

Report

	final.contigs
# contigs (>= 1000 bp)	222
# contigs (>= 5000 bp)	170
# contigs (>= 10000 bp)	139
# contigs (>= 25000 bp)	66
# contigs (>= 50000 bp)	28
Total length (>= 1000 bp)	4793470
Total length (>= 5000 bp)	4643409
Total length (>= 10000 bp)	4413299
Total length (>= 25000 bp)	3276605
Total length (>= 50000 bp)	1962347
# contigs	244
Largest contig	114100
Total length	4809387
Reference length	4857432
GC (℥)	52.20
Reference GC (℥)	52.22
N50	40414
NG50	40414
N75	19584
NG75	19258
L50	39
LG50	39
L75	82
LG75	84
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	98.673
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.27
# indels per 100 kbp	0.00
Largest alignment	114100
NA50	40414
NGA50	40414
NA75	19584
NGA75	19258
LA50	39
LGA50	39
LA75	82
LGA75	84

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

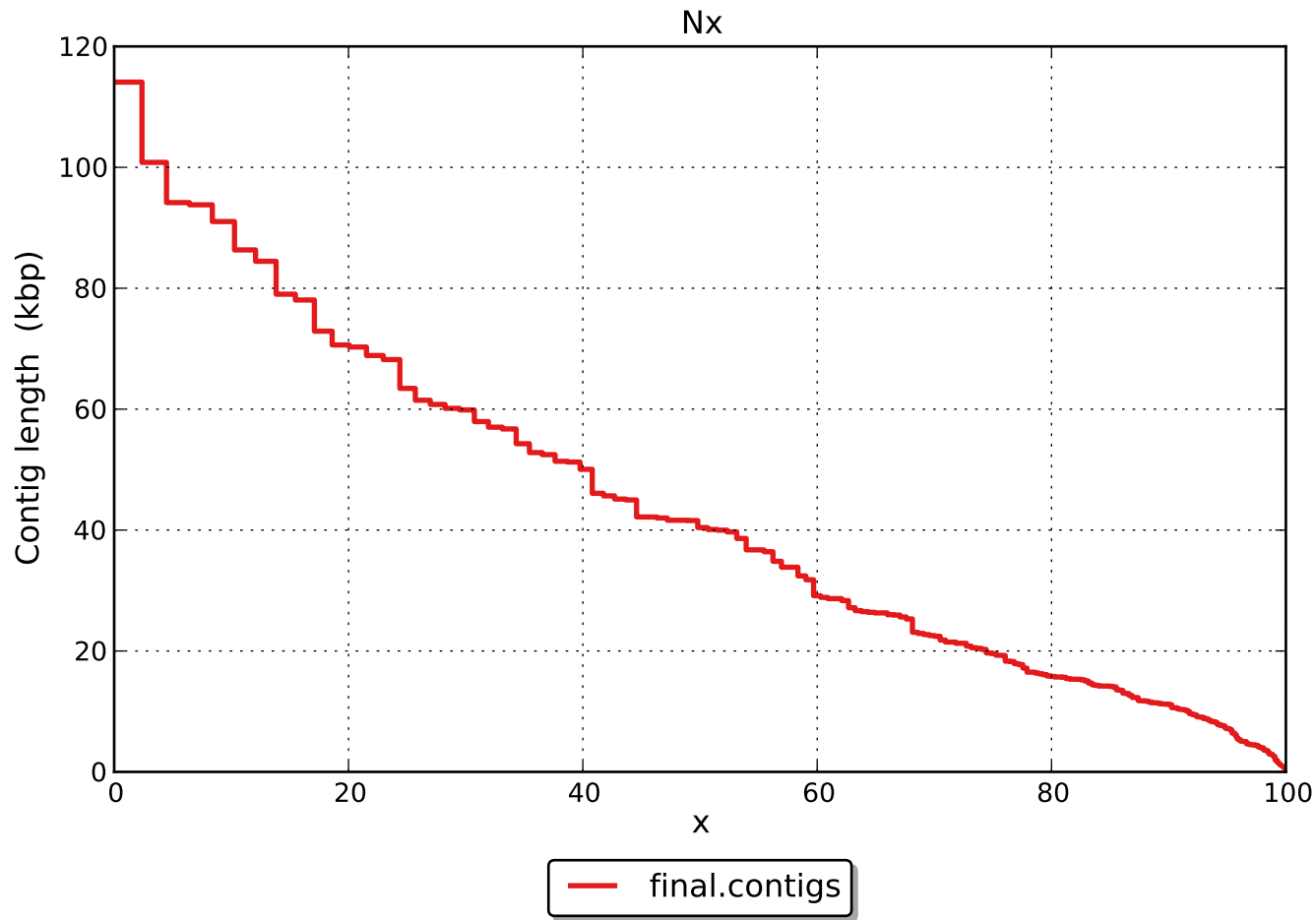
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	61
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

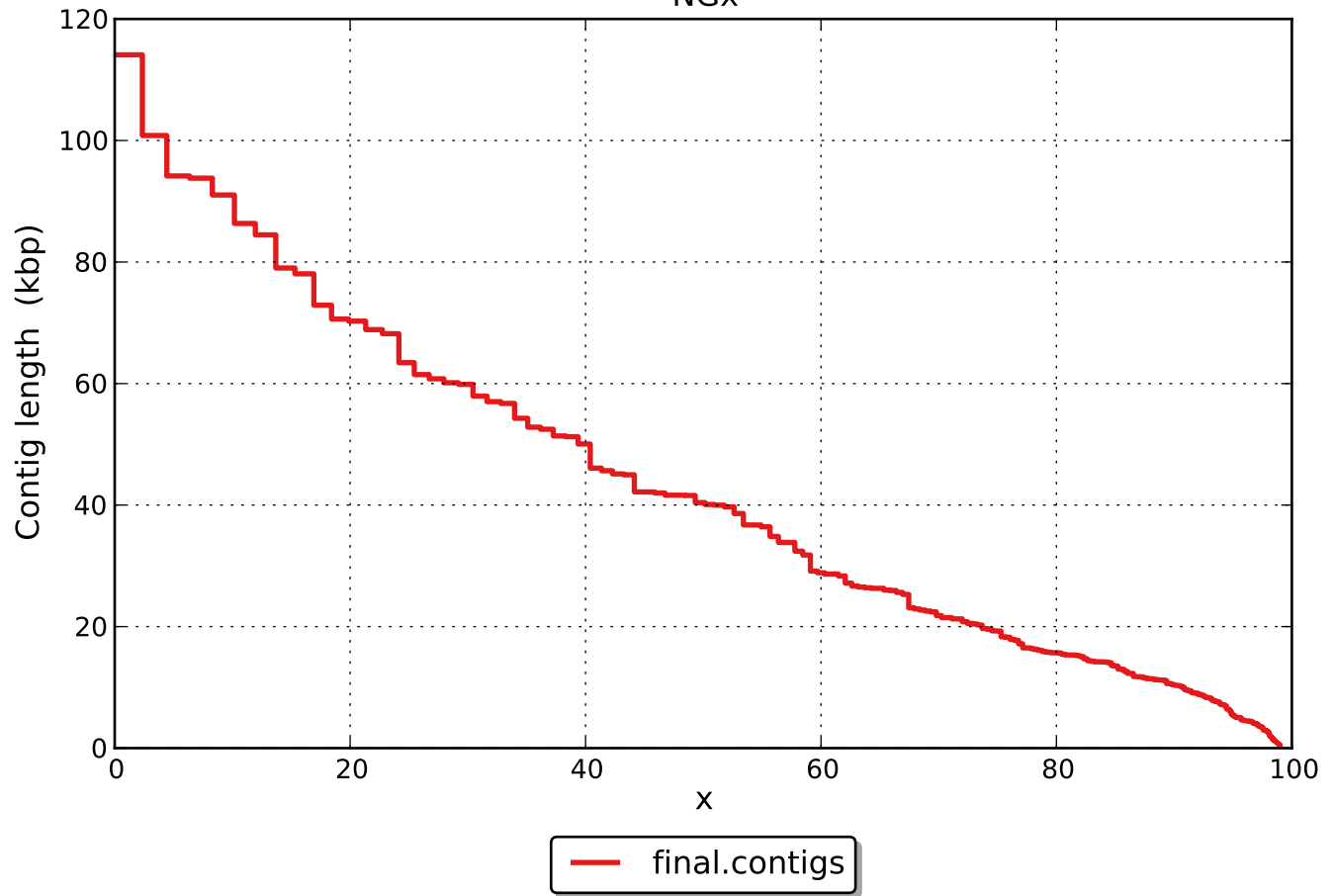
## Unaligned report

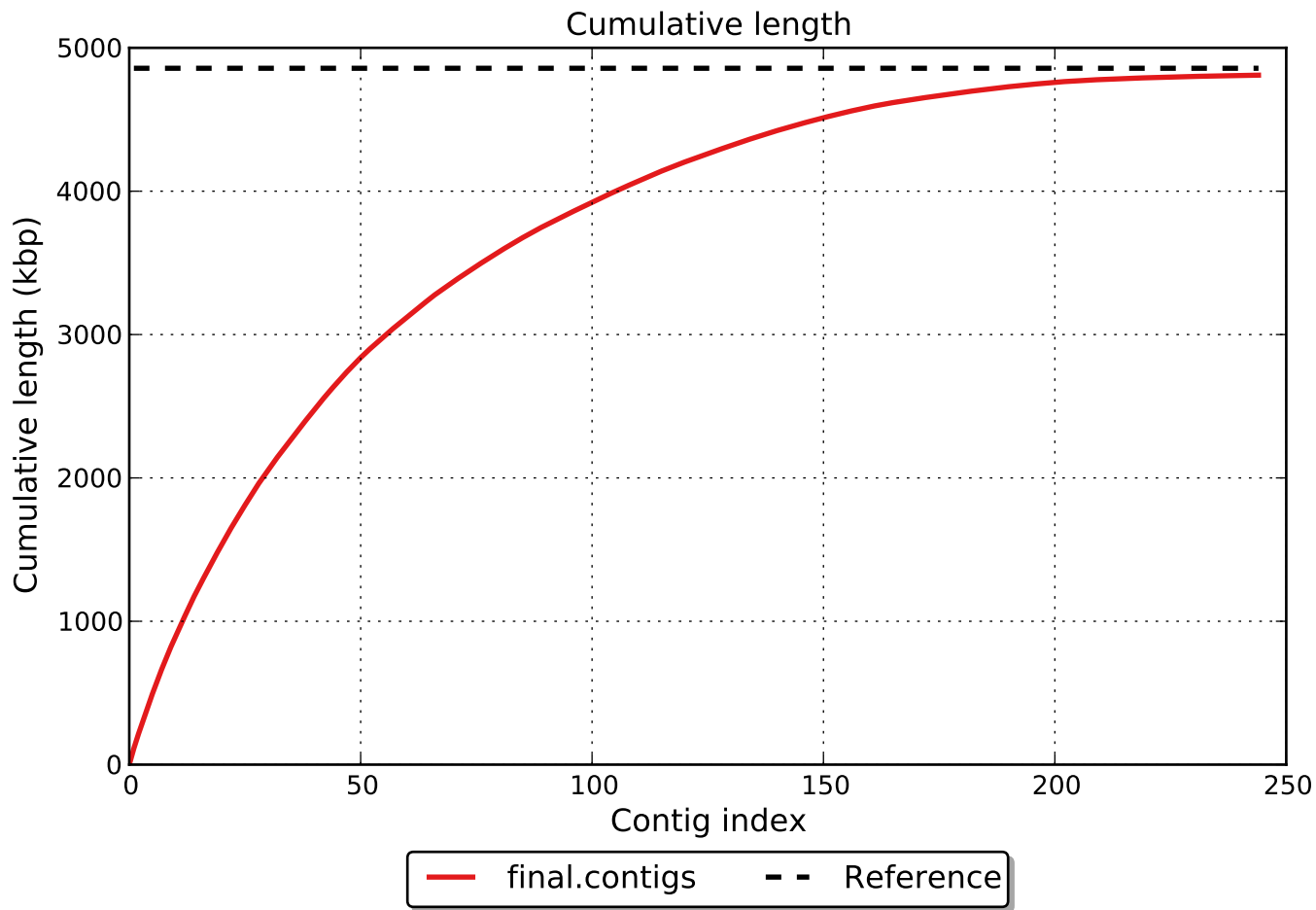
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

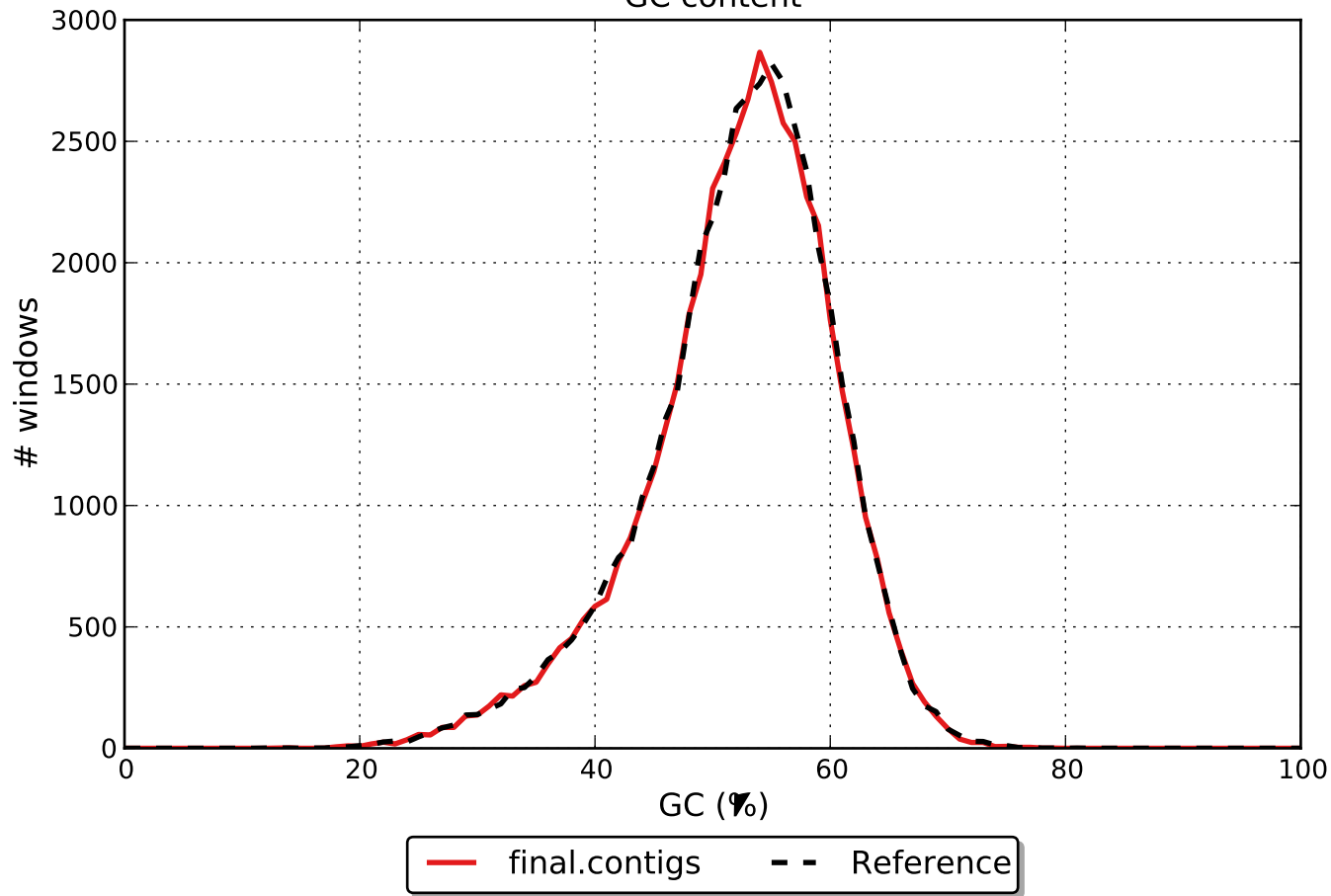


NGx





GC content

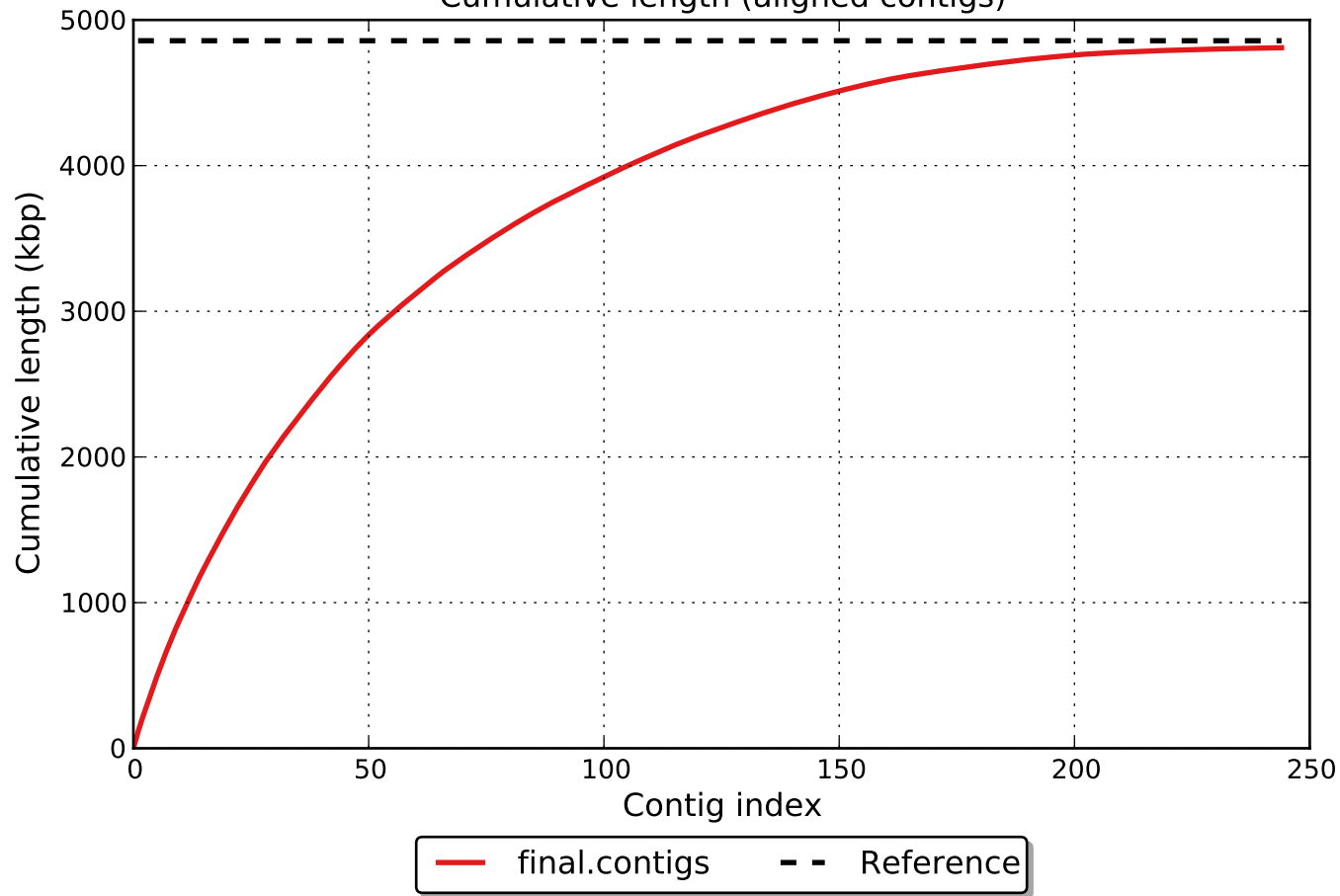


# Misassemblies

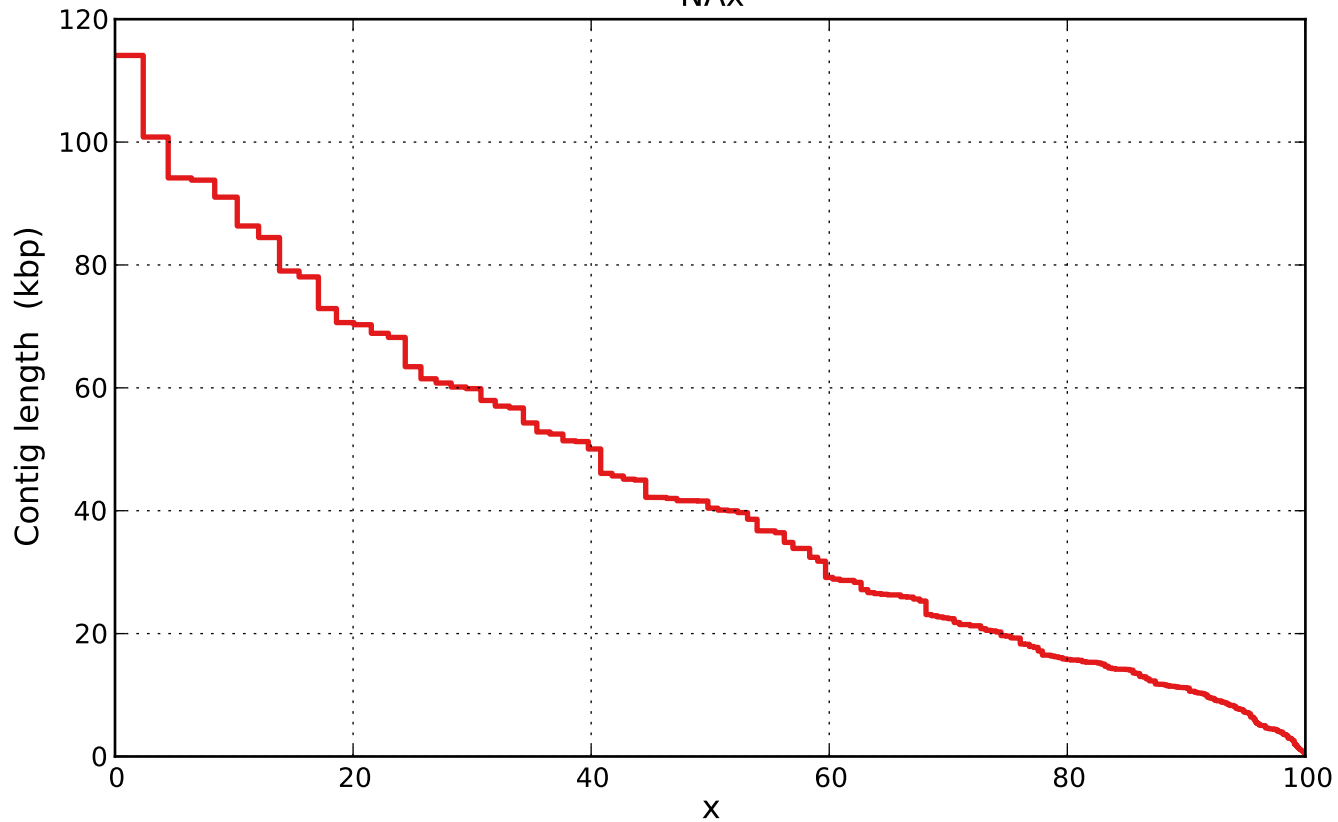




Cumulative length (aligned contigs)

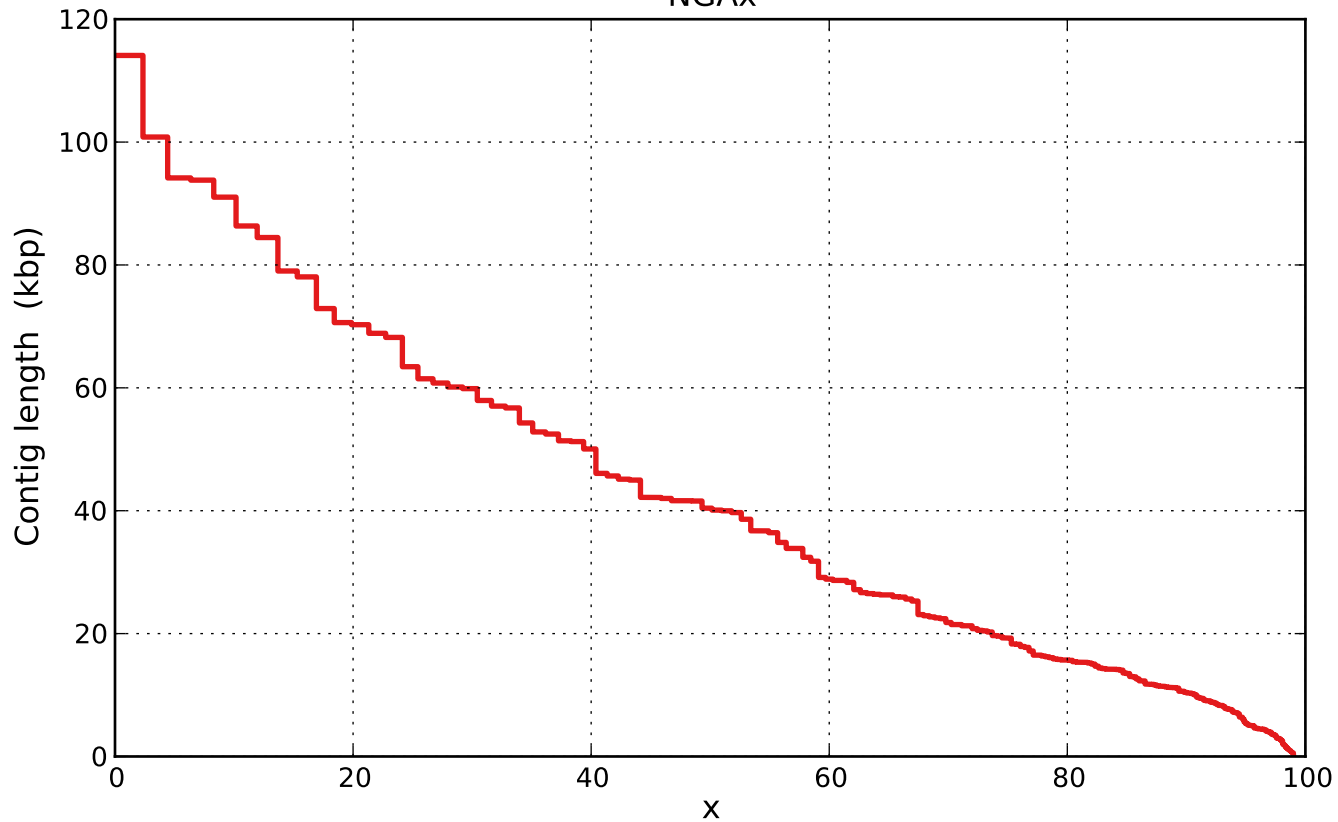


NAx



— final.contigs

# NGAx



— final.contigs