

## Report

	final.contigs
# contigs (>= 0 bp)	2357
# contigs (>= 1000 bp)	1460
# contigs (>= 5000 bp)	99
# contigs (>= 10000 bp)	5
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4161125
Total length (>= 1000 bp)	3606417
Total length (>= 5000 bp)	646728
Total length (>= 10000 bp)	53697
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2051
Largest contig	11619
Total length	4039989
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	2568
NG50	2235
N75	1524
NG75	1134
L50	495
LG50	620
L75	1002
LG75	1344
# misassemblies	7
# misassembled contigs	7
Misassembled contigs length	26458
# local misassemblies	4
# unaligned contigs	0 + 2 part
Unaligned length	142
Genome fraction (%)	86.978
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5.15
# indels per 100 kbp	0.84
Largest alignment	11619
NA50	2563
NGA50	2231
NA75	1515
NGA75	1129
LA50	497
LGA50	623
LA75	1006
LGA75	1348

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

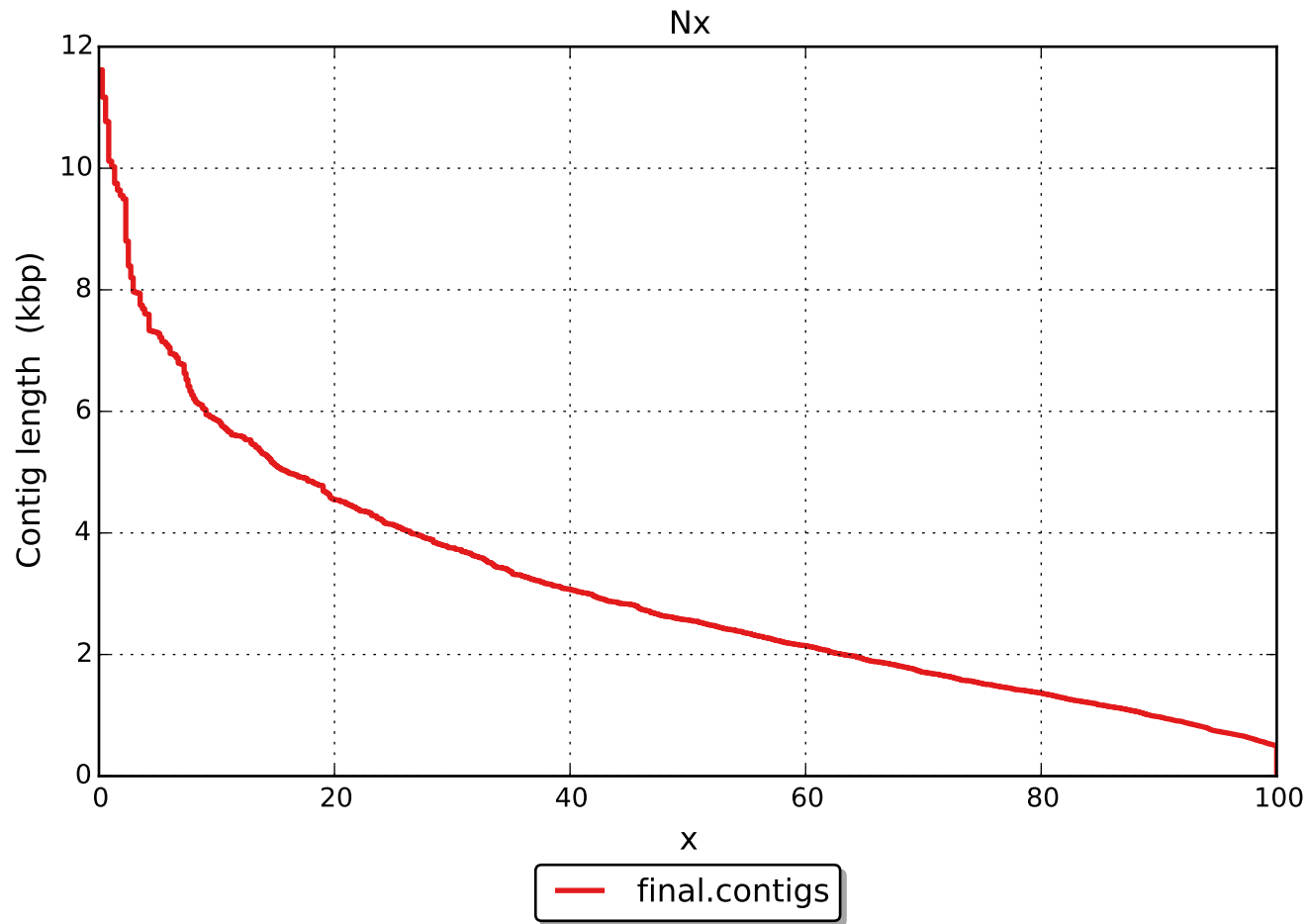
	final.contigs
# misassemblies	7
# relocations	7
# translocations	0
# inversions	0
# misassembled contigs	7
Misassembled contigs length	26458
# local misassemblies	4
# mismatches	208
# indels	34
# short indels	27
# long indels	7
Indels length	195

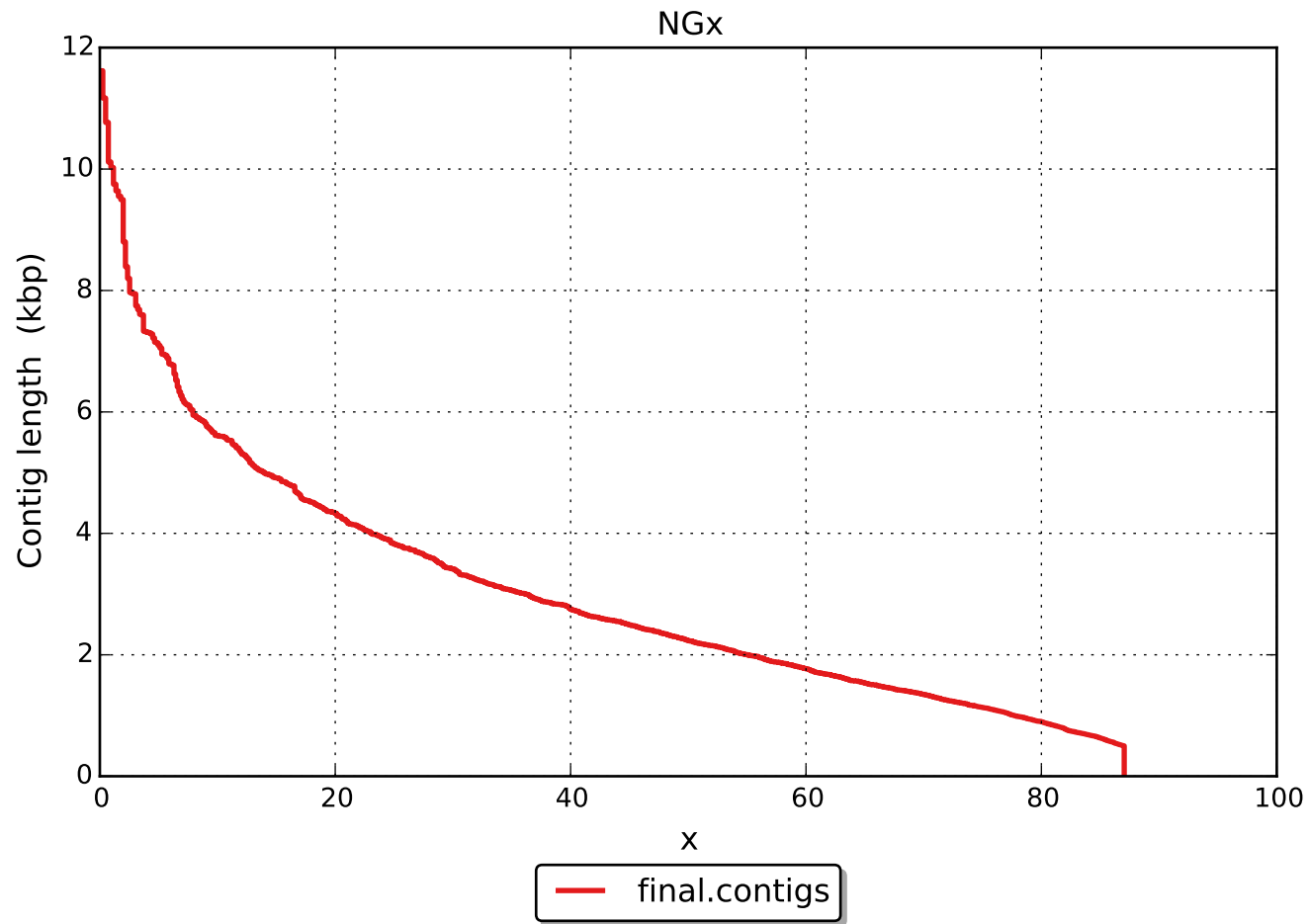
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

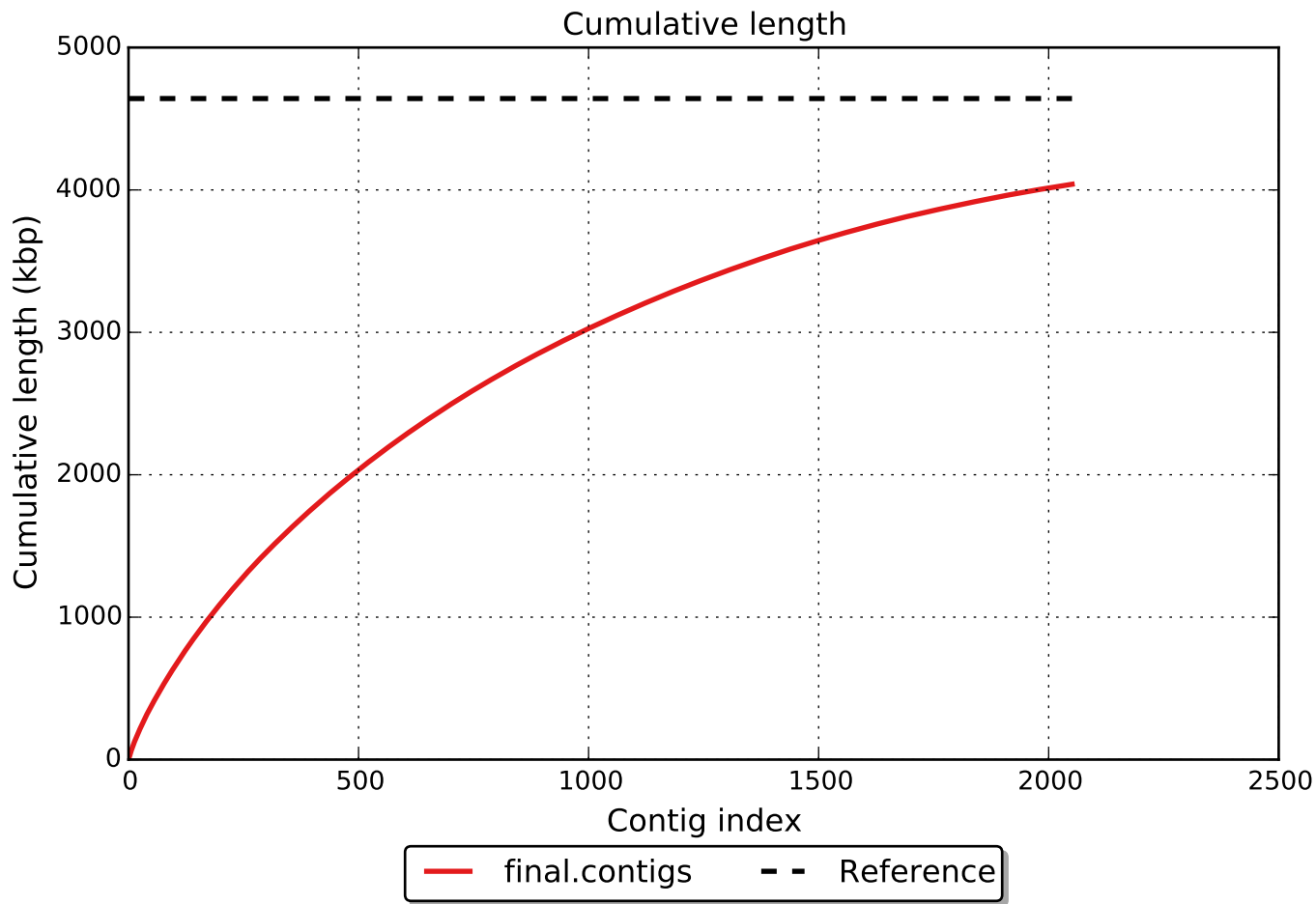
## Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	142
# N's	0

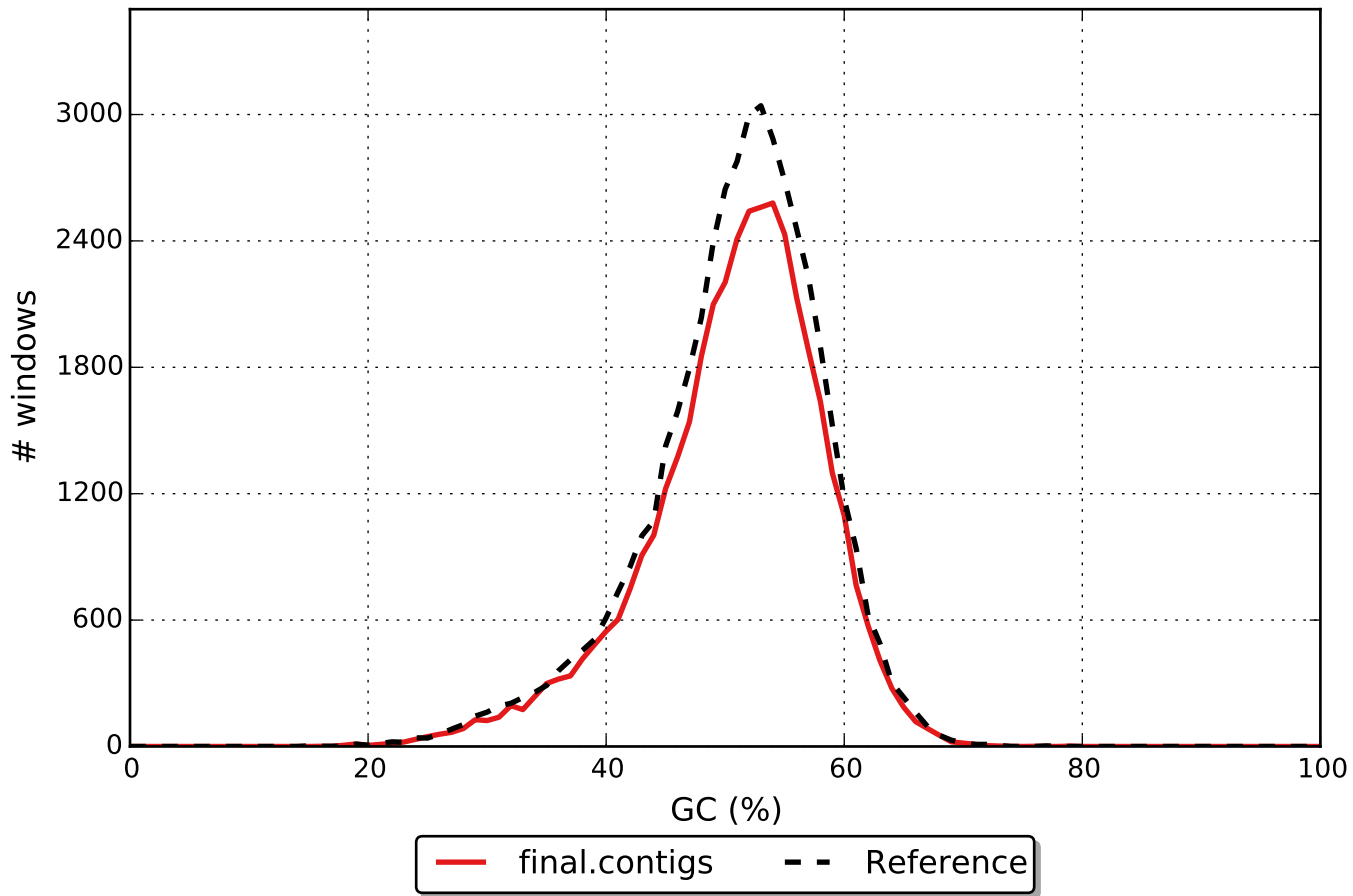
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

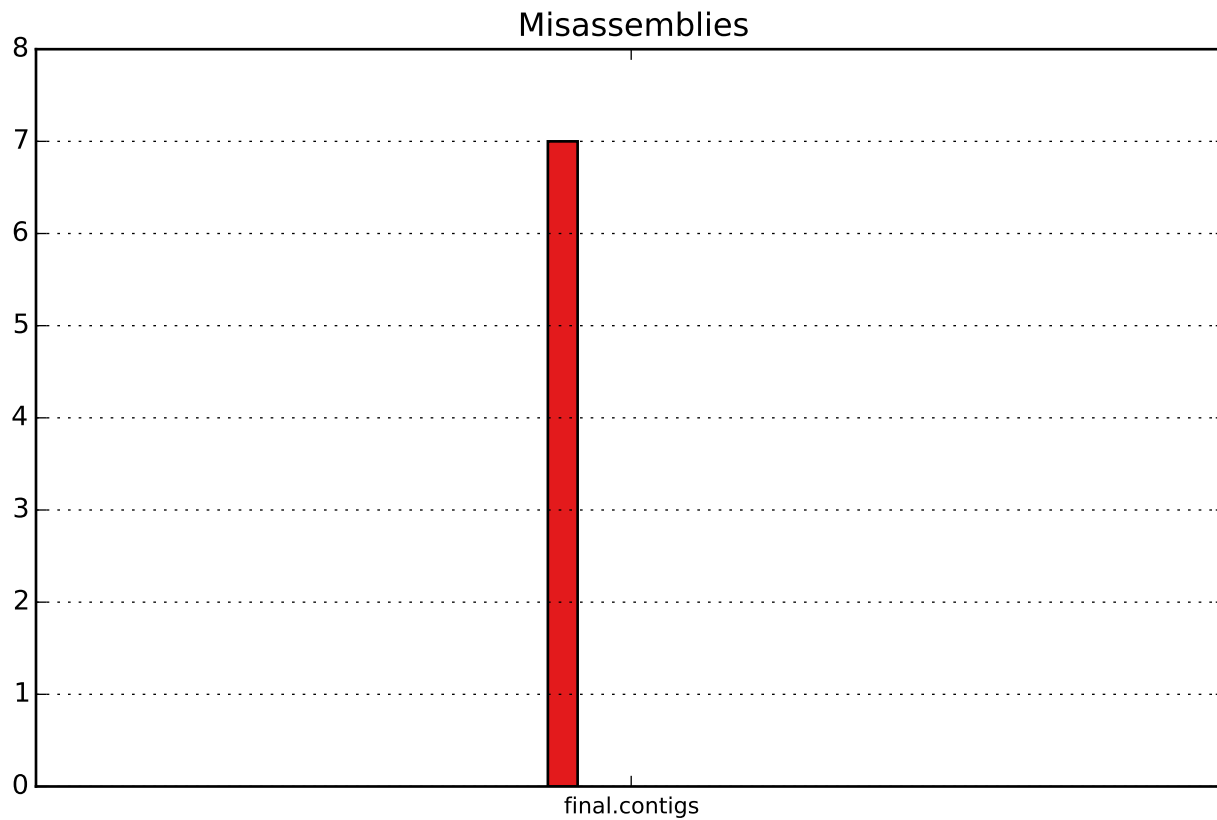






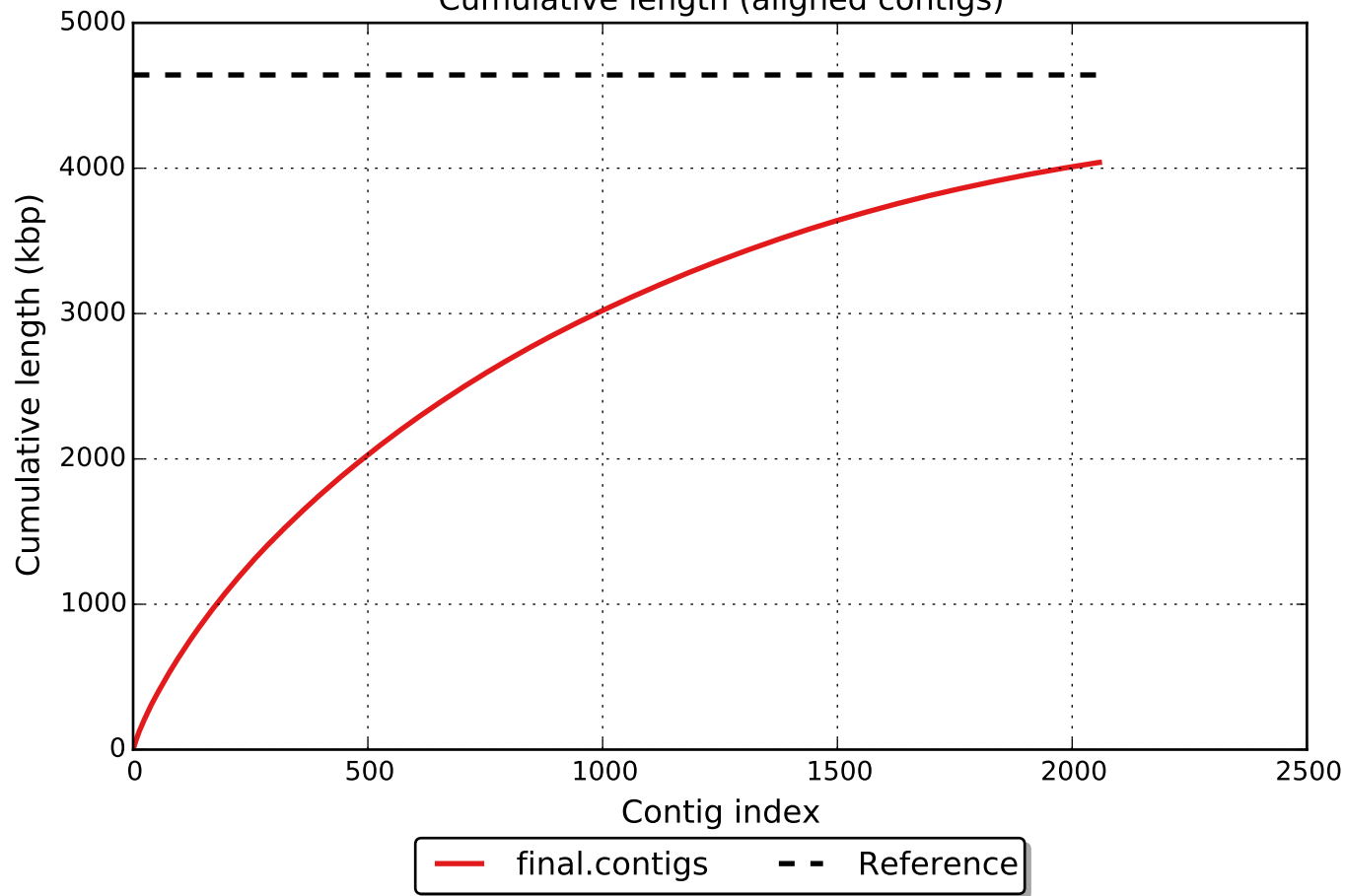
# GC content

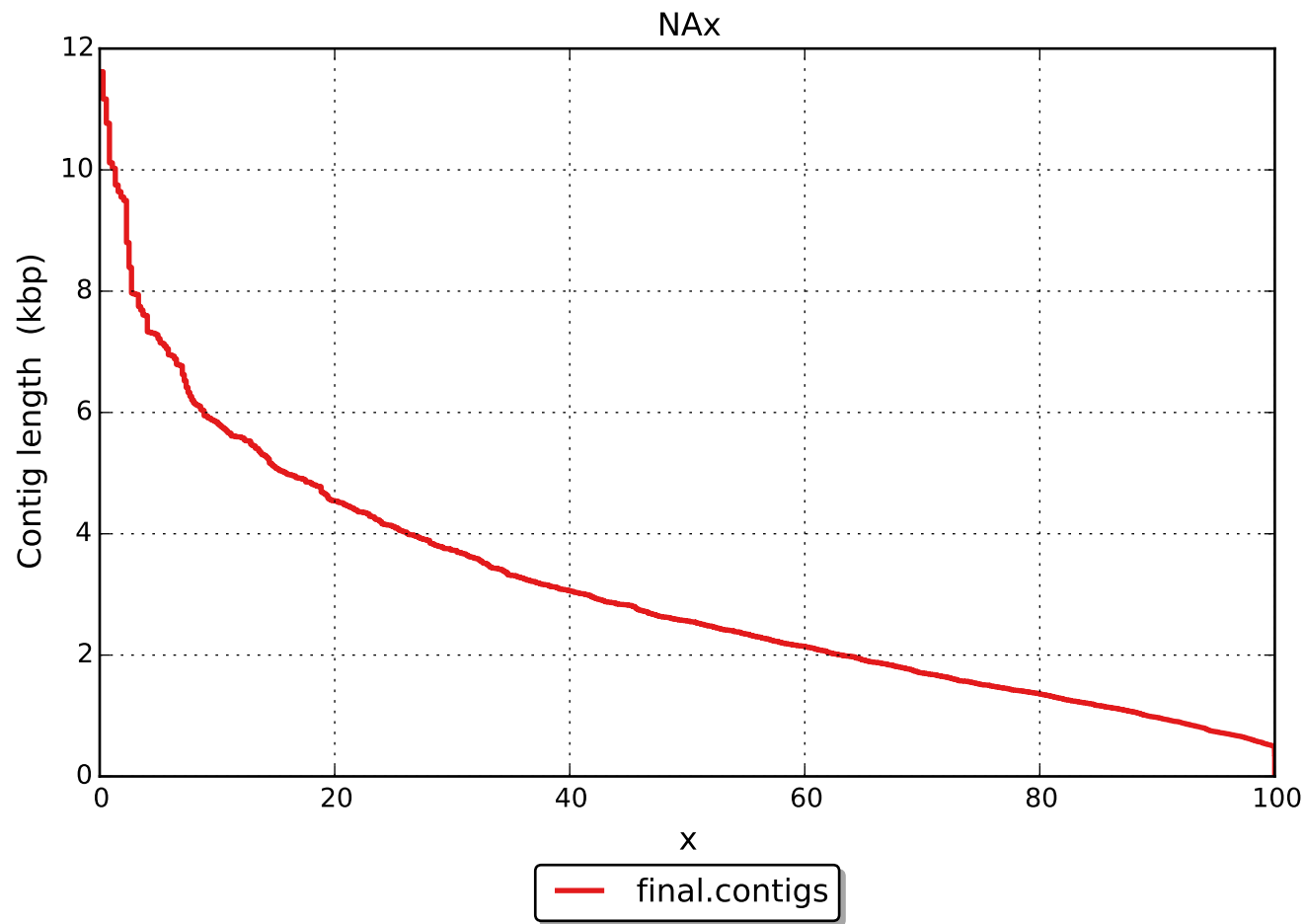






Cumulative length (aligned contigs)





# NGAx

