

## Report

	final.contigs
# contigs (>= 1000 bp)	392
# contigs (>= 5000 bp)	256
# contigs (>= 10000 bp)	160
# contigs (>= 25000 bp)	44
# contigs (>= 50000 bp)	4
Total length (>= 1000 bp)	4564489
Total length (>= 5000 bp)	4180842
Total length (>= 10000 bp)	3481383
Total length (>= 25000 bp)	1631998
Total length (>= 50000 bp)	244358
# contigs	426
Largest contig	76374
Total length	4590017
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	19406
NG50	19123
N75	10387
NG75	10005
L50	75
LG50	76
L75	157
LG75	160
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# unaligned contigs	0 + 1 part
Unaligned length	21
Genome fraction (%)	98.140
Duplication ratio	1.008
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13.11
# indels per 100 kbp	0.09
Largest alignment	76374
NA50	19406
NGA50	19123
NA75	10387
NGA75	10005
LA50	75
LGA50	76
LA75	157
LGA75	160

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

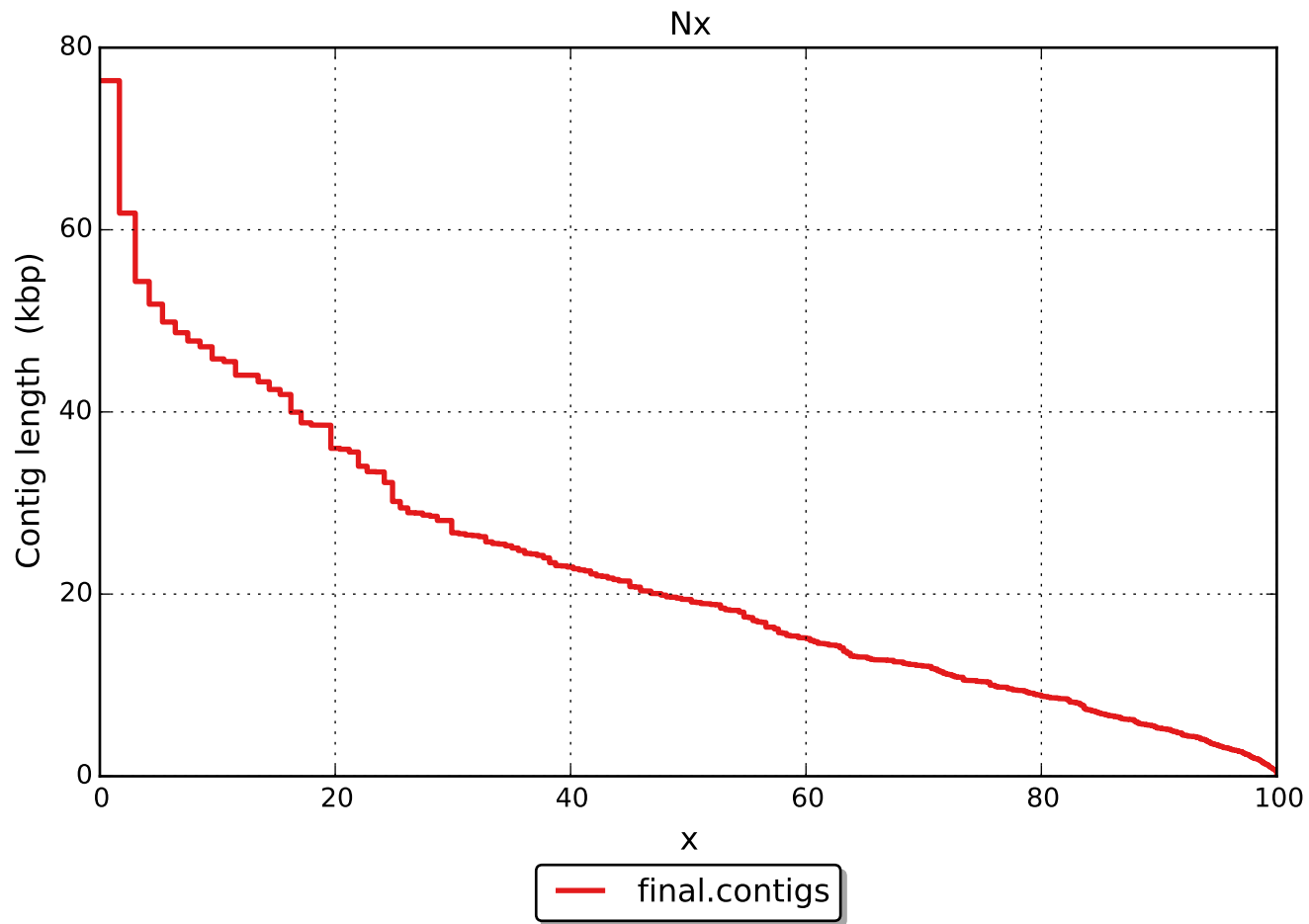
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# mismatches	597
# indels	4
# short indels	4
# long indels	0
Indels length	4

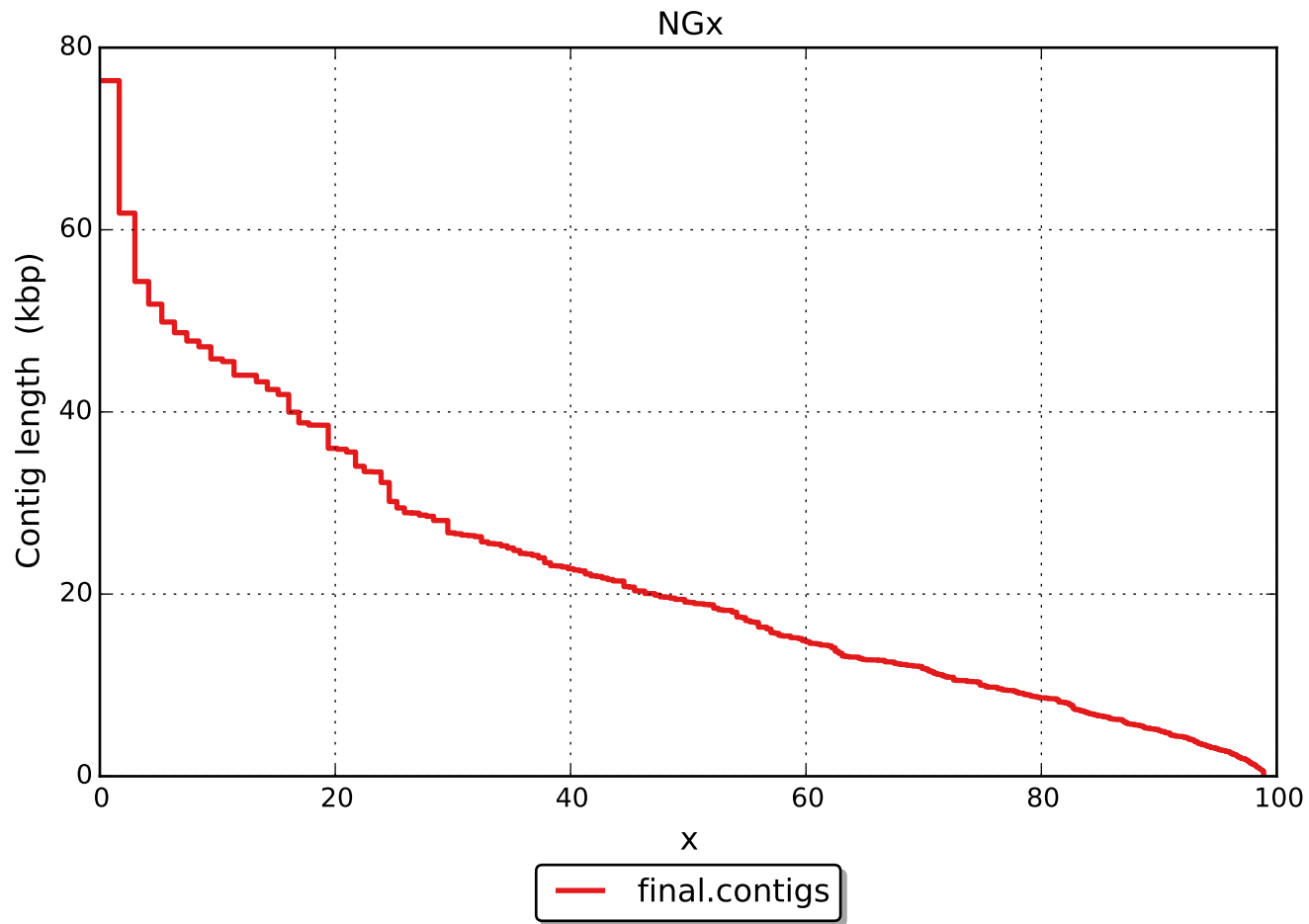
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

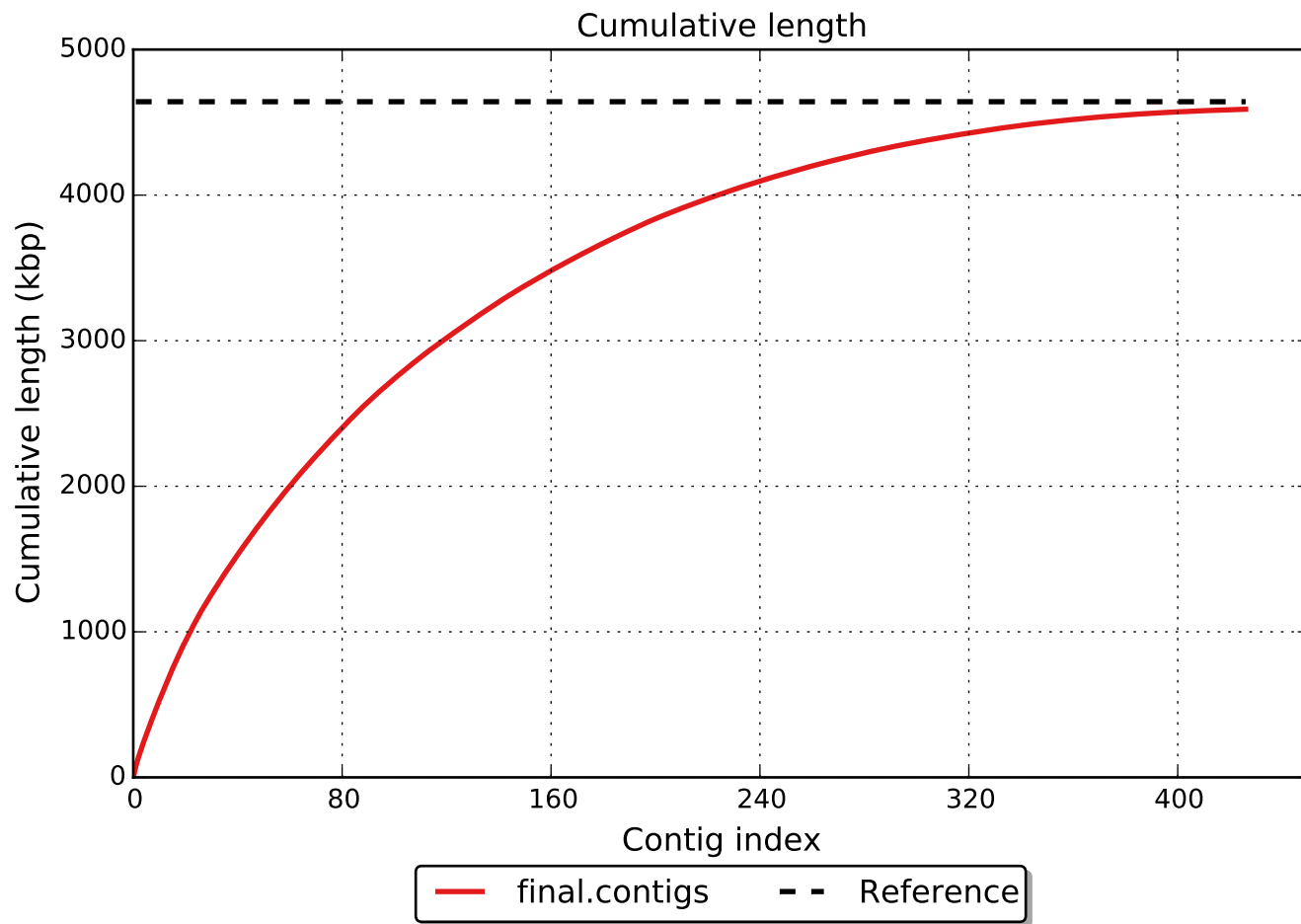
## Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	21
# N's	0

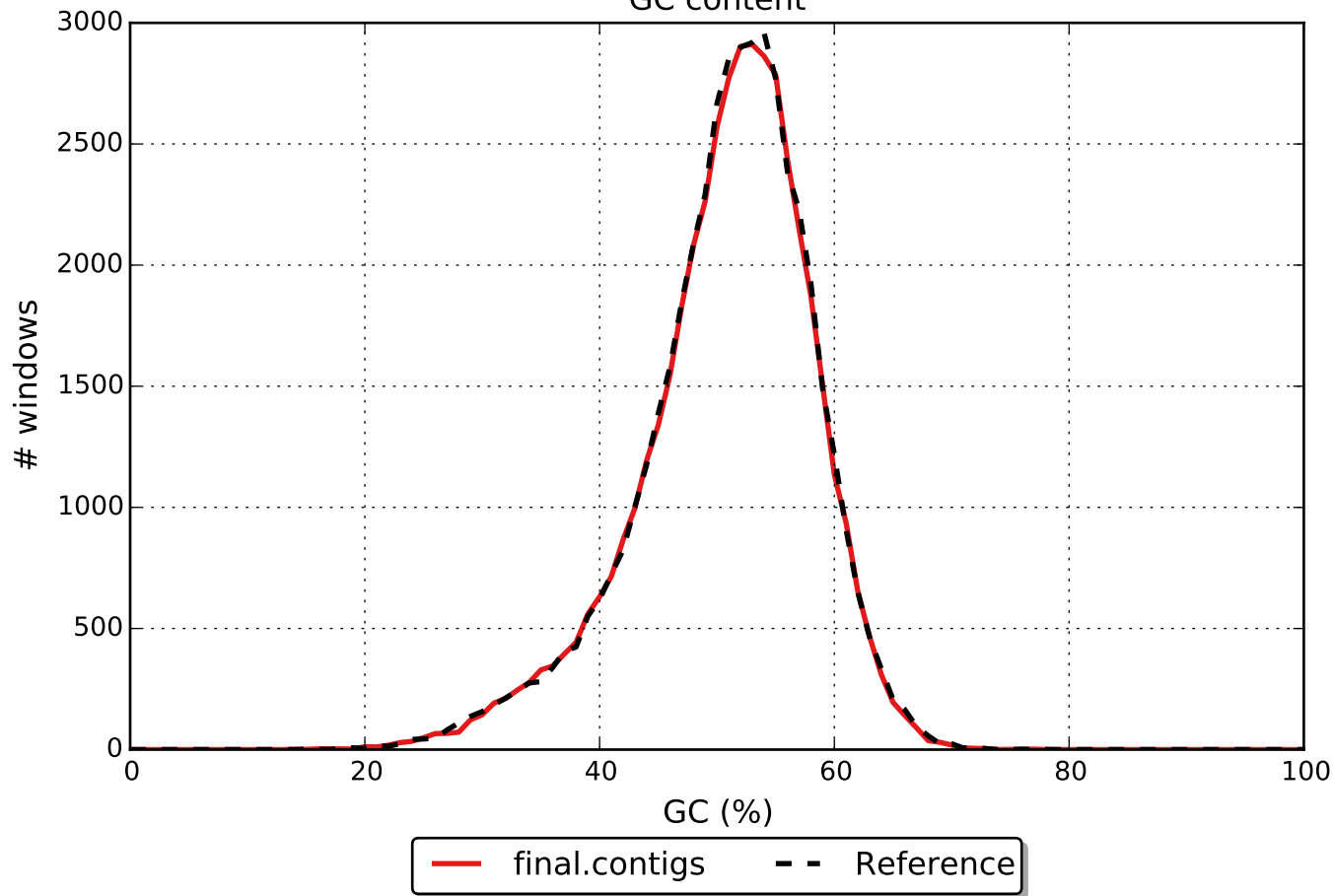
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







GC content

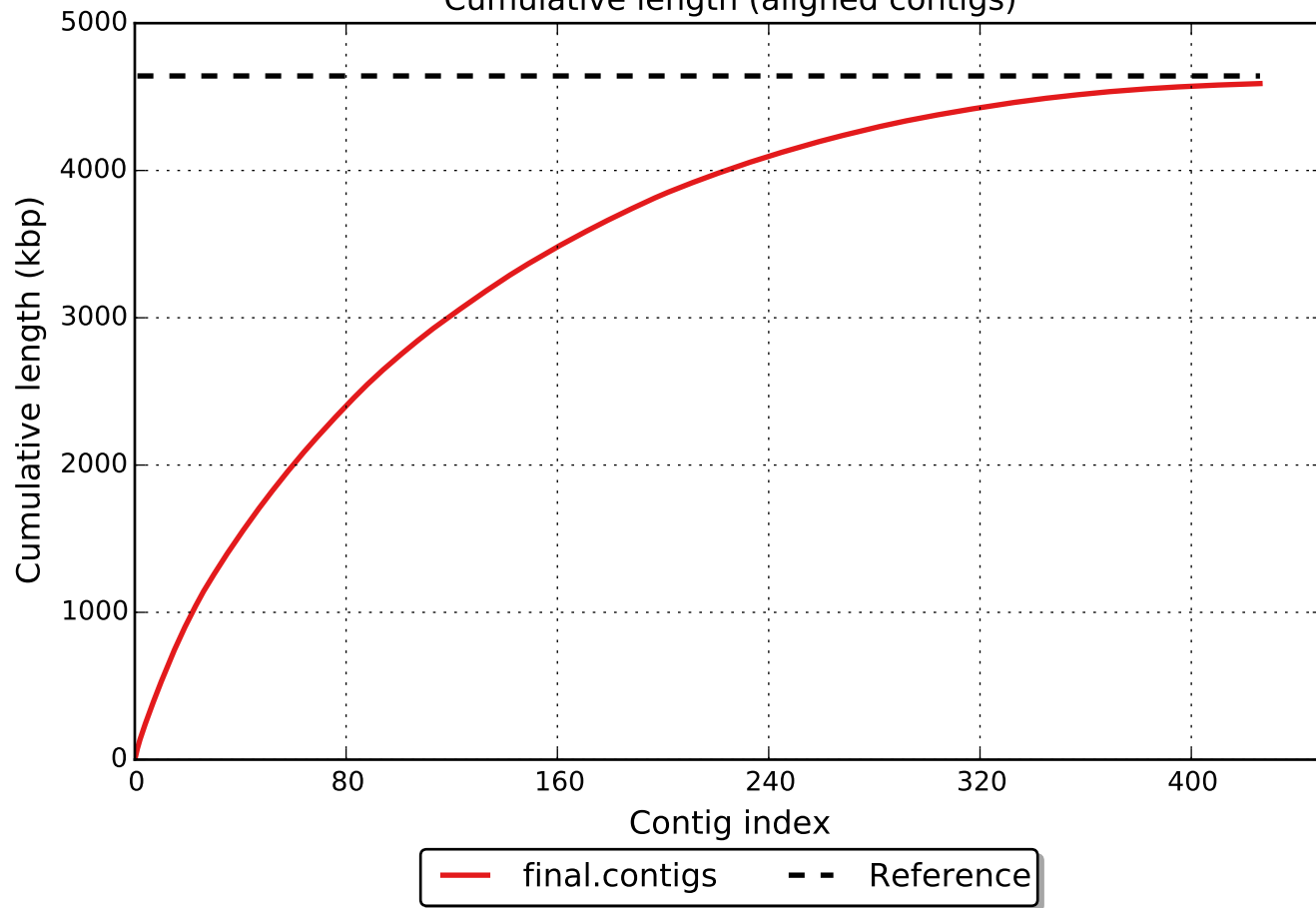


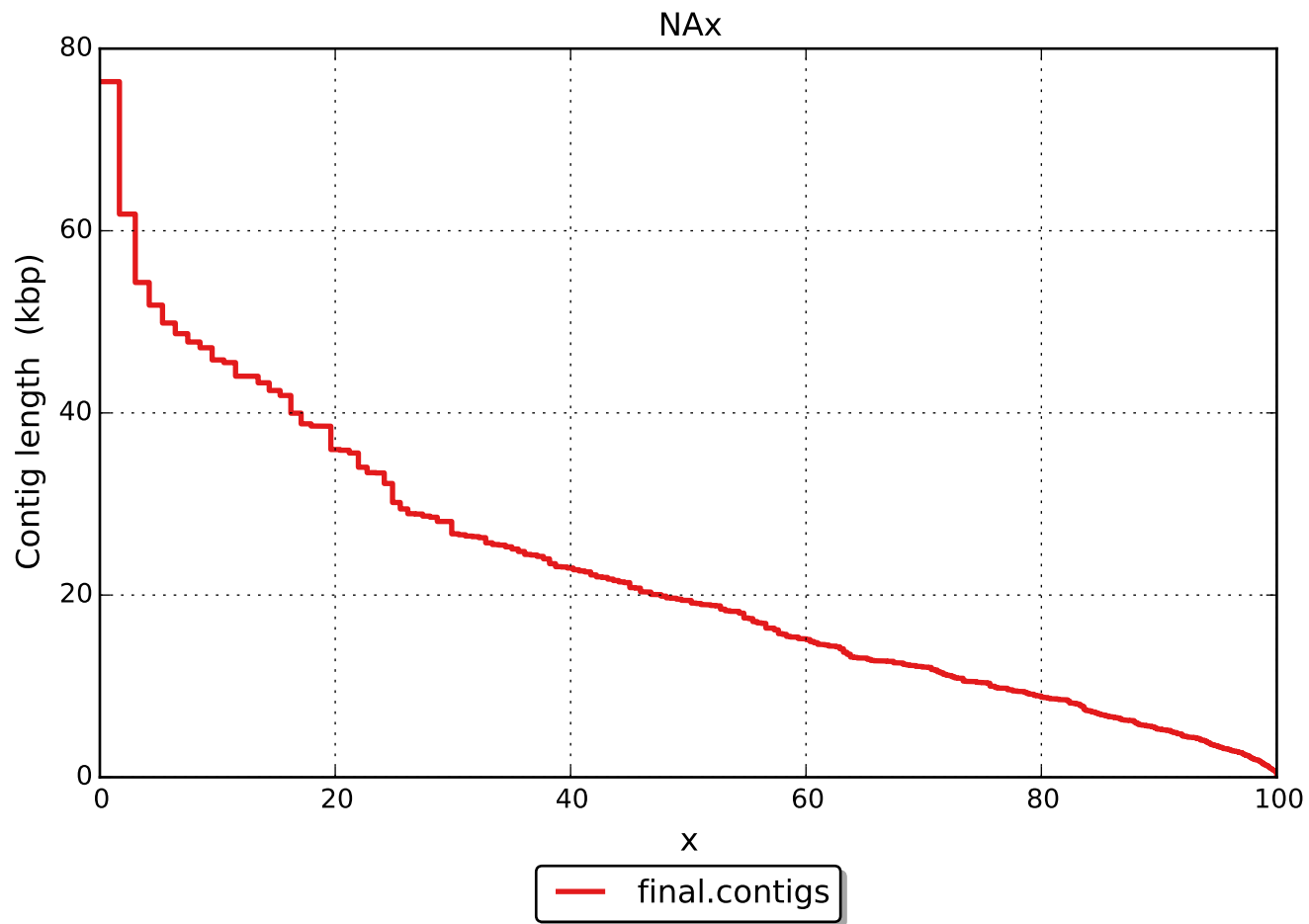
# Misassemblies





Cumulative length (aligned contigs)





# NGAx

