

Report

	scaffolds
# contigs (≥ 1000 bp)	115
# contigs (≥ 5000 bp)	84
# contigs (≥ 10000 bp)	70
# contigs (≥ 25000 bp)	35
# contigs (≥ 50000 bp)	8
Total length (≥ 1000 bp)	2243579
Total length (≥ 5000 bp)	2175356
Total length (≥ 10000 bp)	2067231
Total length (≥ 25000 bp)	1518665
Total length (≥ 50000 bp)	562726
# contigs	135
Largest contig	132022
Total length	2256719
Reference length	4641652
GC (%)	50.83
Reference GC (%)	50.79
N50	32783
N75	17934
L50	23
L75	44
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	152553
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	47.297
Duplication ratio	1.028
# N's per 100 kbp	0.00
# mismatches per 100 kbp	845.83
# indels per 100 kbp	0.14
Largest alignment	132022
NA50	32783
NGA50	-
NA75	17754
LA50	23
LA75	46

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	4
# relocations	4
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	152553
# local misassemblies	2
# mismatches	18569
# indels	3
# short indels	3
# long indels	0
Indels length	5

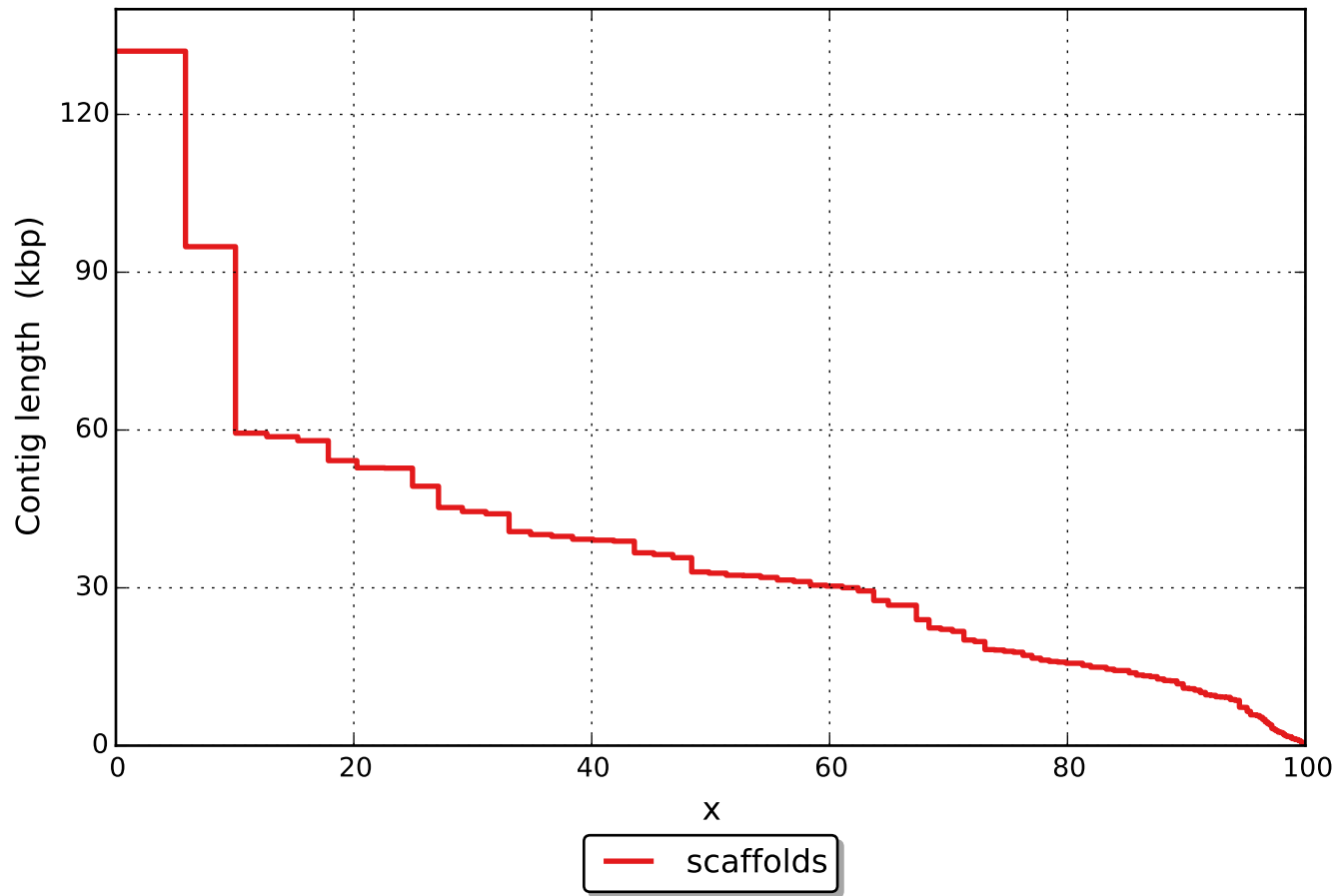
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

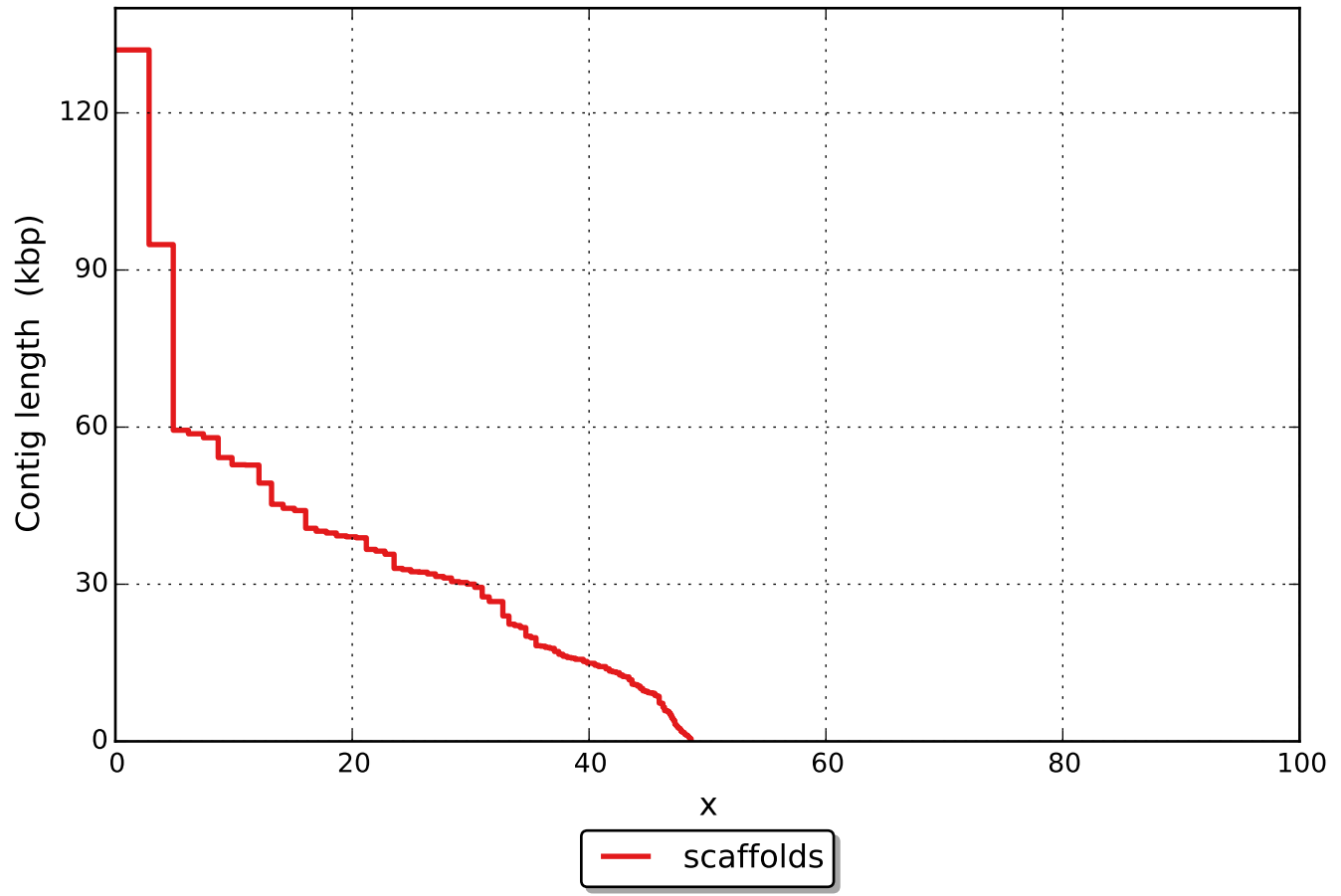
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

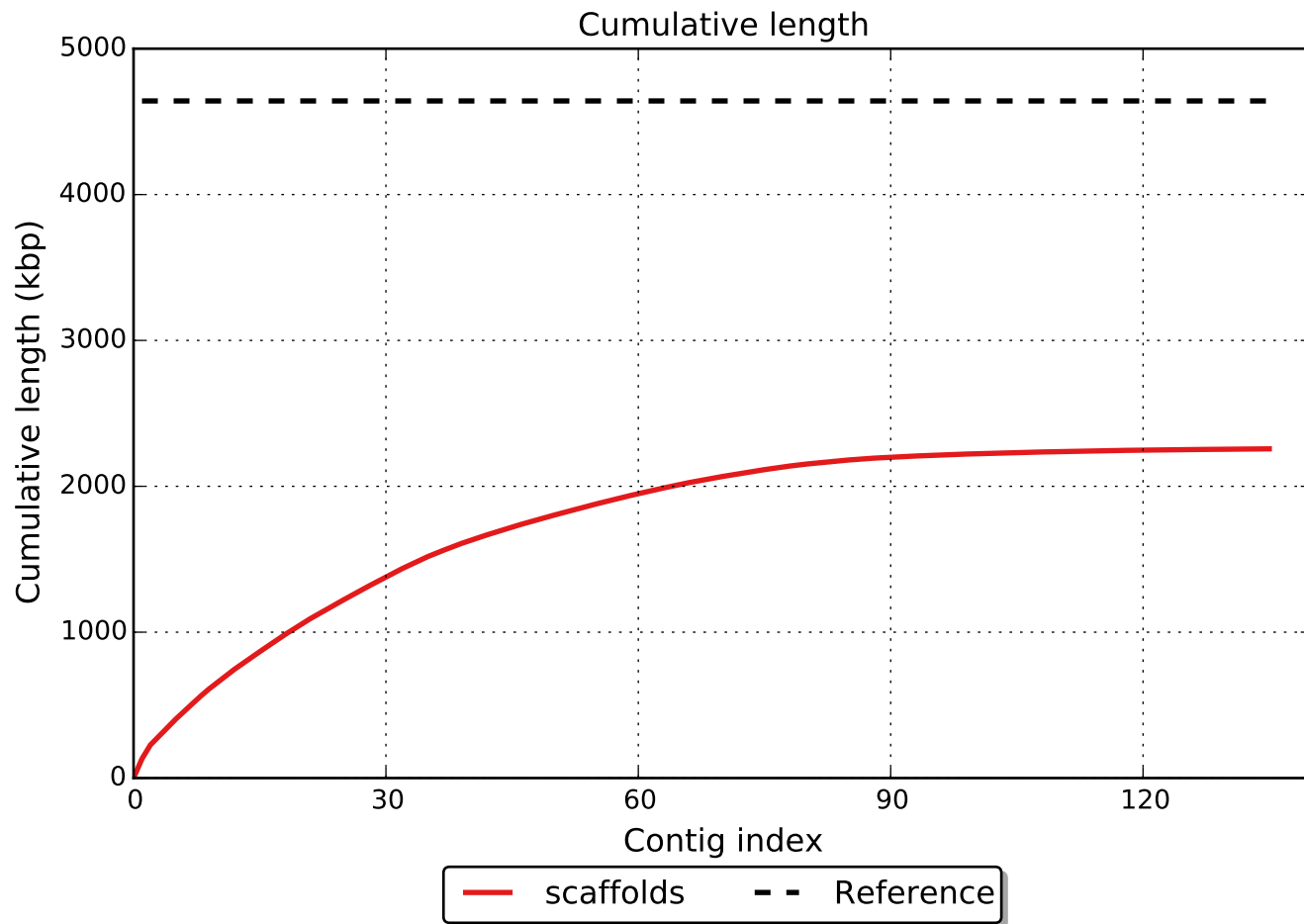
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

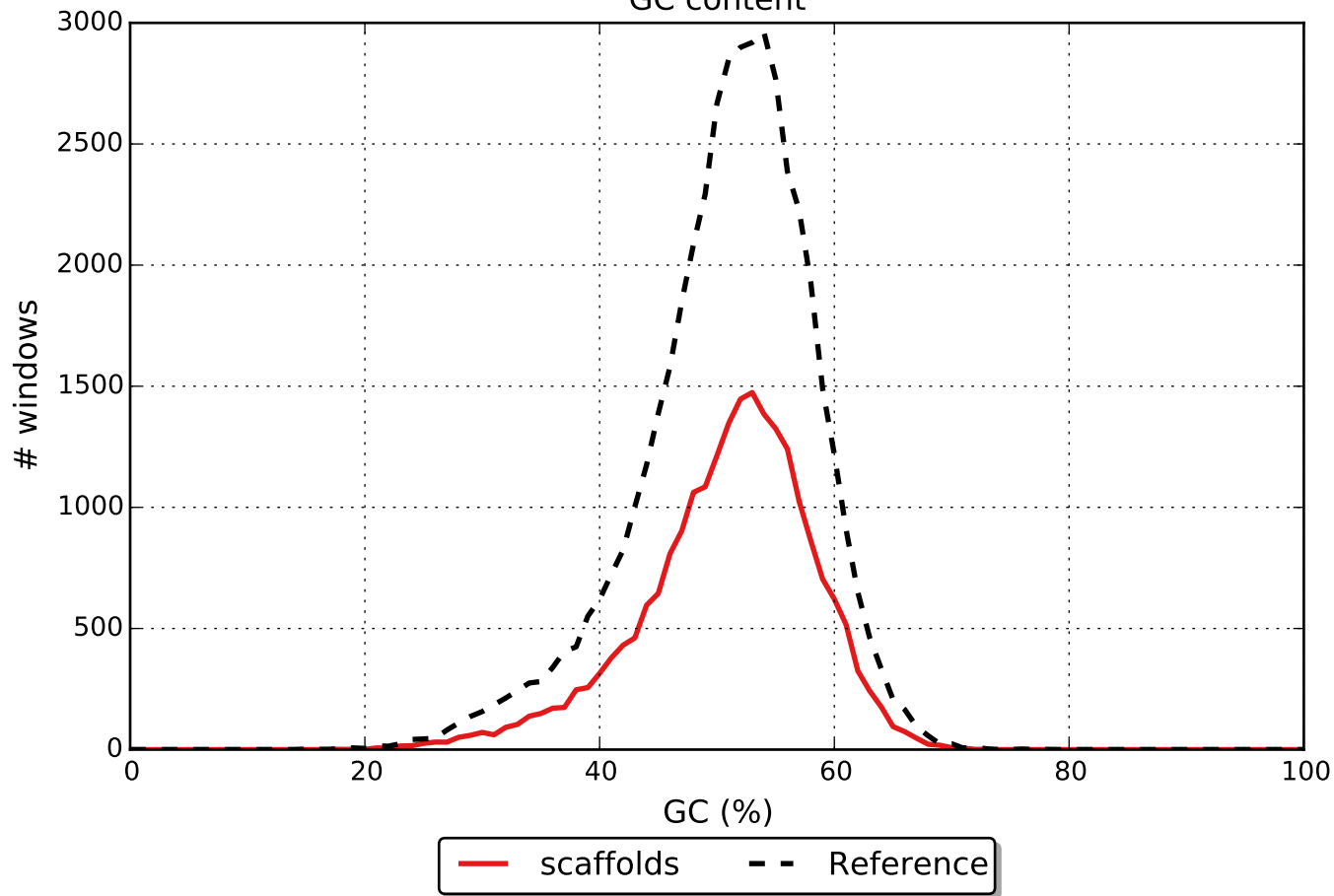


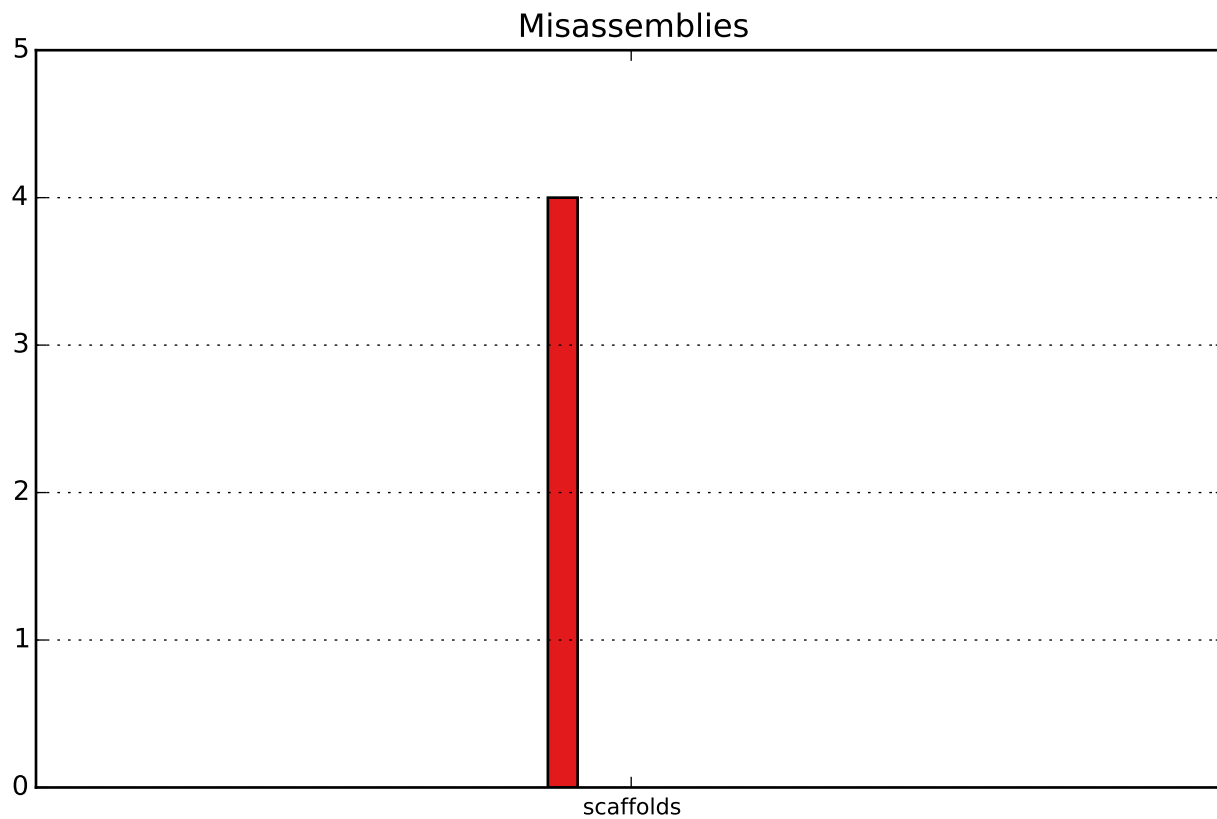
NGx



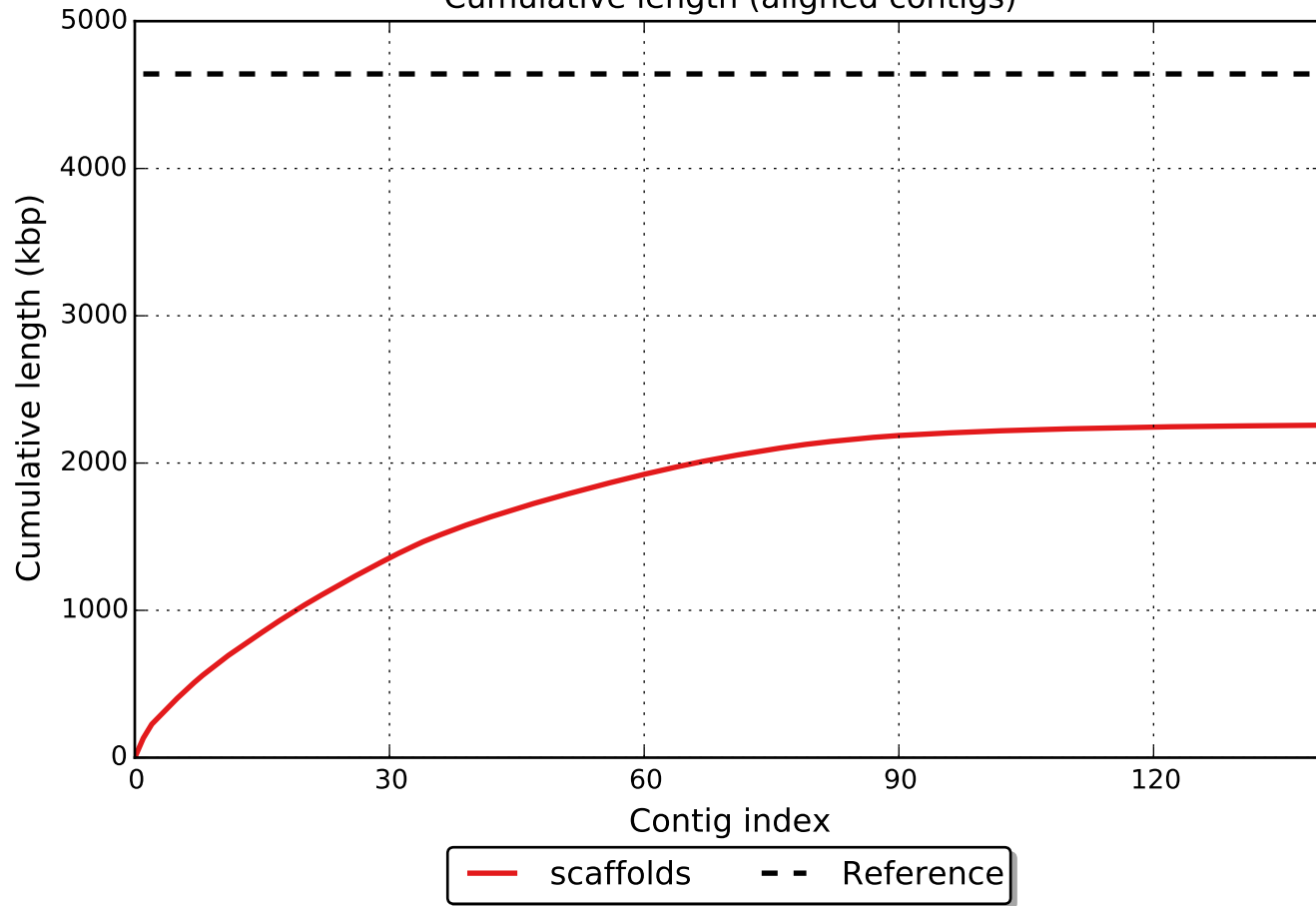


GC content

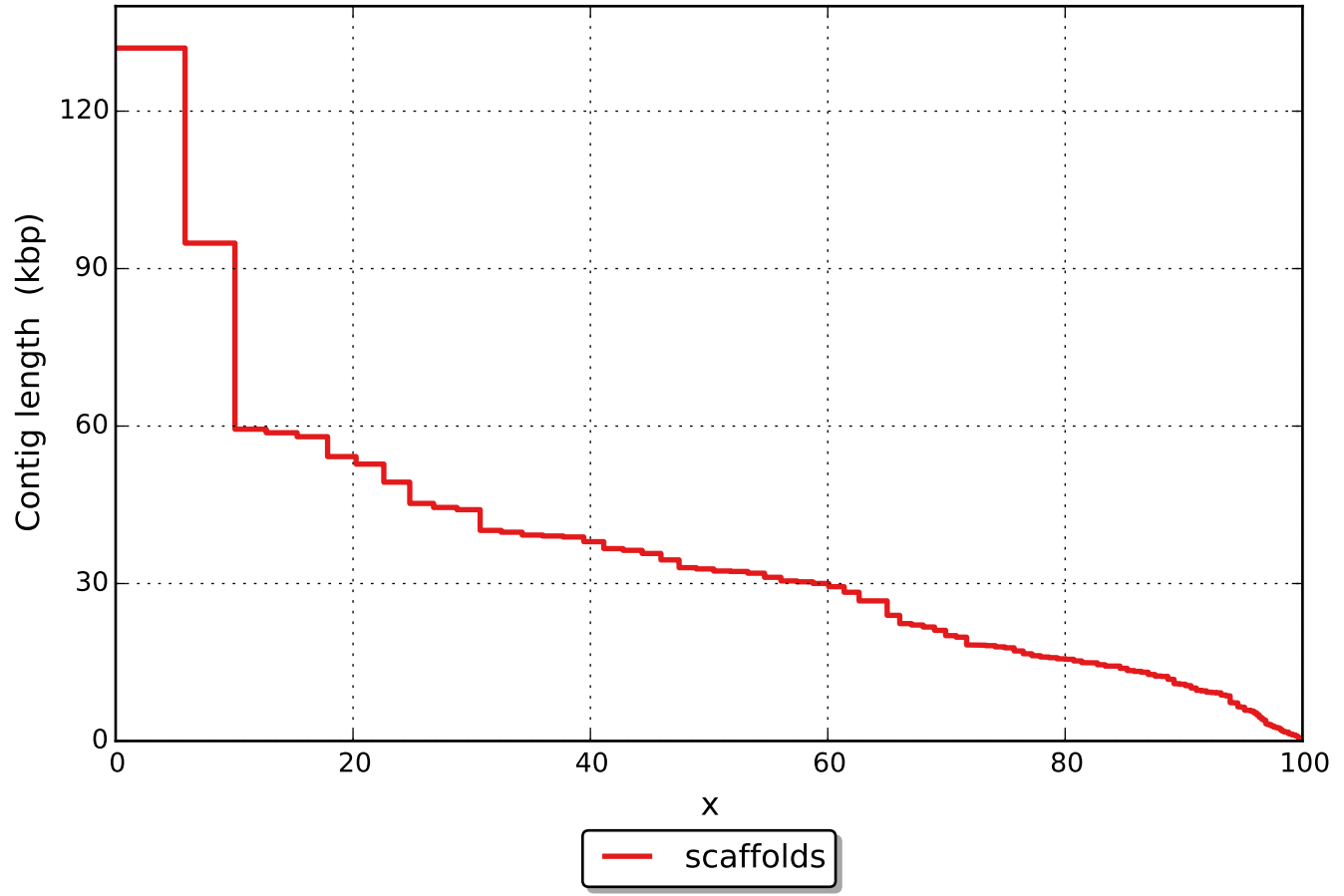




Cumulative length (aligned contigs)



NAx



NGAx

