

Report

	scaffolds
# contigs (≥ 1000 bp)	98
# contigs (≥ 5000 bp)	75
# contigs (≥ 10000 bp)	63
# contigs (≥ 25000 bp)	41
# contigs (≥ 50000 bp)	22
Total length (≥ 1000 bp)	2853519
Total length (≥ 5000 bp)	2802457
Total length (≥ 10000 bp)	2715969
Total length (≥ 25000 bp)	2362896
Total length (≥ 50000 bp)	1700768
# contigs	110
Largest contig	148188
Total length	2861075
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.79
N50	57888
NG50	26461
N75	32953
L50	18
LG50	40
L75	34
# misassemblies	5
# misassembled contigs	5
Misassembled contigs length	475557
# local misassemblies	1
# unaligned contigs	0 + 1 part
Unaligned length	55
Genome fraction (%)	60.241
Duplication ratio	1.023
# N's per 100 kbp	0.00
# mismatches per 100 kbp	711.50
# indels per 100 kbp	0.36
Largest alignment	118781
NA50	55862
NGA50	24598
NA75	27744
LA50	19
LGA50	45
LA75	38

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	19895
# indels	10
# short indels	10
# long indels	0
Indels length	11

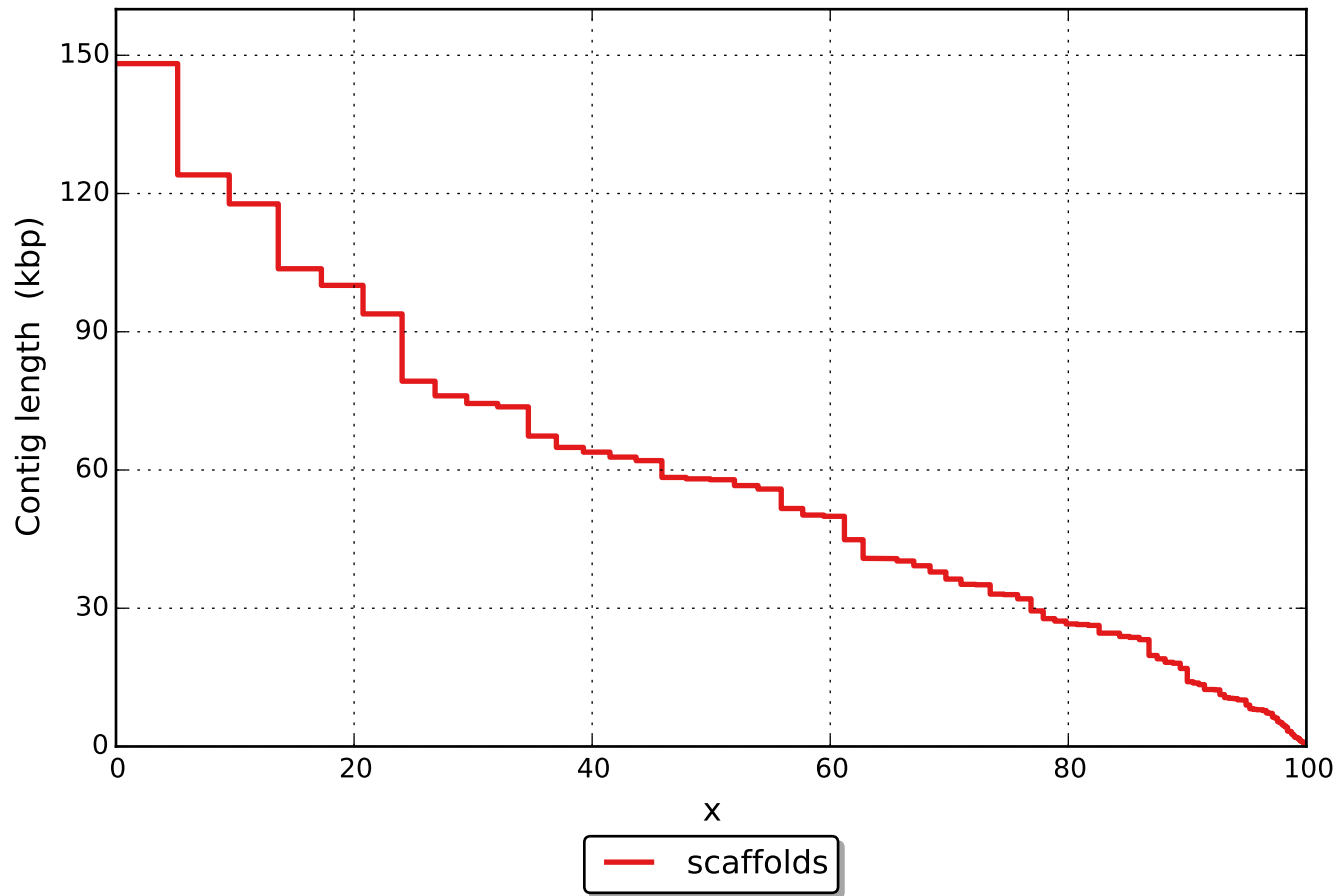
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

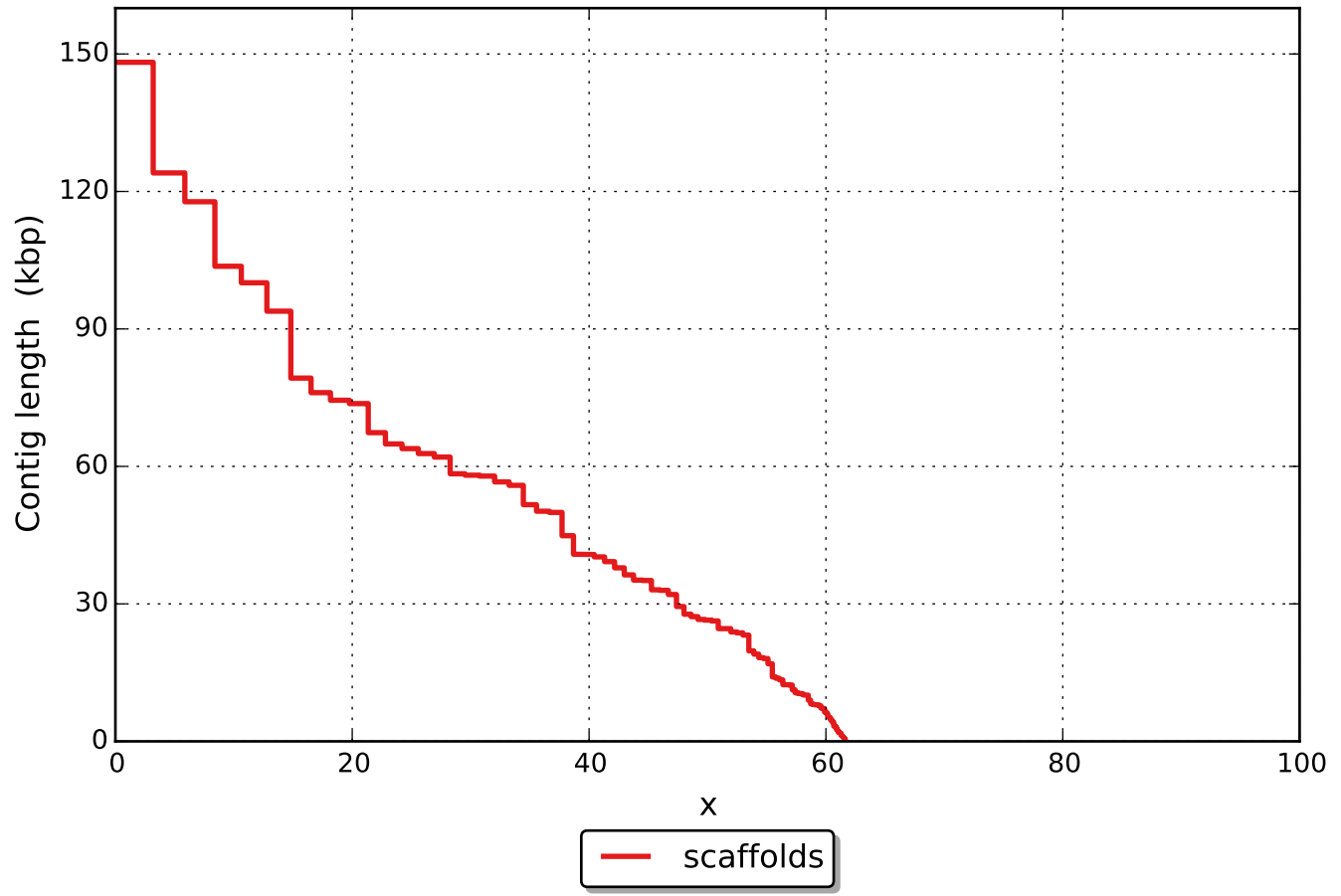
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	55
# N's	0

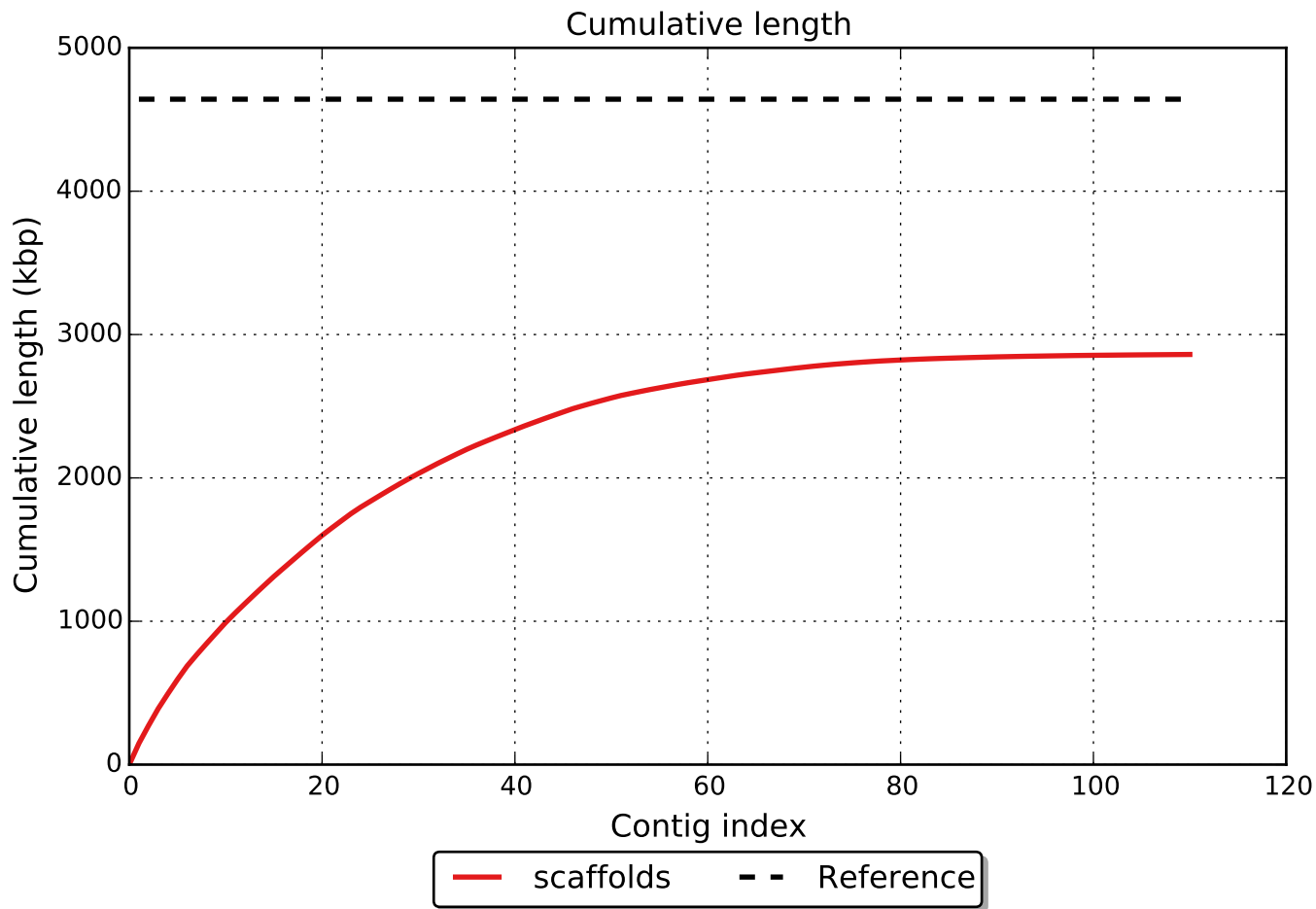
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

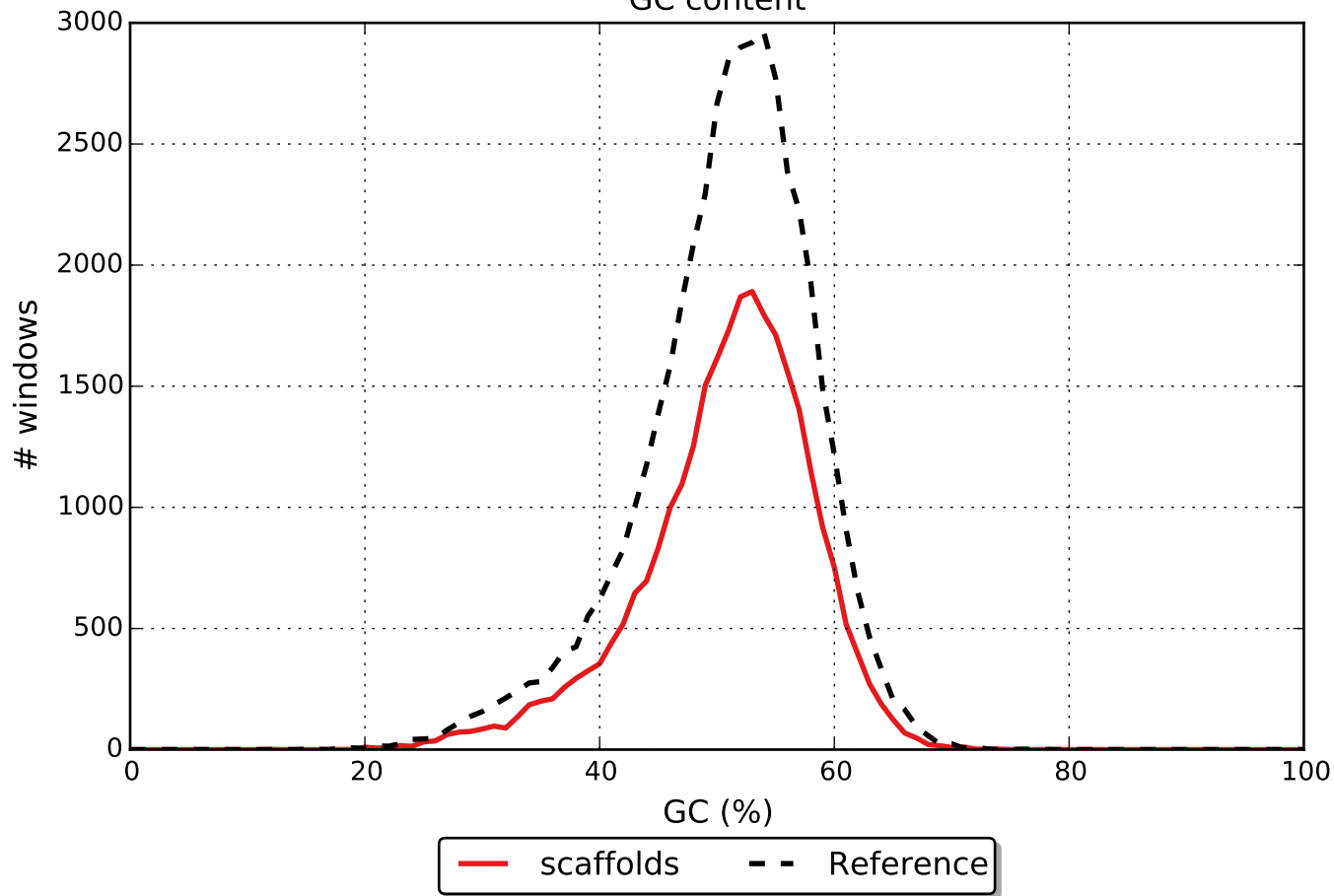


NGx

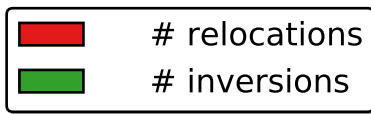
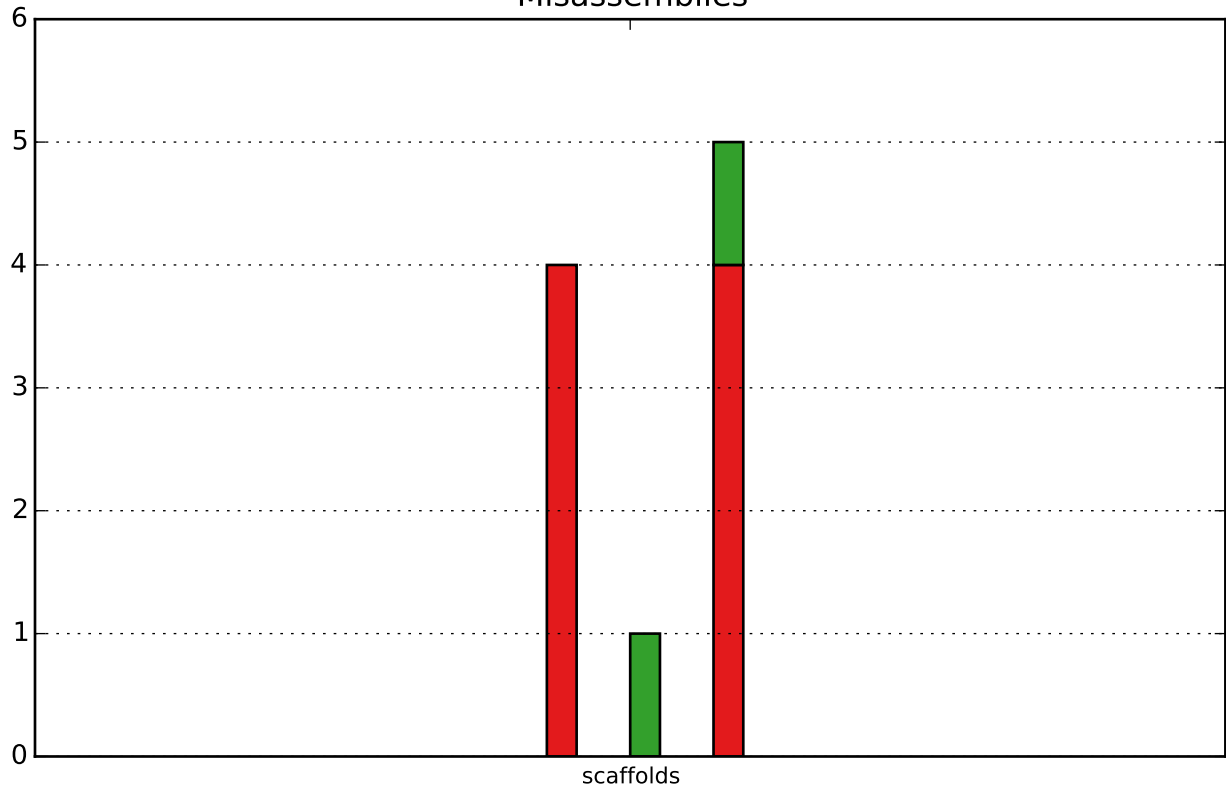




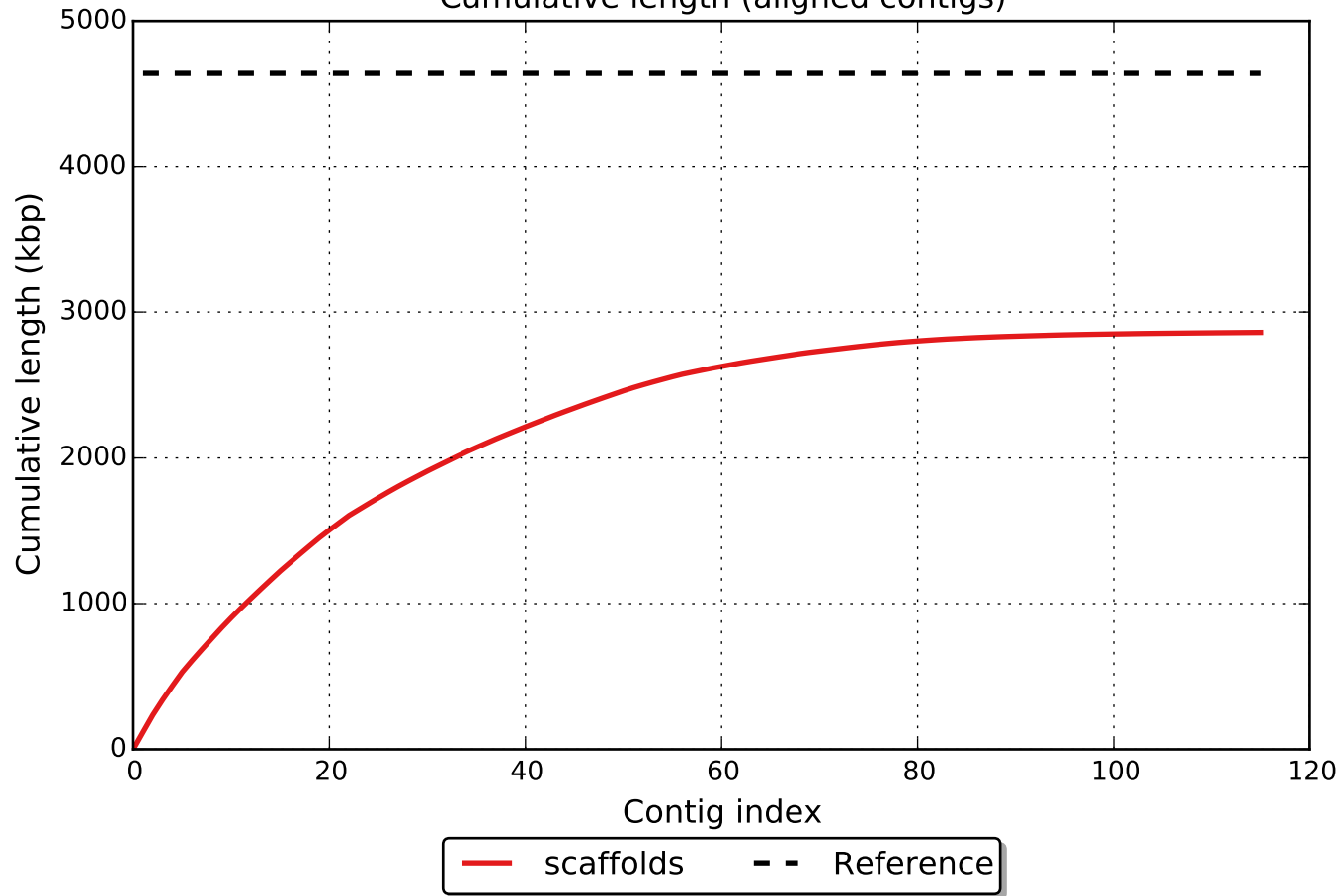
GC content



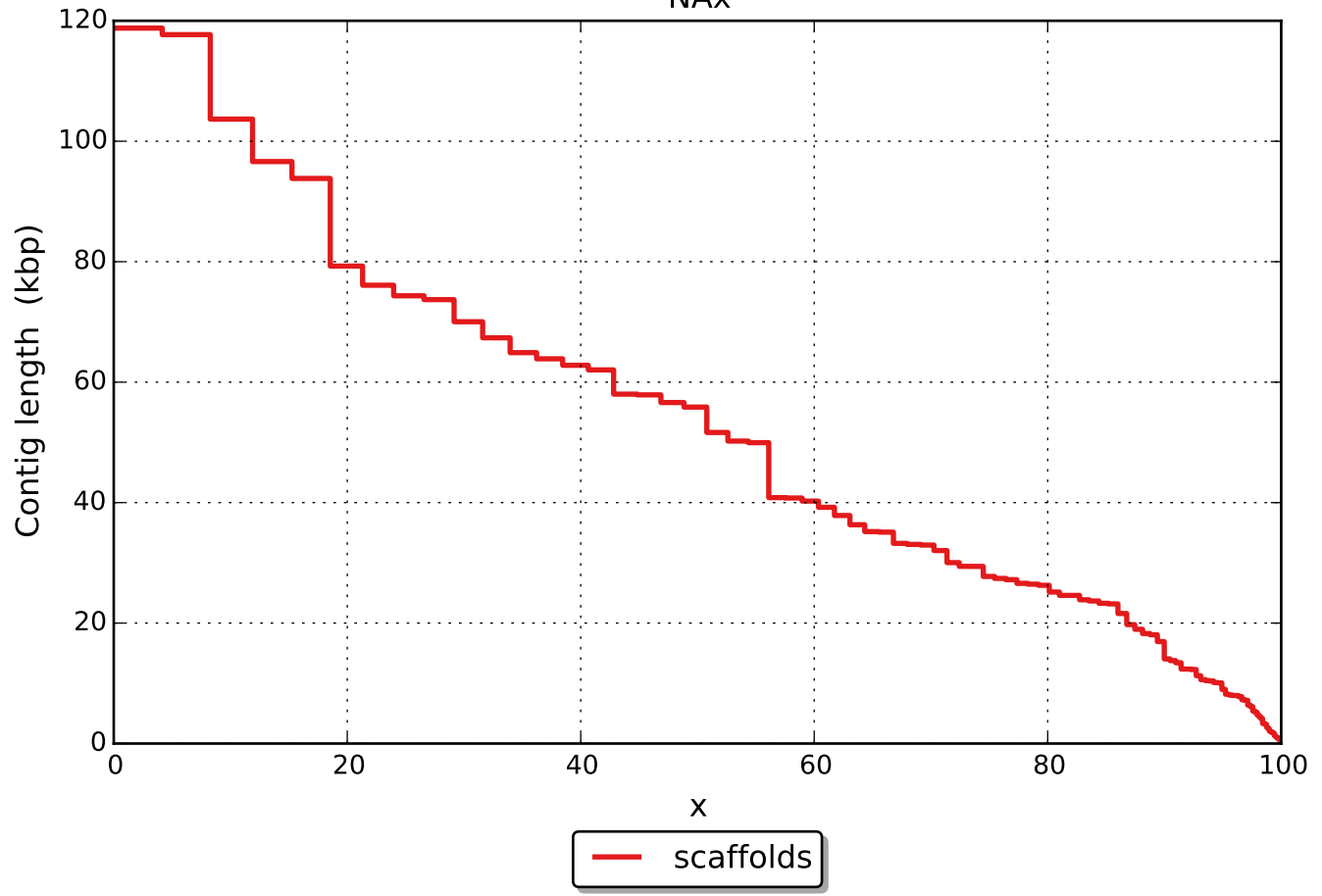
Misassemblies



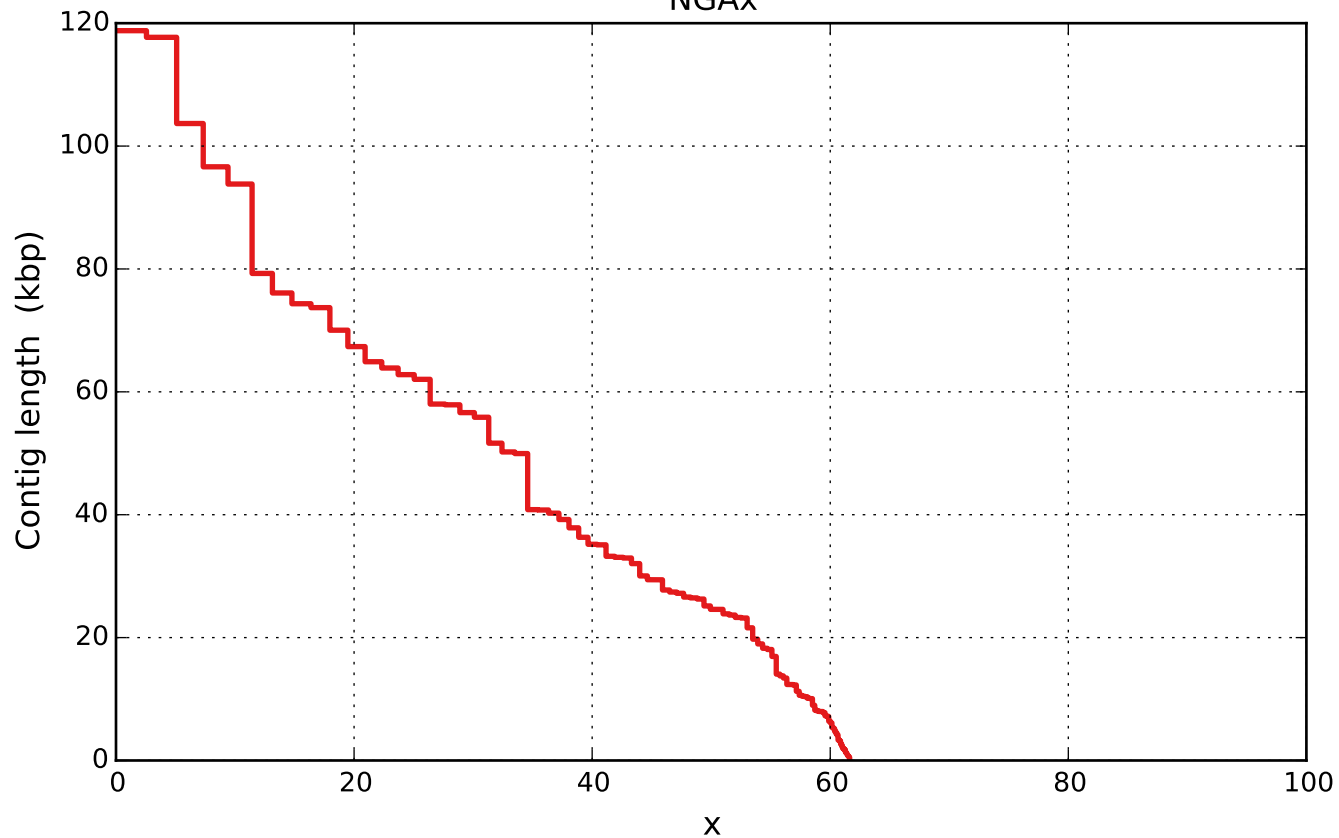
Cumulative length (aligned contigs)



NAx



NGAx



— scaffolds