

Report

	final.contigs
# contigs (>= 1000 bp)	107
# contigs (>= 5000 bp)	80
# contigs (>= 10000 bp)	71
# contigs (>= 25000 bp)	50
# contigs (>= 50000 bp)	34
Total length (>= 1000 bp)	4555575
Total length (>= 5000 bp)	4492569
Total length (>= 10000 bp)	4426372
Total length (>= 25000 bp)	4091857
Total length (>= 50000 bp)	3531445
# contigs	115
Largest contig	313863
Total length	4560765
Reference length	4641652
GC (℥)	50.74
Reference GC (℥)	50.79
N50	95512
NG50	95512
N75	54949
NG75	52342
L50	16
LG50	16
L75	32
LG75	34
# misassemblies	3
# misassembled contigs	2
Misassembled contigs length	84874
# local misassemblies	12
# unaligned contigs	0 + 1 part
Unaligned length	53
Genome fraction (℥)	98.199
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	61.30
# indels per 100 kbp	10.16
Largest alignment	313863
NA50	95512
NGA50	95512
NA75	54949
NGA75	52342
LA50	16
LGA50	16
LA75	32
LGA75	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).

Misassemblies report

	final.contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	84874
# local misassemblies	12
# mismatches	2794
# indels	463
# short indels	462
# long indels	1
Indels length	740

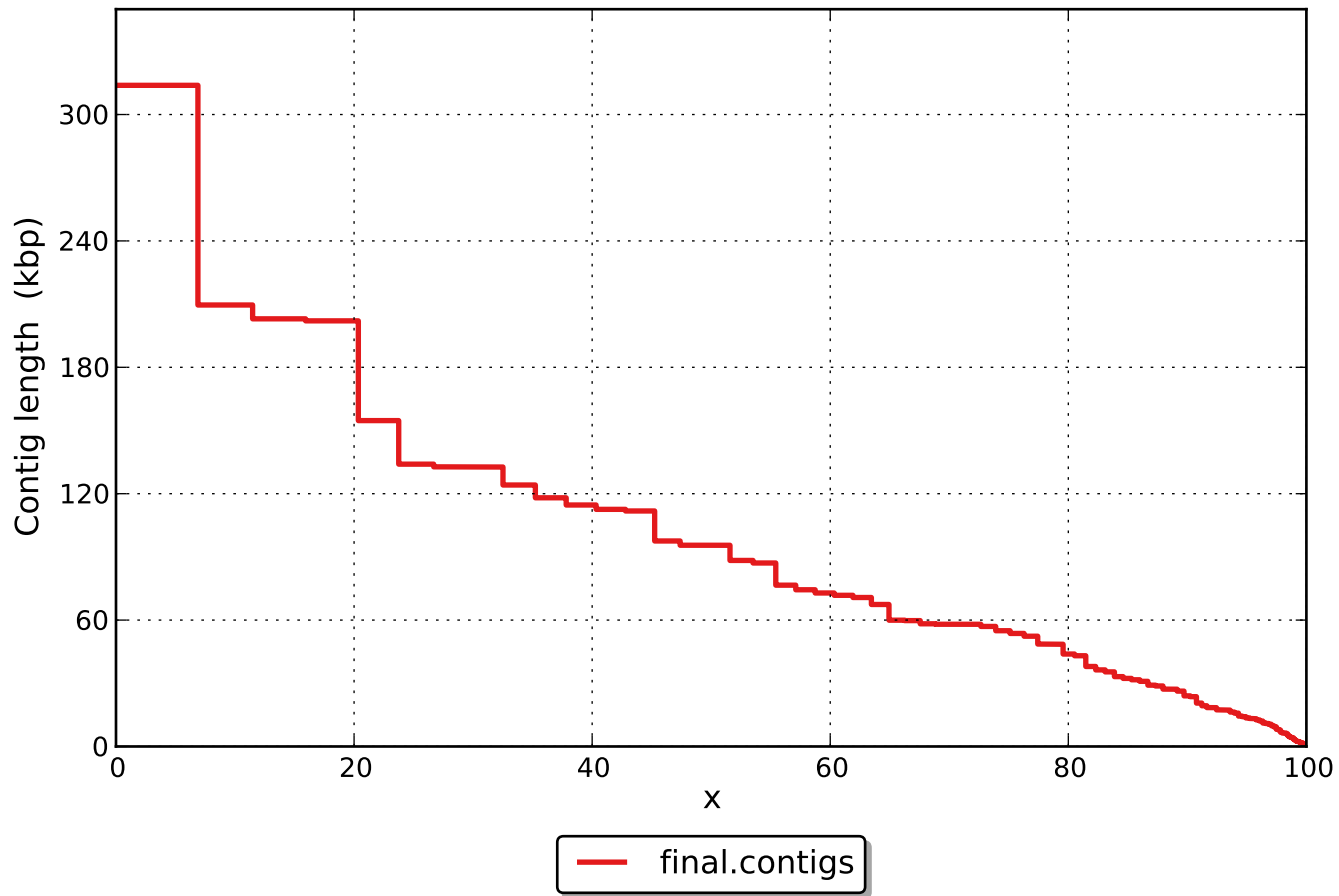
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

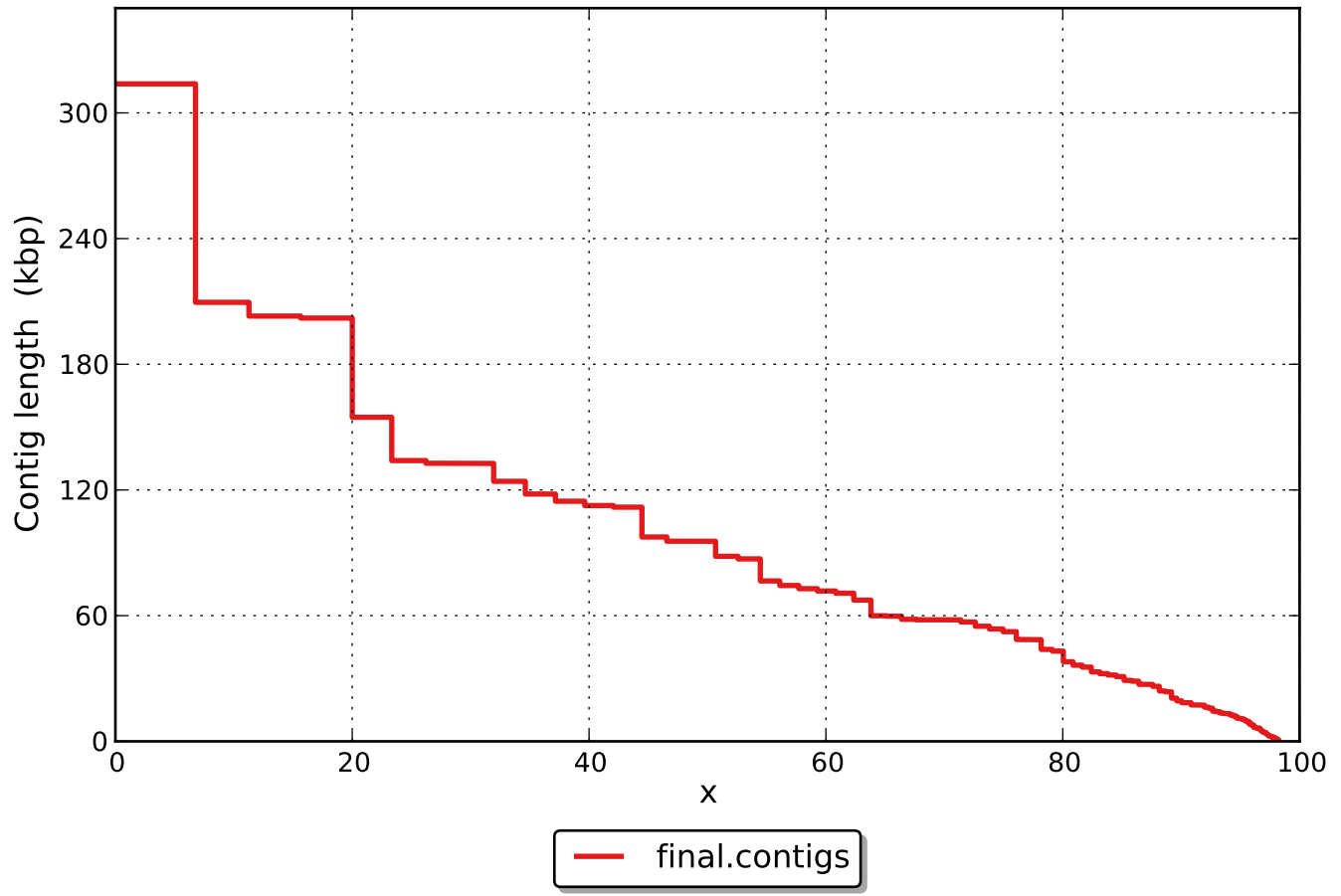
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	53
# N's	0

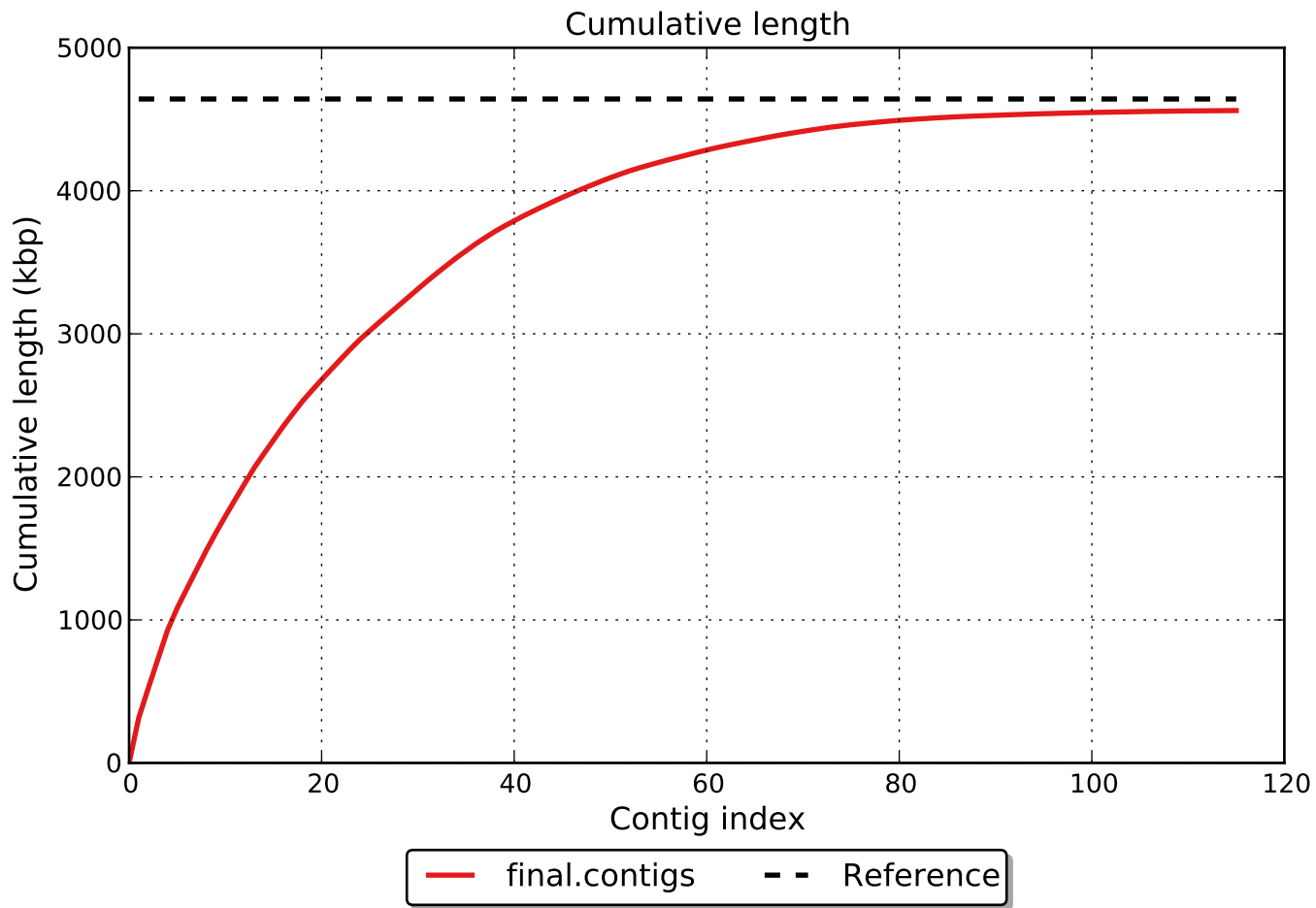
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

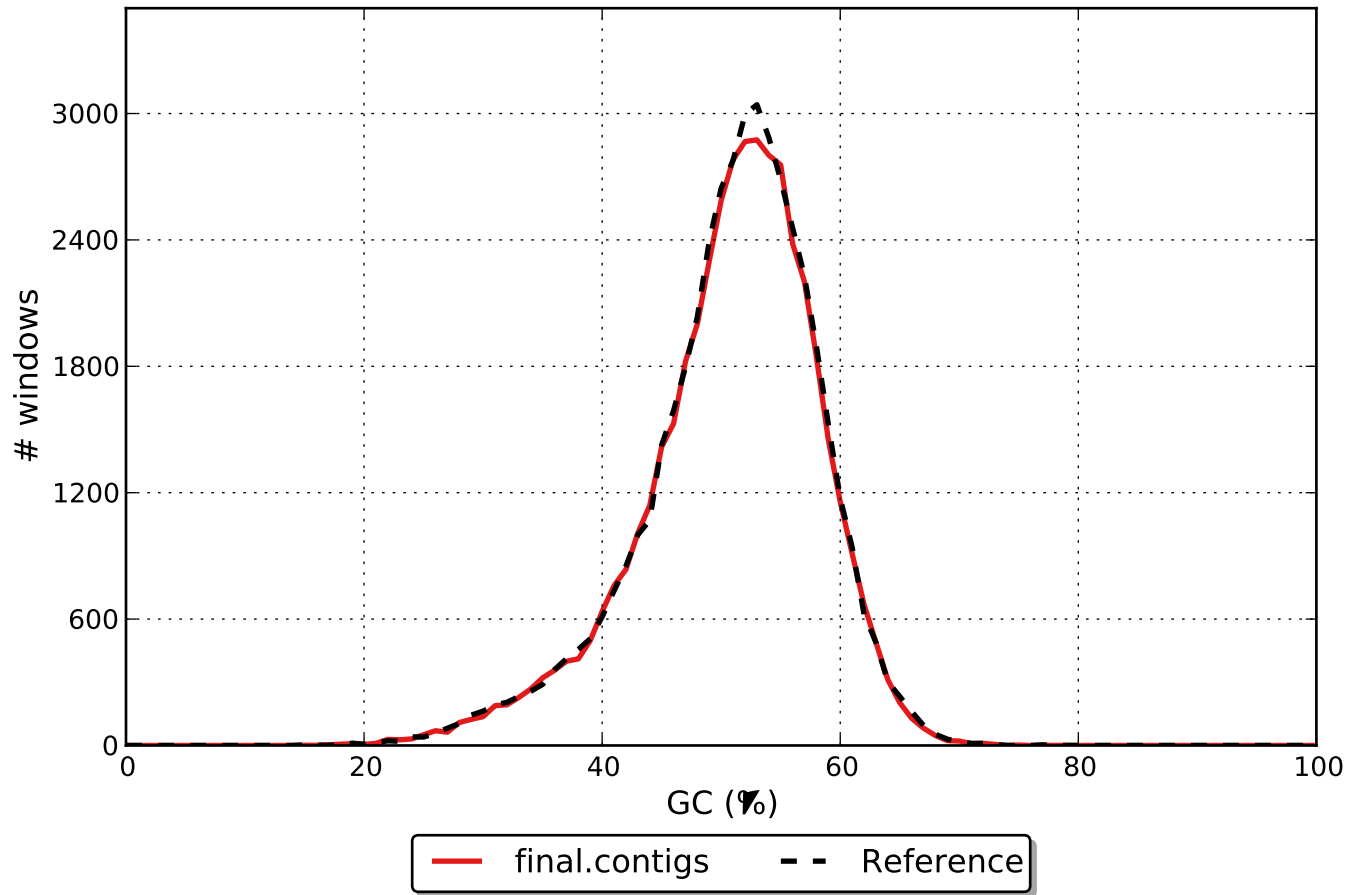


NGx

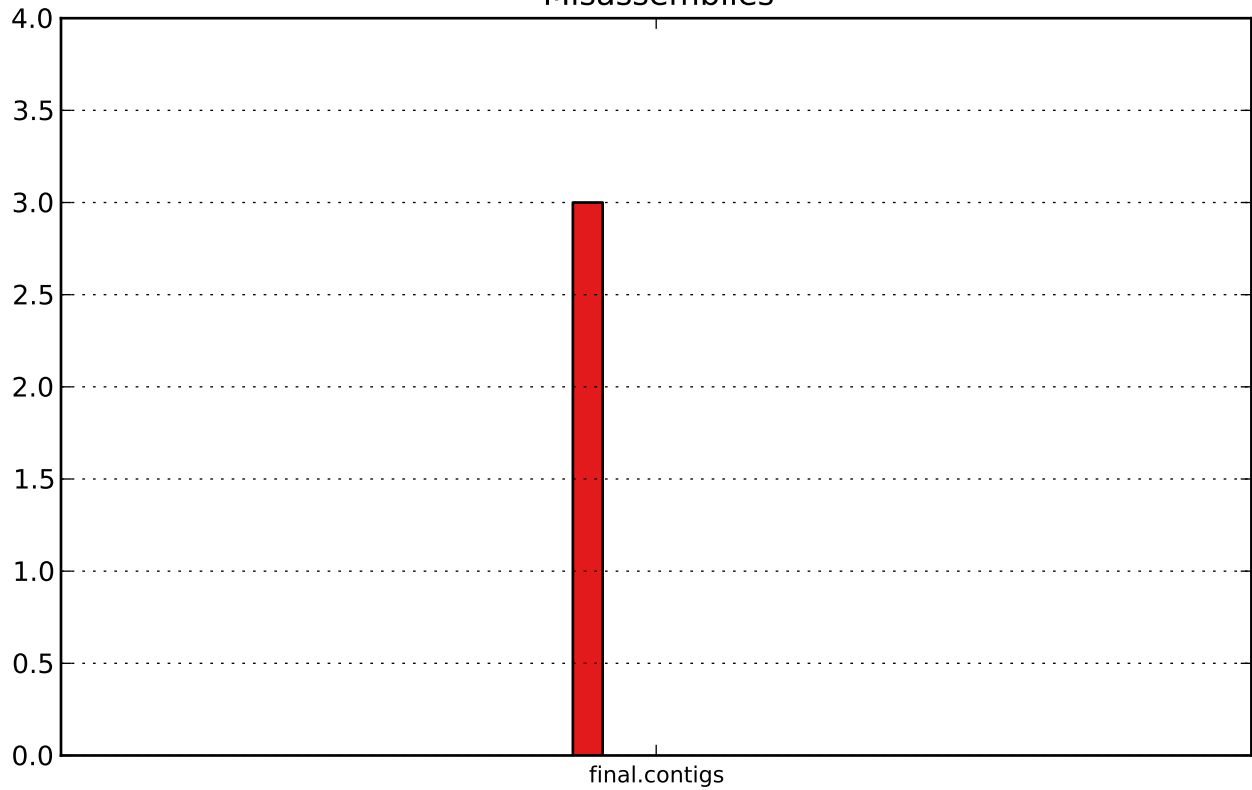




GC content

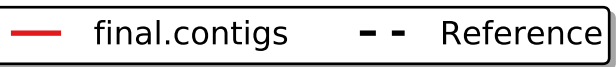
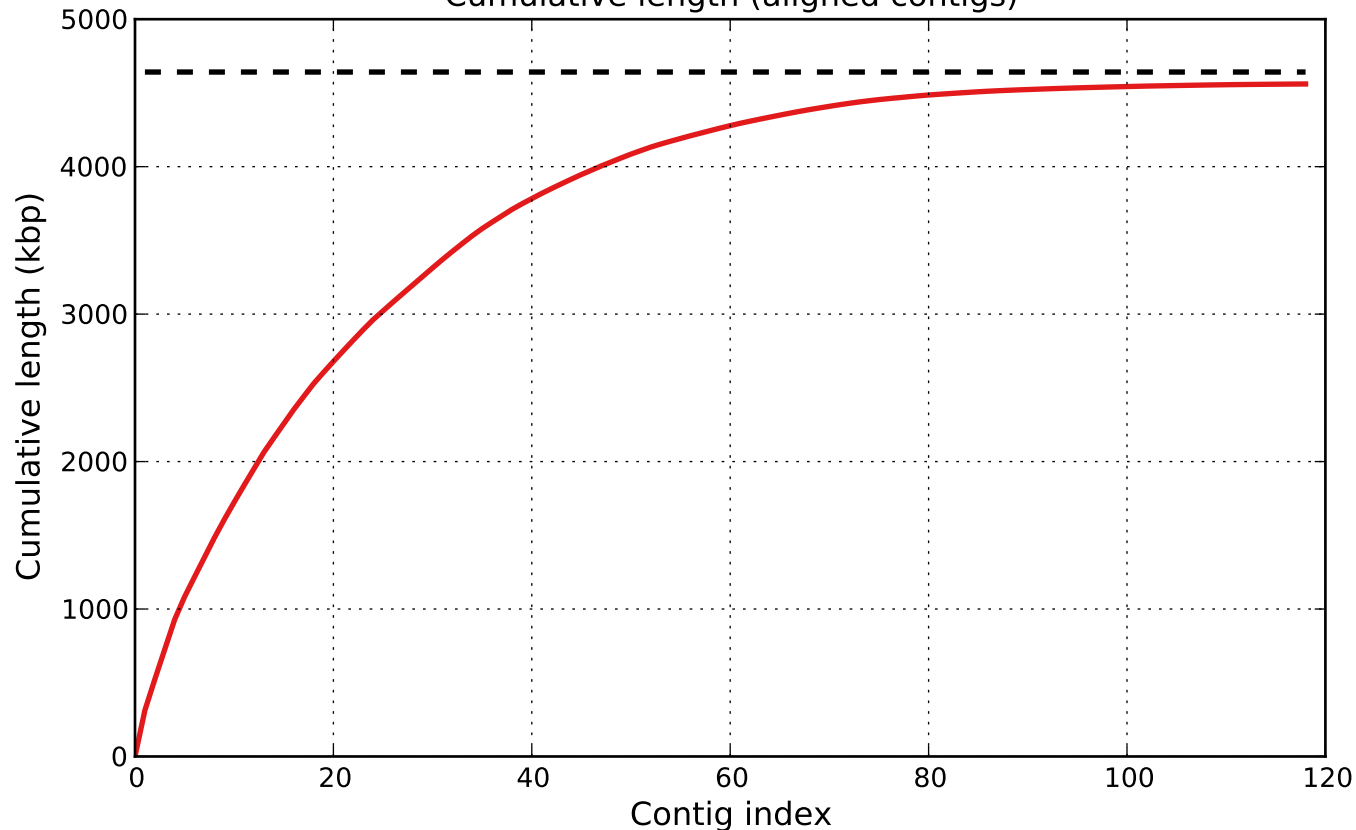


Misassemblies

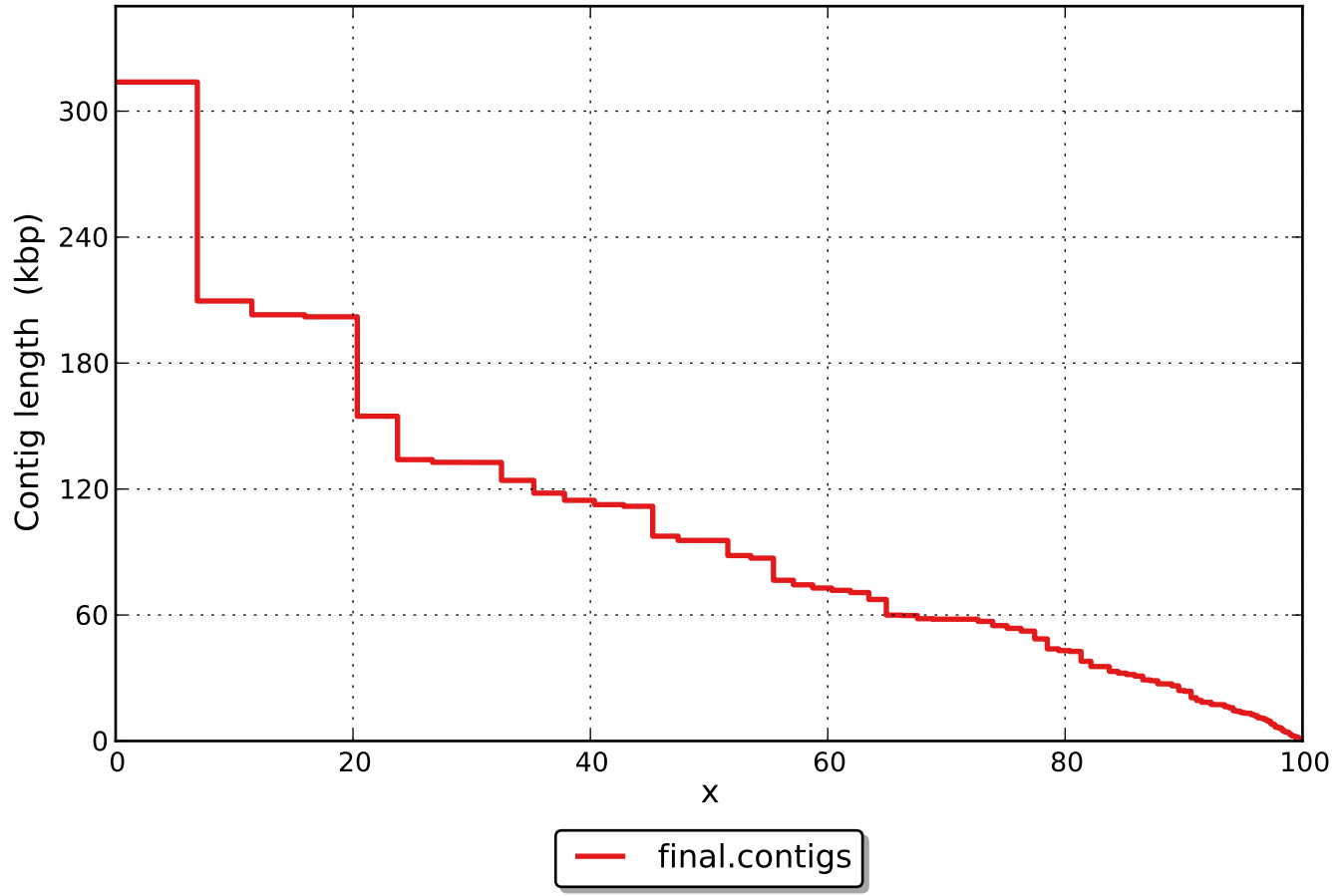


 # relocations

Cumulative length (aligned contigs)



NAx



NGAx

