

## Report

	final.contigs
# contigs (>= 1000 bp)	904
# contigs (>= 5000 bp)	358
# contigs (>= 10000 bp)	107
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4761330
Total length (>= 5000 bp)	3310842
Total length (>= 10000 bp)	1546885
Total length (>= 25000 bp)	130185
Total length (>= 50000 bp)	0
# contigs	1043
Largest contig	27020
Total length	4861099
Reference length	4857432
GC (%)	52.21
Reference GC (%)	52.22
N50	7315
NG50	7315
N75	4266
NG75	4281
L50	211
LG50	211
L75	431
LG75	430
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 1 part
Unaligned length	252
Genome fraction (%)	98.233
Duplication ratio	1.019
# N's per 100 kbp	0.00
# mismatches per 100 kbp	23.77
# indels per 100 kbp	0.00
Largest alignment	27020
NA50	7315
NGA50	7315
NA75	4266
NGA75	4281
LA50	211
LGA50	211
LA75	431
LGA75	430

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

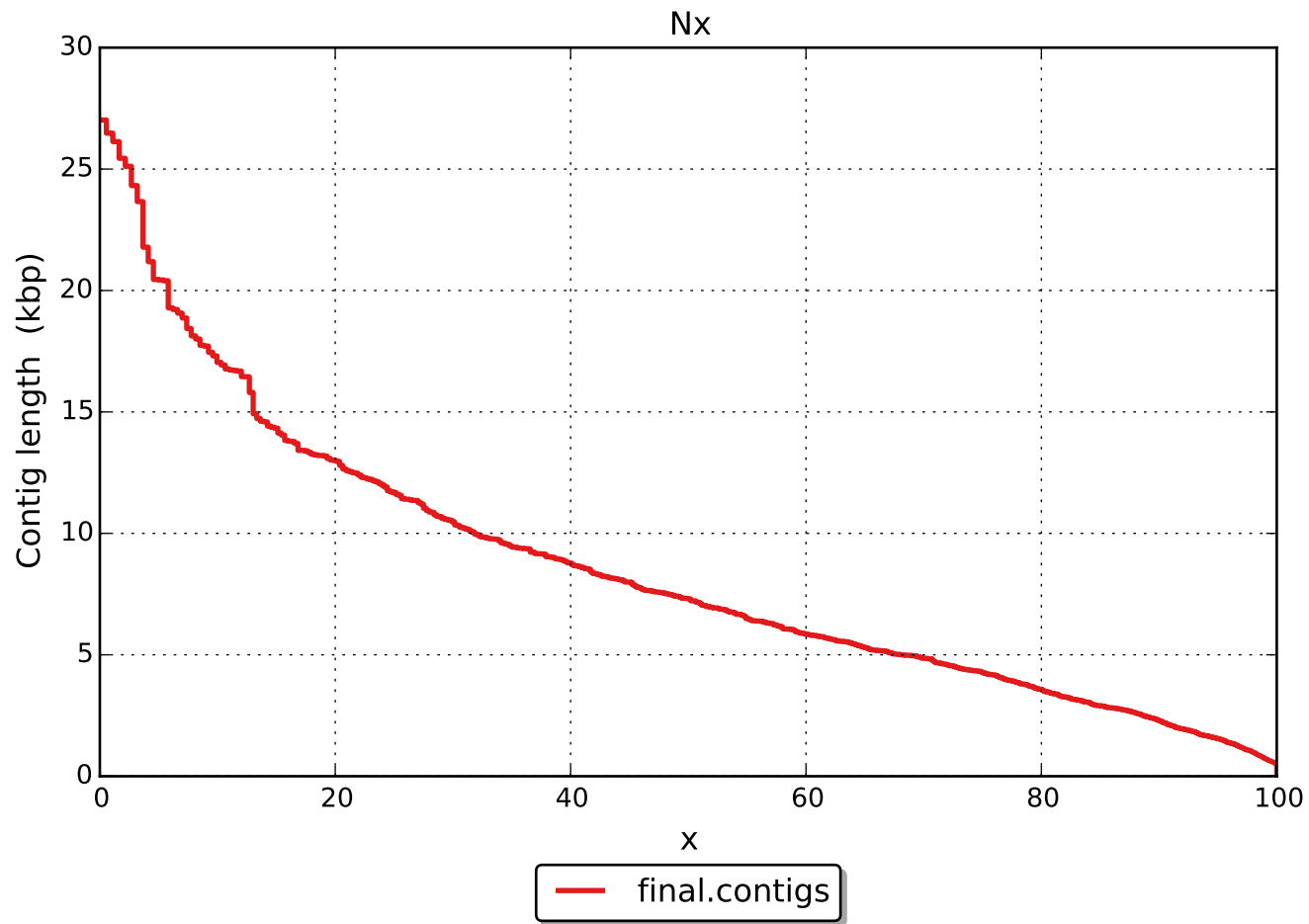
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	1134
# indels	0
# short indels	0
# long indels	0
Indels length	0

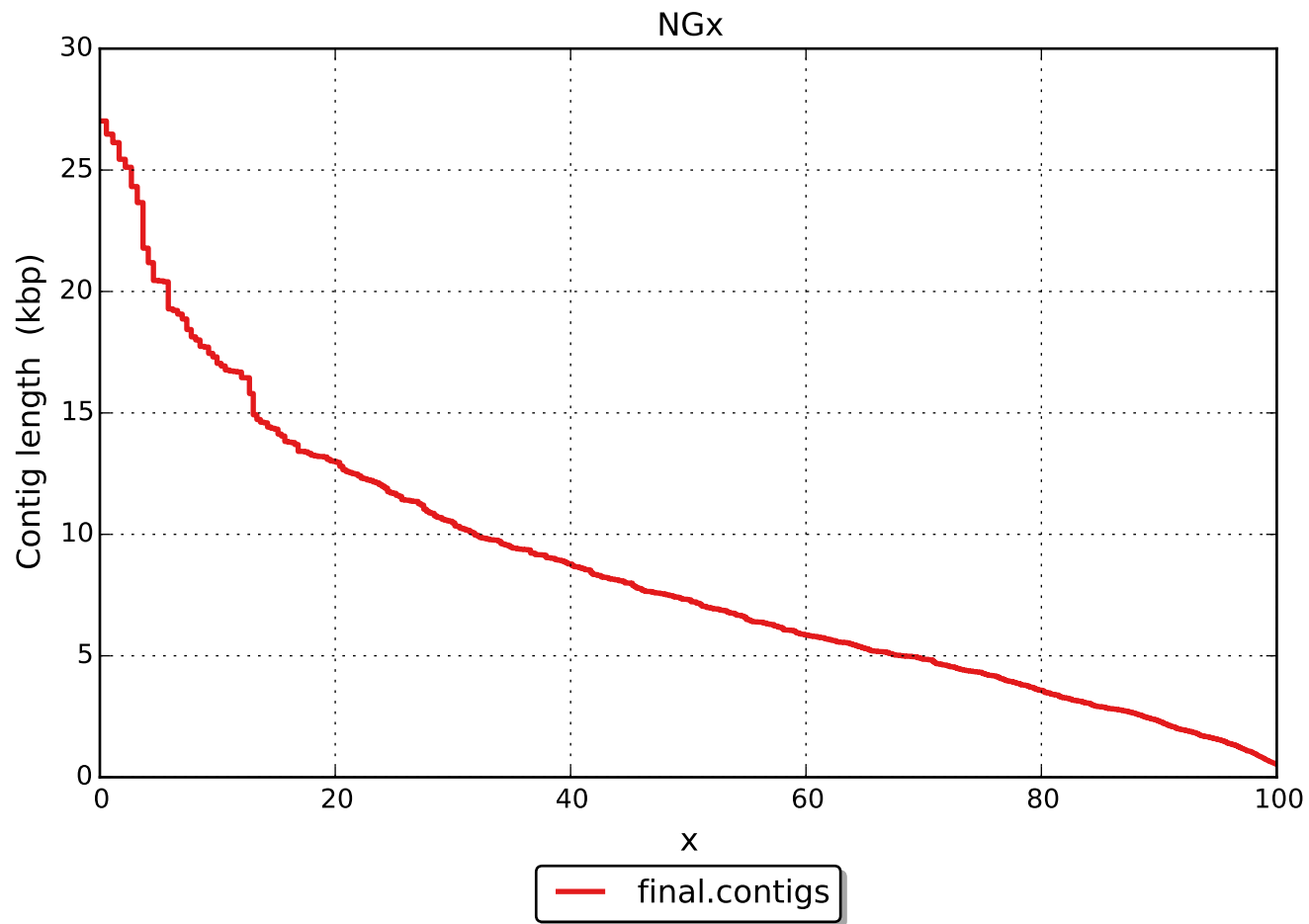
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

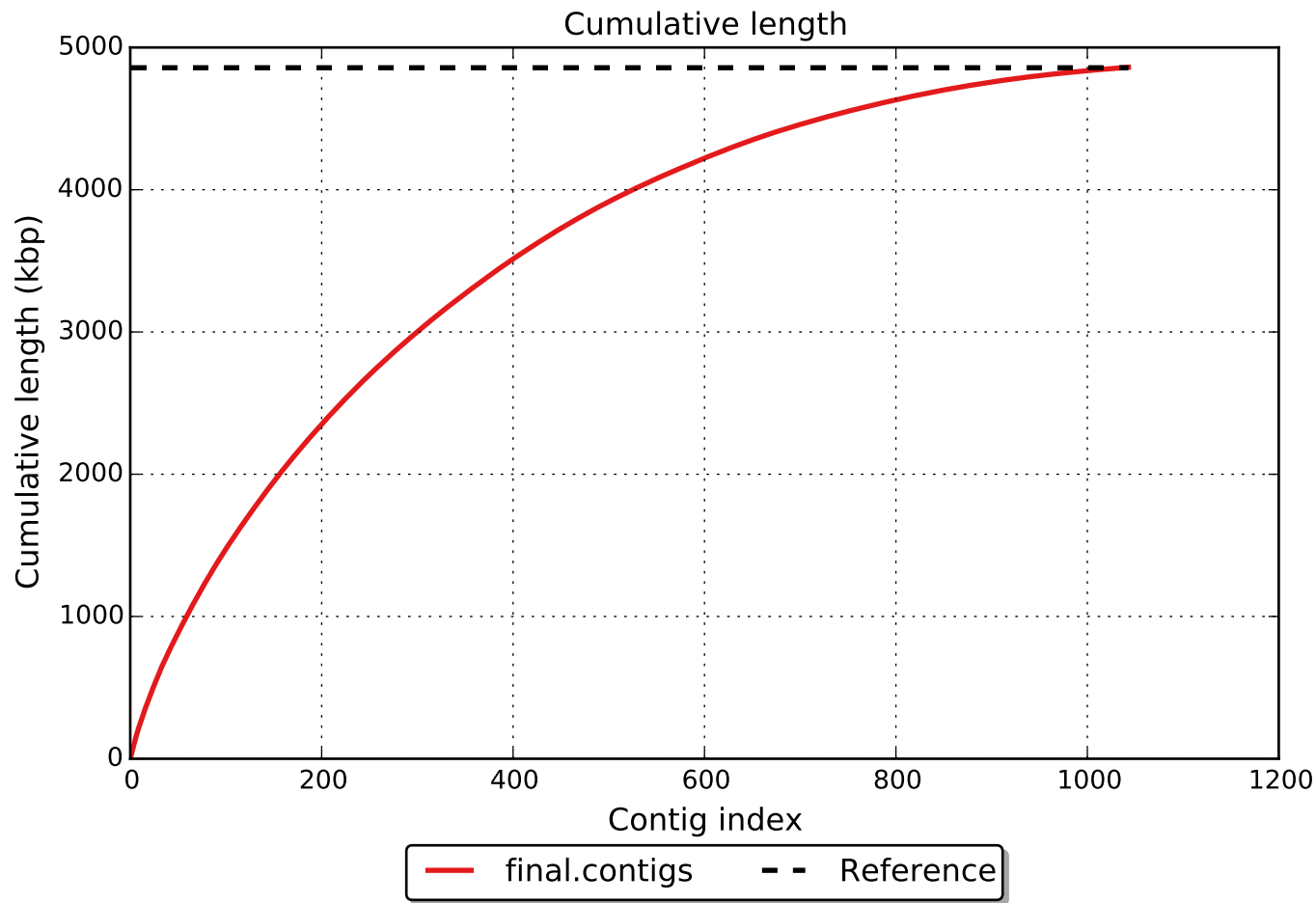
## Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	252
# N's	0

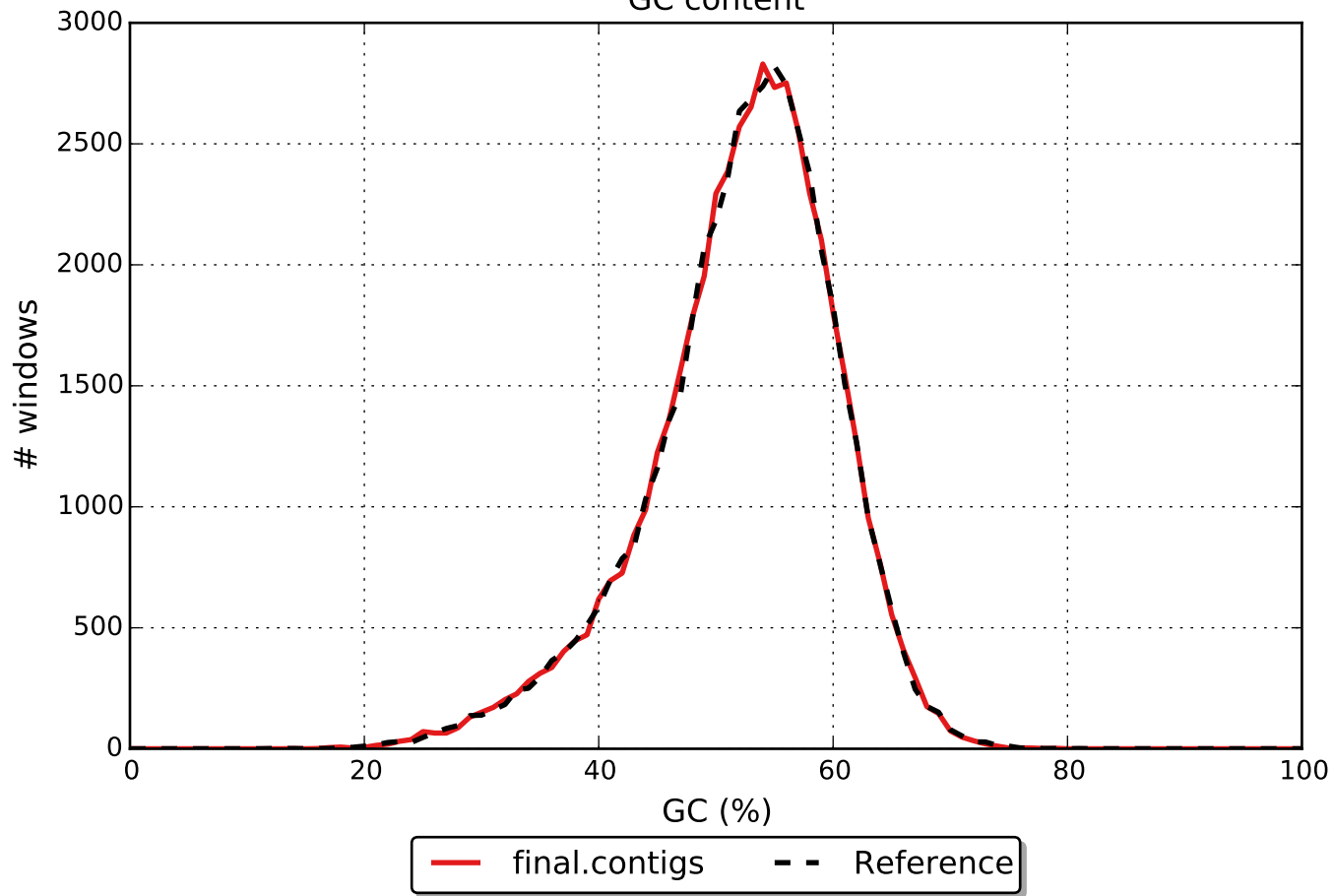
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







GC content

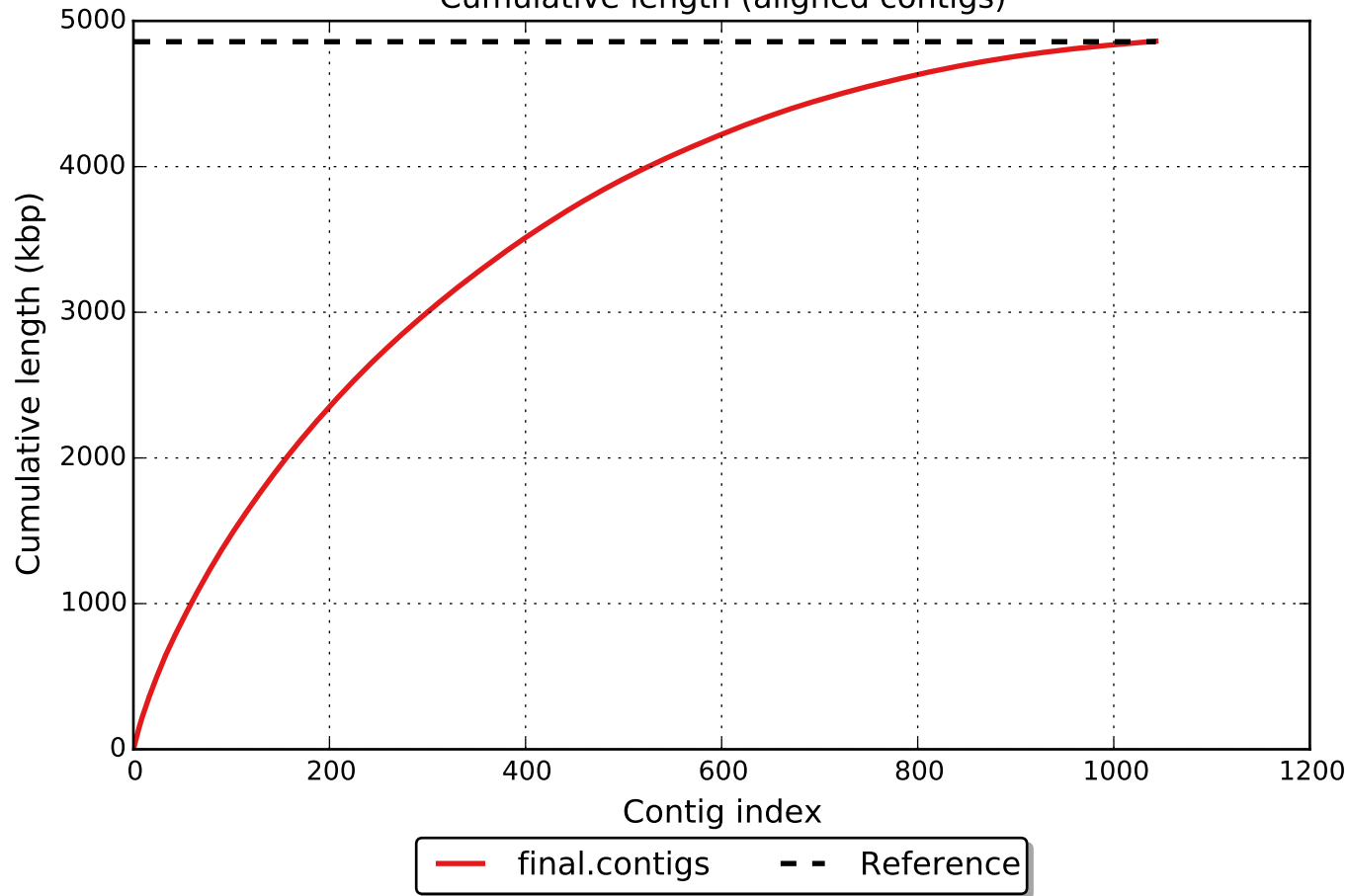


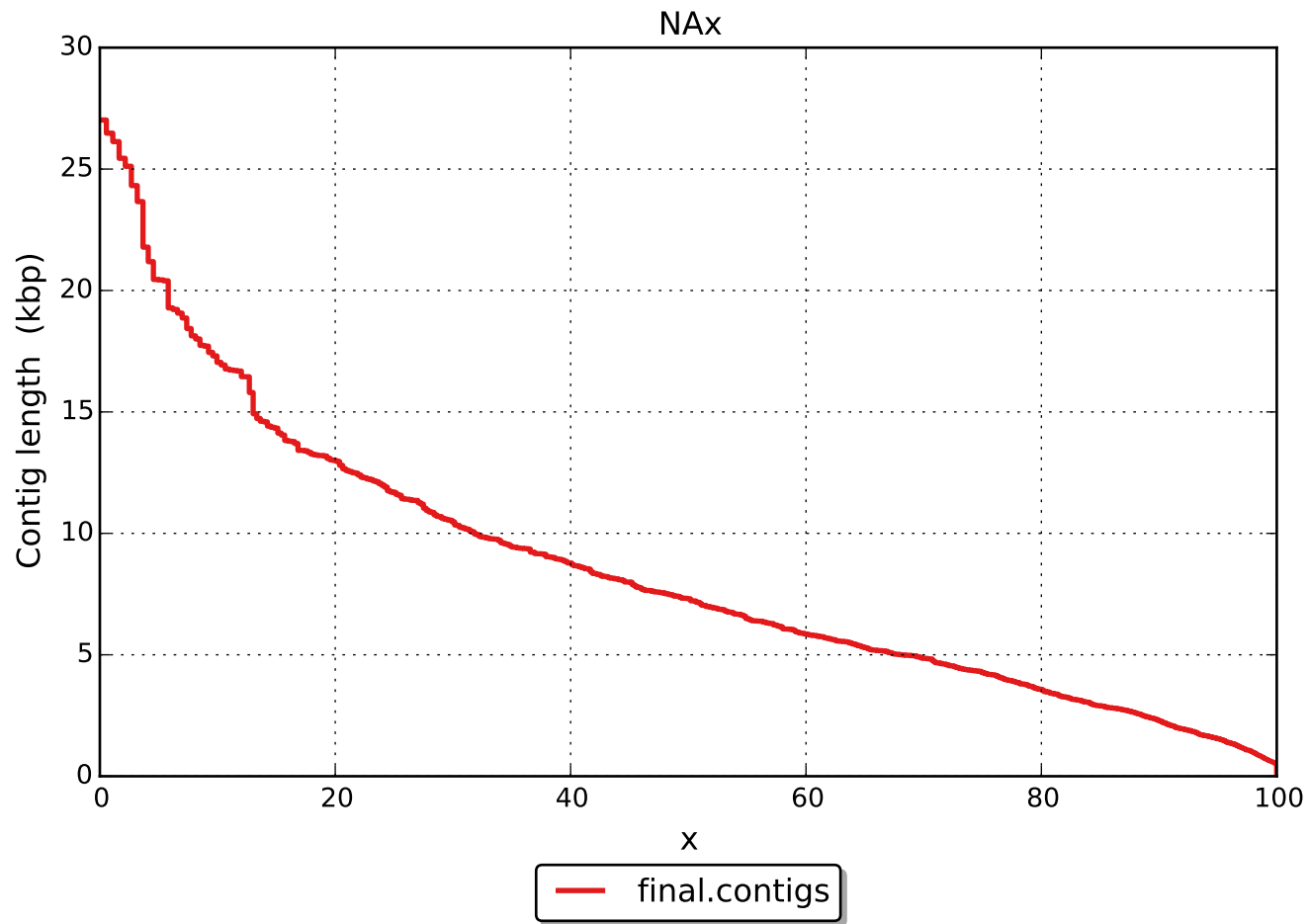
# Misassemblies





Cumulative length (aligned contigs)





# NGAx

