

## Report

	final.contigs
# contigs (>= 0 bp)	12122
# contigs (>= 1000 bp)	1560
# contigs (>= 5000 bp)	14
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	6709677
Total length (>= 1000 bp)	2972934
Total length (>= 5000 bp)	88998
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2811
Largest contig	9644
Total length	3879340
Reference length	4641652
GC (%)	50.83
Reference GC (%)	50.79
N50	1672
NG50	1390
N75	1032
NG75	724
L50	755
LG50	1005
L75	1498
LG75	2153
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	1 + 0 part
Unaligned length	516
Genome fraction (%)	82.323
Duplication ratio	1.015
# N's per 100 kbp	0.00
# mismatches per 100 kbp	8.03
# indels per 100 kbp	0.00
Largest alignment	9644
NA50	1672
NGA50	1390
NA75	1032
NGA75	724
LA50	755
LGA50	1005
LA75	1498
LGA75	2153

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

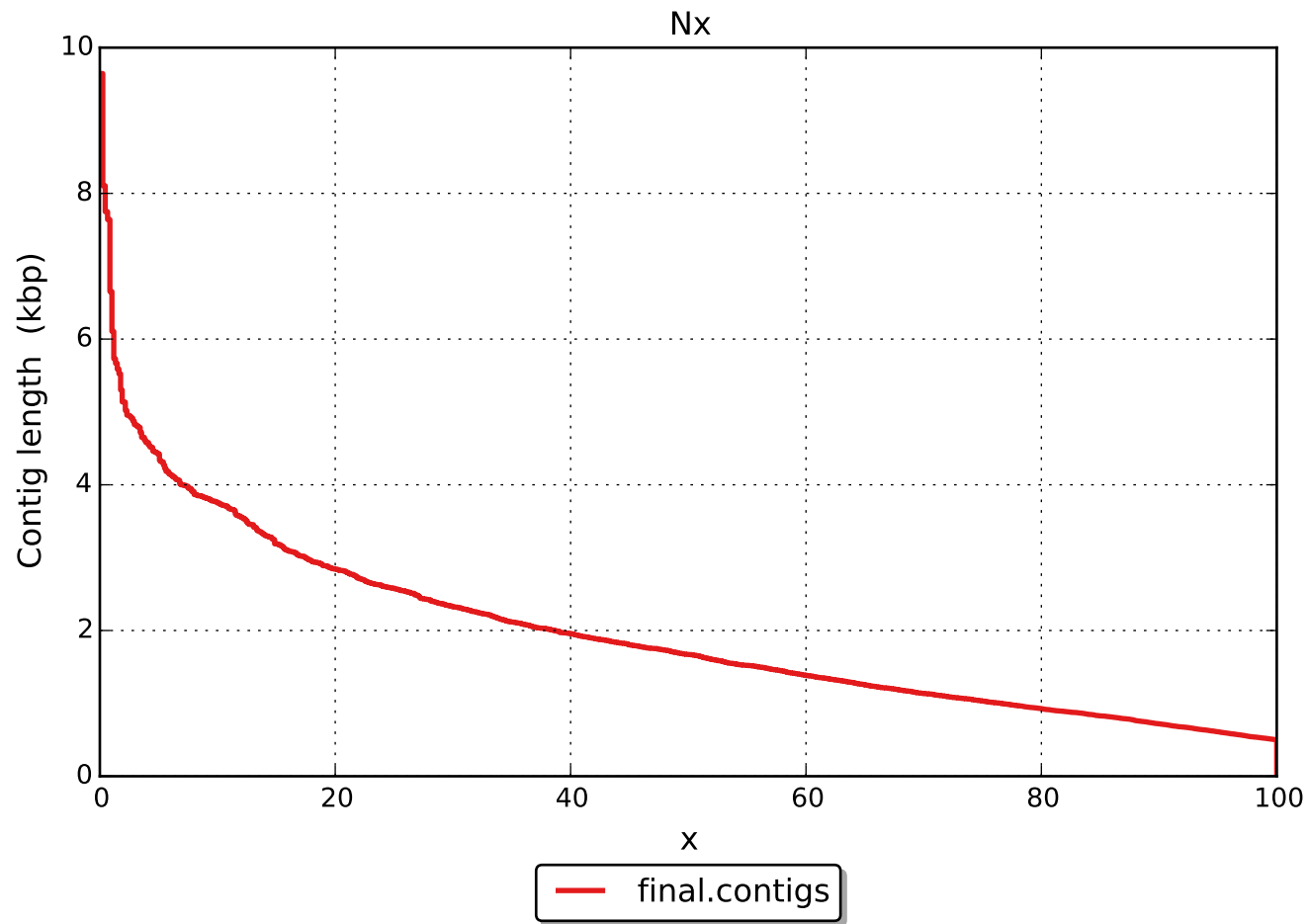
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	307
# indels	0
# short indels	0
# long indels	0
Indels length	0

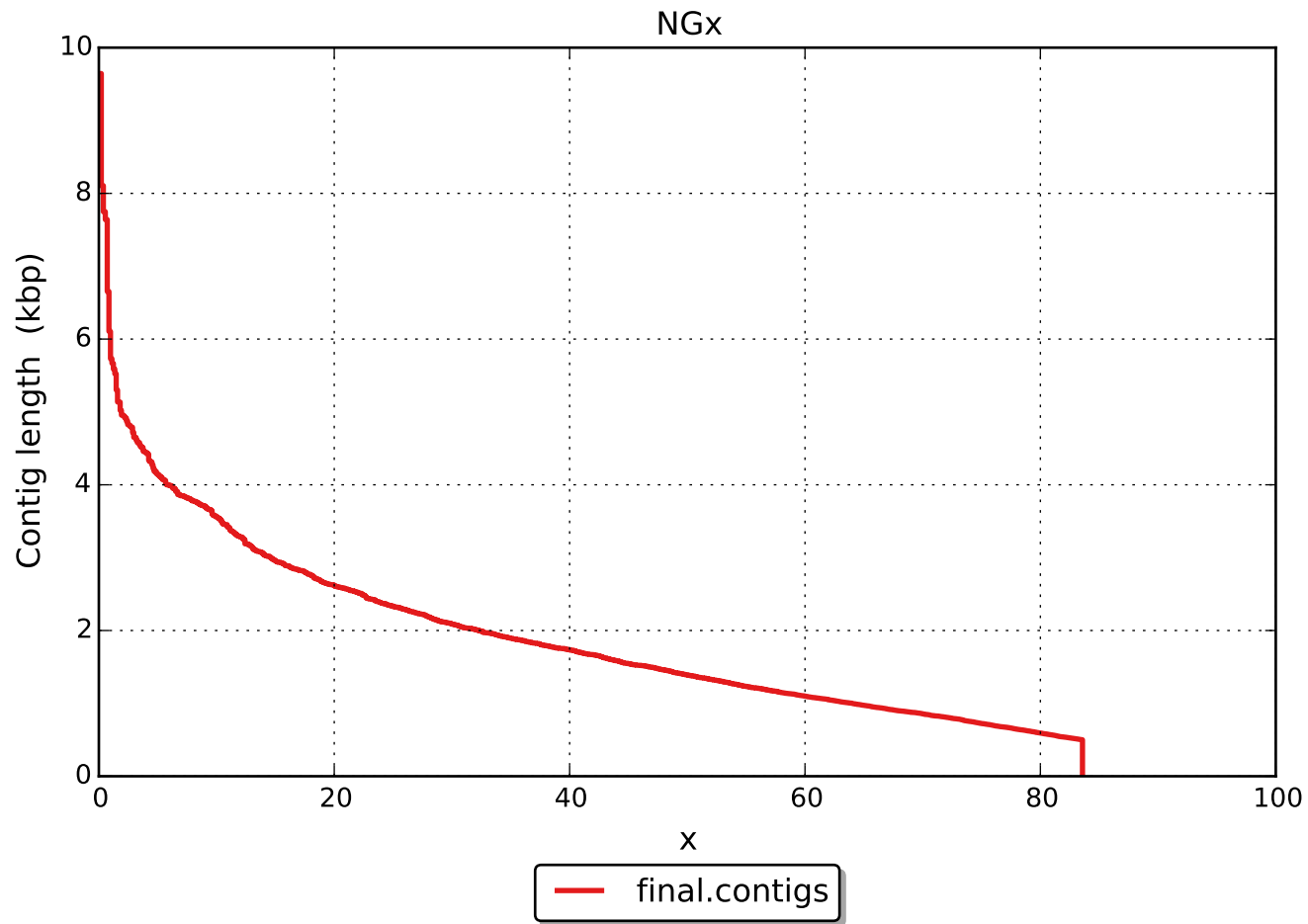
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

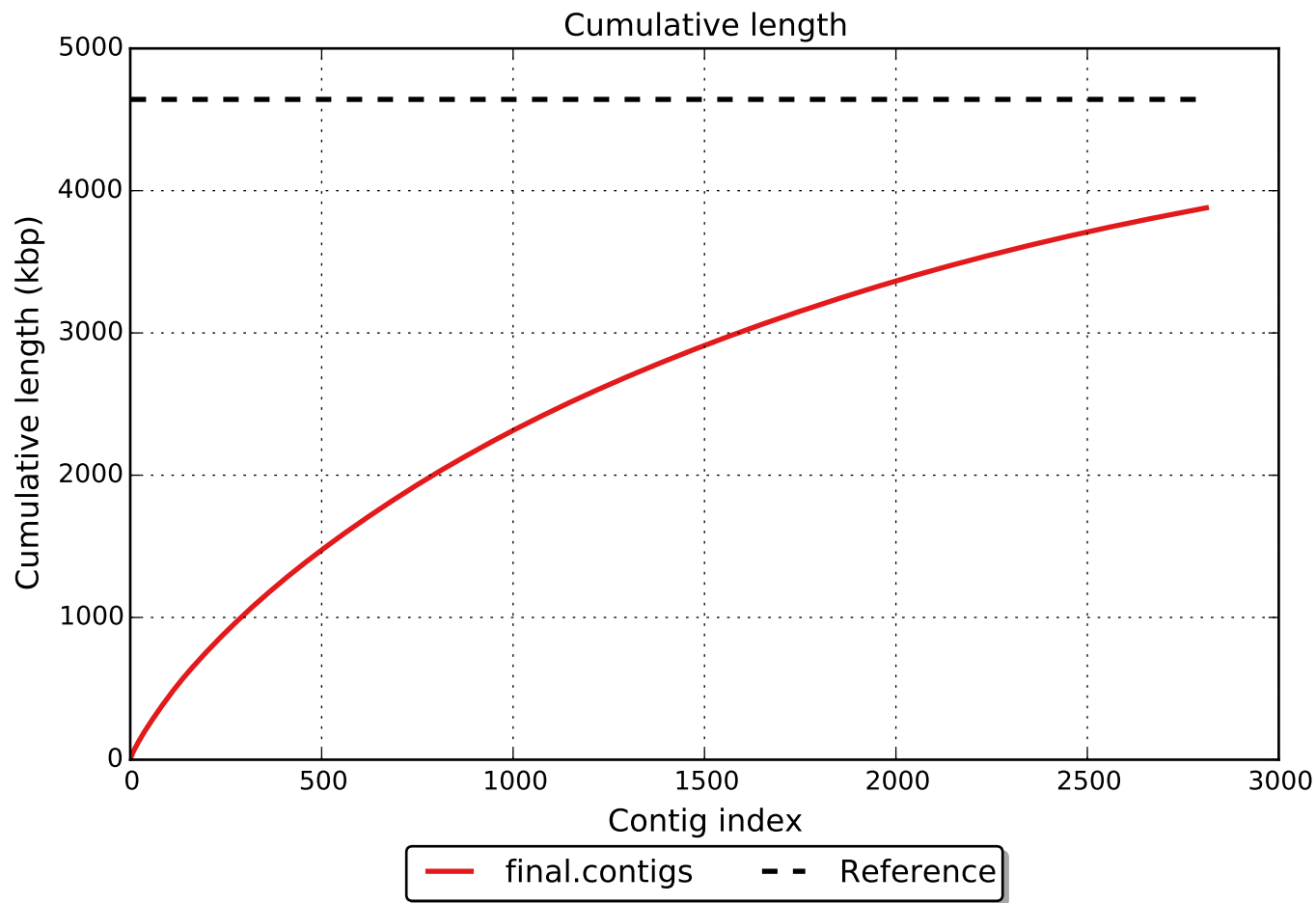
## Unaligned report

	final.contigs
# fully unaligned contigs	1
Fully unaligned length	516
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

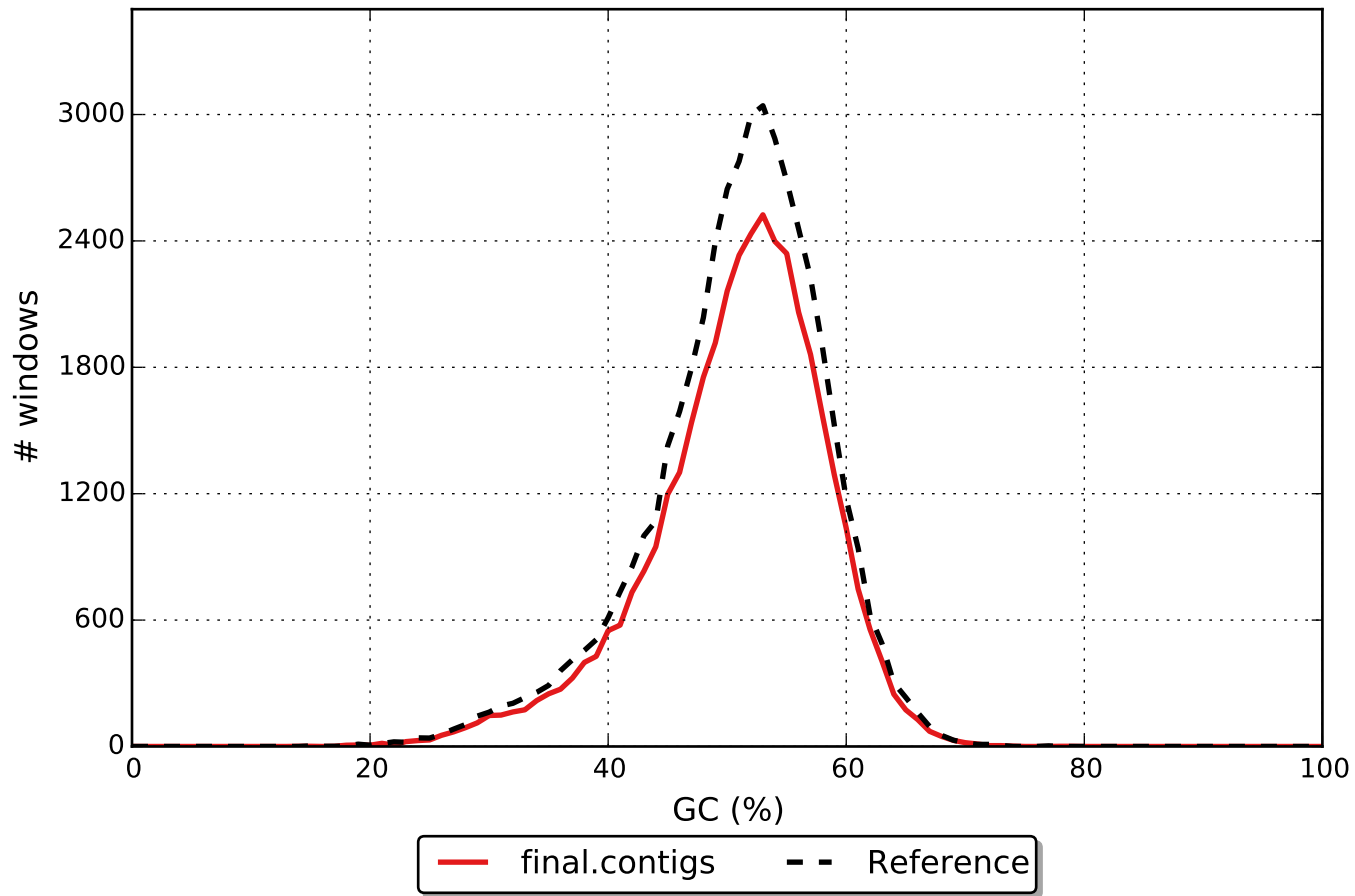
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







# GC content

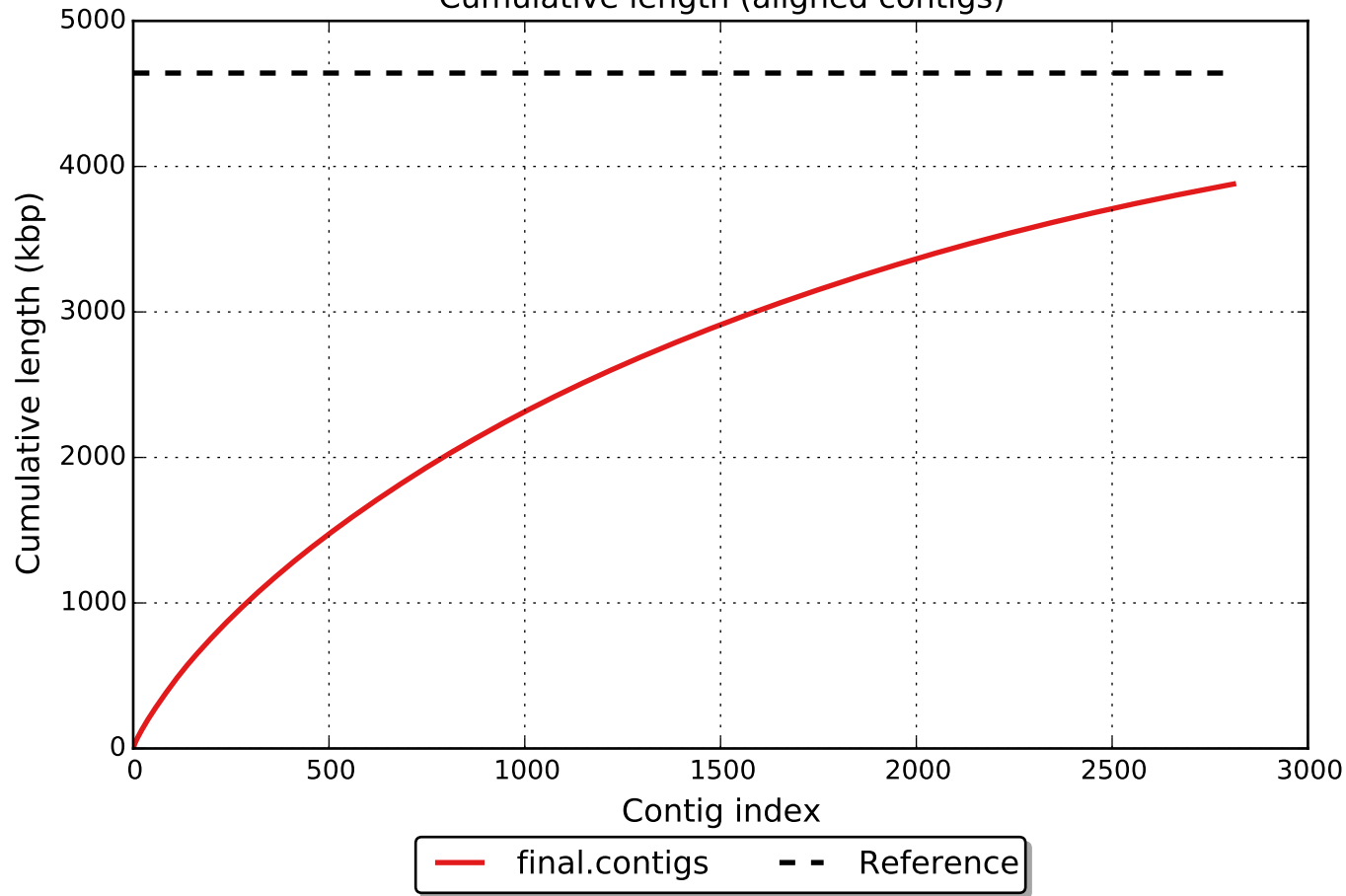


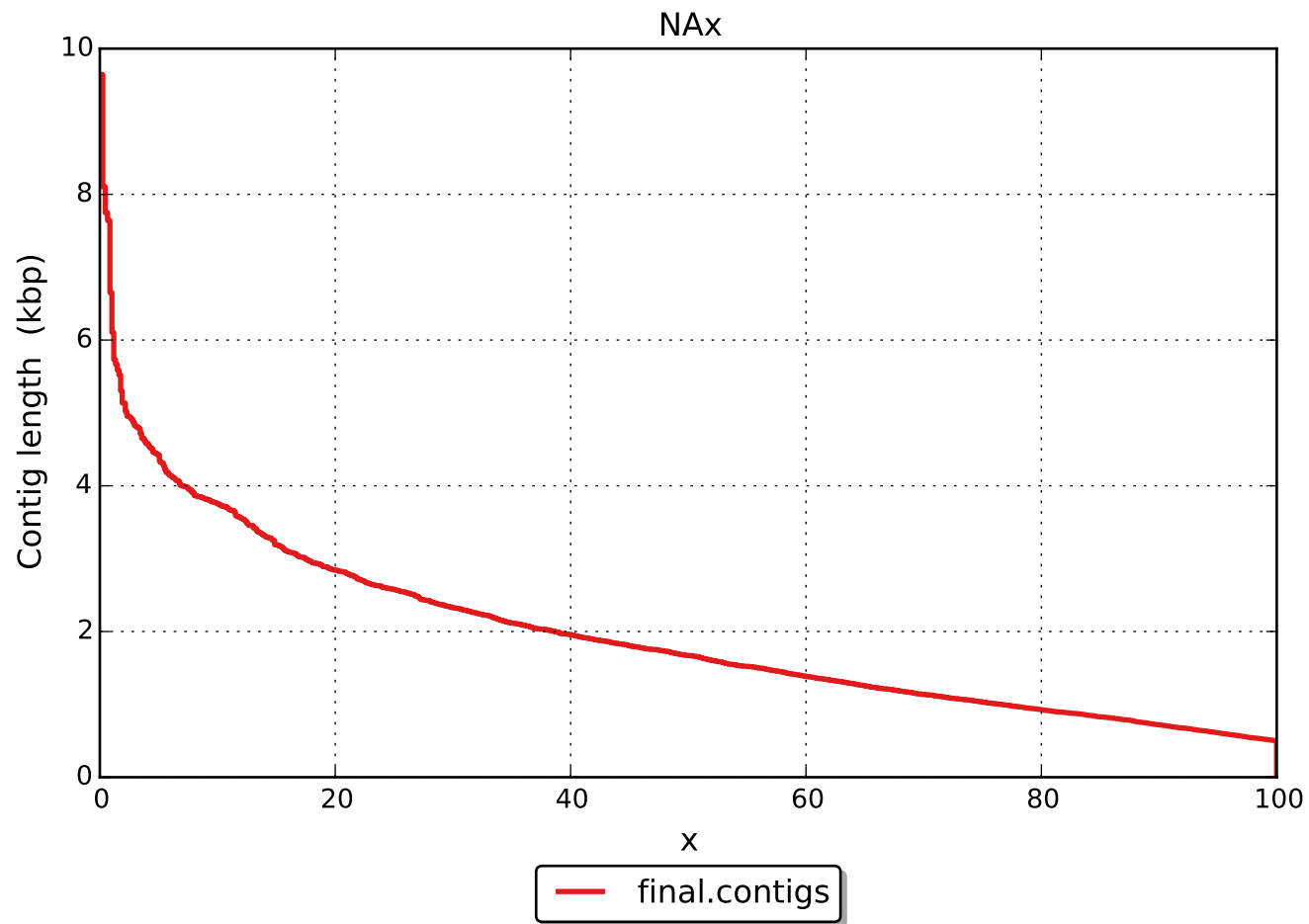
# Misassemblies





Cumulative length (aligned contigs)





NGAx

