

Report

	scaffolds
# contigs (>= 1000 bp)	67
# contigs (>= 5000 bp)	49
# contigs (>= 10000 bp)	46
# contigs (>= 25000 bp)	40
# contigs (>= 50000 bp)	27
Total length (>= 1000 bp)	4559920
Total length (>= 5000 bp)	4520879
Total length (>= 10000 bp)	4496826
Total length (>= 25000 bp)	4407539
Total length (>= 50000 bp)	3946955
# contigs	73
Largest contig	327051
Total length	4564385
Reference length	4641652
GC (▼)	50.74
Reference GC (▼)	50.79
N50	173974
NG50	173974
N75	87051
NG75	87051
L50	10
LG50	10
L75	20
LG75	20
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	98.283
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	61.22
# indels per 100 kbp	8.46
Largest alignment	327051
NA50	173974
NGA50	173974
NA75	87051
NGA75	87051
LA50	10
LGA50	10
LA75	20
LGA75	20

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	2793
# indels	386
# short indels	386
# long indels	0
Indels length	555

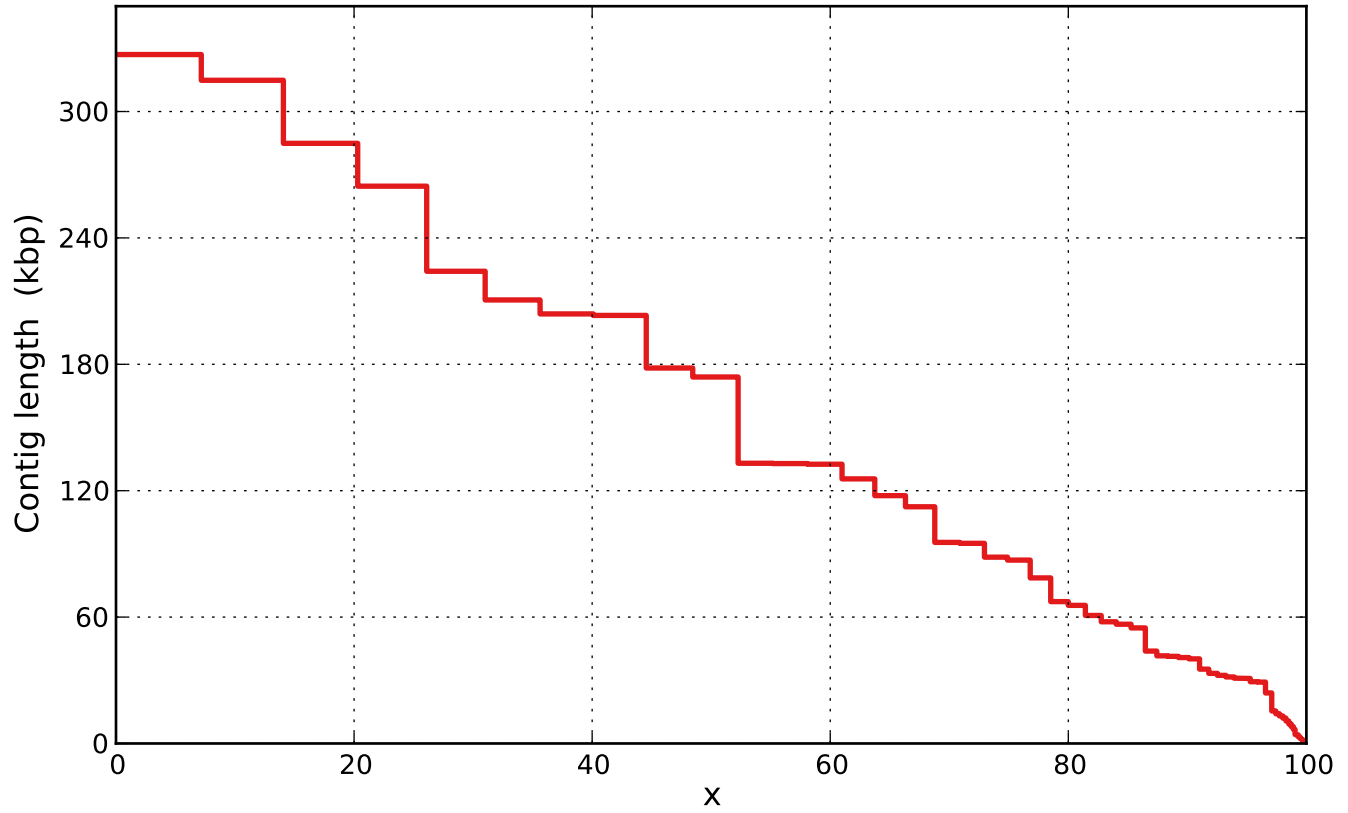
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

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

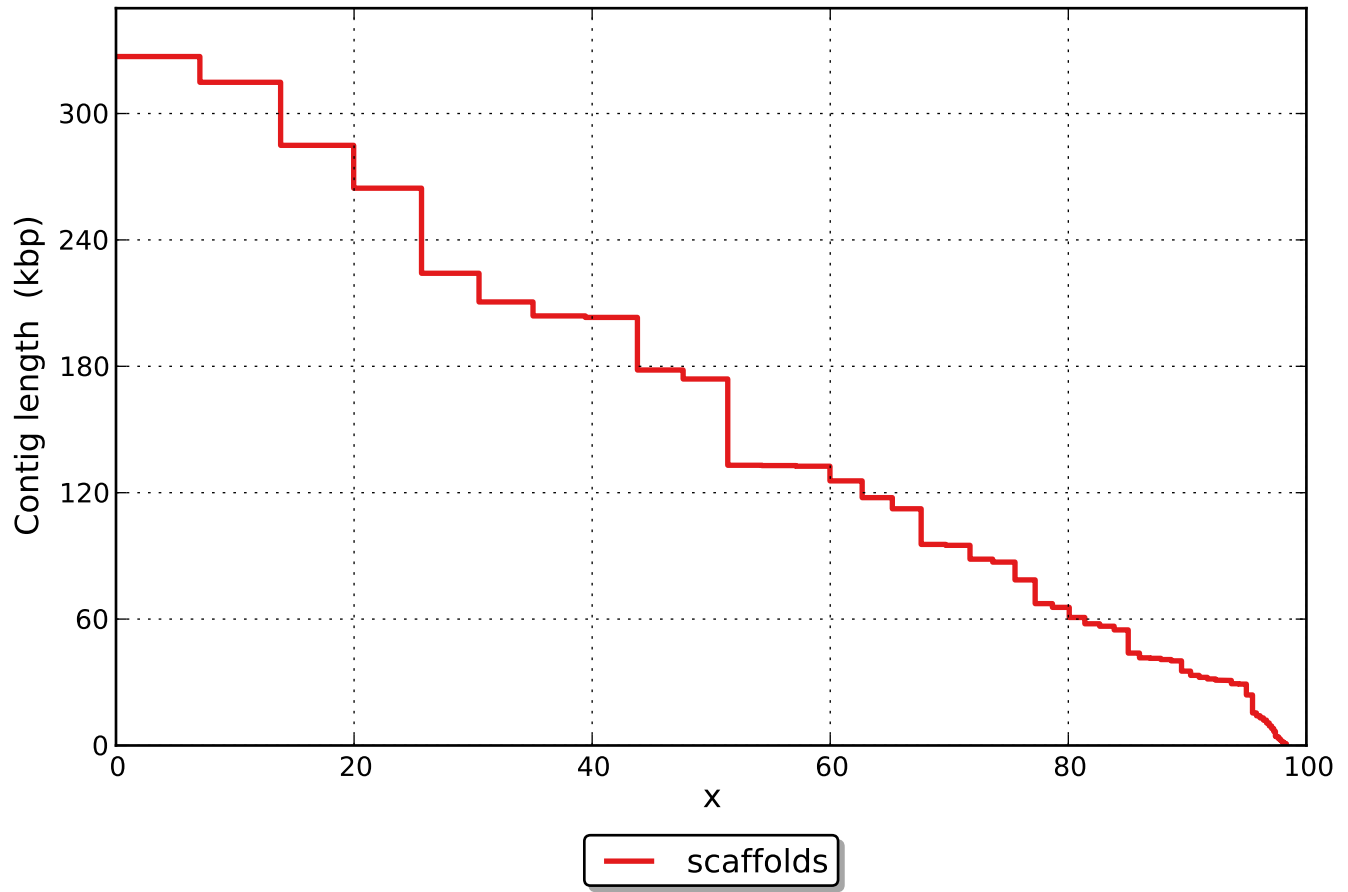
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

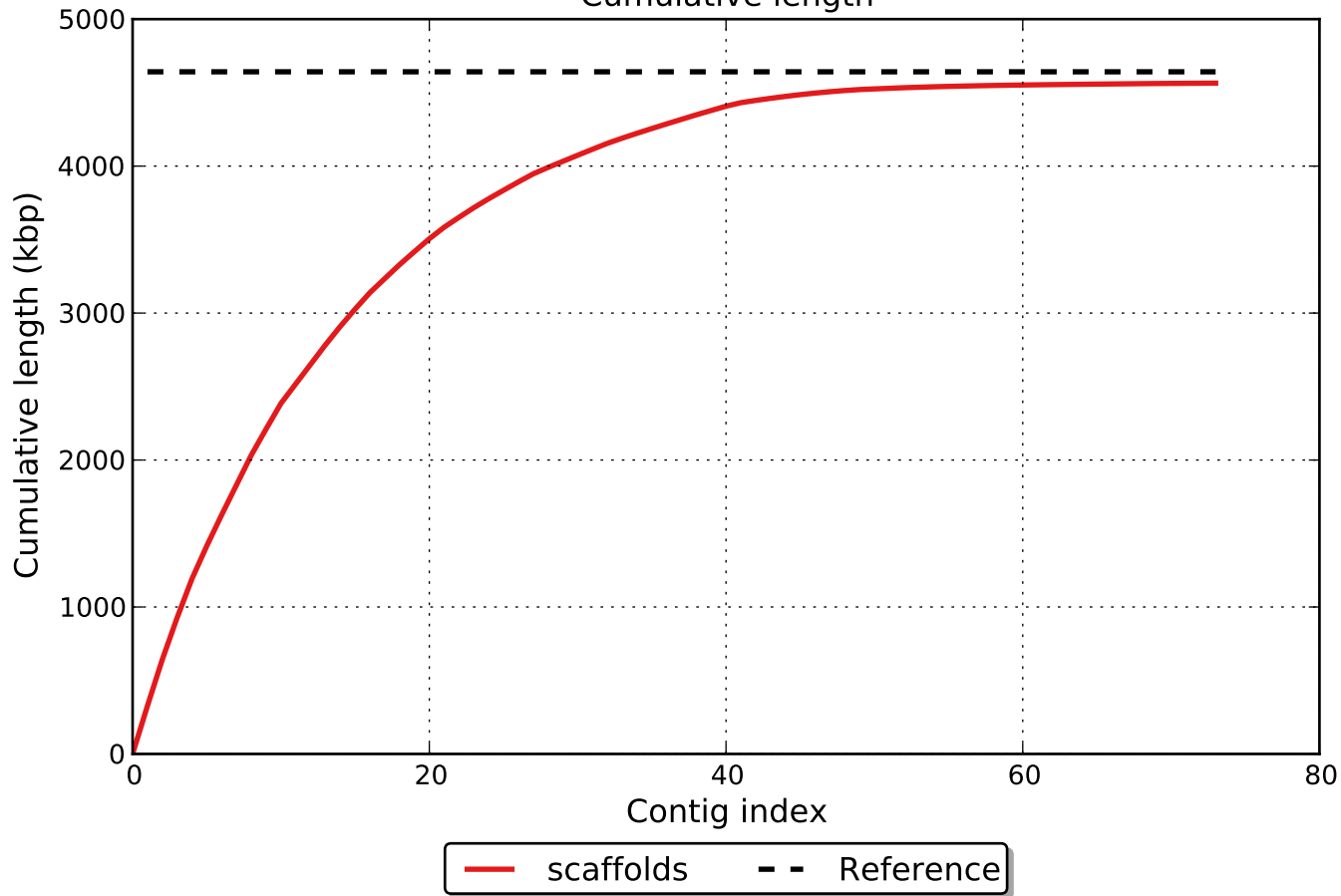


scaffolds

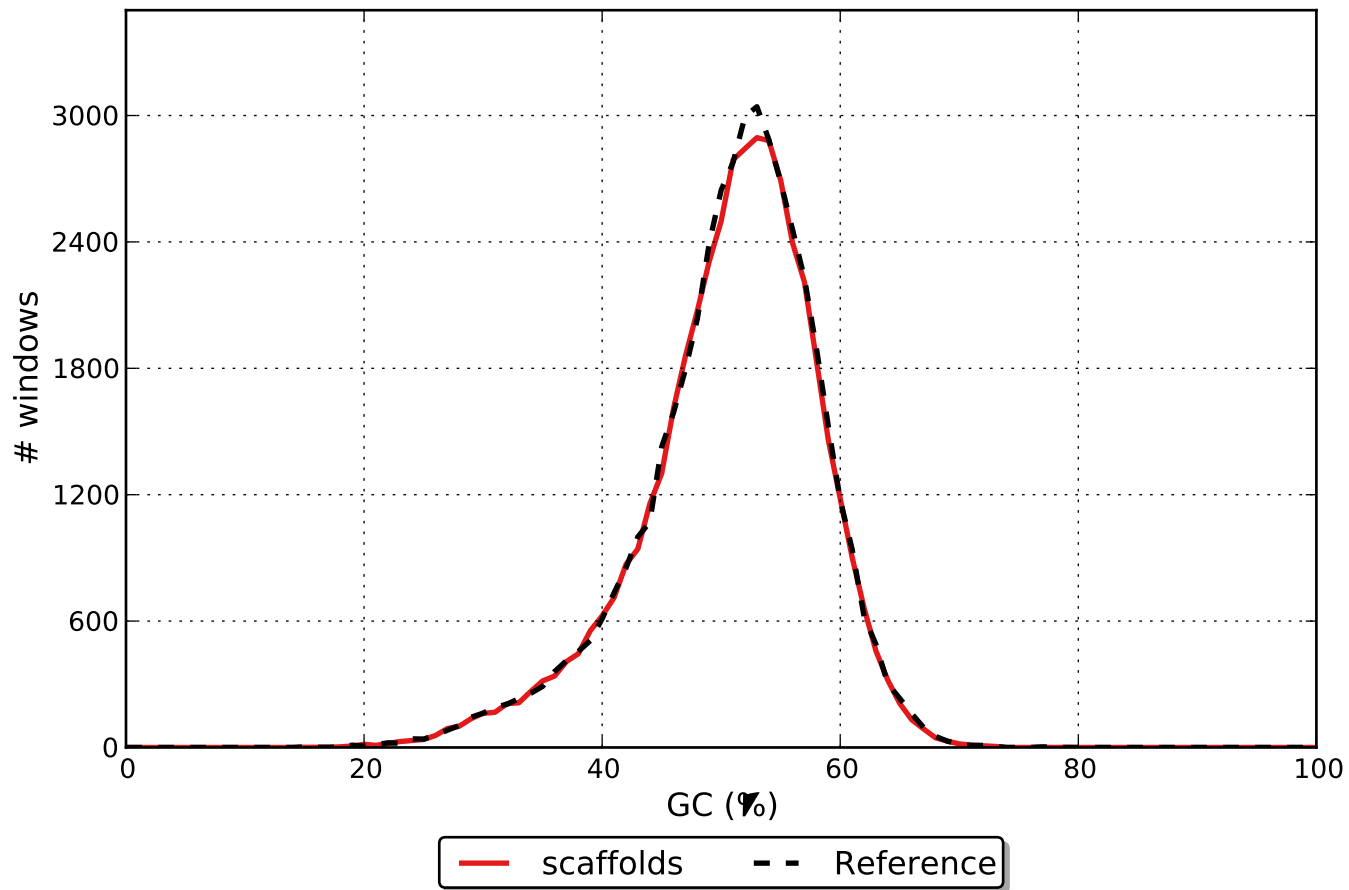
NGx



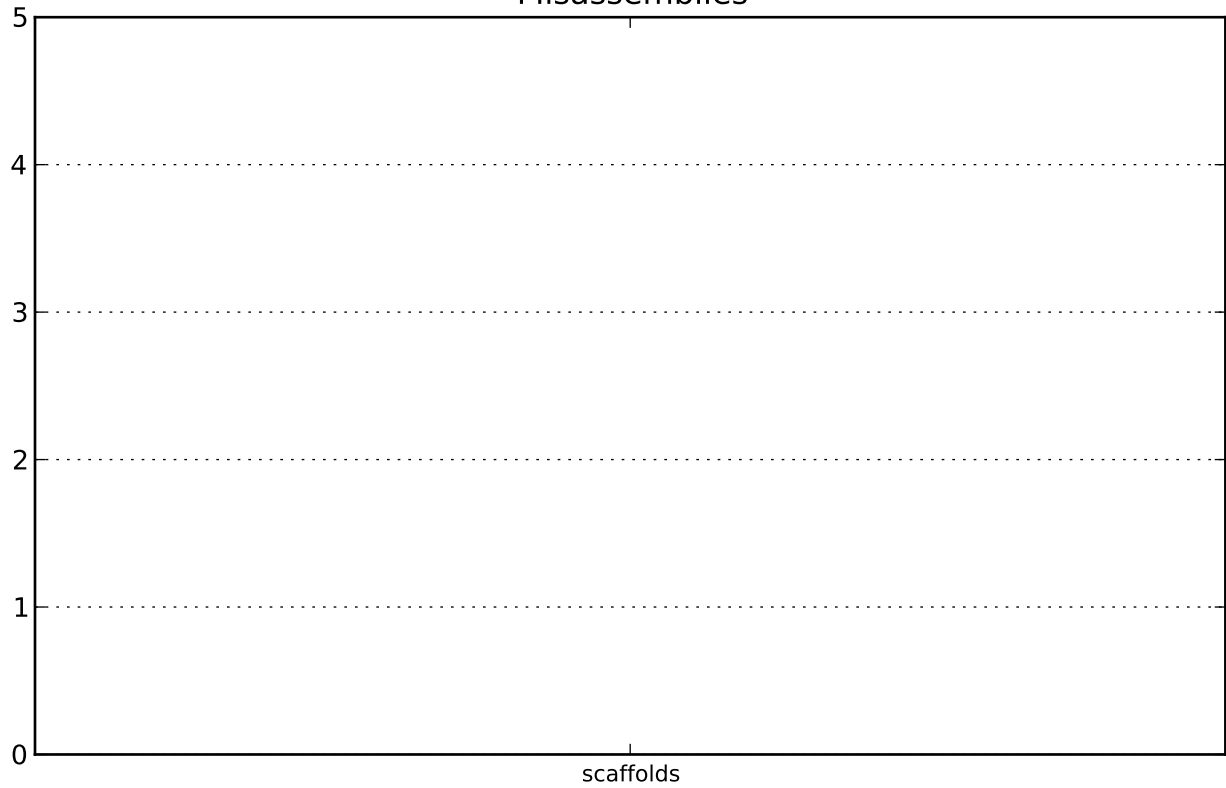
Cumulative length



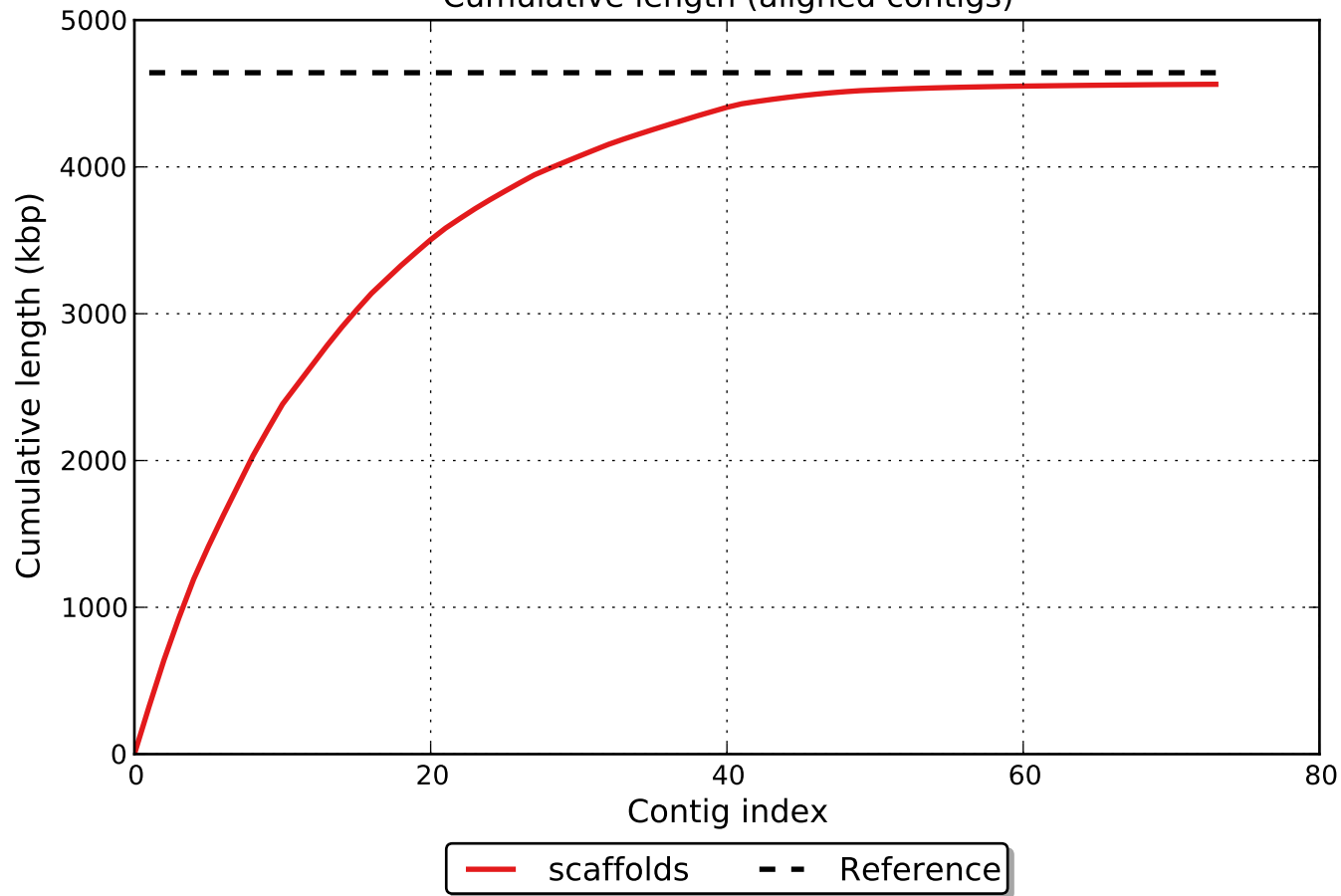
GC content



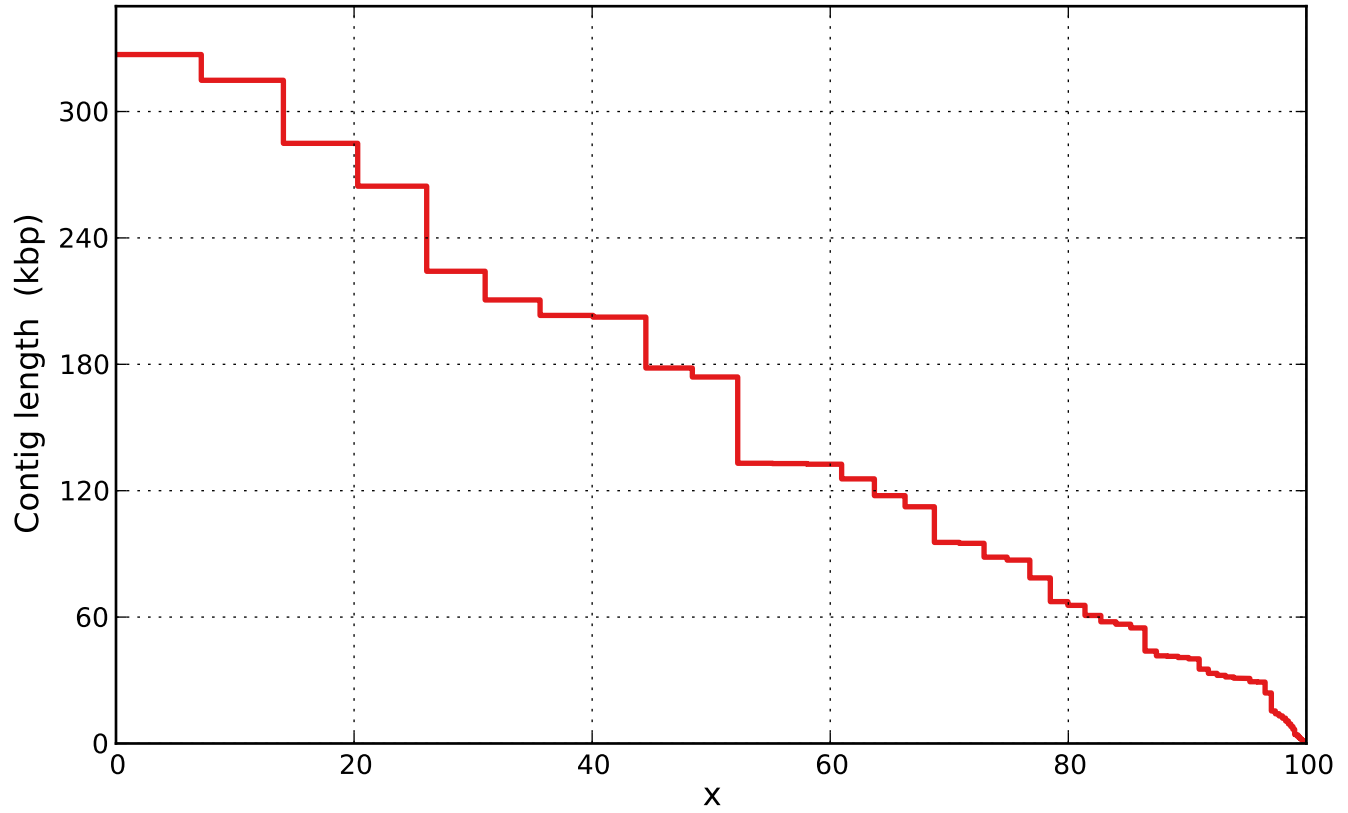
Misassemblies



Cumulative length (aligned contigs)



NAx



— scaffolds

NGAx

