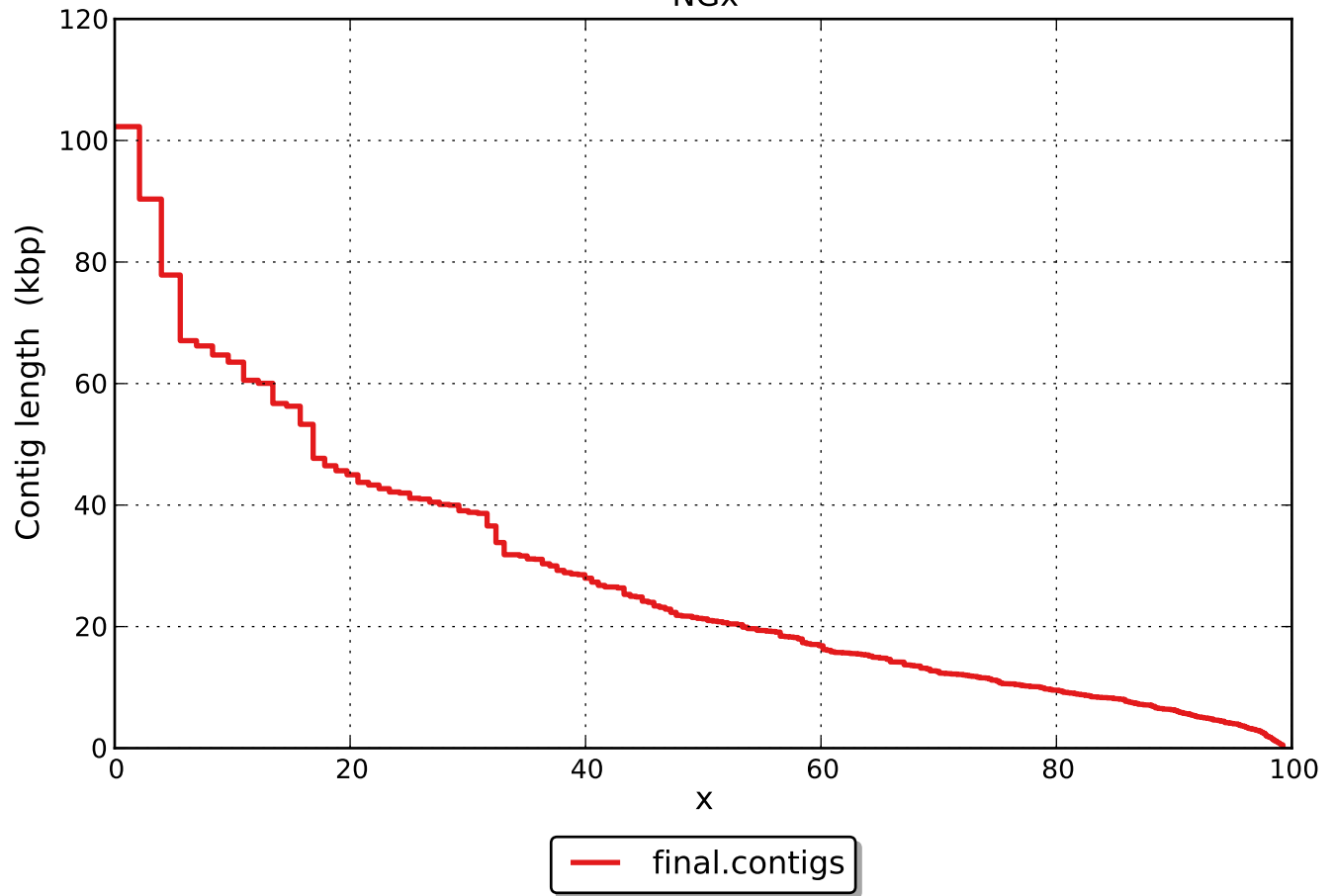
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

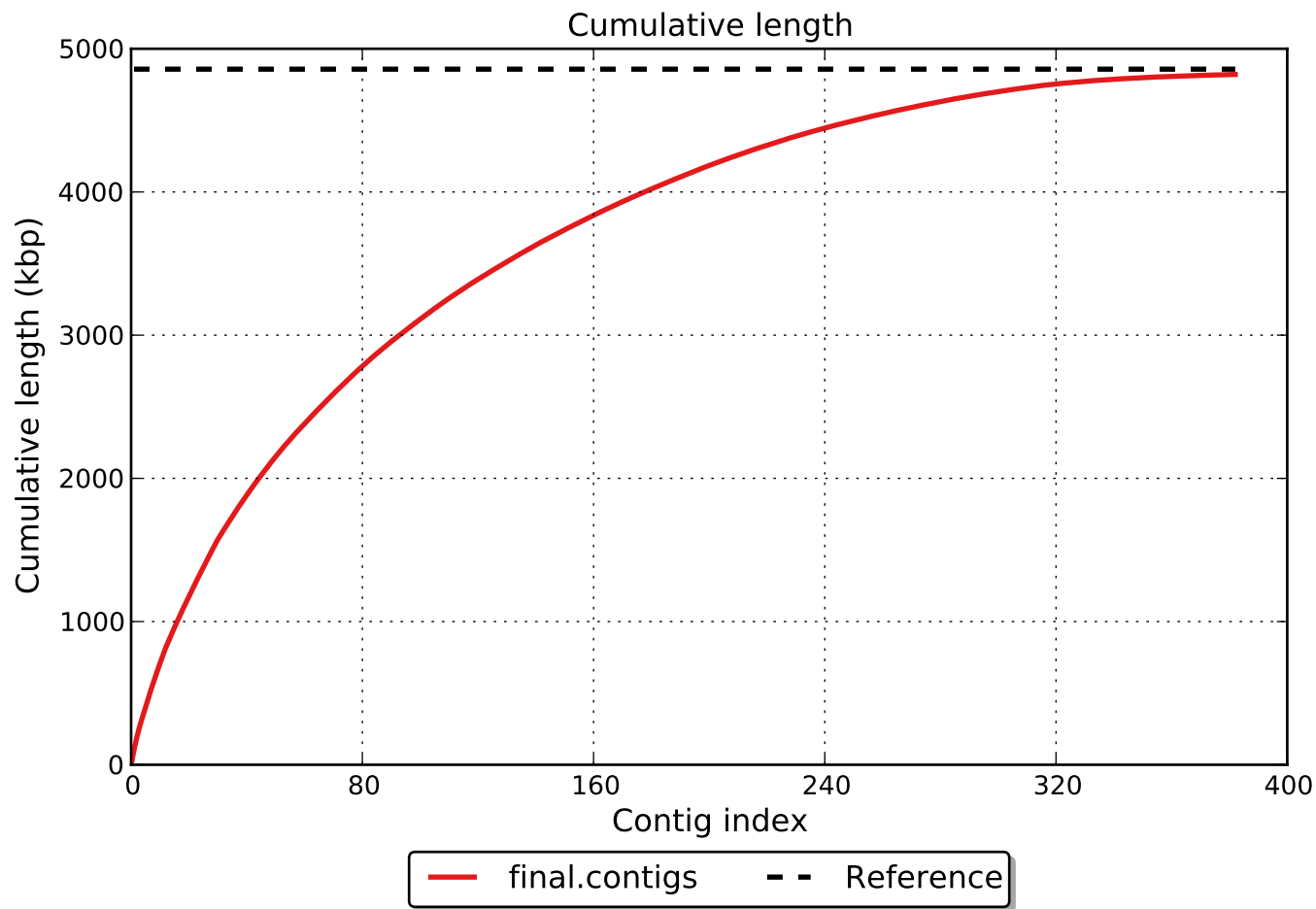
Nx



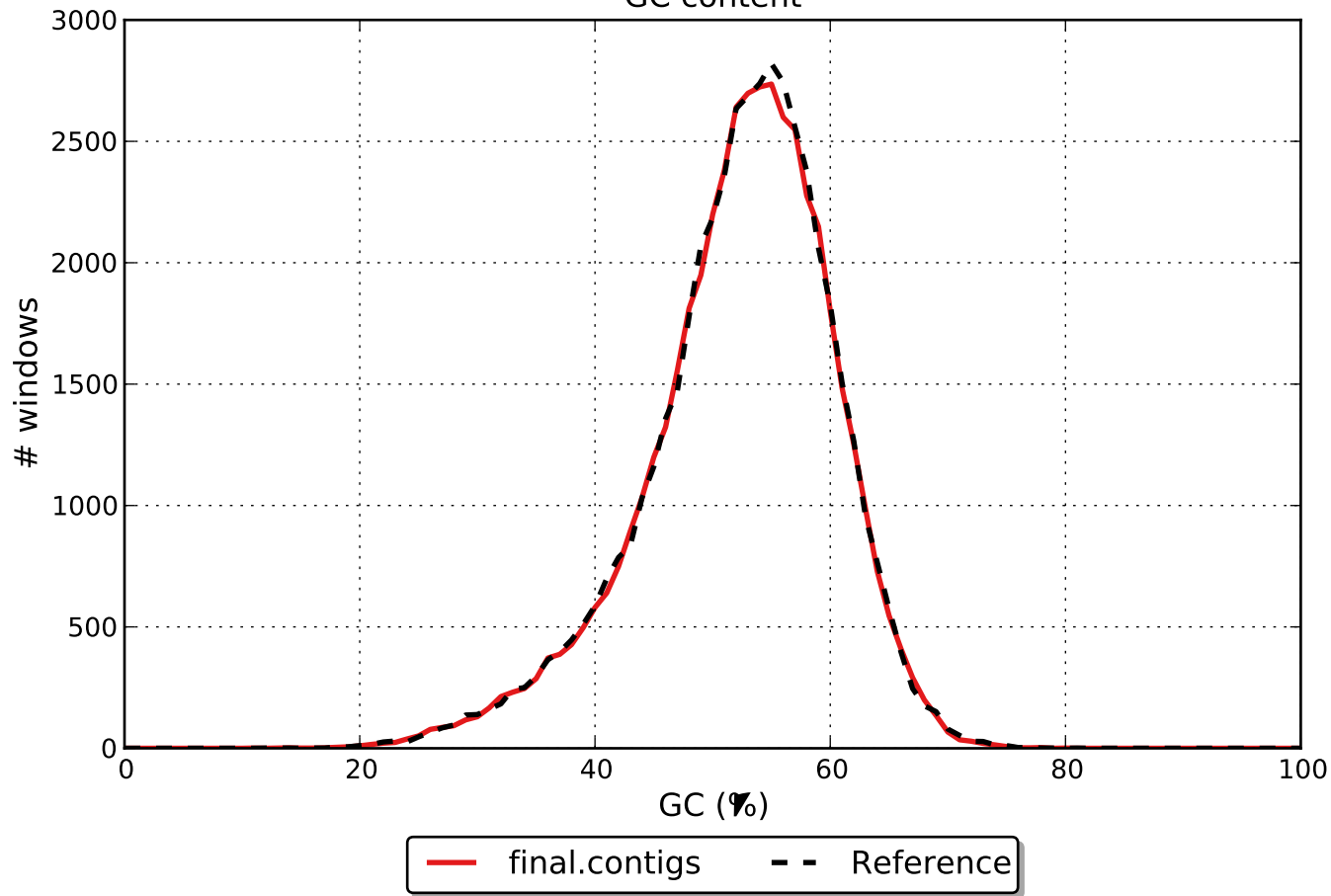
— final.contigs

NGx





GC content

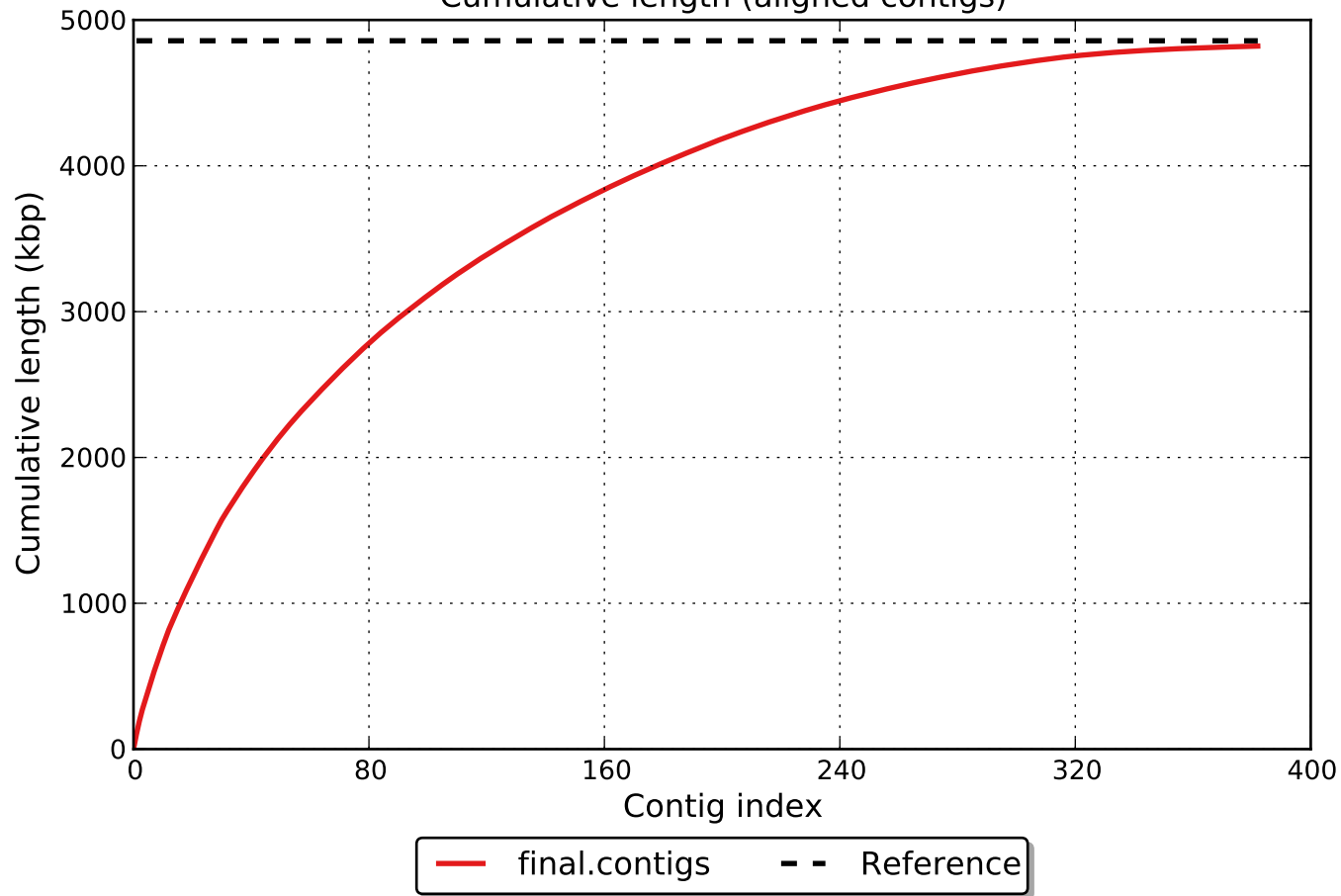


# Misassemblies

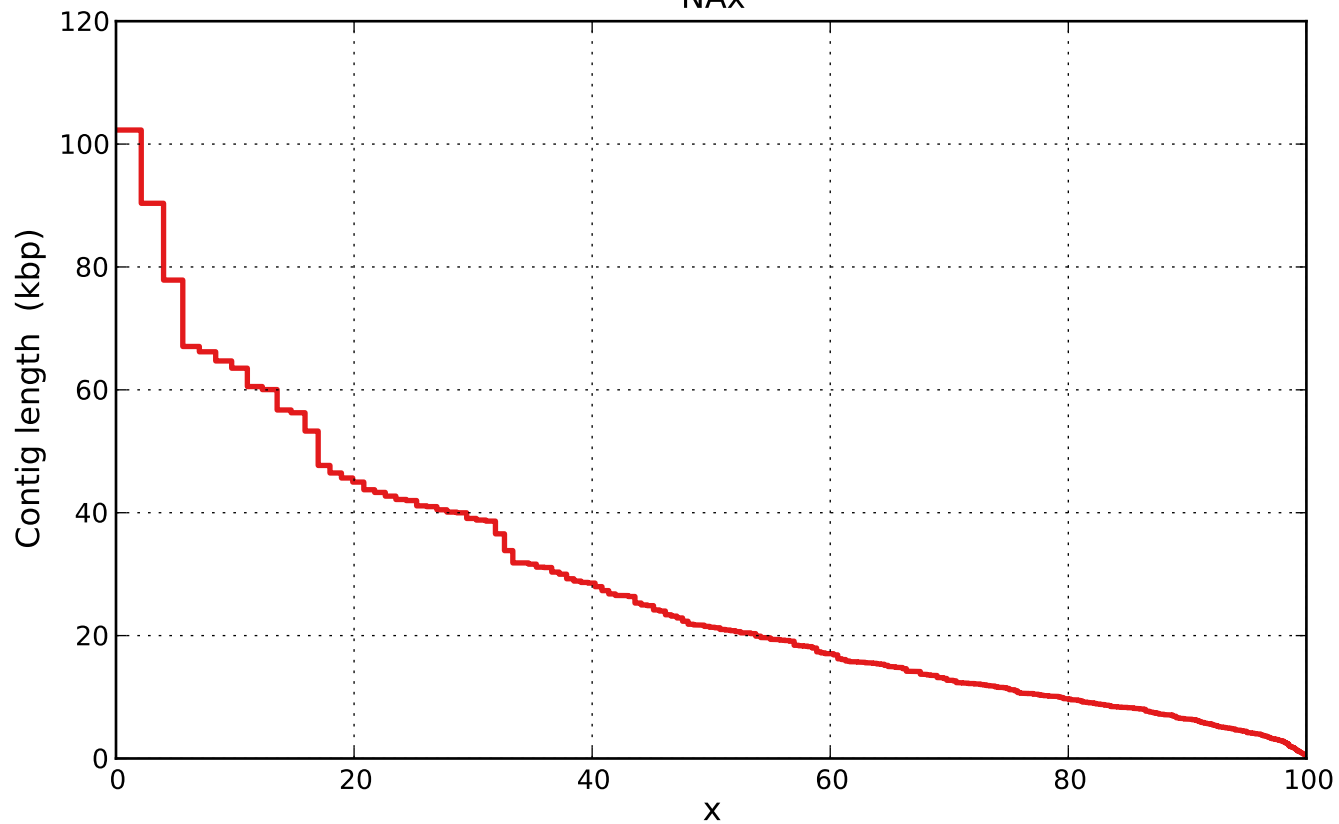




Cumulative length (aligned contigs)

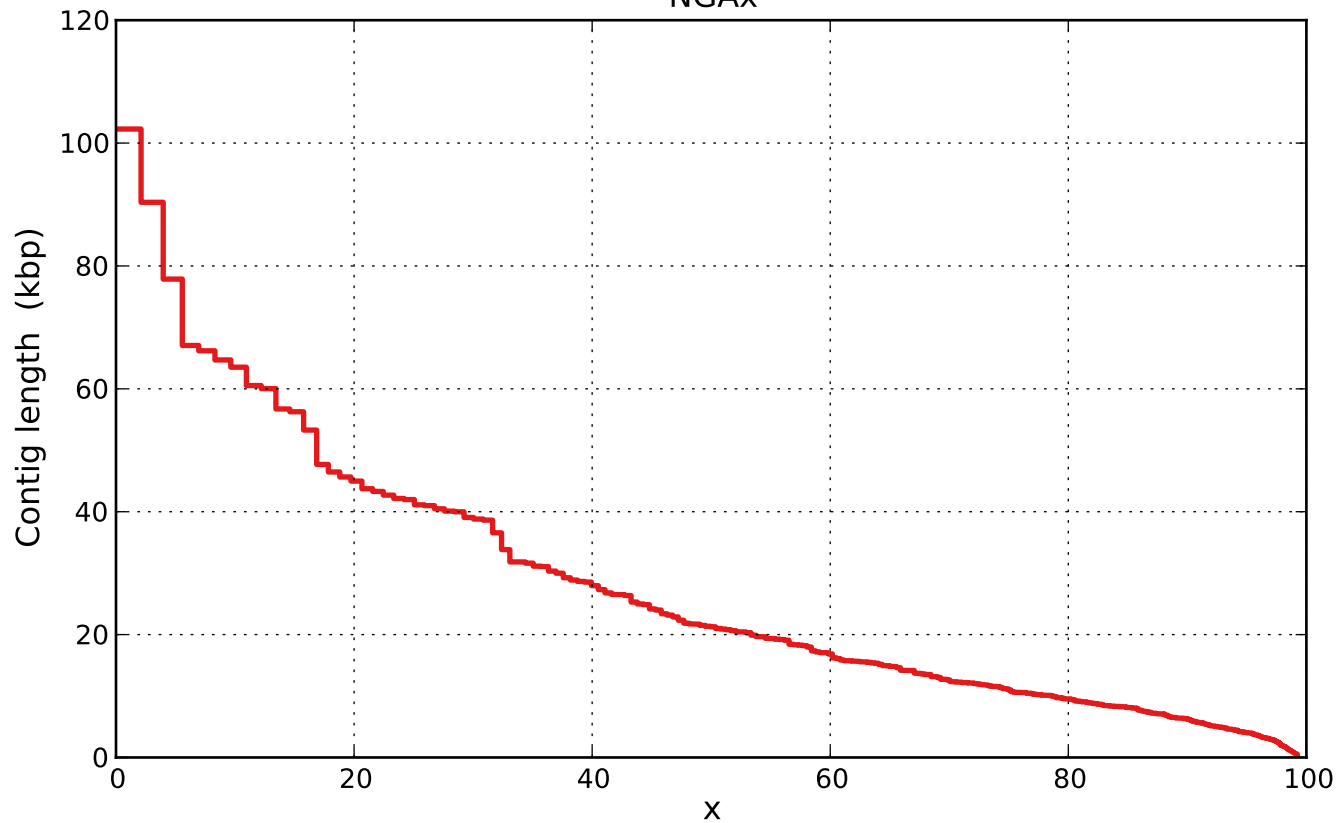


NAx



— final.contigs

NGAx



— final.contigs