

Report

	scaffolds
# contigs (>= 1000 bp)	69
# contigs (>= 5000 bp)	50
# contigs (>= 10000 bp)	47
# contigs (>= 25000 bp)	41
# contigs (>= 50000 bp)	27
Total length (>= 1000 bp)	4560368
Total length (>= 5000 bp)	4516394
Total length (>= 10000 bp)	4492442
Total length (>= 25000 bp)	4401257
Total length (>= 50000 bp)	3919865
# contigs	73
Largest contig	327046
Total length	4563284
Reference length	4641652
GC (▼)	50.75
Reference GC (▼)	50.79
N50	173984
NG50	173984
N75	87058
NG75	78609
L50	10
LG50	10
L75	20
LG75	21
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	98.259
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	61.55
# indels per 100 kbp	8.75
Largest alignment	327046
NA50	173064
NGA50	173064
NA75	87058
NGA75	78609
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	2
# mismatches	2807
# indels	399
# short indels	399
# long indels	0
Indels length	568

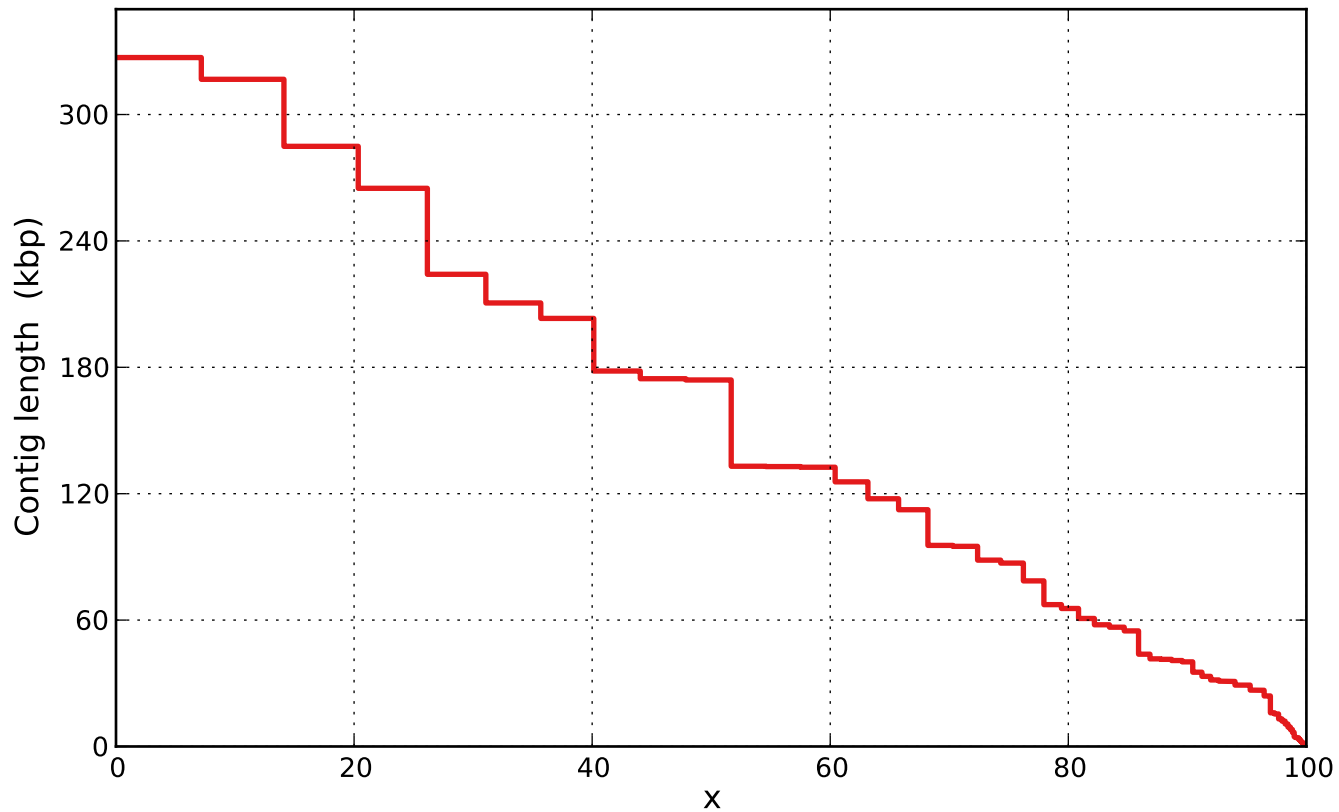
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

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

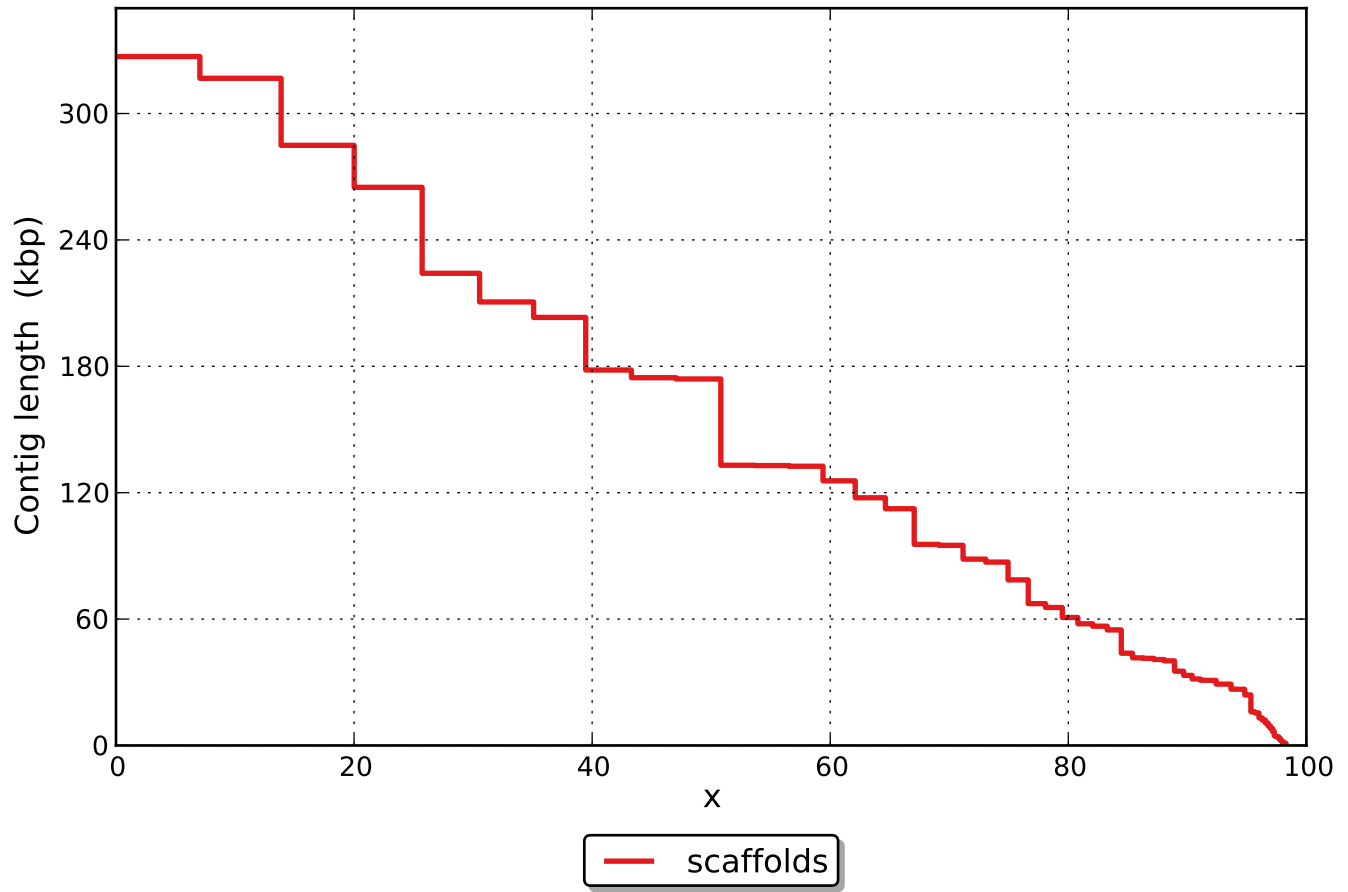
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

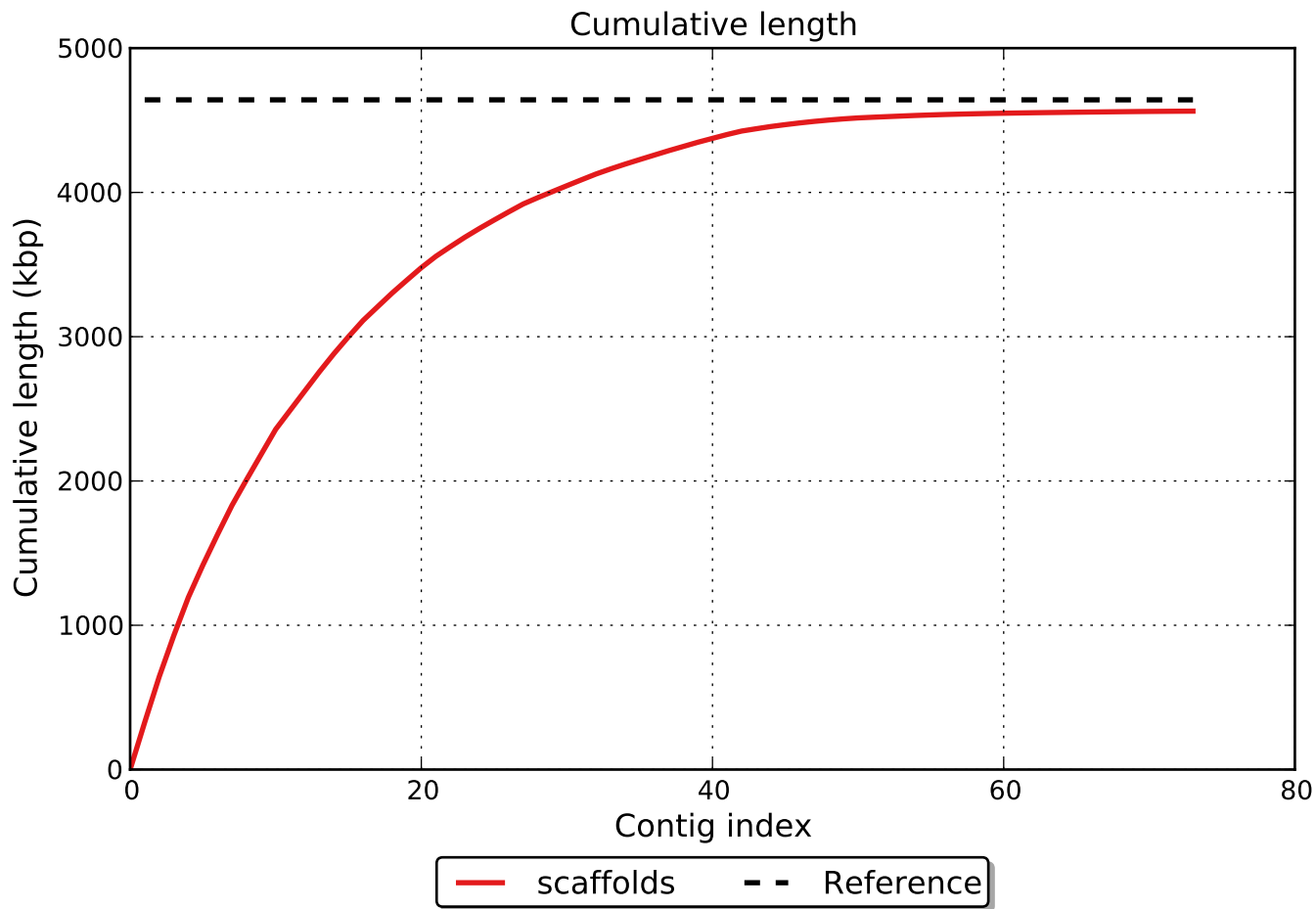
Nx



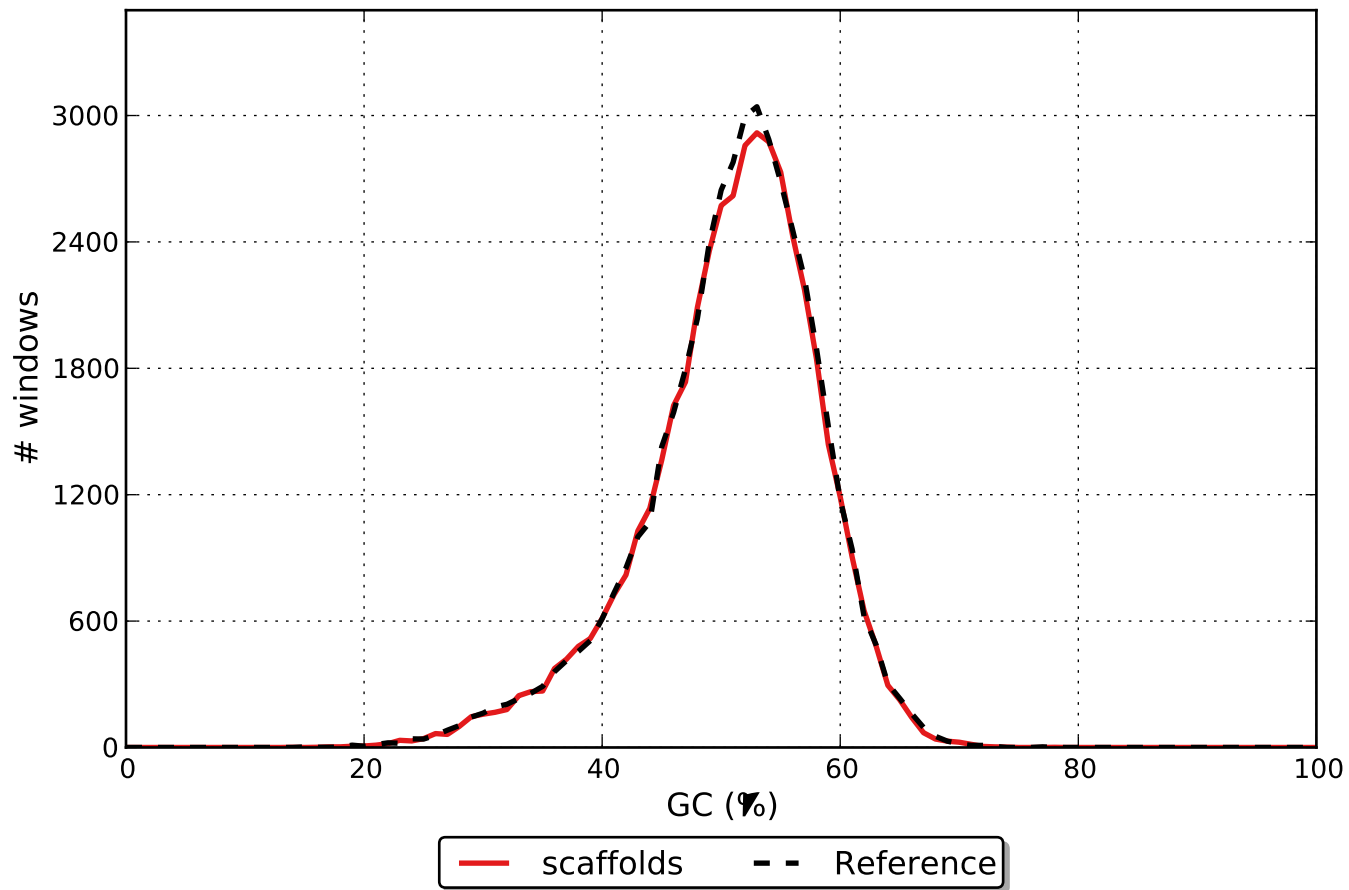
scaffolds

NGx

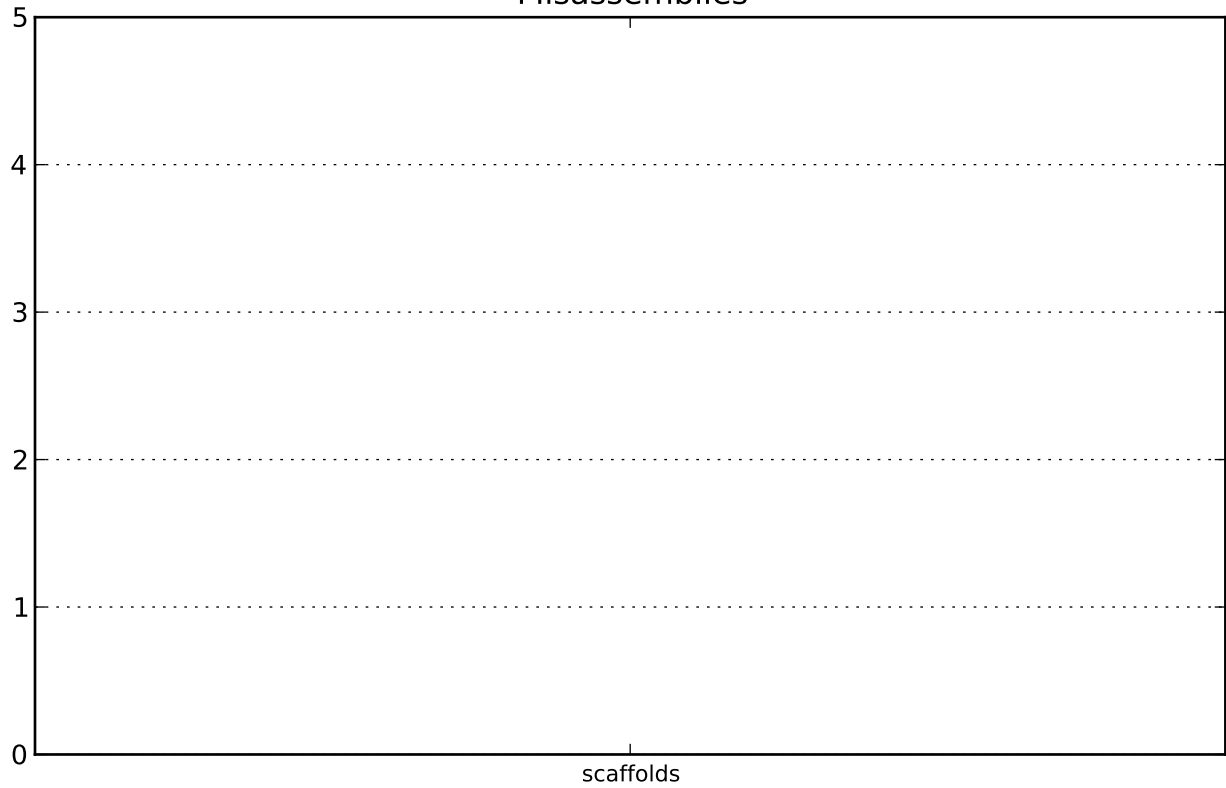




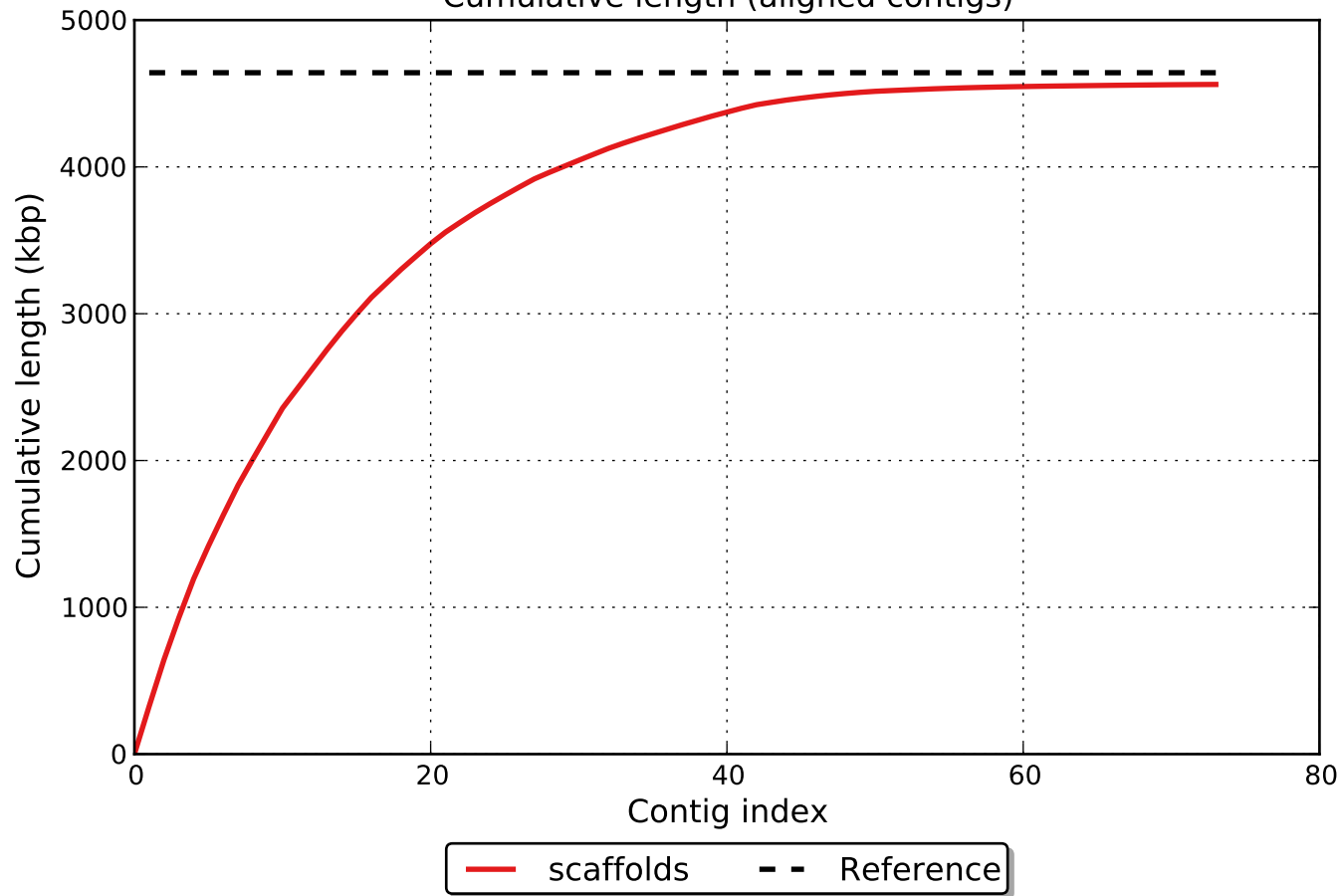
GC content



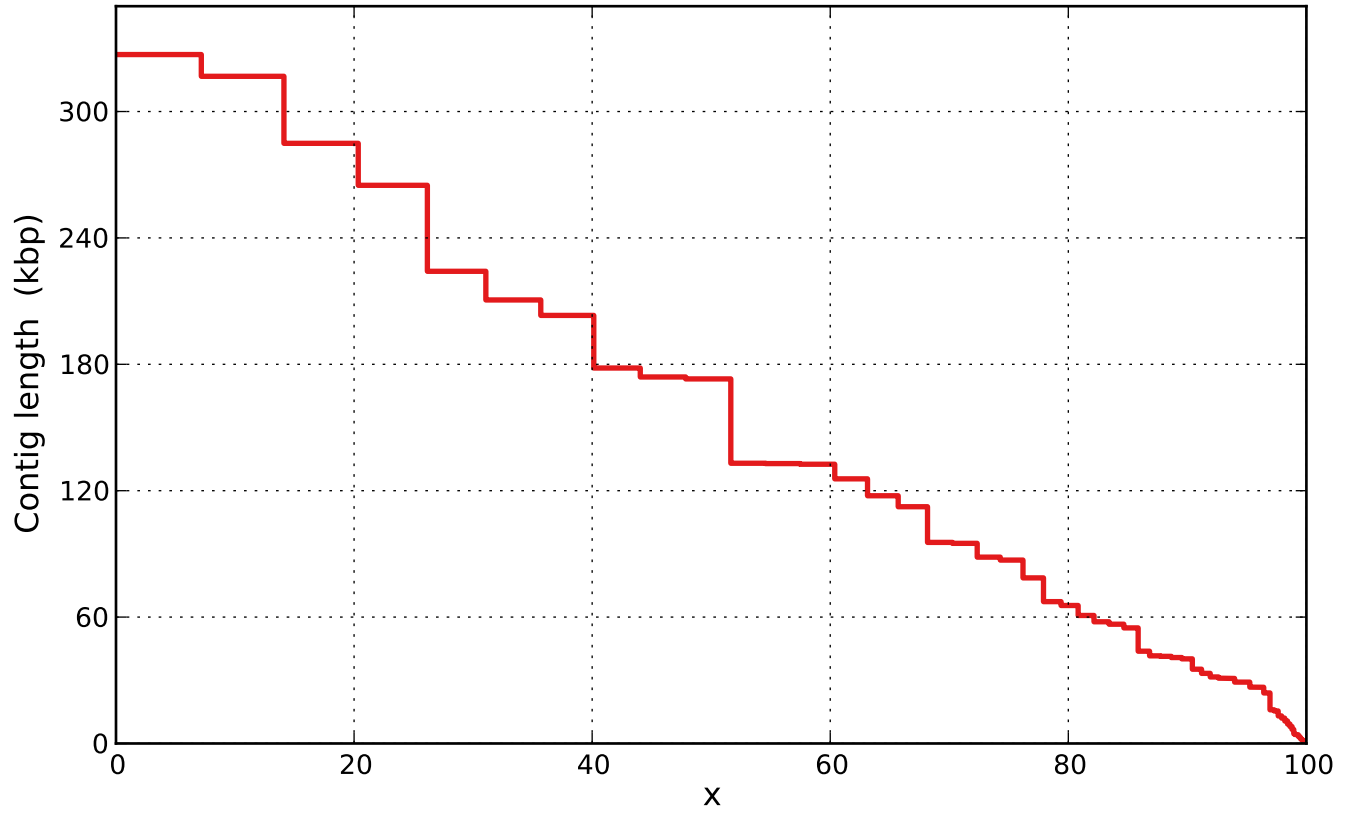
Misassemblies



Cumulative length (aligned contigs)



NAx



— scaffolds

NGAx

