

## Report

	final.contigs
# contigs (>= 1000 bp)	1067
# contigs (>= 5000 bp)	296
# contigs (>= 10000 bp)	56
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4398761
Total length (>= 5000 bp)	2365934
Total length (>= 10000 bp)	729582
Total length (>= 25000 bp)	29835
Total length (>= 50000 bp)	0
# contigs	1242
Largest contig	29835
Total length	4530525
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	5245
NG50	5122
N75	3128
NG75	2996
L50	277
LG50	288
L75	554
LG75	582
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	22834
# local misassemblies	7
# unaligned contigs	0 + 8 part
Unaligned length	381
Genome fraction (%)	95.681
Duplication ratio	1.020
# N's per 100 kbp	0.00
# mismatches per 100 kbp	220.89
# indels per 100 kbp	9.37
Largest alignment	29835
NA50	5240
NGA50	5118
NA75	3115
NGA75	2994
LA50	278
LGA50	288
LA75	556
LGA75	583

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

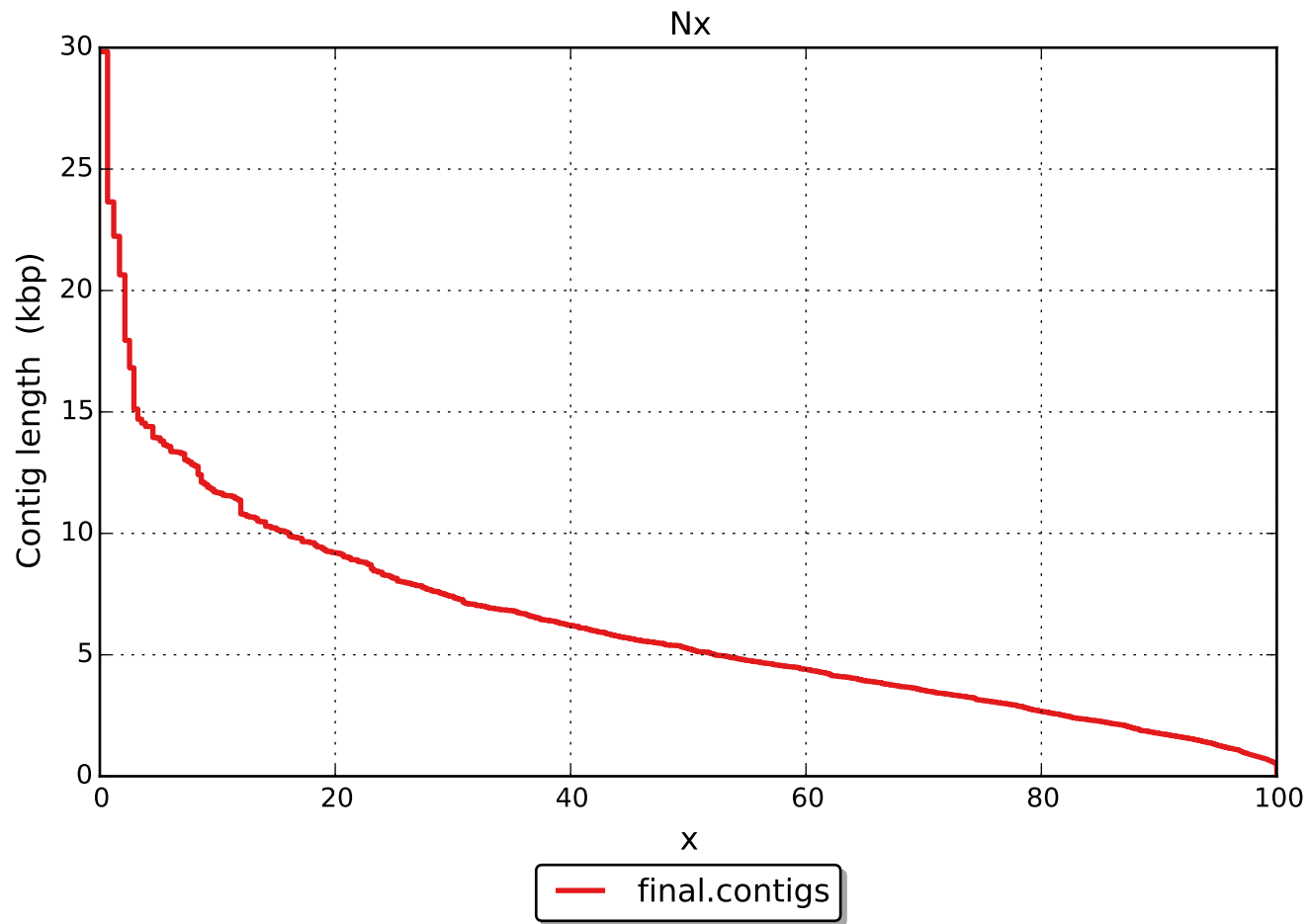
	final.contigs
# misassemblies	4
# relocations	4
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	22834
# local misassemblies	7
# mismatches	9810
# indels	416
# short indels	414
# long indels	2
Indels length	681

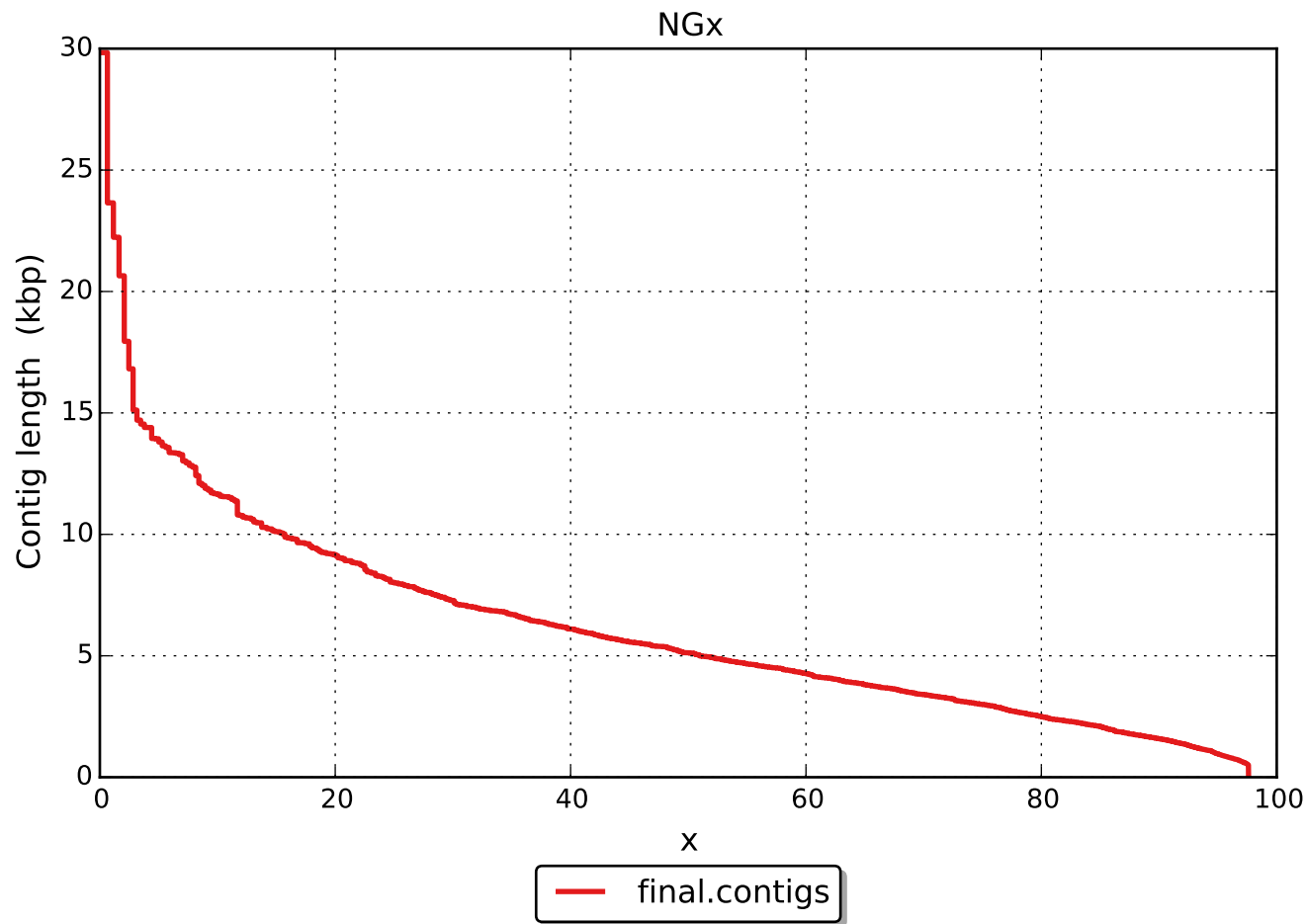
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

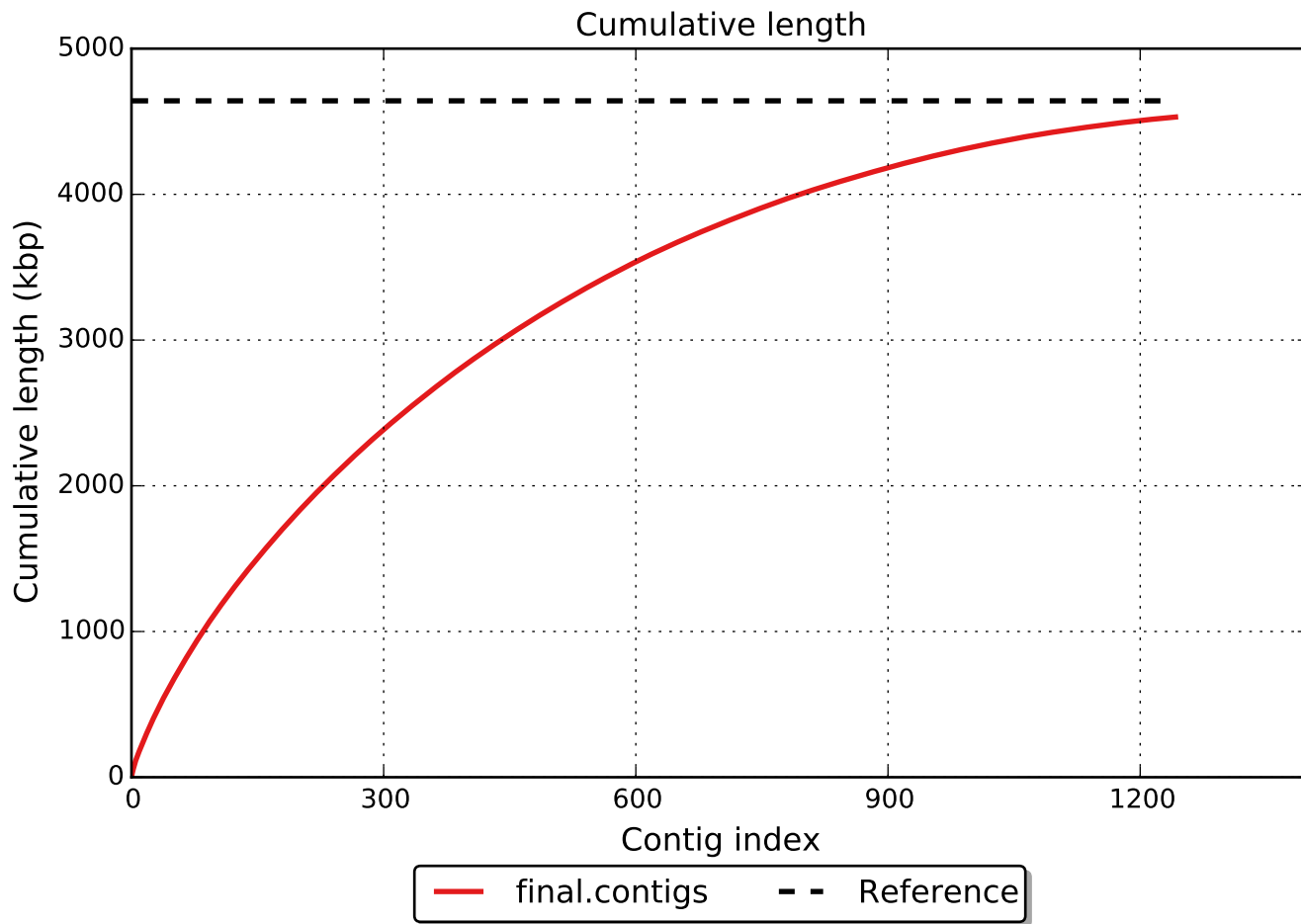
## Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	8
# with misassembly	0
# both parts are significant	0
Partially unaligned length	381
# N's	0

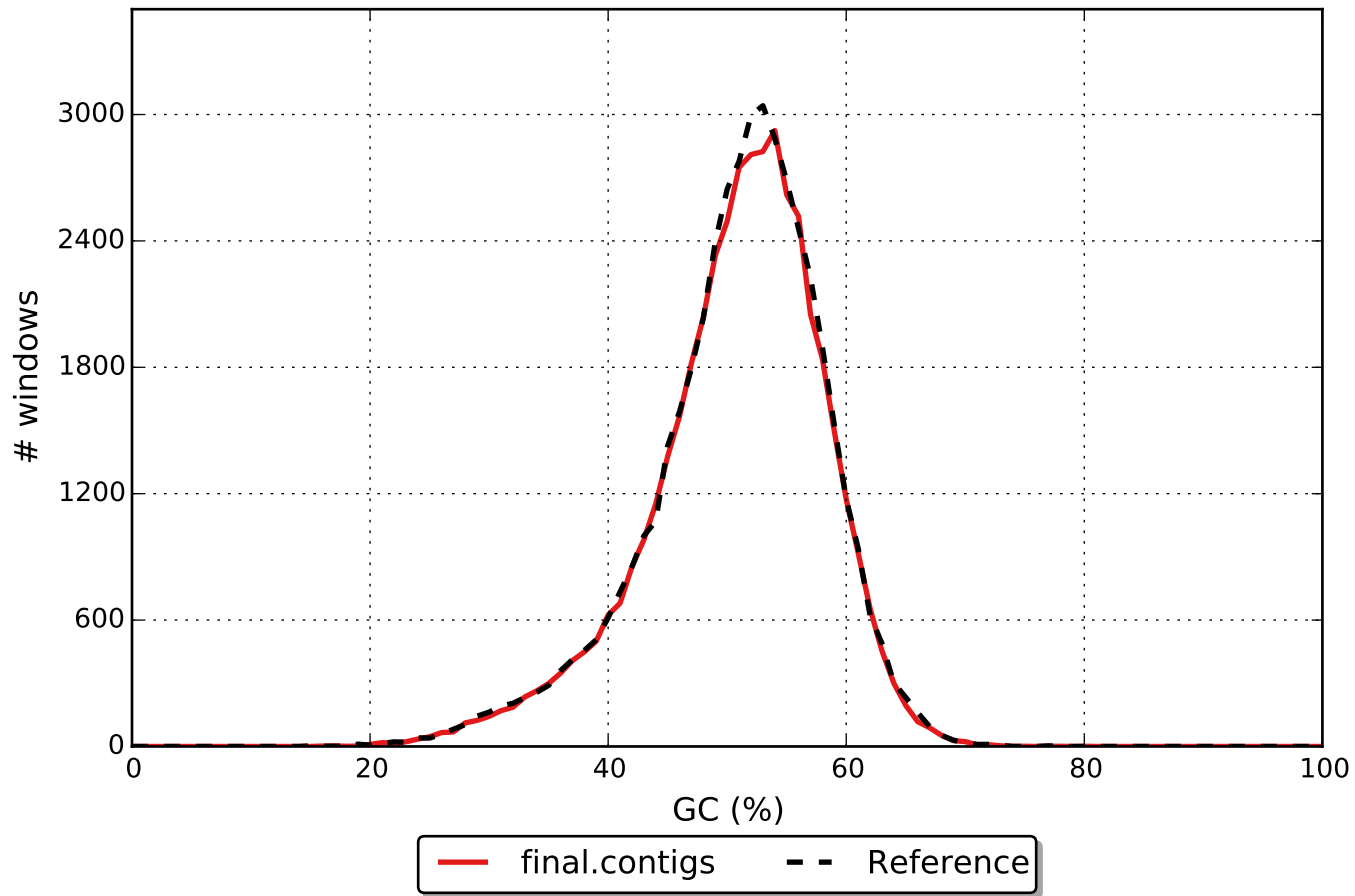
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

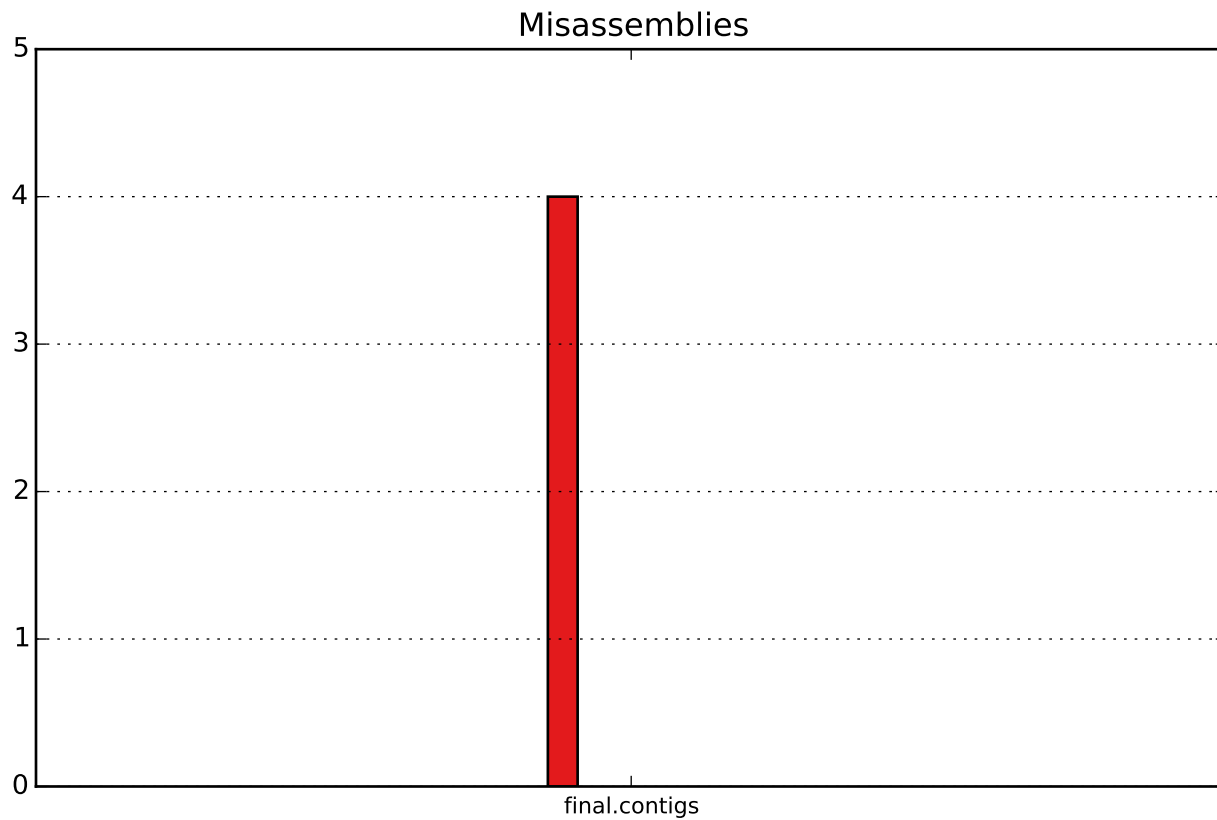






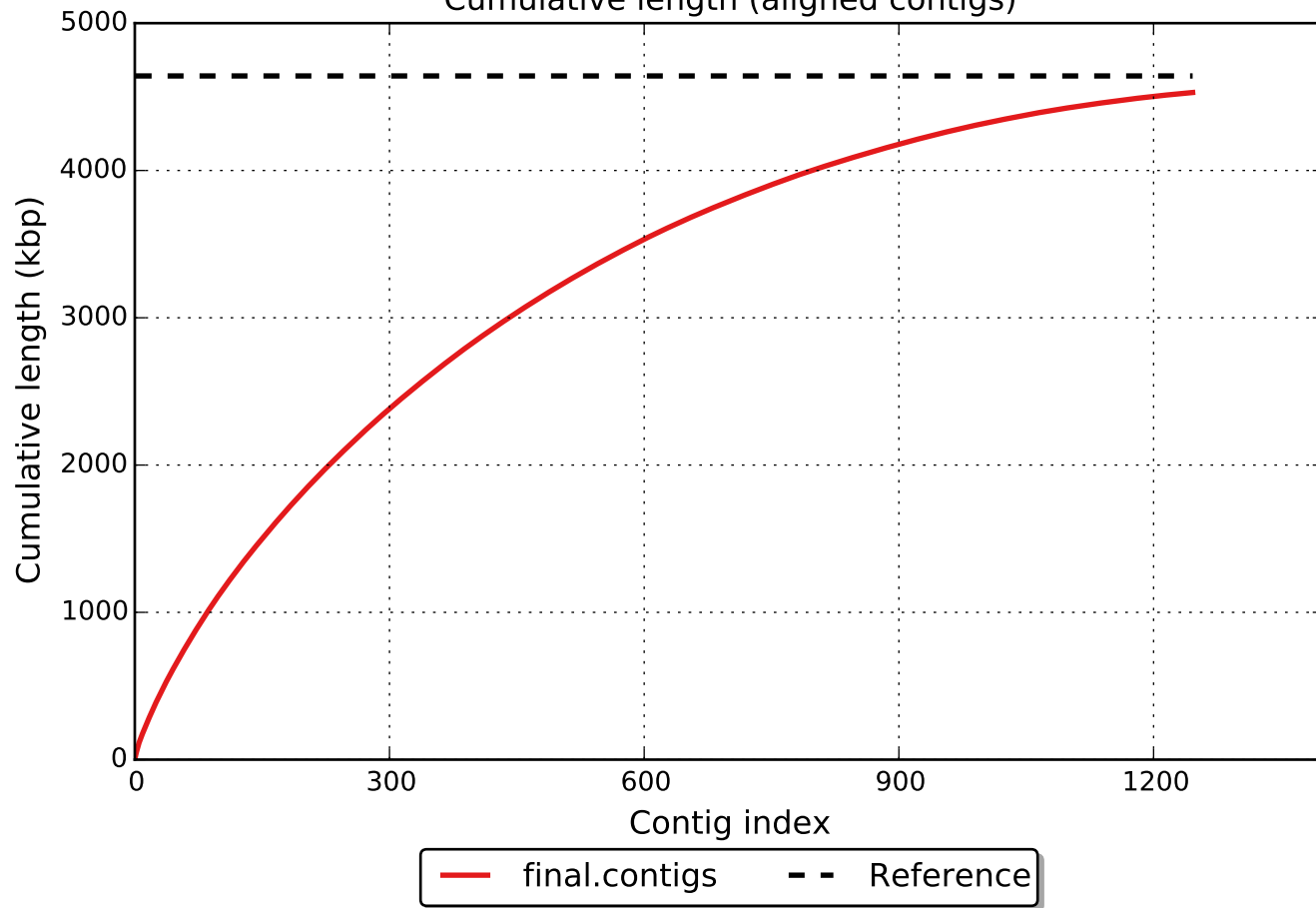
GC content

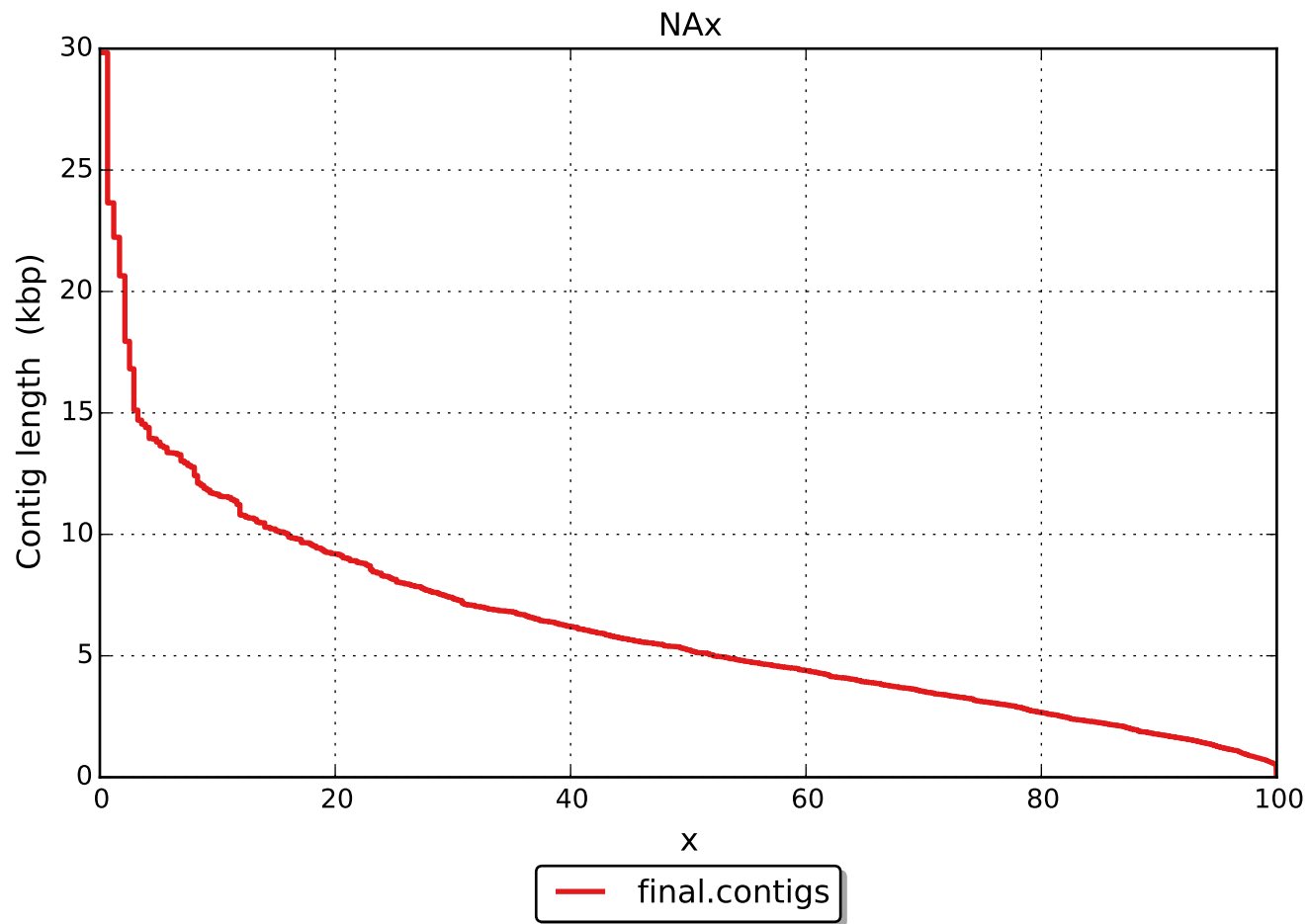






Cumulative length (aligned contigs)





# NGAx

