

Report

	scaffolds
# contigs (≥ 1000 bp)	100
# contigs (≥ 5000 bp)	81
# contigs (≥ 10000 bp)	67
# contigs (≥ 25000 bp)	49
# contigs (≥ 50000 bp)	30
Total length (≥ 1000 bp)	4546459
Total length (≥ 5000 bp)	4504936
Total length (≥ 10000 bp)	4403489
Total length (≥ 25000 bp)	4111791
Total length (≥ 50000 bp)	3453079
# contigs	103
Largest contig	327367
Total length	4548491
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	105658
NG50	105658
N75	53520
NG75	48989
L50	14
LG50	14
L75	30
LG75	31
# misassemblies	10
# misassembled contigs	10
Misassembled contigs length	624215
# local misassemblies	8
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.962
Duplication ratio	1.000
# N's per 100 kbp	27.77
# mismatches per 100 kbp	64.86
# indels per 100 kbp	9.65
Largest alignment	327367
NA50	95467
NGA50	82766
NA75	43798
NGA75	42166
LA50	14
LGA50	15
LA75	32
LGA75	34

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	10
# relocations	10
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	10
Misassembled contigs length	624215
# local misassemblies	8
# mismatches	2949
# indels	439
# short indels	409
# long indels	30
Indels length	1107

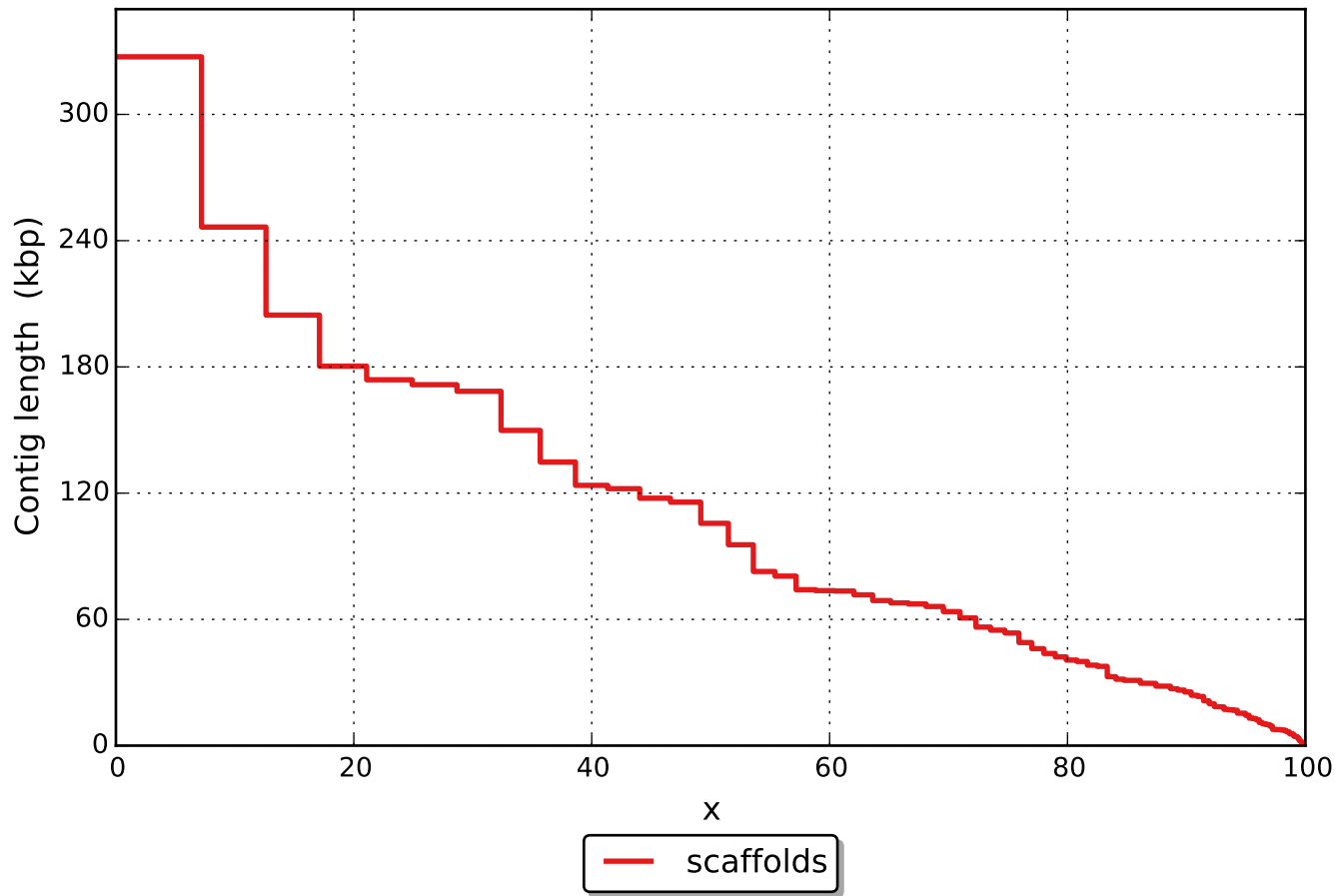
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

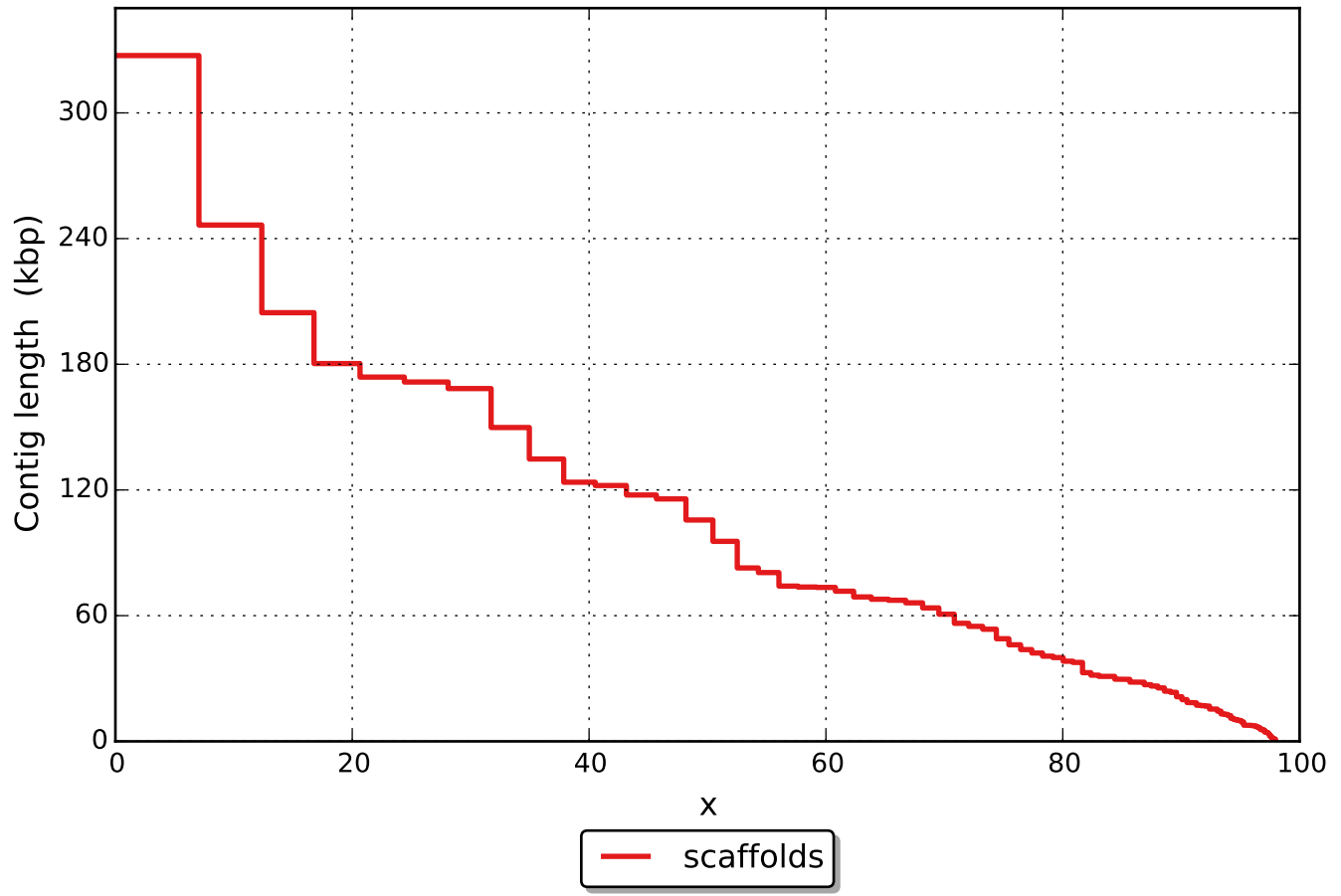
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	1263

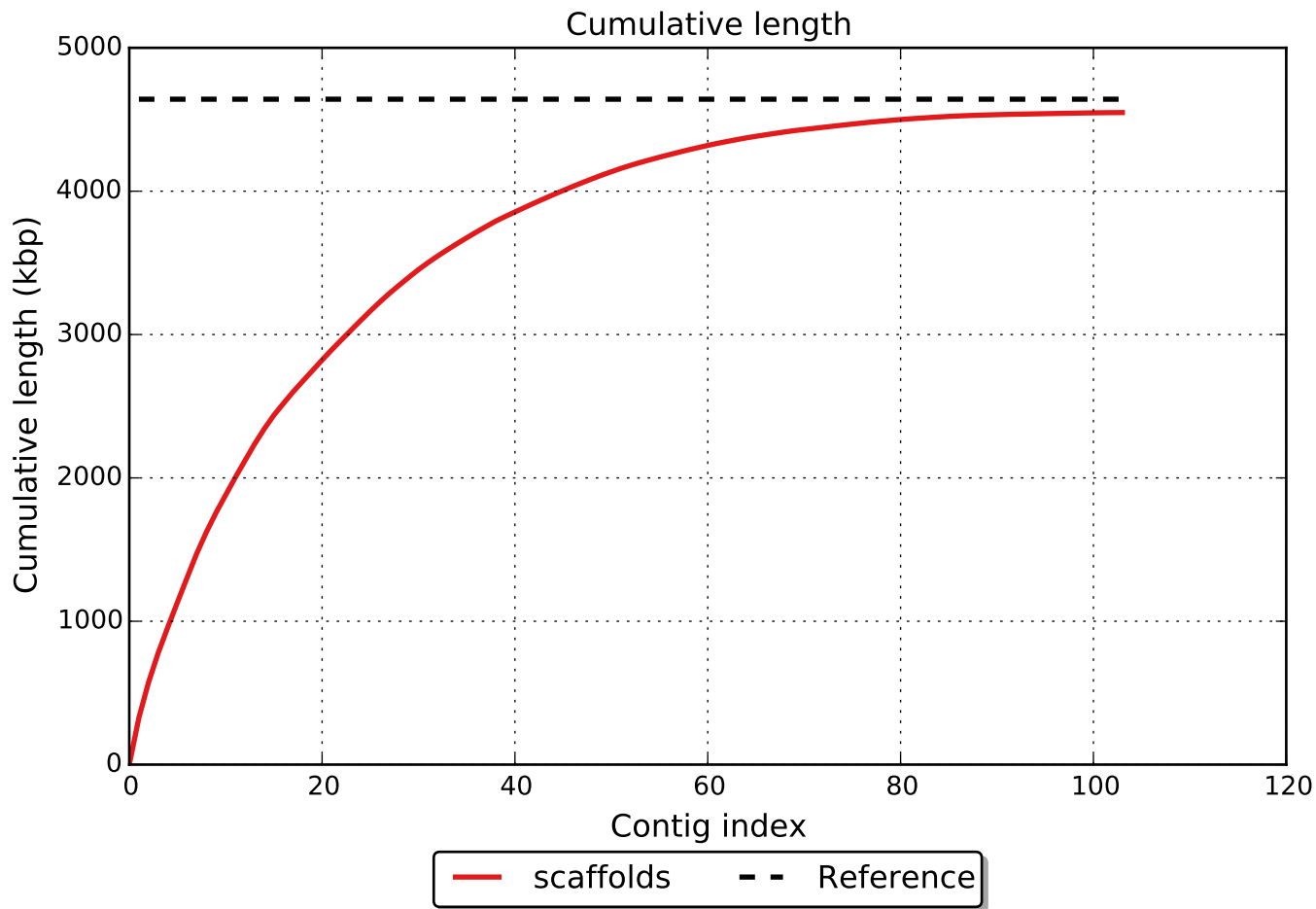
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

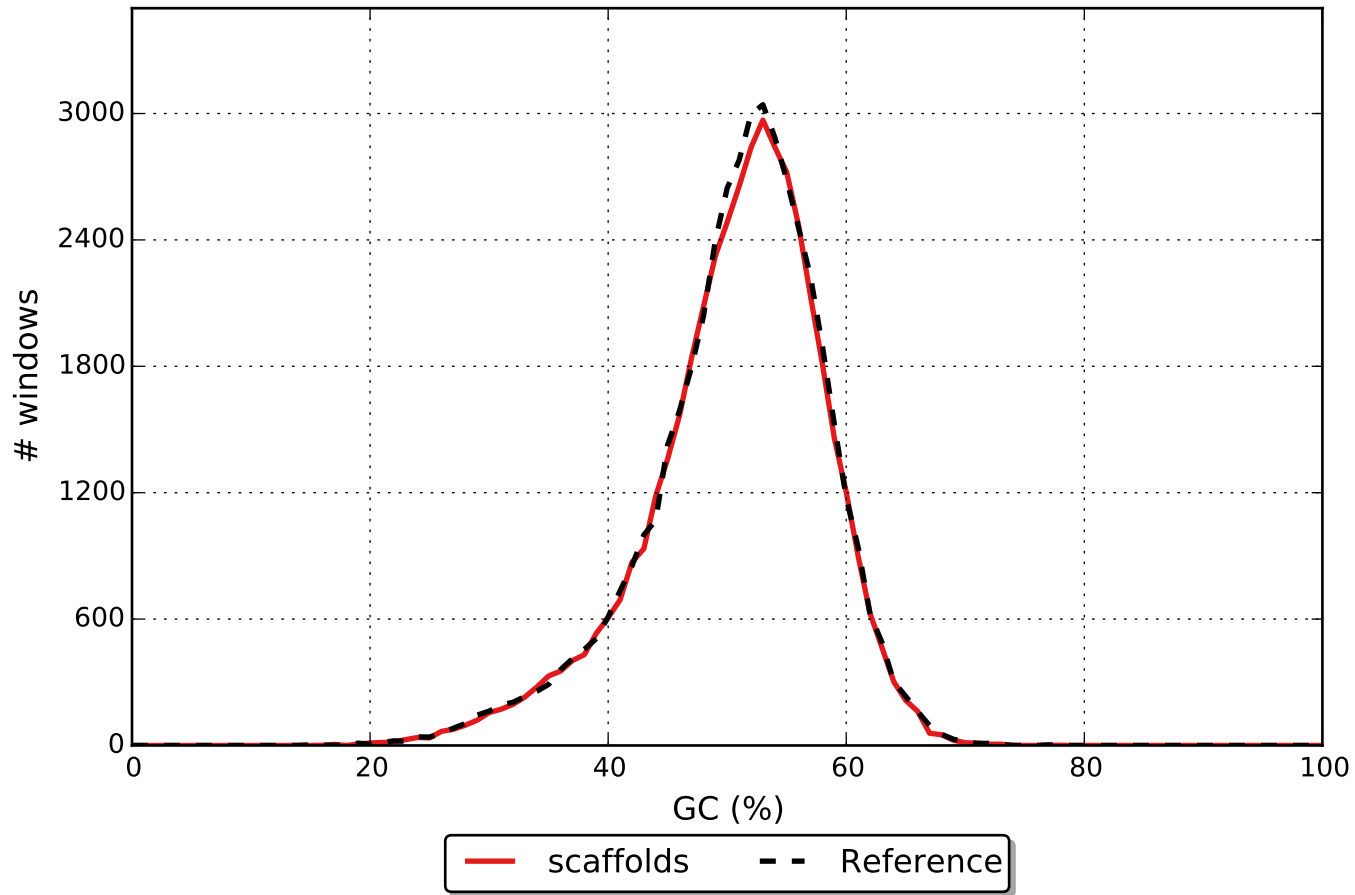


NGx

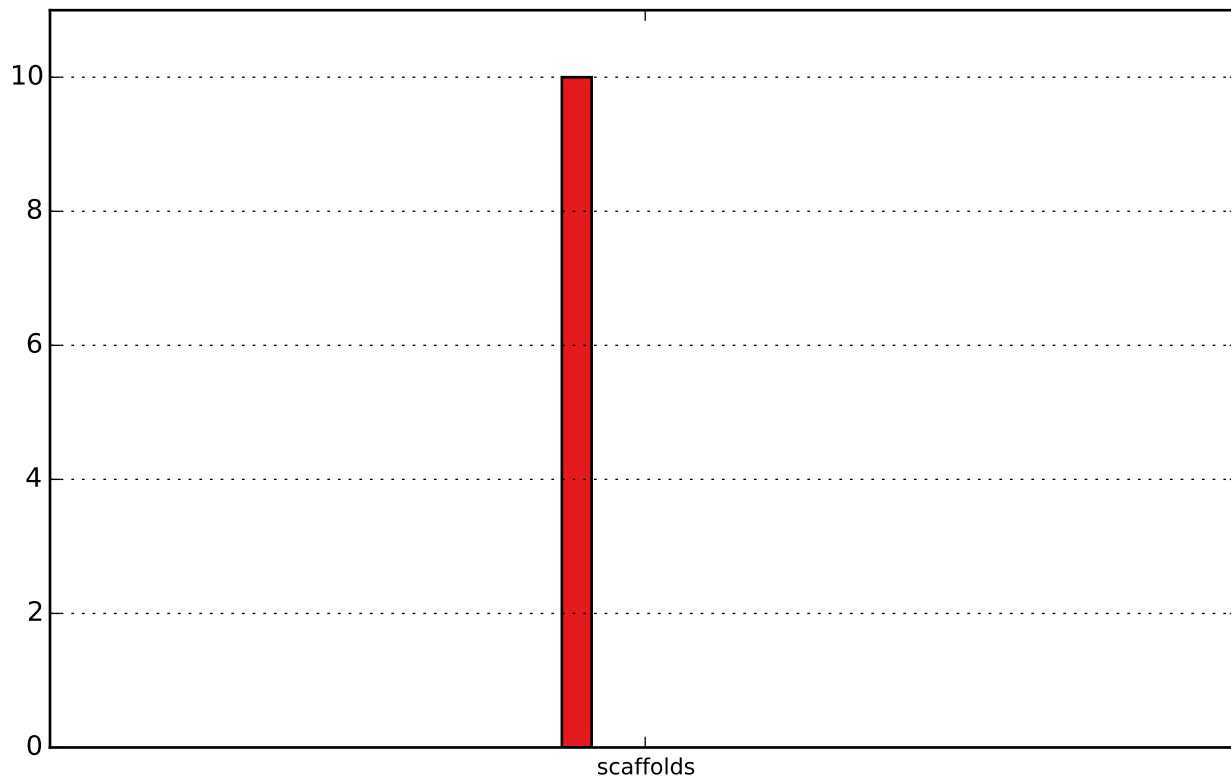




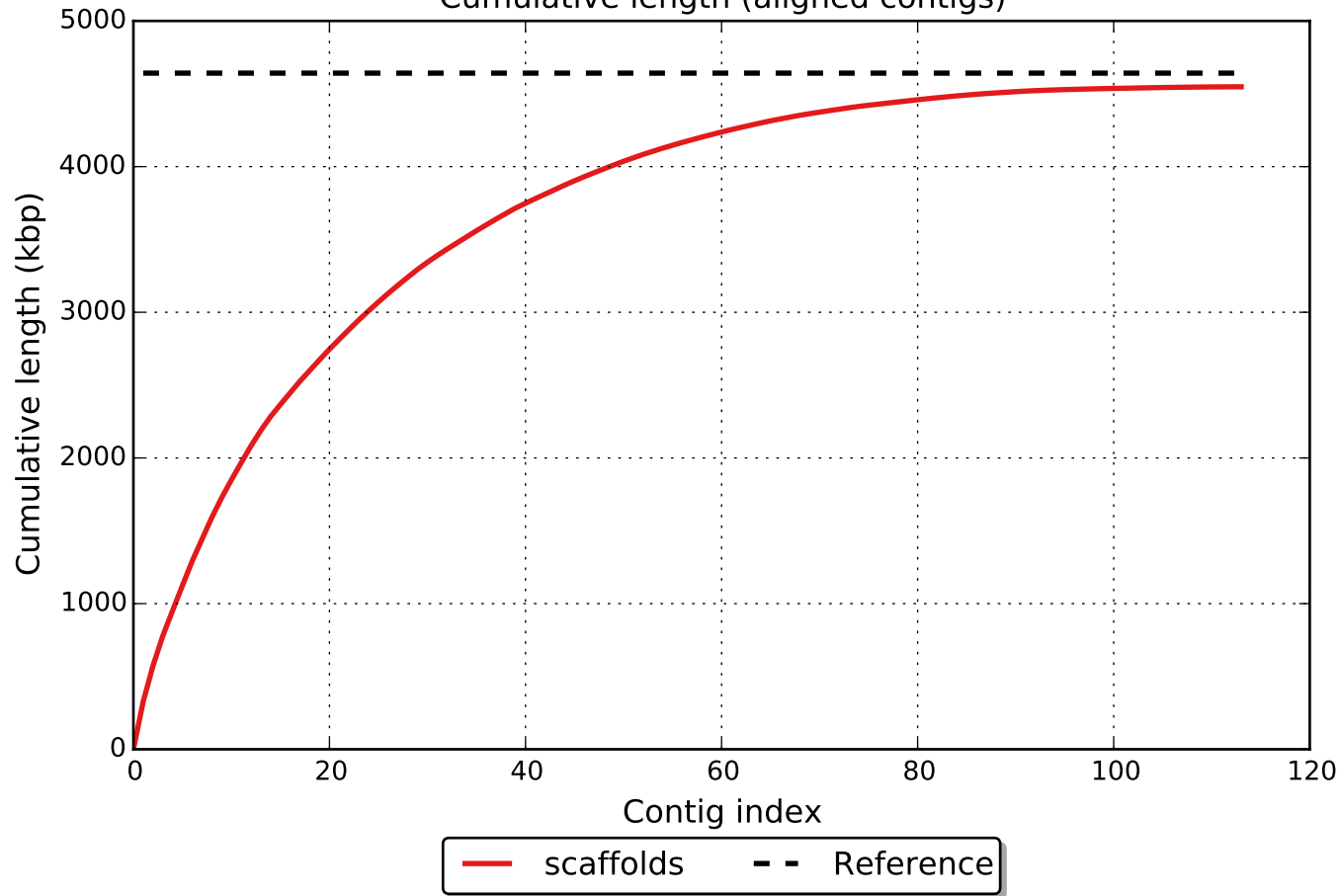
GC content



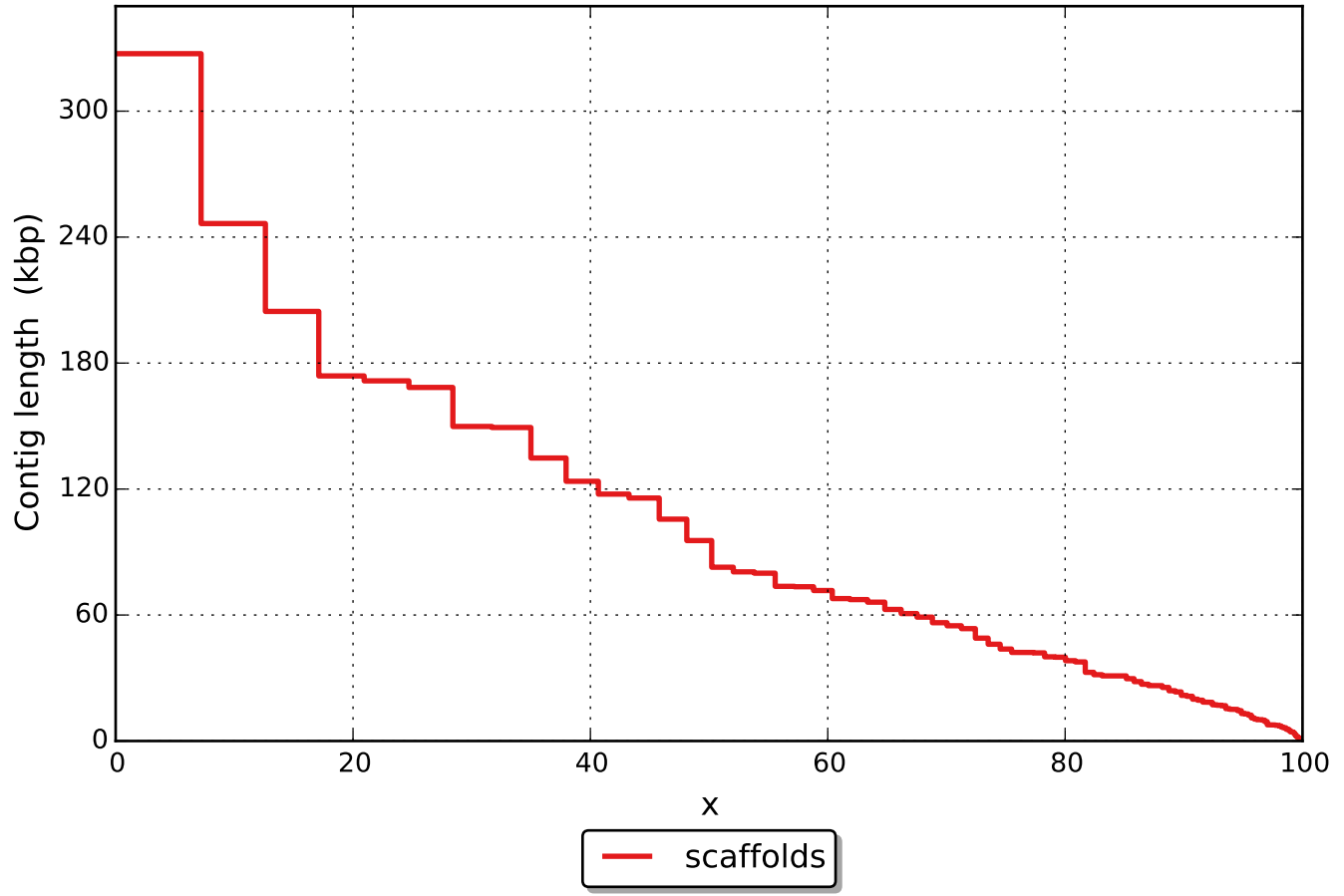
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

