

## Report

	final.contigs
# contigs (>= 1000 bp)	1353
# contigs (>= 5000 bp)	230
# contigs (>= 10000 bp)	33
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4409473
Total length (>= 5000 bp)	1689295
Total length (>= 10000 bp)	392908
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1670
Largest contig	24045
Total length	4641621
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	3876
NG50	3876
N75	2313
NG75	2313
L50	375
LG50	375
L75	760
LG75	760
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 1 part
Unaligned length	58
Genome fraction (%)	97.107
Duplication ratio	1.030
# N's per 100 kbp	0.00
# mismatches per 100 kbp	33.39
# indels per 100 kbp	0.07
Largest alignment	24045
NA50	3876
NGA50	3876
NA75	2313
NGA75	2313
LA50	375
LGA50	375
LA75	760
LGA75	760

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

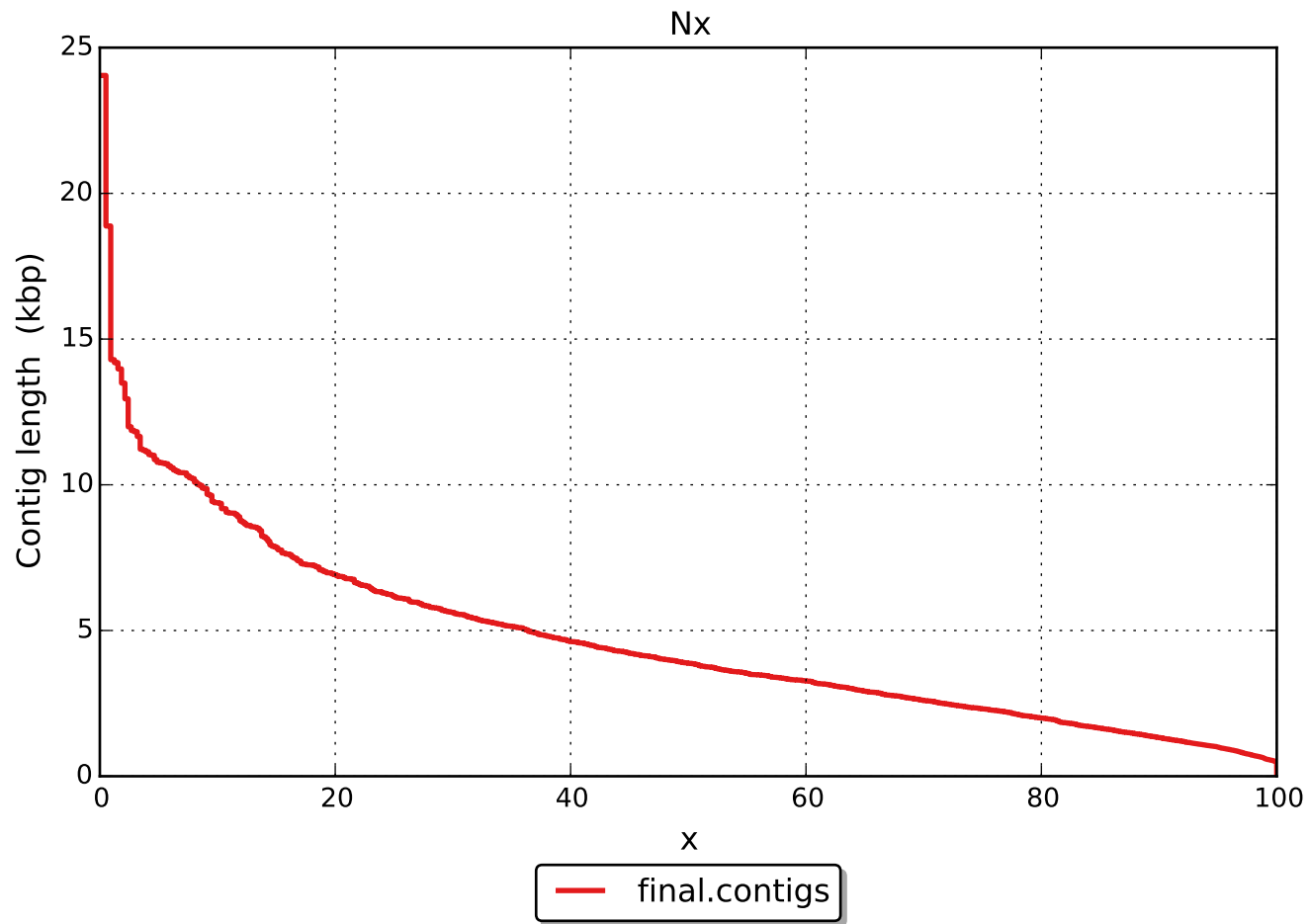
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	1505
# indels	3
# short indels	3
# long indels	0
Indels length	3

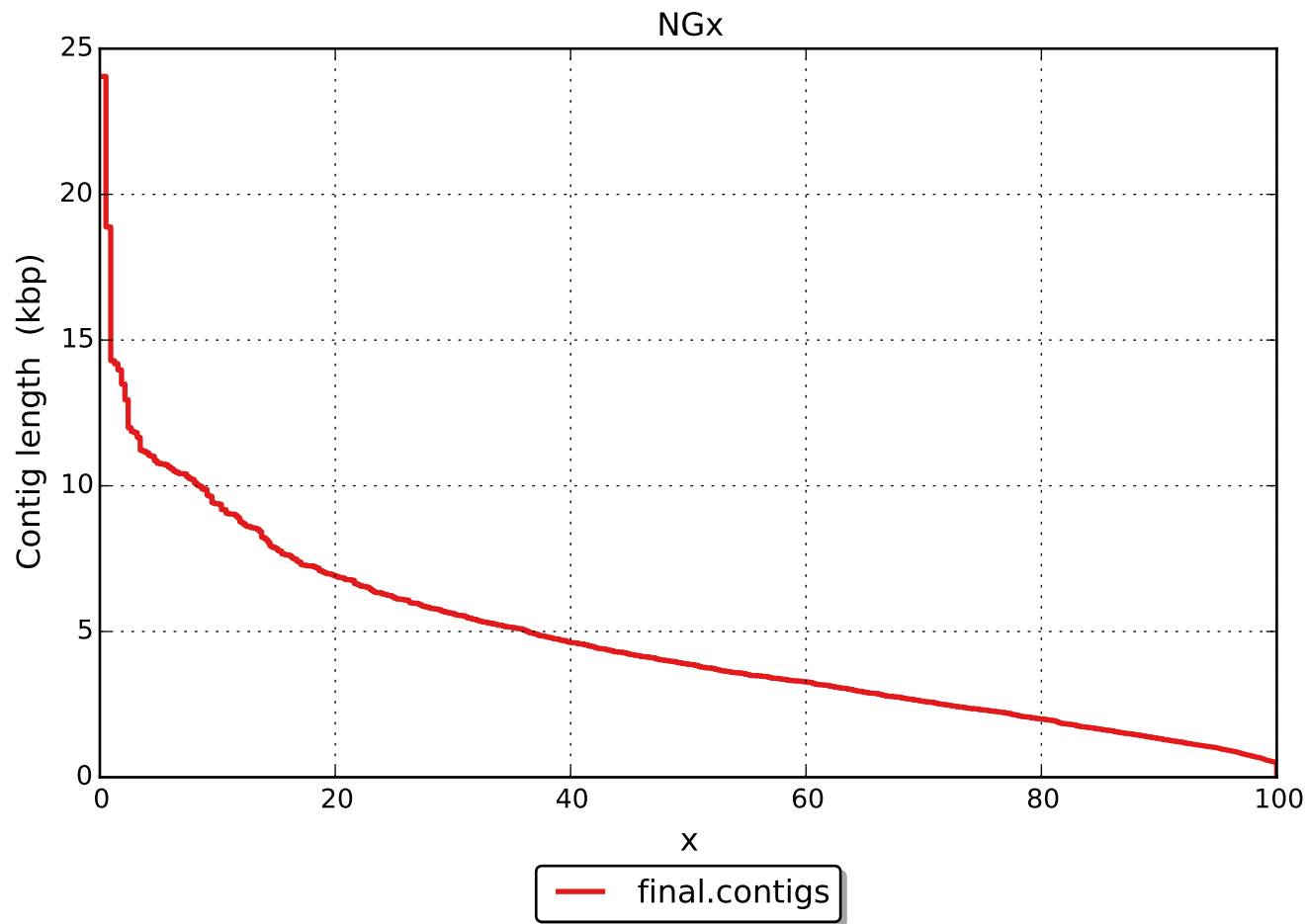
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

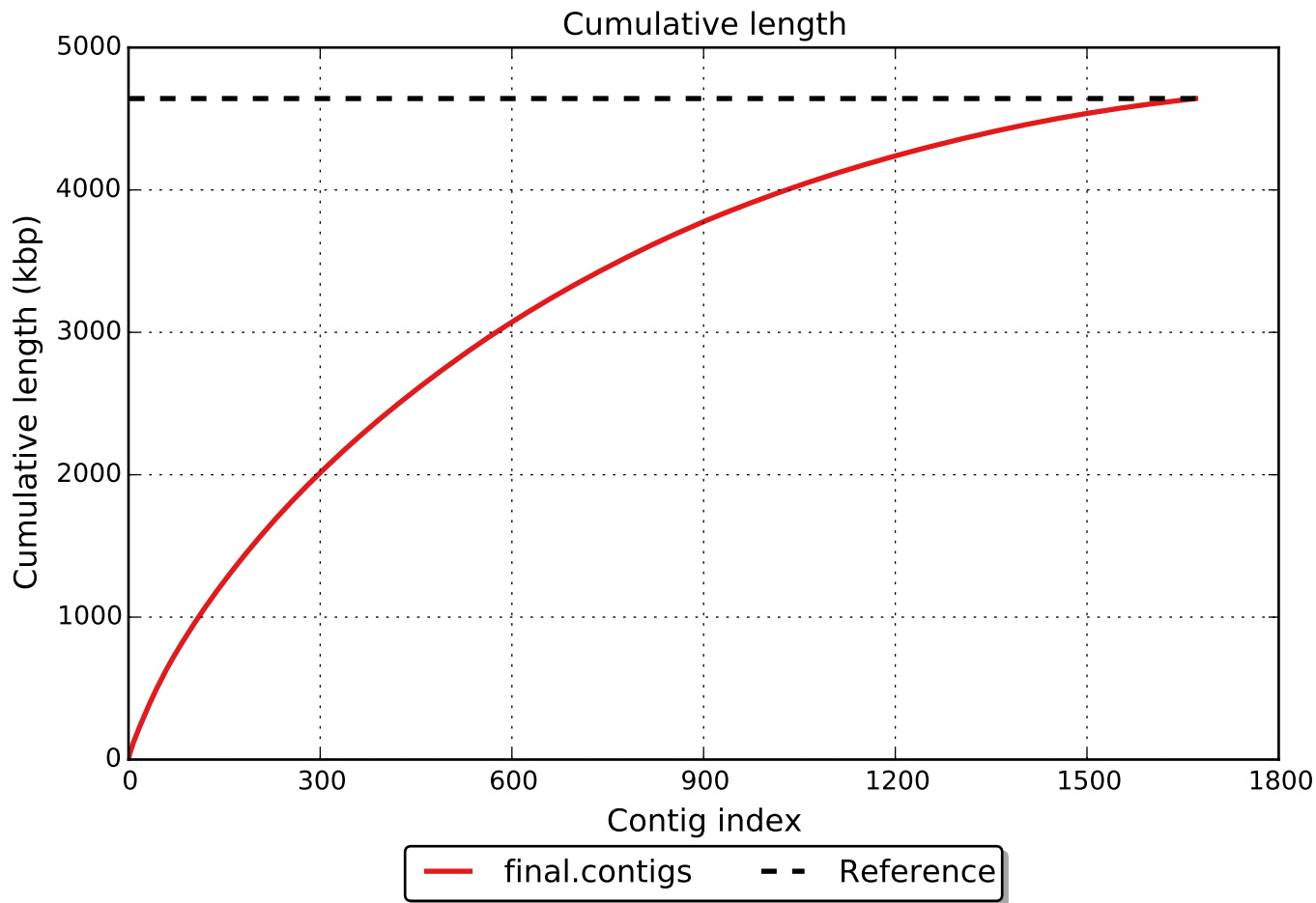
## Unaligned report

	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	58
# N's	0

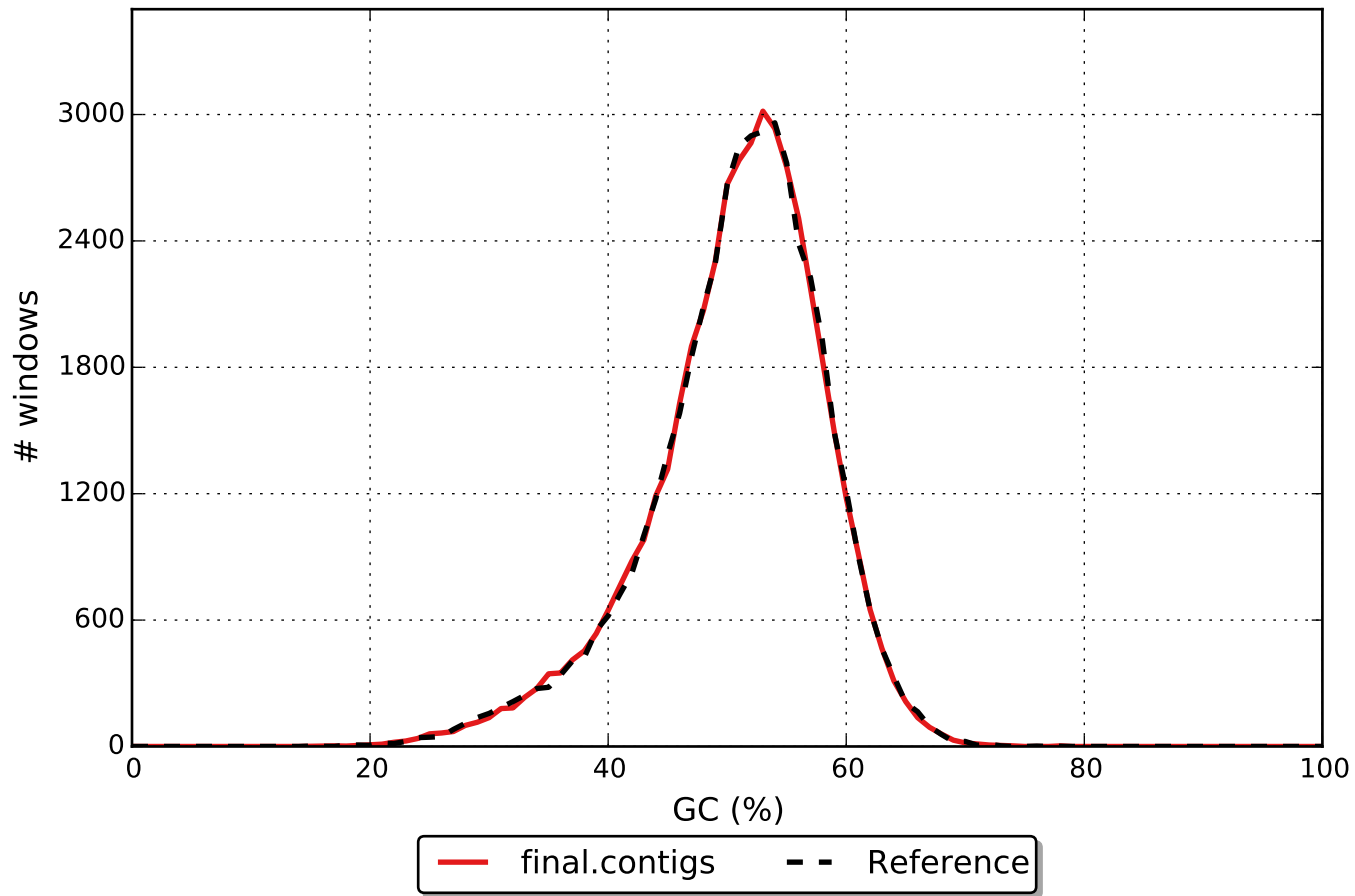
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







GC content

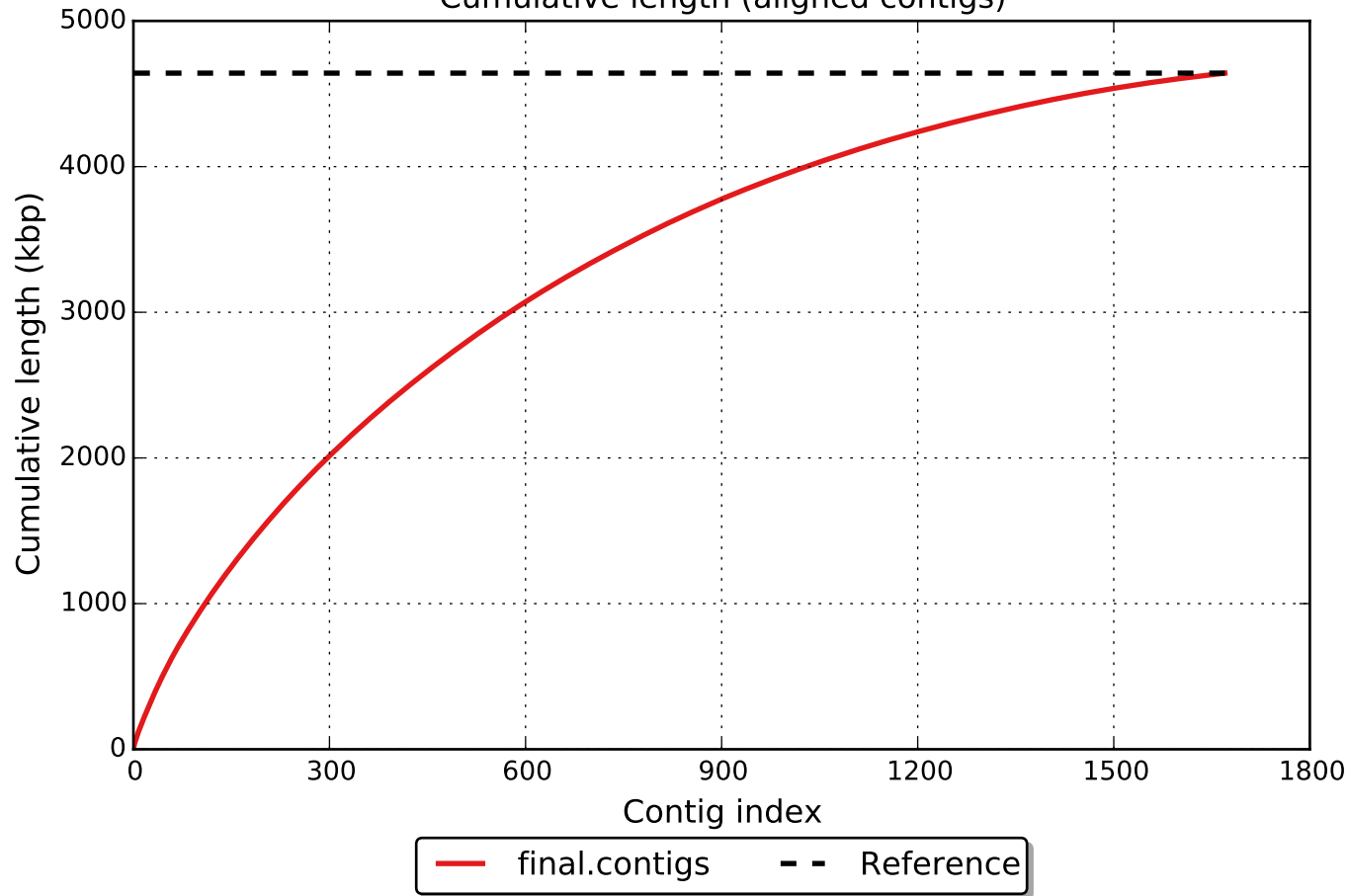


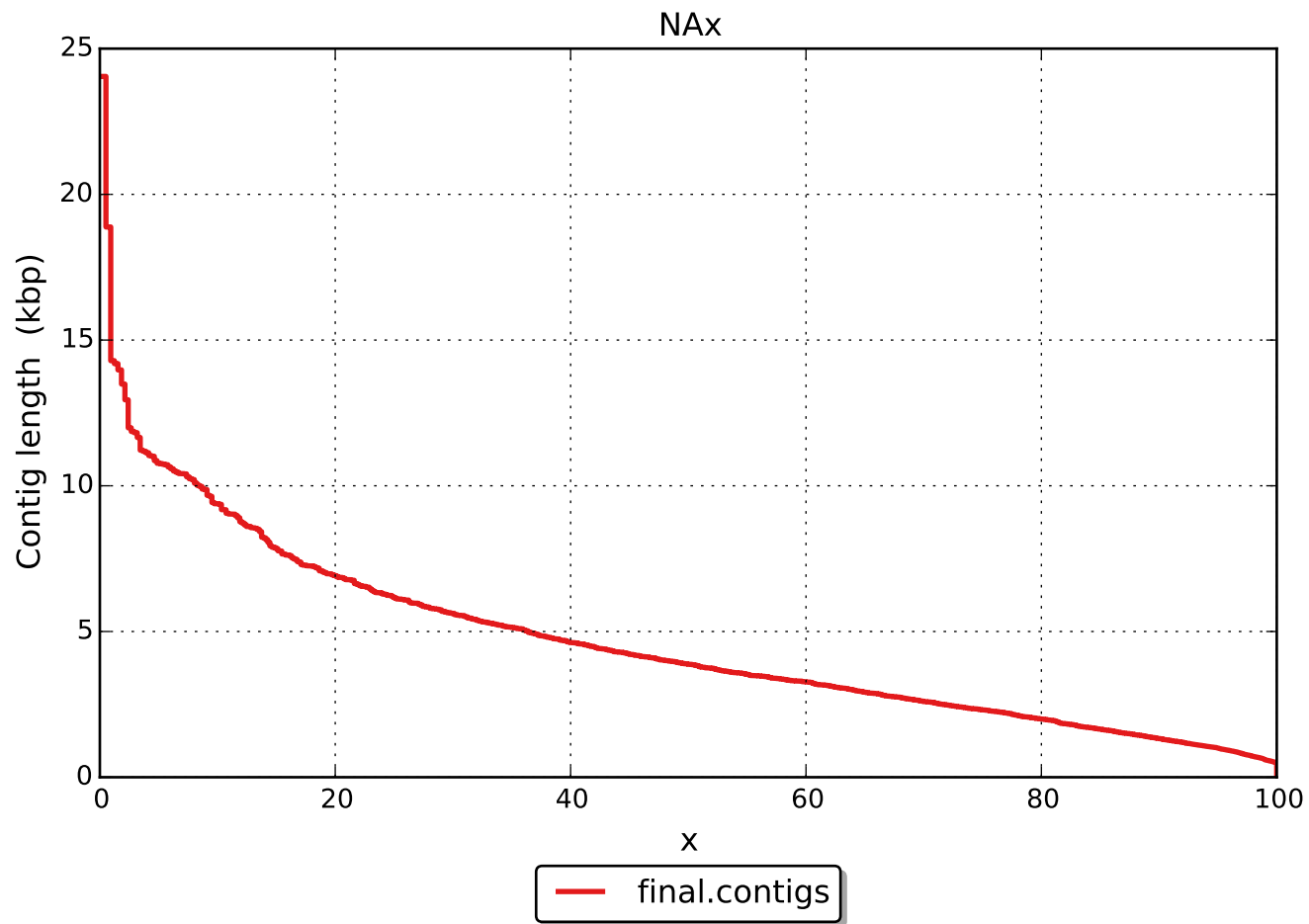
# Misassemblies





Cumulative length (aligned contigs)





# NGAx

