

# Report

	final.contigs
# contigs ( $\geq 0$ bp)	4321
# contigs ( $\geq 1000$ bp)	27
# 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)	1948663
Total length ( $\geq 1000$ bp)	33234
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	4321
Largest contig	1965
Total length	1948663
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	450
N75	374
L50	1684
L75	2876
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	4299 + 4 part
Unaligned length	1938660
Genome fraction (%)	0.215
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	710.28
# indels per 100 kbp	0.00
Largest alignment	1337
NGA50	-

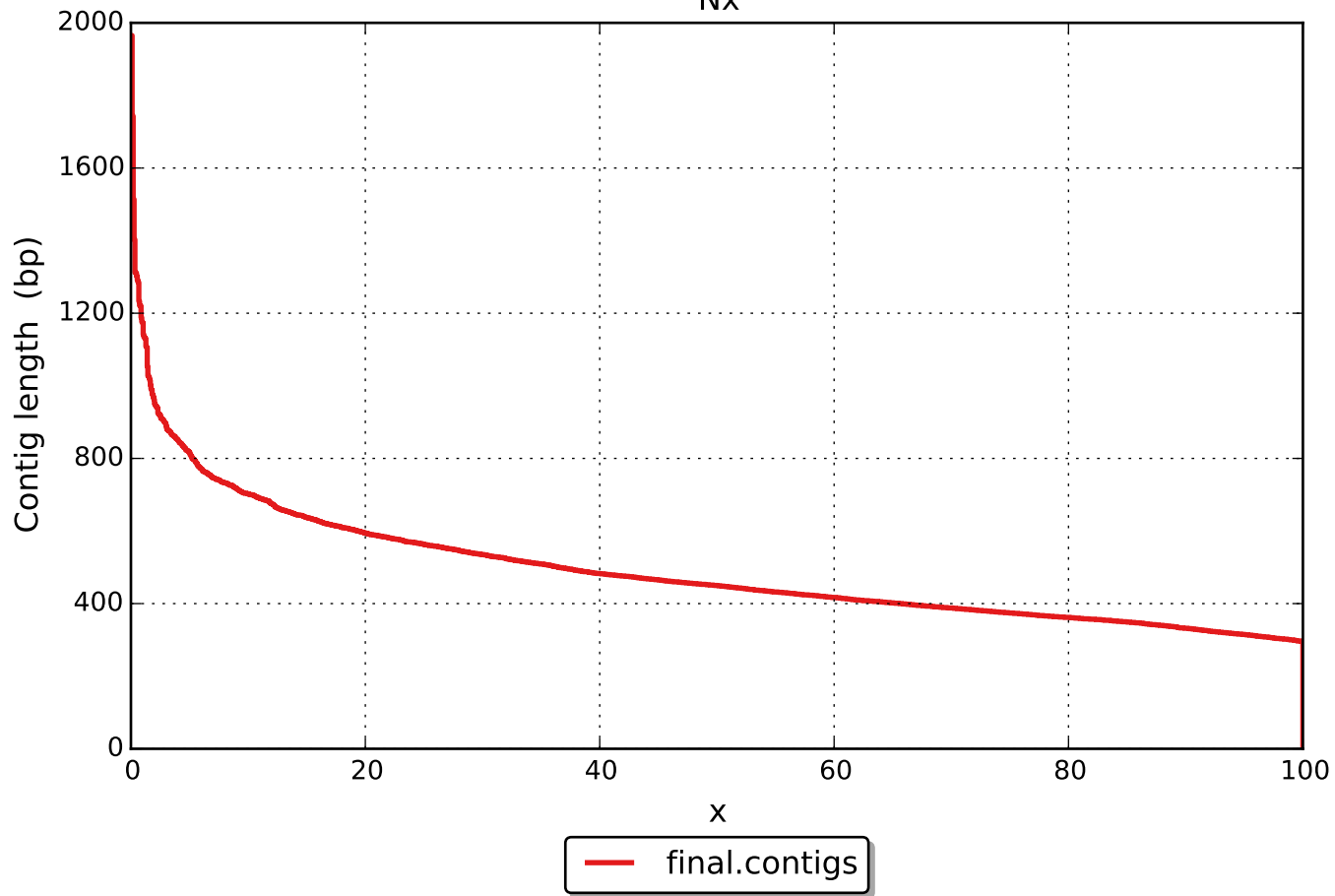
## Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	71
# indels	0
# short indels	0
# long indels	0
Indels length	0

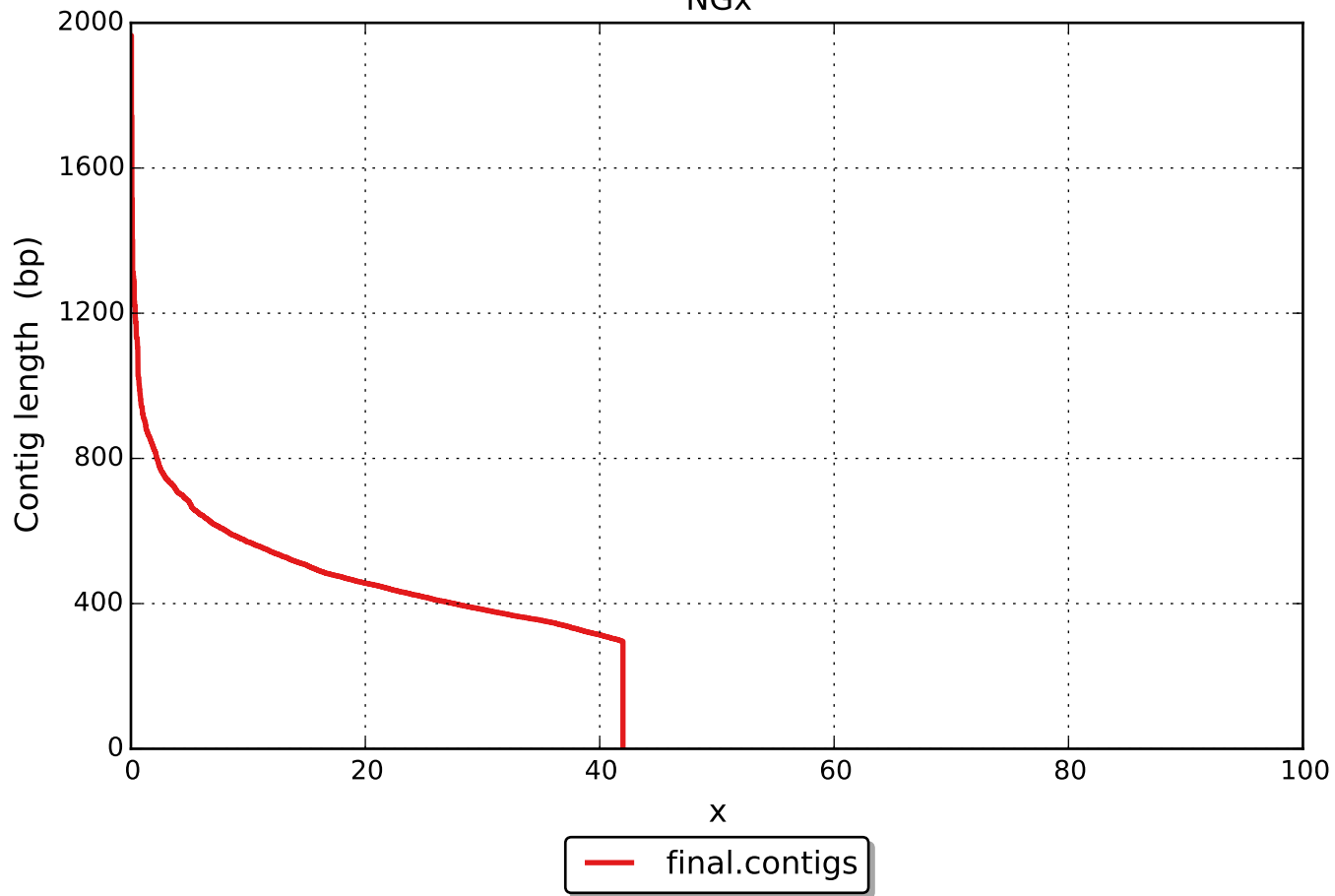
## Unaligned report

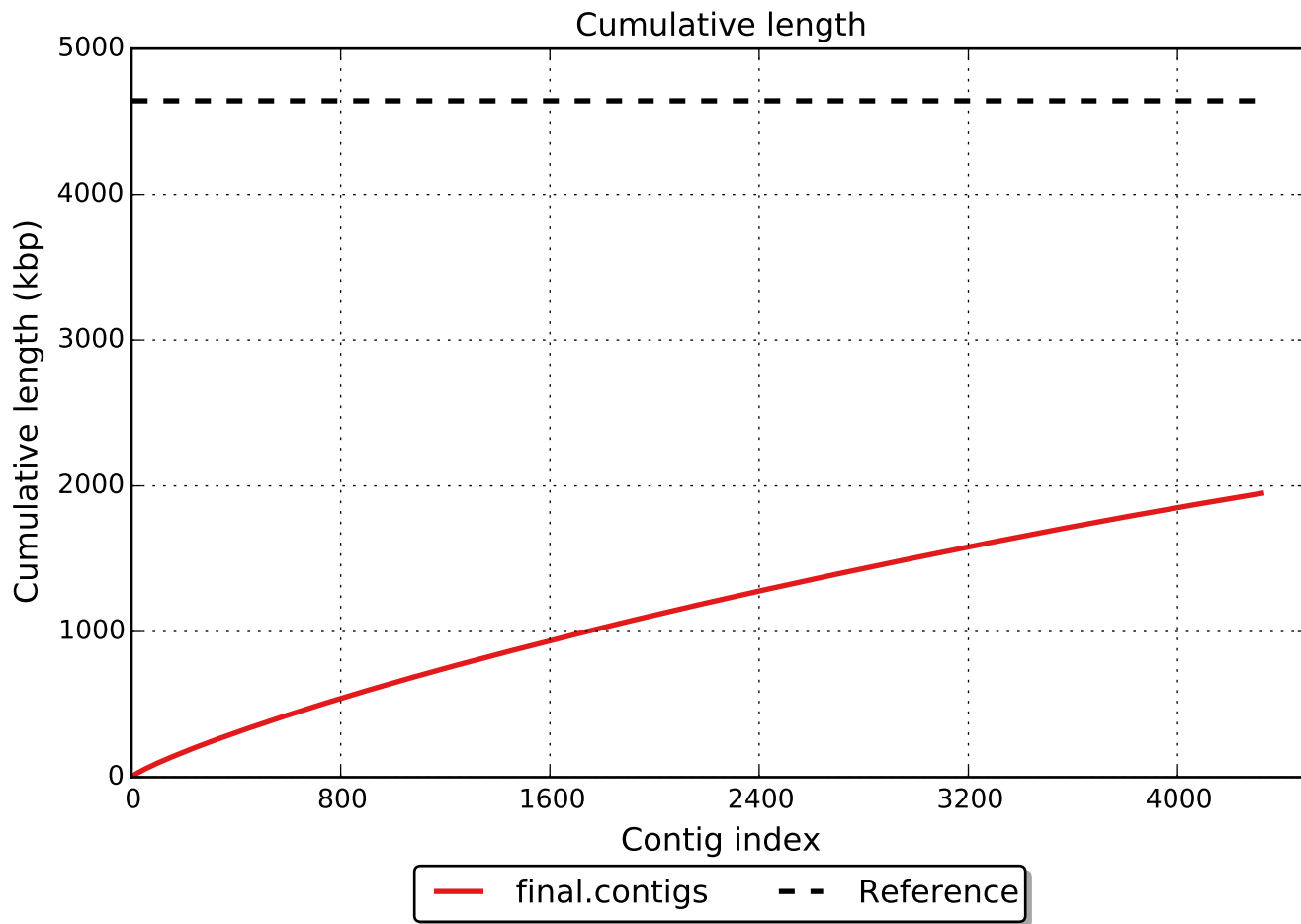
	final.contigs
# fully unaligned contigs	4299
Fully unaligned length	1937351
# partially unaligned contigs	4
# with misassembly	1
# both parts are significant	4
Partially unaligned length	1309
# N's	0

Nx

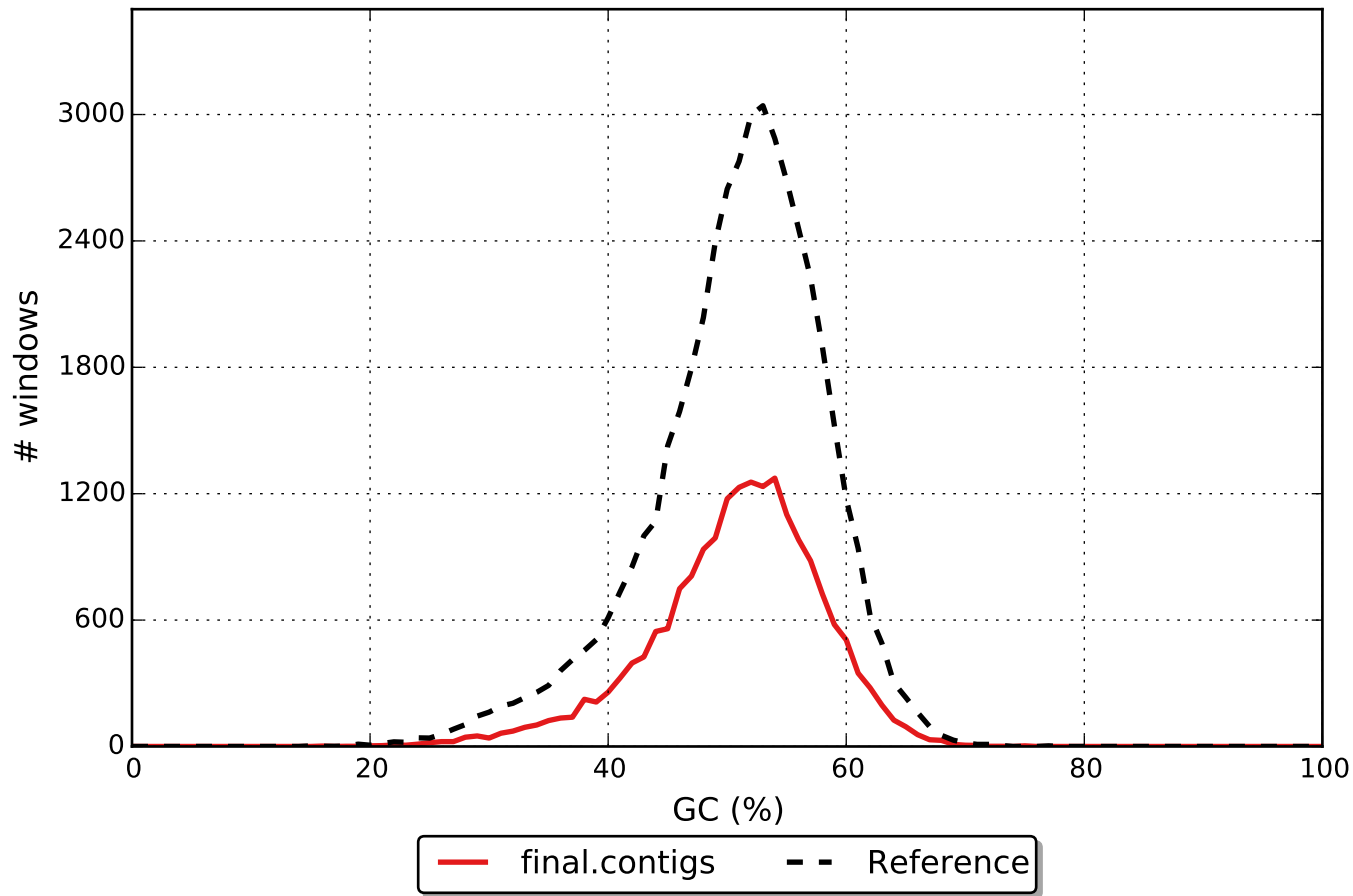


NGx





GC content

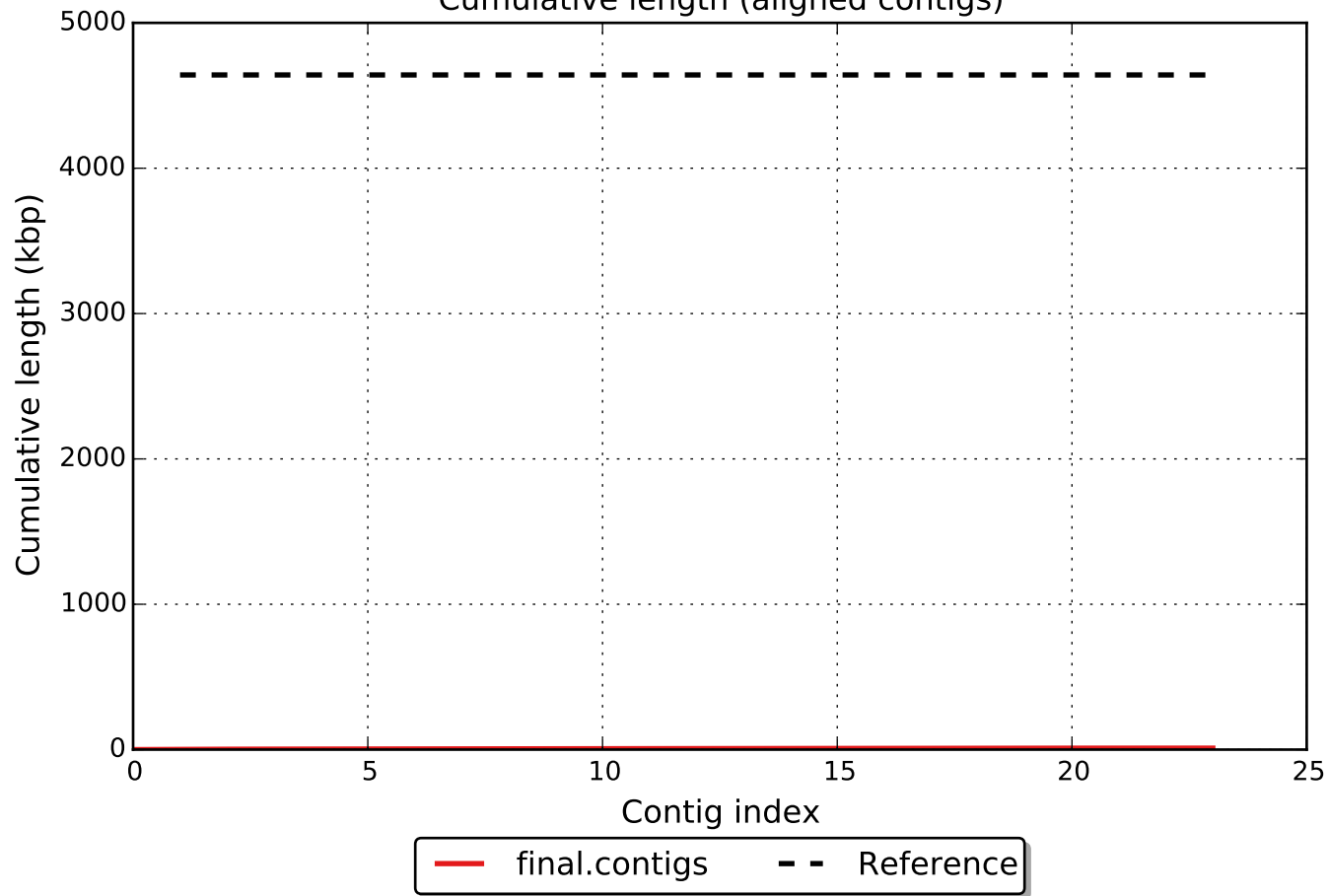


# Misassemblies

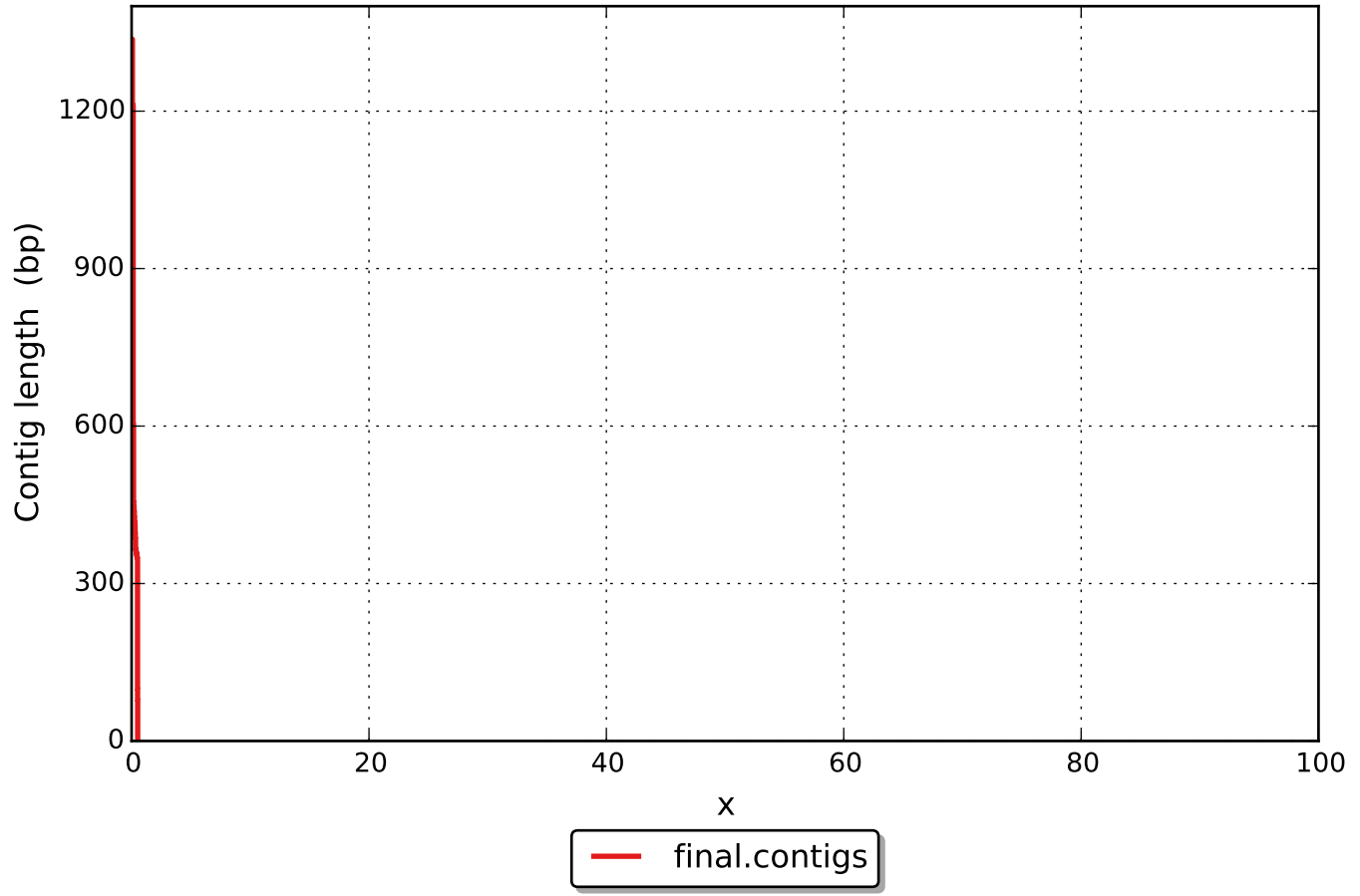




Cumulative length (aligned contigs)



NAx



NGAx

