

Report

	final.contigs
# contigs (≥ 0 bp)	148
# contigs (≥ 1000 bp)	97
# contigs (≥ 5000 bp)	74
# contigs (≥ 10000 bp)	66
# contigs (≥ 25000 bp)	53
# contigs (≥ 50000 bp)	29
Total length (≥ 0 bp)	4592530
Total length (≥ 1000 bp)	4571305
Total length (≥ 5000 bp)	4520844
Total length (≥ 10000 bp)	4460643
Total length (≥ 25000 bp)	4258917
Total length (≥ 50000 bp)	3398643
# contigs	106
Largest contig	327315
Total length	4577521
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	97687
NG50	97687
N75	48864
NG75	47677
L50	15
LG50	15
L75	30
LG75	31
# misassemblies	5
# misassembled contigs	4
Misassembled contigs length	314605
# local misassemblies	6
# unaligned contigs	0 + 1 part
Unaligned length	122
Genome fraction (%)	98.428
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	8.73
# indels per 100 kbp	0.15
Largest alignment	327315
NA50	96494
NGA50	96494
NA75	48864
NGA75	47677
LA50	16
LGA50	16
LA75	31
LGA75	32

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	5
# relocations	5
# translocations	0
# inversions	0
# misassembled contigs	4
Misassembled contigs length	314605
# local misassemblies	6
# mismatches	399
# indels	7
# short indels	6
# long indels	1
Indels length	34

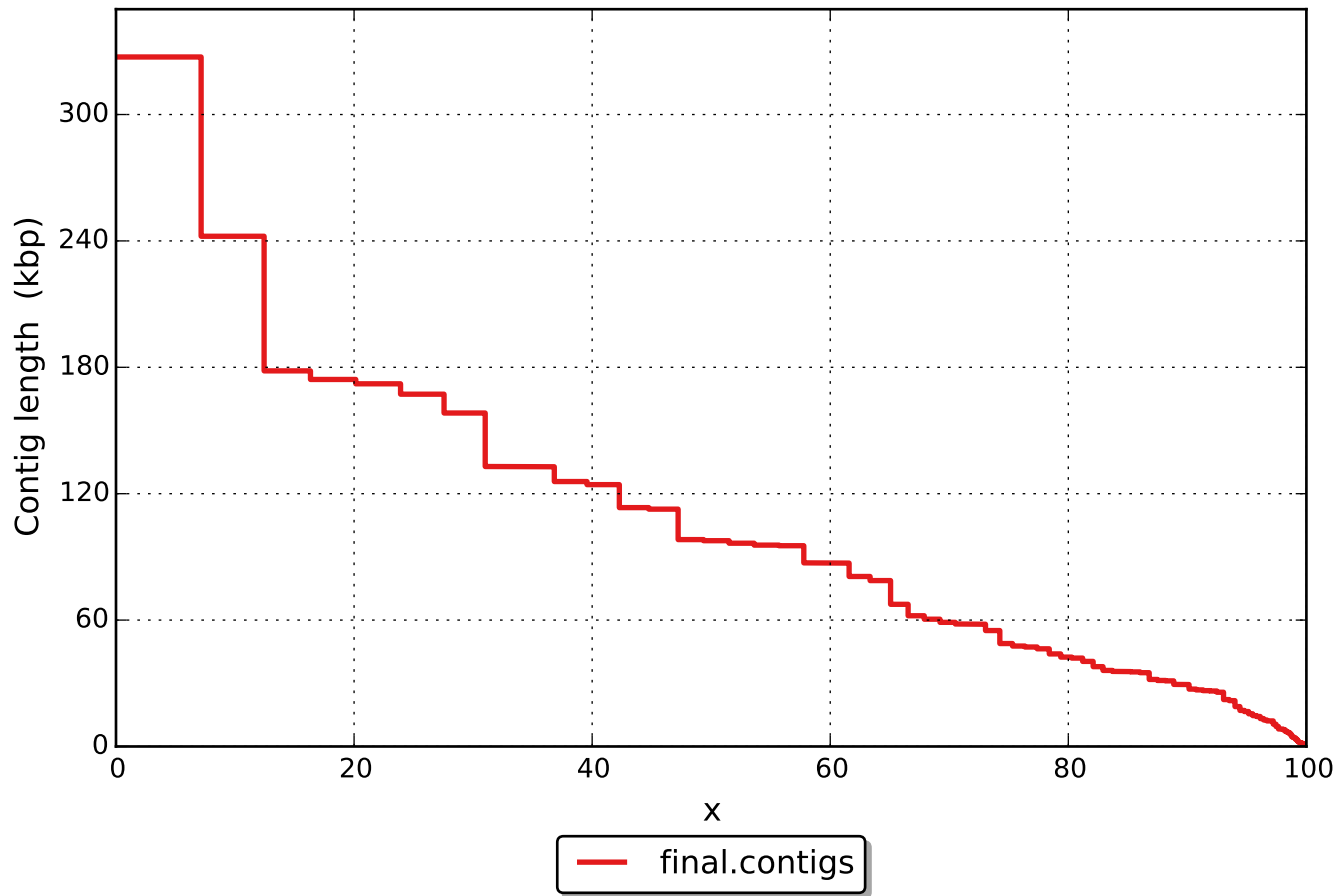
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

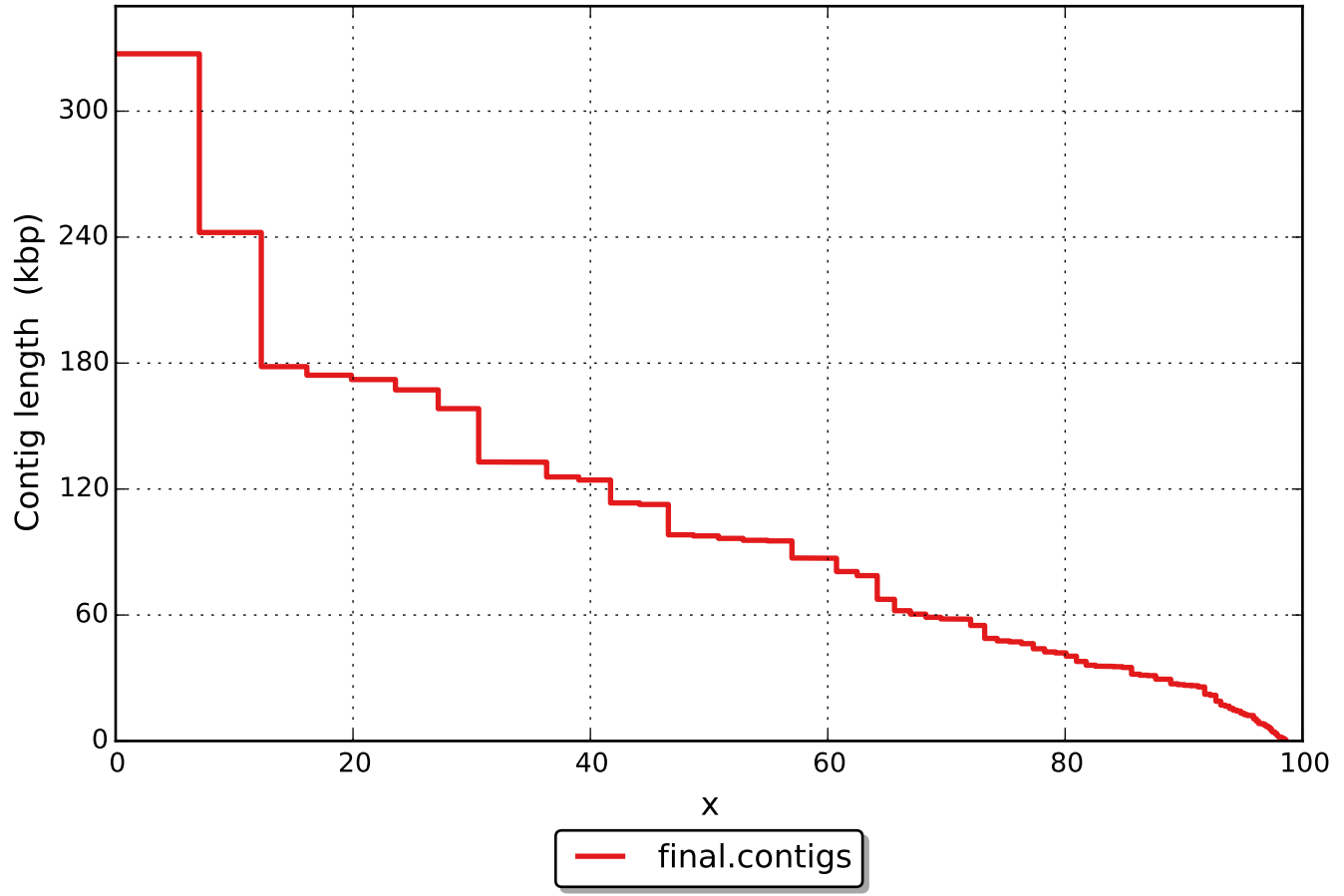
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	122
# N's	0

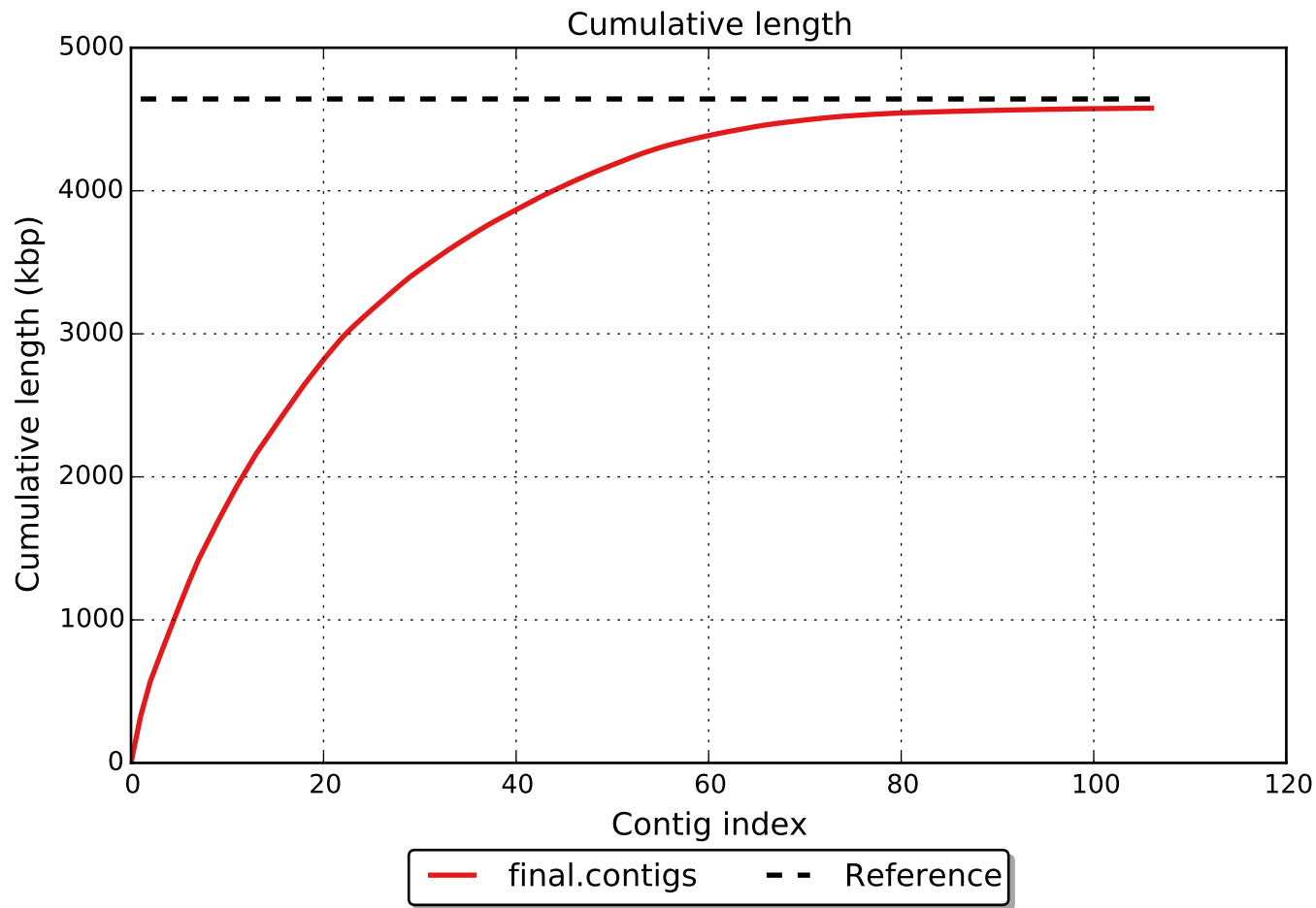
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

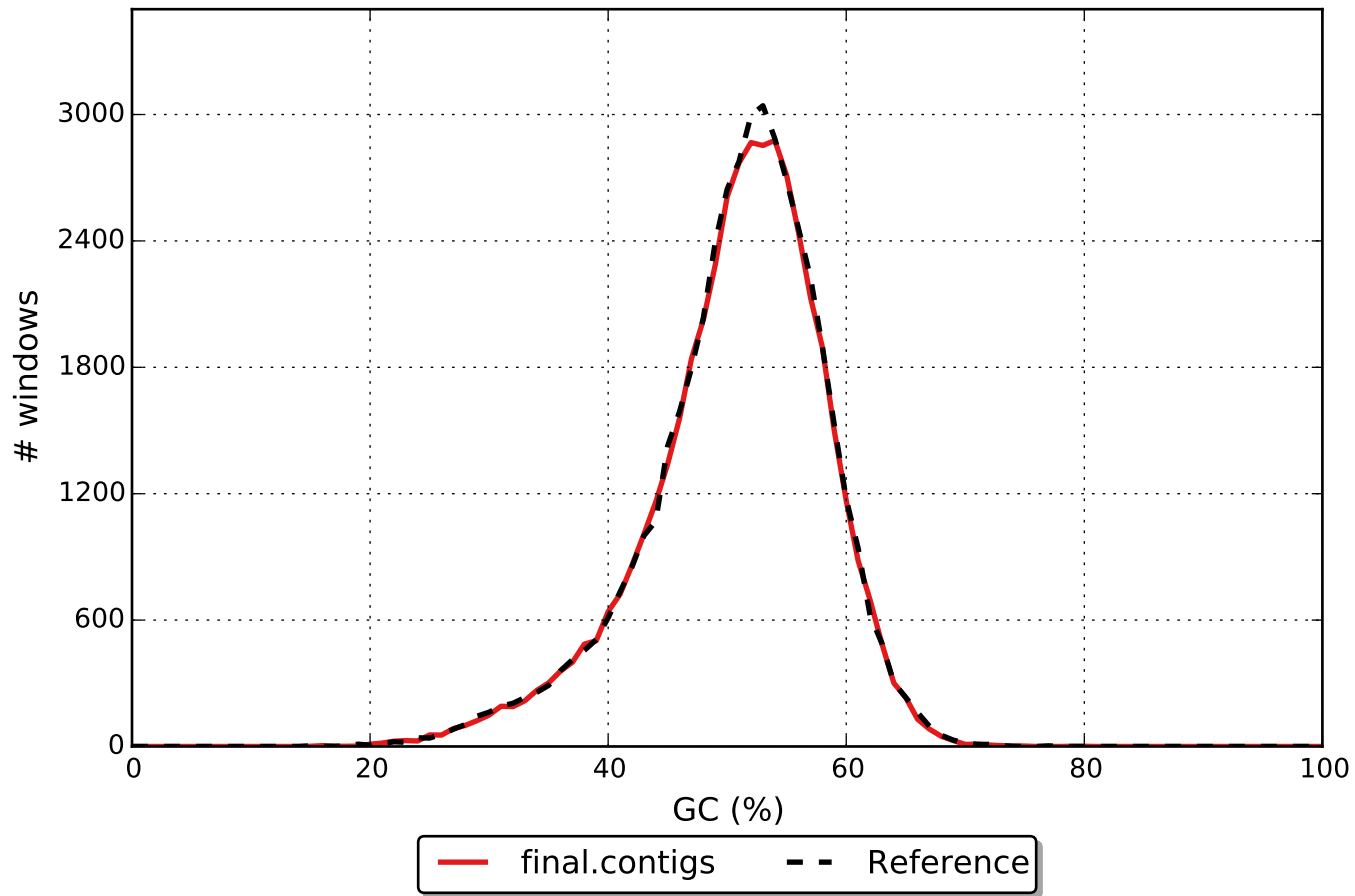


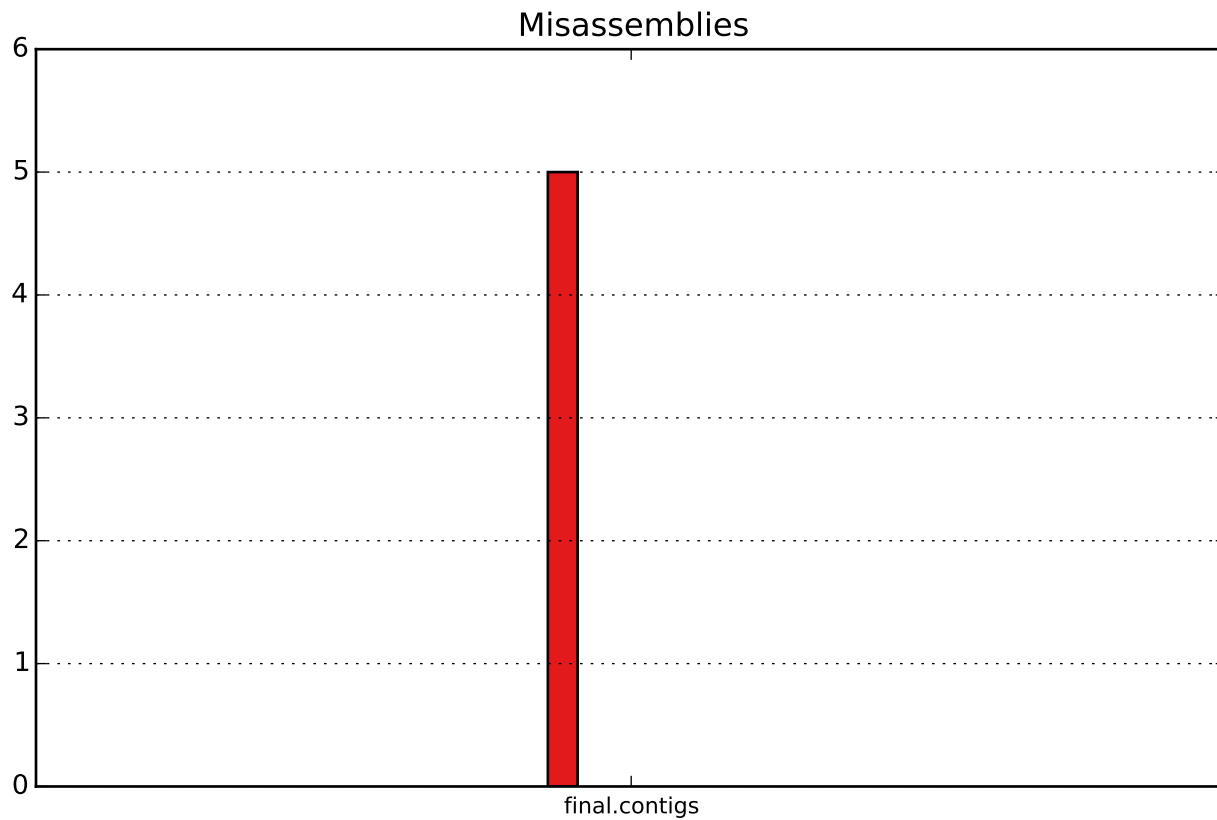
NGx



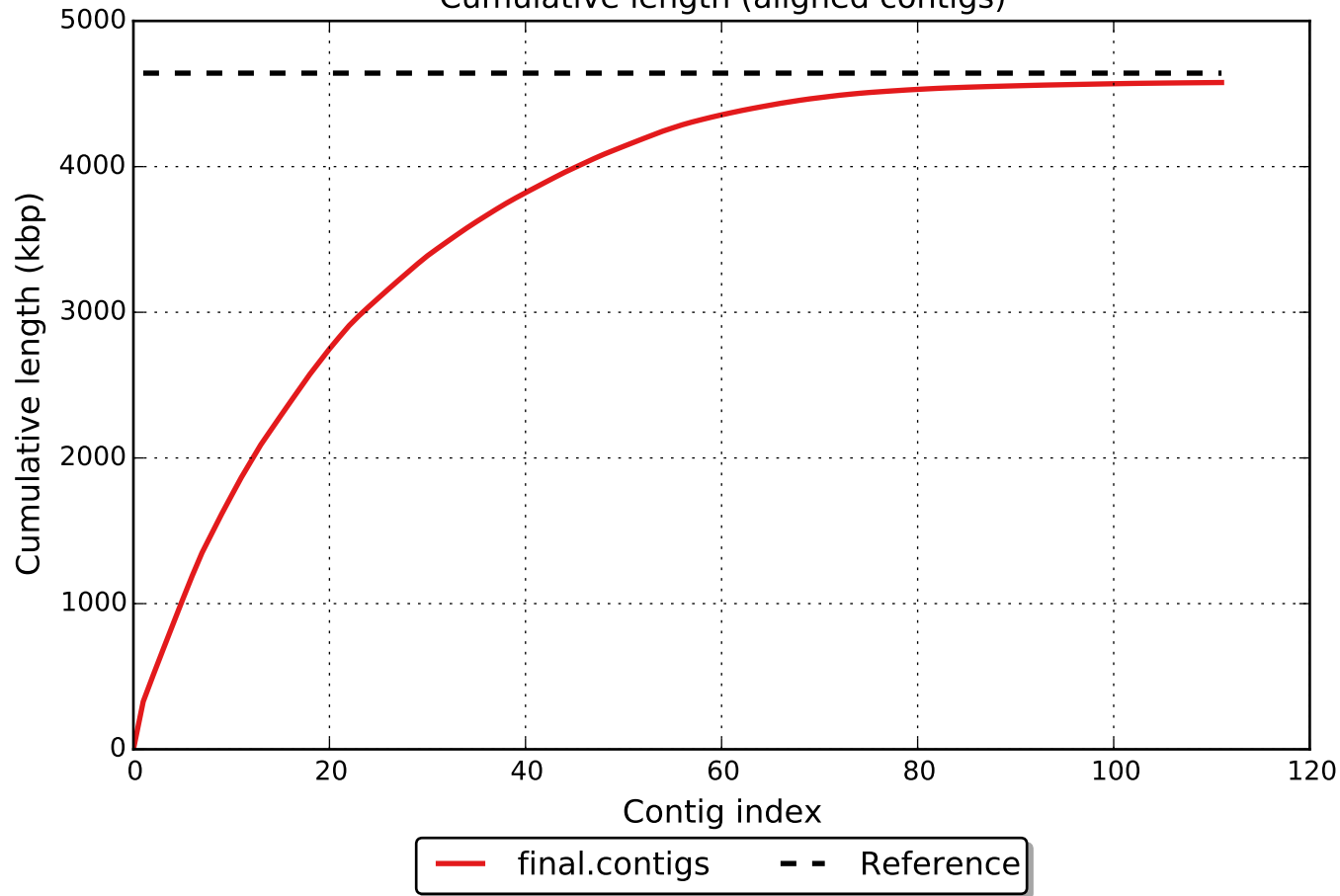


GC content

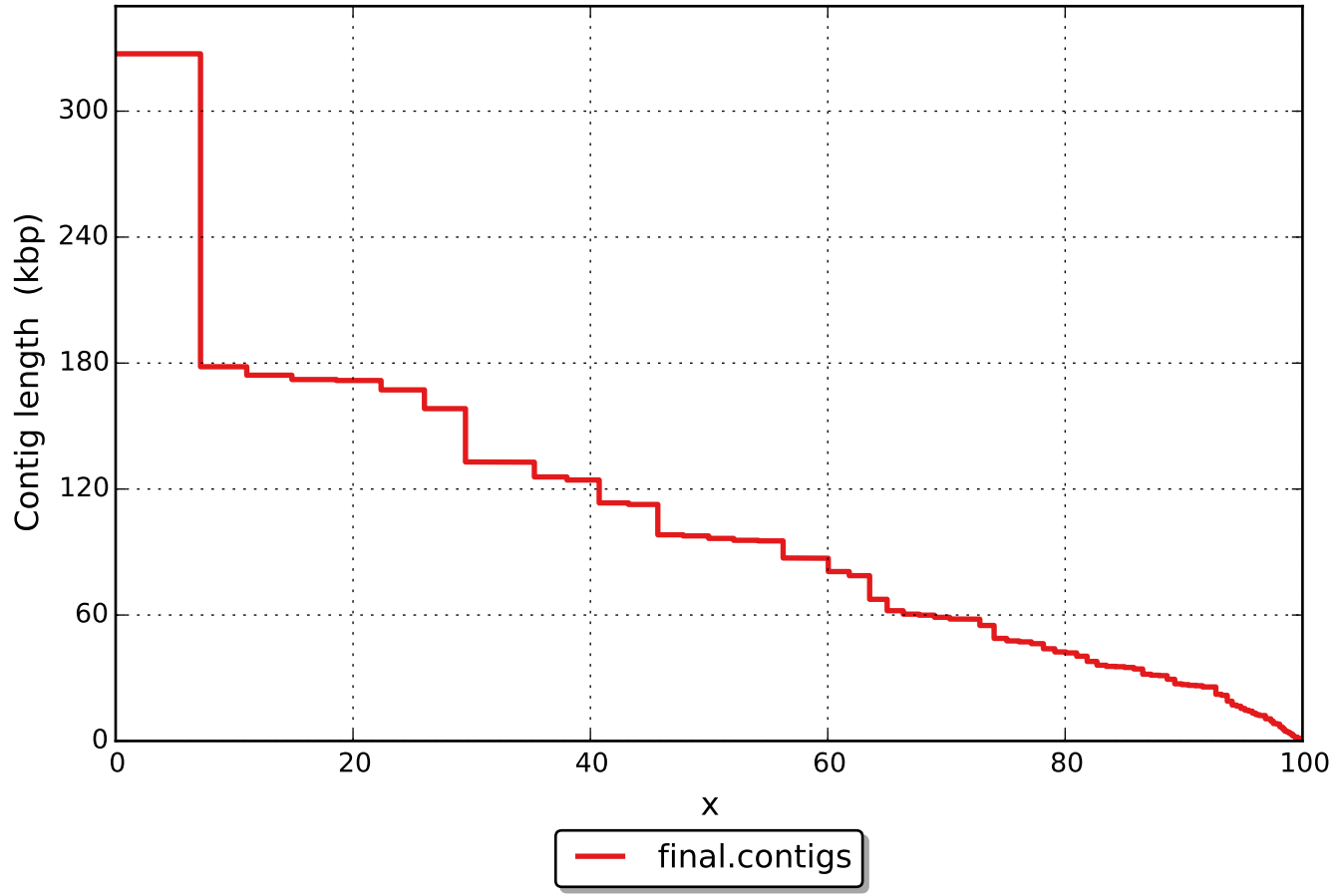




Cumulative length (aligned contigs)



NAx



NGAx

