

## Report

	final.contigs
# contigs (>= 1000 bp)	332
# contigs (>= 5000 bp)	233
# contigs (>= 10000 bp)	160
# contigs (>= 25000 bp)	56
# contigs (>= 50000 bp)	14
Total length (>= 1000 bp)	4818071
Total length (>= 5000 bp)	4526351
Total length (>= 10000 bp)	4007013
Total length (>= 25000 bp)	2341474
Total length (>= 50000 bp)	926148
# contigs	356
Largest contig	88870
Total length	4834776
Reference length	4857432
GC (%)	52.20
Reference GC (%)	52.22
N50	22554
NG50	22554
N75	13770
NG75	13693
L50	60
LG50	60
L75	128
LG75	129
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.578
Duplication ratio	1.010
# N's per 100 kbp	0.00
# mismatches per 100 kbp	33.06
# indels per 100 kbp	0.13
Largest alignment	88870
NA50	22554
NGA50	22554
NA75	13770
NGA75	13585
LA50	60
LGA50	60
LA75	128
LGA75	130

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

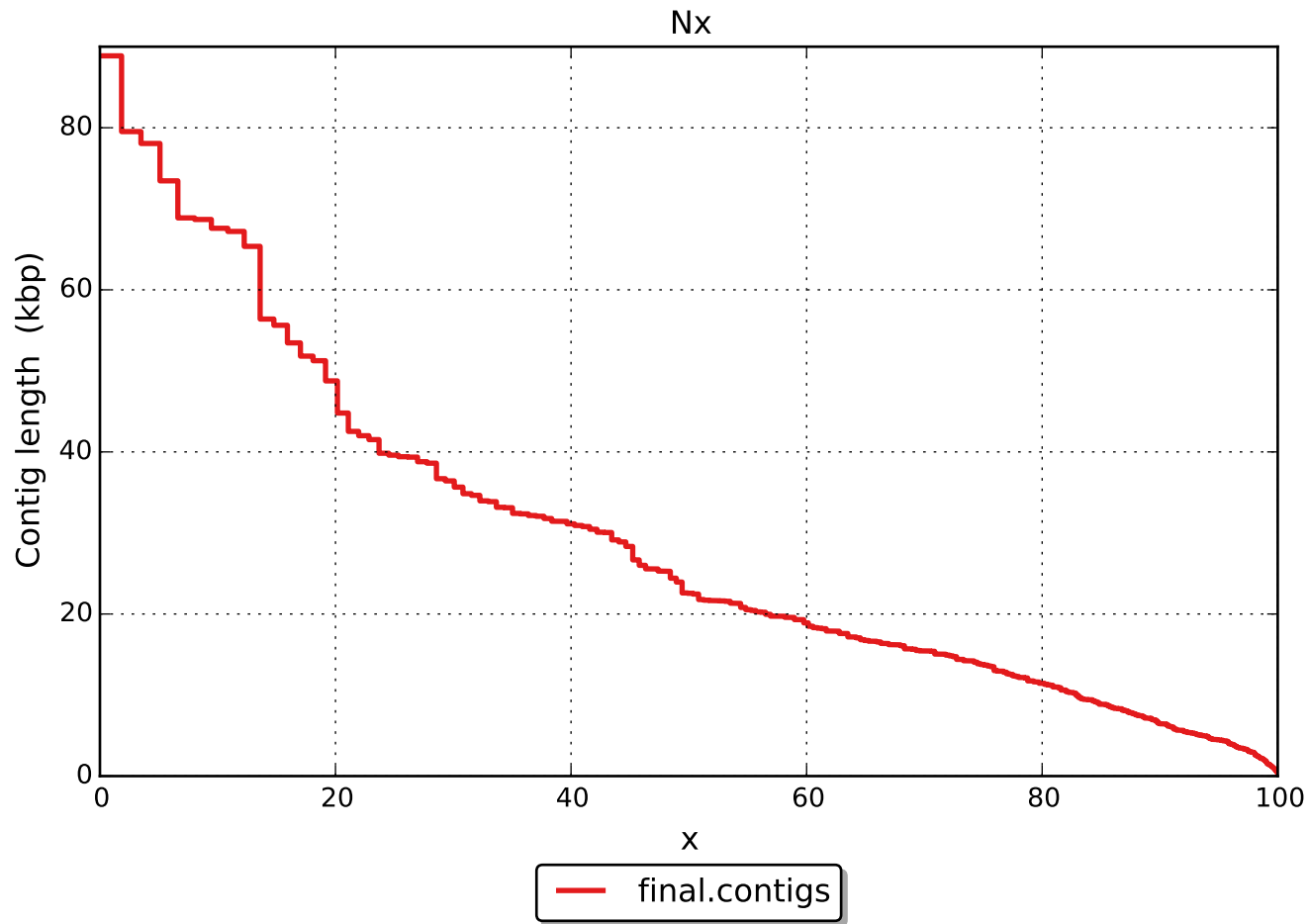
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	1583
# indels	6
# short indels	5
# long indels	1
Indels length	14

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).

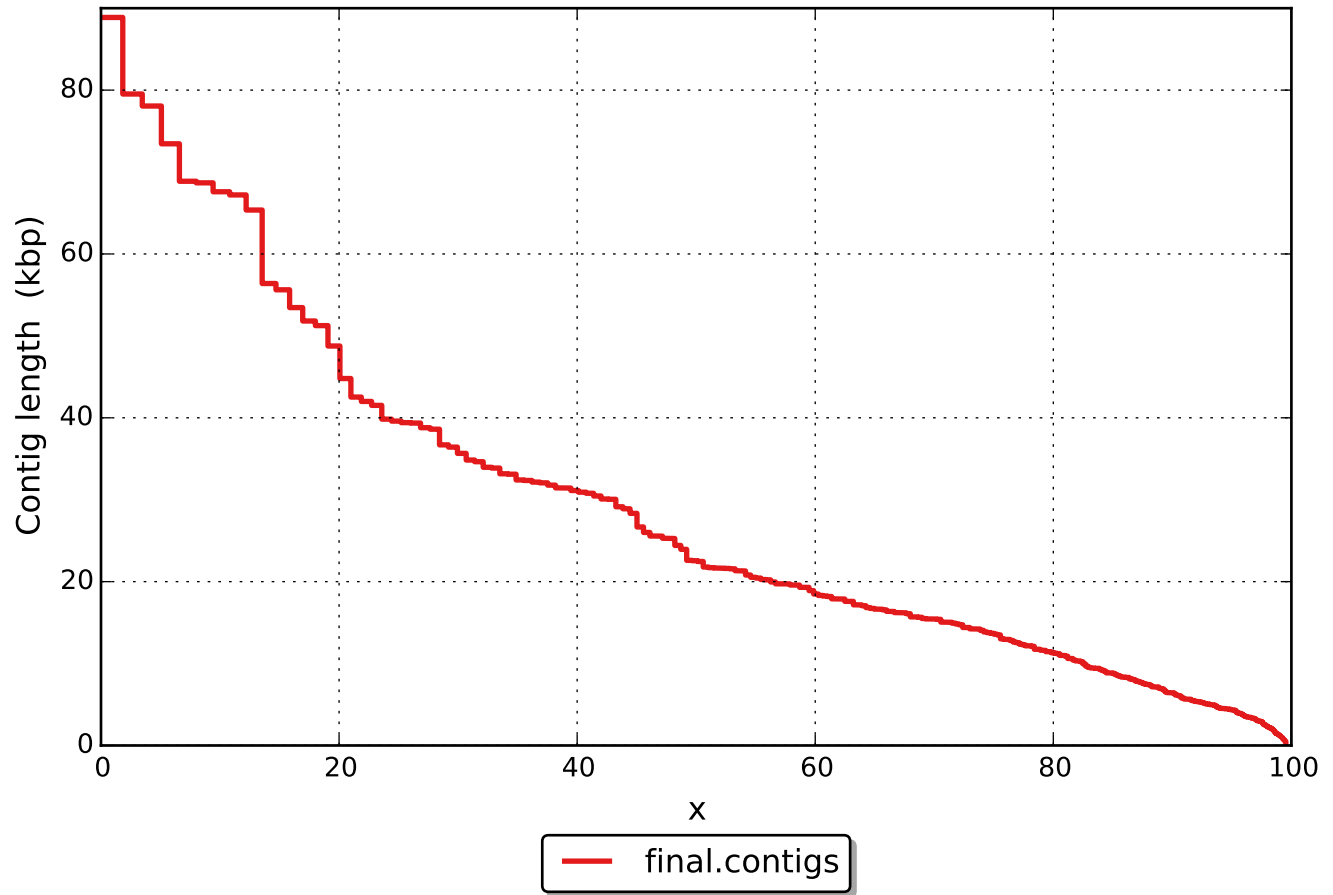
## Unaligned report

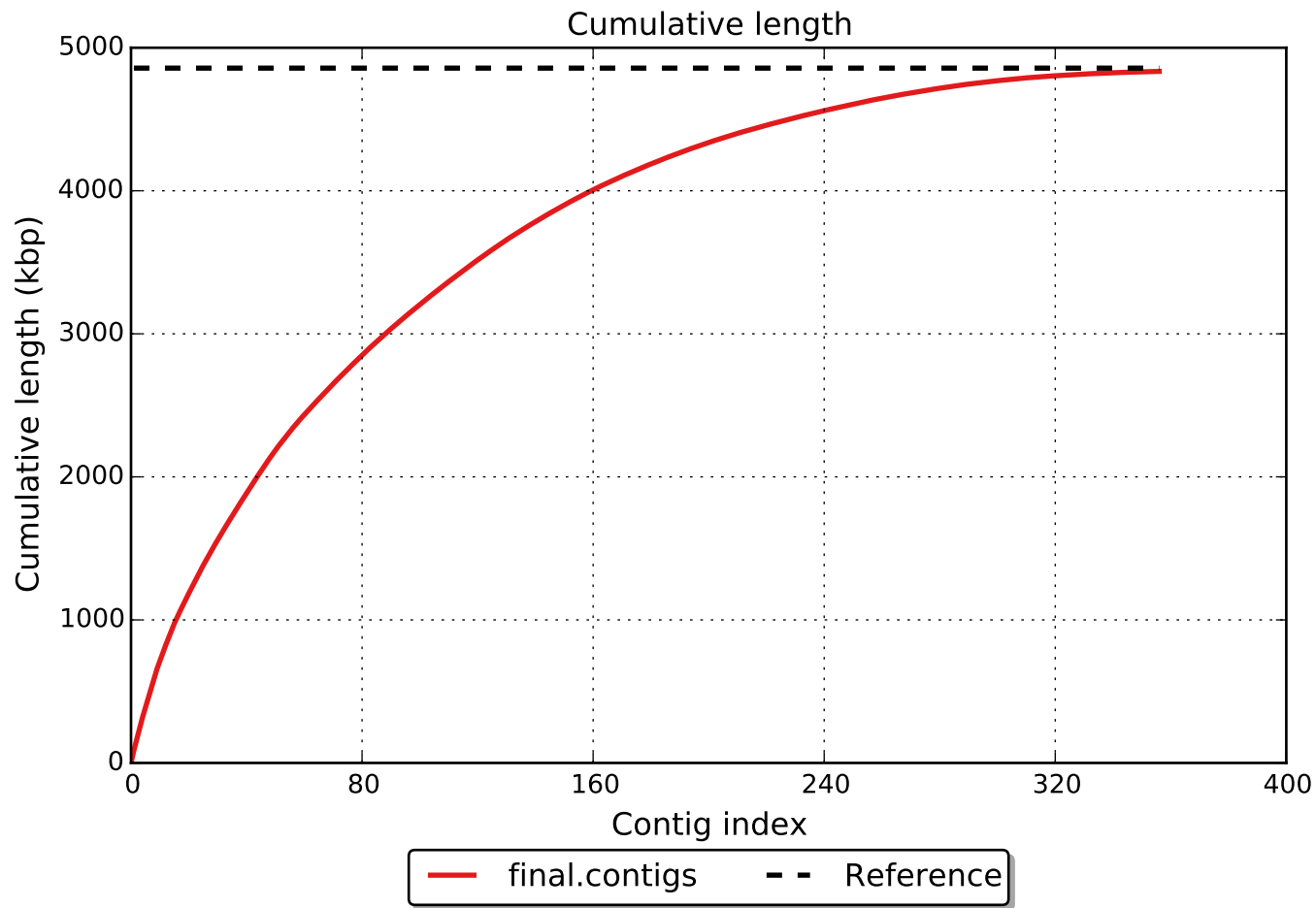
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

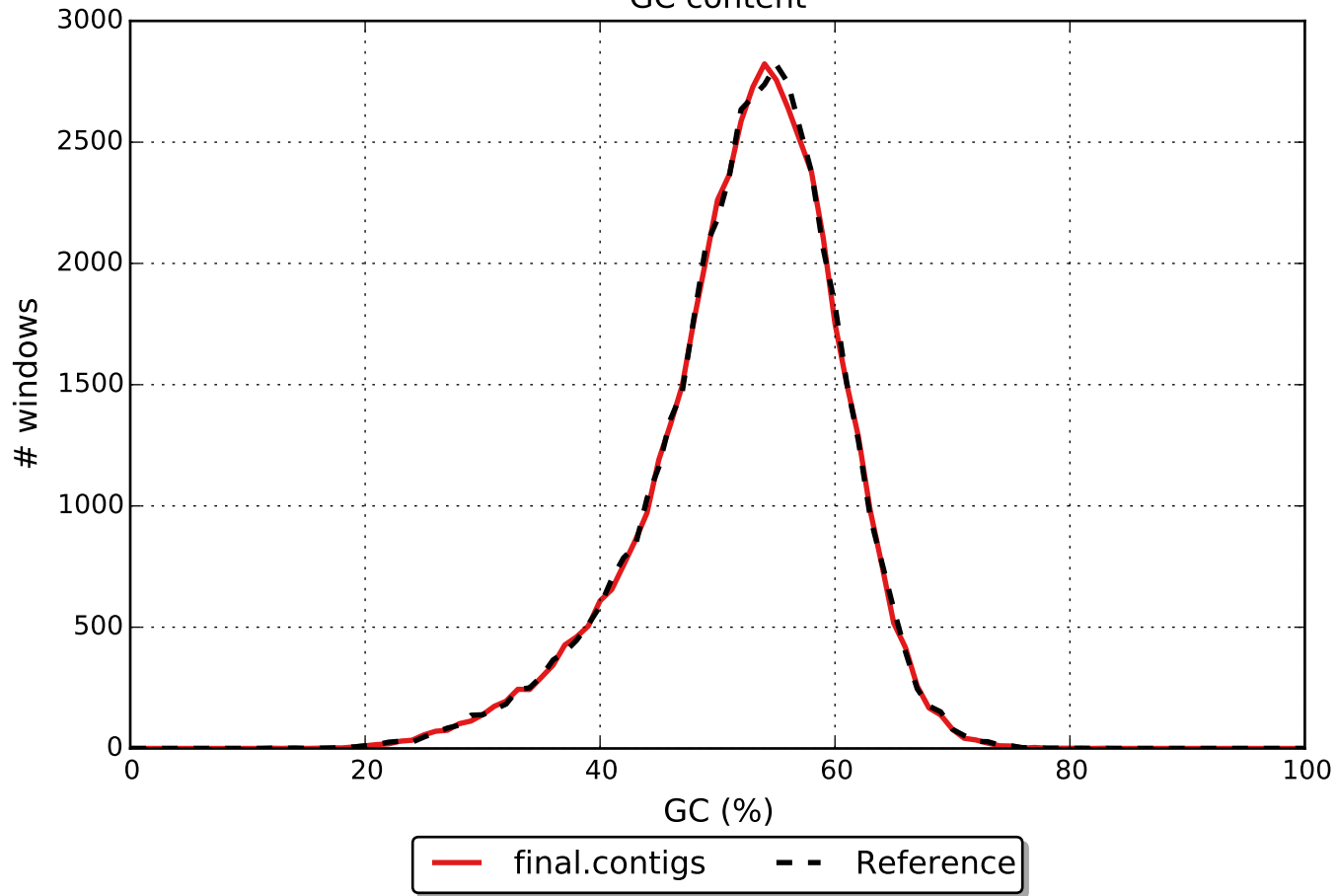


NGx





GC content

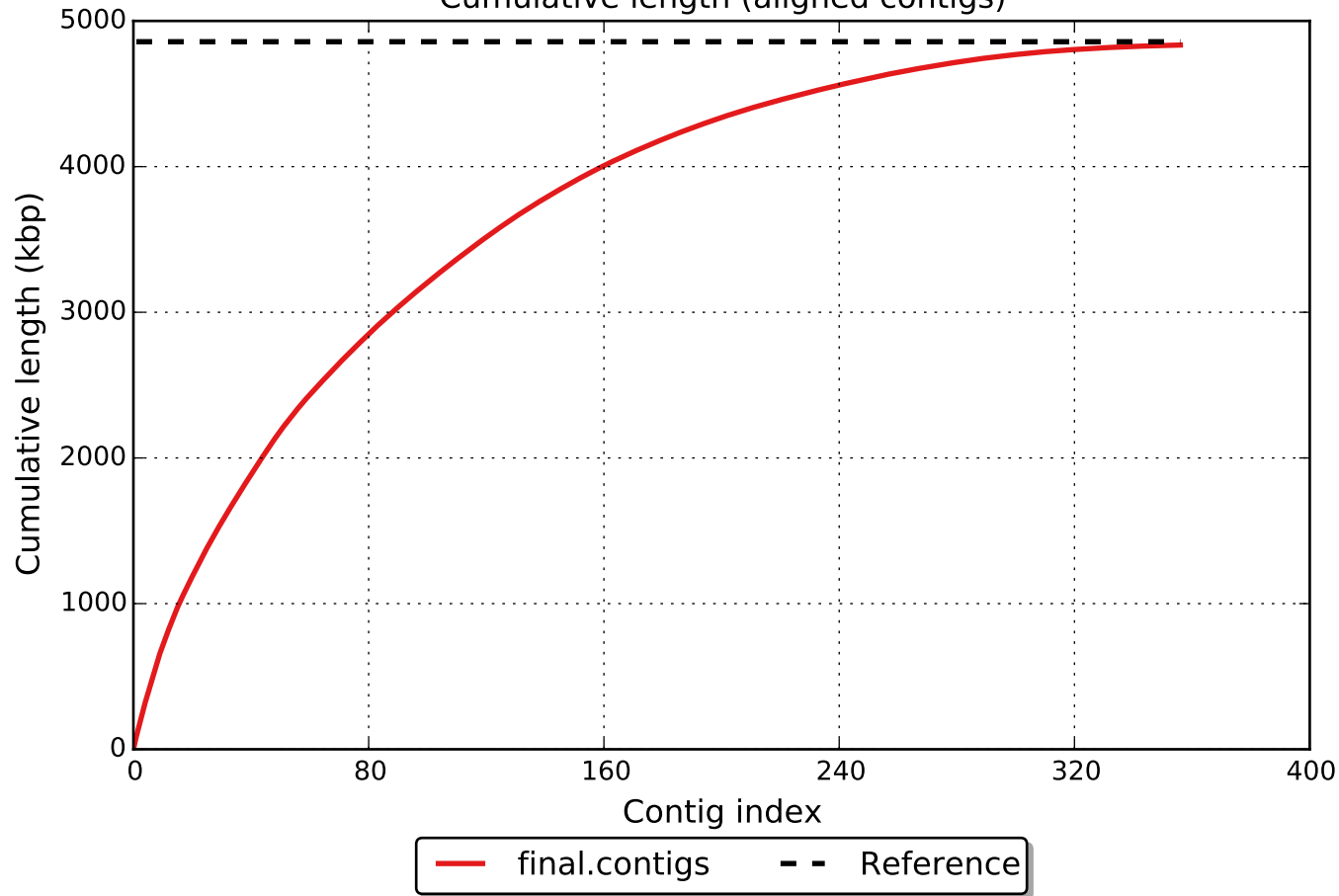


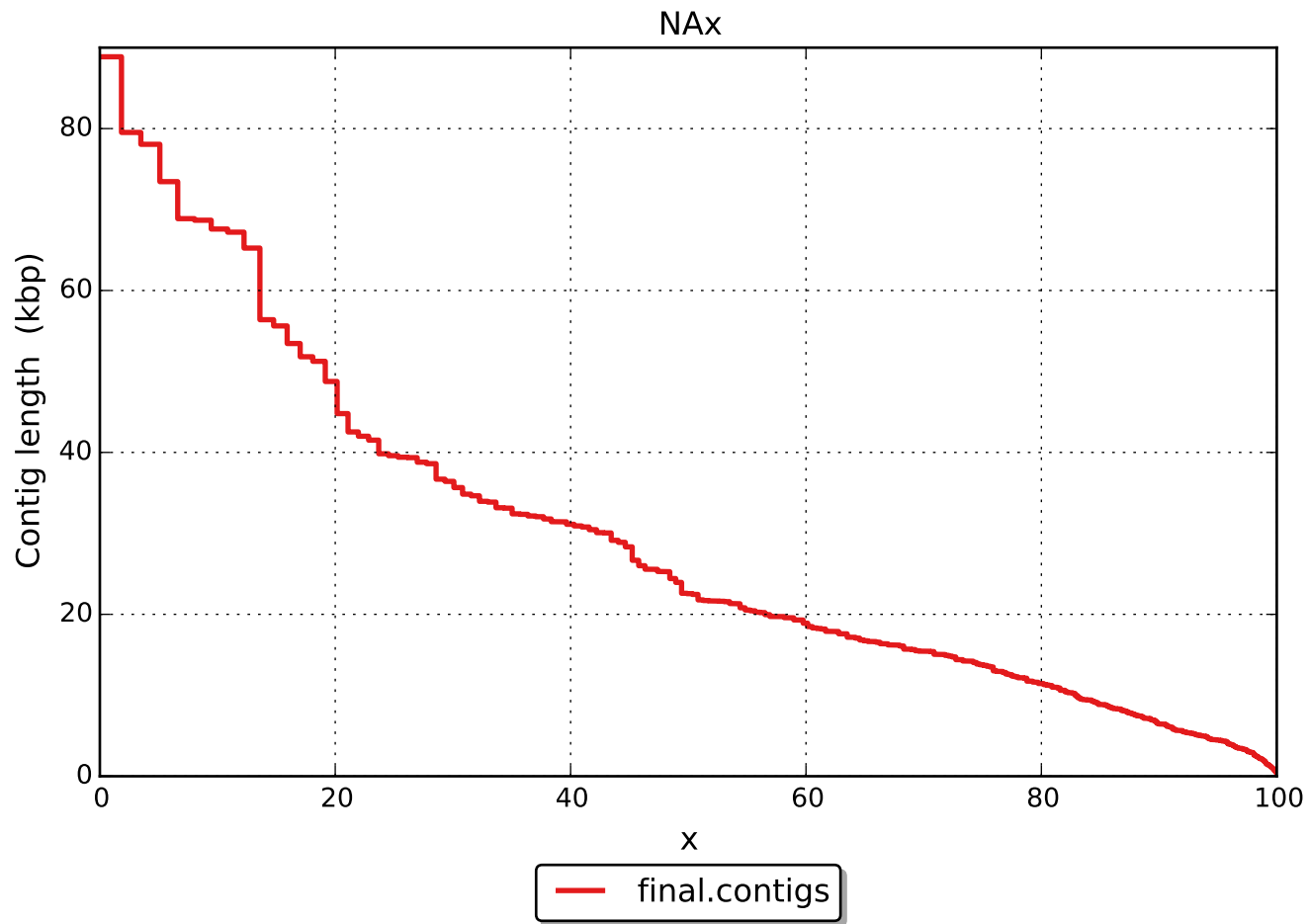
# Misassemblies





Cumulative length (aligned contigs)





# NGAx

