

Report

	scaffolds
# contigs (≥ 1000 bp)	146
# contigs (≥ 5000 bp)	117
# contigs (≥ 10000 bp)	93
# contigs (≥ 25000 bp)	58
# contigs (≥ 50000 bp)	26
Total length (≥ 1000 bp)	3925106
Total length (≥ 5000 bp)	3850531
Total length (≥ 10000 bp)	3681144
Total length (≥ 25000 bp)	3130123
Total length (≥ 50000 bp)	1957319
# contigs	157
Largest contig	148188
Total length	3932767
Reference length	4641652
GC (%)	50.69
Reference GC (%)	50.78
N50	49952
NG50	40252
N75	32043
NG75	13768
L50	27
LG50	35
L75	52
LG75	77
# misassemblies	5
# misassembled contigs	5
Misassembled contigs length	475557
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	83.212
Duplication ratio	1.018
# N's per 100 kbp	93.80
# mismatches per 100 kbp	746.56
# indels per 100 kbp	0.80
Largest alignment	122264
NA50	48914
NGA50	39220
NA75	29421
NGA75	13365
LA50	29
LGA50	38
LA75	56
LGA75	81

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	2
# misassembled contigs	5
Misassembled contigs length	475557
# local misassemblies	4
# mismatches	28835
# indels	31
# short indels	20
# long indels	11
Indels length	631

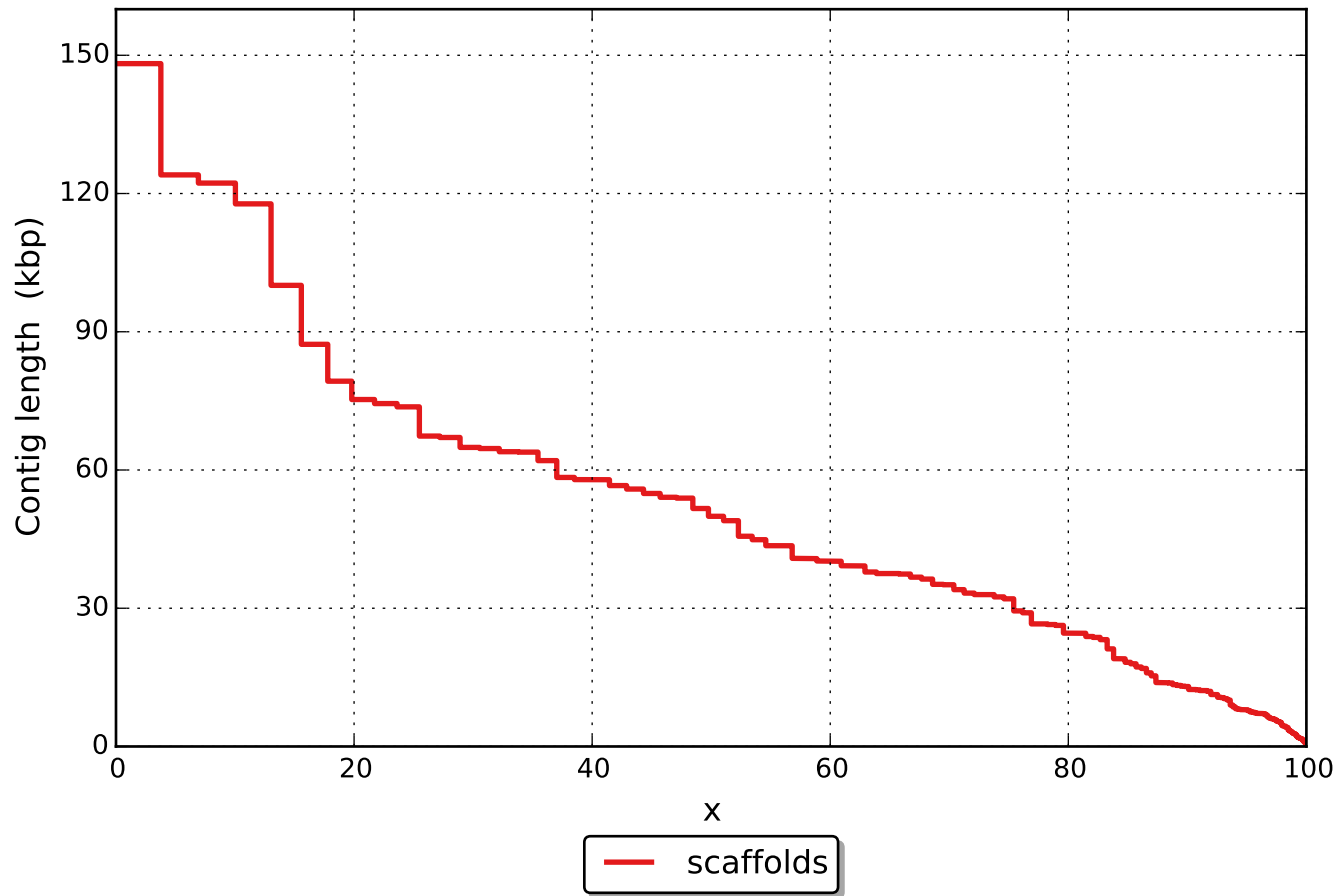
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

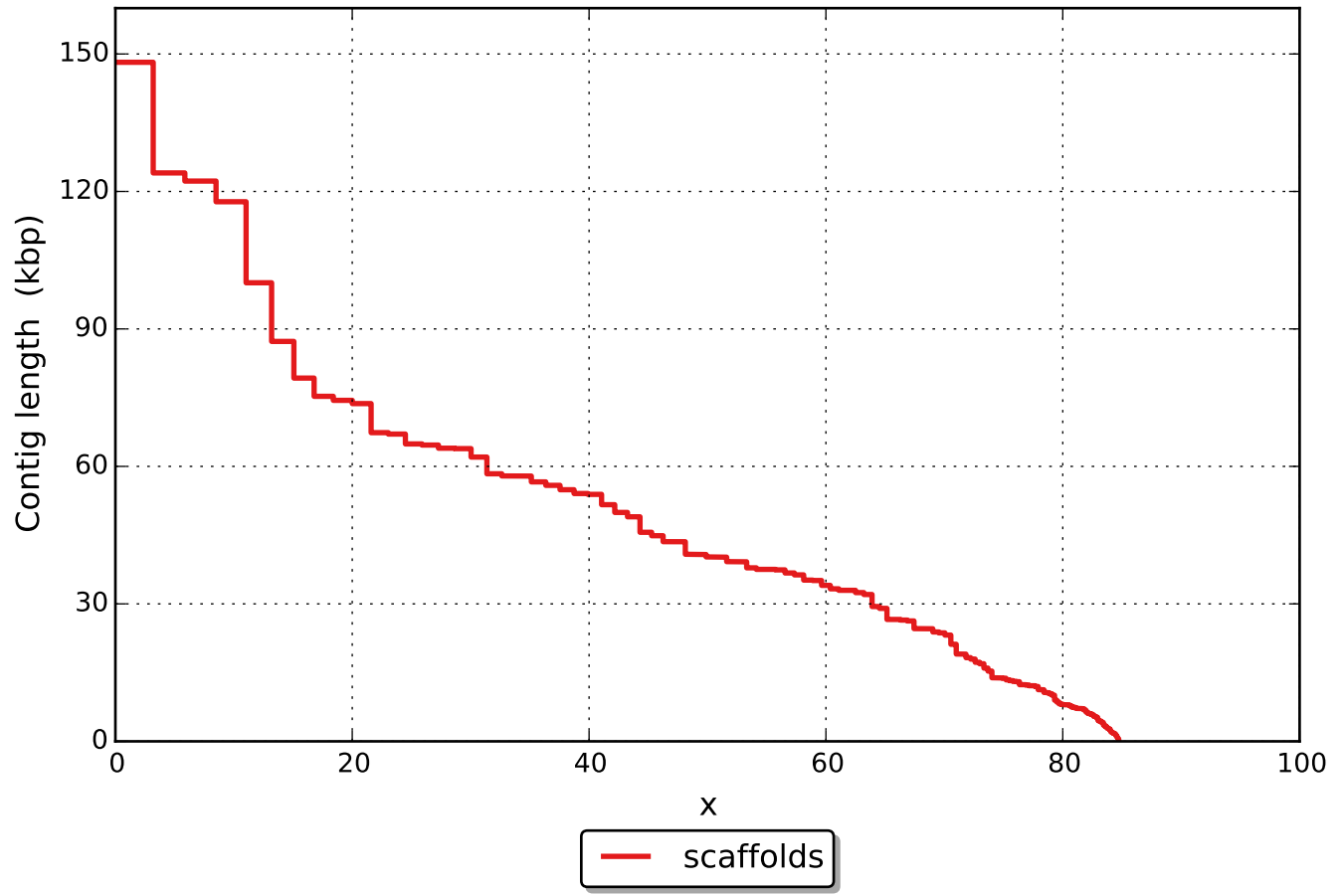
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	3689

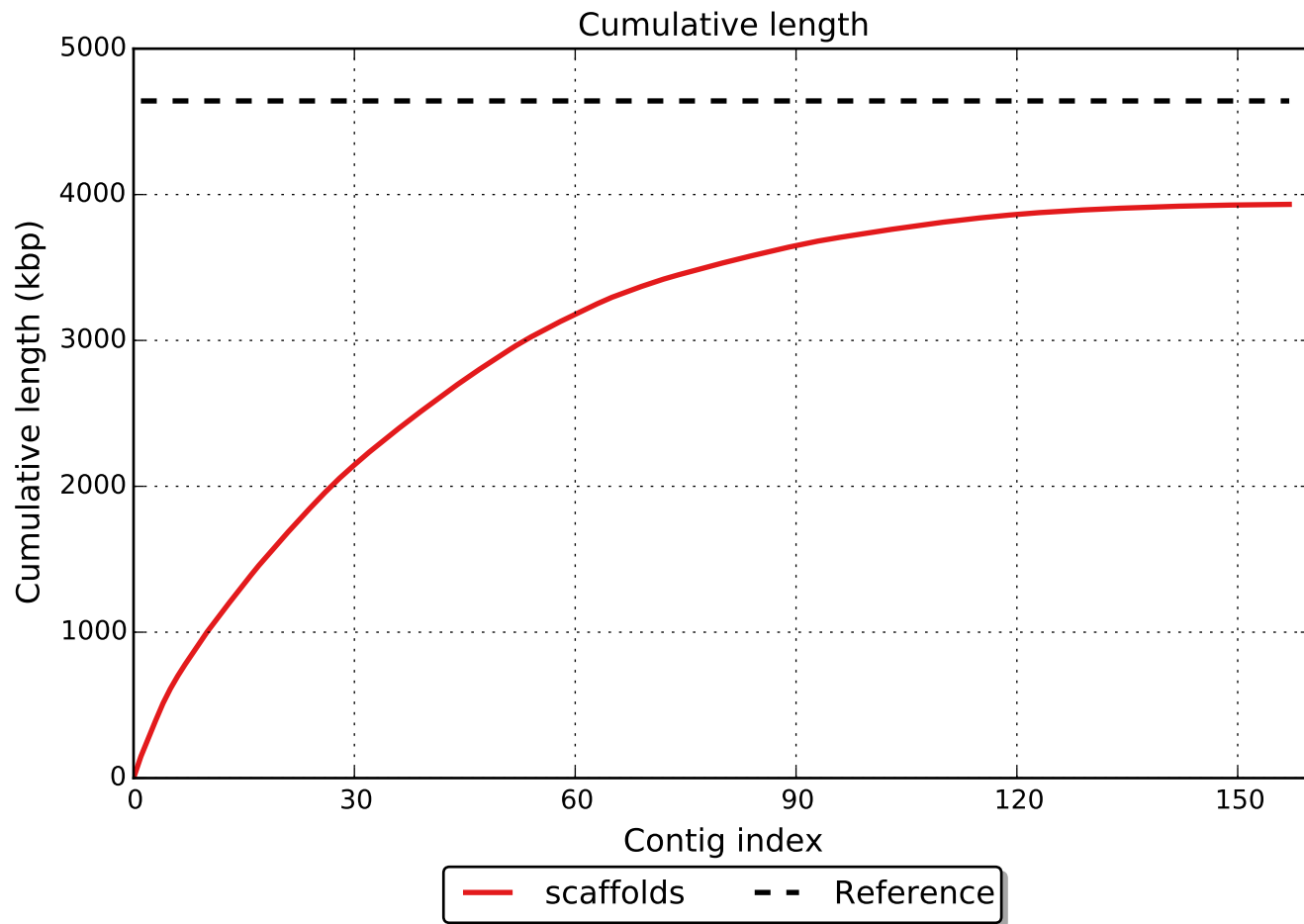
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

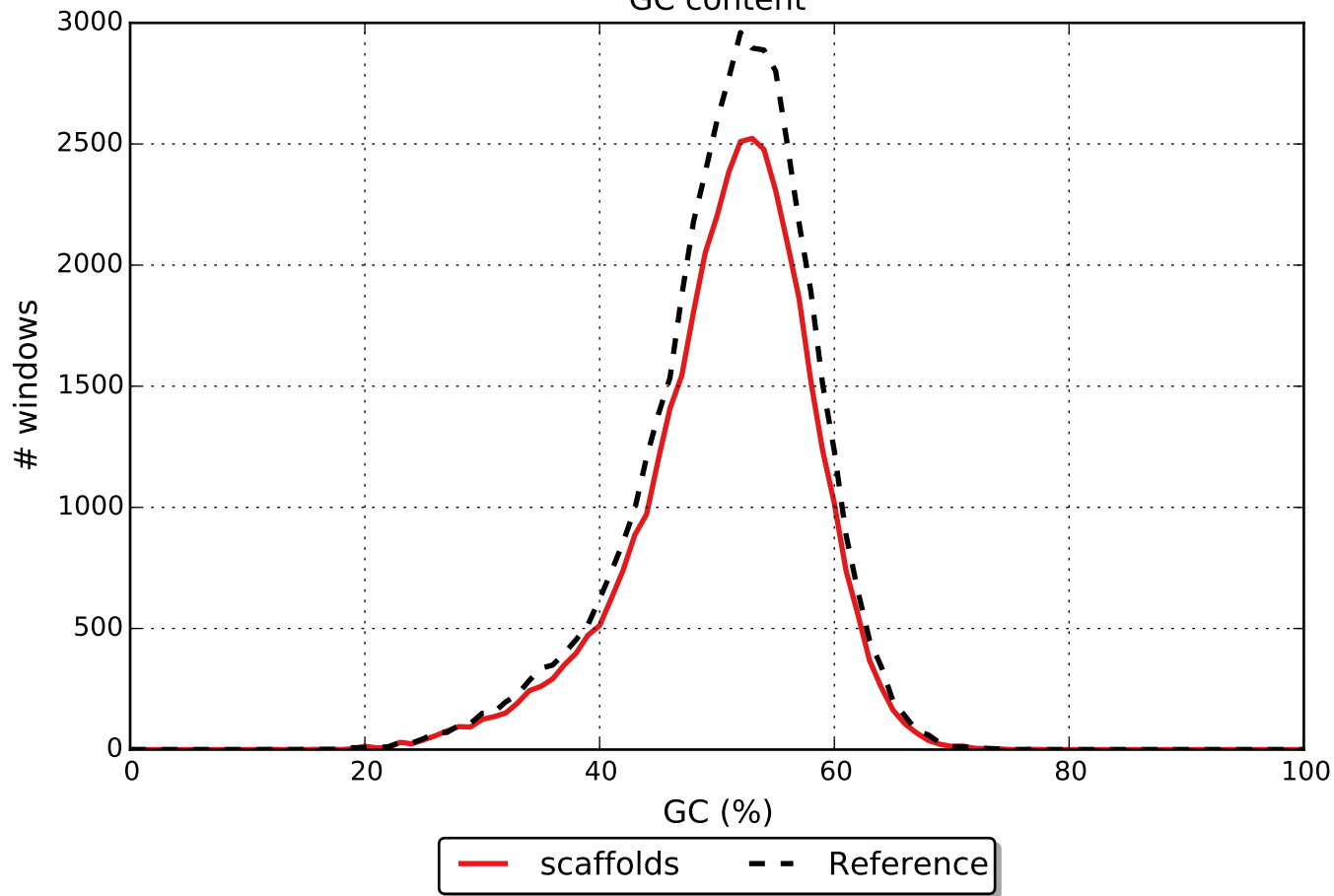


NGx

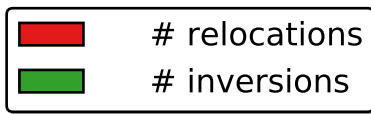
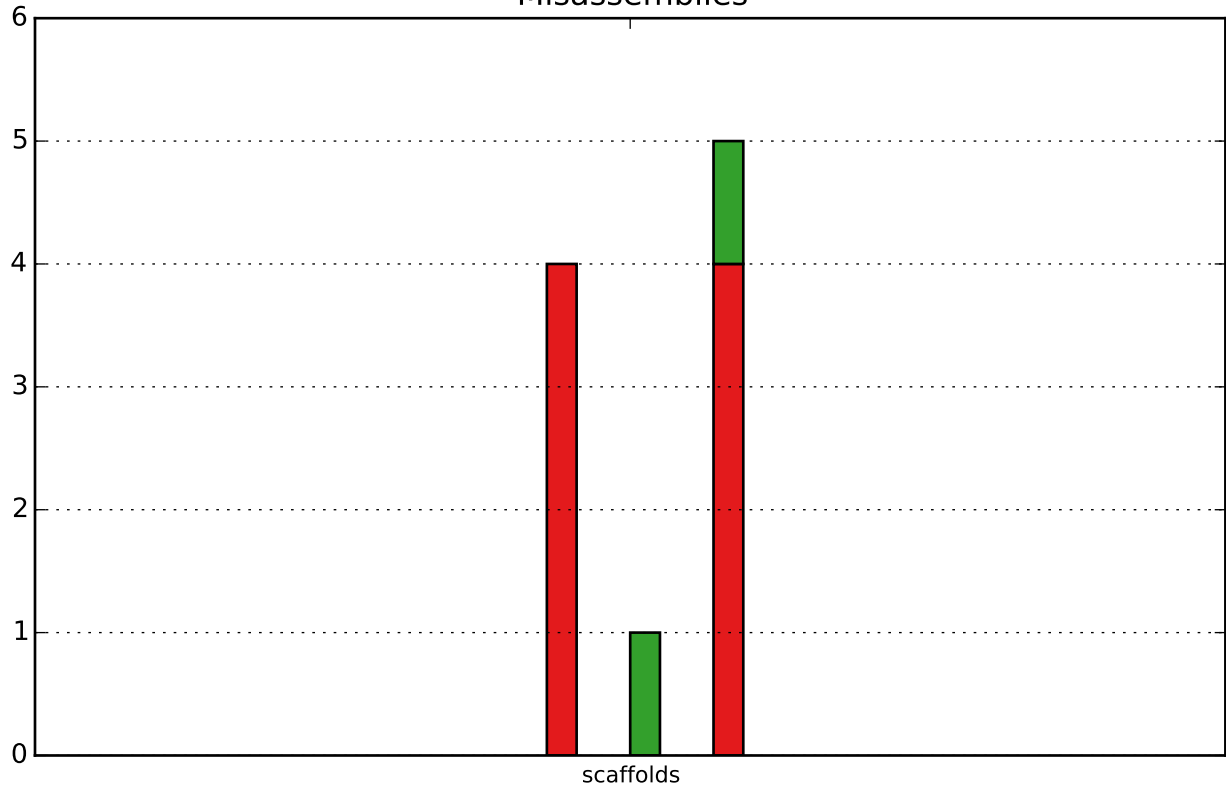




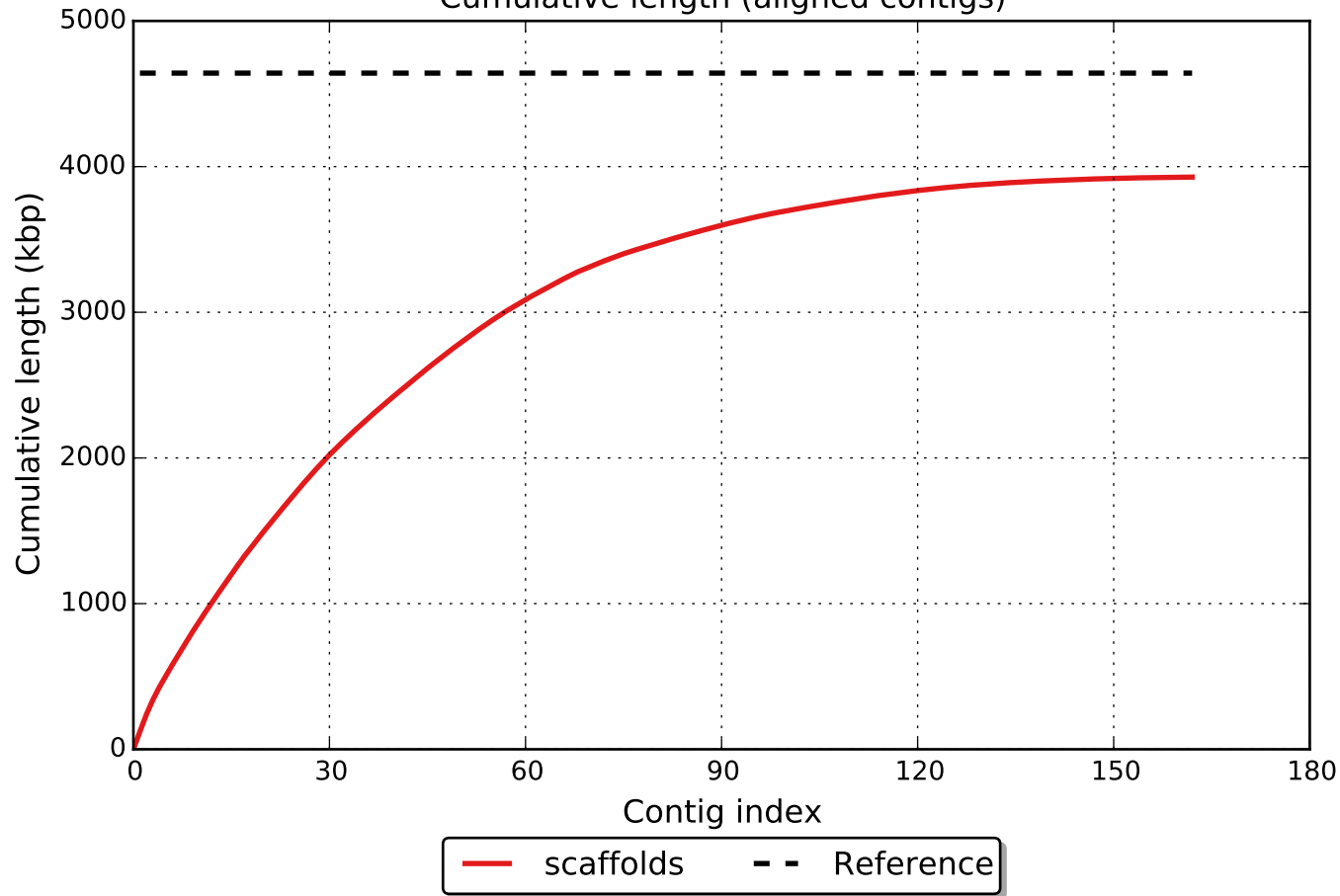
GC content



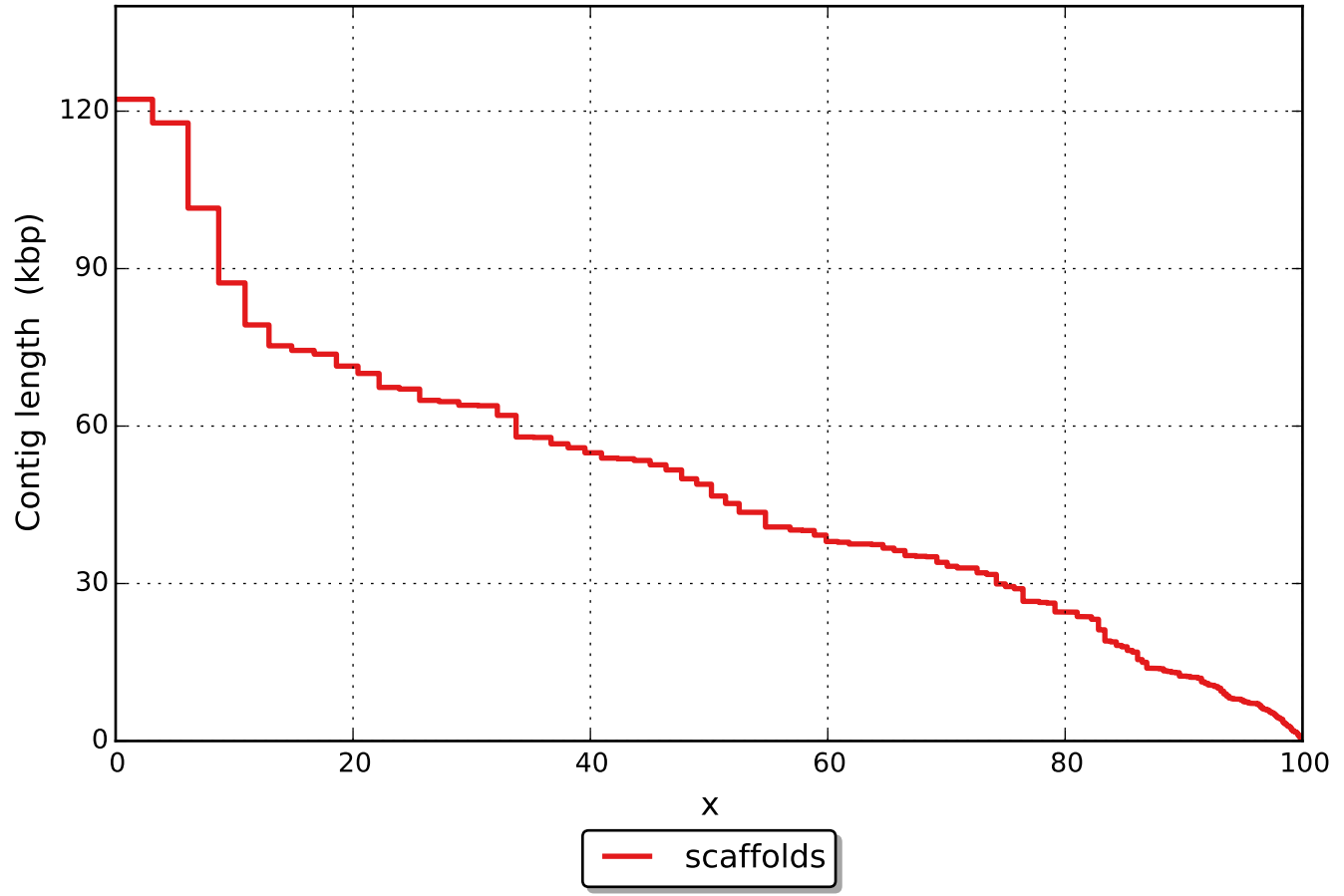
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

