

## Report

	scaffolds
# contigs (>= 1000 bp)	111
# contigs (>= 5000 bp)	90
# contigs (>= 10000 bp)	86
# contigs (>= 25000 bp)	76
# contigs (>= 50000 bp)	60
Total length (>= 1000 bp)	8993398
Total length (>= 5000 bp)	8949107
Total length (>= 10000 bp)	8917074
Total length (>= 25000 bp)	8752641
Total length (>= 50000 bp)	8226933
# contigs	136
Largest contig	332068
Total length	9009669
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.79
N50	164195
NG50	228178
N75	91954
NG75	178199
L50	21
LG50	9
L75	39
LG75	15
# misassemblies	268
# misassembled contigs	38
Misassembled contigs length	4252810
# local misassemblies	6
# unaligned contigs	0 + 1 part
Unaligned length	447
Genome fraction (%)	98.674
Duplication ratio	1.967
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1041.09
# indels per 100 kbp	1.38
Largest alignment	300358
NA50	62146
NGA50	159904
NA75	22580
NGA75	92493
LA50	34
LGA50	11
LA75	94
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	268
# relocations	236
# translocations	0
# inversions	32
# possibly misassembled contigs	4
# misassembled contigs	38
Misassembled contigs length	4252810
# local misassemblies	6
# mismatches	47683
# indels	63
# short indels	62
# long indels	1
Indels length	72

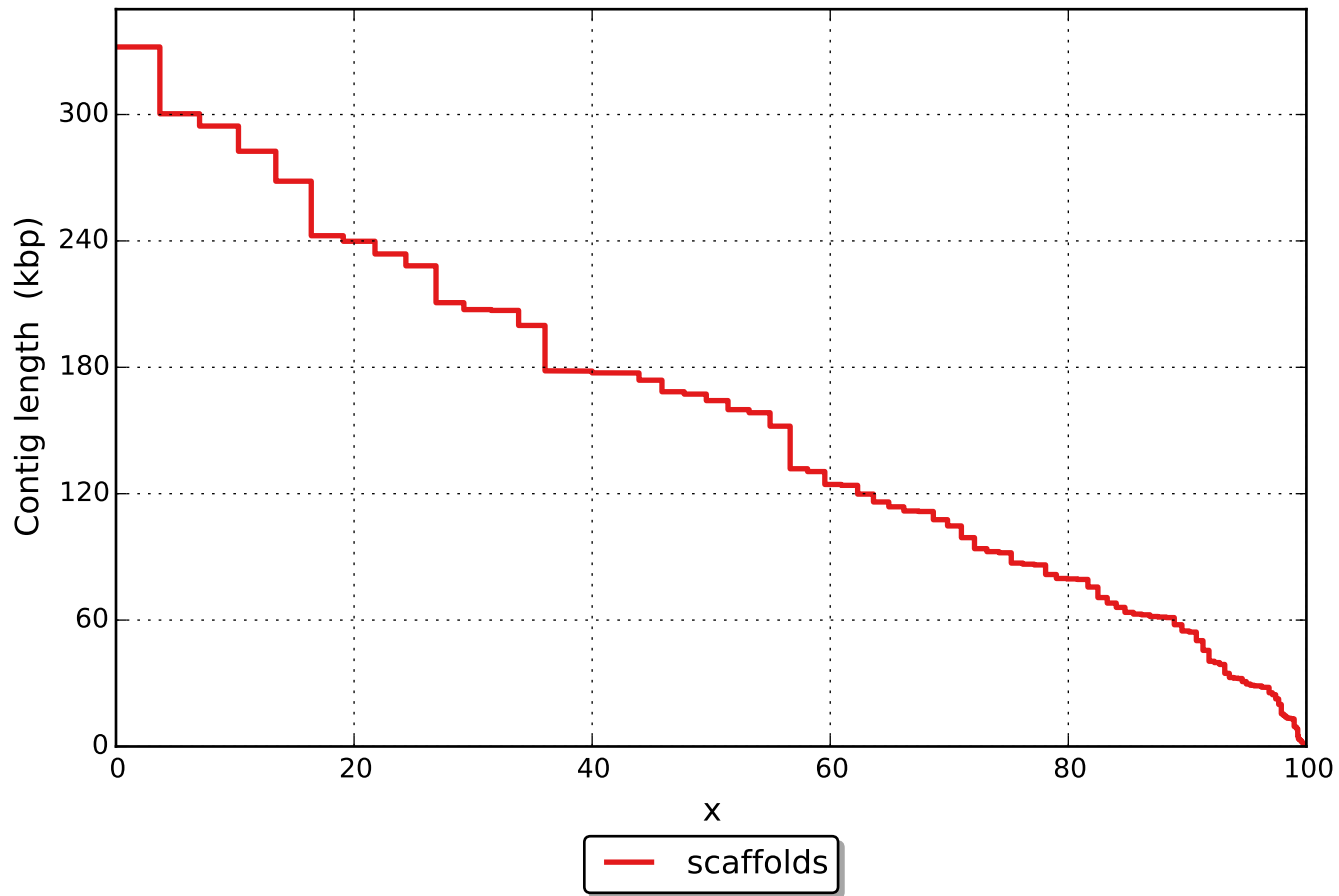
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

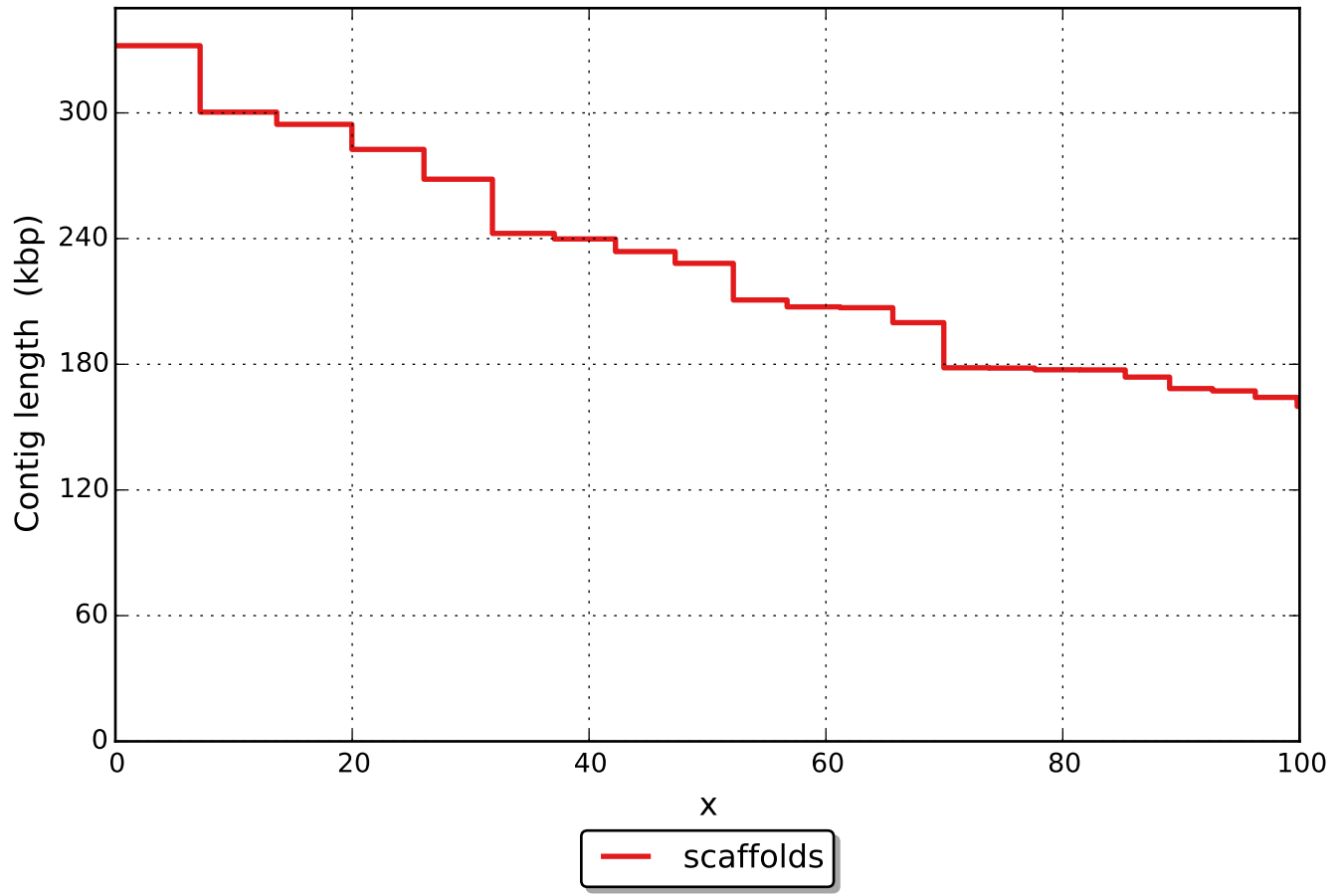
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	447
# N's	0

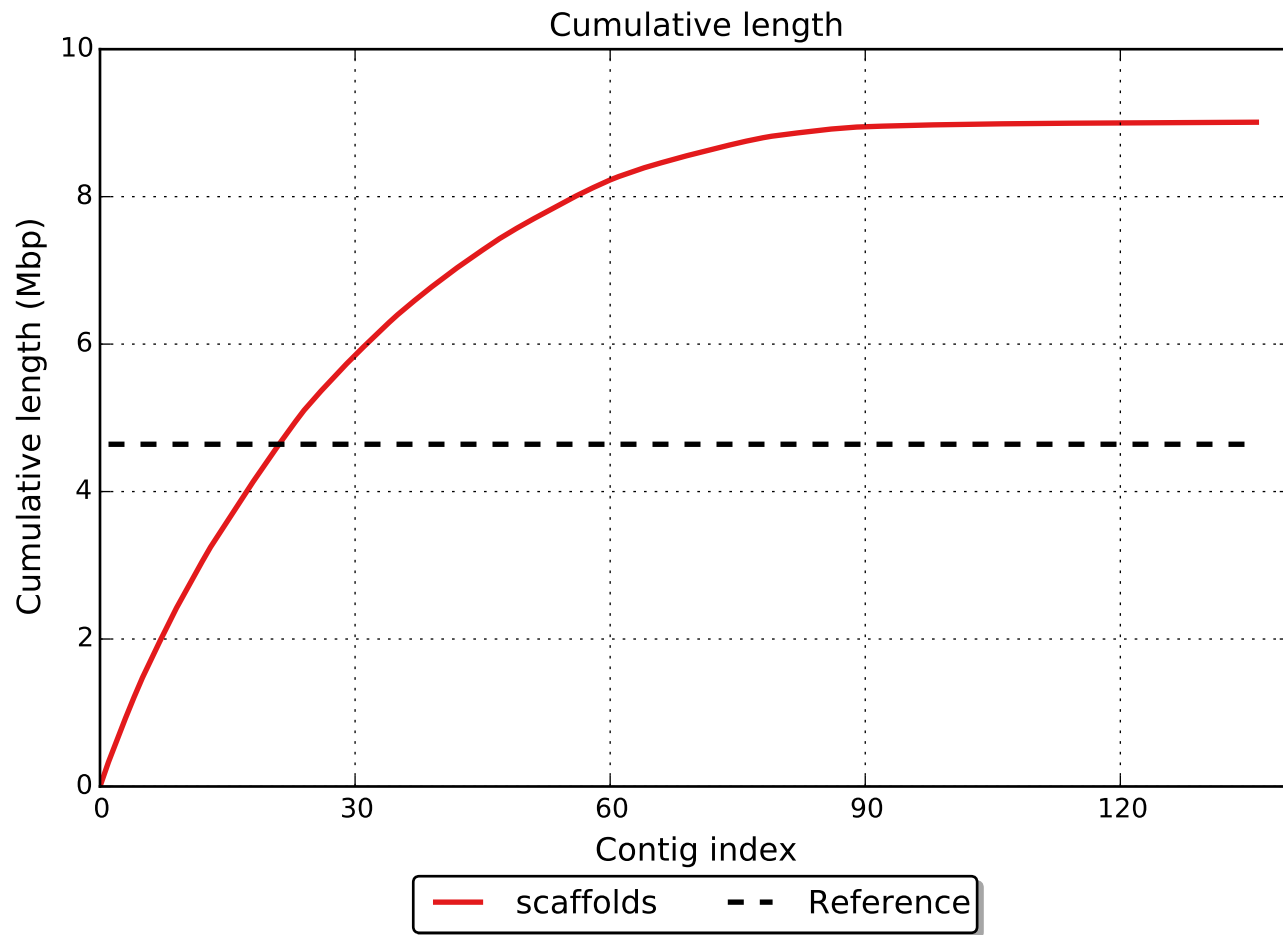
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

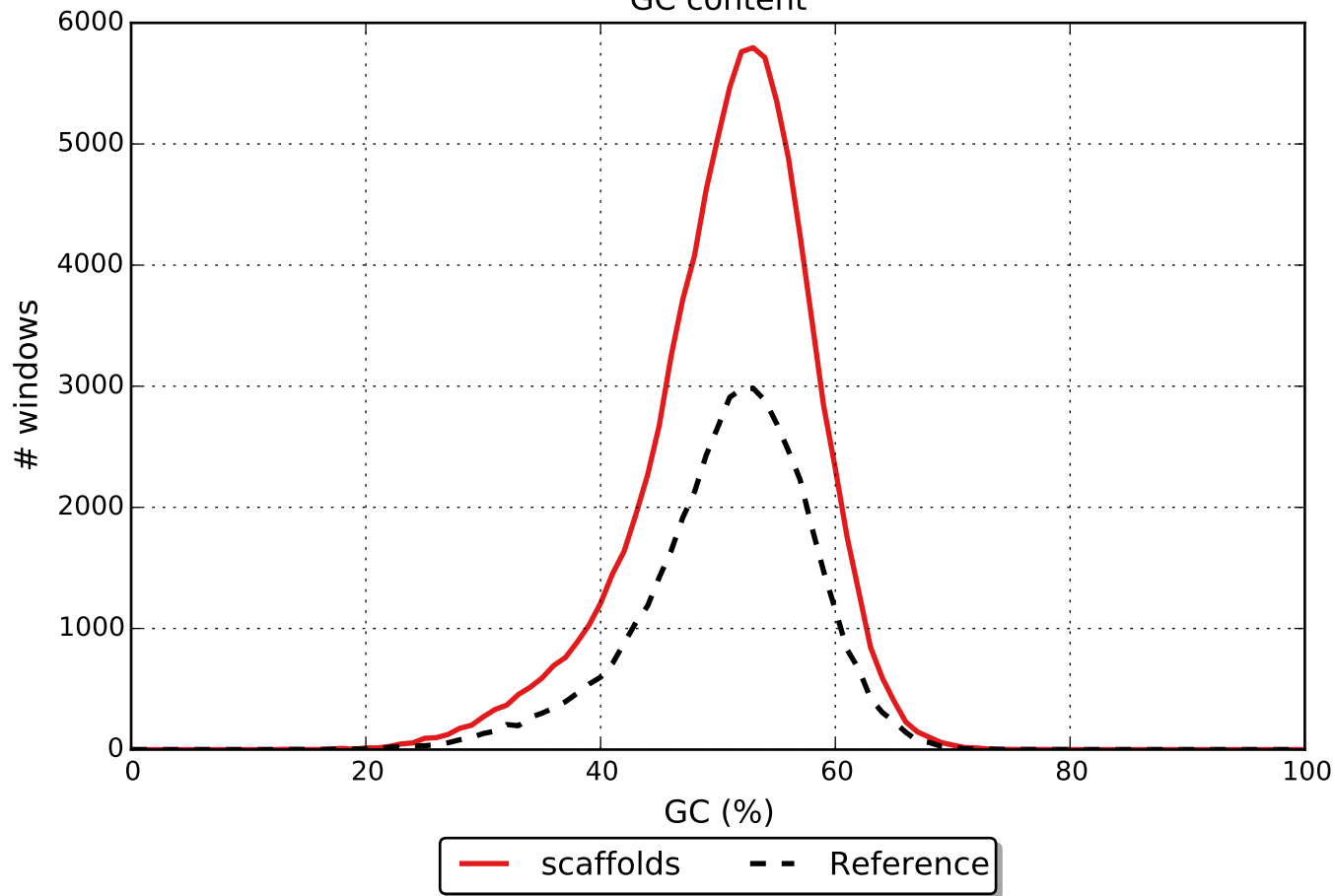


NGx

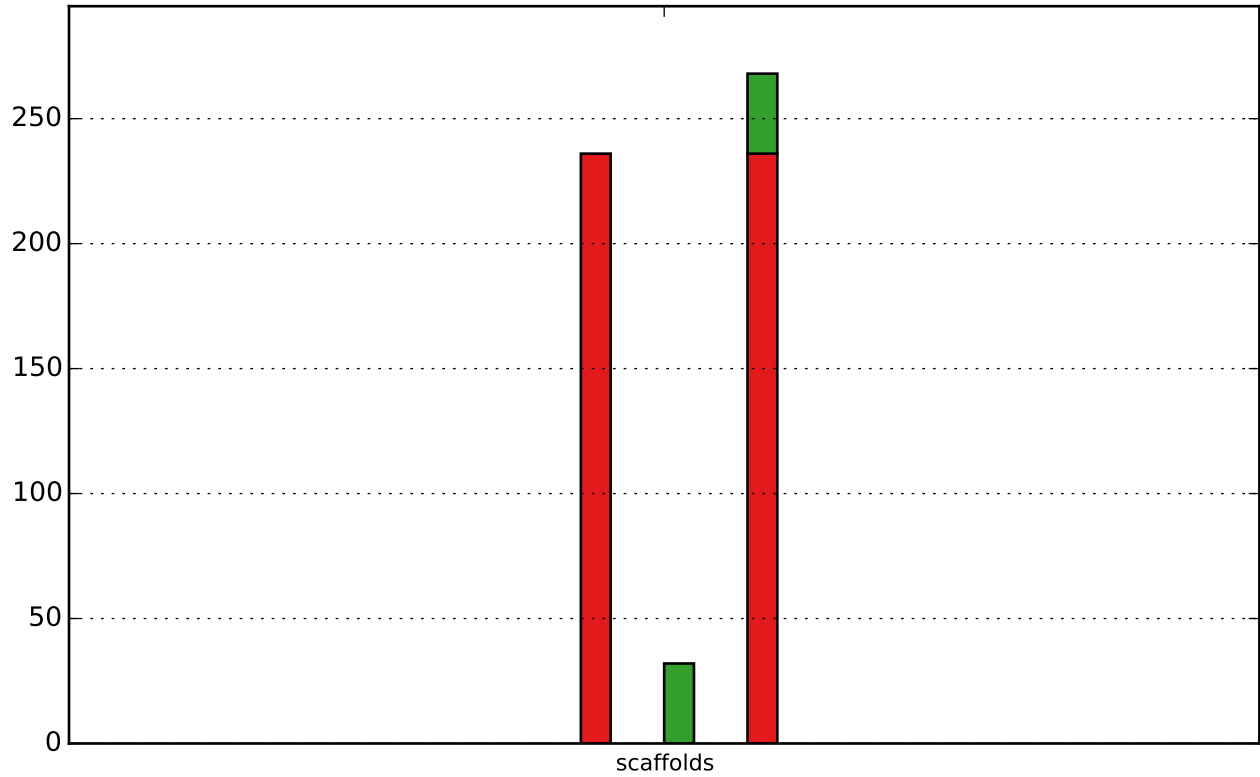




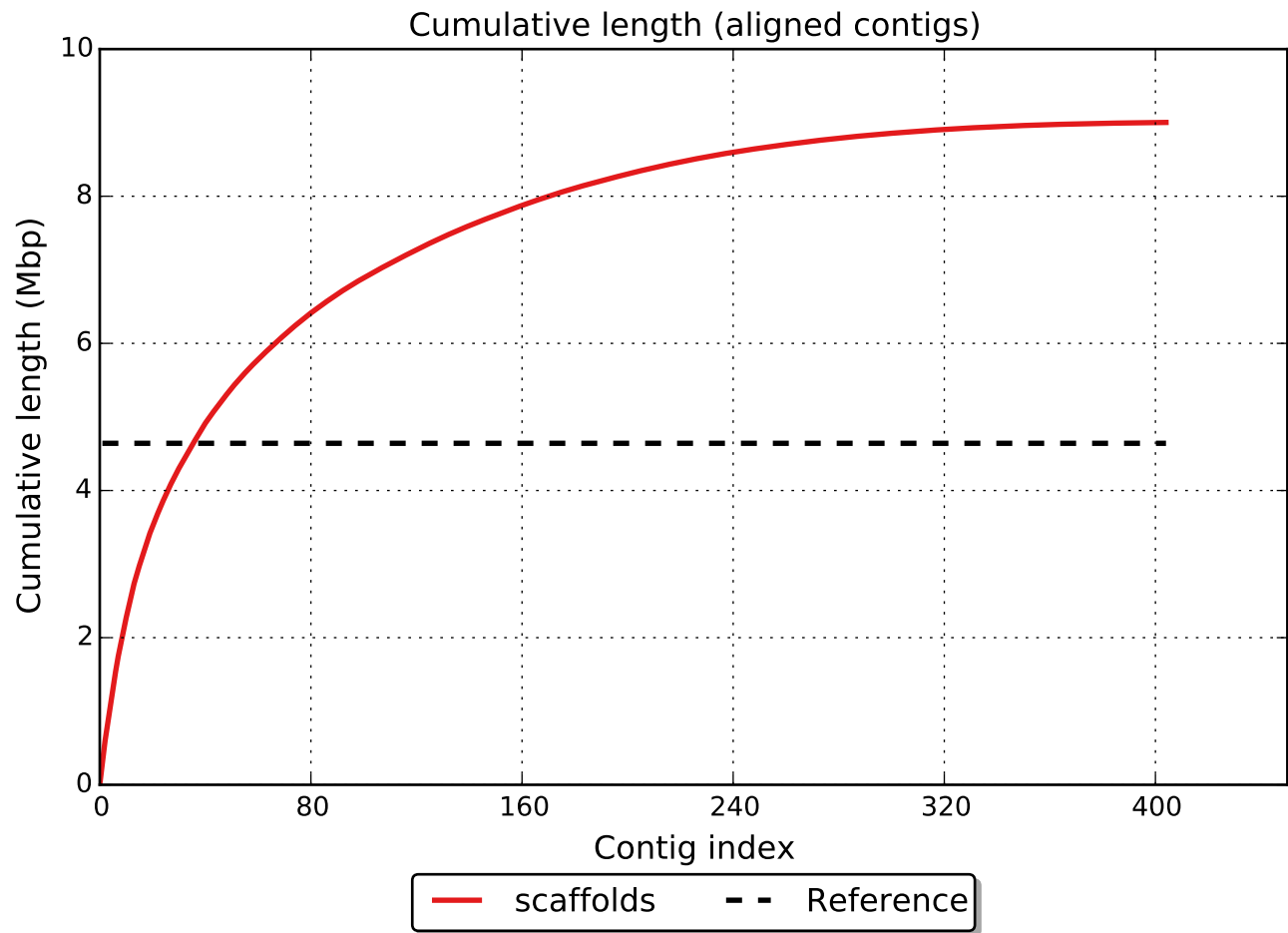
# GC content



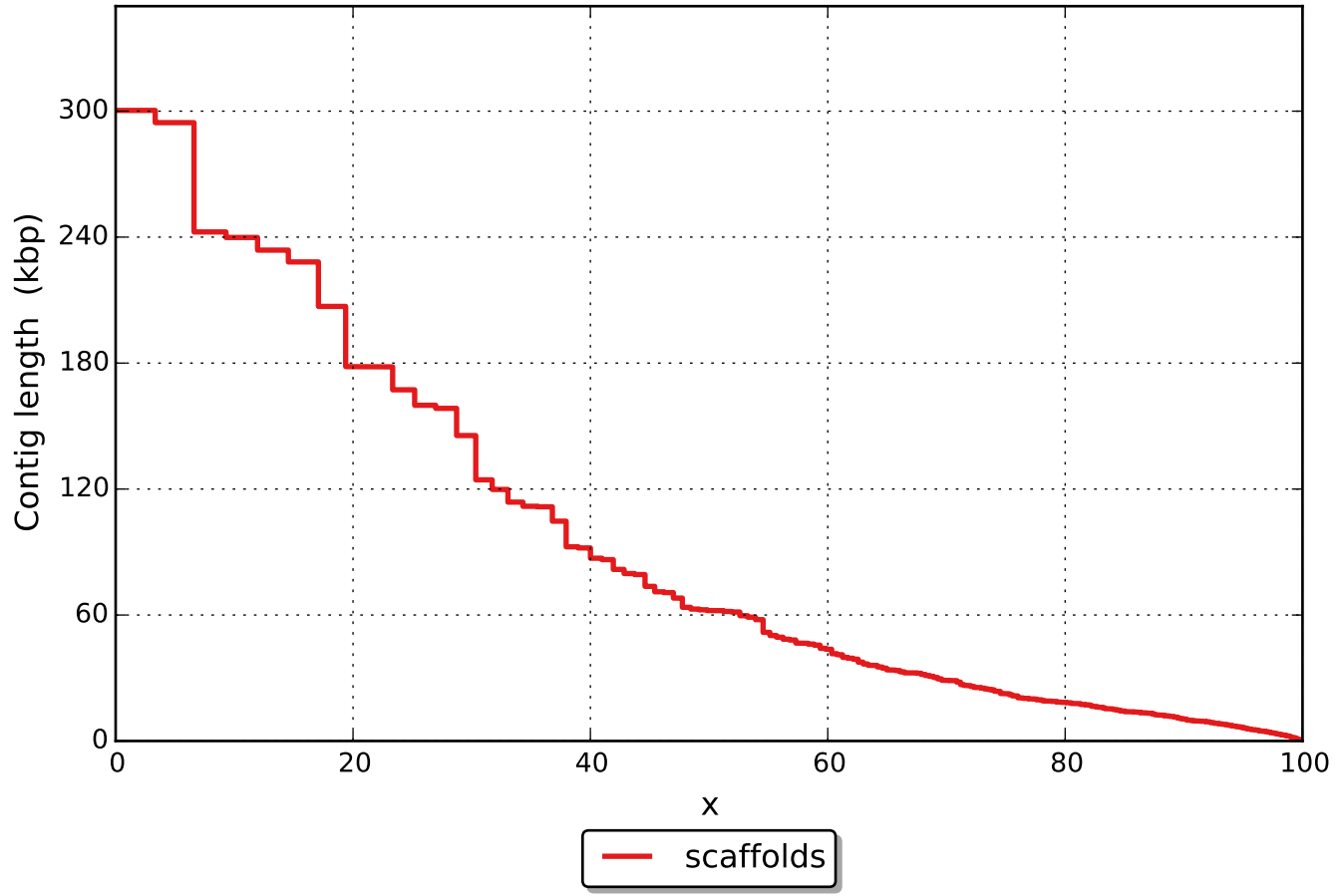
# Misassemblies







NAx



# NGAx

