

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)	4557596
Total length (>= 5000 bp)	4517905
Total length (>= 10000 bp)	4493834
Total length (>= 25000 bp)	4404514
Total length (>= 50000 bp)	3947084
# contigs	73
Largest contig	327052
Total length	4561806
Reference length	4641652
GC (▼)	50.75
Reference GC (▼)	50.79
N50	173973
NG50	173973
N75	87064
NG75	87064
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 (▼)	98.228
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	61.19
# indels per 100 kbp	8.31
Largest alignment	327052
NA50	173973
NGA50	173973
NA75	87064
NGA75	87064
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	2790
# indels	379
# short indels	379
# long indels	0
Indels length	543

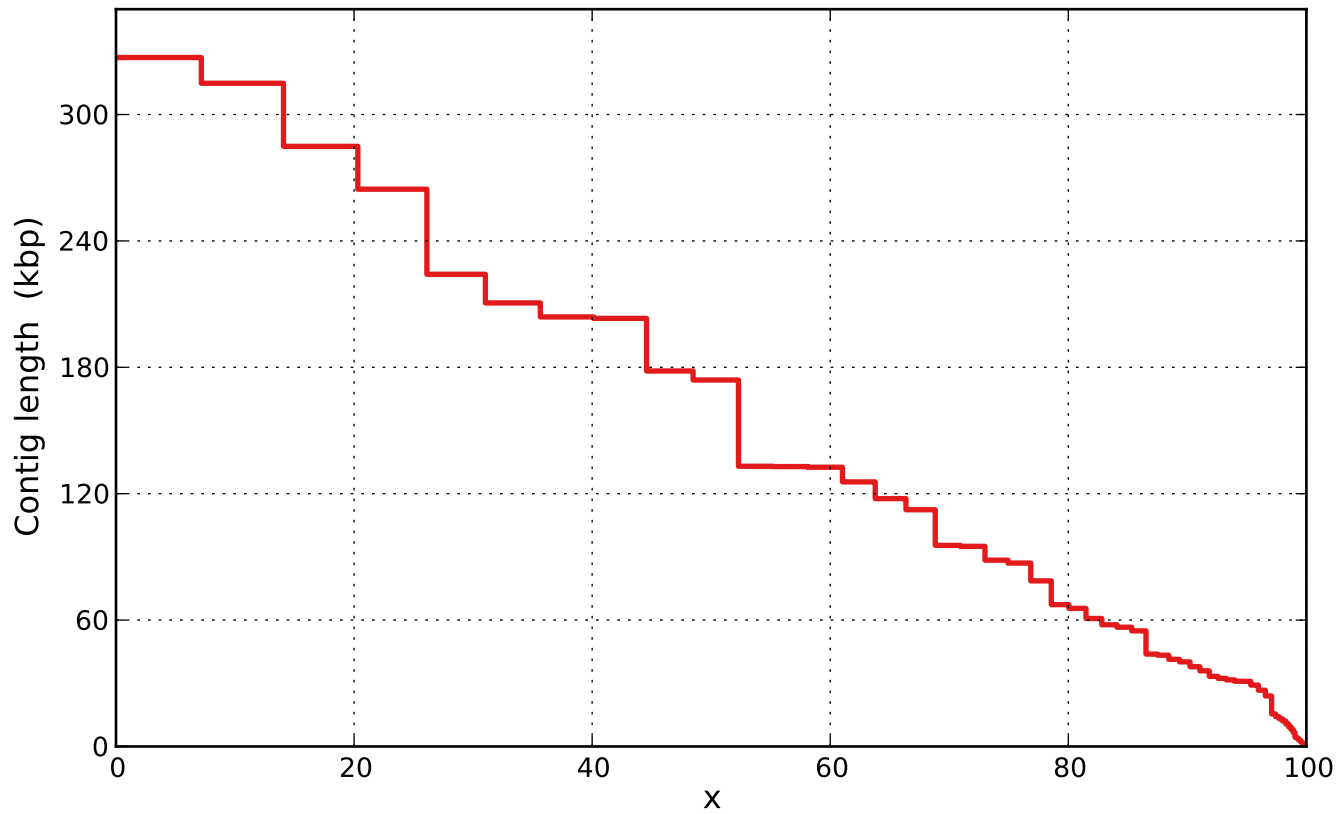
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

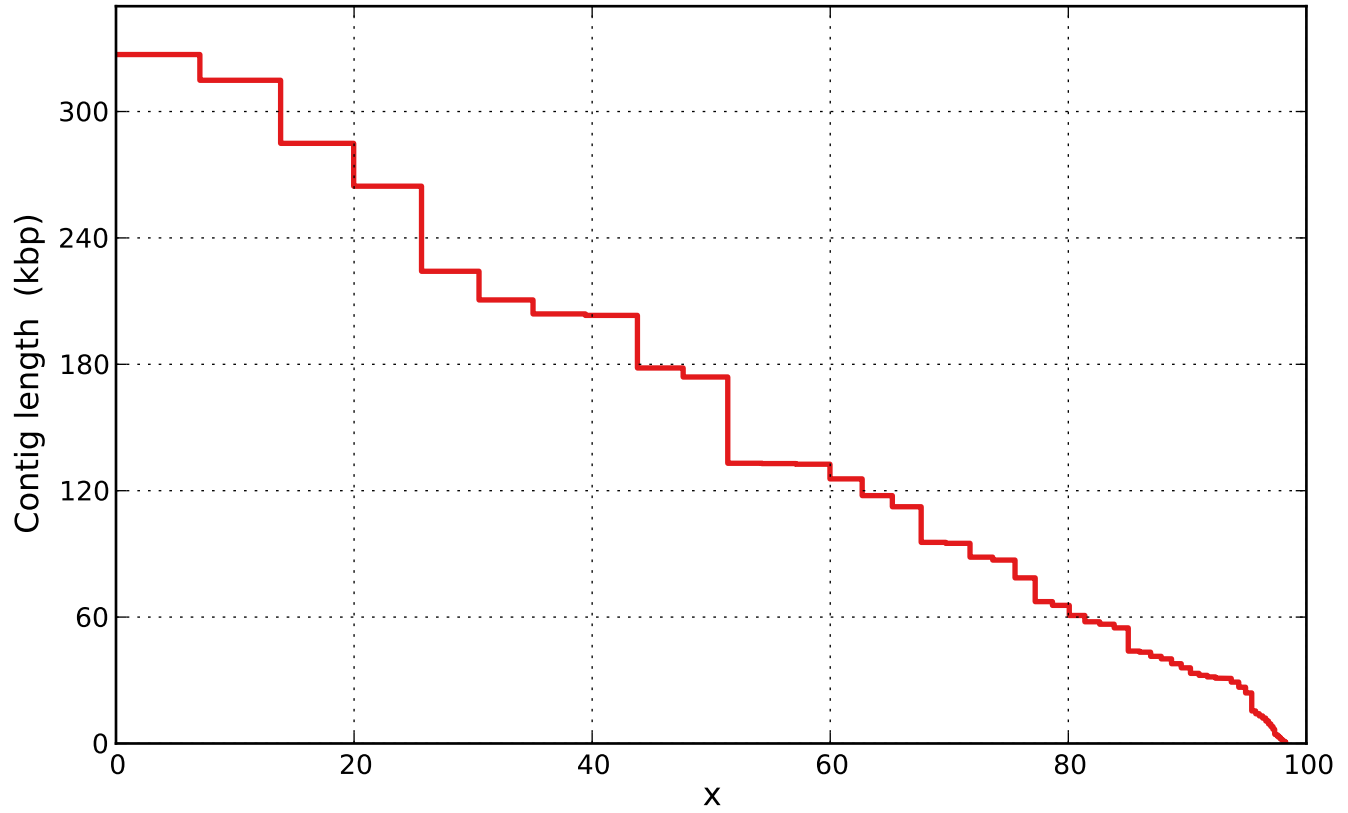
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

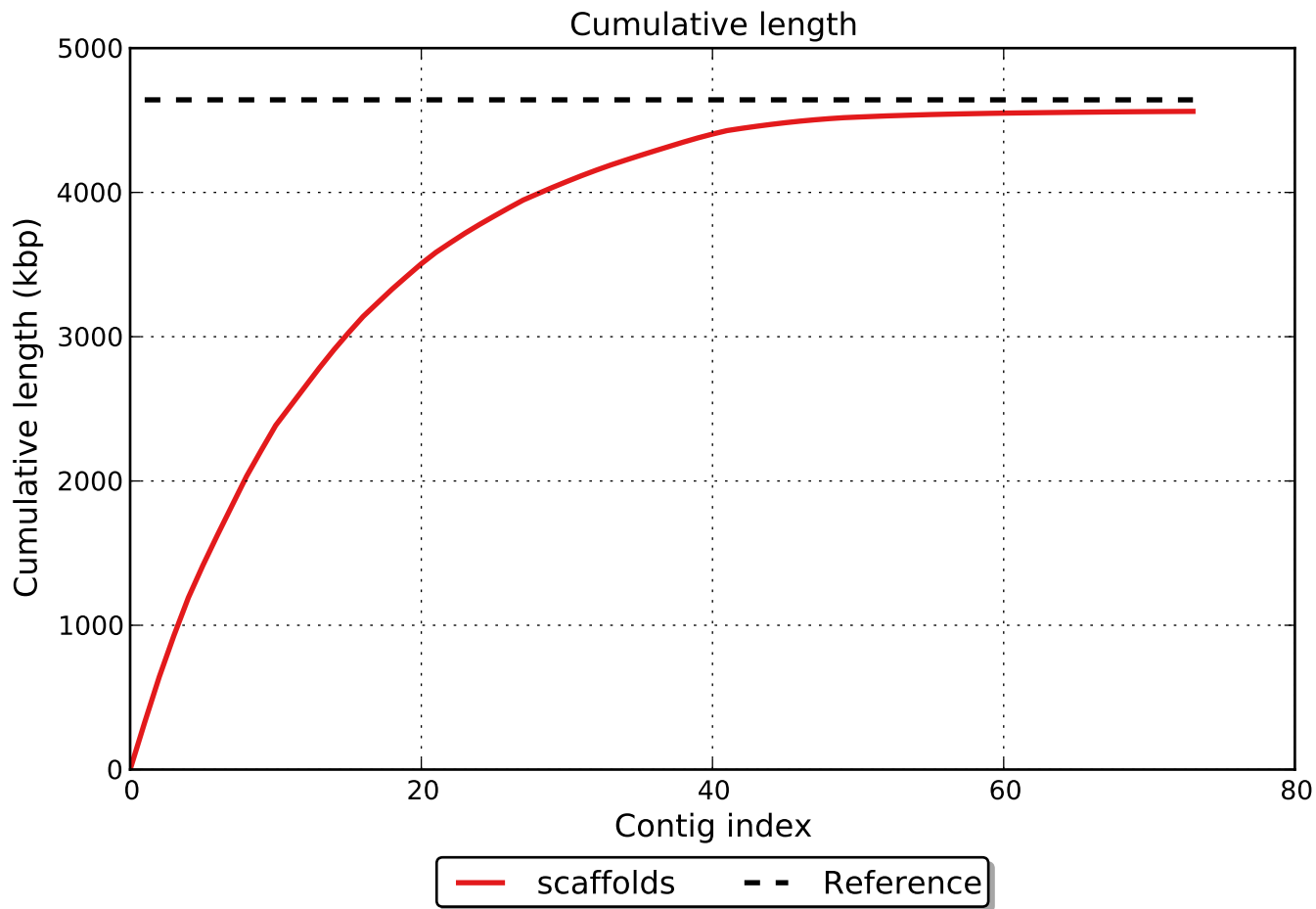
Nx



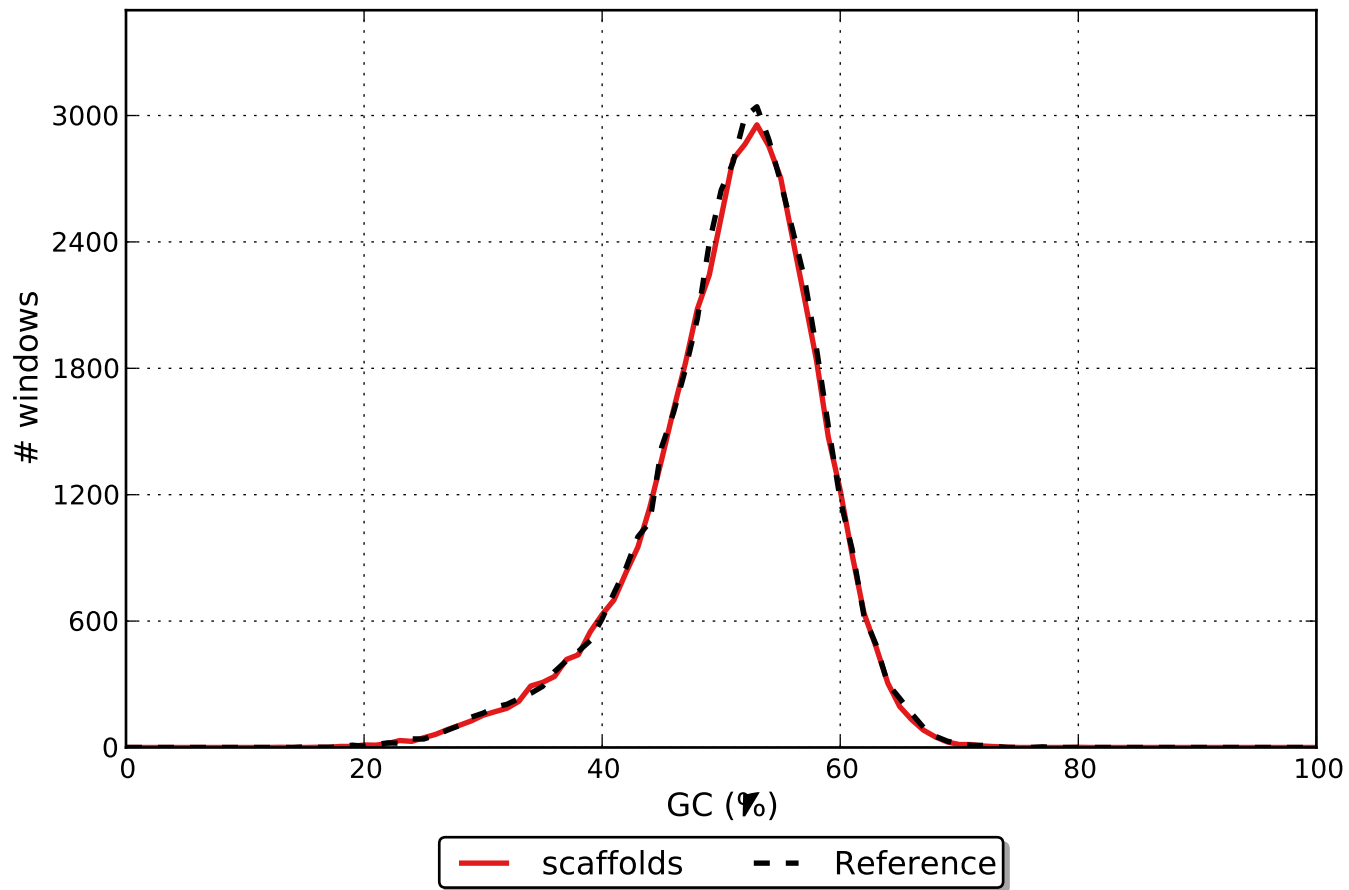
NGx



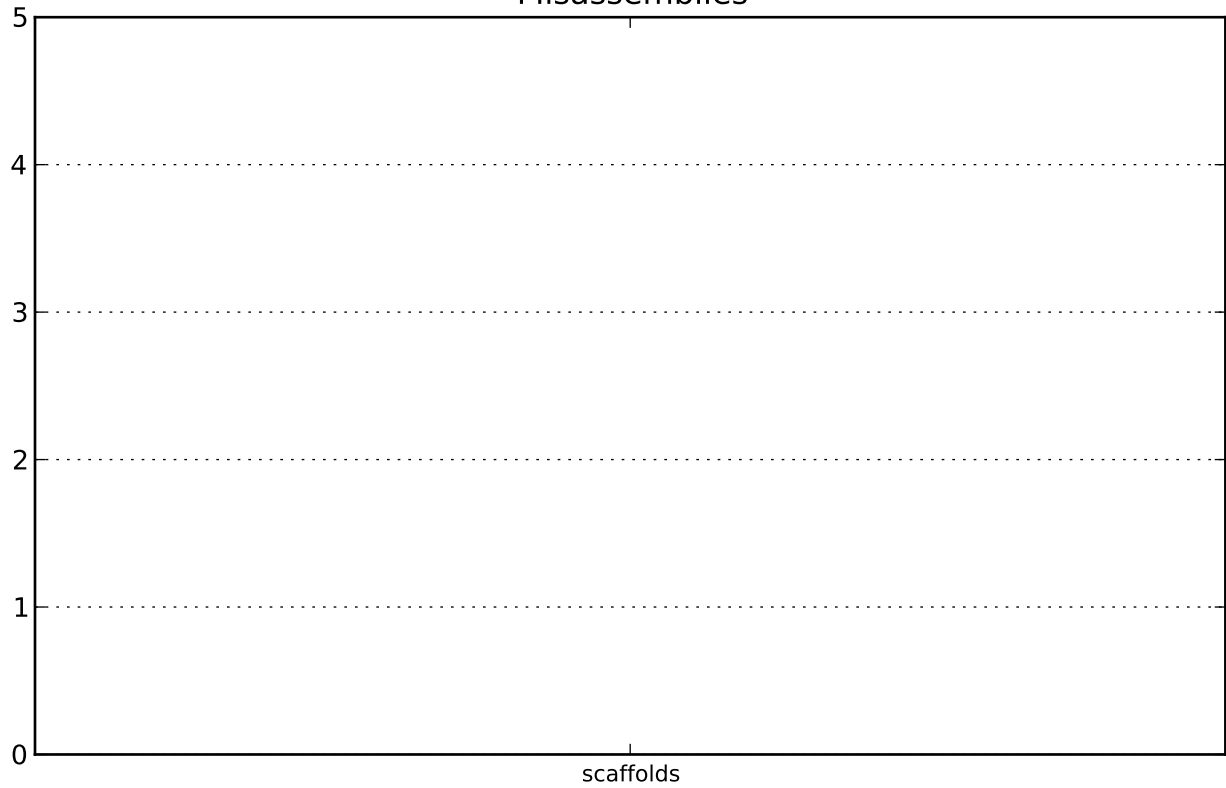
— scaffolds



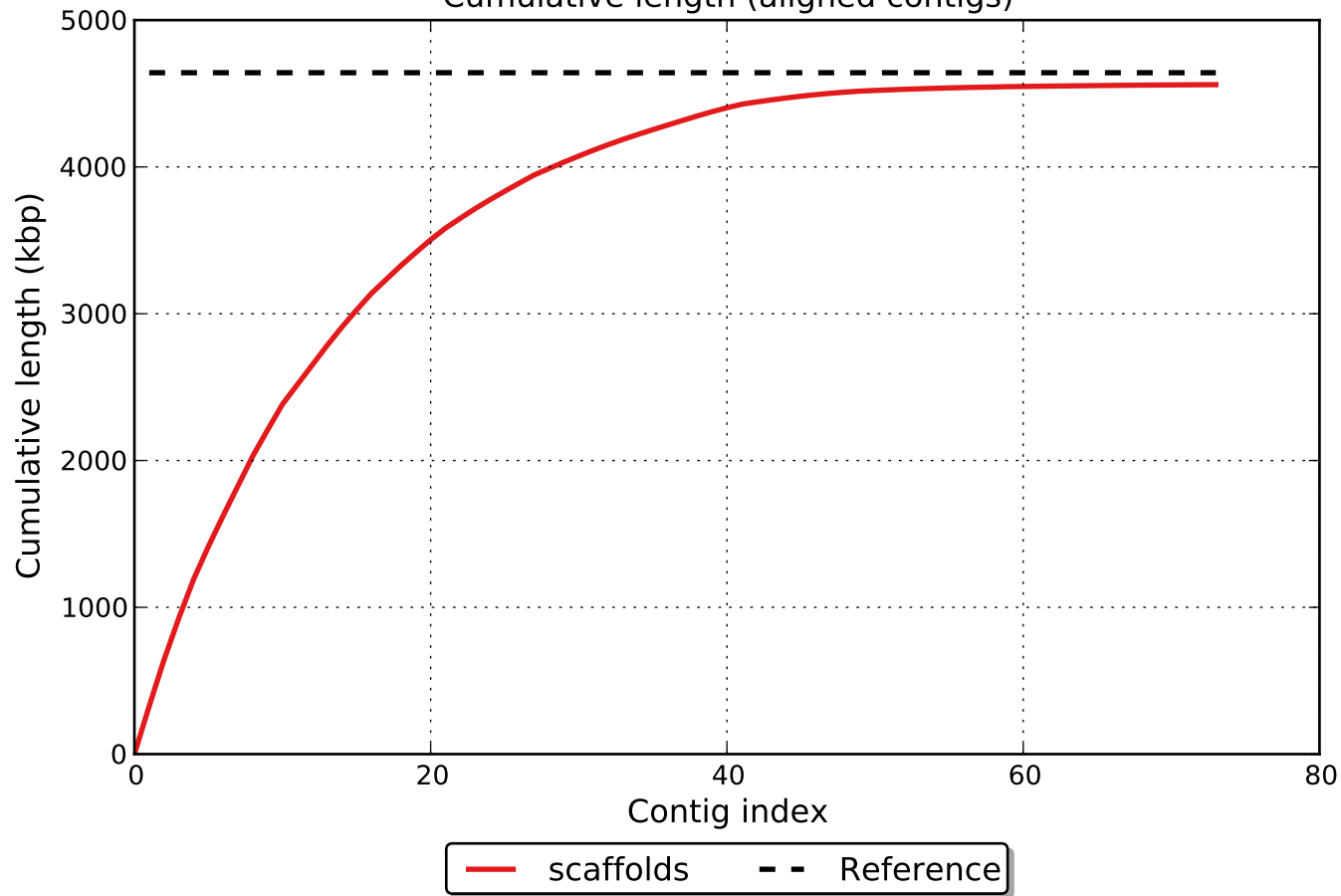
GC content



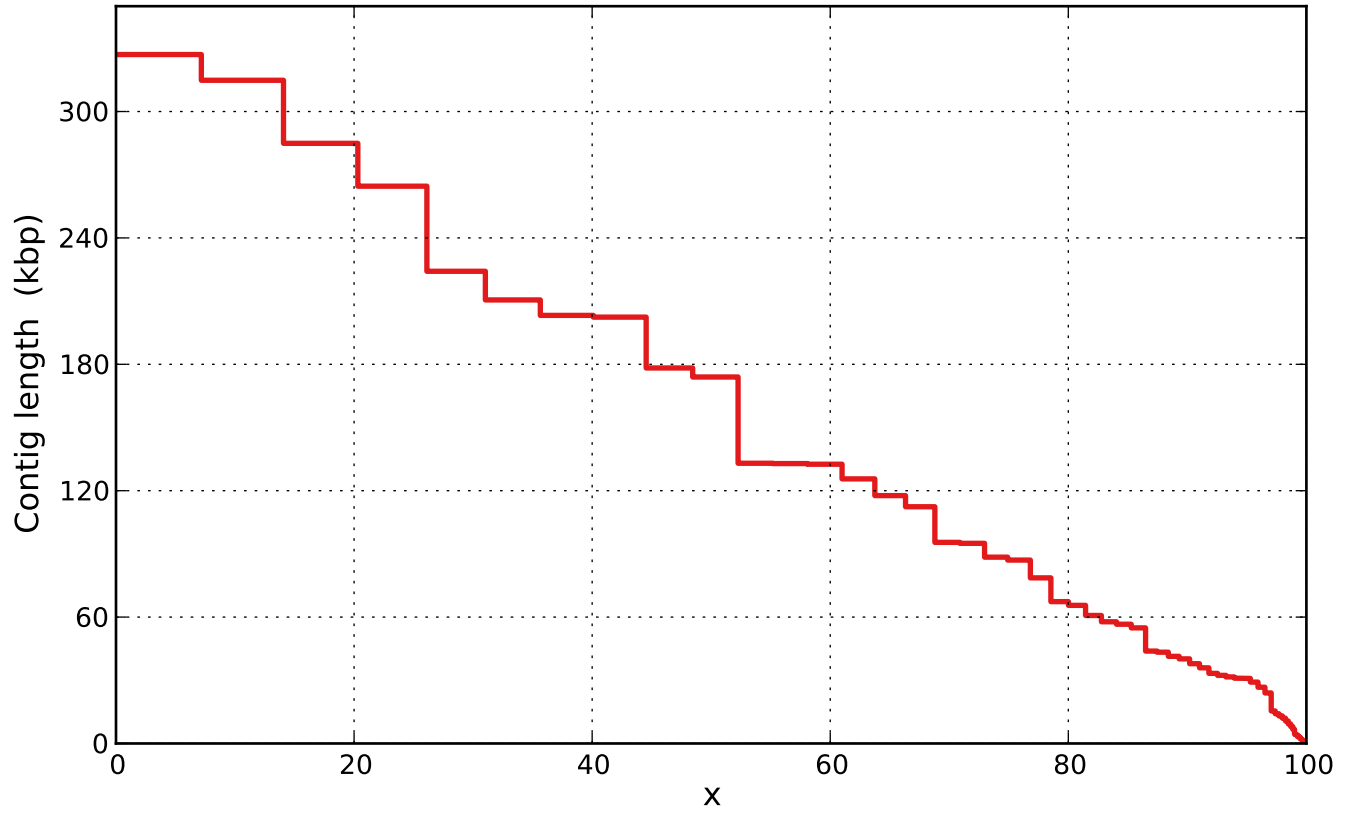
Misassemblies



Cumulative length (aligned contigs)



NAx



scaffolds

NGAx

