

Report

	scaffolds
# contigs (>= 1000 bp)	72
# contigs (>= 5000 bp)	50
# contigs (>= 10000 bp)	47
# contigs (>= 25000 bp)	41
# contigs (>= 50000 bp)	28
Total length (>= 1000 bp)	4554625
Total length (>= 5000 bp)	4504386
Total length (>= 10000 bp)	4480443
Total length (>= 25000 bp)	4391325
Total length (>= 50000 bp)	3942965
# contigs	79
Largest contig	327056
Total length	4559734
Reference length	4641652
GC (▼)	50.75
Reference GC (▼)	50.79
N50	173981
NG50	173981
N75	78600
NG75	67331
L50	10
LG50	10
L75	20
LG75	21
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	98.180
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	59.73
# indels per 100 kbp	8.65
Largest alignment	327056
NA50	173981
NGA50	173981
NA75	78600
NGA75	67331
LA50	10
LGA50	10
LA75	20
LGA75	21

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

	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	2722
# indels	394
# short indels	394
# long indels	0
Indels length	534

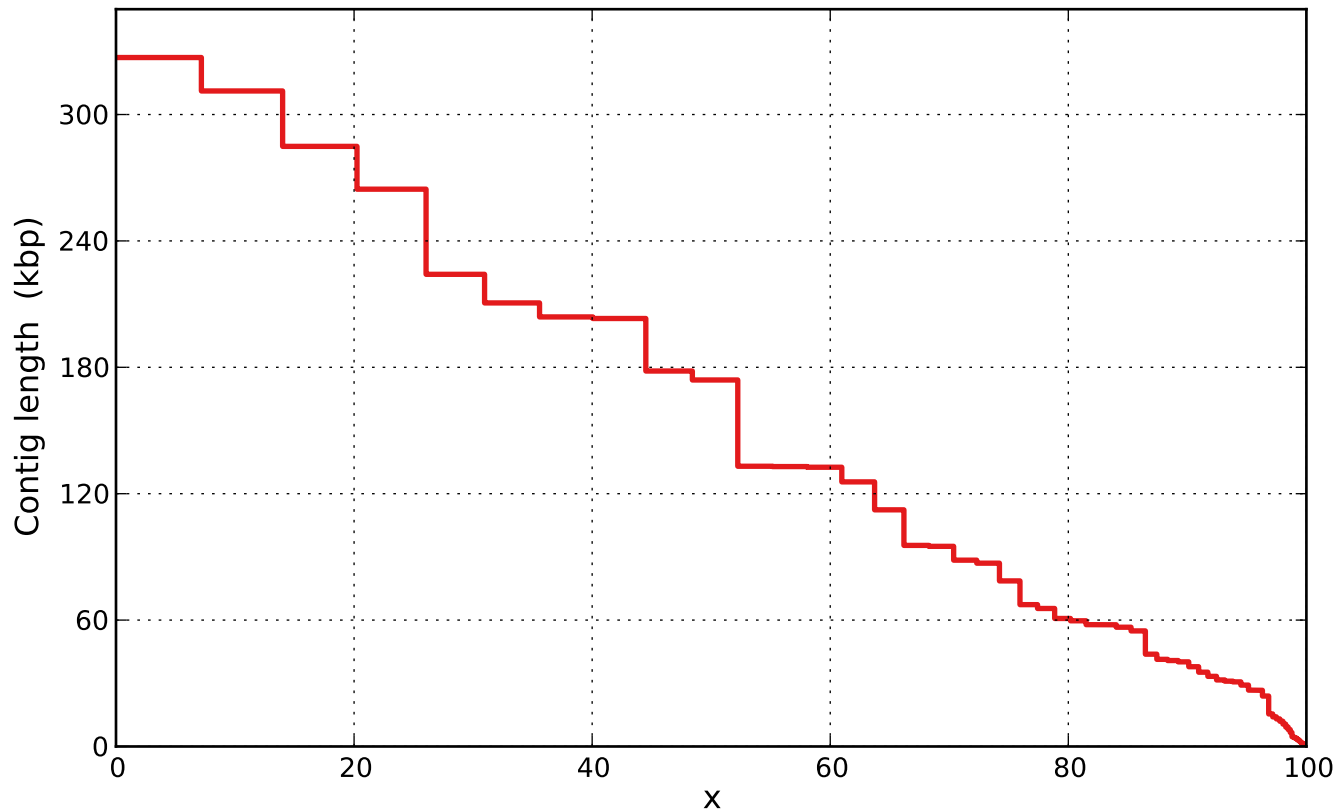
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

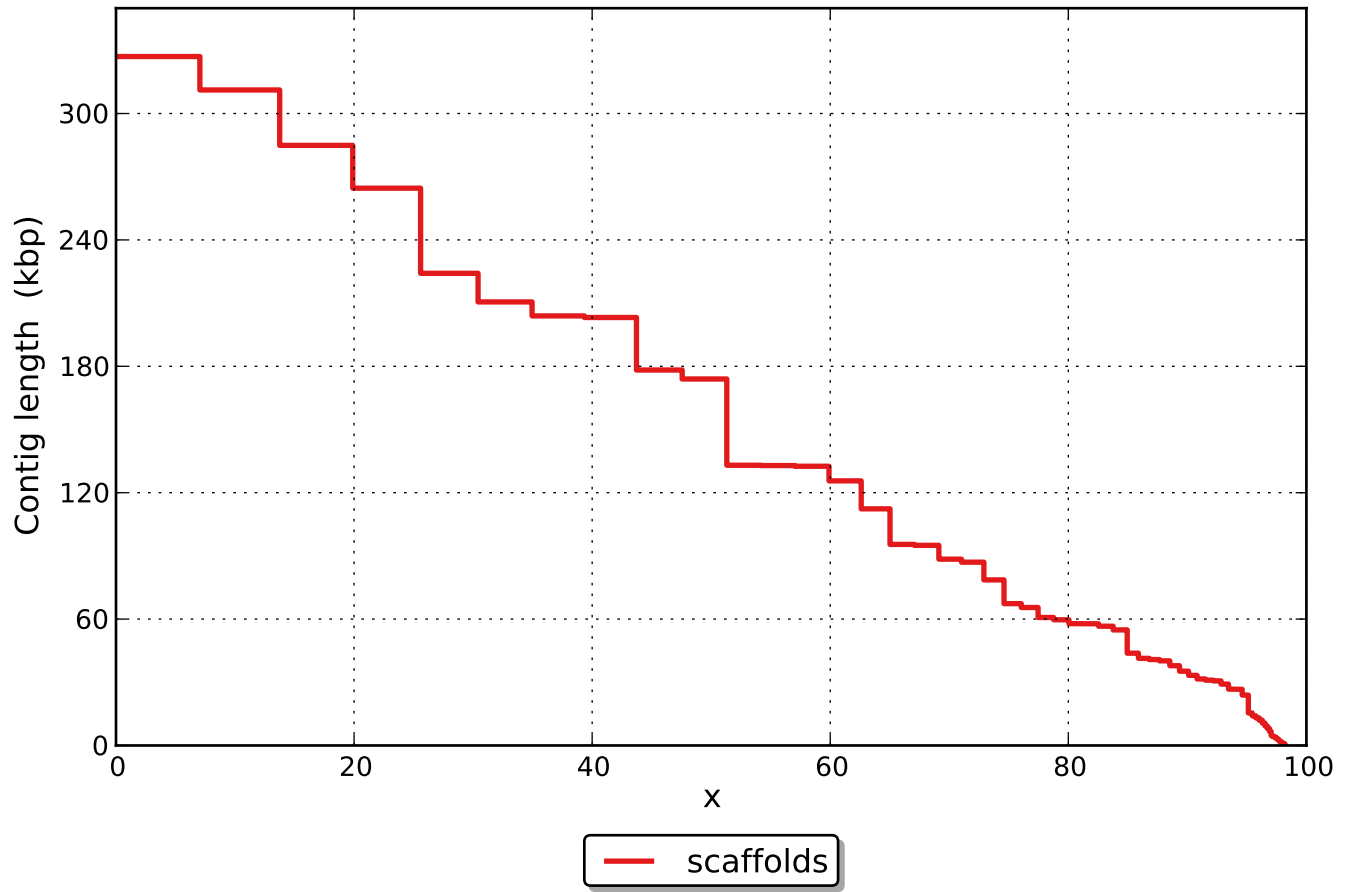
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

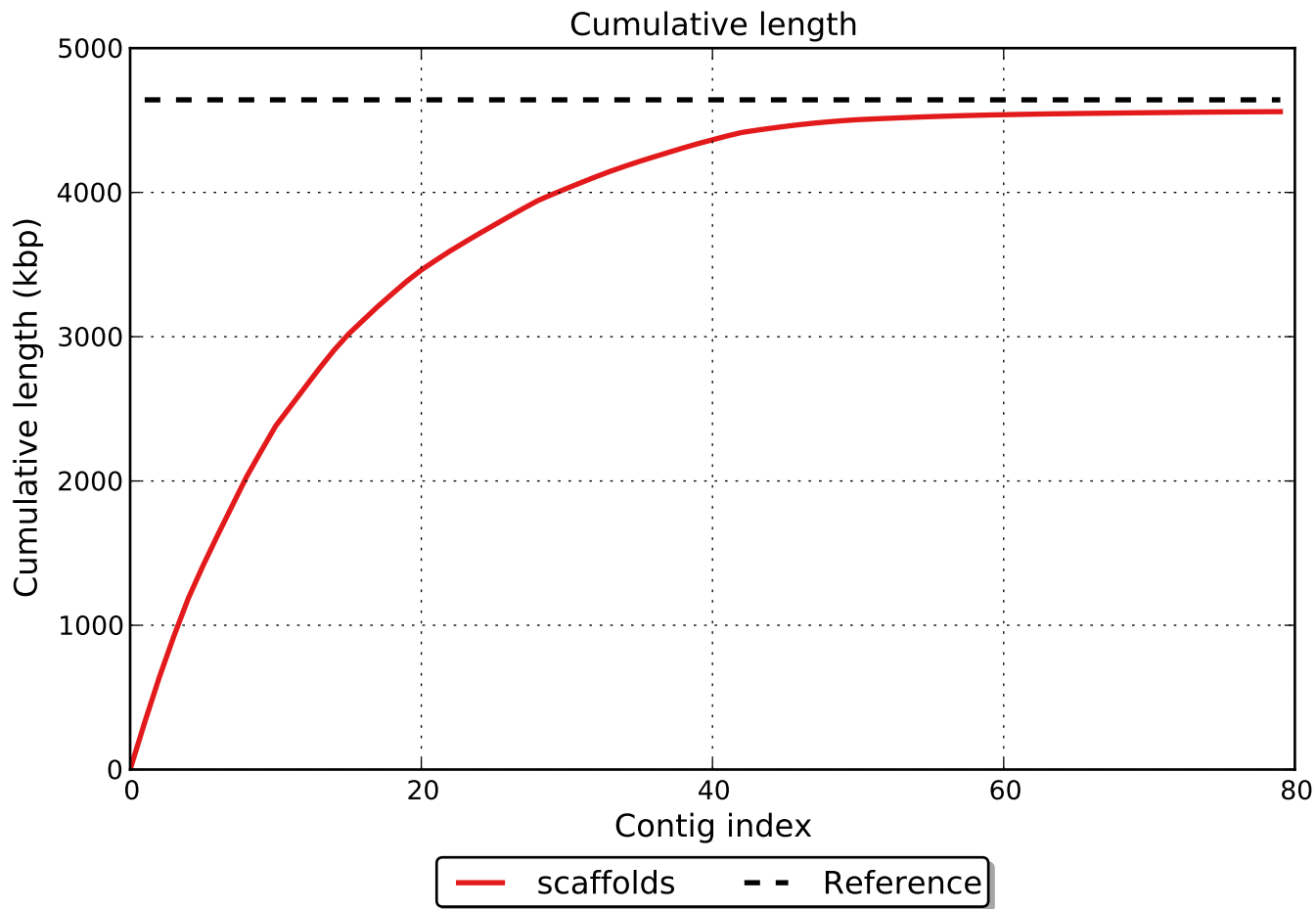
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

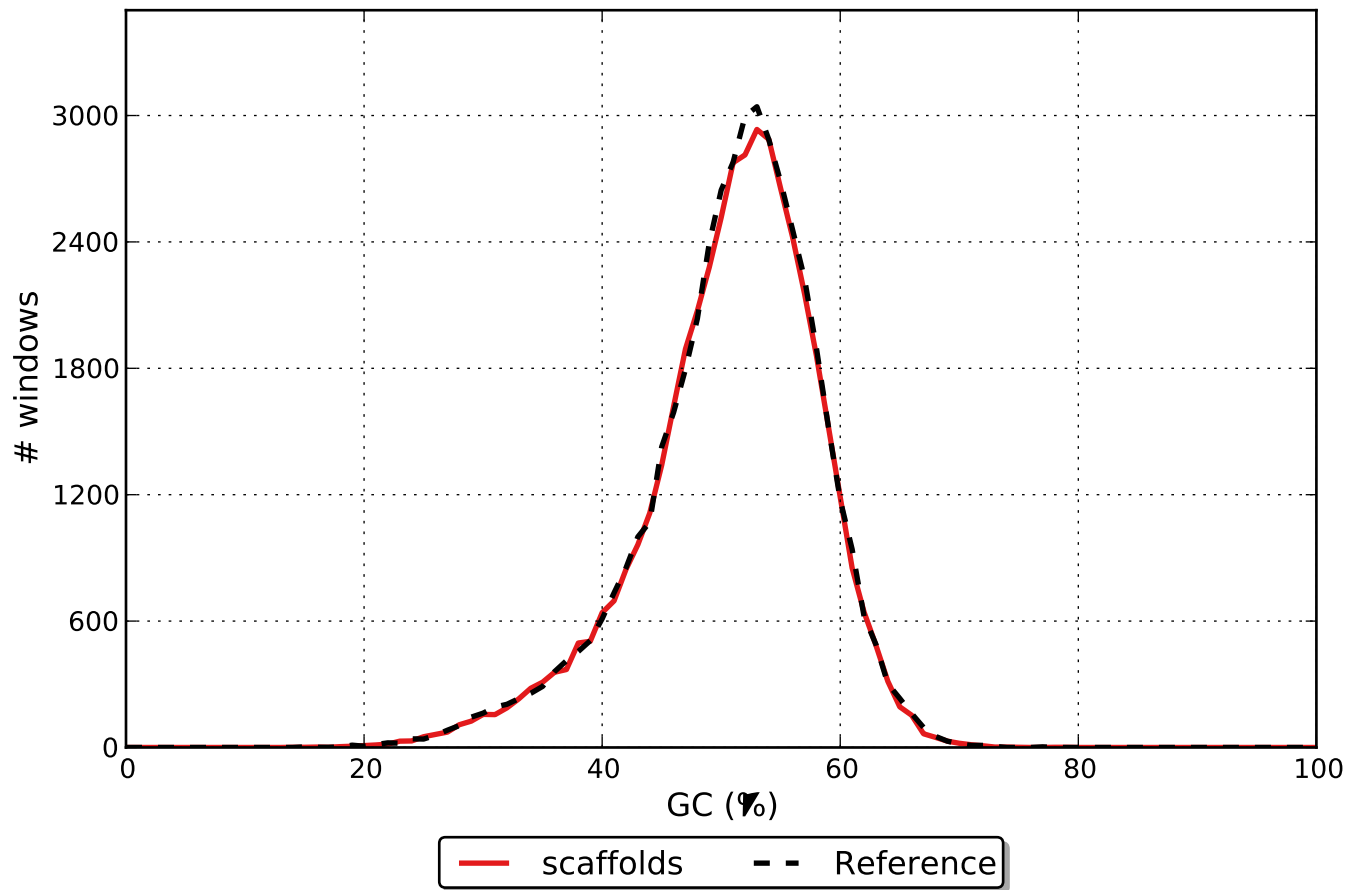


NGx

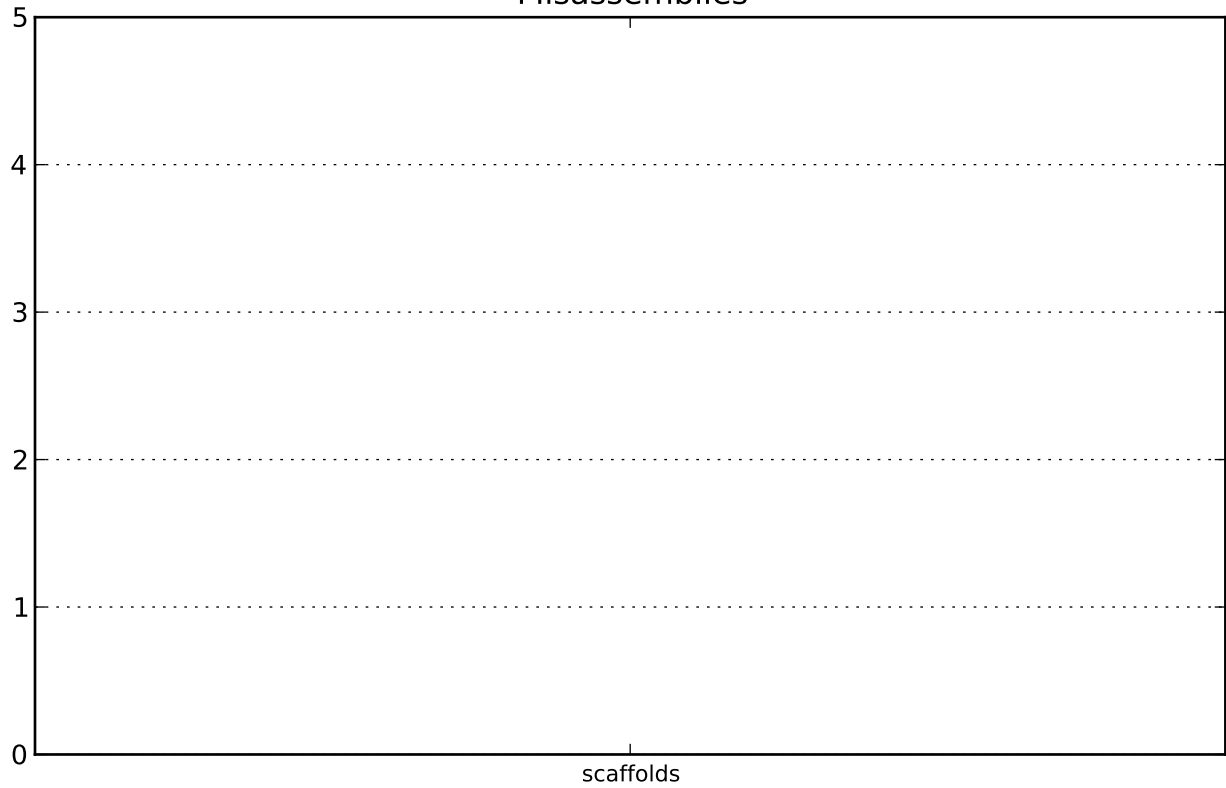




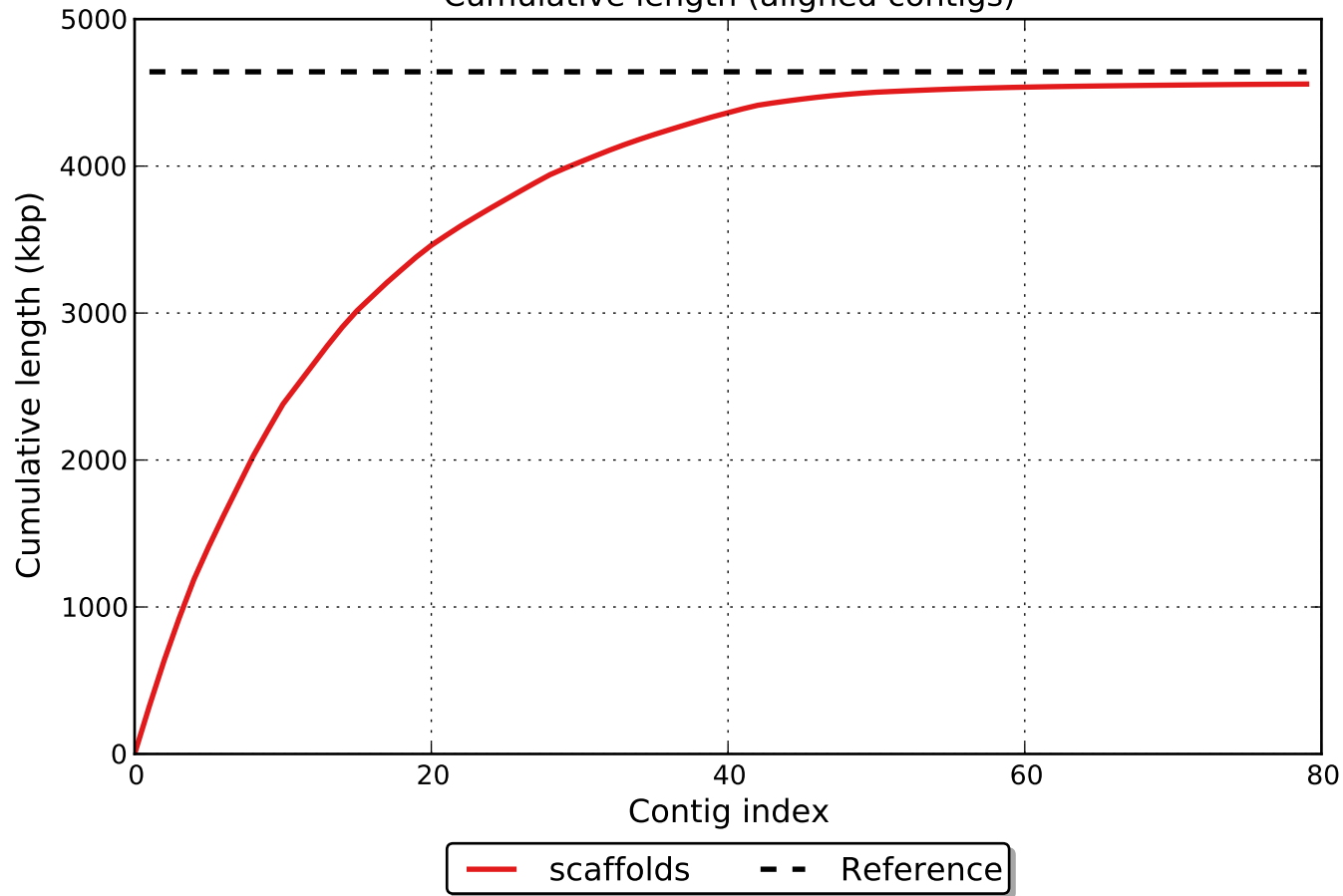
GC content



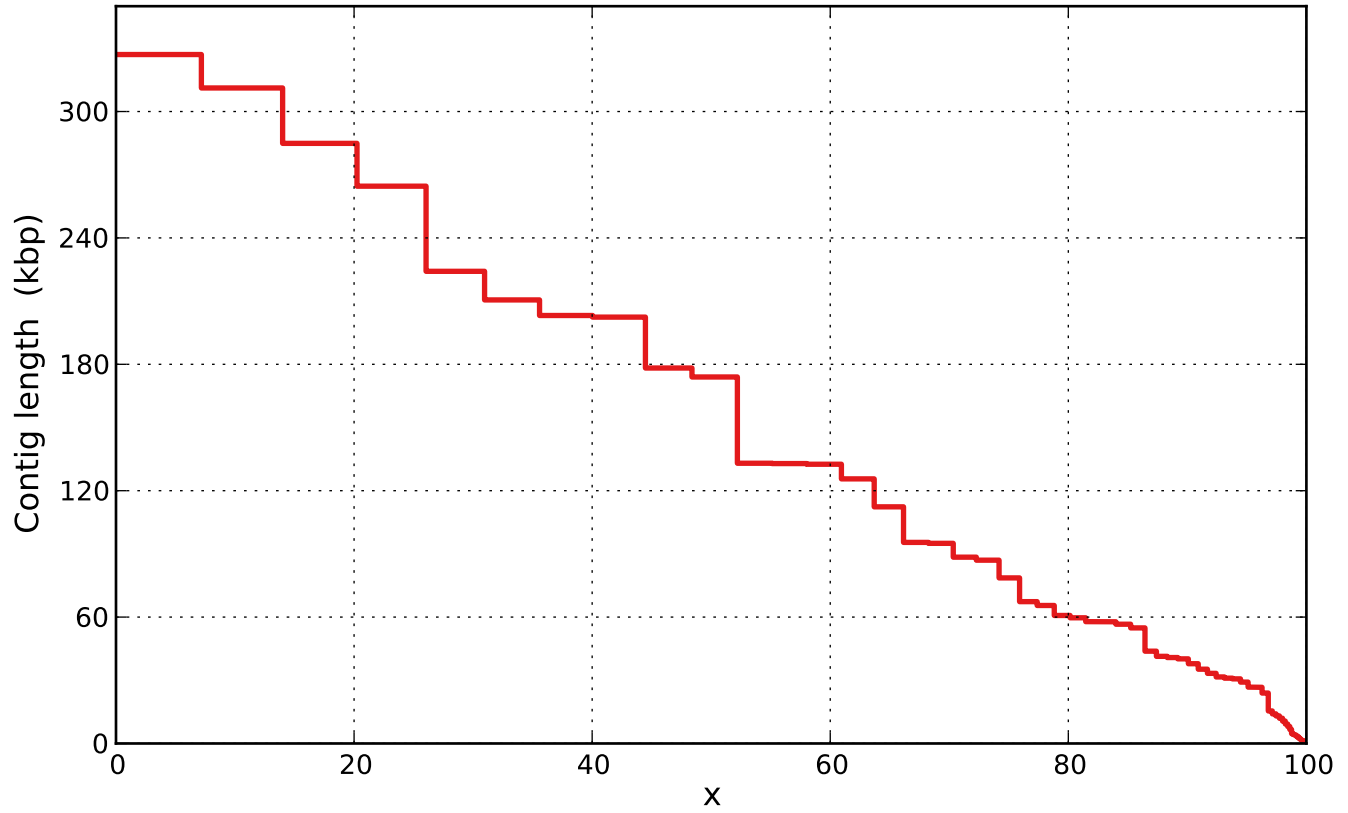
Misassemblies



Cumulative length (aligned contigs)



NAx



— scaffolds

NGAx

