

## Report

	final.contigs
# contigs (>= 1000 bp)	870
# contigs (>= 5000 bp)	362
# contigs (>= 10000 bp)	115
# contigs (>= 25000 bp)	8
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4871278
Total length (>= 5000 bp)	3487188
Total length (>= 10000 bp)	1767563
Total length (>= 25000 bp)	227736
Total length (>= 50000 bp)	0
# contigs	964
Largest contig	32238
Total length	4939120
Reference length	4857432
GC (%)	52.23
Reference GC (%)	52.22
N50	7581
NG50	7673
N75	4546
NG75	4681
L50	196
LG50	191
L75	408
LG75	395
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	6669
Genome fraction (%)	99.689
Duplication ratio	1.019
# N's per 100 kbp	0.00
# mismatches per 100 kbp	25.13
# indels per 100 kbp	0.00
Largest alignment	32238
NA50	7581
NGA50	7673
NA75	4512
NGA75	4664
LA50	196
LGA50	191
LA75	408
LGA75	395

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

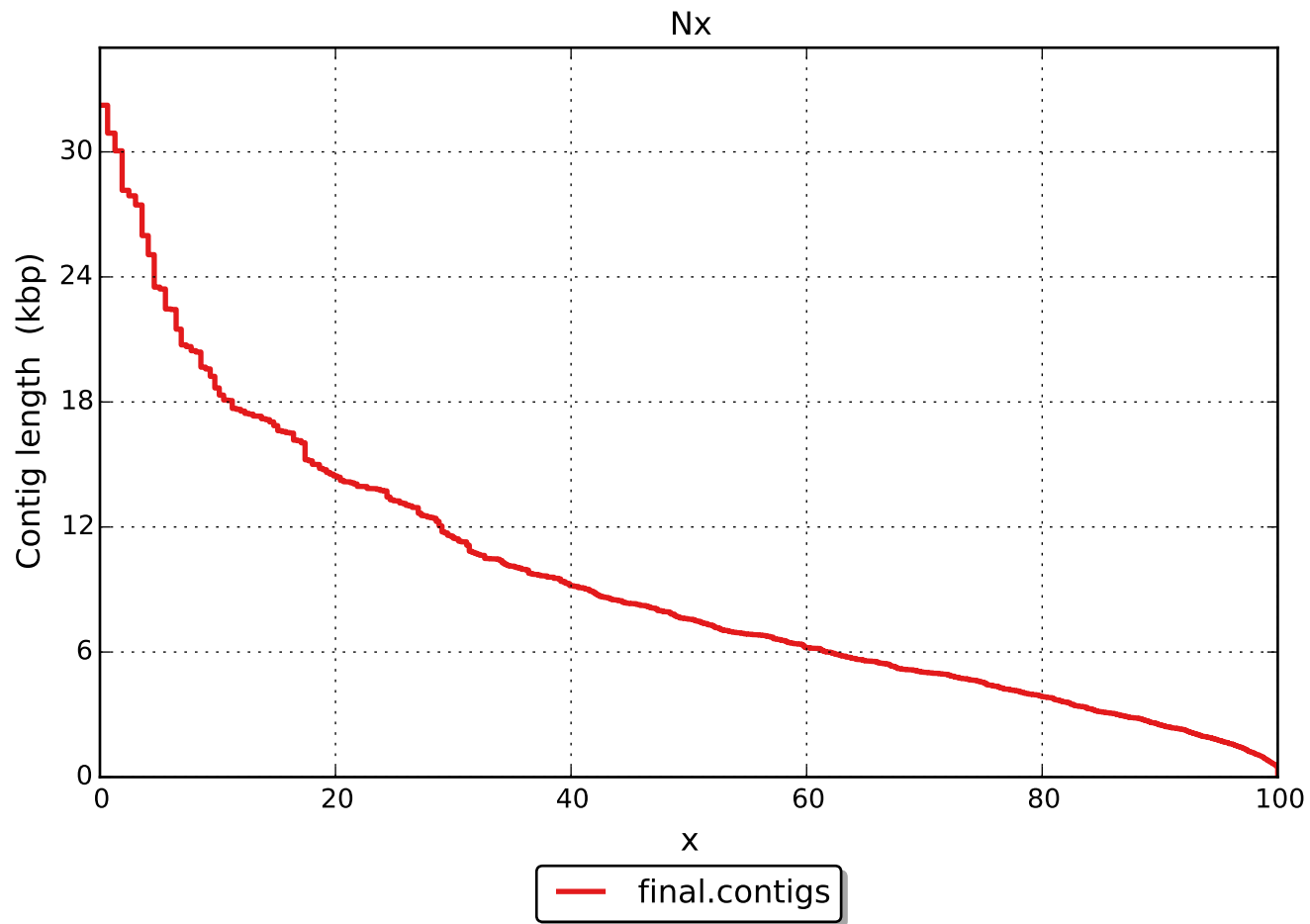
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1217
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

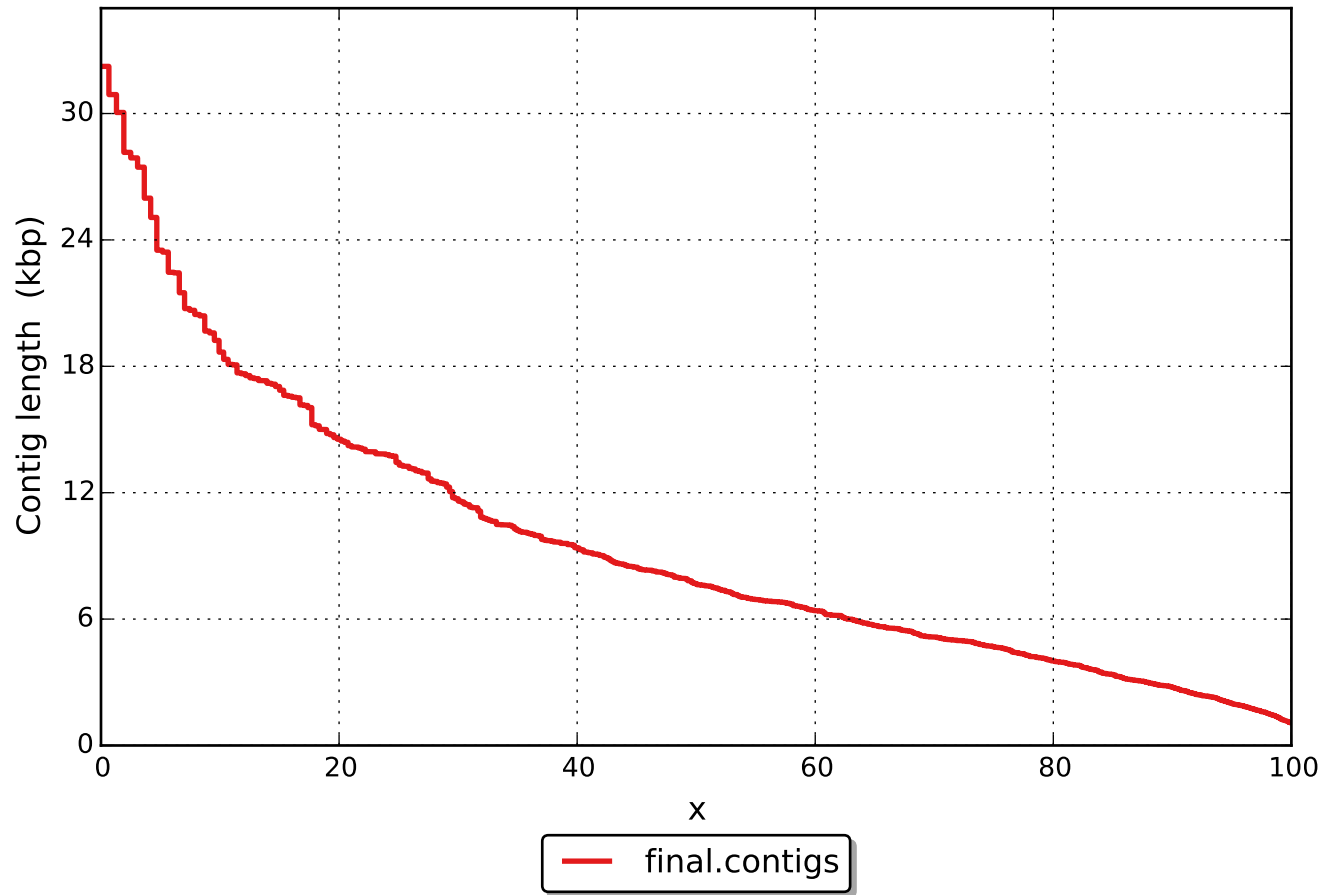
## Unaligned report

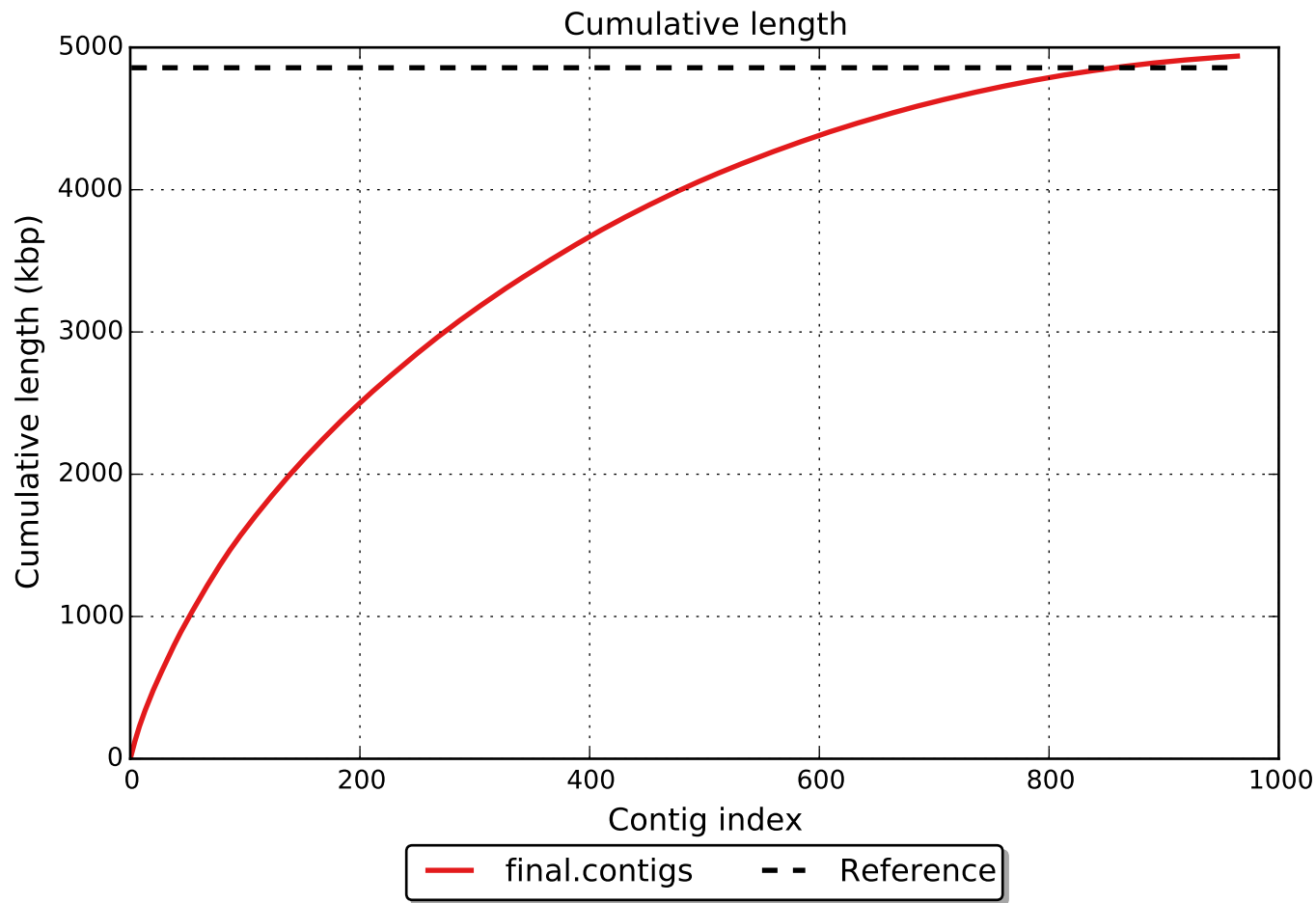
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	6669
# N's	0

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).

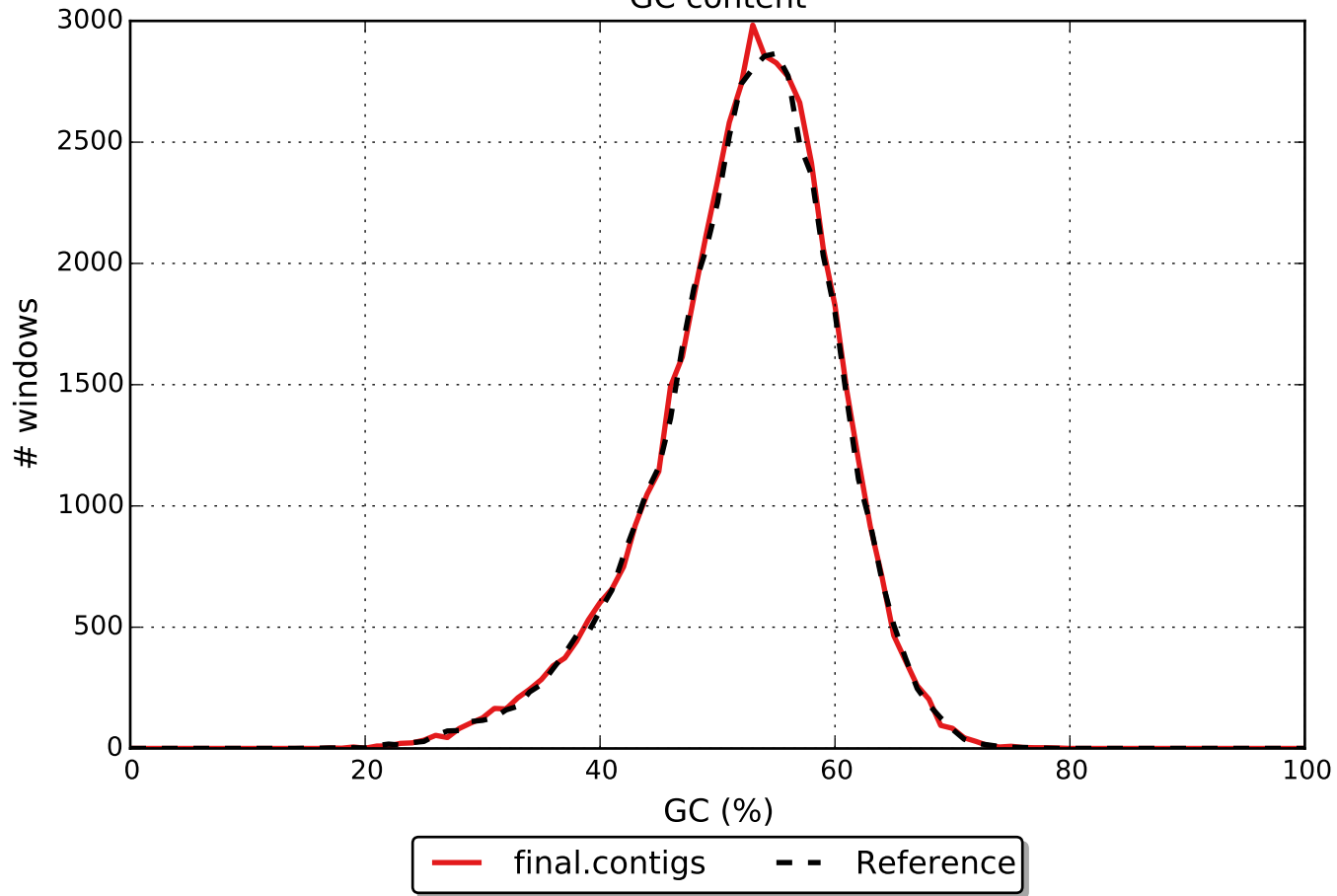


NGx





GC content

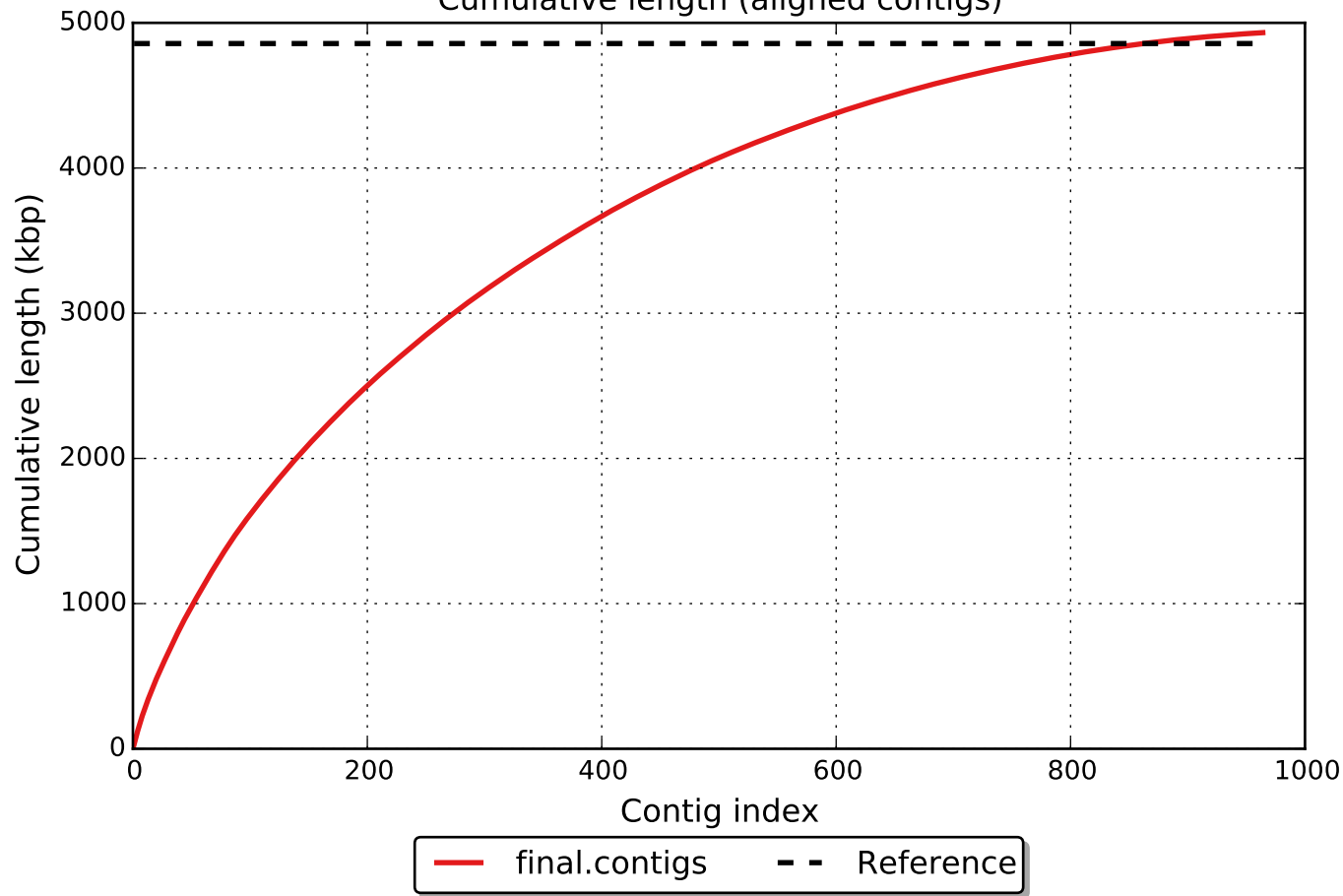


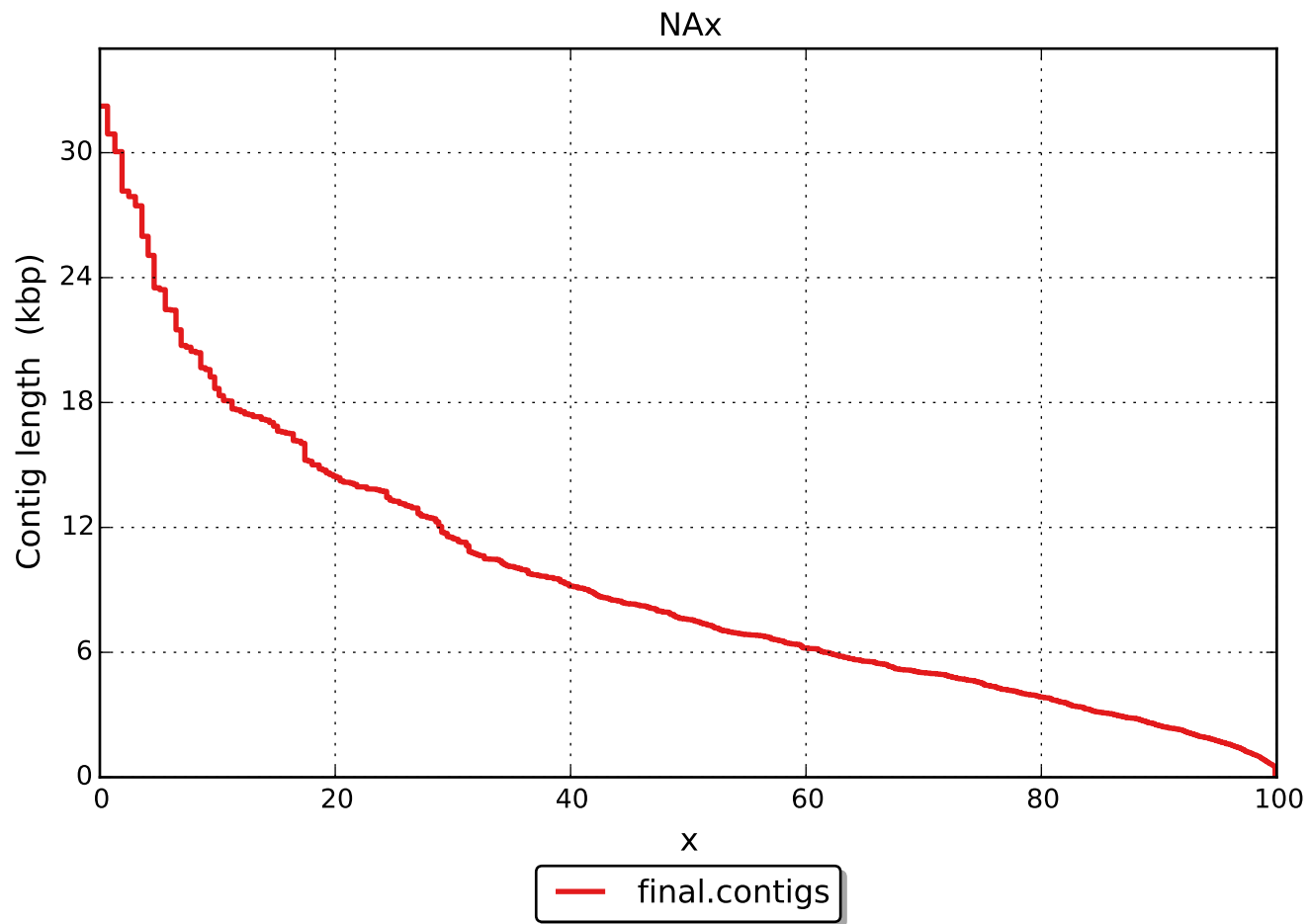
# Misassemblies





Cumulative length (aligned contigs)





# NGAx

