

## Report

	scaffolds
# contigs (>= 1000 bp)	27
# contigs (>= 5000 bp)	23
# contigs (>= 10000 bp)	22
# contigs (>= 25000 bp)	20
# contigs (>= 50000 bp)	18
Total length (>= 1000 bp)	4991117
Total length (>= 5000 bp)	4981319
Total length (>= 10000 bp)	4971881
Total length (>= 25000 bp)	4937716
Total length (>= 50000 bp)	4873077
# contigs	30
Largest contig	1053360
Total length	4992889
Reference length	4641652
GC (%)	50.85
Reference GC (%)	50.79
N50	451601
NG50	451601
N75	178093
NG75	210555
L50	4
LG50	4
L75	8
LG75	7
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 6 part
Unaligned length	377311
Genome fraction (%)	99.321
Duplication ratio	1.001
# N's per 100 kbp	0.20
# mismatches per 100 kbp	181.84
# indels per 100 kbp	0.72
Largest alignment	1053360
NA50	451601
NGA50	451601
NA75	146456
NGA75	178093
LA50	4
LGA50	4
LA75	9
LGA75	7

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	3
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	8383
# indels	33
# short indels	31
# long indels	2
Indels length	109

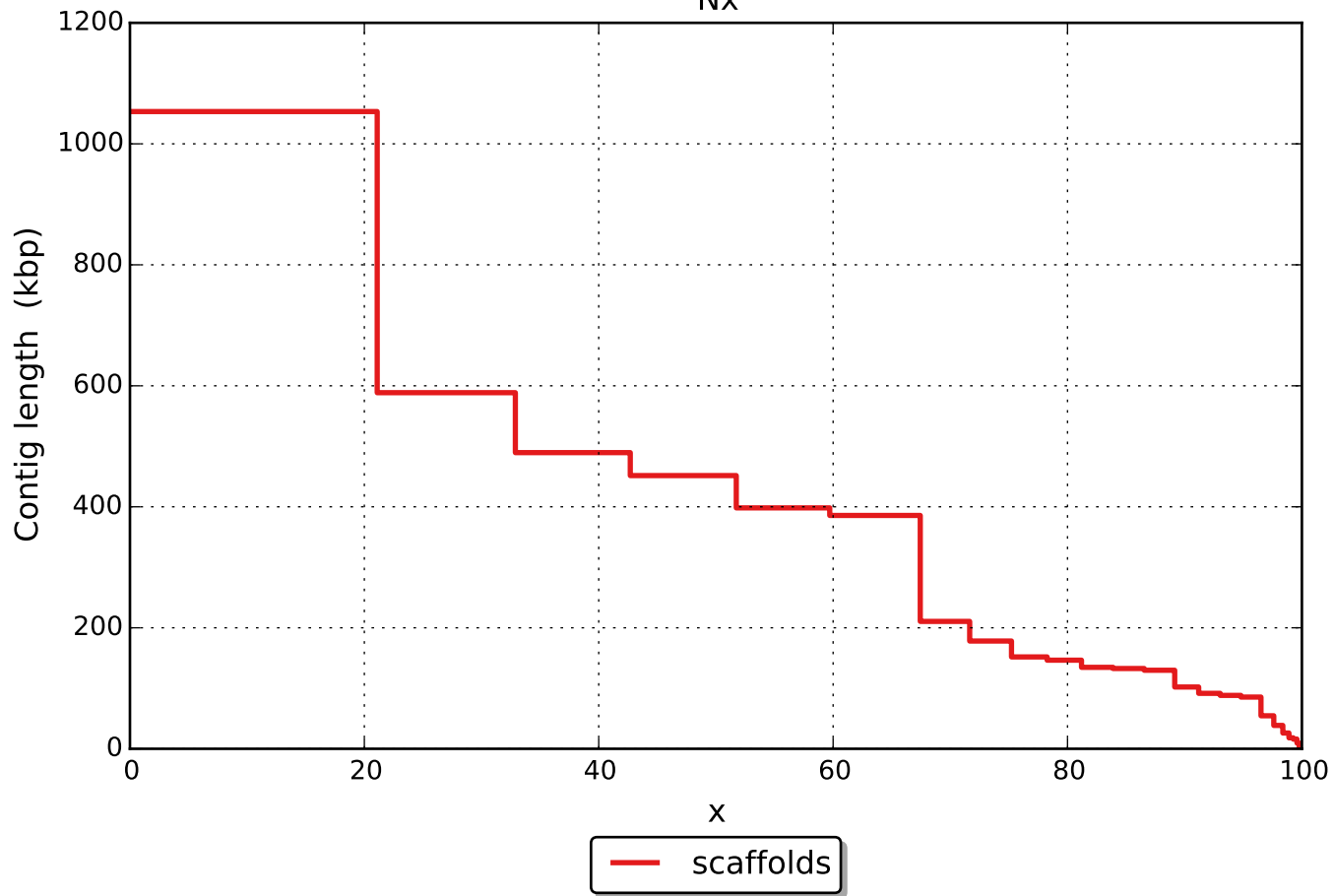
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

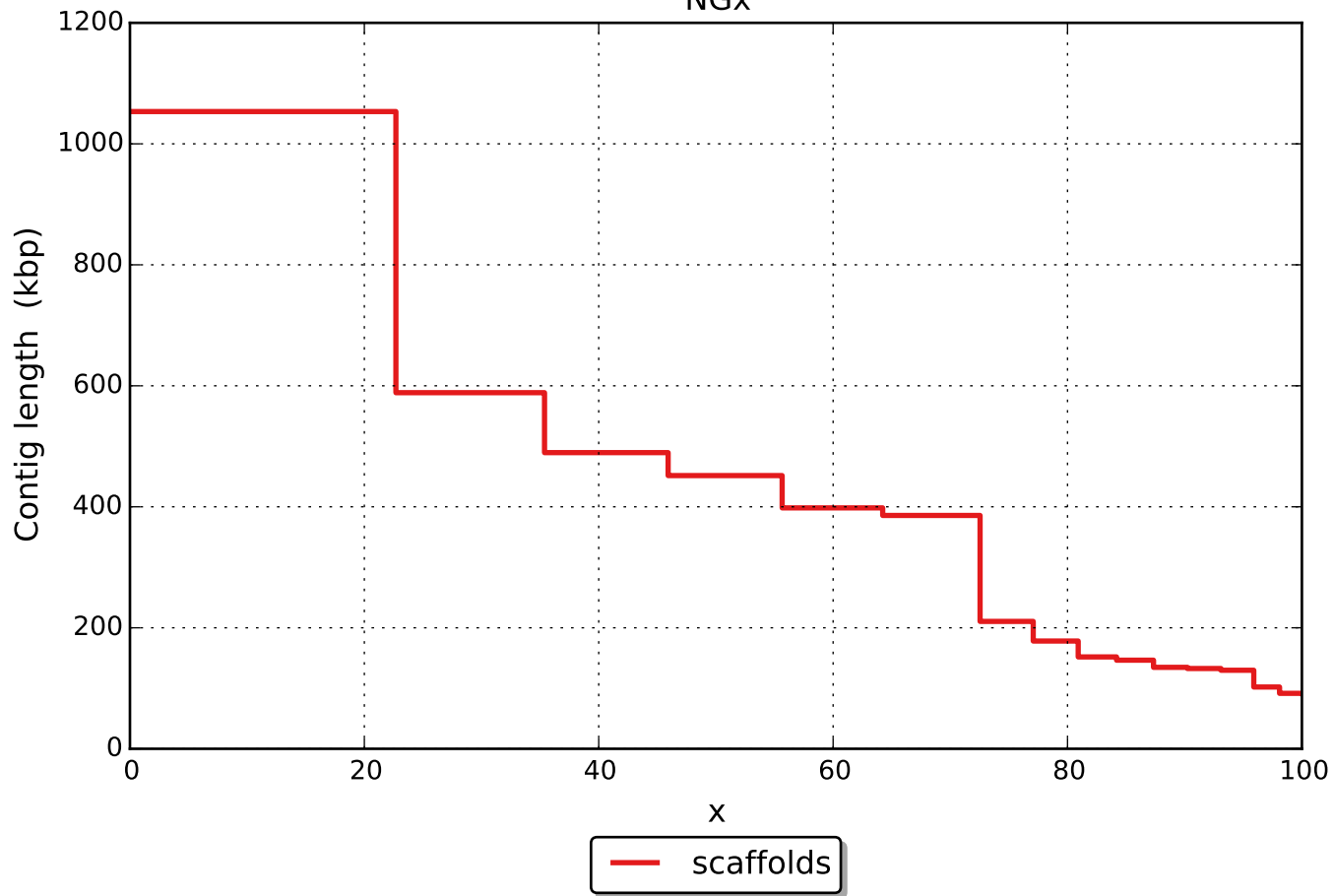
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	6
# with misassembly	1
# both parts are significant	3
Partially unaligned length	377311
# N's	10

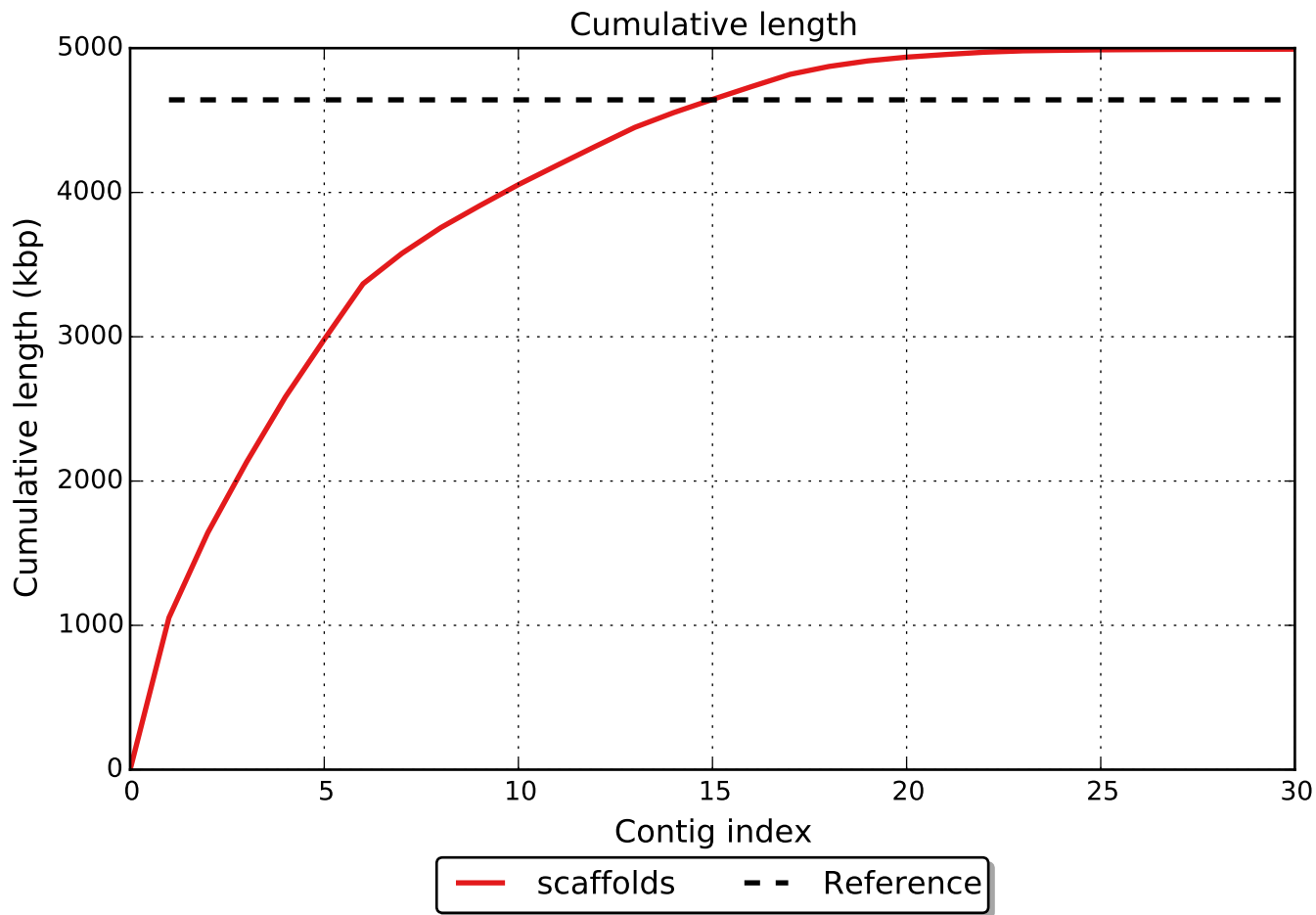
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

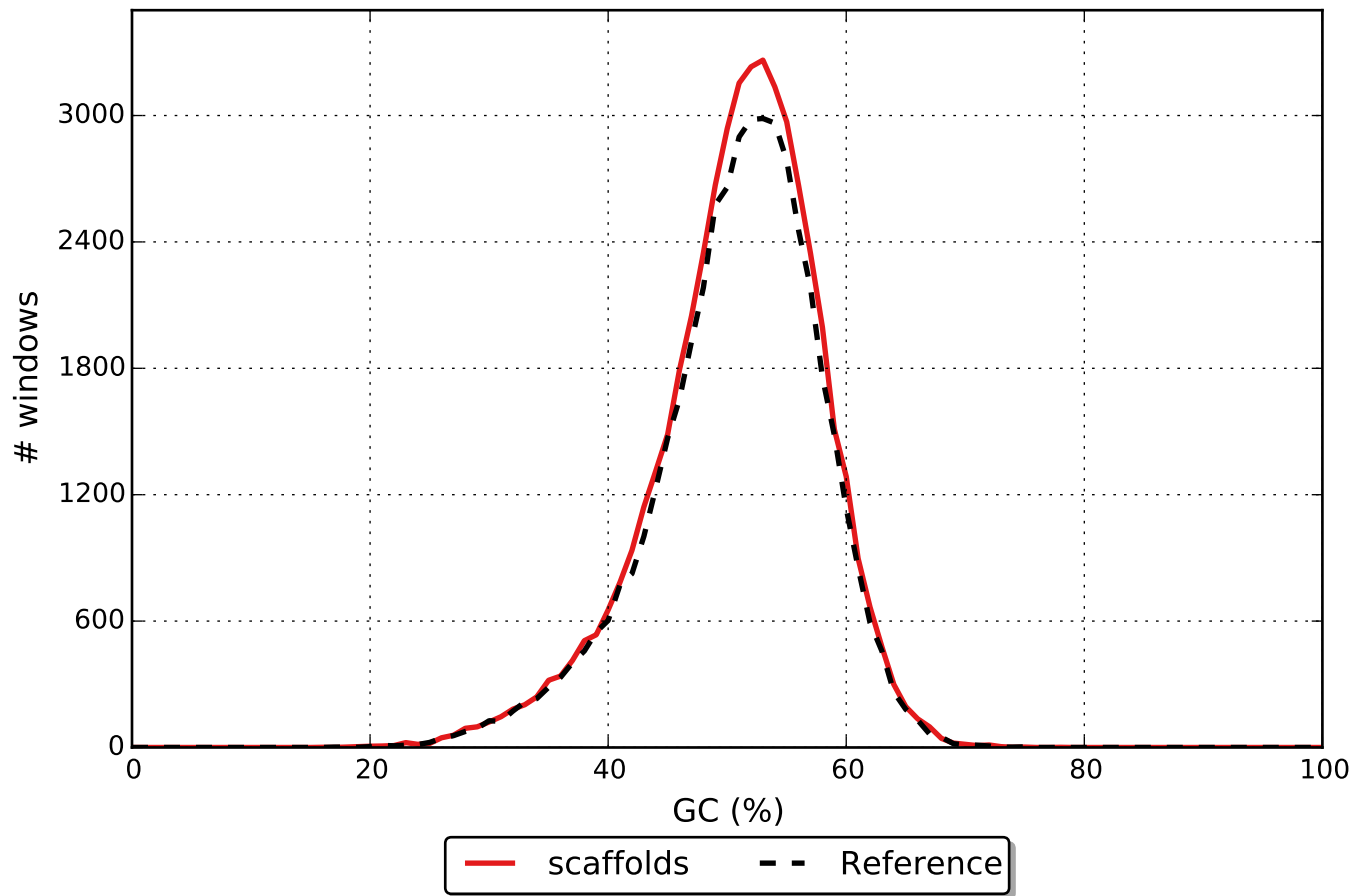


NGx





GC content

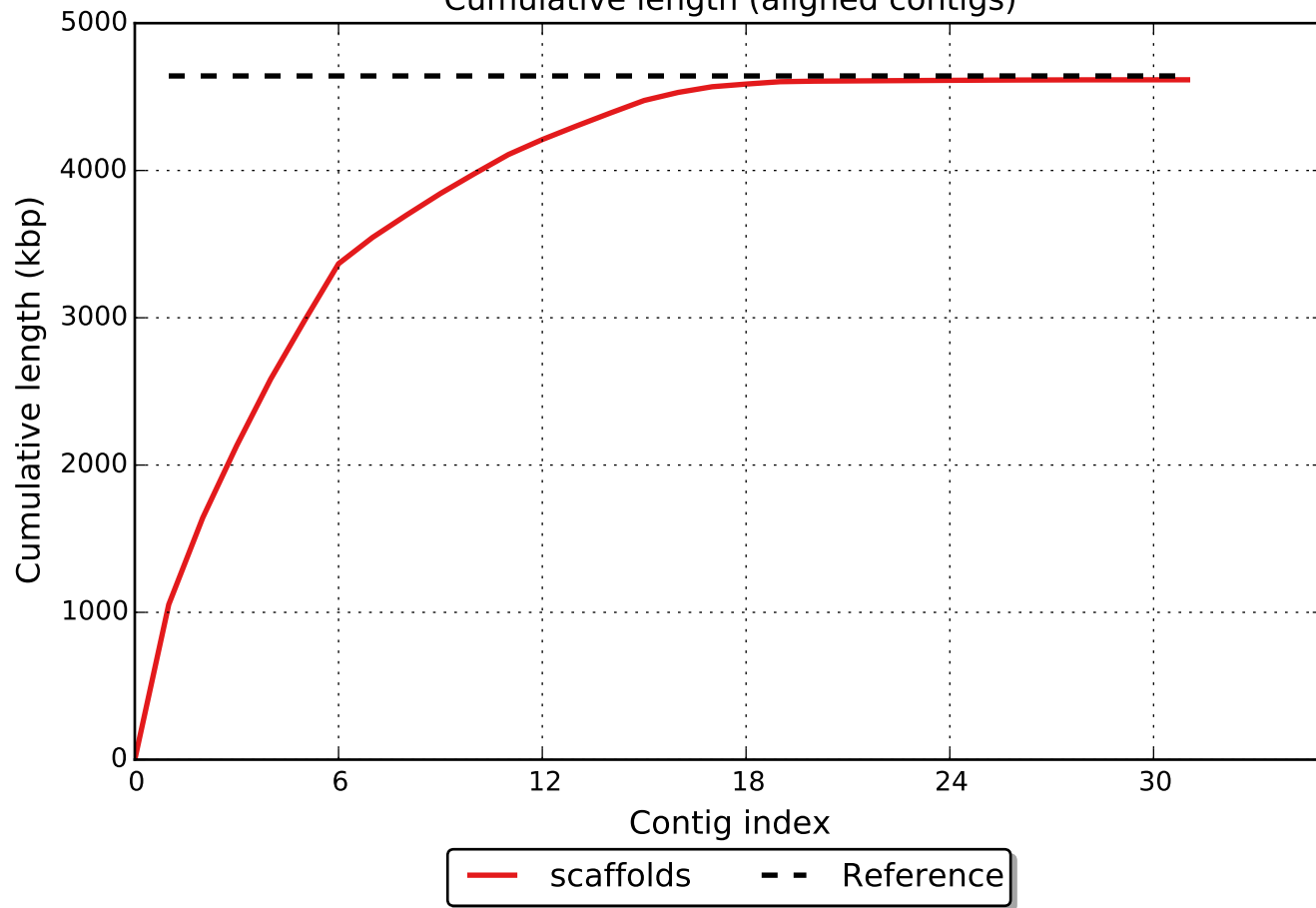


# Misassemblies

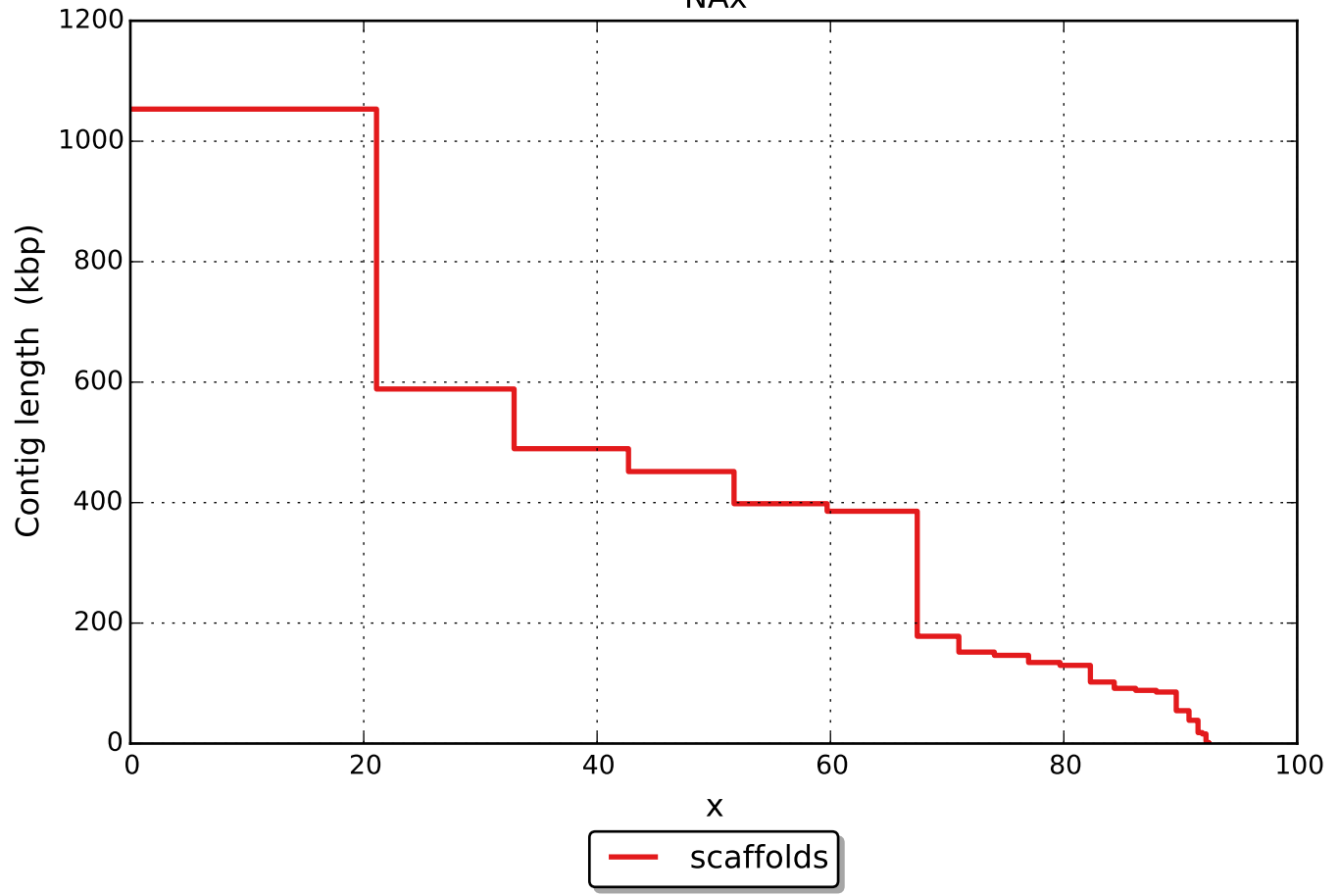




Cumulative length (aligned contigs)



NAx



# NGAx

