

## Report

	final.contigs
# contigs (>= 1000 bp)	871
# contigs (>= 5000 bp)	348
# contigs (>= 10000 bp)	99
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4629898
Total length (>= 5000 bp)	3188828
Total length (>= 10000 bp)	1449764
Total length (>= 25000 bp)	127866
Total length (>= 50000 bp)	0
# contigs	992
Largest contig	39629
Total length	4720114
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.79
N50	7054
NG50	7186
N75	4145
NG75	4314
L50	209
LG50	204
L75	425
LG75	411
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.691
Duplication ratio	1.020
# N's per 100 kbp	0.00
# mismatches per 100 kbp	20.01
# indels per 100 kbp	0.00
Largest alignment	39629
NA50	7054
NGA50	7186
NA75	4145
NGA75	4314
LA50	209
LGA50	204
LA75	425
LGA75	411

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

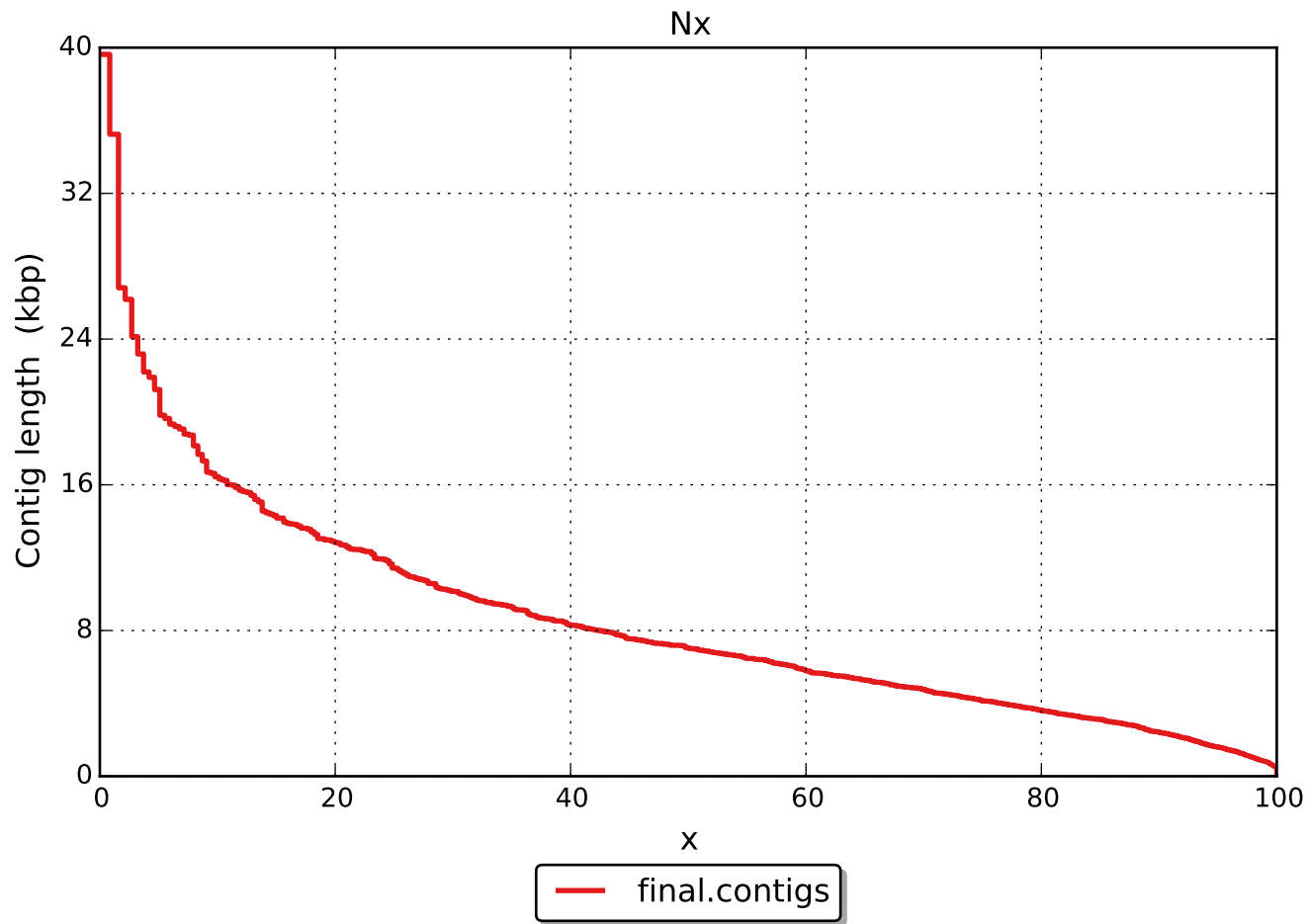
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	926
# indels	0
# short indels	0
# long indels	0
Indels length	0

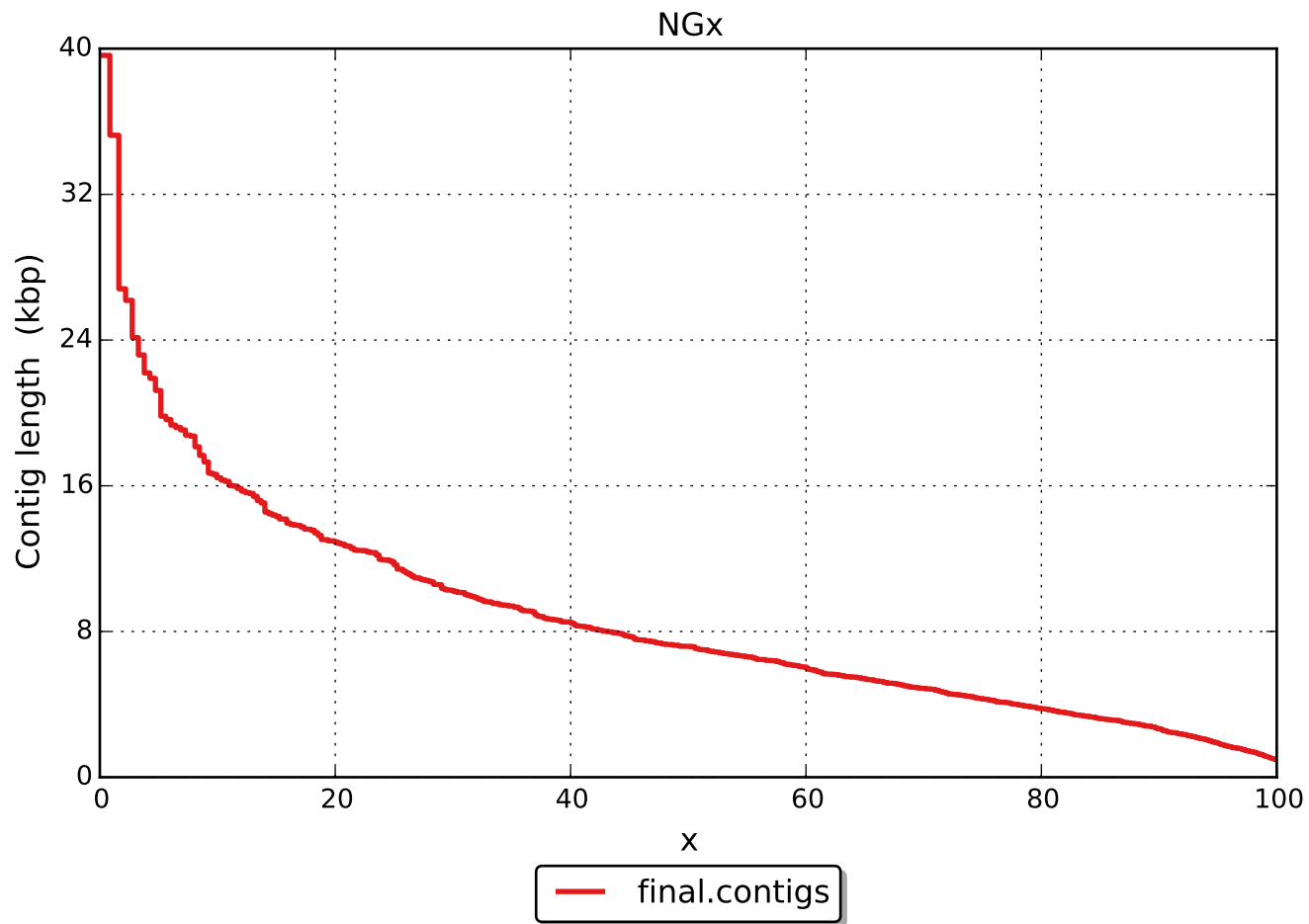
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

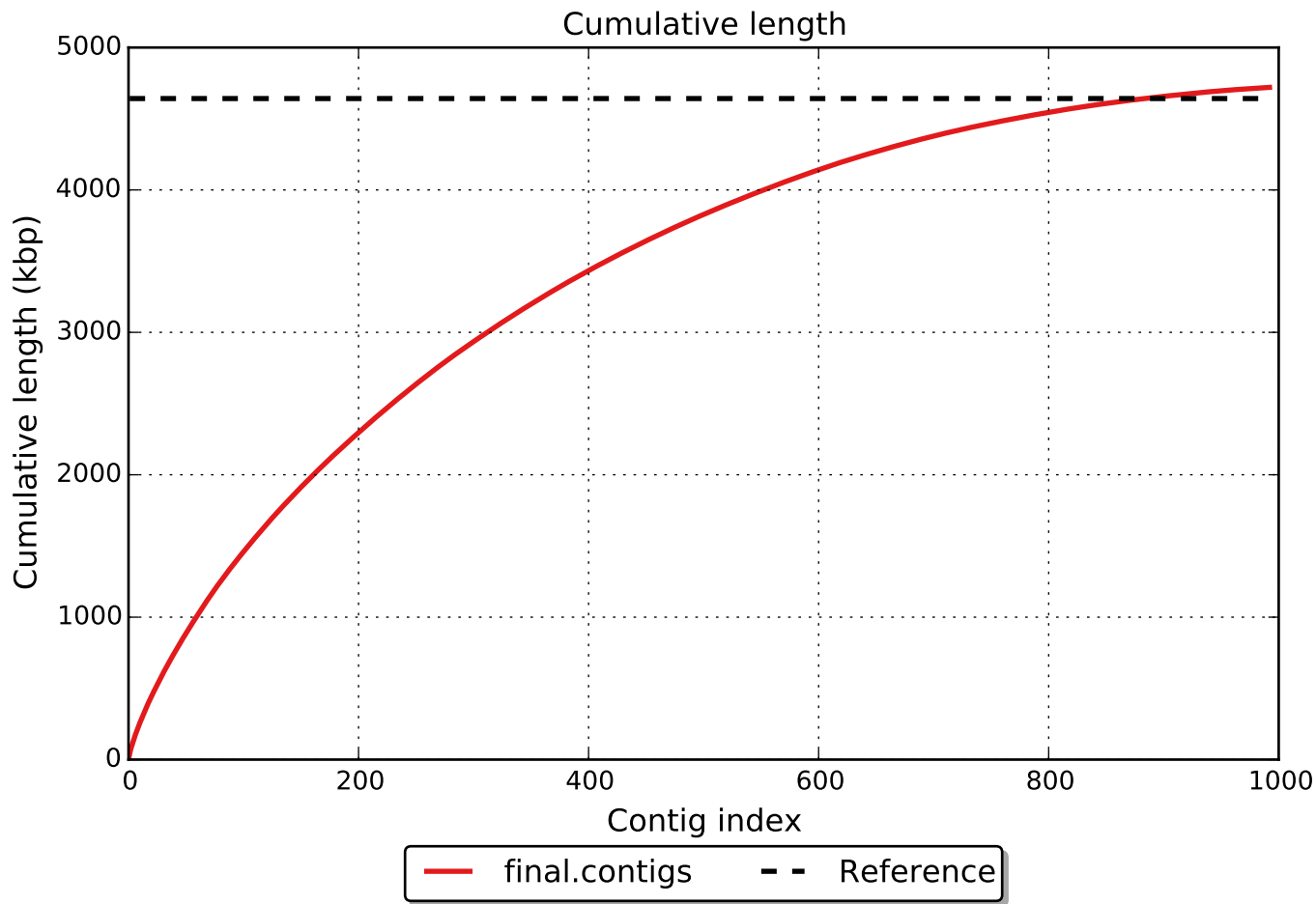
## Unaligned report

	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

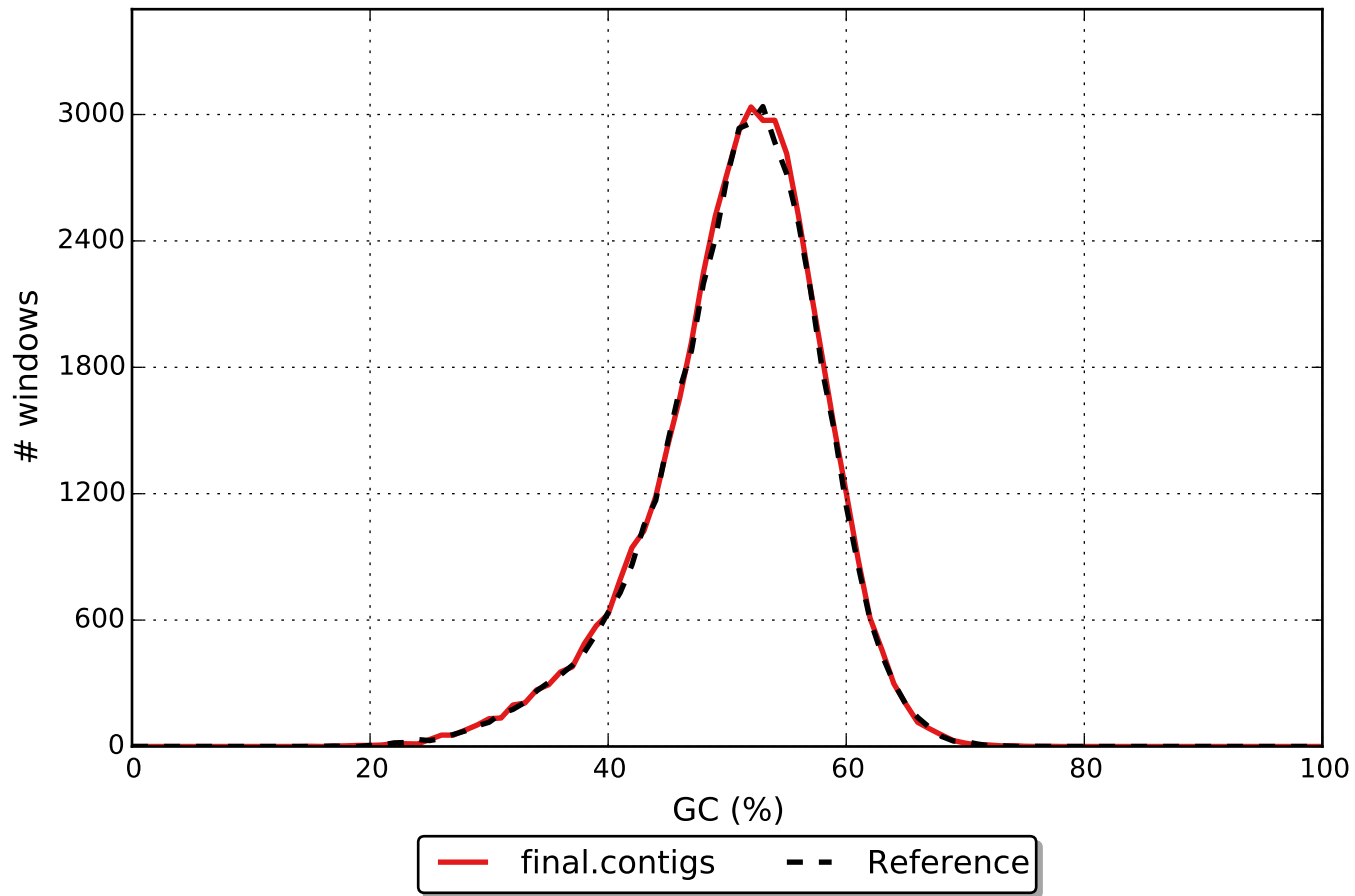
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







GC content

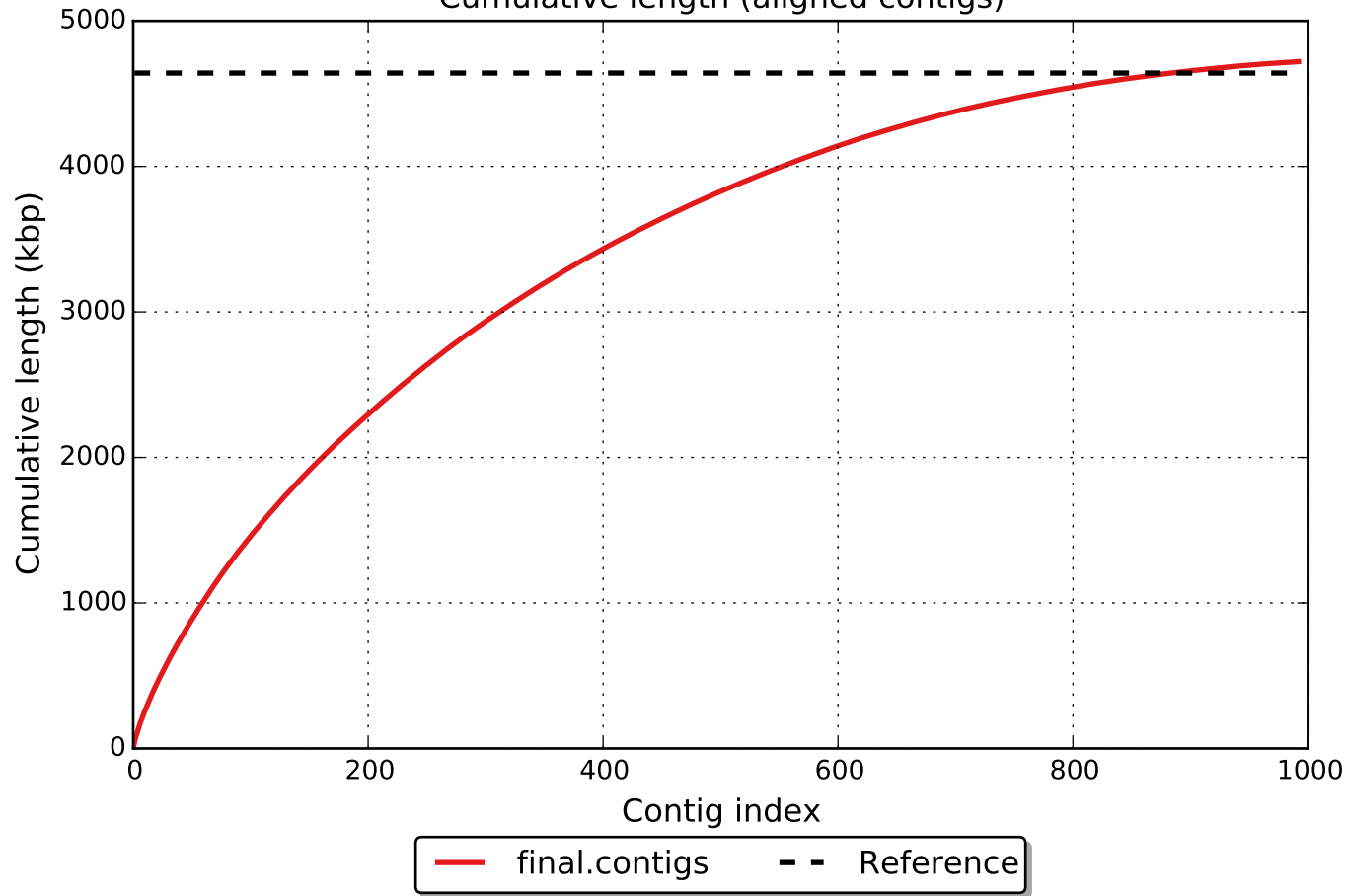


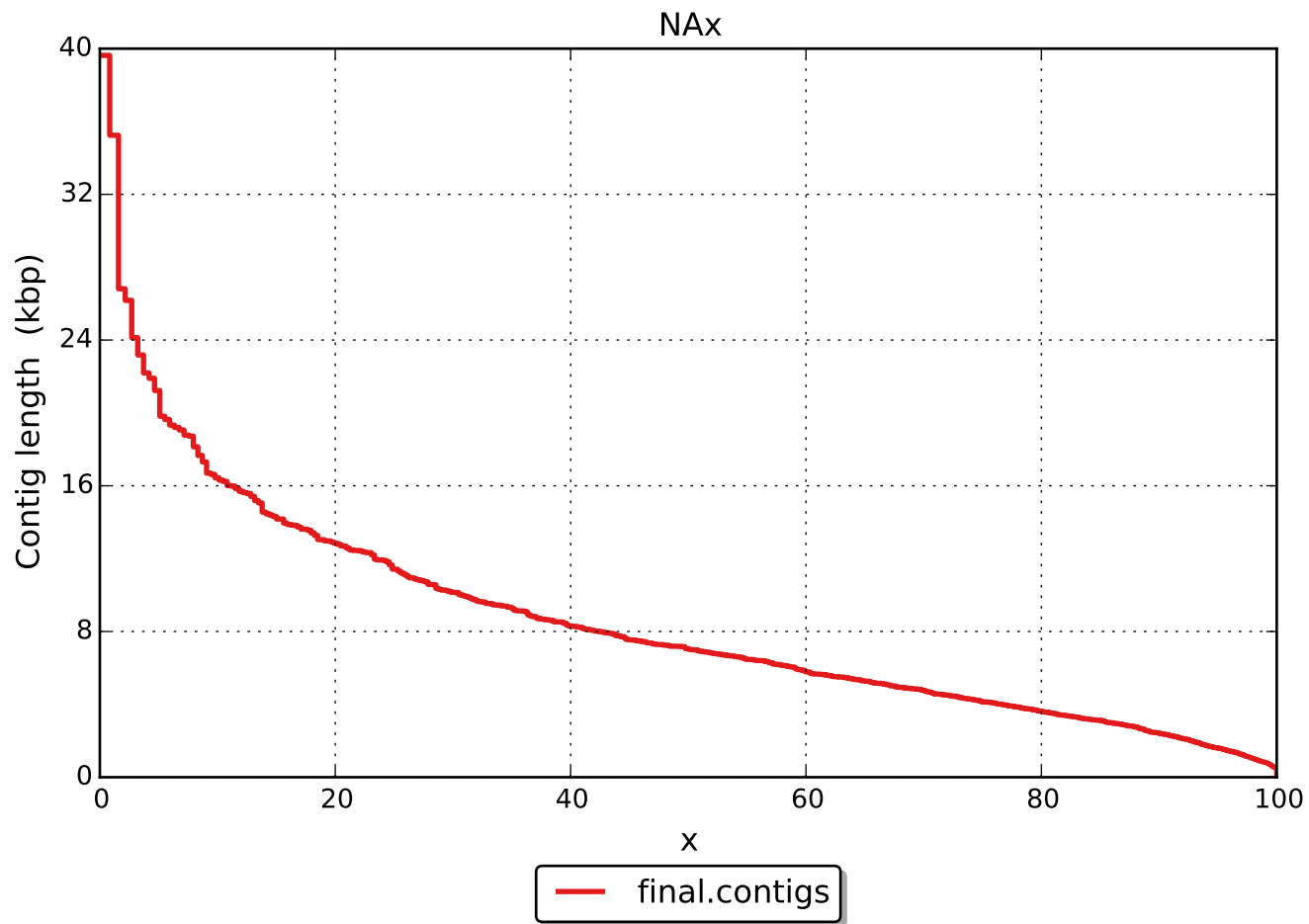
# Misassemblies





Cumulative length (aligned contigs)





# NGAx

