

Report

	scaffolds
# contigs (>= 1000 bp)	72
# contigs (>= 5000 bp)	51
# contigs (>= 10000 bp)	48
# contigs (>= 25000 bp)	42
# contigs (>= 50000 bp)	28
Total length (>= 1000 bp)	4558404
Total length (>= 5000 bp)	4513119
Total length (>= 10000 bp)	4489168
Total length (>= 25000 bp)	4398036
Total length (>= 50000 bp)	3914279
# contigs	77
Largest contig	327064
Total length	4561971
Reference length	4641652
GC (▼)	50.75
Reference GC (▼)	50.79
N50	133023
NG50	133023
N75	87064
NG75	78609
L50	11
LG50	11
L75	21
LG75	22
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	98.227
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.75
# indels per 100 kbp	0.39
Largest alignment	327064
NA50	133023
NGA50	133023
NA75	87064
NGA75	78609
LA50	11
LGA50	11
LA75	21
LGA75	22

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	171
# indels	18
# short indels	18
# long indels	0
Indels length	25

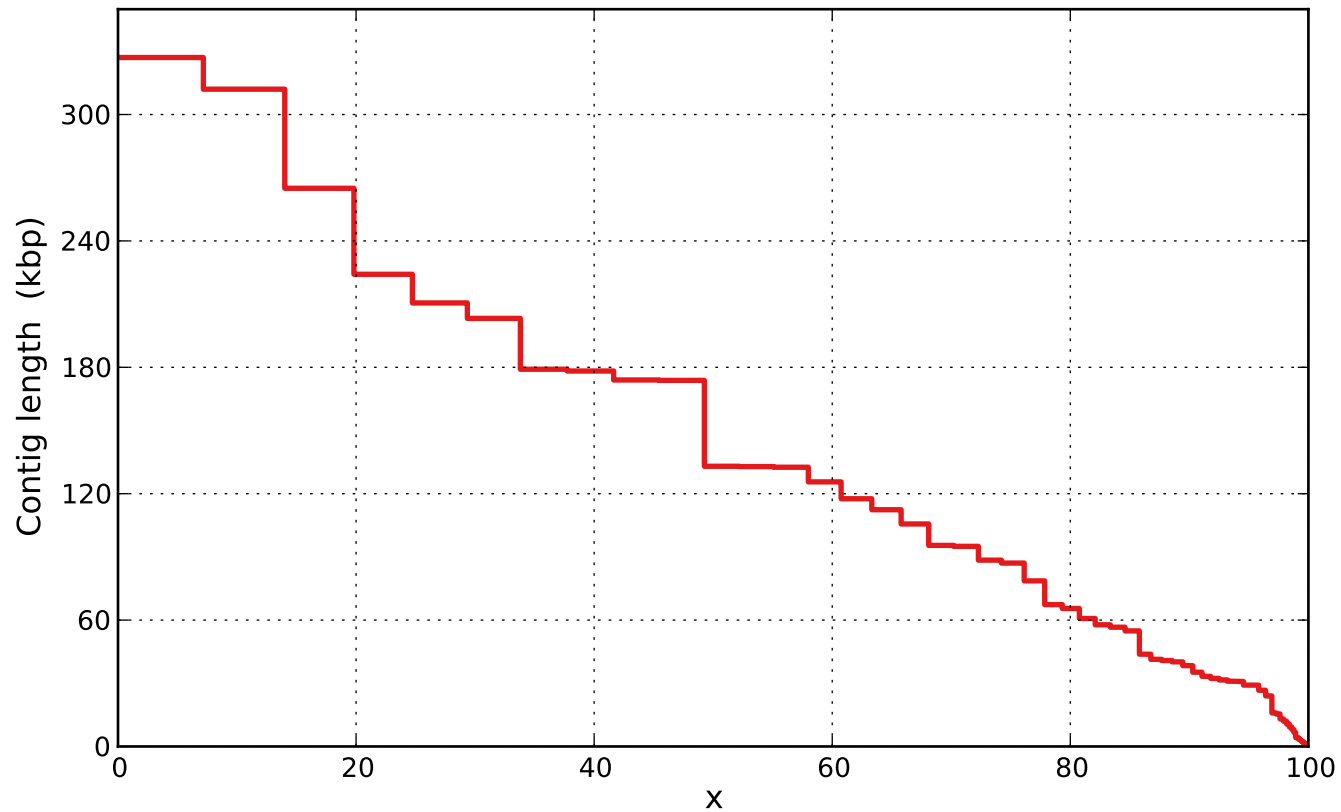
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

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

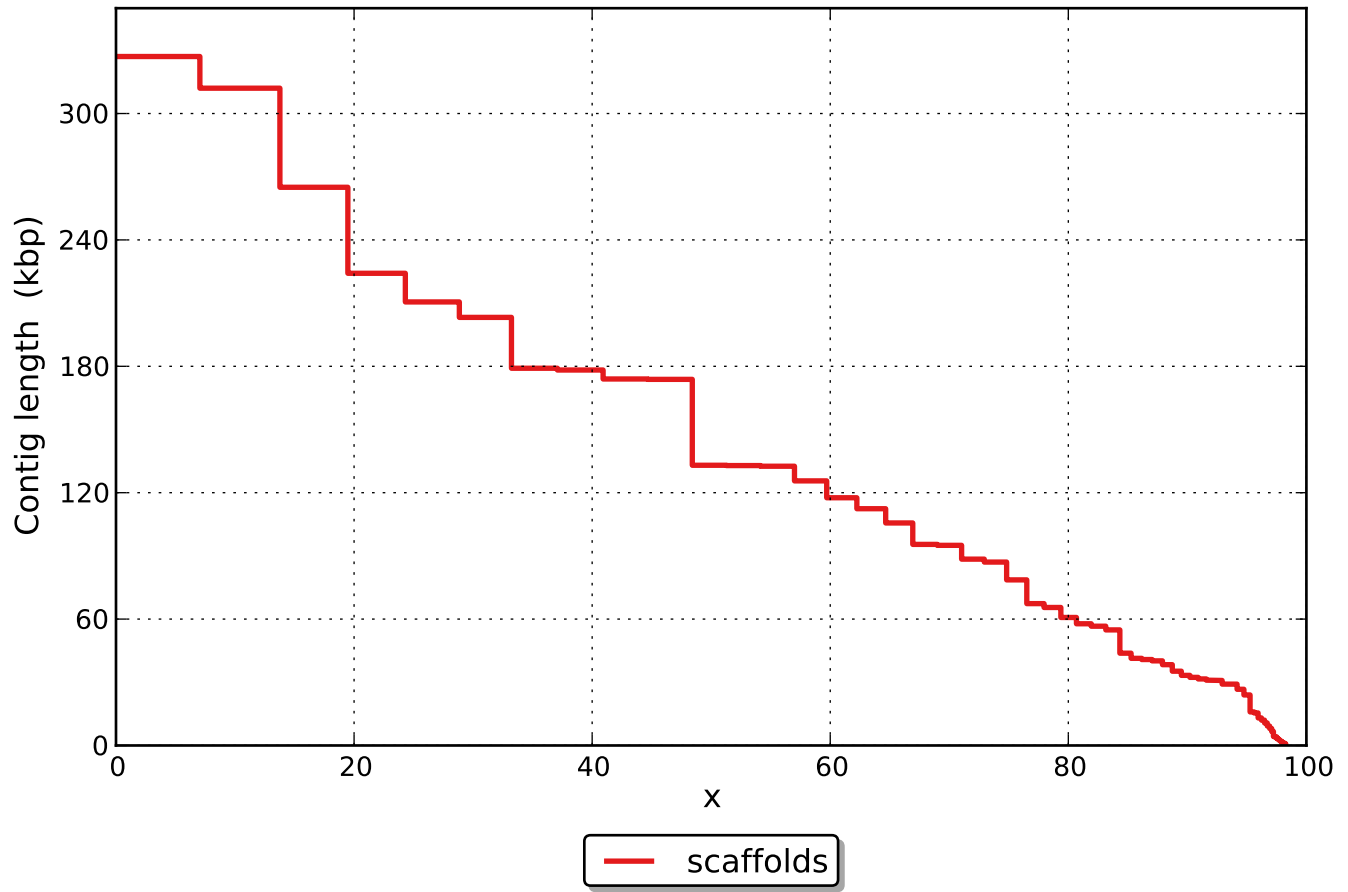
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

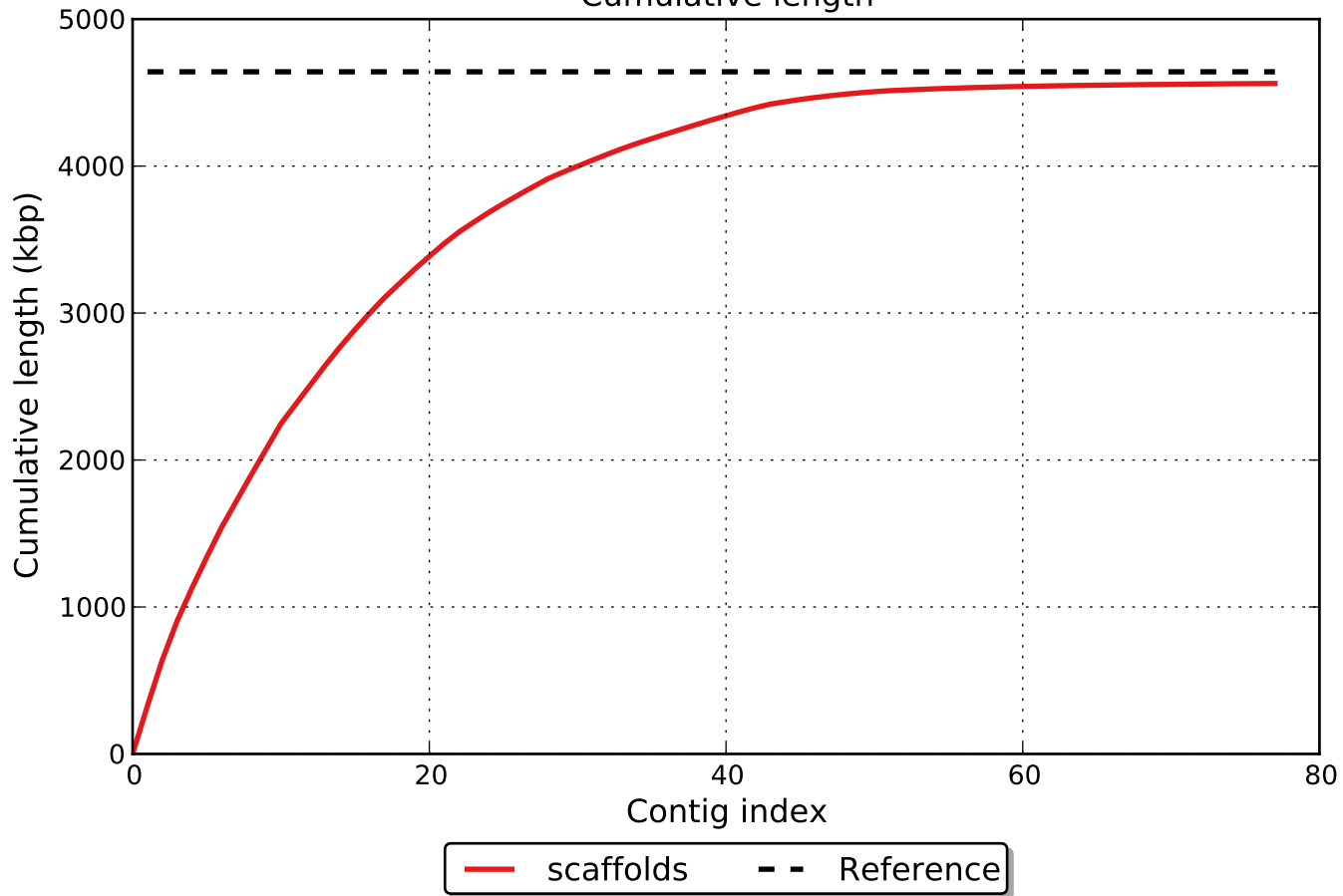


scaffolds

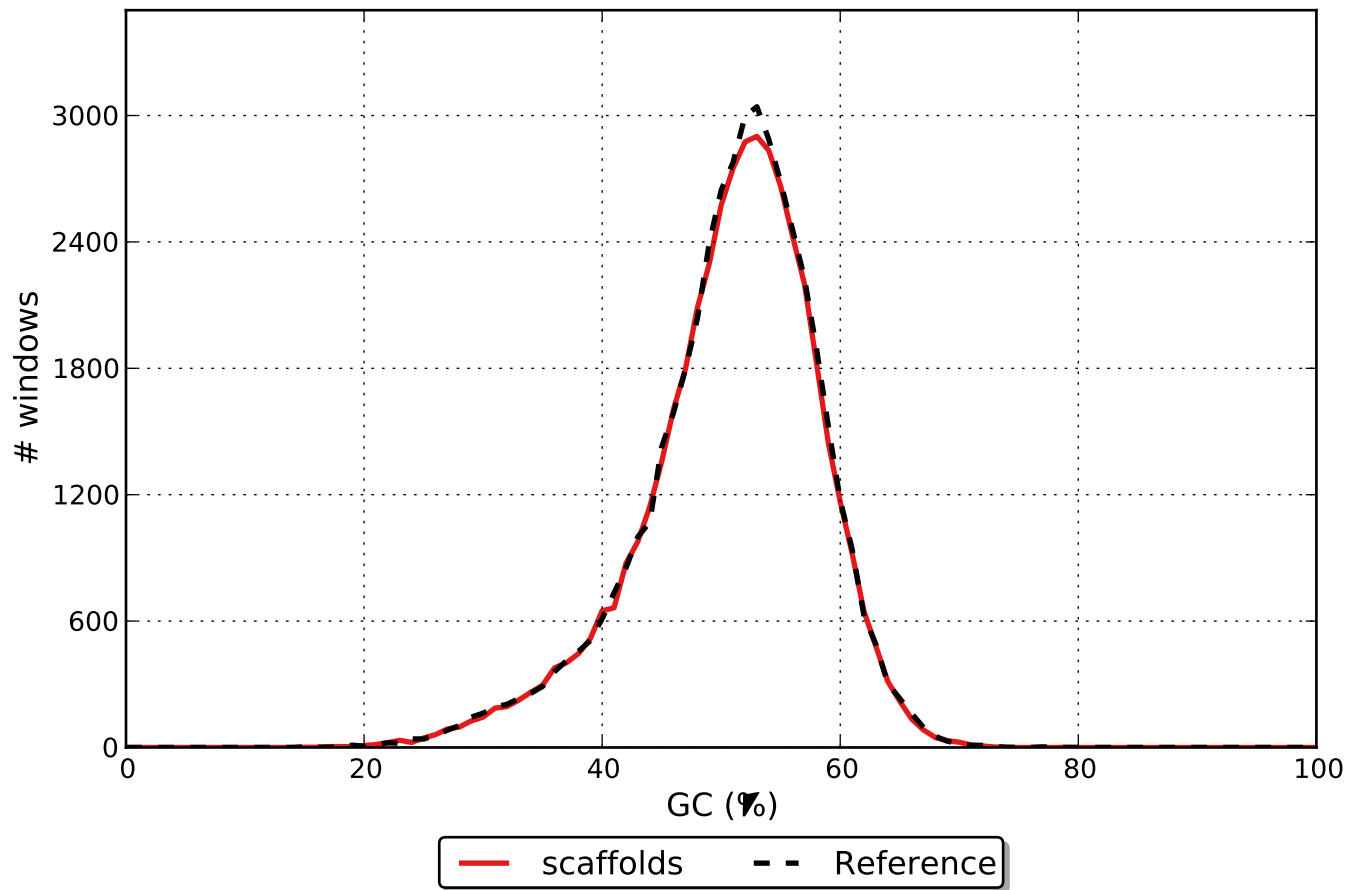
NGx



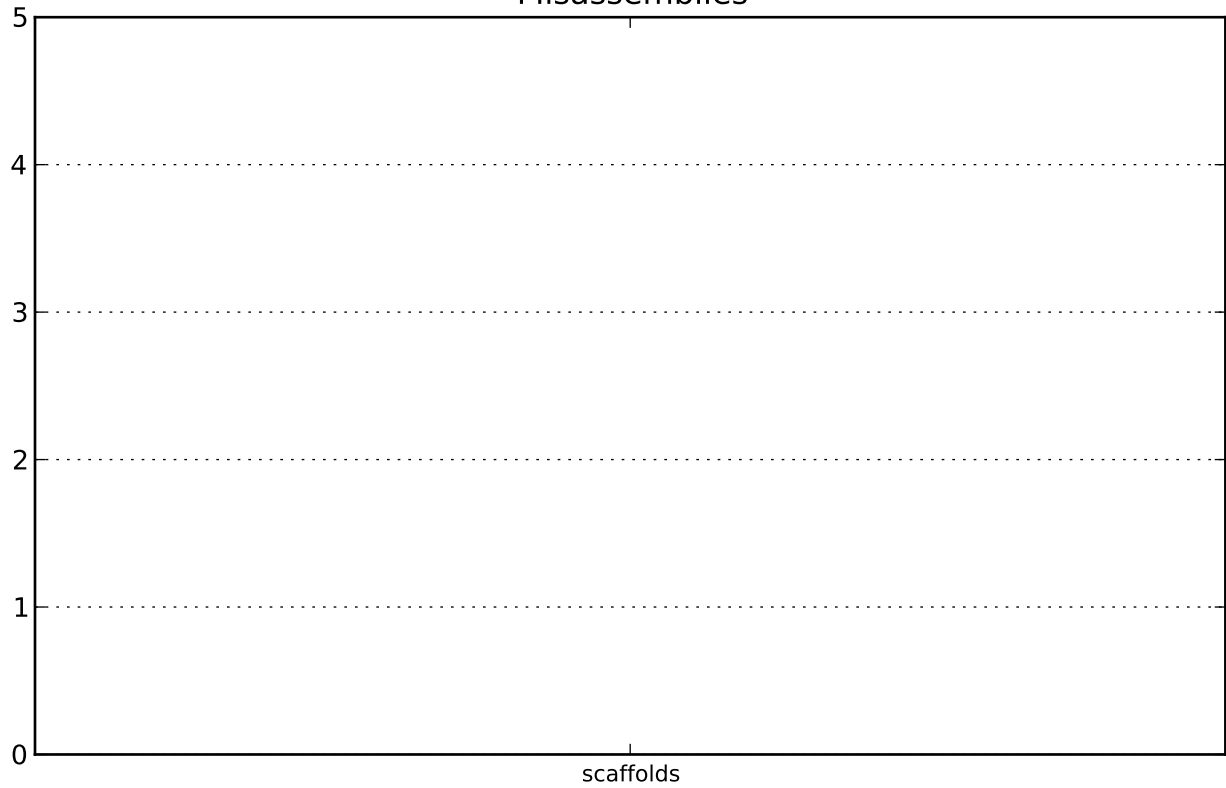
Cumulative length



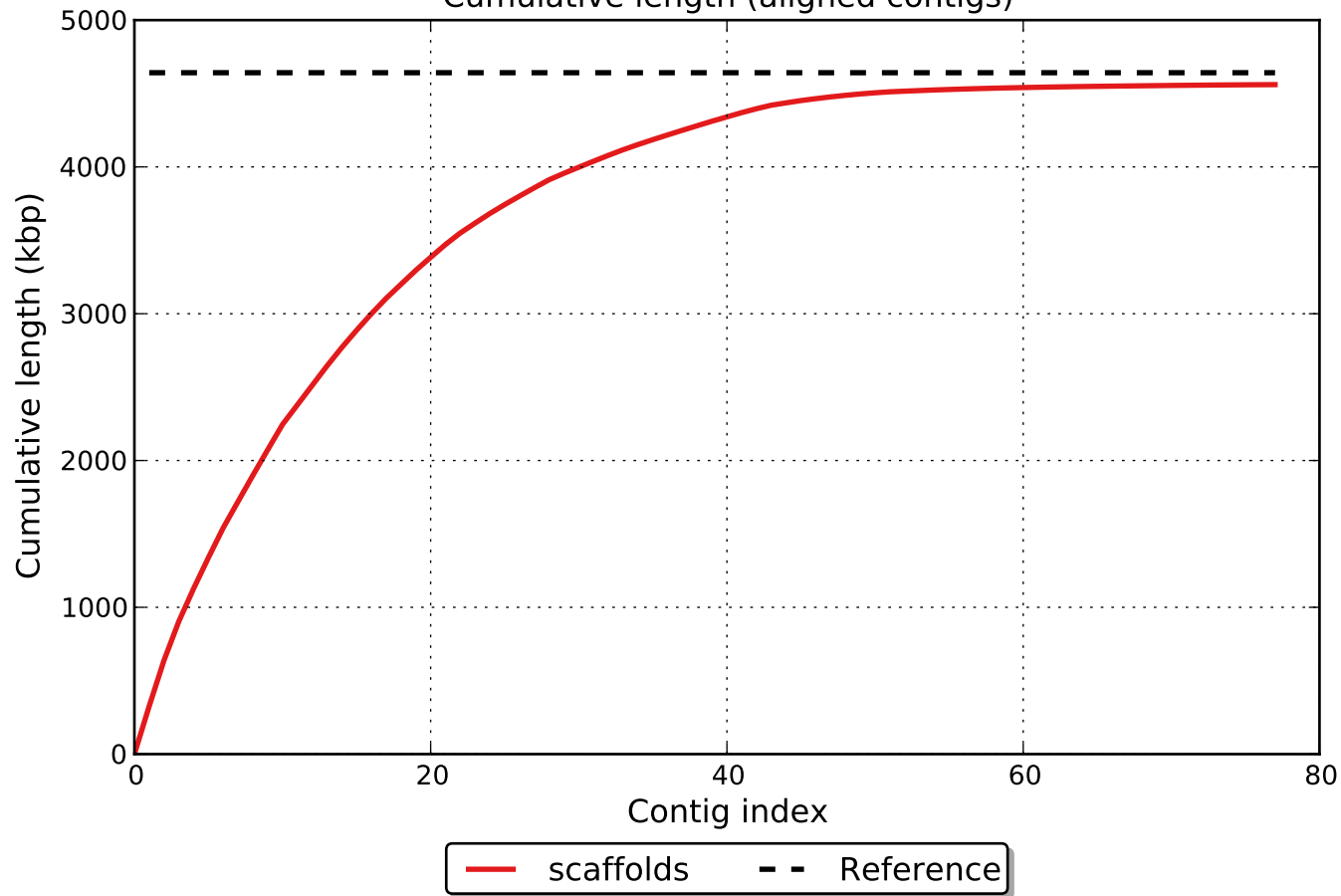
GC content



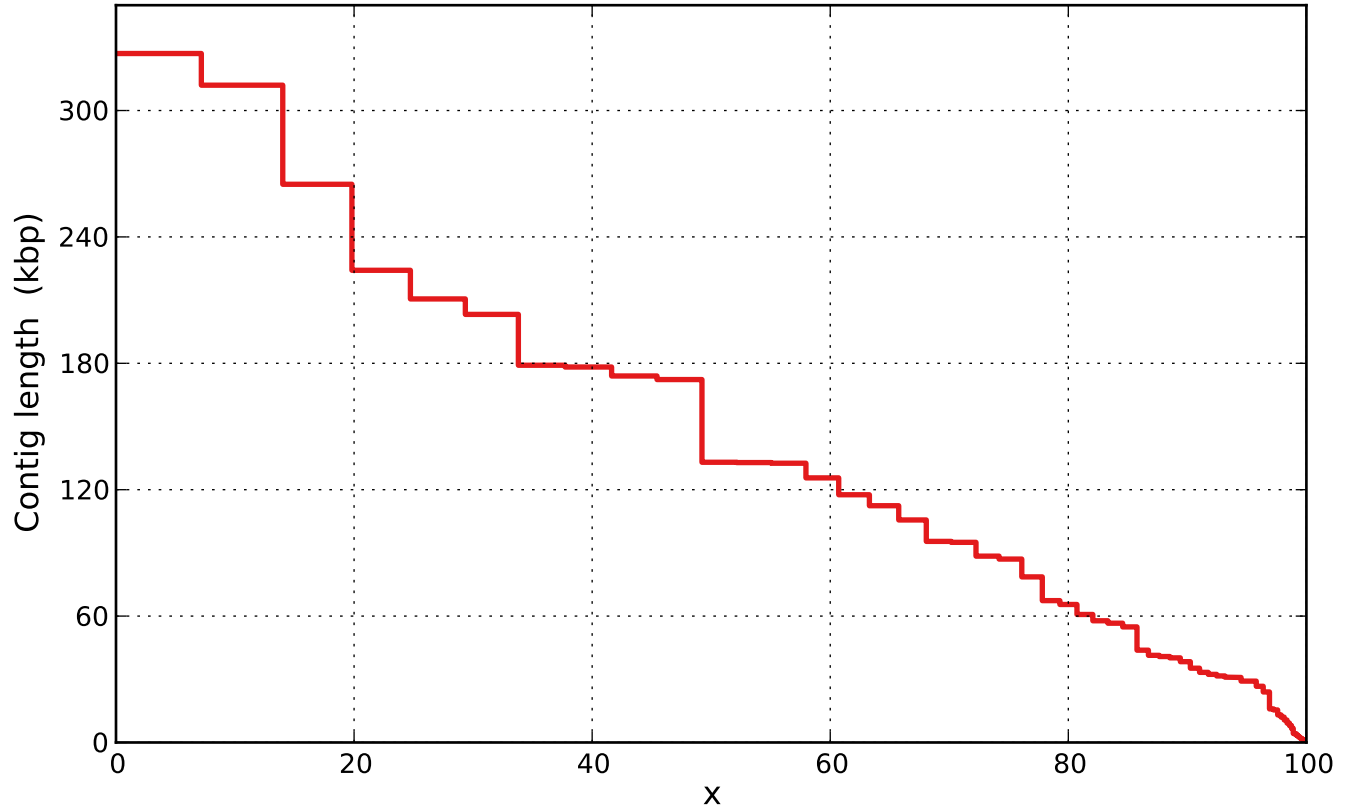
Misassemblies



Cumulative length (aligned contigs)



NAx



— scaffolds

NGAx

