

Report

	scaffolds
# contigs (≥ 1000 bp)	148
# contigs (≥ 5000 bp)	116
# contigs (≥ 10000 bp)	93
# contigs (≥ 25000 bp)	58
# contigs (≥ 50000 bp)	29
Total length (≥ 1000 bp)	4047801
Total length (≥ 5000 bp)	3969556
Total length (≥ 10000 bp)	3805004
Total length (≥ 25000 bp)	3260655
Total length (≥ 50000 bp)	2226729
# contigs	163
Largest contig	148188
Total length	4058103
Reference length	4641652
GC (%)	50.68
Reference GC (%)	50.79
N50	54906
NG50	44872
N75	32043
NG75	18062
L50	26
LG50	31
L75	51
LG75	69
# misassemblies	5
# misassembled contigs	5
Misassembled contigs length	475557
# local misassemblies	1
# unaligned contigs	0 + 1 part
Unaligned length	55
Genome fraction (%)	85.973
Duplication ratio	1.017
# N's per 100 kbp	0.00
# mismatches per 100 kbp	732.41
# indels per 100 kbp	0.28
Largest alignment	122264
NA50	51643
NGA50	40252
NA75	27744
NGA75	18062
LA50	27
LGA50	34
LA75	55
LGA75	74

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	5
# relocations	4
# translocations	0
# inversions	1
# possibly misassembled contigs	0
# misassembled contigs	5
Misassembled contigs length	475557
# local misassemblies	1
# mismatches	29227
# indels	11
# short indels	11
# long indels	0
Indels length	12

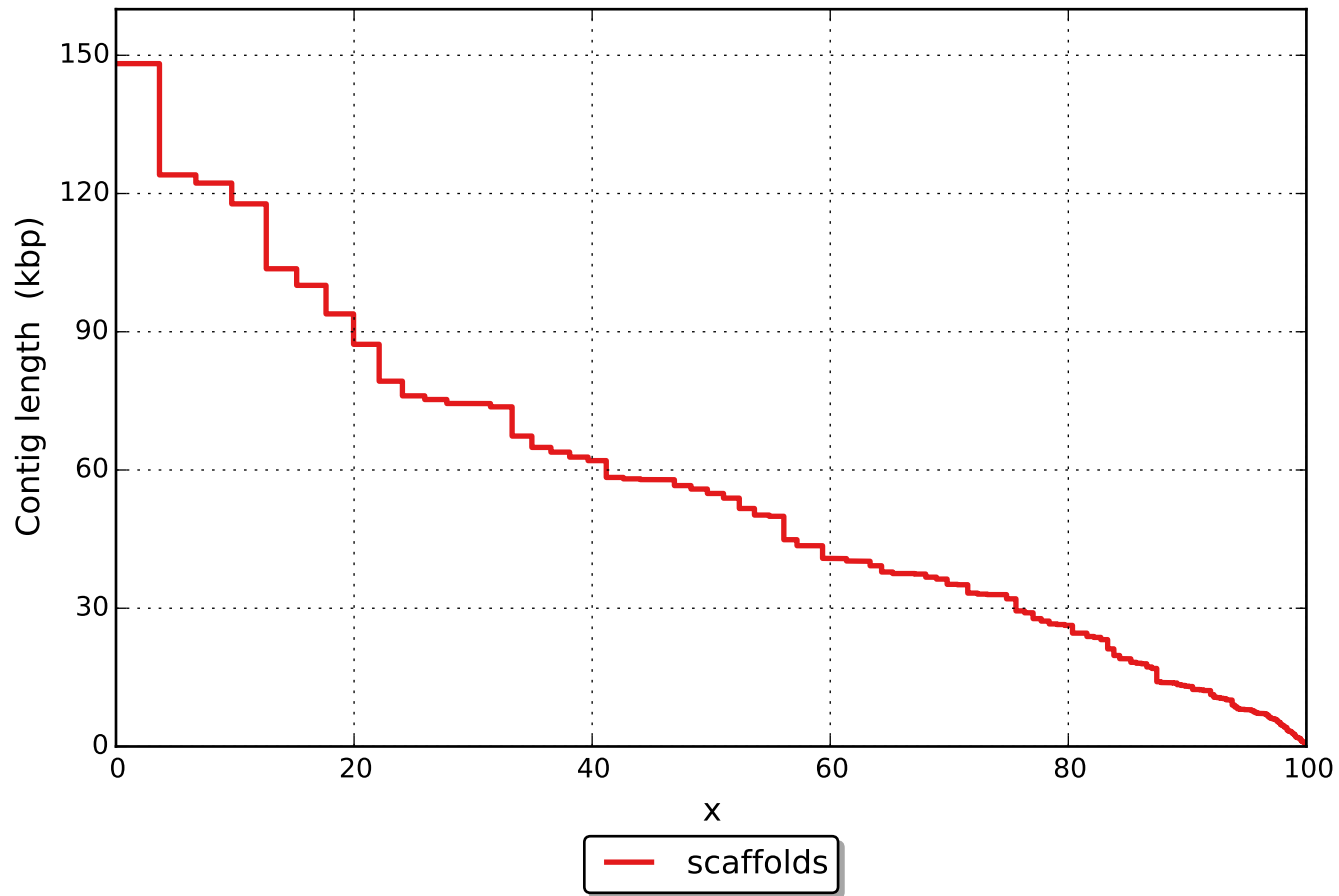
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

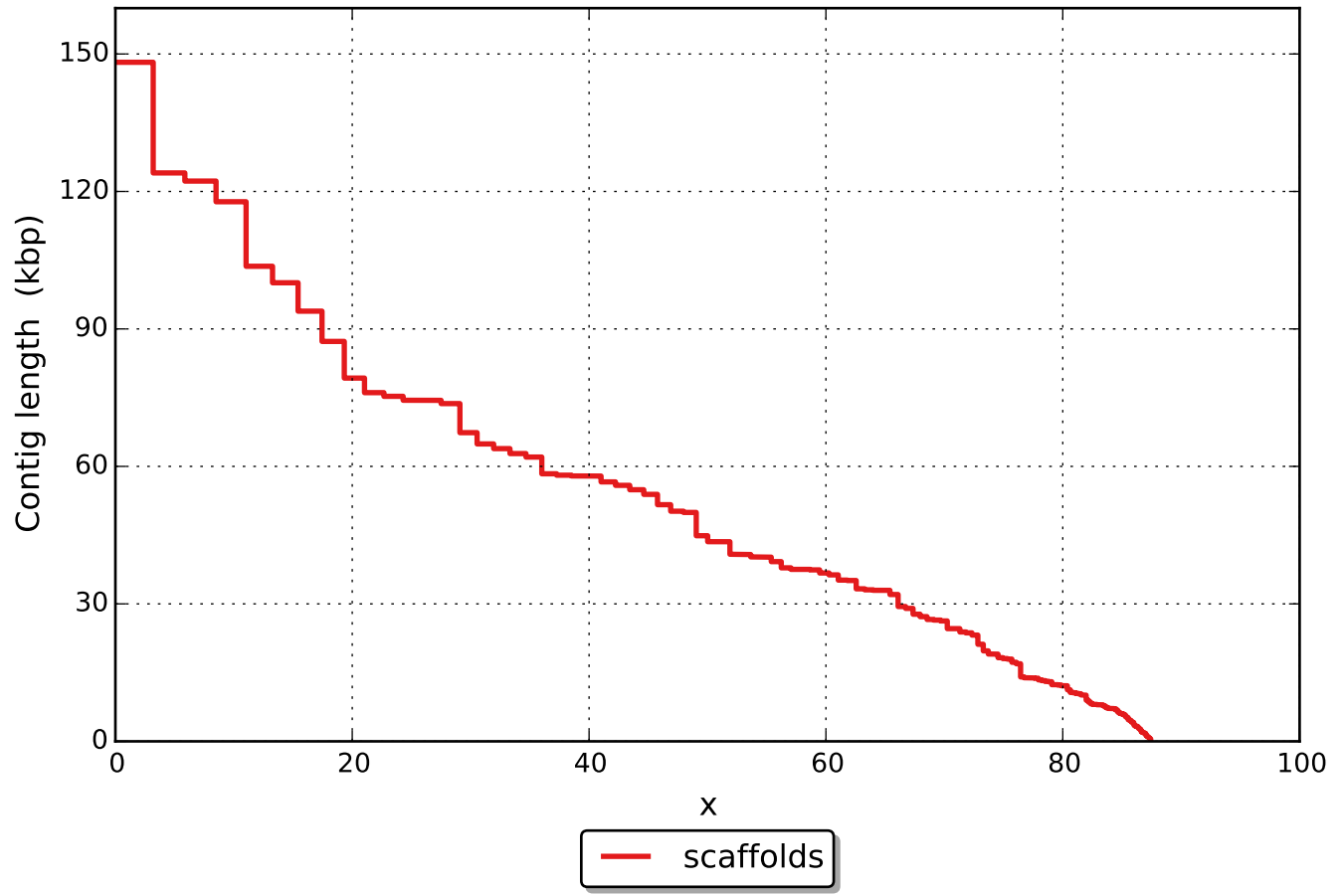
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	55
# N's	0

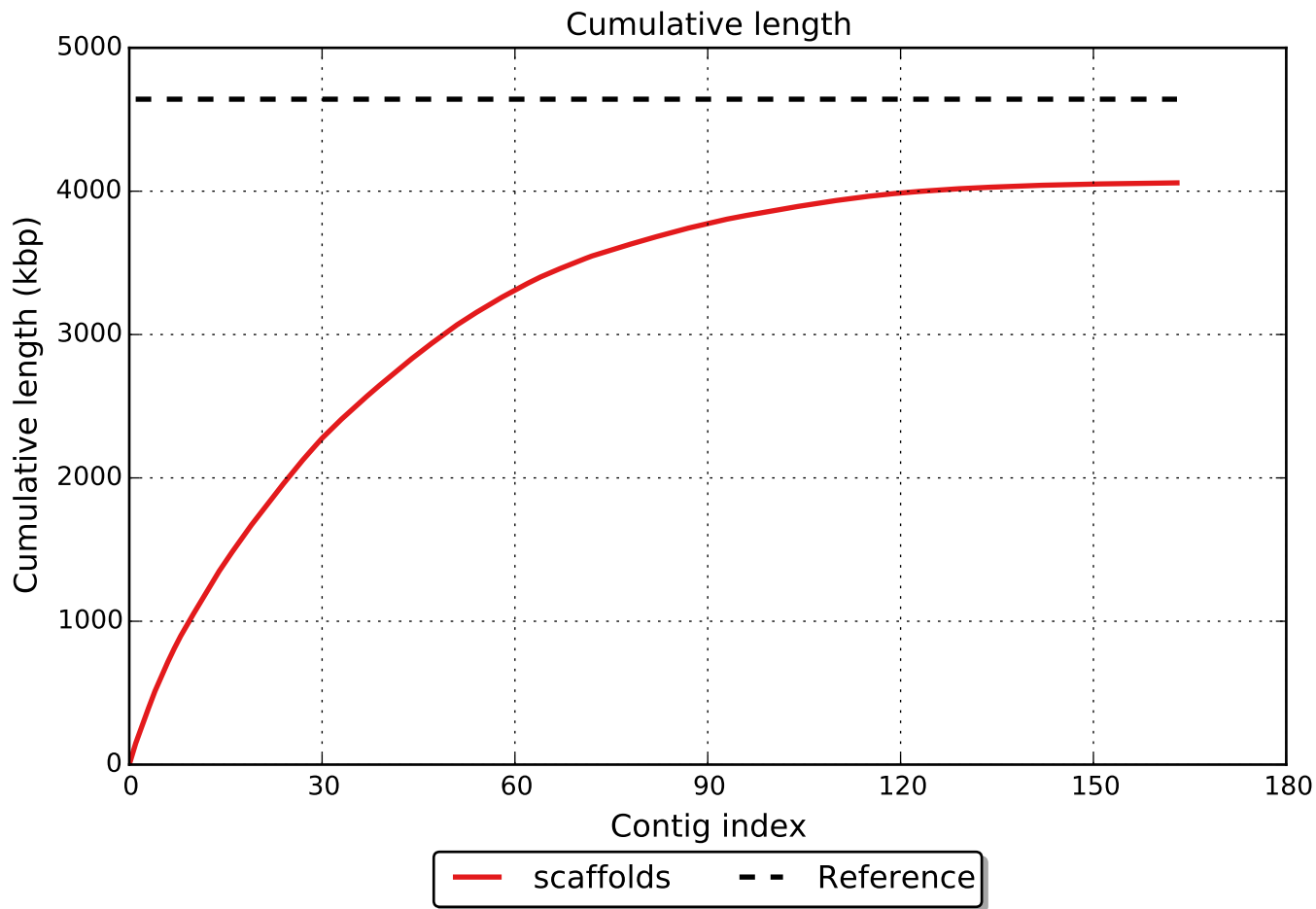
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

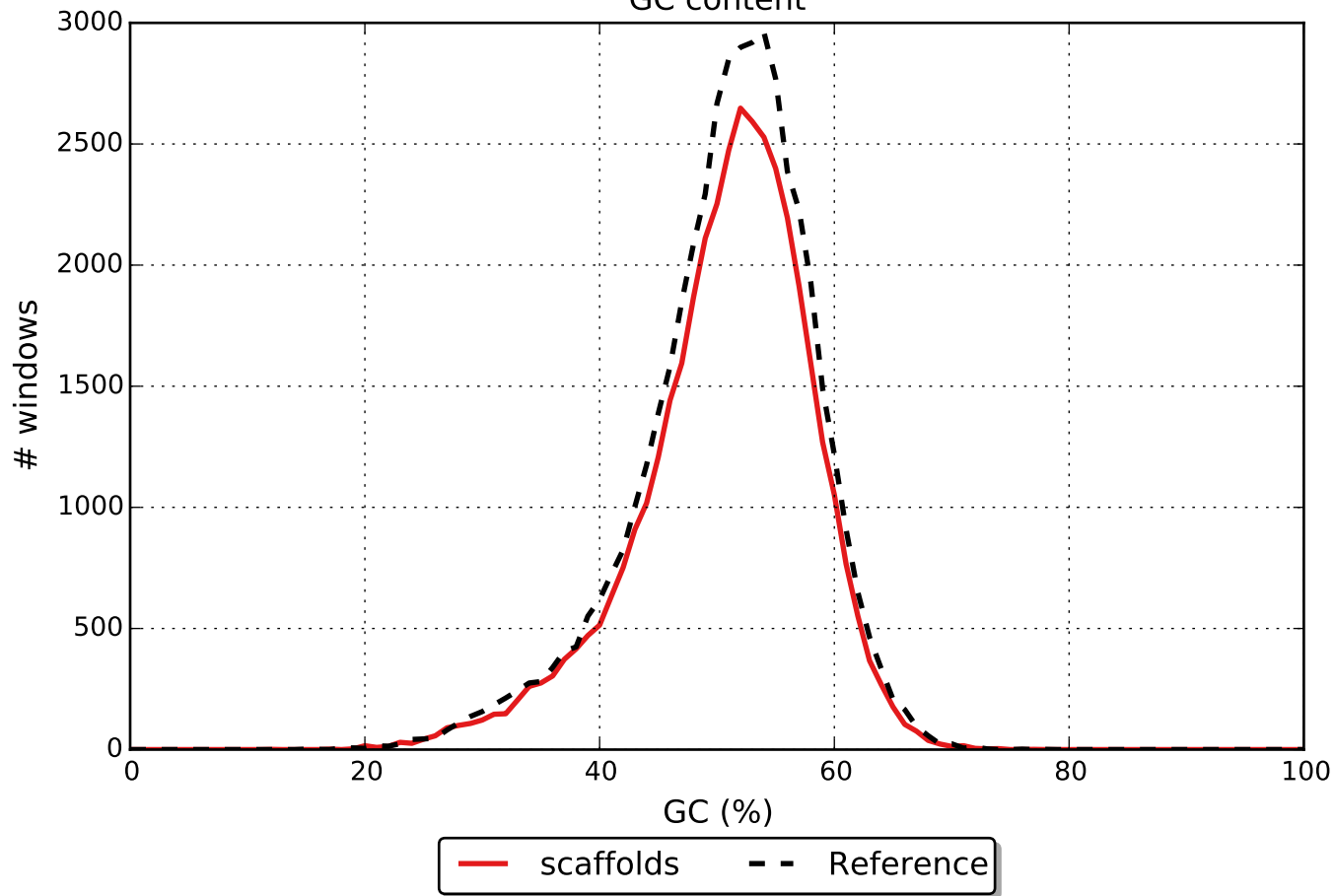


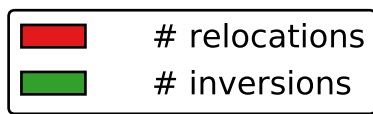
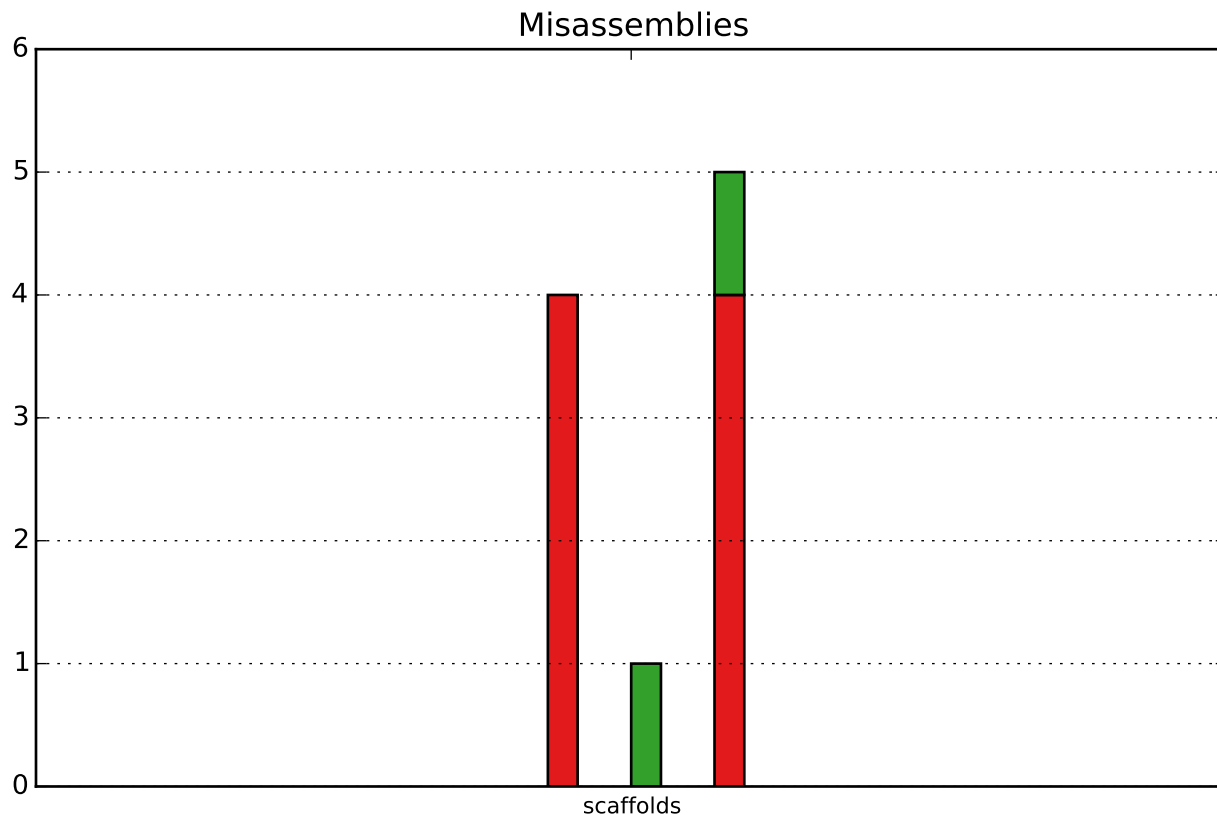
NGx



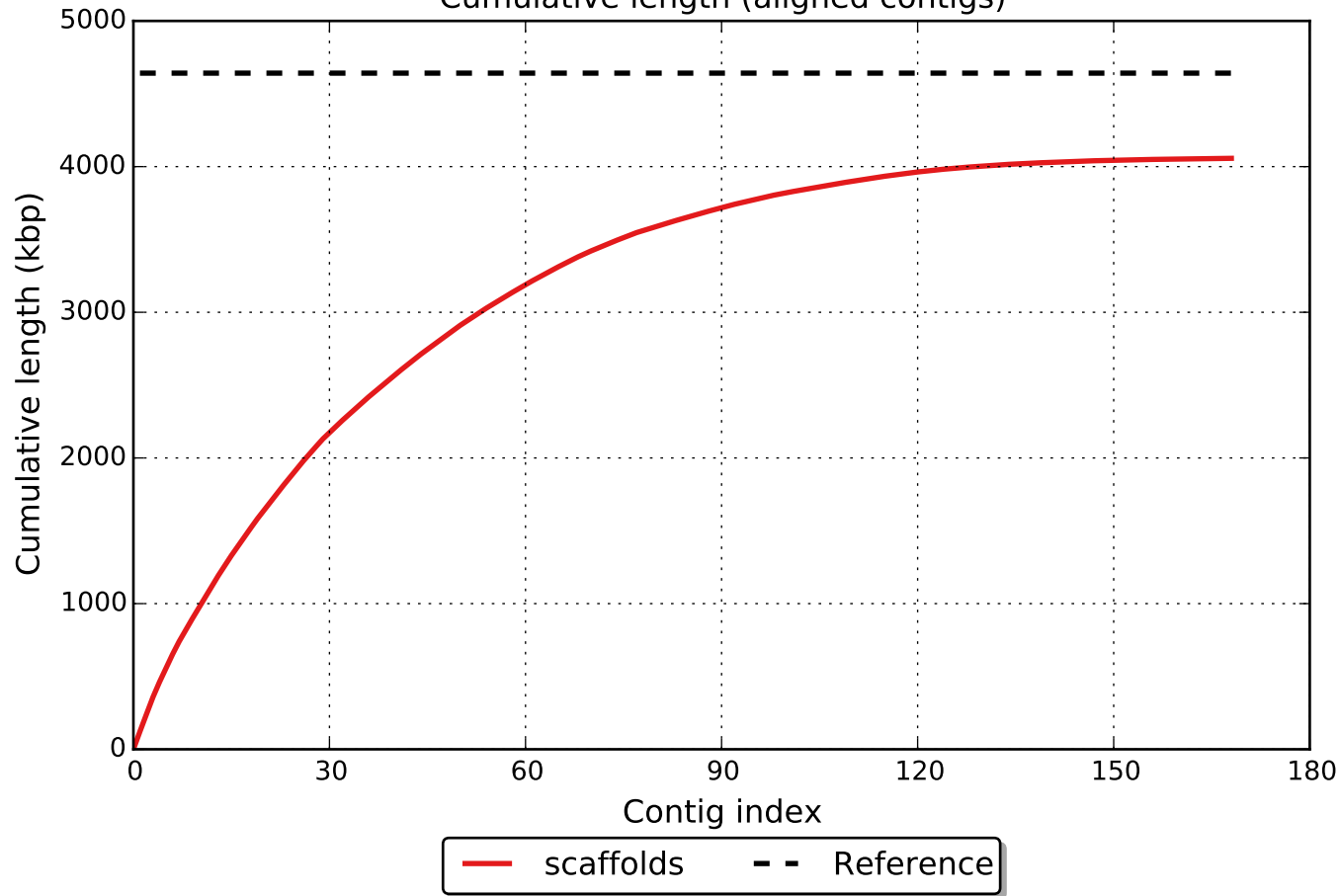


GC content

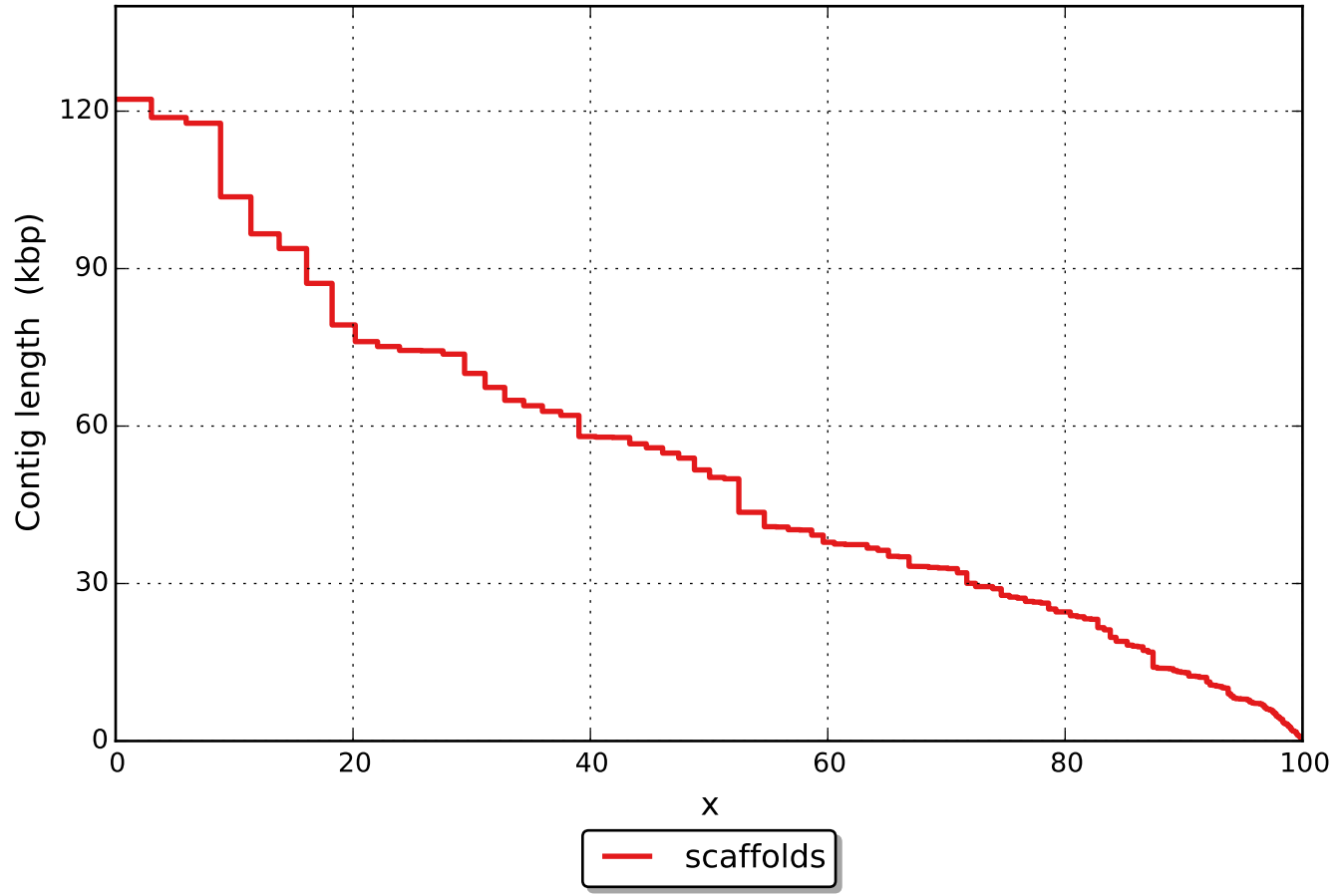




Cumulative length (aligned contigs)



NAx



NGAx

