

Report

	final.contigs
# contigs (>= 0 bp)	55818
# contigs (>= 1000 bp)	0
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	16992122
Total length (>= 1000 bp)	0
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	550
Largest contig	778
Total length	297680
Reference length	4641652
GC (%)	51.06
Reference GC (%)	50.79
N50	531
N75	511
L50	260
L75	403
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	538 + 0 part
Unaligned length	291079
Genome fraction (%)	0.142
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	242.39
# indels per 100 kbp	0.00
Largest alignment	642
NGA50	-

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
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	16
# indels	0
# short indels	0
# long indels	0
Indels length	0

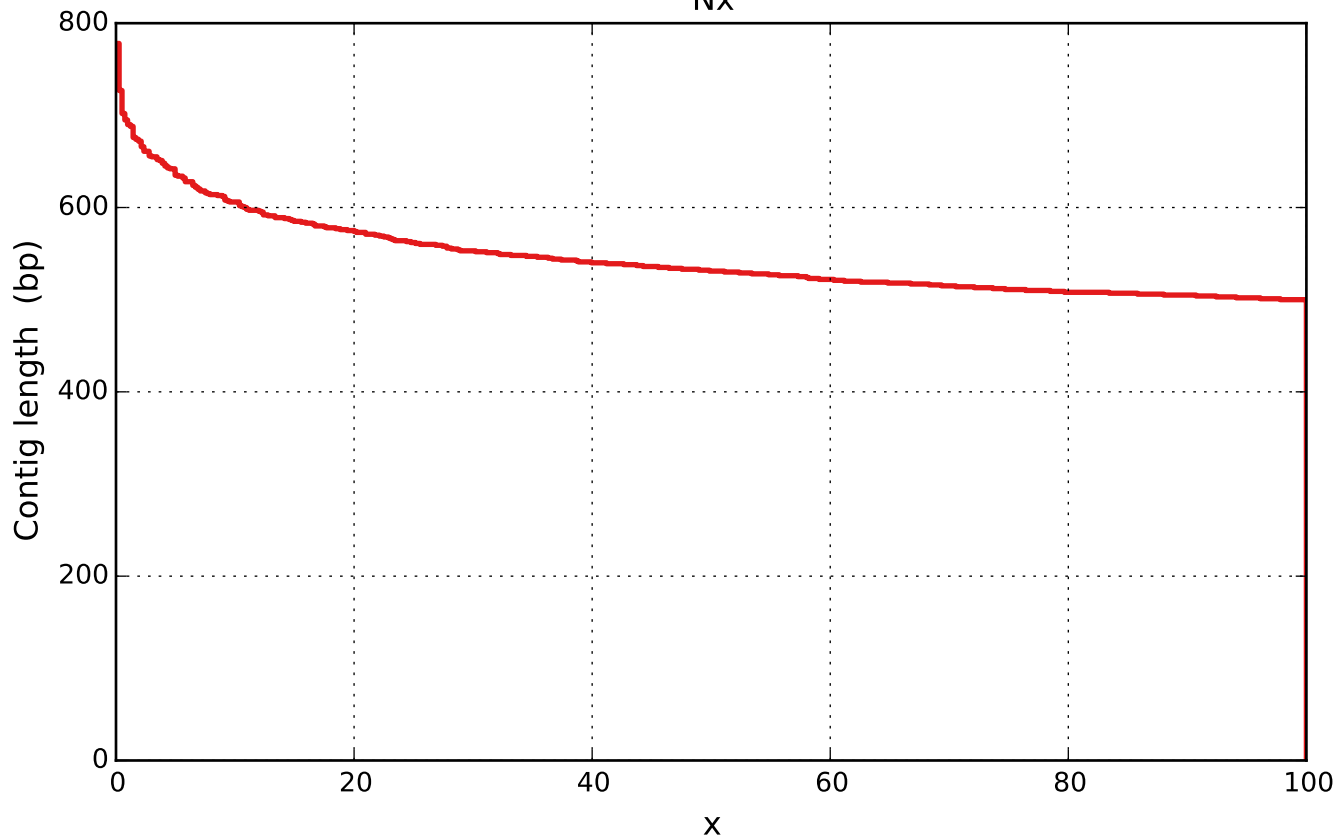
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	538
Fully unaligned length	291079
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

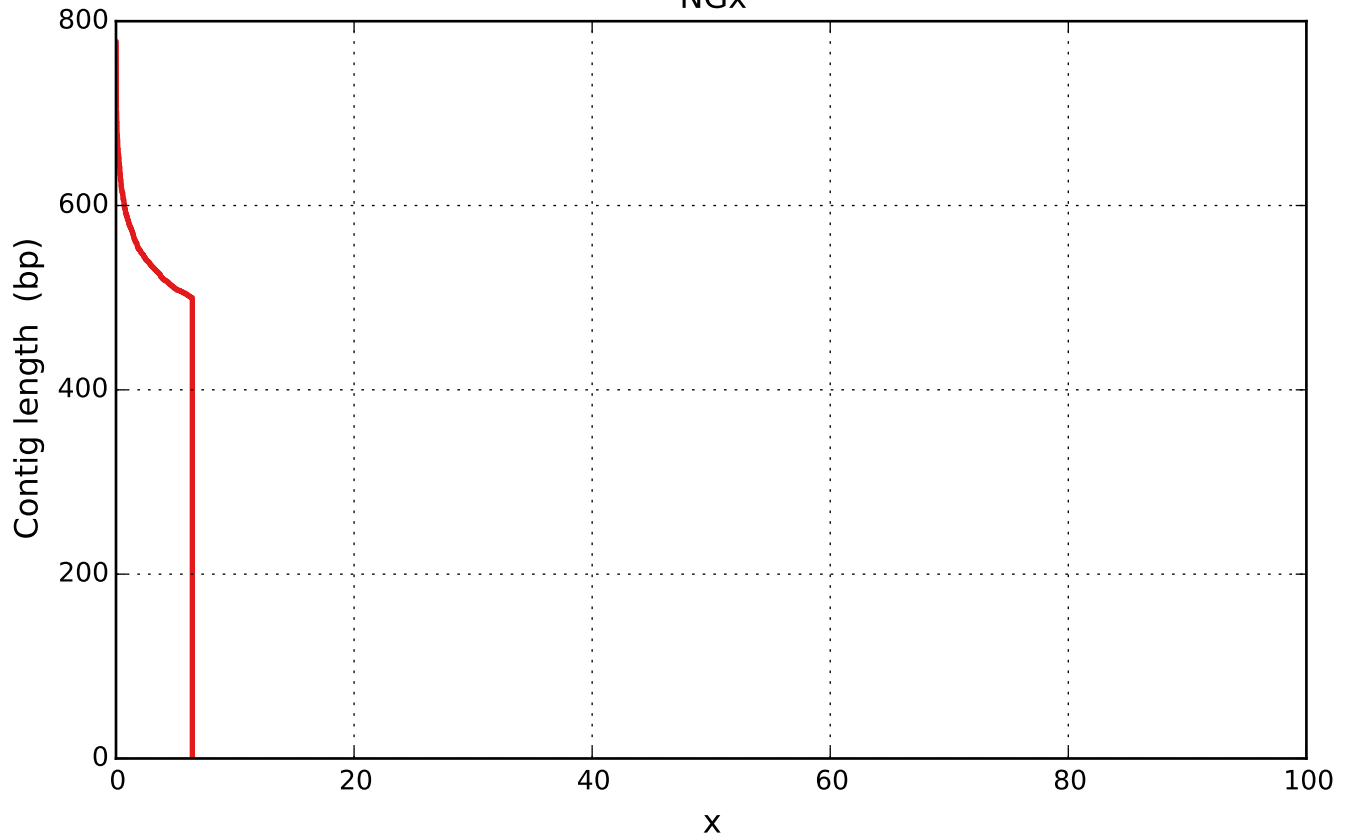
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

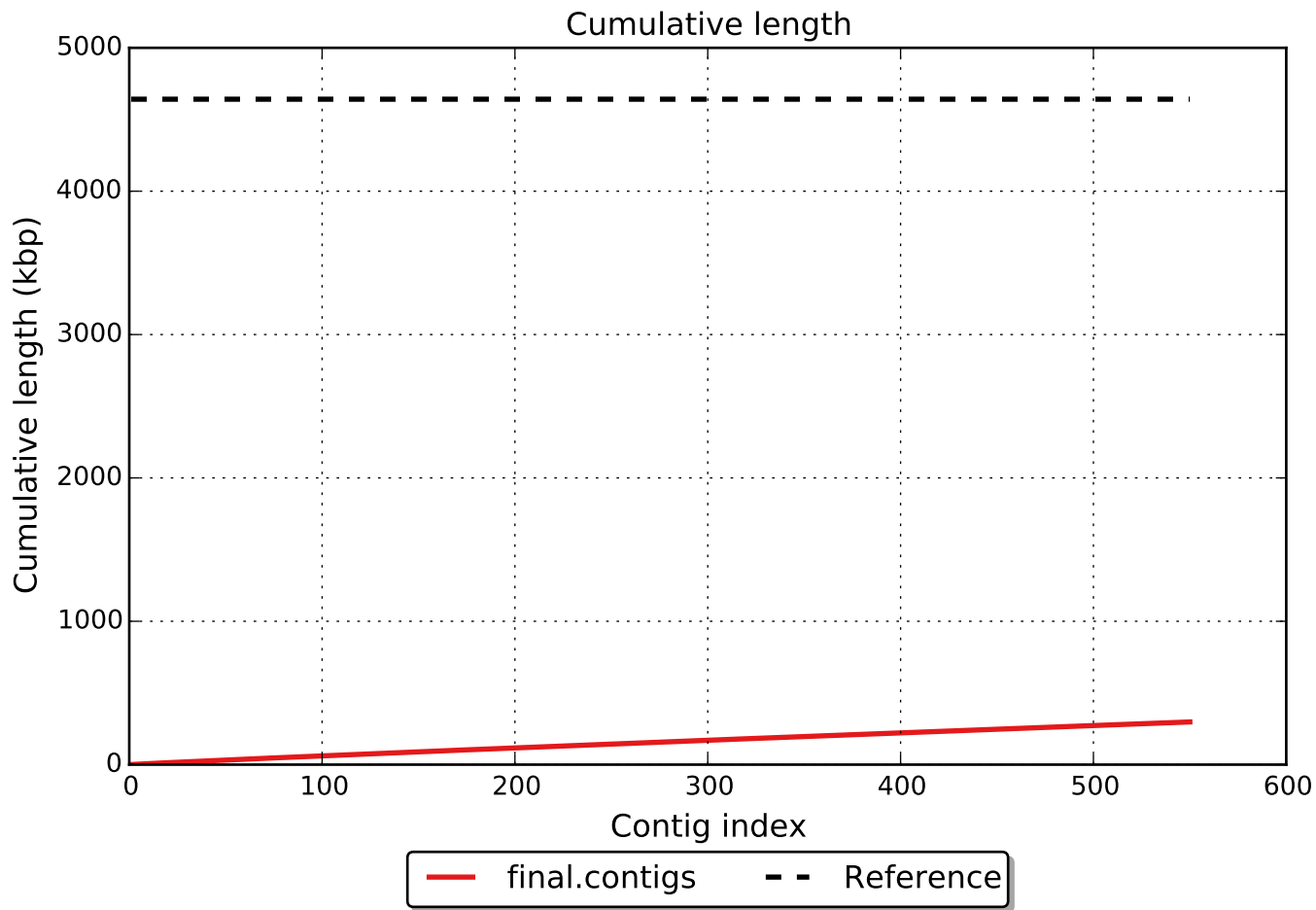


— final.contigs

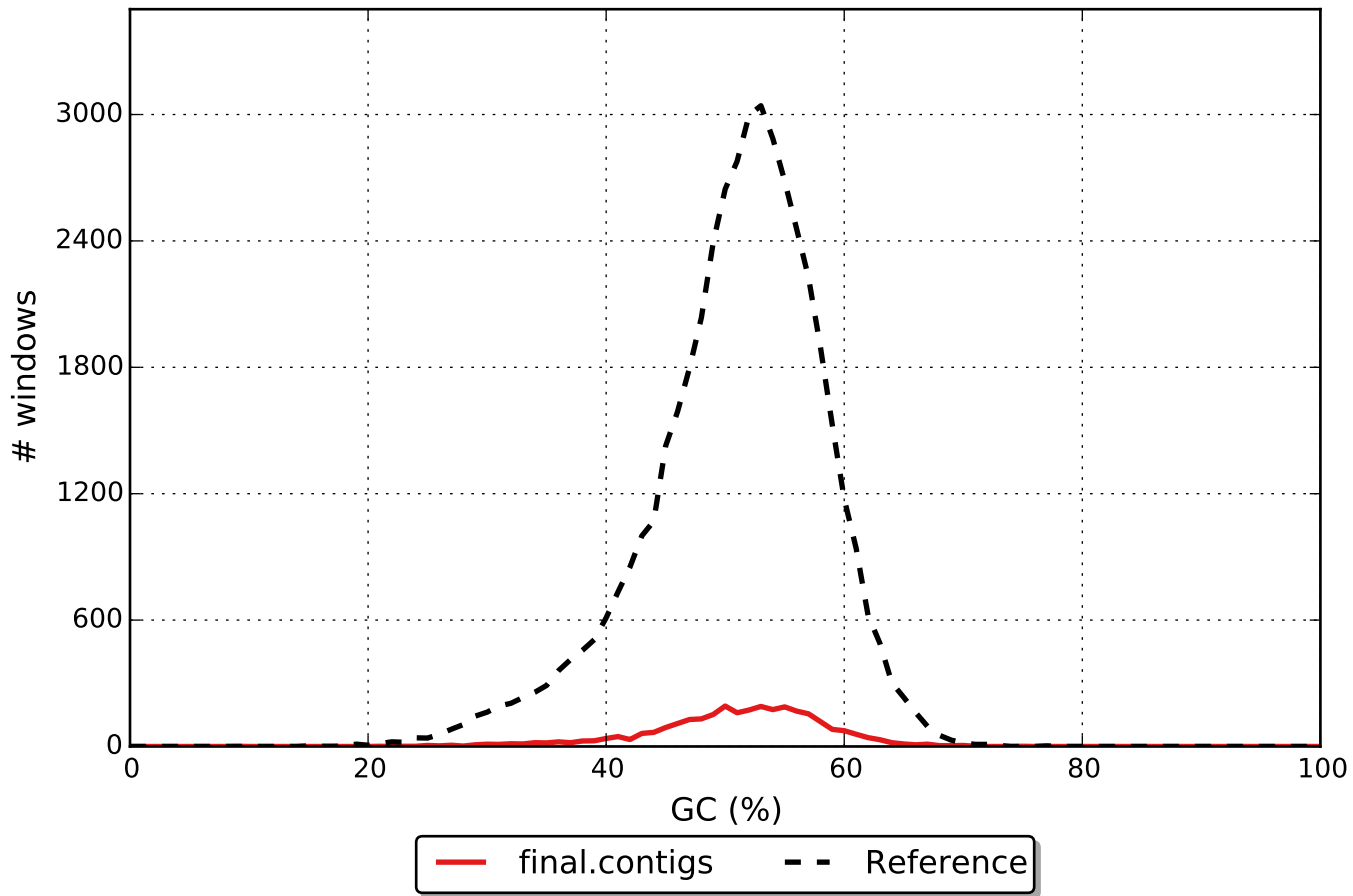
NGx



— final.contigs



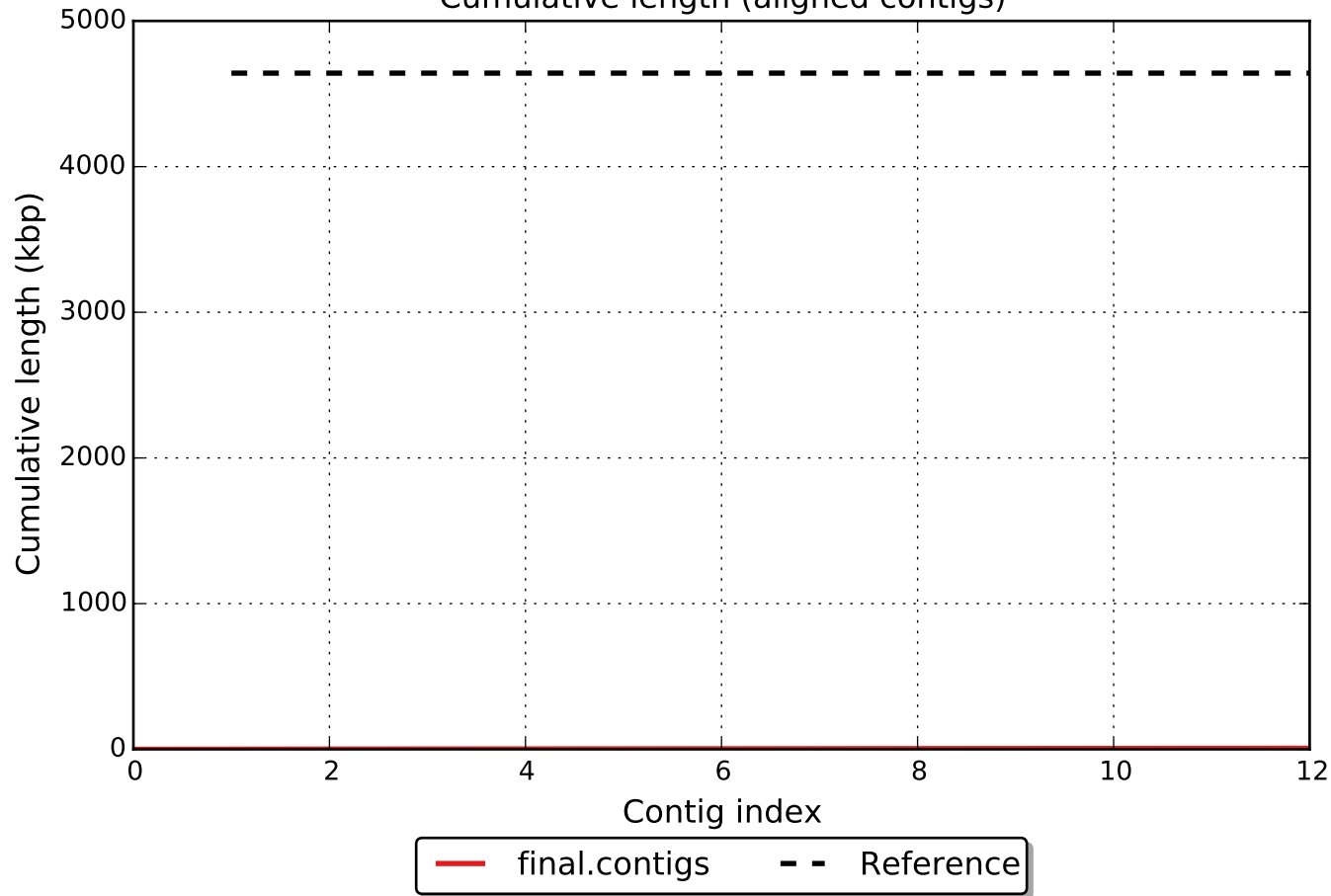
GC content



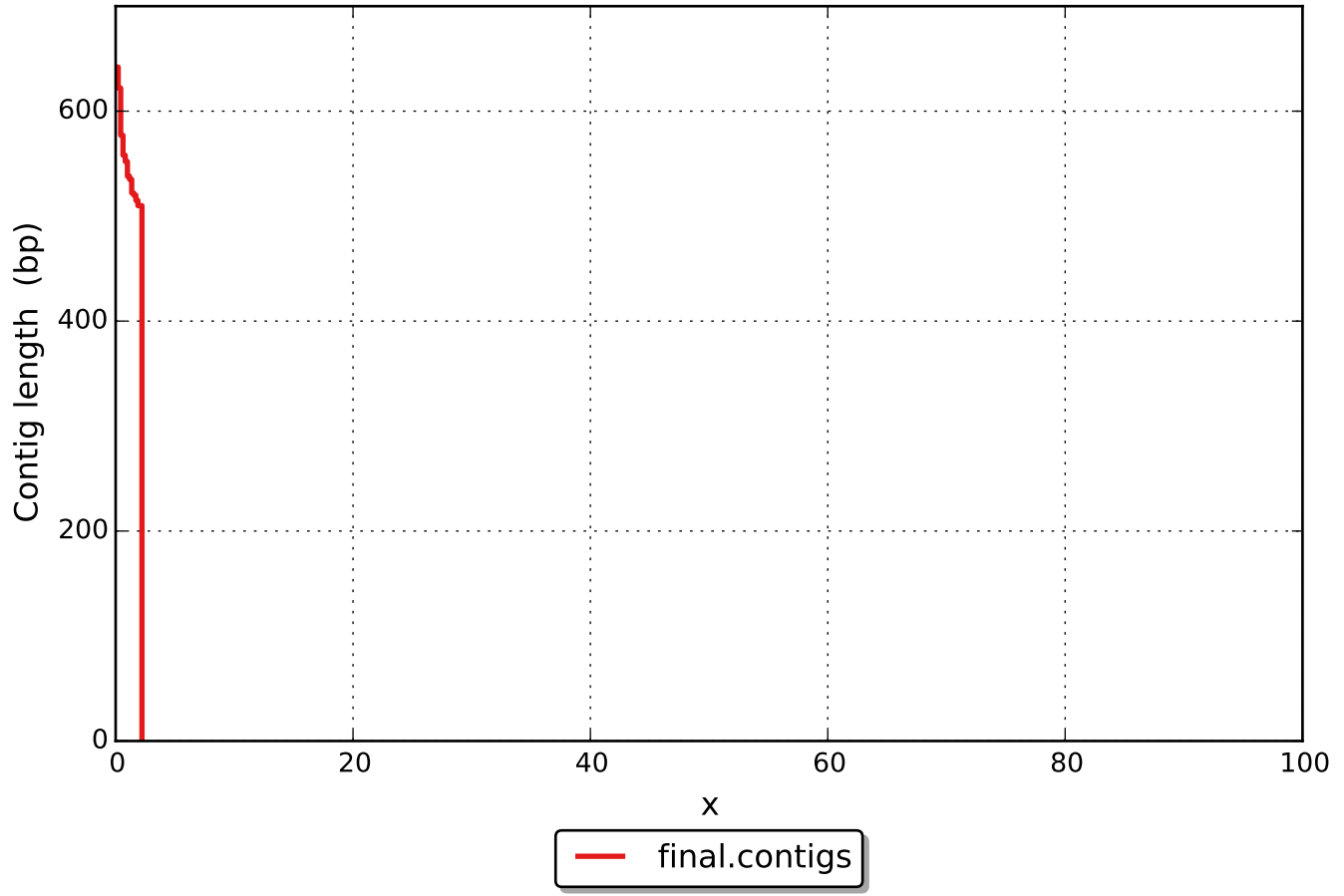
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

