

Report

	final.contigs
# contigs (>= 1000 bp)	280
# contigs (>= 5000 bp)	213
# contigs (>= 10000 bp)	157
# contigs (>= 25000 bp)	59
# contigs (>= 50000 bp)	13
Total length (>= 1000 bp)	4796746
Total length (>= 5000 bp)	4610121
Total length (>= 10000 bp)	4178896
Total length (>= 25000 bp)	2563469
Total length (>= 50000 bp)	858501
# contigs	305
Largest contig	117058
Total length	4814773
Reference length	4857432
GC (℥)	52.20
Reference GC (℥)	52.22
N50	26532
NG50	26532
N75	15137
NG75	14922
L50	54
LG50	54
L75	112
LG75	114
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	98.674
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.15
# indels per 100 kbp	0.00
Largest alignment	117058
NA50	26532
NGA50	26532
NA75	15137
NGA75	14922
LA50	54
LGA50	54
LA75	112
LGA75	114

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

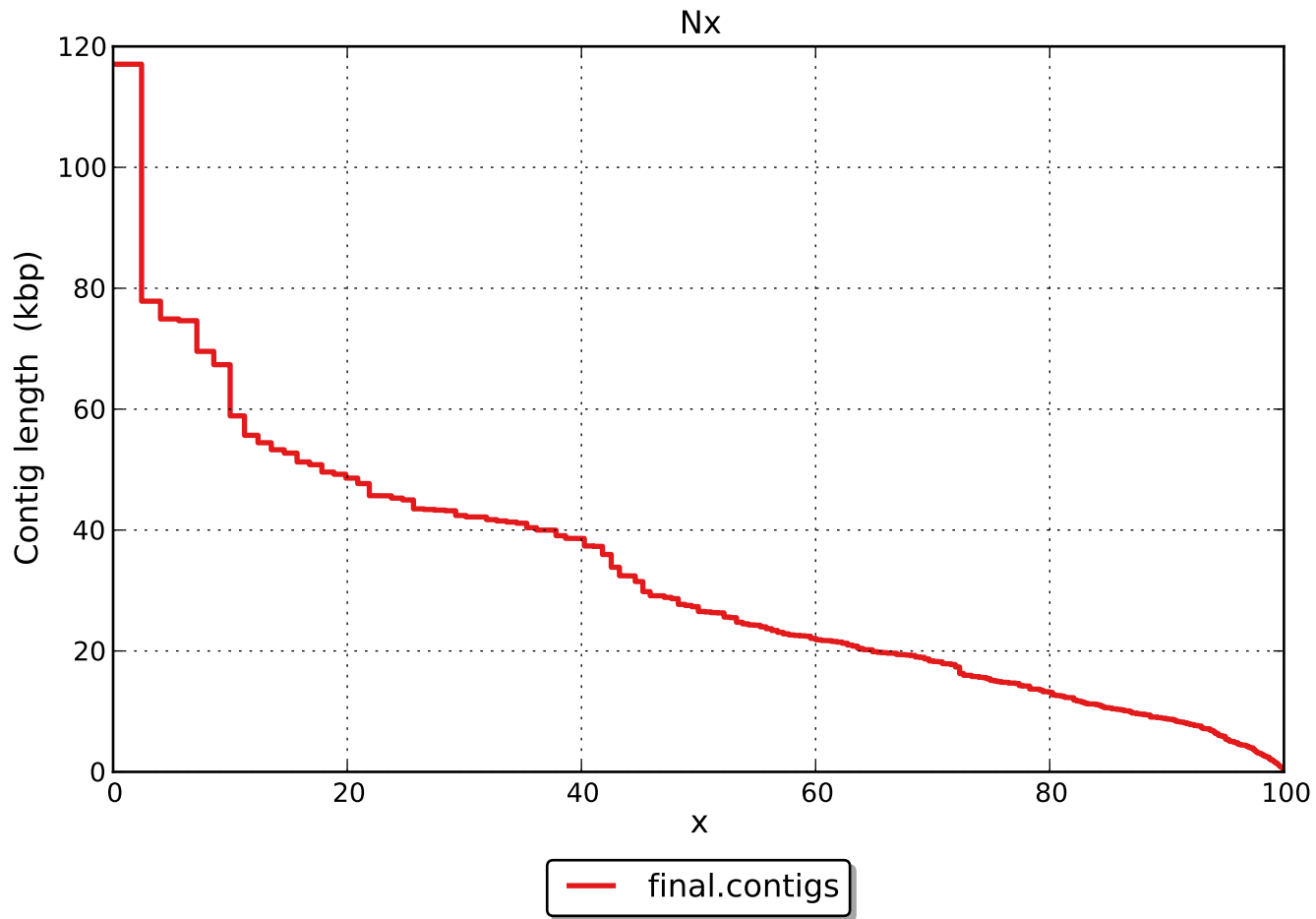
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	55
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

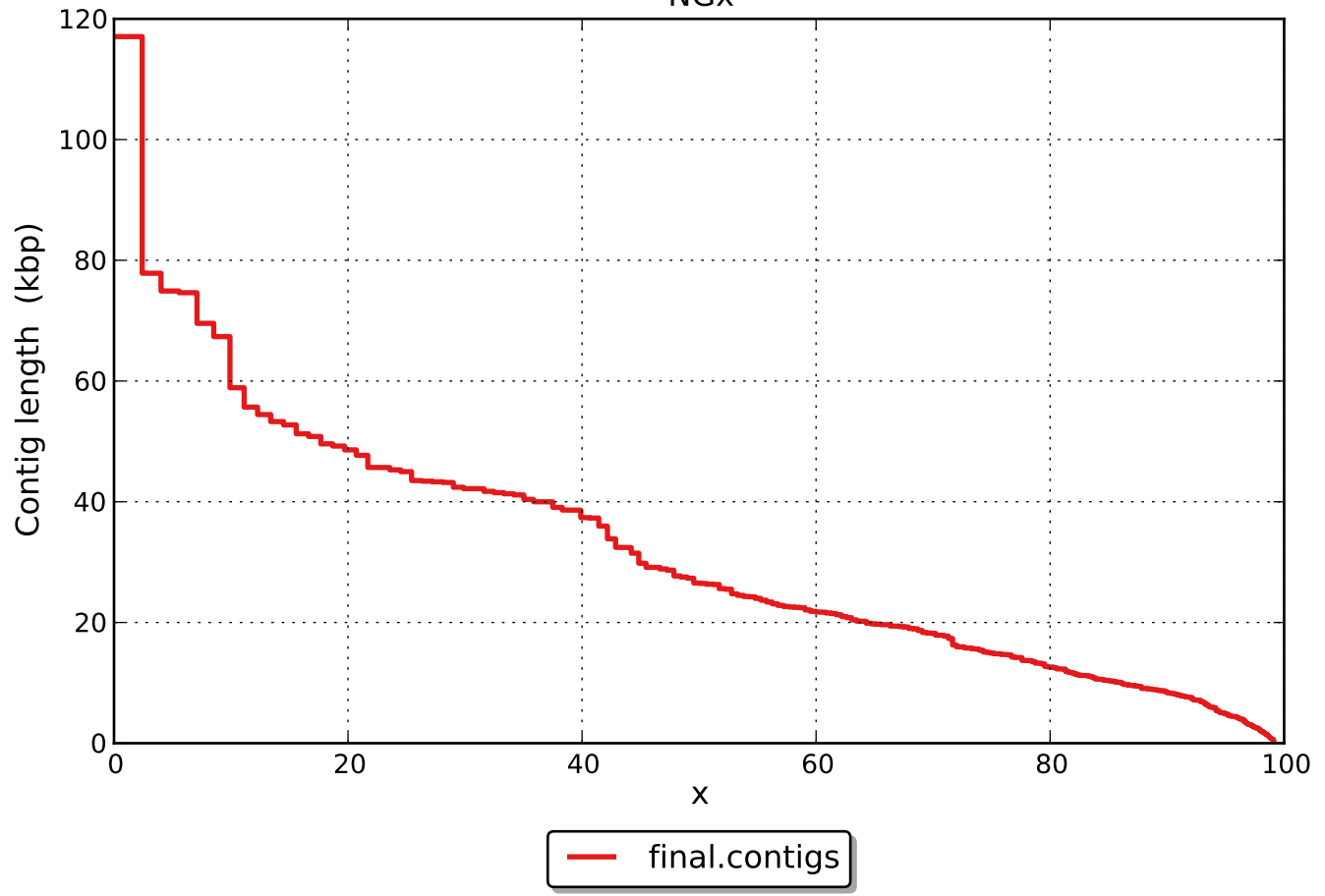
## Unaligned report

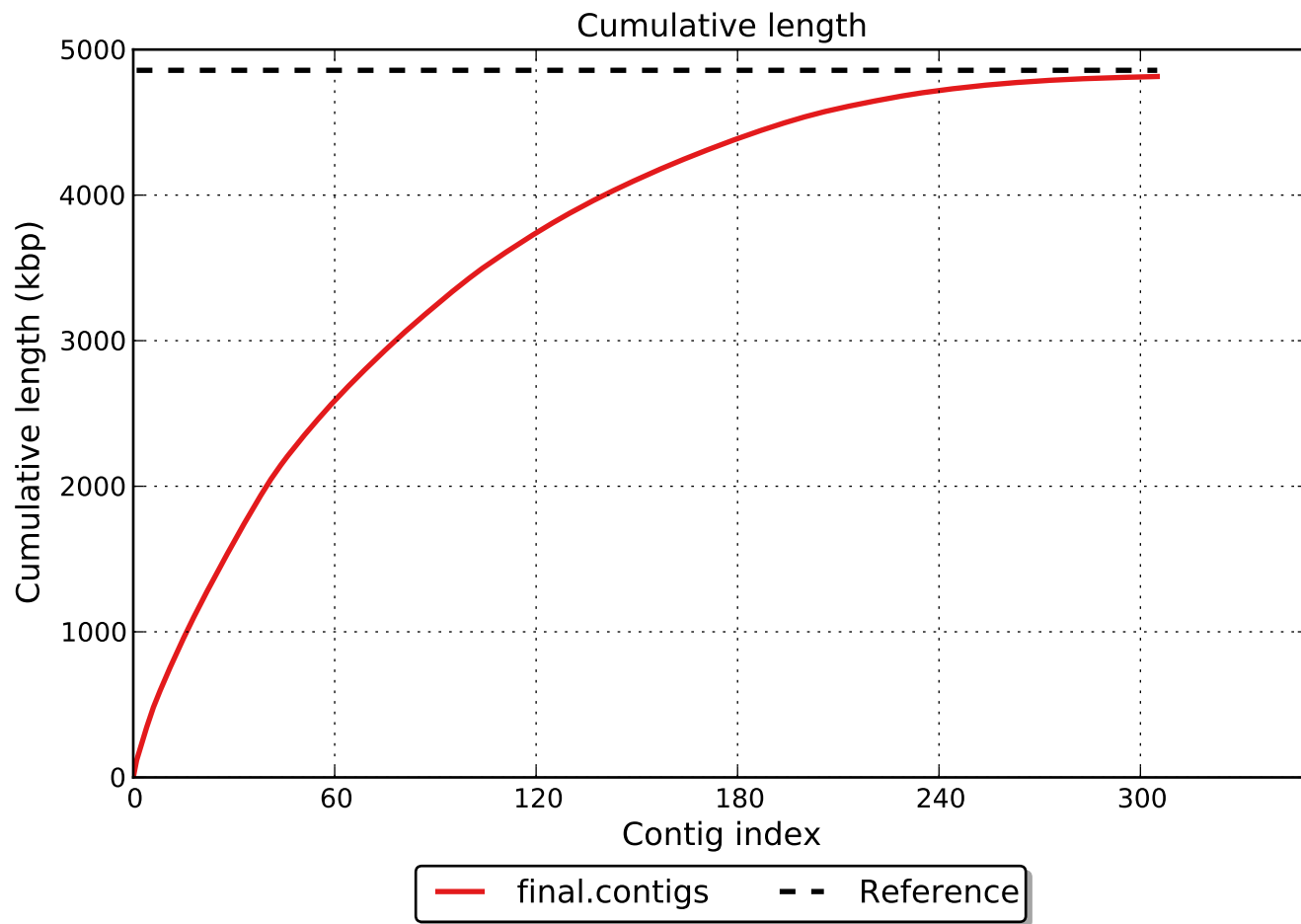
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

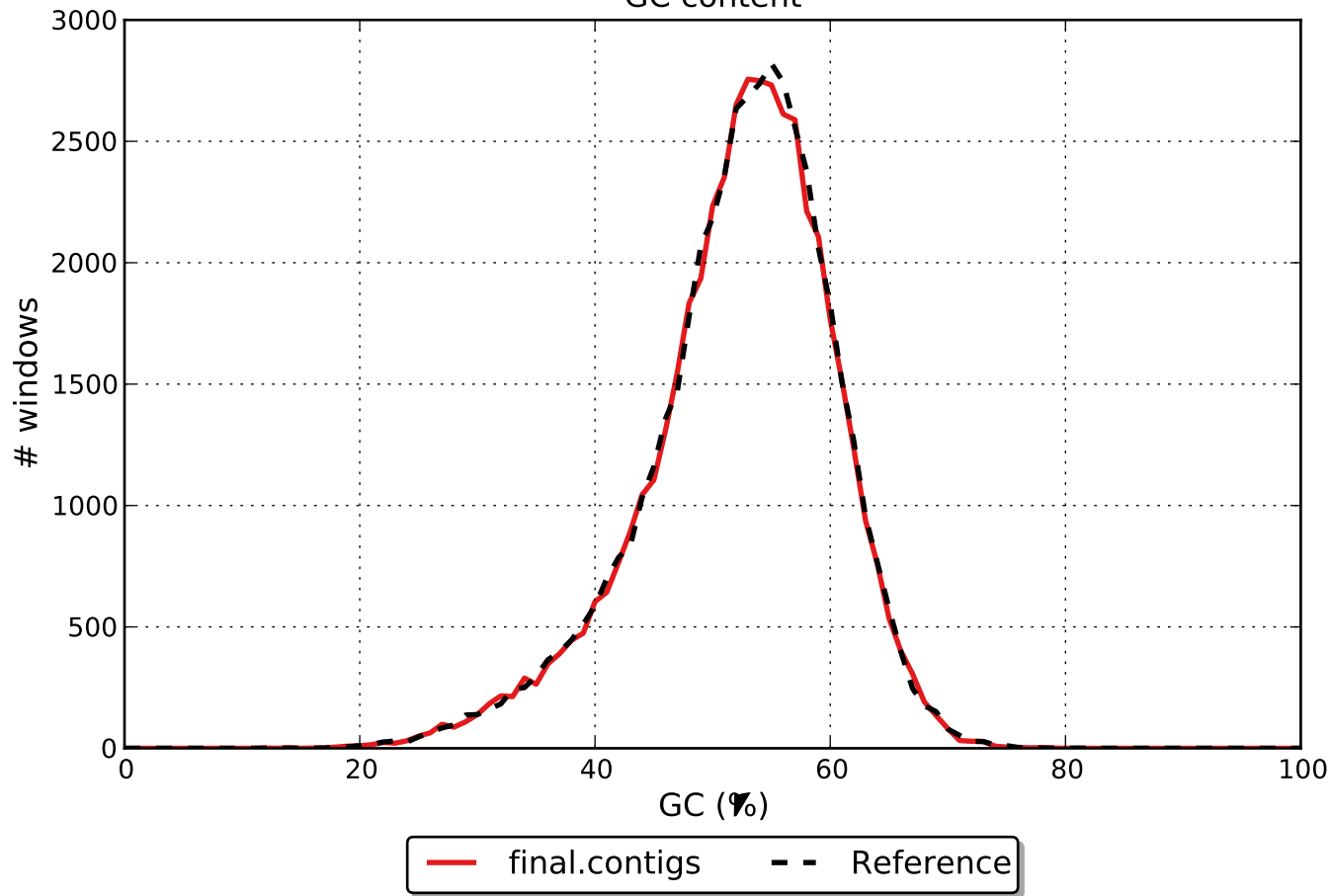


NGx





GC content

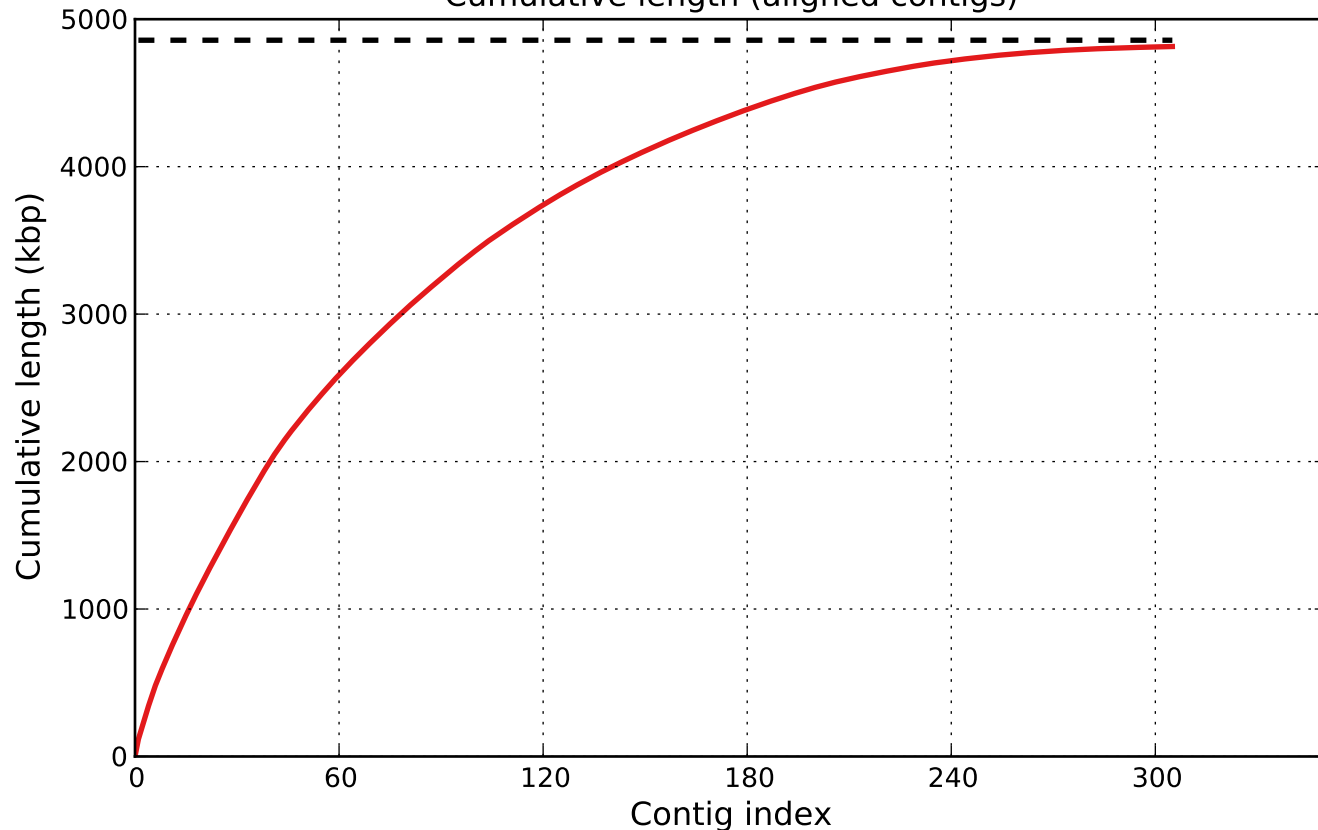


# Misassemblies



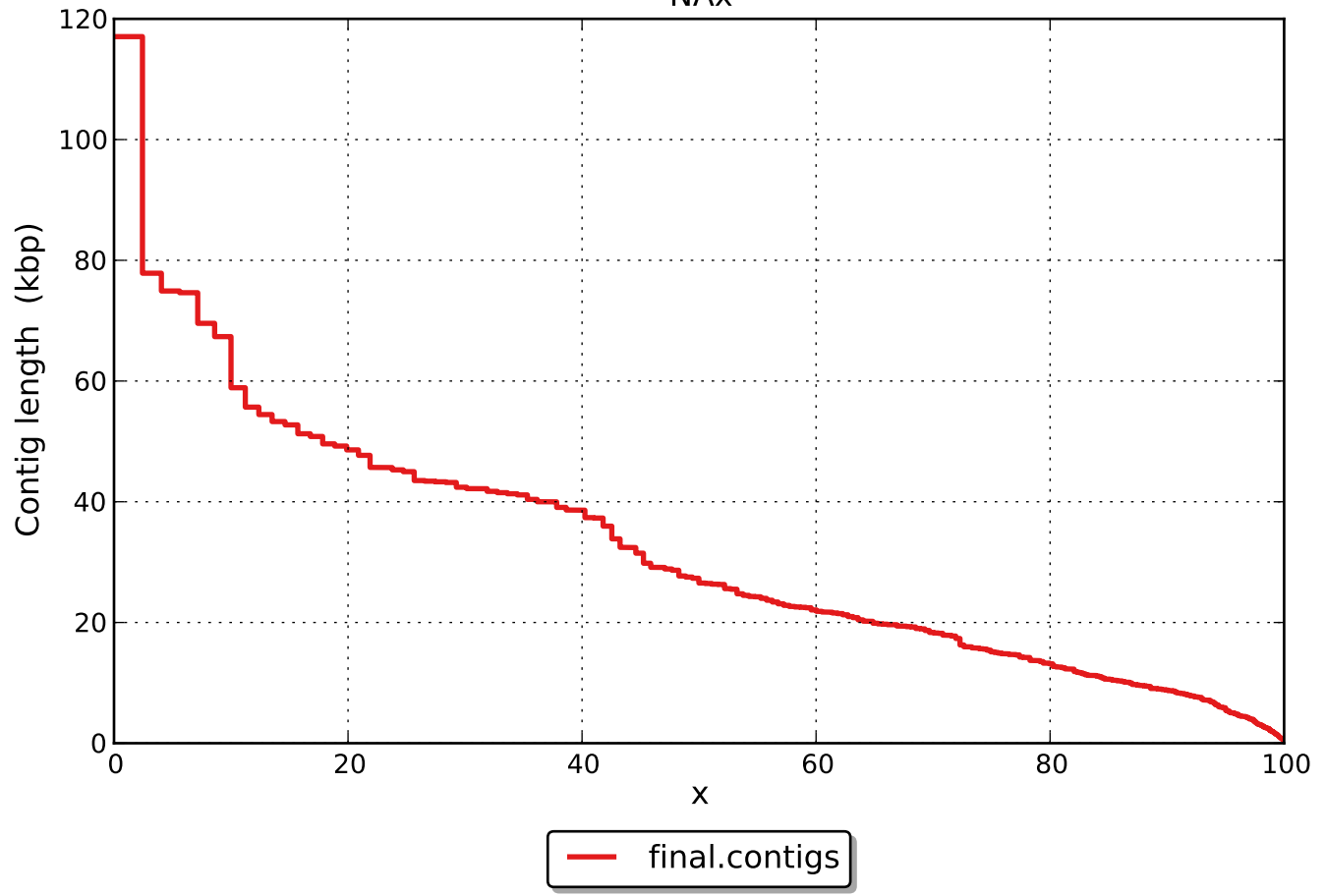


Cumulative length (aligned contigs)



— final.contigs    - - Reference

NAx



# NGAx

