

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	5215
# contigs ( $\geq 1000$ bp)	90
# contigs ( $\geq 5000$ bp)	0
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	2509768
Total length ( $\geq 1000$ bp)	107666
Total length ( $\geq 5000$ bp)	0
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	1723
Largest contig	1933
Total length	1147927
Reference length	4641652
GC (%)	50.84
Reference GC (%)	50.79
N50	647
N75	559
L50	702
L75	1180
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	1674
# local misassemblies	1
# unaligned contigs	99 + 10 part
Unaligned length	58933
Genome fraction (%)	23.107
Duplication ratio	1.015
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3236.16
# indels per 100 kbp	2.80
Largest alignment	1933
NA50	642
NGA50	-
NA75	550
LA50	705
LA75	1190

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).

## Misassemblies report

	final.contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# misassembled contigs	3
Misassembled contigs length	1674
# local misassemblies	1
# mismatches	34709
# indels	30
# short indels	30
# long indels	0
Indels length	30

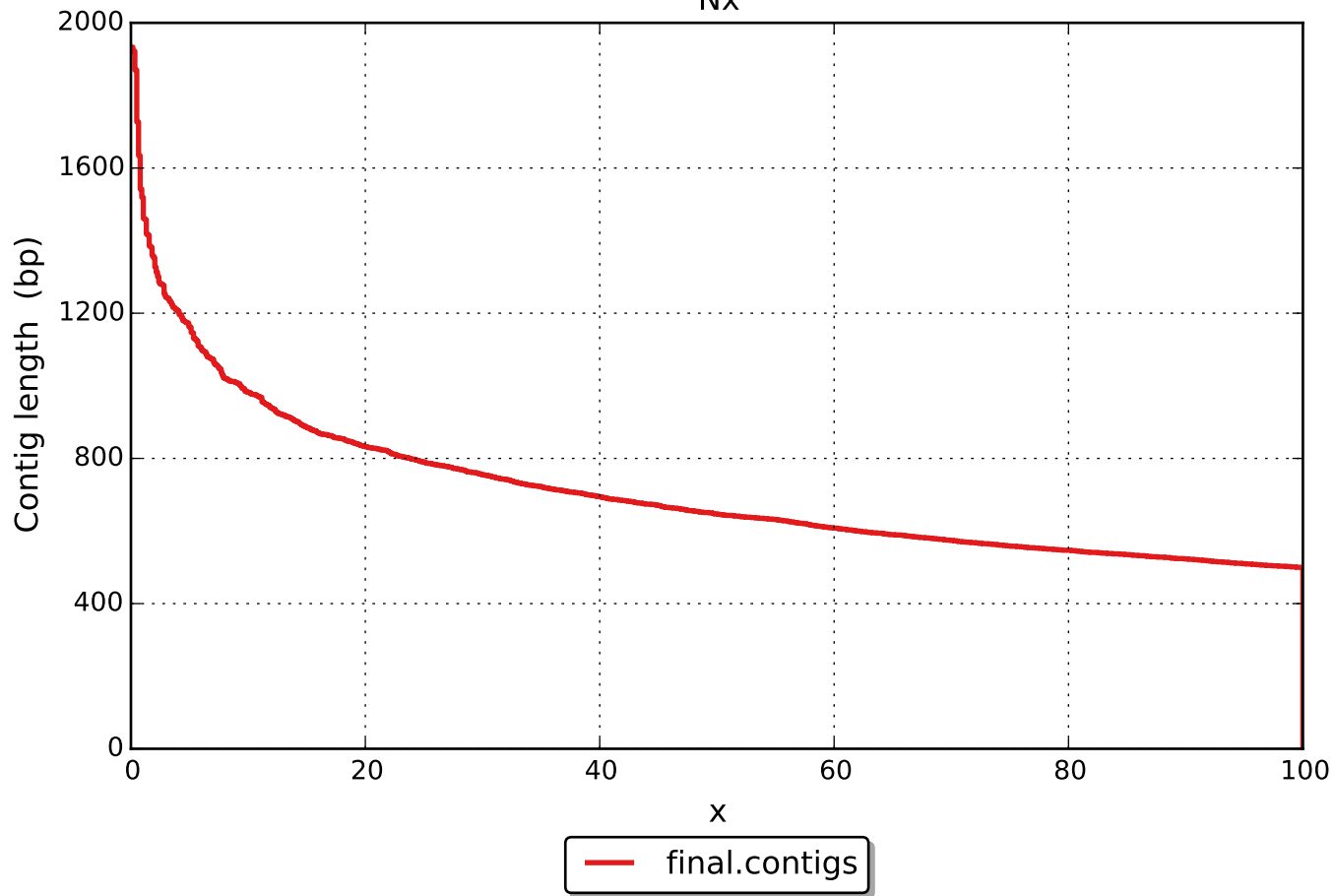
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

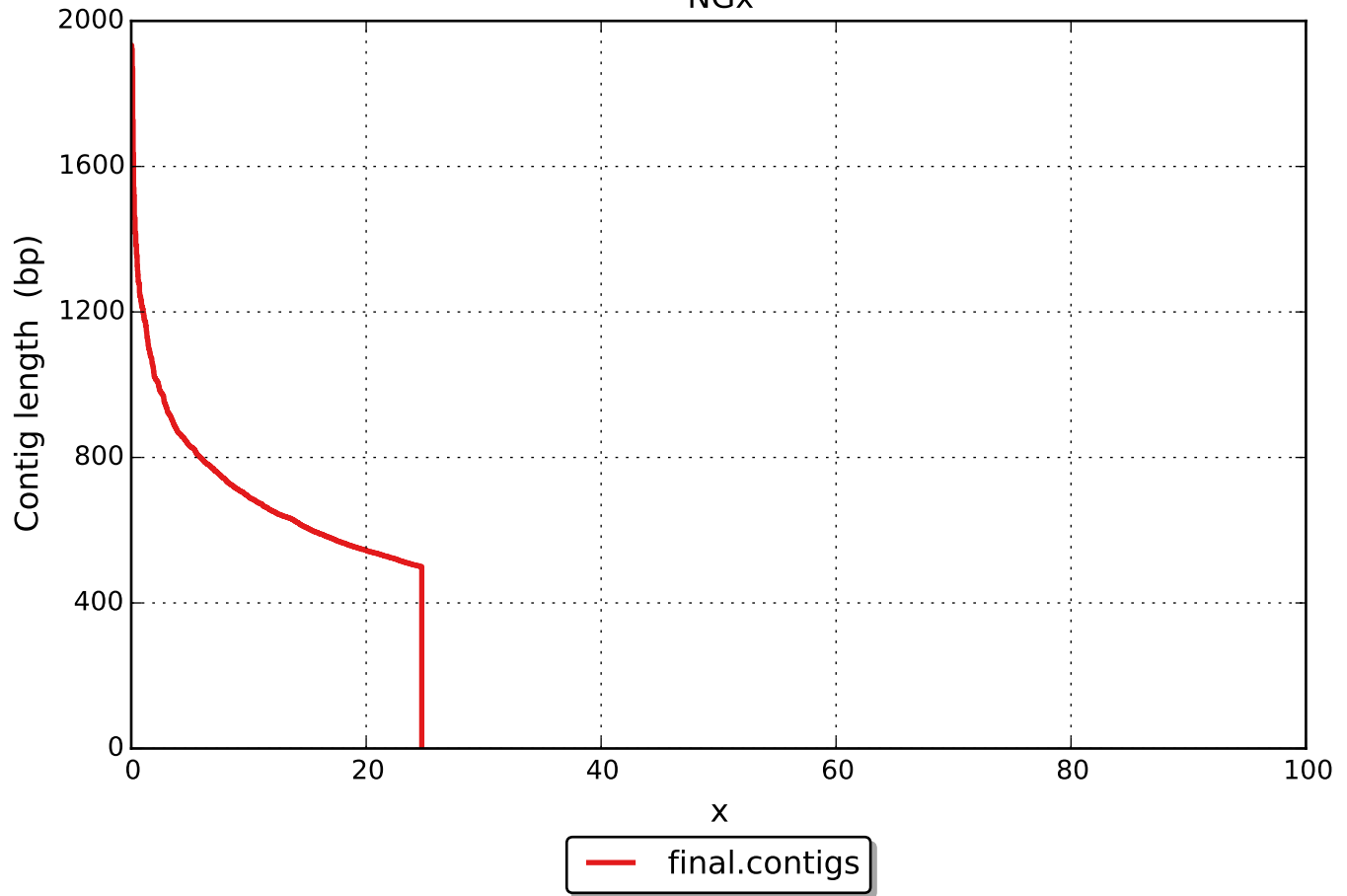
	final.contigs
# fully unaligned contigs	99
Fully unaligned length	58105
# partially unaligned contigs	10
# with misassembly	0
# both parts are significant	0
Partially unaligned length	828
# N's	0

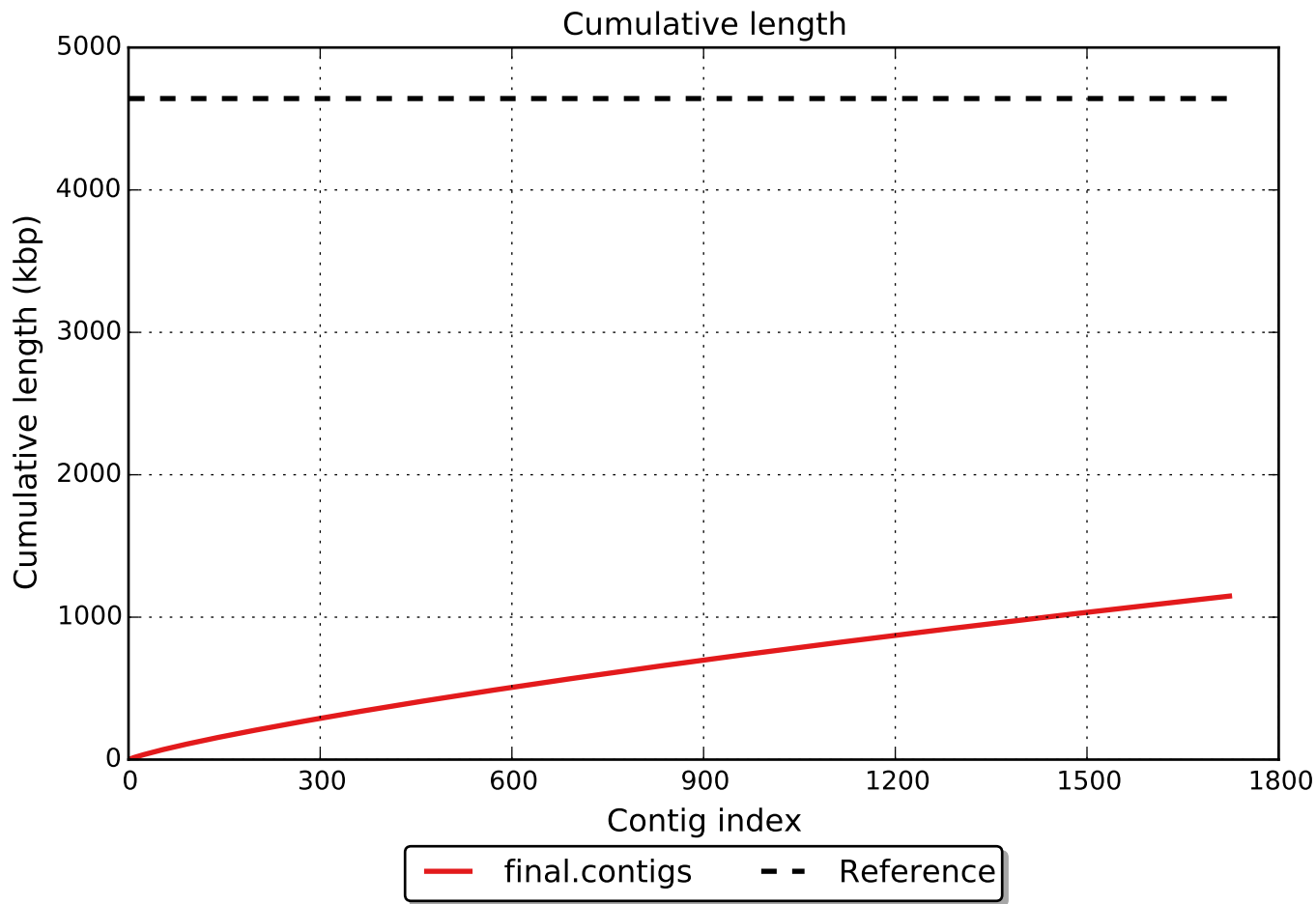
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

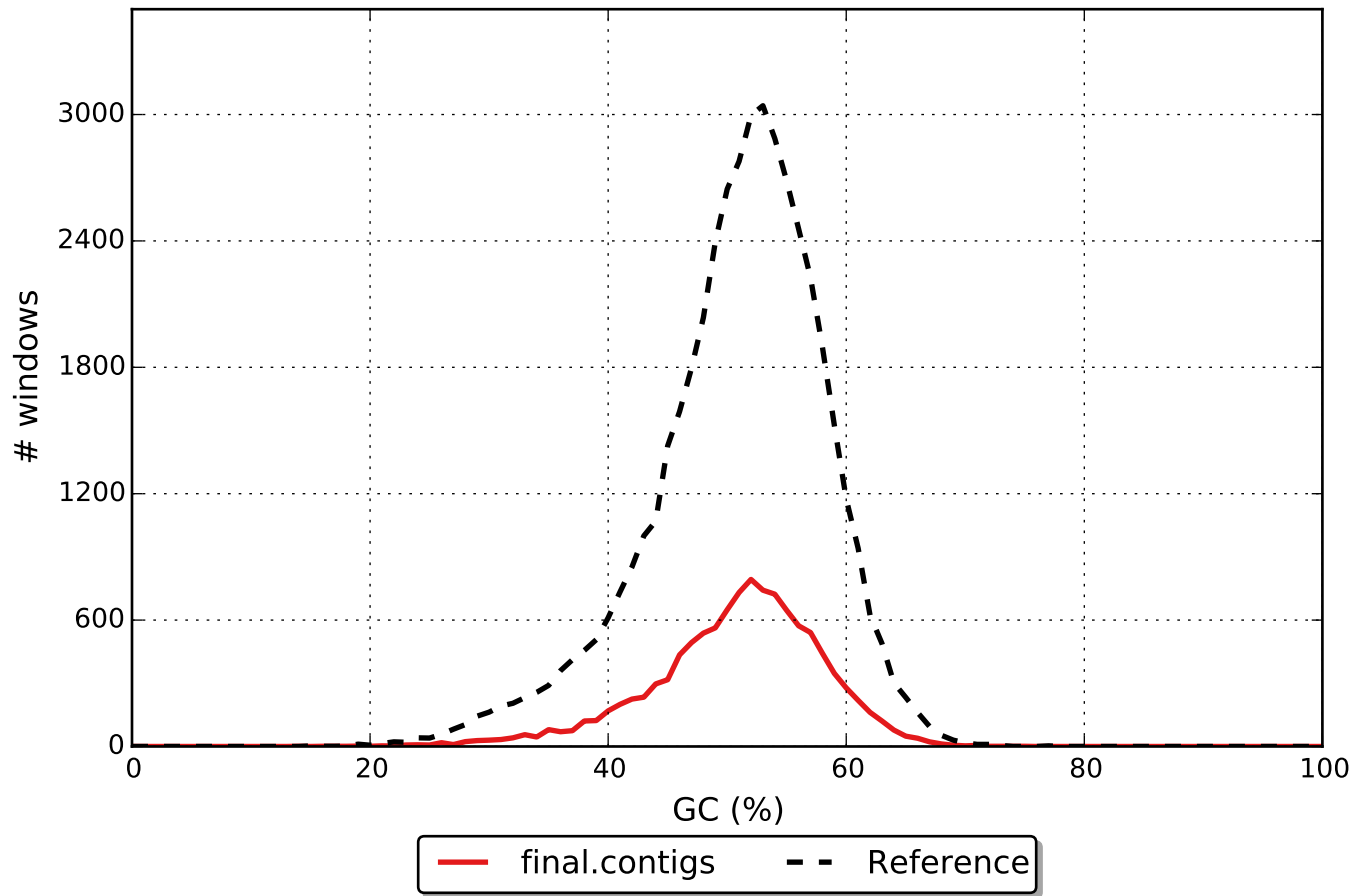


NGx

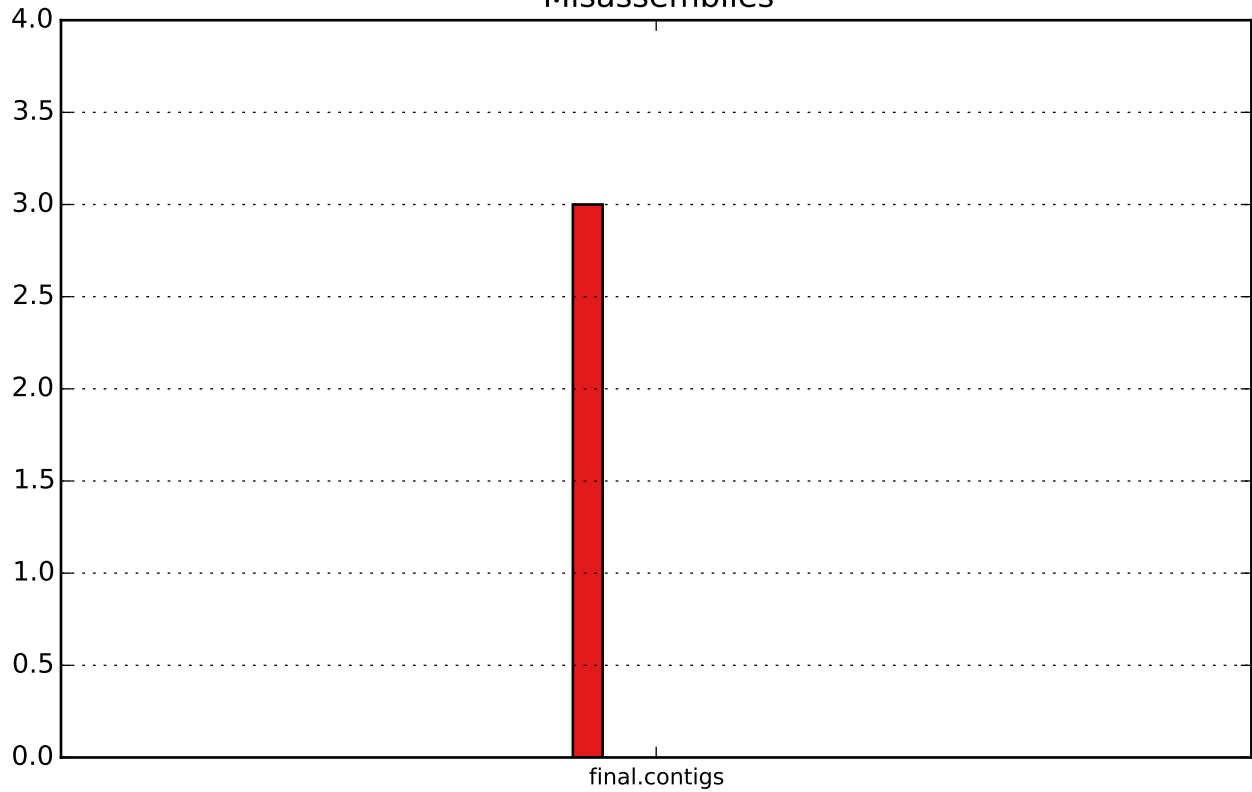




GC content

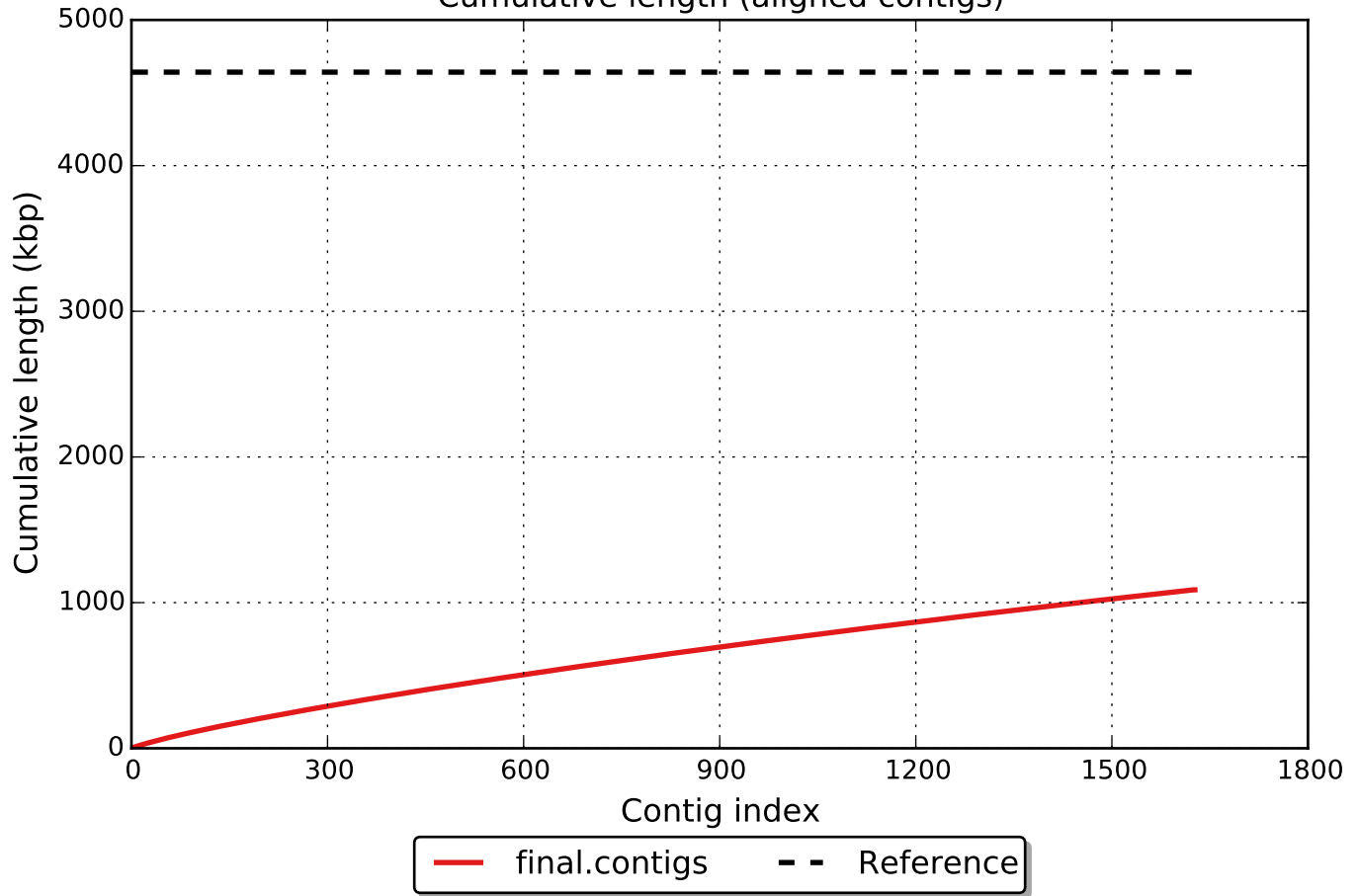


# Misassemblies

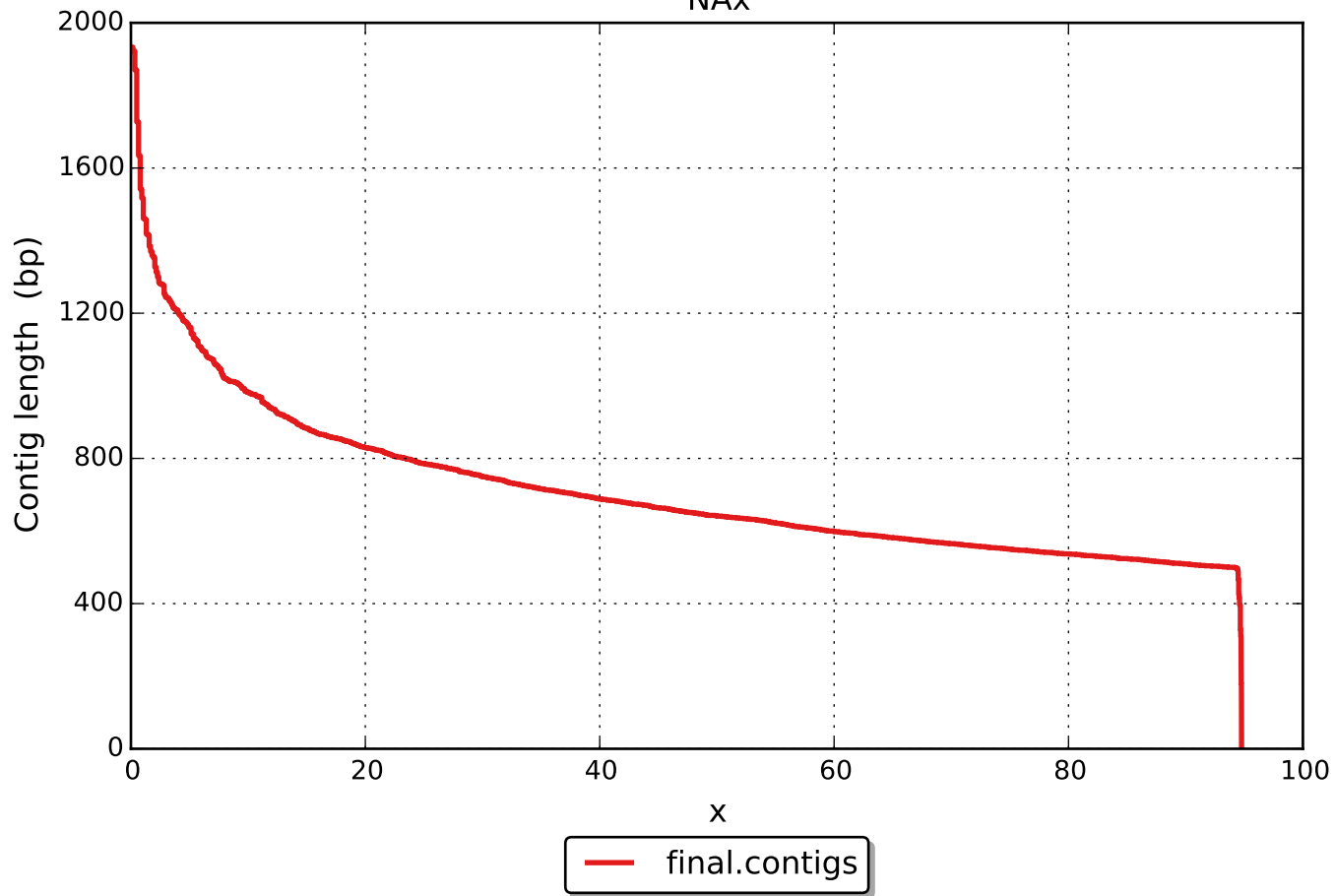




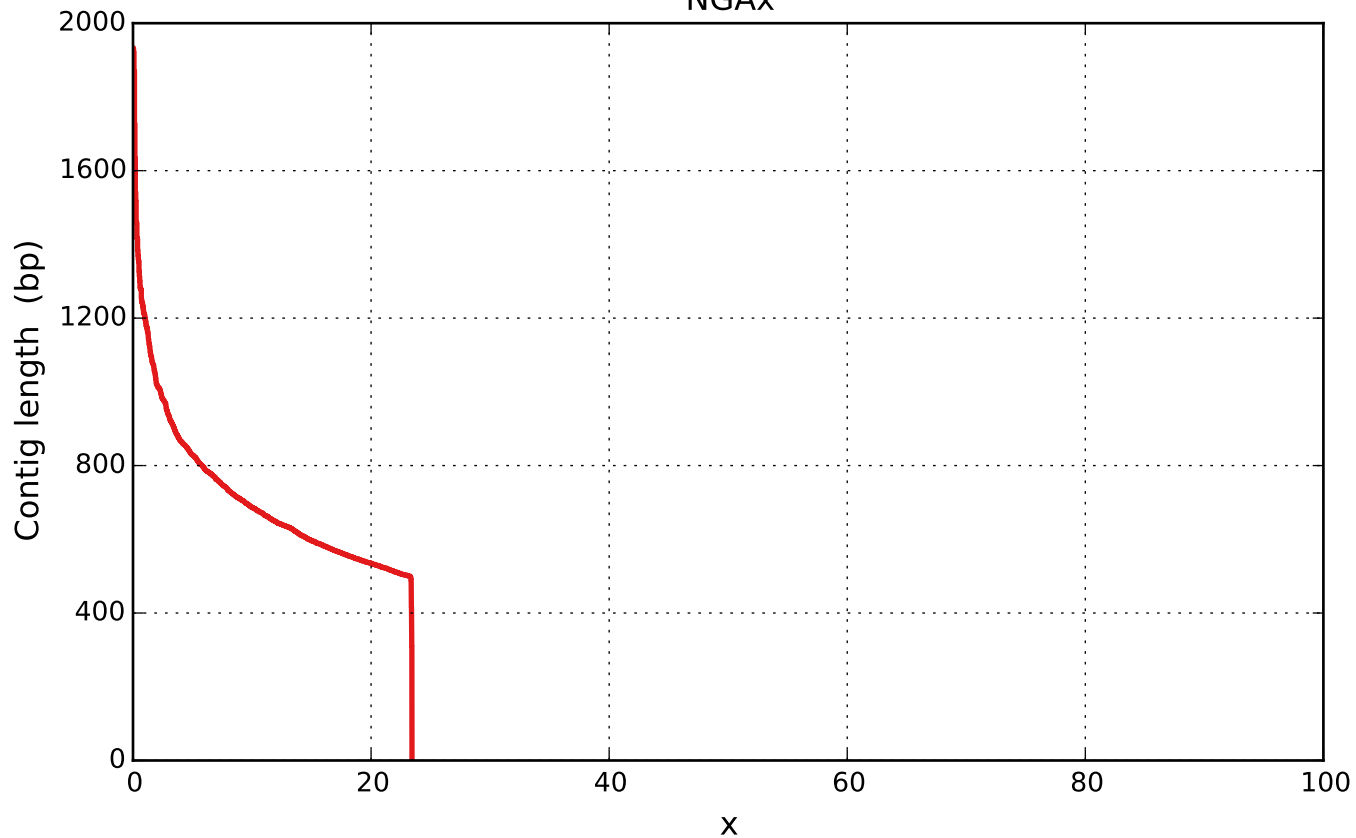
Cumulative length (aligned contigs)



NAx



NGAx



— final.contigs