

Report

	scaffolds
# contigs (≥ 1000 bp)	57
# contigs (≥ 5000 bp)	50
# contigs (≥ 10000 bp)	50
# contigs (≥ 25000 bp)	47
# contigs (≥ 50000 bp)	43
Total length (≥ 1000 bp)	8055135
Total length (≥ 5000 bp)	8047447
Total length (≥ 10000 bp)	8047447
Total length (≥ 25000 bp)	8001492
Total length (≥ 50000 bp)	7873706
# contigs	62
Largest contig	529642
Total length	8058538
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	264862
NG50	324227
N75	157835
NG75	288223
L50	12
LG50	6
L75	22
LG75	10
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 27 part
Unaligned length	3033062
Genome fraction (%)	99.195
Duplication ratio	1.091
# N's per 100 kbp	0.37
# mismatches per 100 kbp	449.26
# indels per 100 kbp	0.98
Largest alignment	529642
NA50	111062
NGA50	291704
NGA75	240233
LA50	14
LGA50	6
LGA75	10

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	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	26
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	20685
# indels	45
# short indels	45
# long indels	0
Indels length	48

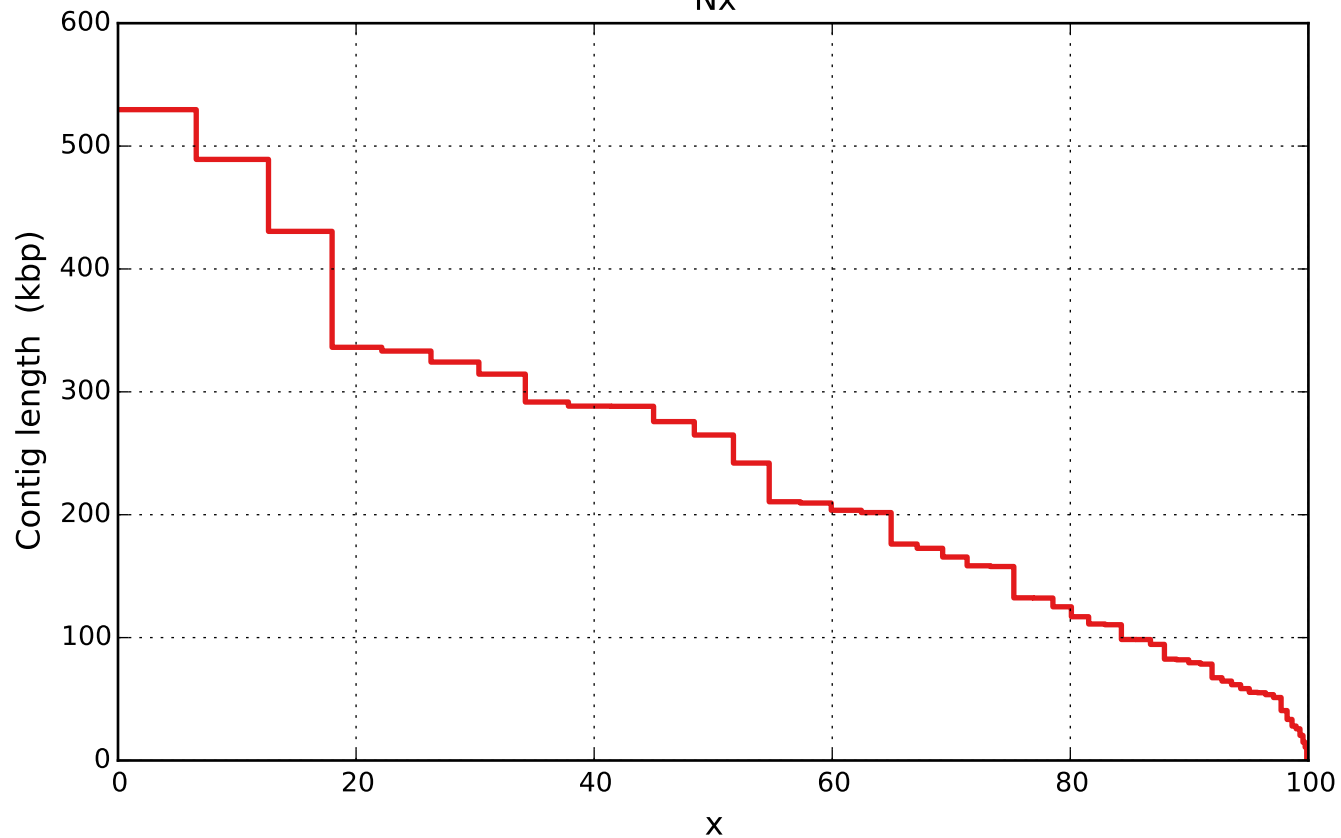
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

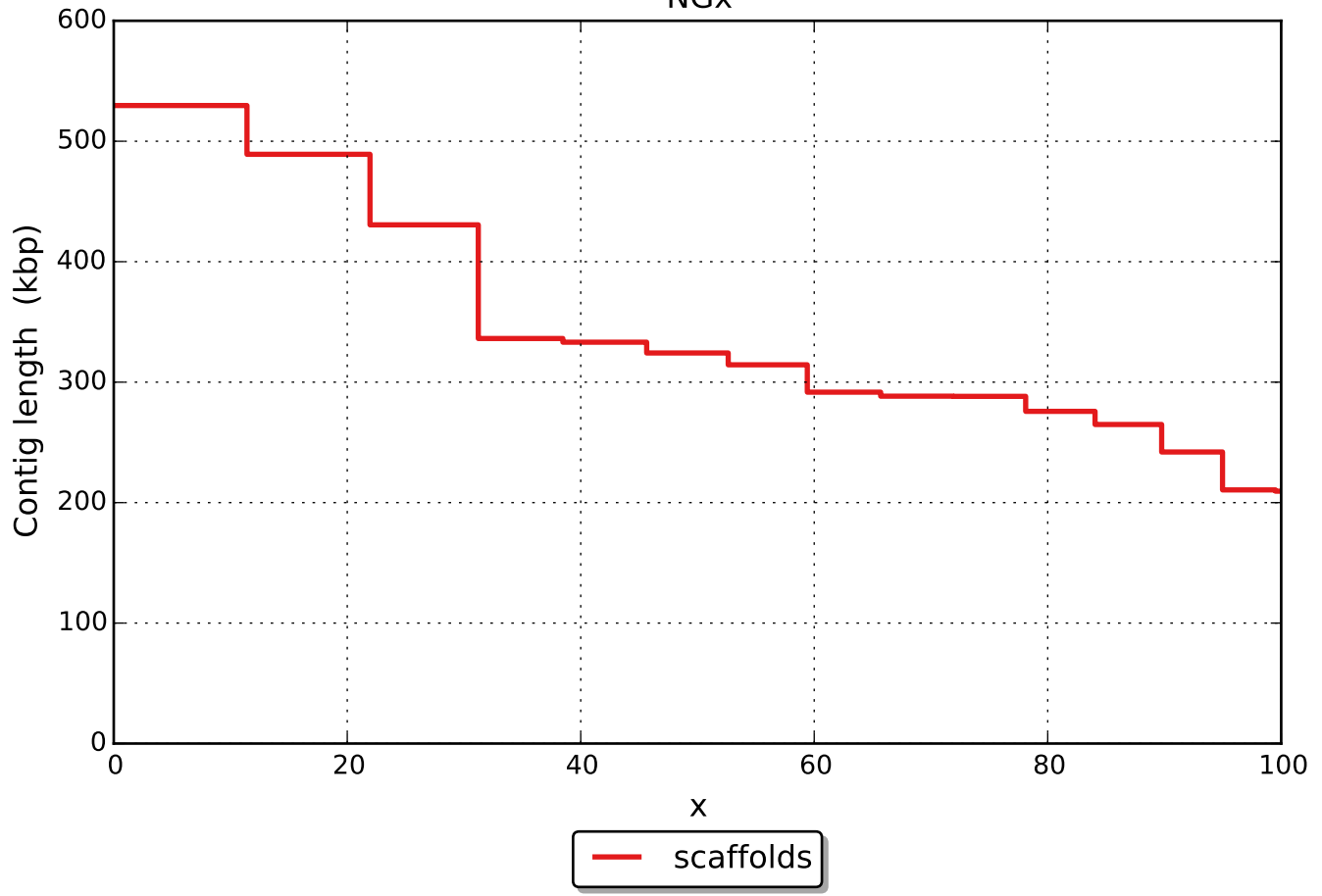
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	27
# with misassembly	20
# both parts are significant	26
Partially unaligned length	3033062
# N's	30

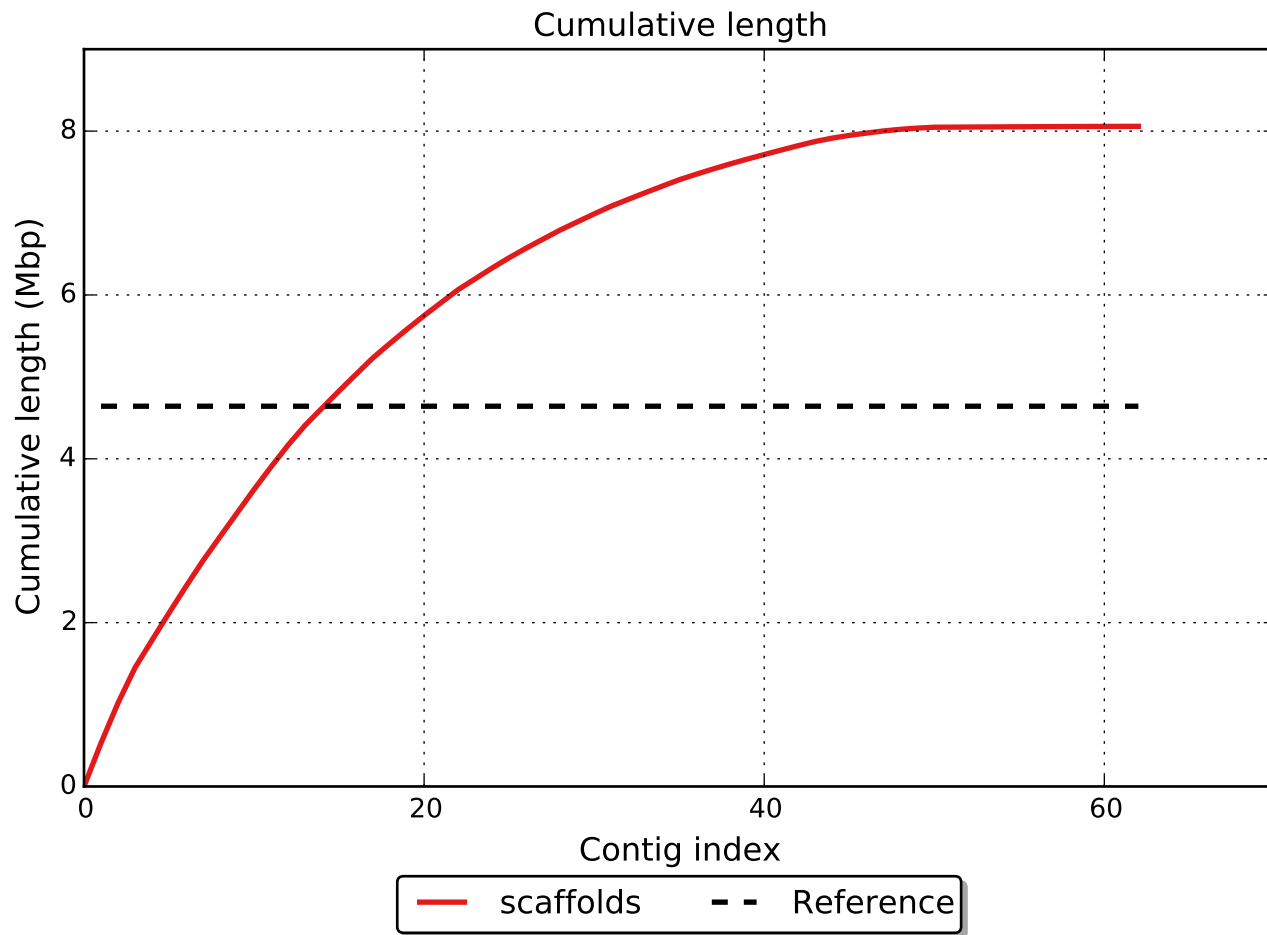
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

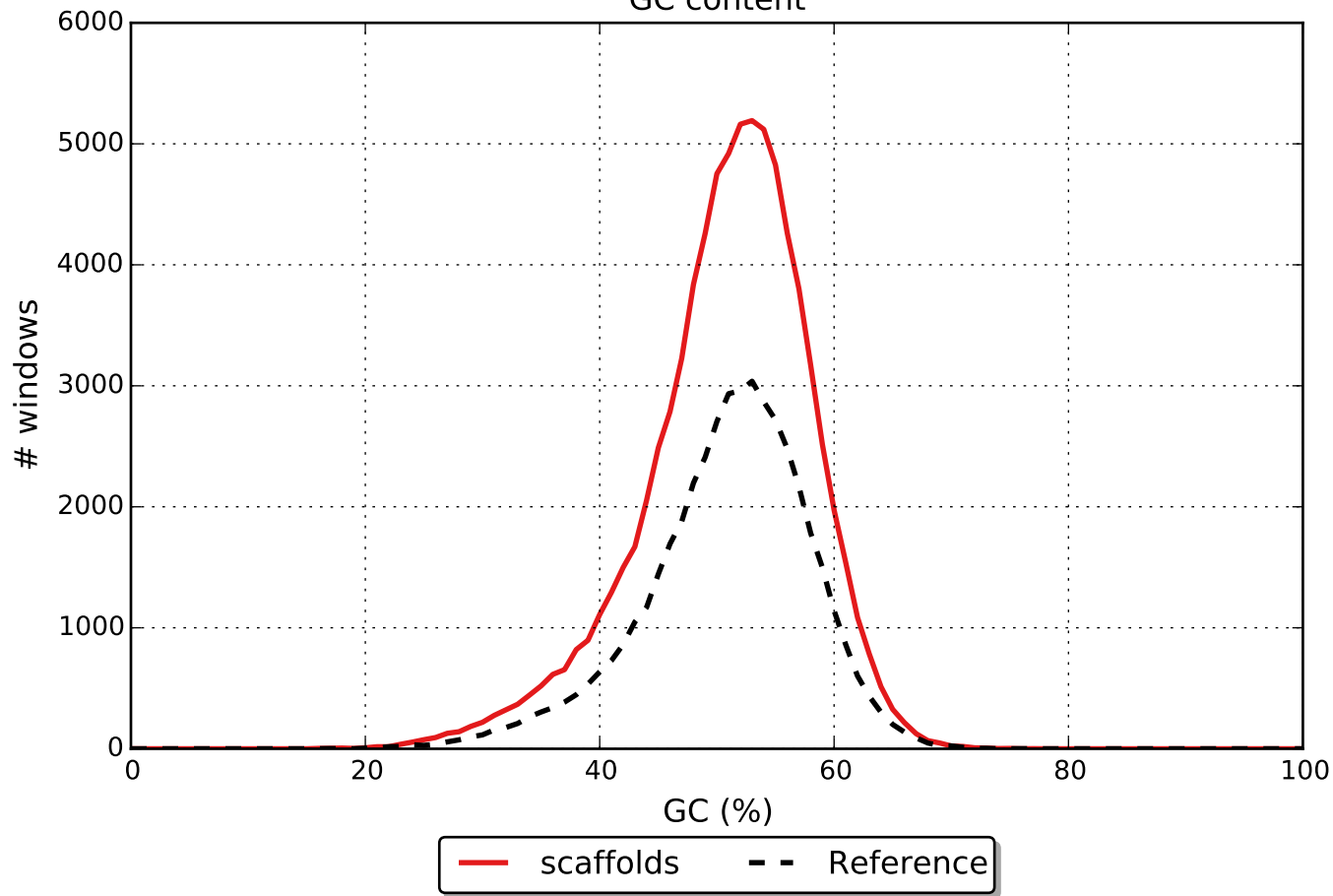


NGx



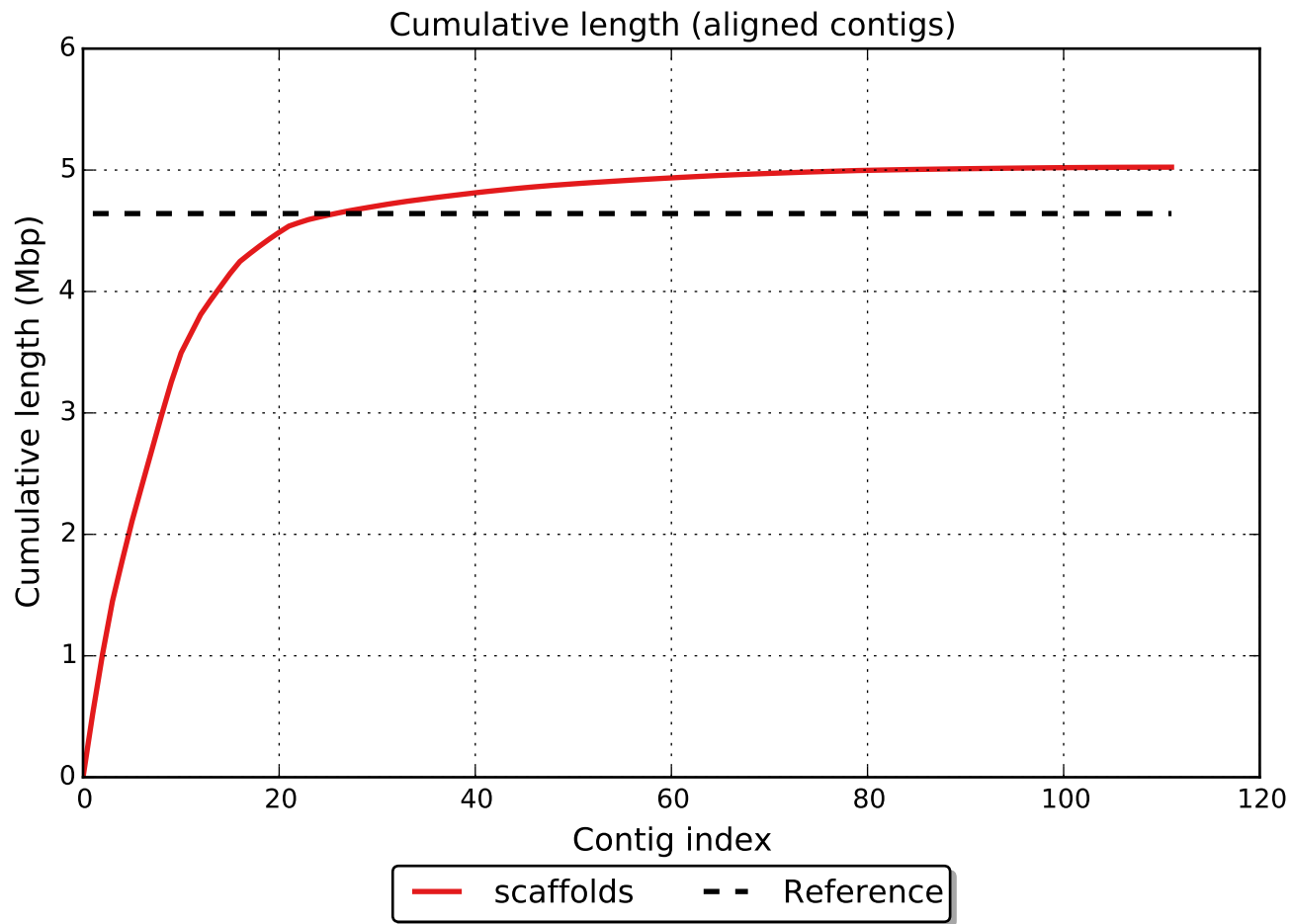


GC content

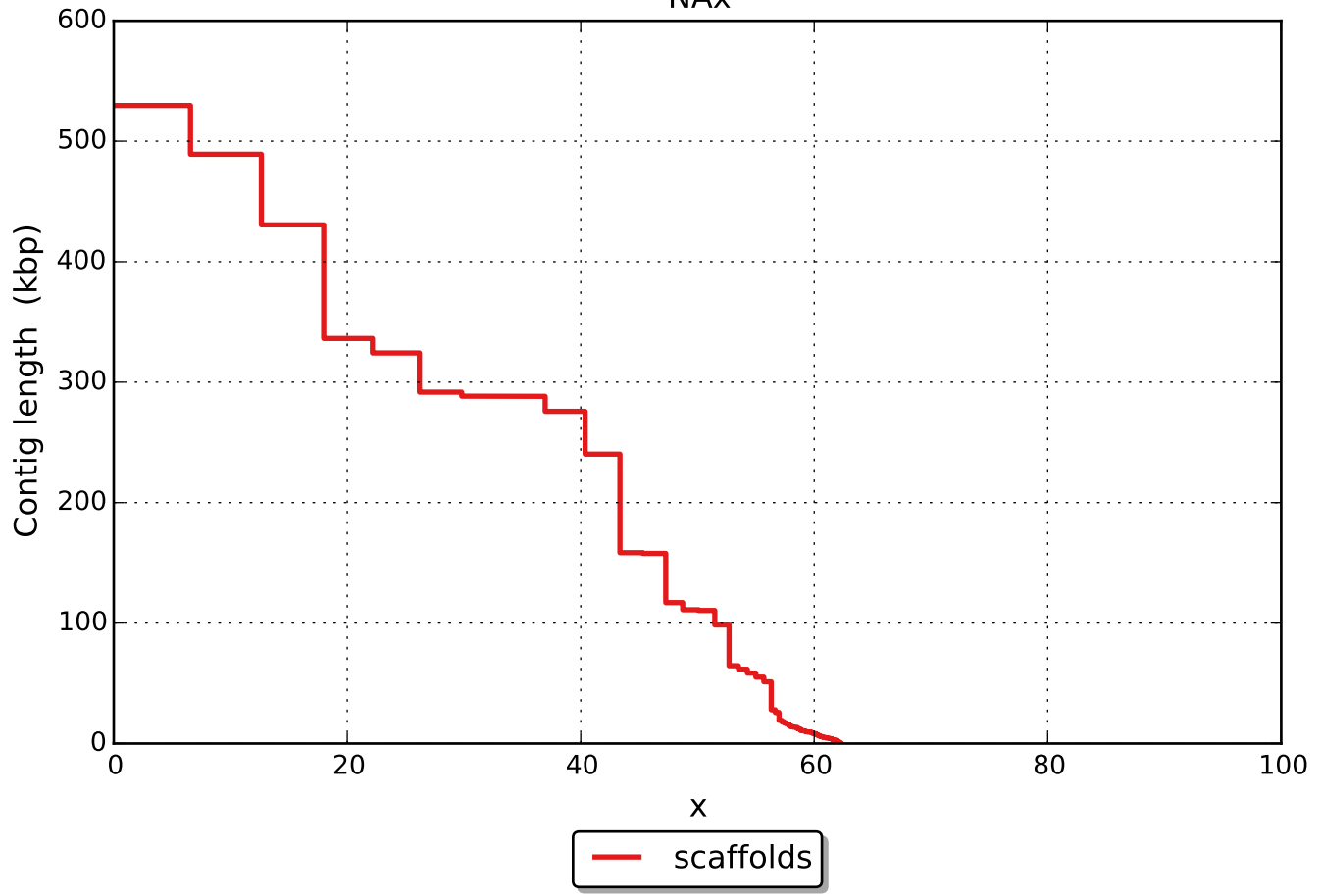


Misassemblies





NAx



NGAx

