

Report

	final.contigs
# contigs (>= 0 bp)	134
# contigs (>= 1000 bp)	91
# contigs (>= 5000 bp)	72
# contigs (>= 10000 bp)	65
# contigs (>= 25000 bp)	54
# contigs (>= 50000 bp)	28
Total length (>= 0 bp)	4591150
Total length (>= 1000 bp)	4570998
Total length (>= 5000 bp)	4528141
Total length (>= 10000 bp)	4473587
Total length (>= 25000 bp)	4320441
Total length (>= 50000 bp)	3373671
# contigs	108
Largest contig	327193
Total length	4582280
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	95665
NG50	95665
N75	47412
NG75	46929
L50	14
LG50	14
L75	30
LG75	31
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	271086
# local misassemblies	6
# unaligned contigs	0 + 1 part
Unaligned length	321
Genome fraction (%)	98.553
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10.69
# indels per 100 kbp	0.15
Largest alignment	327193
NA50	95665
NGA50	95665
NA75	47412
NGA75	46929
LA50	14
LGA50	14
LA75	30
LGA75	31

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
# misassembled contigs	4
Misassembled contigs length	271086
# local misassemblies	6
# mismatches	489
# indels	7
# short indels	7
# long indels	0
Indels length	7

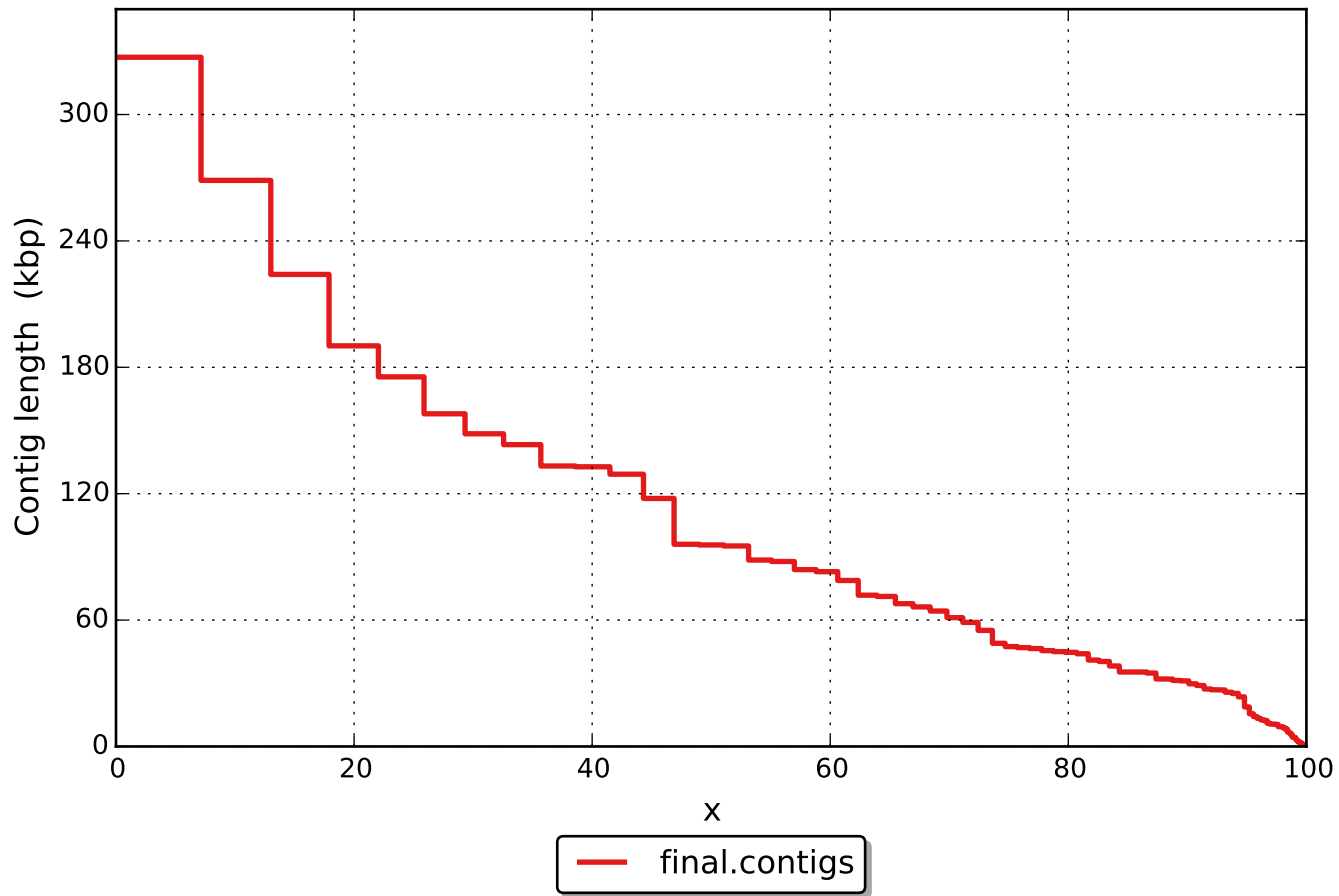
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

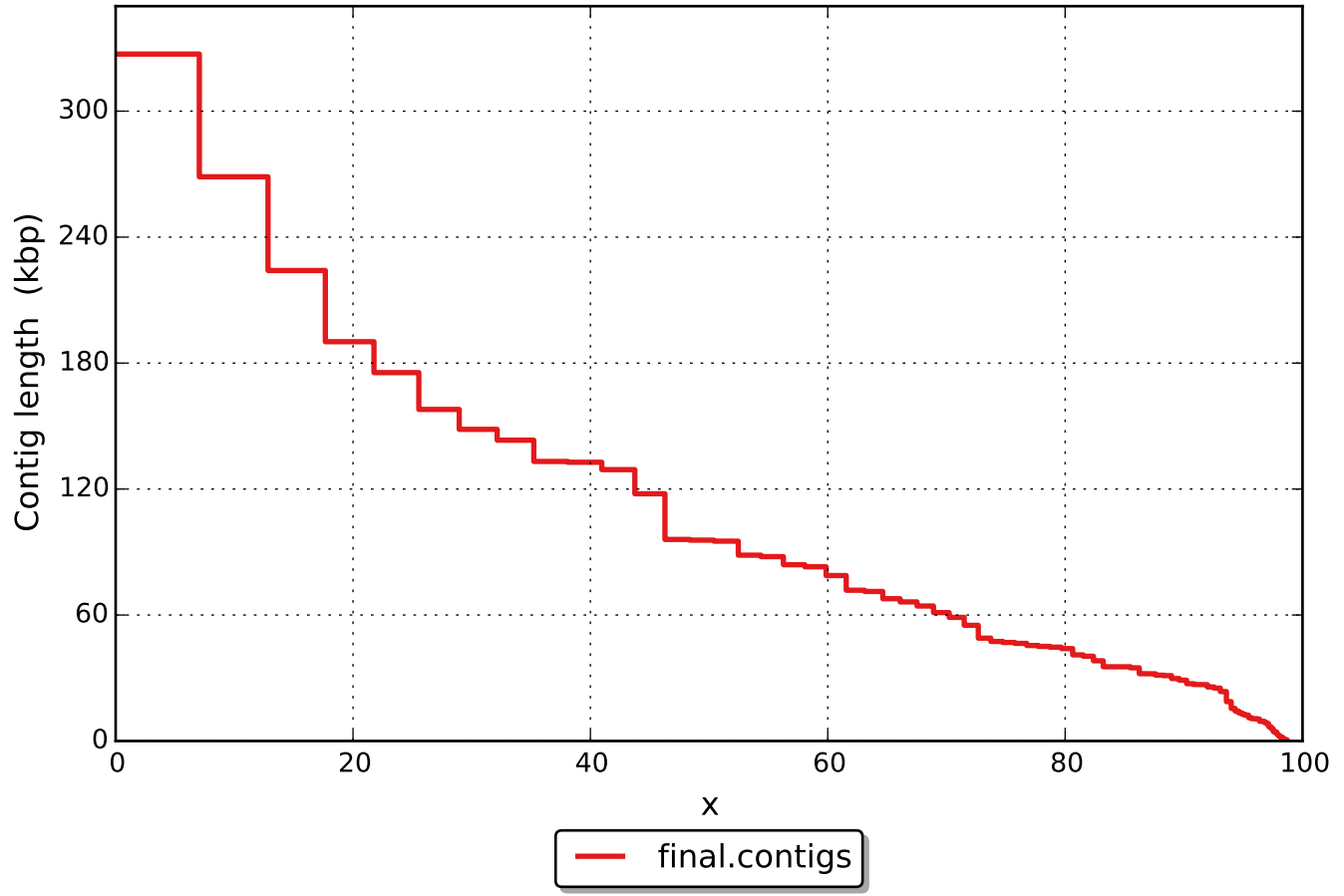
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	321
# N's	0

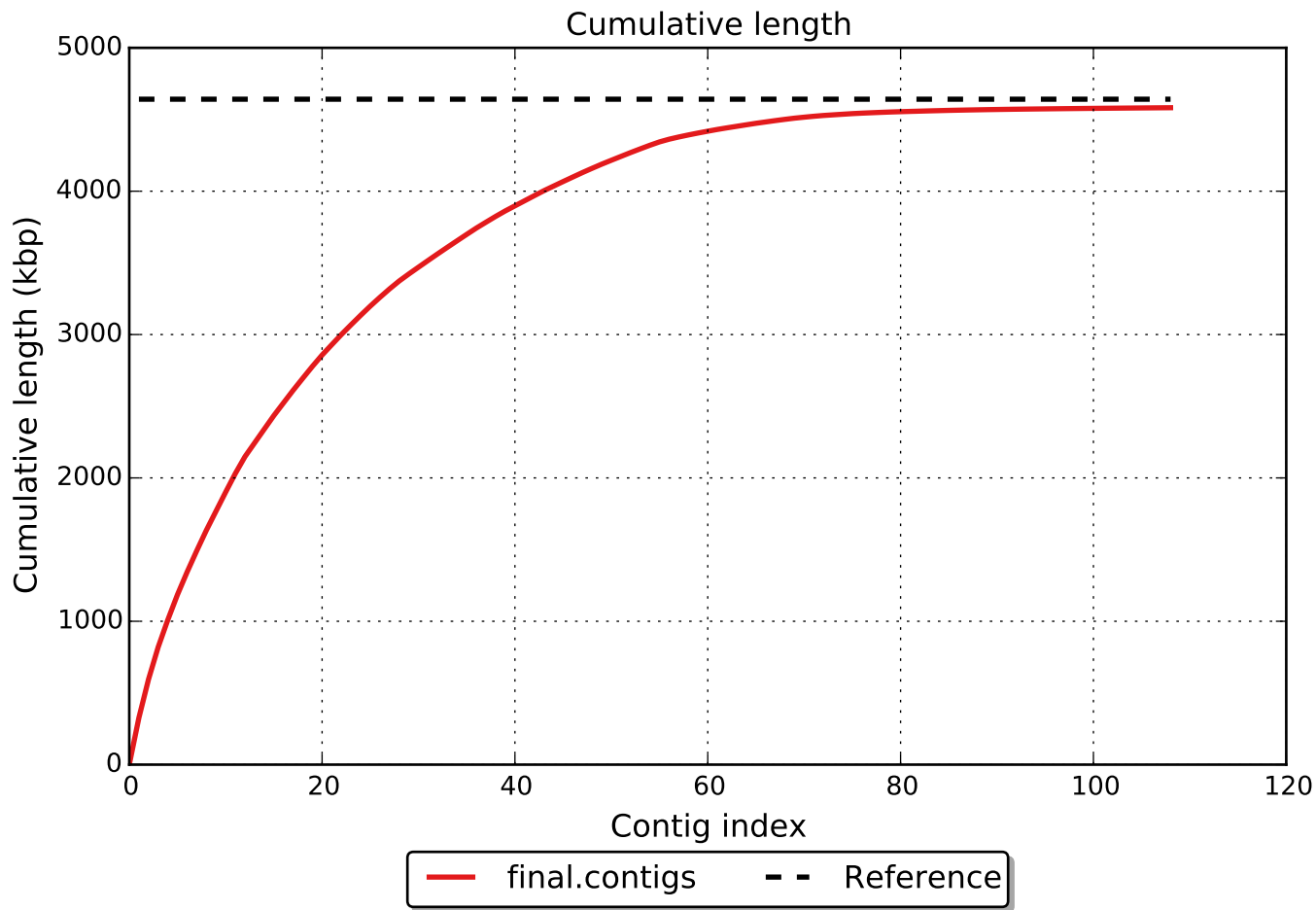
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

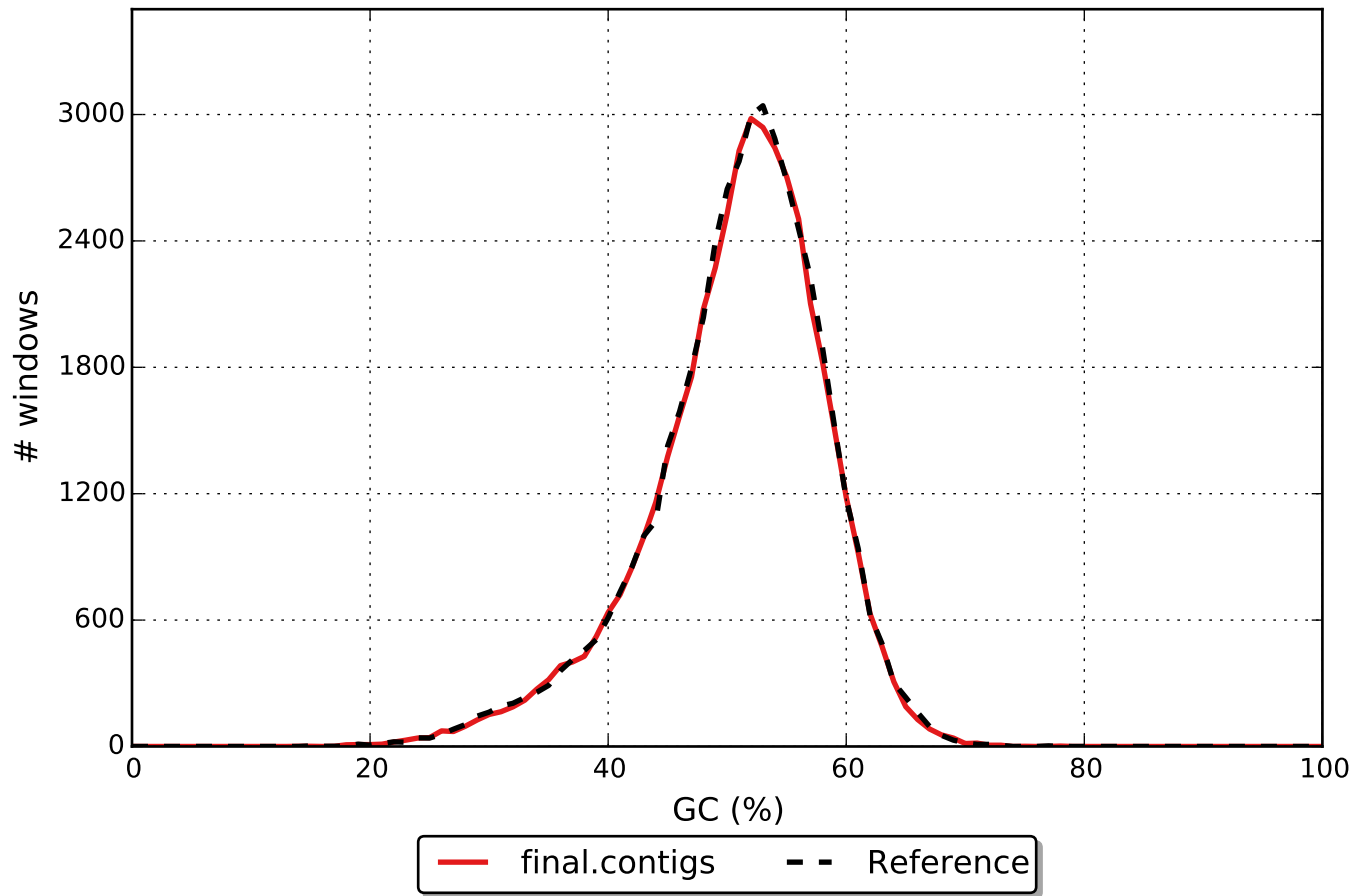


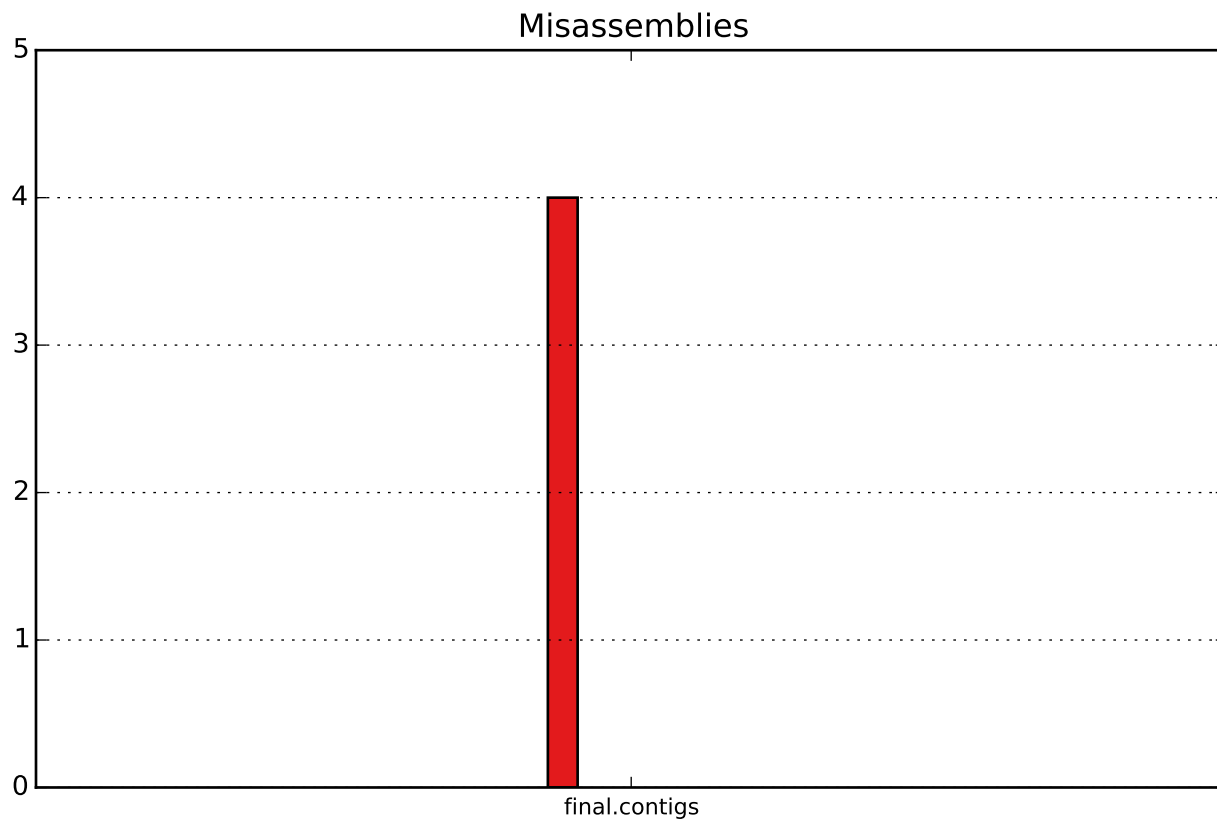
NGx



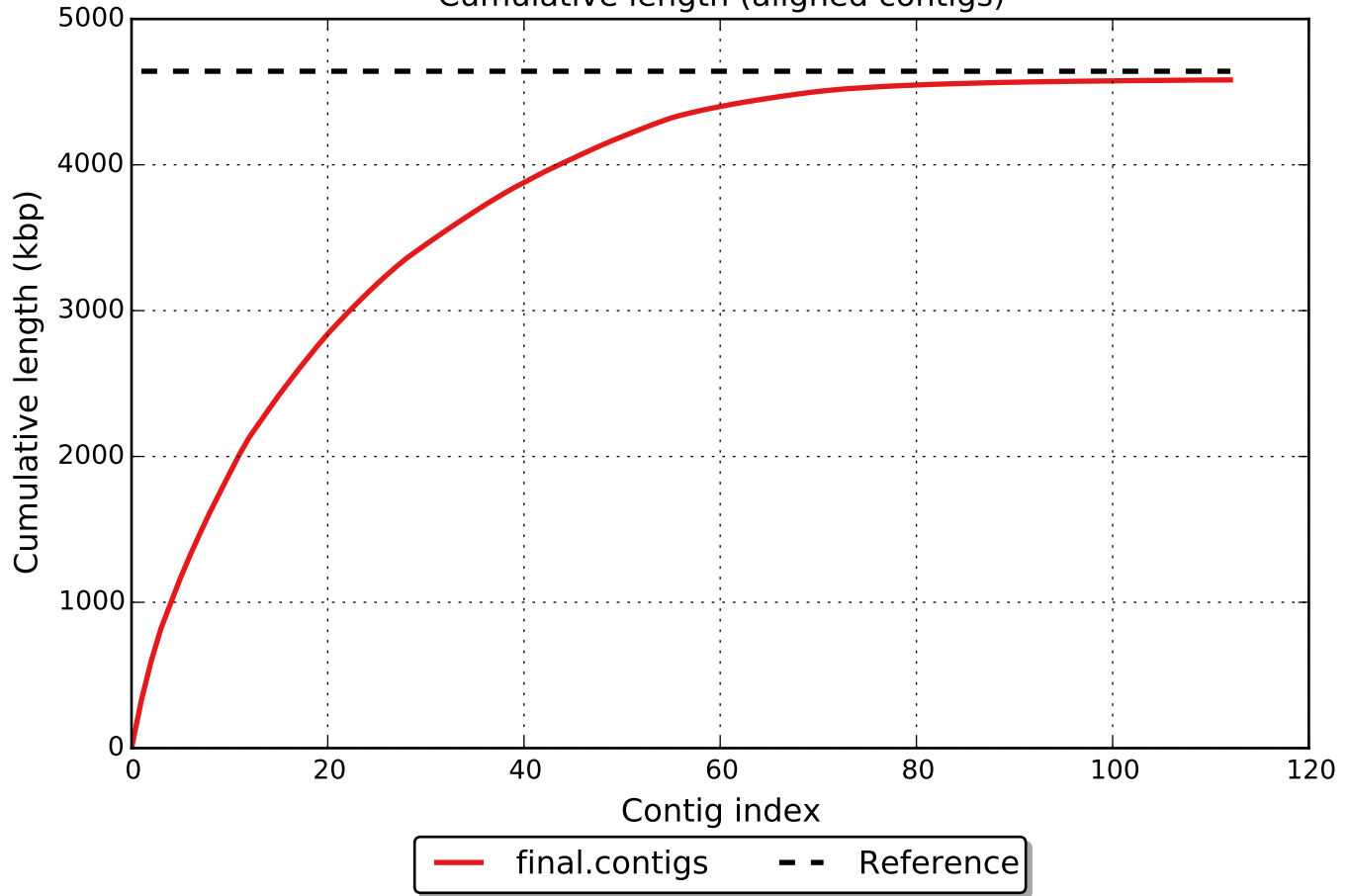


GC content

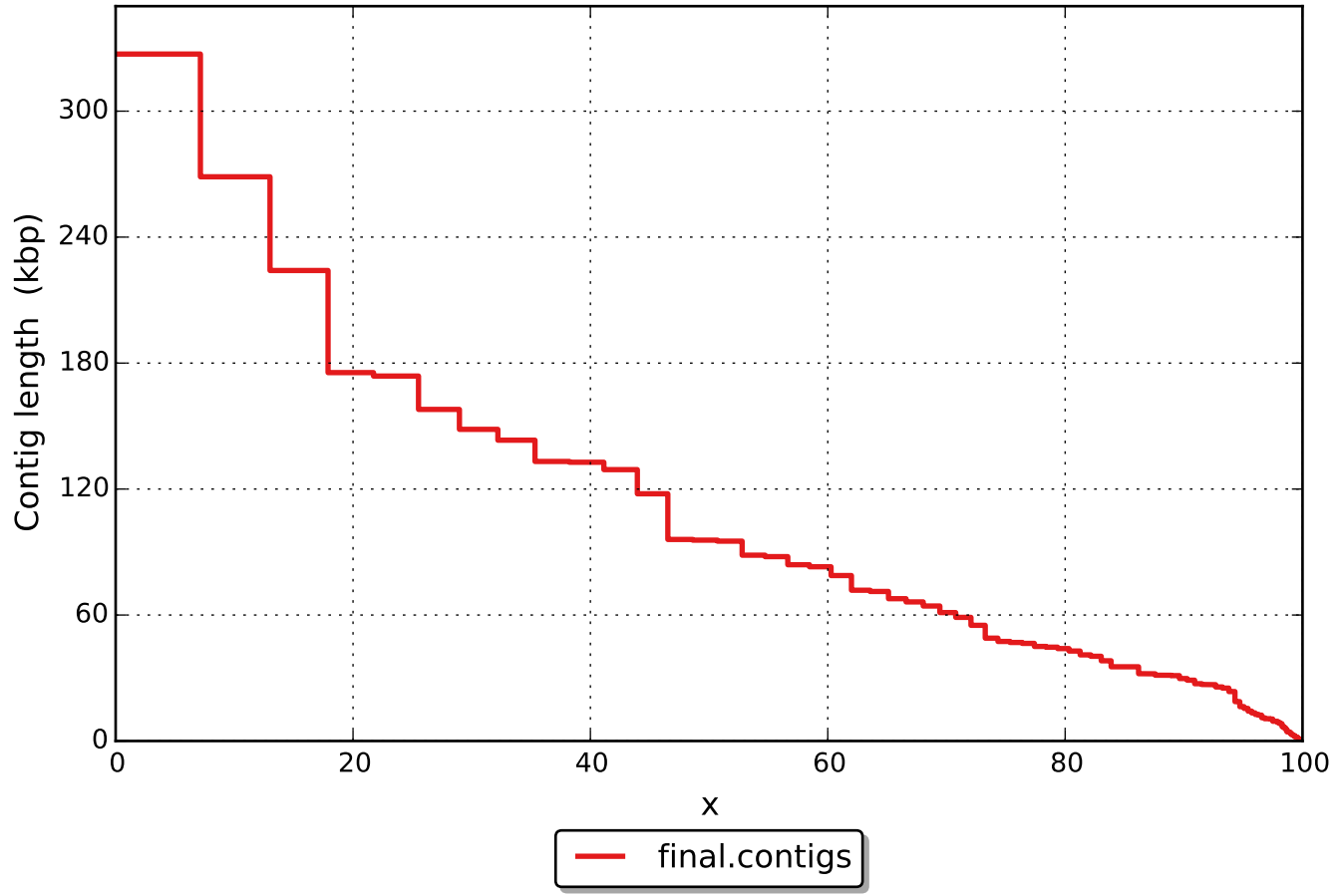




Cumulative length (aligned contigs)



NAx



NGAx

