

## Report

	final.contigs
# contigs (>= 1000 bp)	593
# contigs (>= 5000 bp)	325
# contigs (>= 10000 bp)	159
# contigs (>= 25000 bp)	18
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4547923
Total length (>= 5000 bp)	3839633
Total length (>= 10000 bp)	2663052
Total length (>= 25000 bp)	543484
Total length (>= 50000 bp)	0
# contigs	666
Largest contig	39323
Total length	4602039
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	11798
NG50	11742
N75	6571
NG75	6459
L50	126
LG50	128
L75	258
LG75	263
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 2 part
Unaligned length	1273
Genome fraction (%)	97.863
Duplication ratio	1.013
# N's per 100 kbp	0.00
# mismatches per 100 kbp	16.00
# indels per 100 kbp	0.04
Largest alignment	39323
NA50	11798
NGA50	11742
NA75	6571
NGA75	6459
LA50	126
LGA50	128
LA75	258
LGA75	263

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

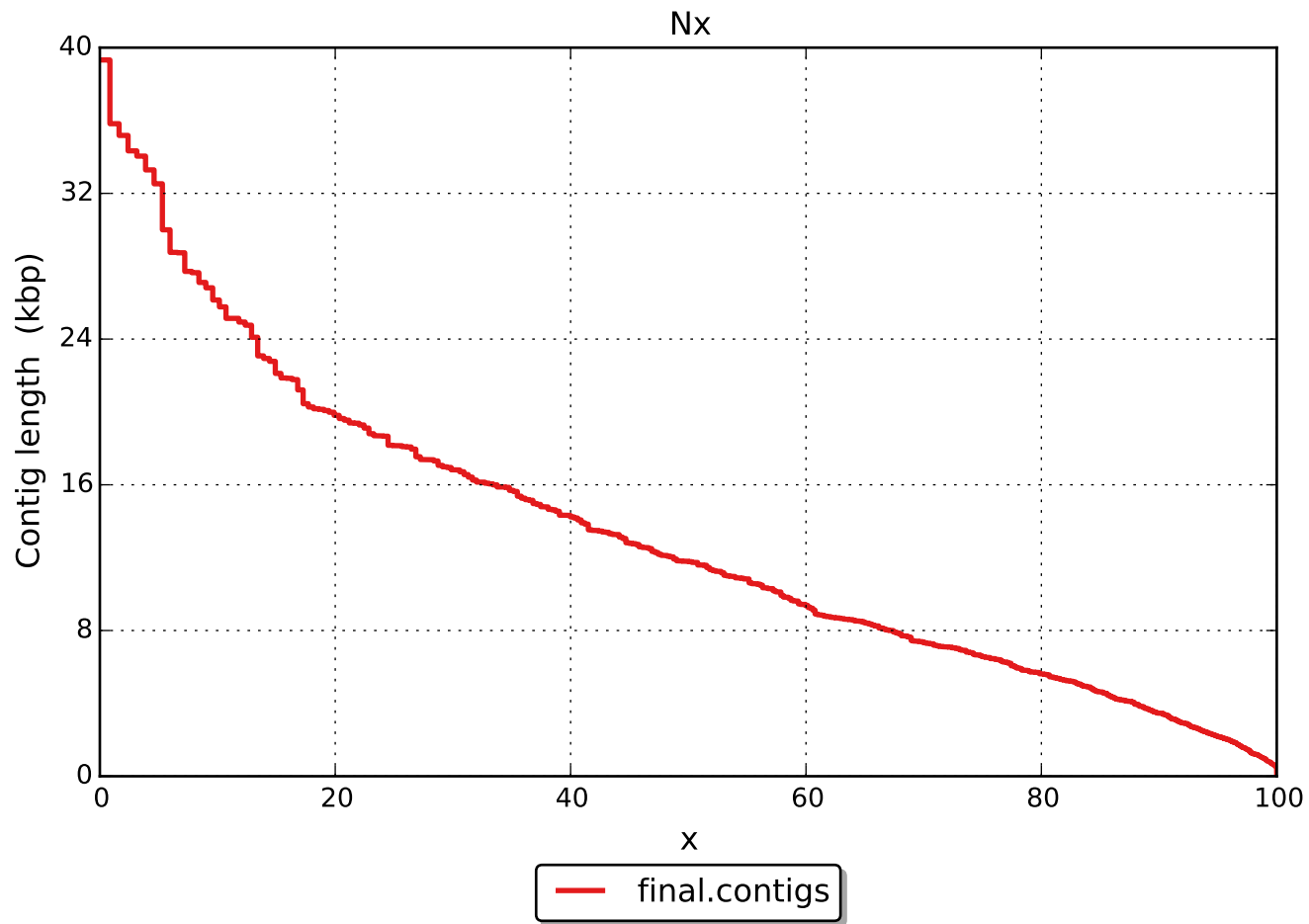
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	727
# indels	2
# short indels	2
# long indels	0
Indels length	2

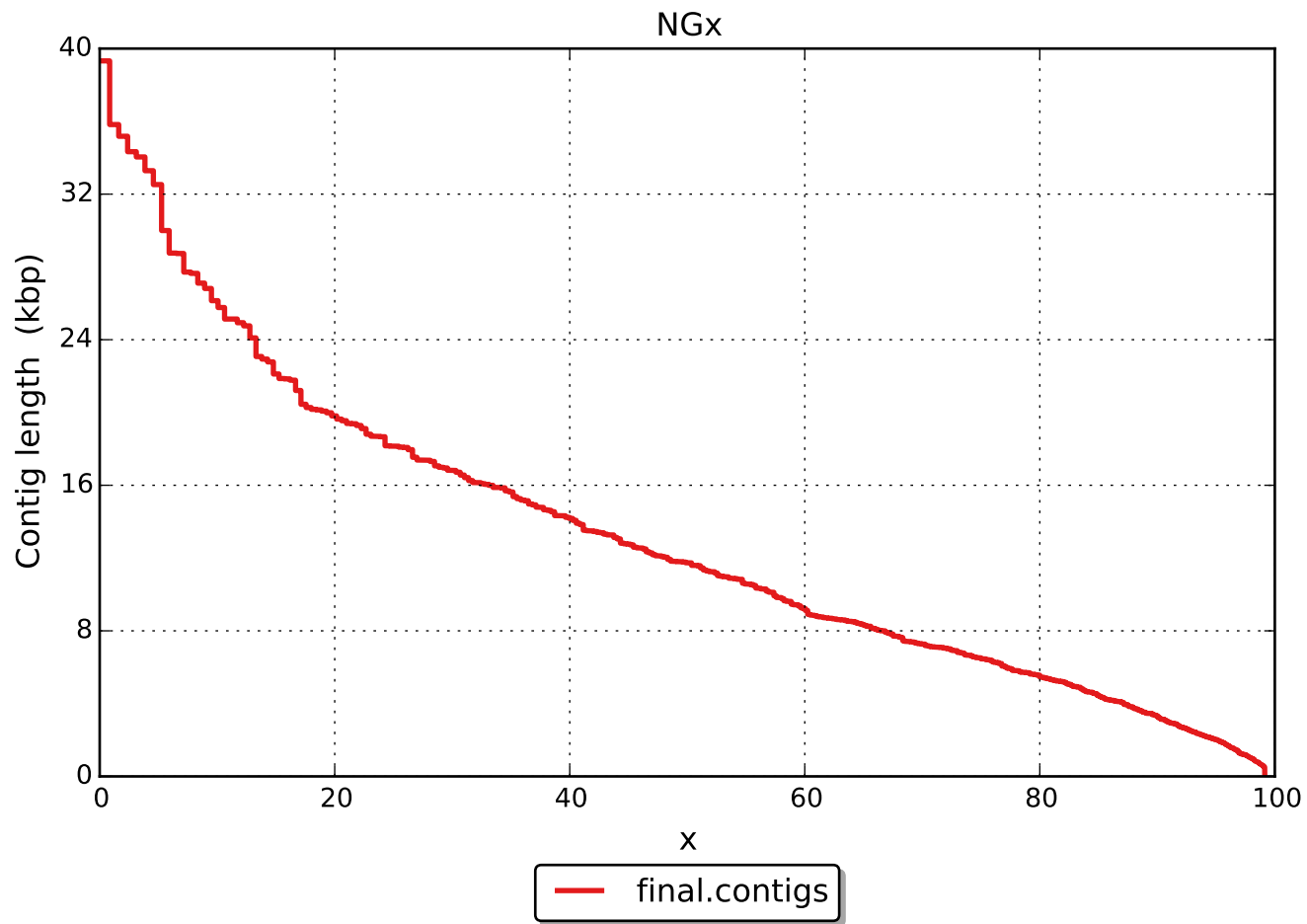
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

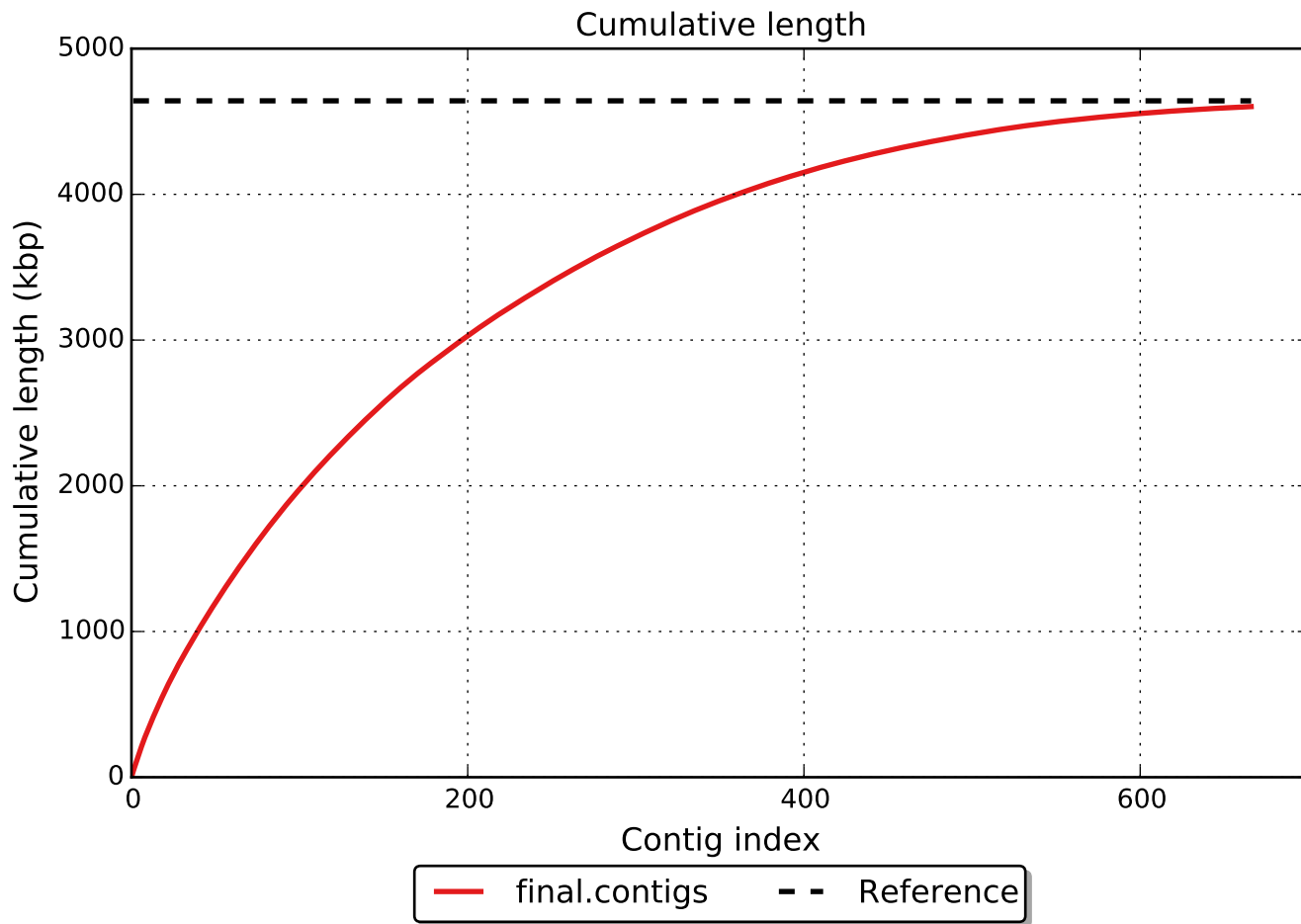
## Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	1
Partially unaligned length	1273
# N's	0

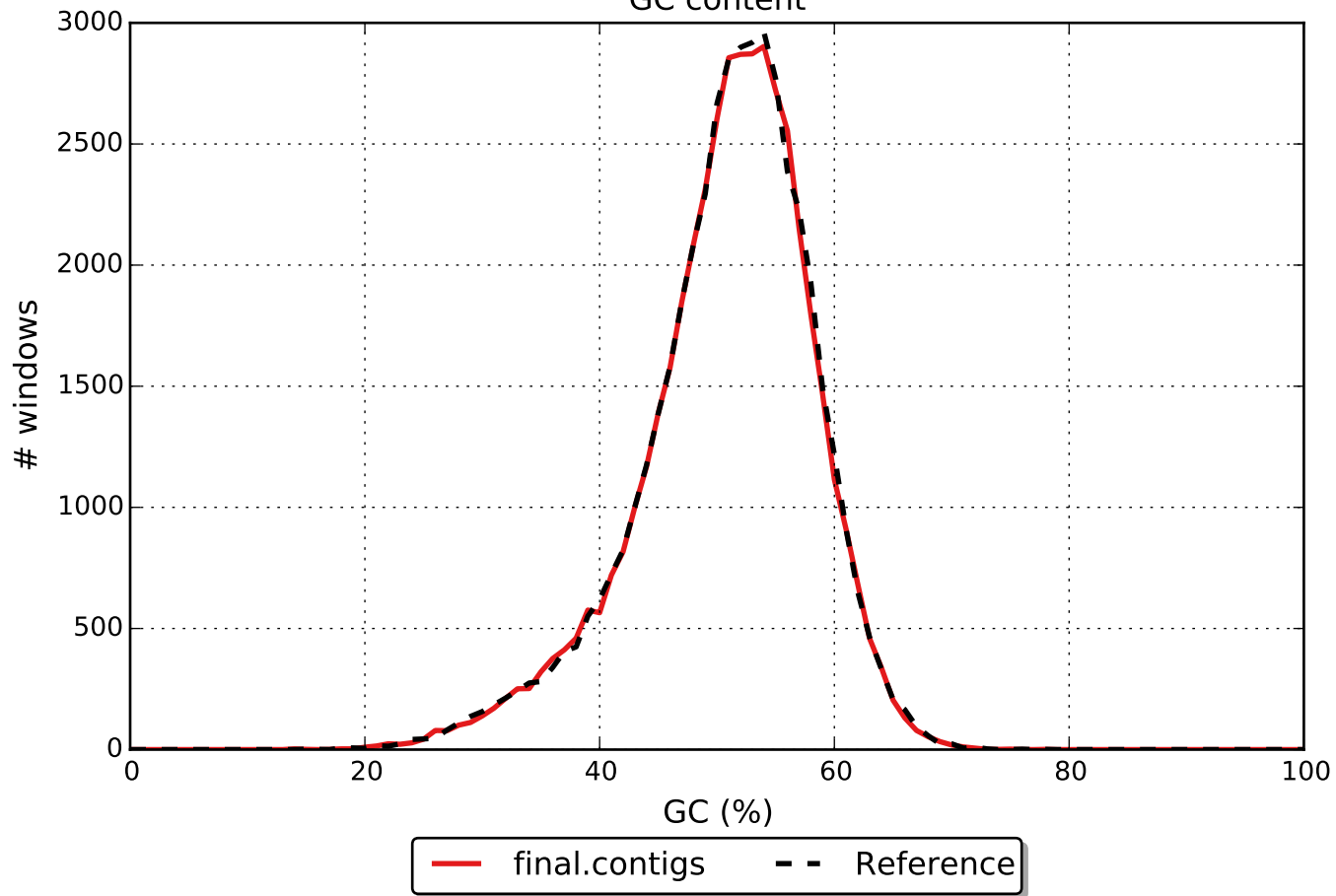
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







GC content

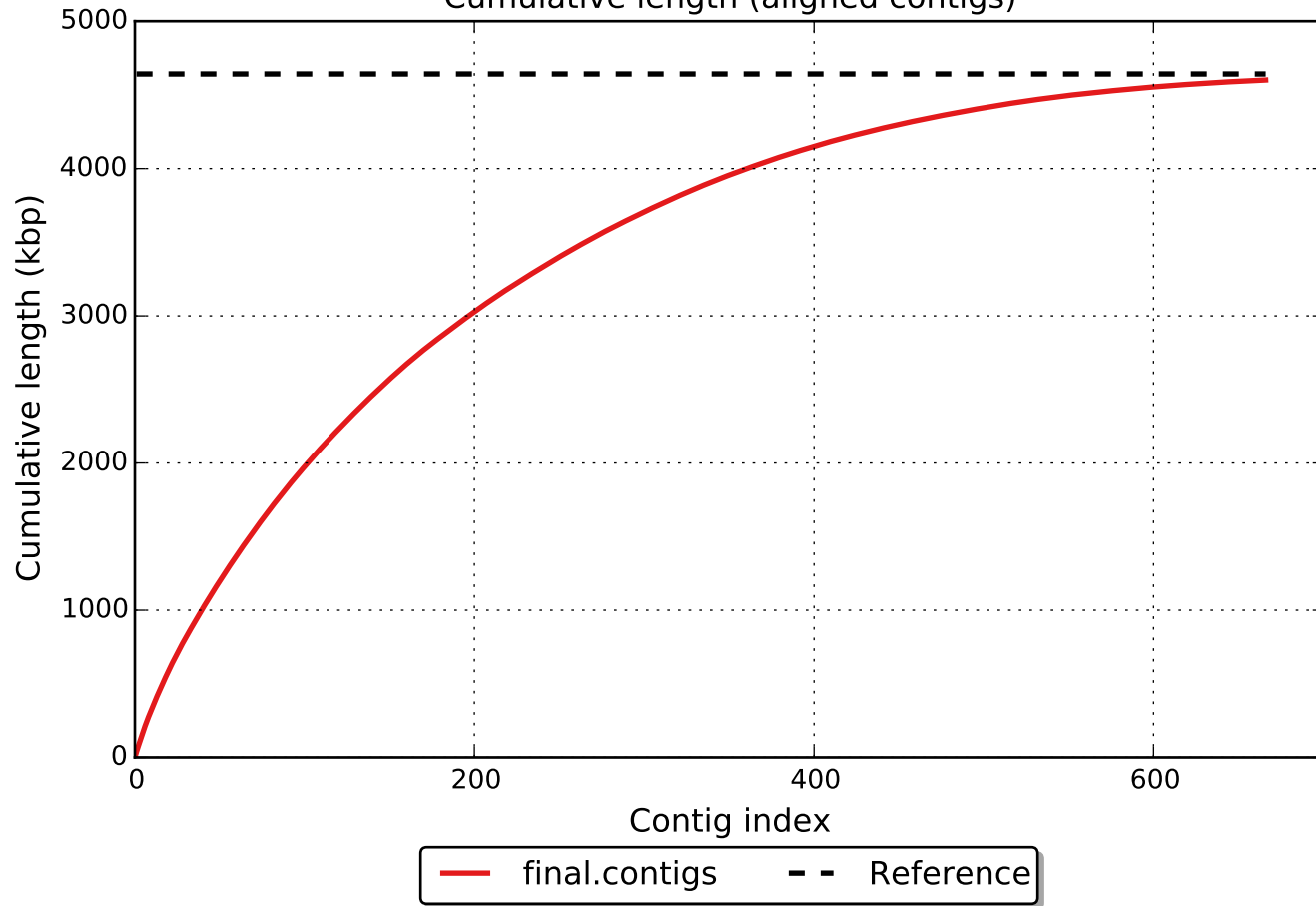


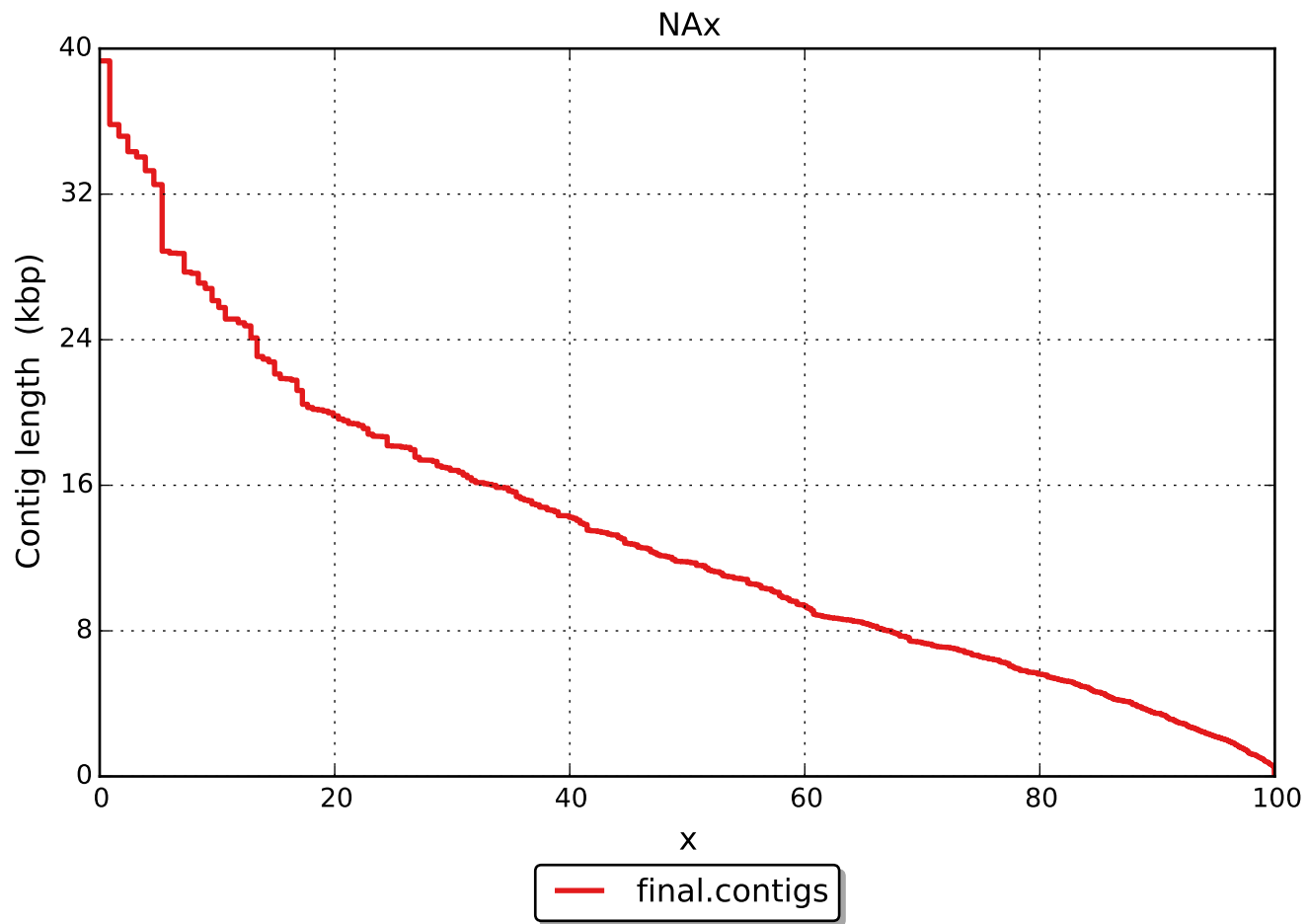
# Misassemblies





Cumulative length (aligned contigs)





# NGAx

