

Report

	scaffolds
# contigs (≥ 1000 bp)	90
# contigs (≥ 5000 bp)	67
# contigs (≥ 10000 bp)	58
# contigs (≥ 25000 bp)	47
# contigs (≥ 50000 bp)	29
Total length (≥ 1000 bp)	4552031
Total length (≥ 5000 bp)	4502499
Total length (≥ 10000 bp)	4436896
Total length (≥ 25000 bp)	4255107
Total length (≥ 50000 bp)	3632805
# contigs	97
Largest contig	327072
Total length	4556946
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	132558
NG50	132558
N75	57779
NG75	56752
L50	12
LG50	12
L75	26
LG75	27
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	127522
# local misassemblies	7
# unaligned contigs	0 + 1 part
Unaligned length	189
Genome fraction (%)	98.105
Duplication ratio	1.001
# N's per 100 kbp	6.14
# mismatches per 100 kbp	62.32
# indels per 100 kbp	8.78
Largest alignment	327072
NA50	132558
NGA50	132558
NA75	56344
NGA75	54877
LA50	12
LGA50	12
LA75	26
LGA75	27

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	2
# relocations	2
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	127522
# local misassemblies	7
# mismatches	2838
# indels	400
# short indels	385
# long indels	15
Indels length	831

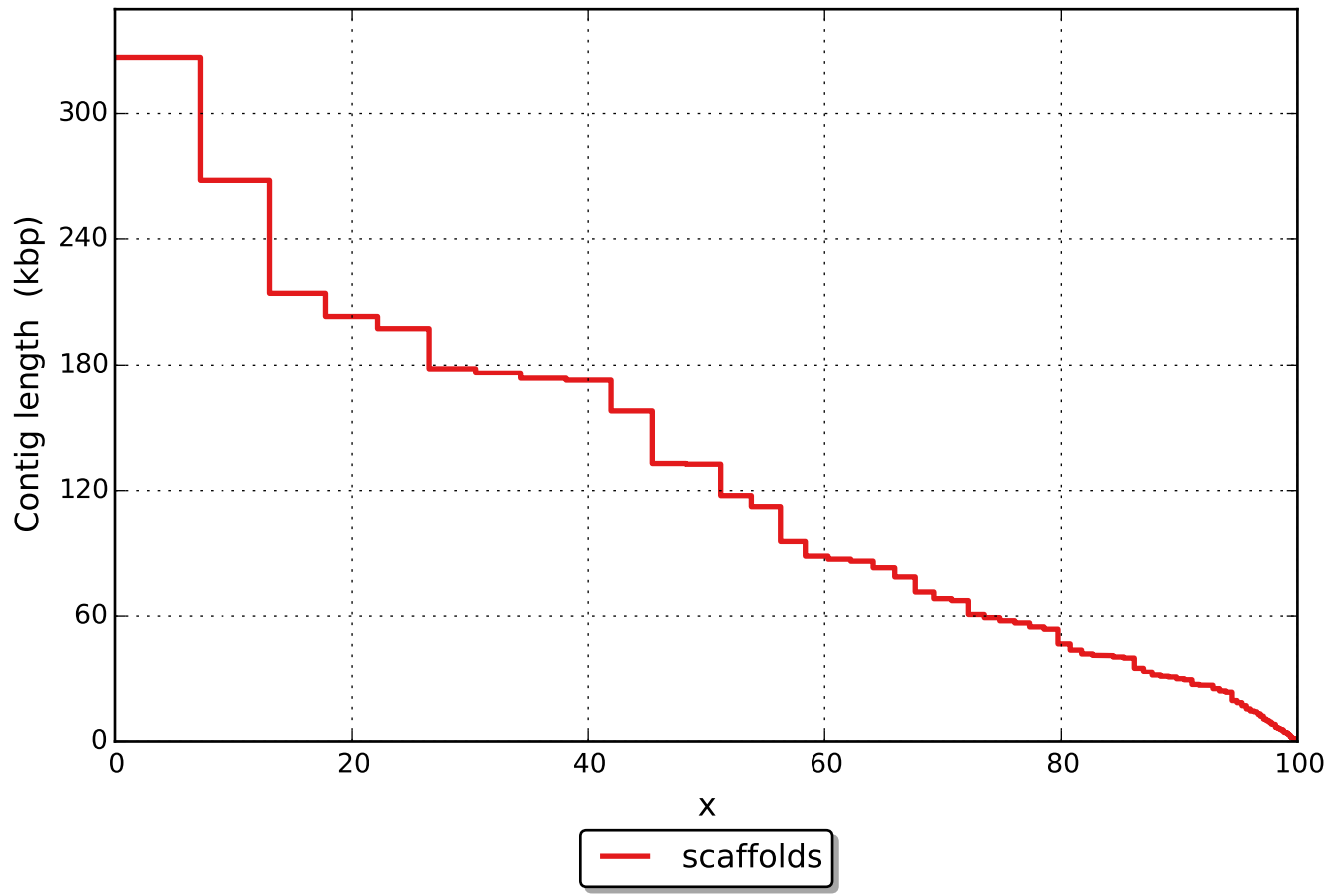
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

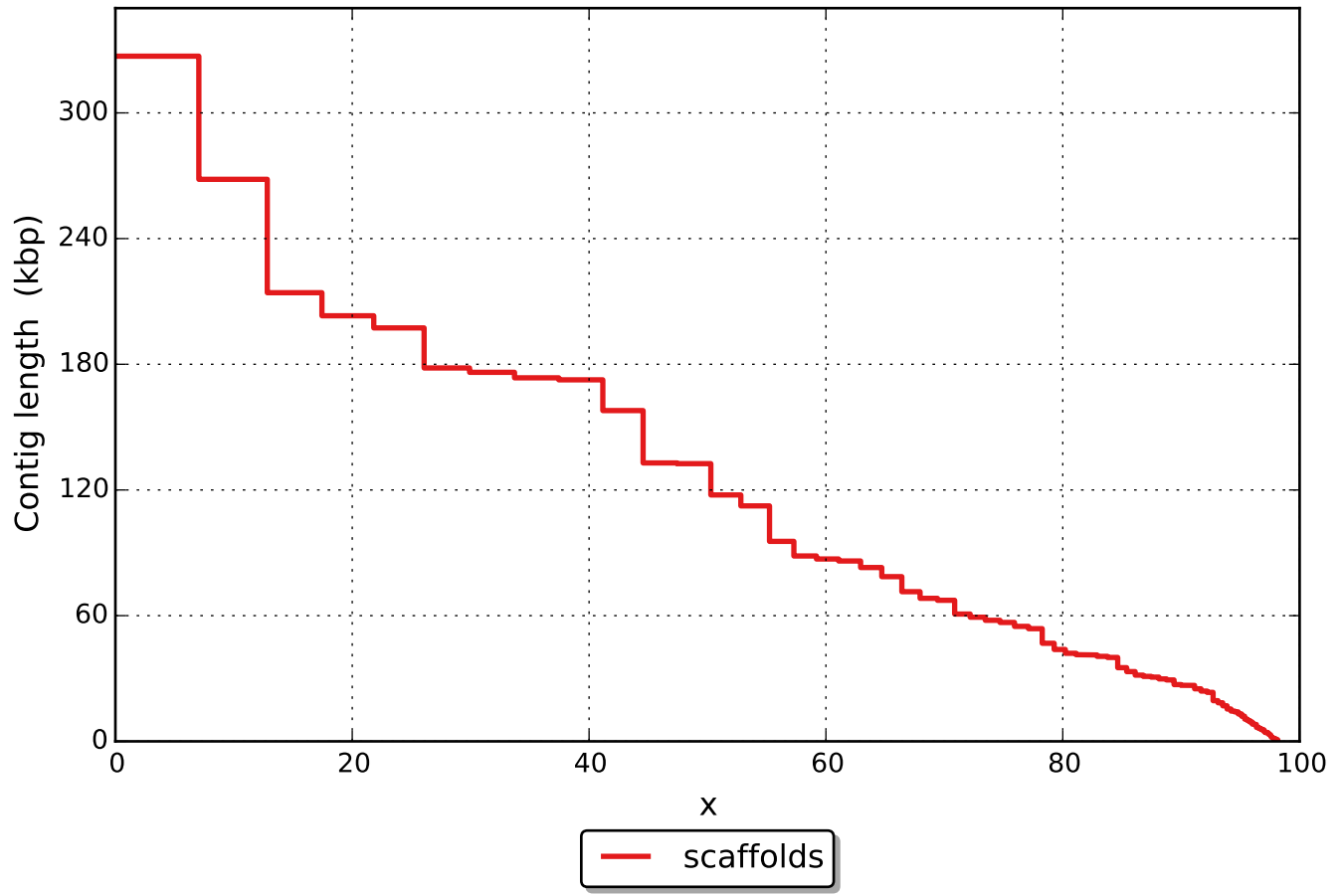
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	189
# N's	280

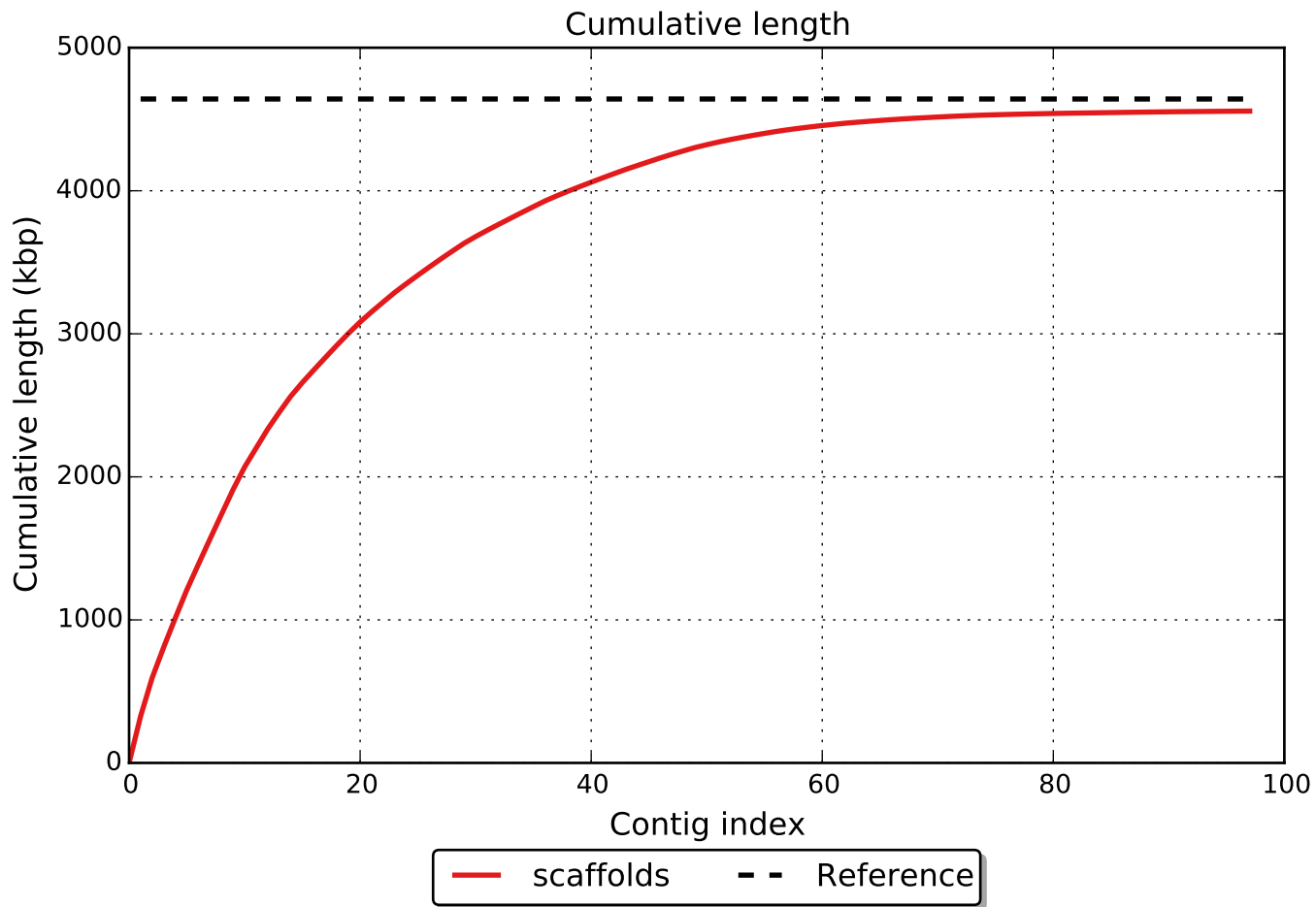
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

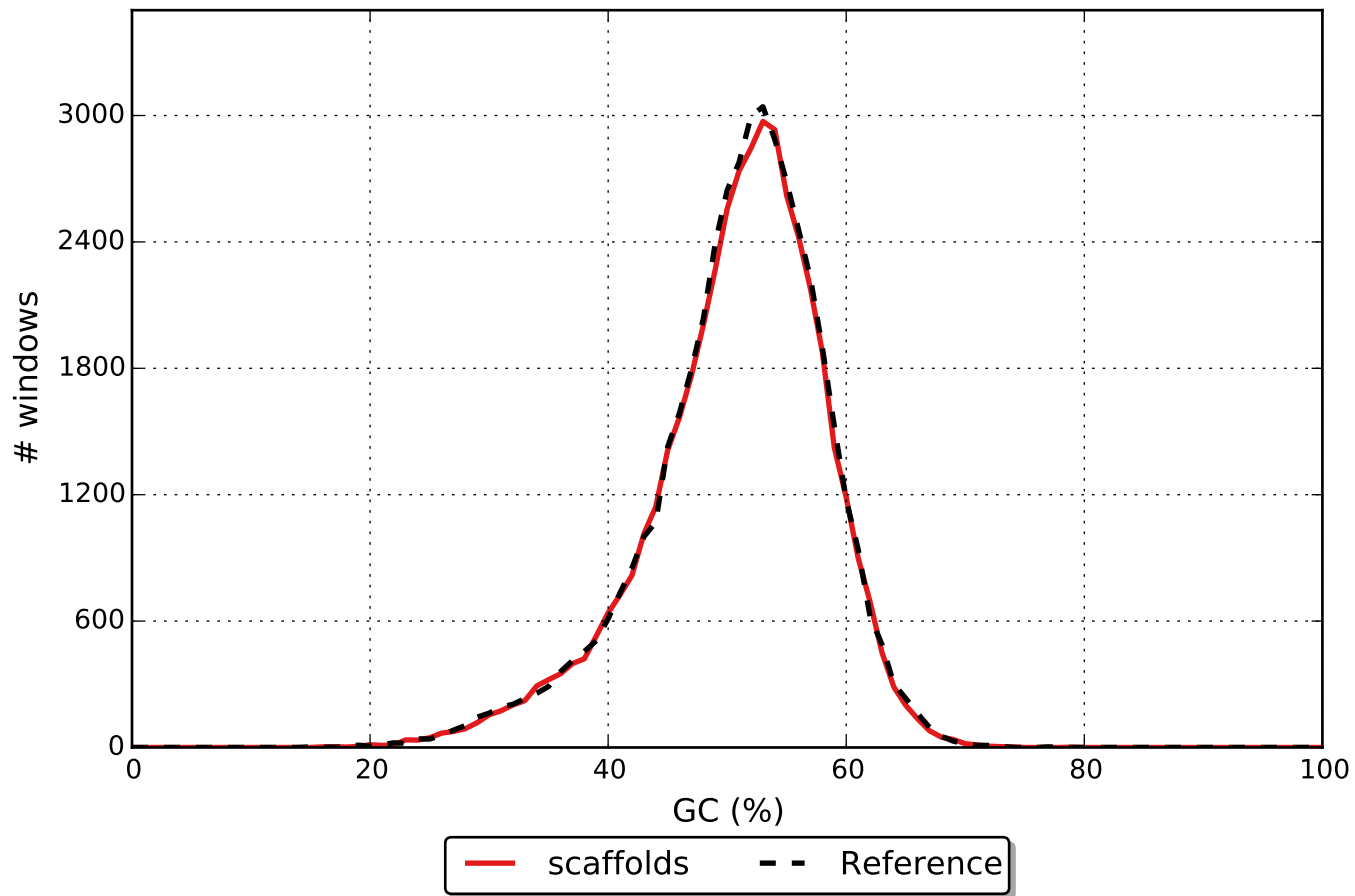


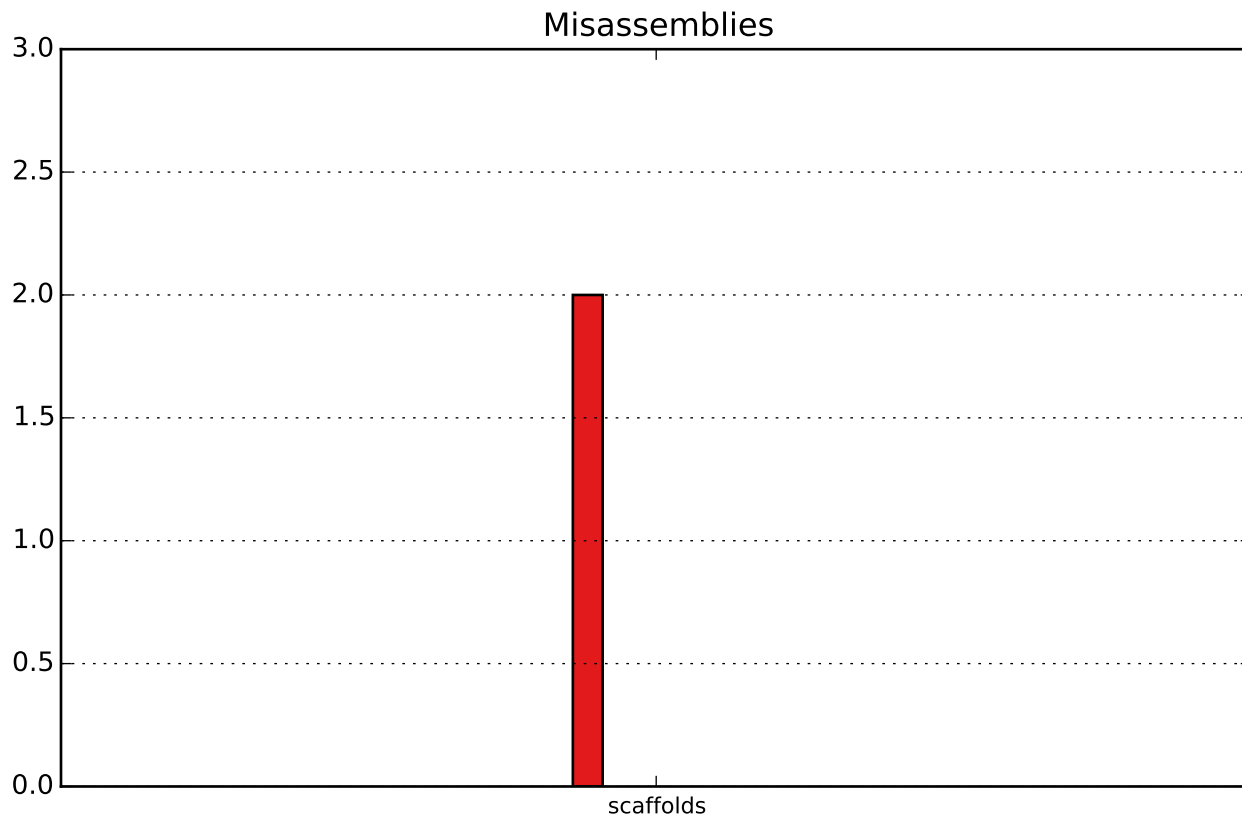
NGx



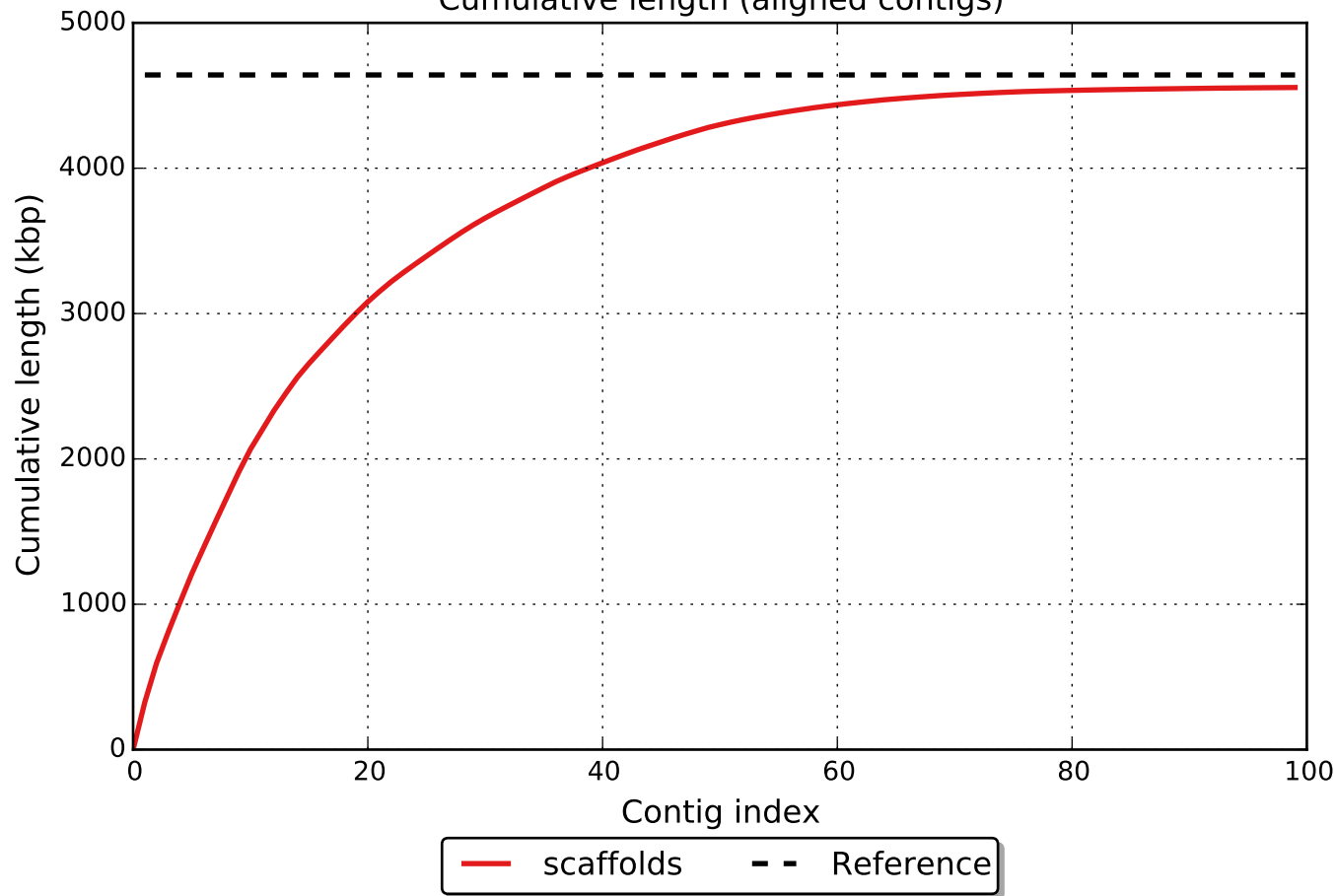


GC content

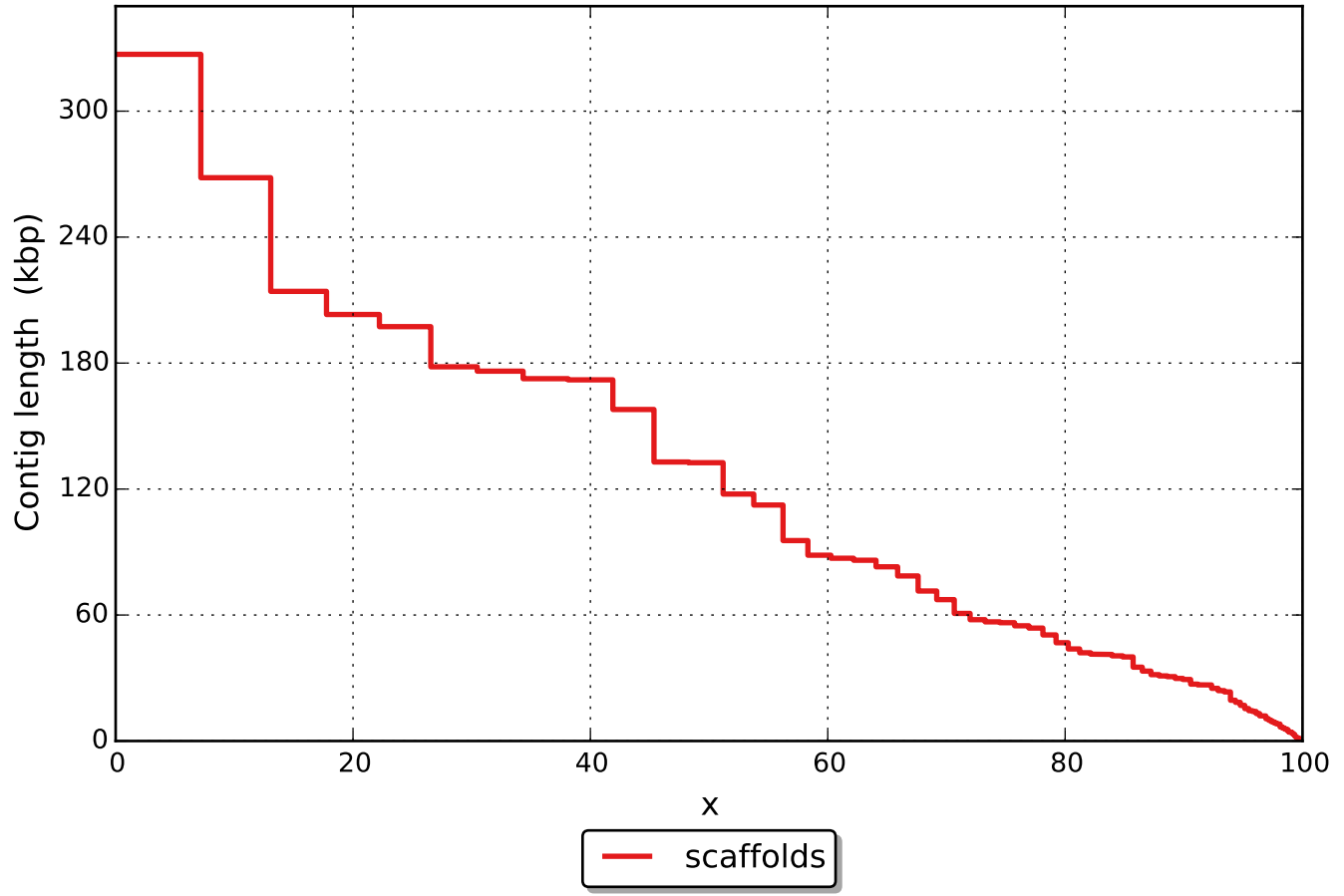




Cumulative length (aligned contigs)



NAx



NGAx

