

## Report

	scaffolds
# contigs ( $\geq 1000$ bp)	8
# contigs ( $\geq 5000$ bp)	8
# contigs ( $\geq 10000$ bp)	7
# contigs ( $\geq 25000$ bp)	6
# contigs ( $\geq 50000$ bp)	5
Total length ( $\geq 1000$ bp)	1378579
Total length ( $\geq 5000$ bp)	1378579
Total length ( $\geq 10000$ bp)	1368823
Total length ( $\geq 25000$ bp)	1354351
Total length ( $\geq 50000$ bp)	1325023
# contigs	9
Largest contig	478751
Total length	1379388
Reference length	4641652
GC (%)	50.32
Reference GC (%)	50.78
N50	284387
N75	176518
L50	2
L75	4
# misassemblies	14
# misassembled contigs	1
Misassembled contigs length	478751
# local misassemblies	0
# unaligned contigs	0 + 7 part
Unaligned length	886674
Genome fraction (%)	7.157
Duplication ratio	1.483
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2107.93
# indels per 100 kbp	2.11
Largest alignment	46257
NGA50	-

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).

## Misassemblies report

	scaffolds
# misassemblies	14
# relocations	12
# translocations	0
# inversions	2
# possibly misassembled contigs	6
# misassembled contigs	1
Misassembled contigs length	478751
# local misassemblies	0
# mismatches	7003
# indels	7
# short indels	6
# long indels	1
Indels length	18

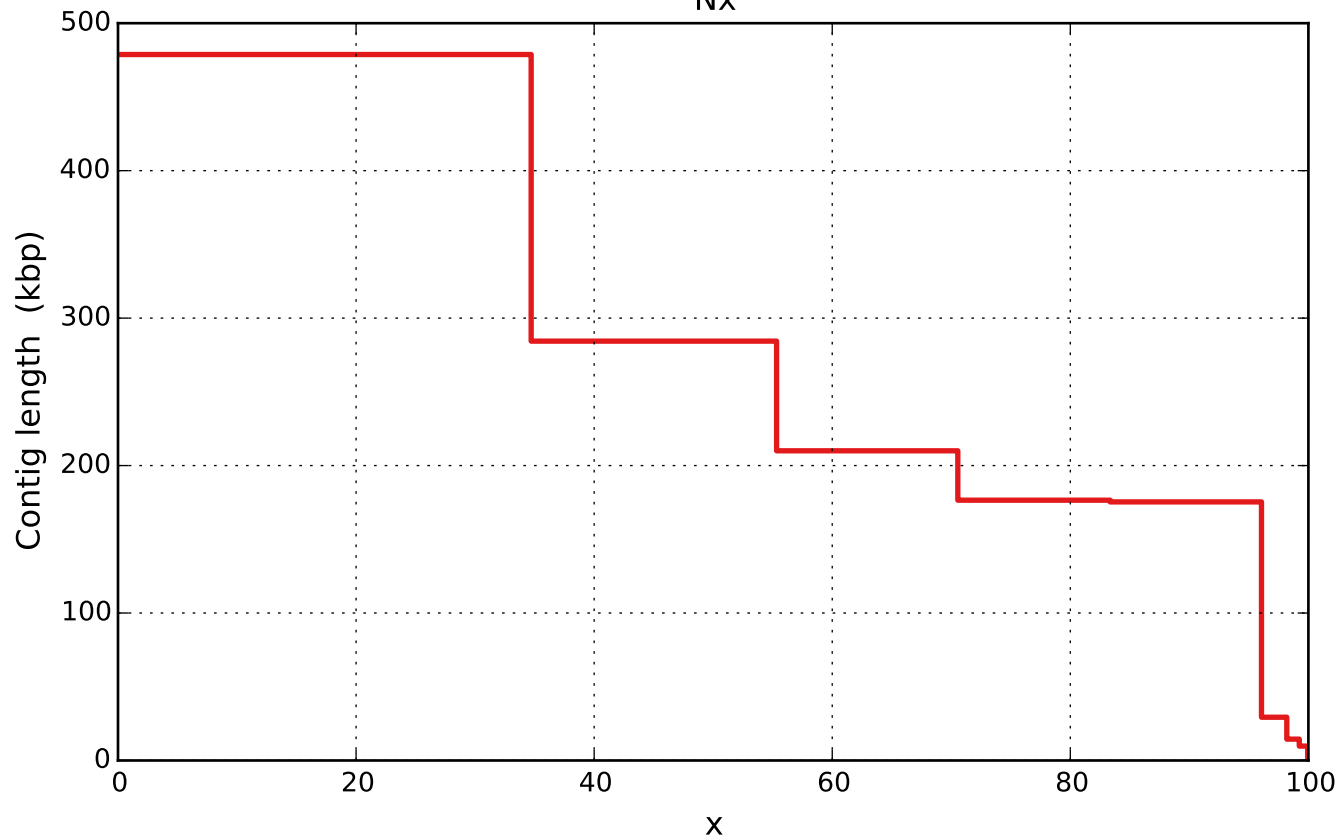
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	7
# with misassembly	2
# both parts are significant	5
Partially unaligned length	886674
# N's	0

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).

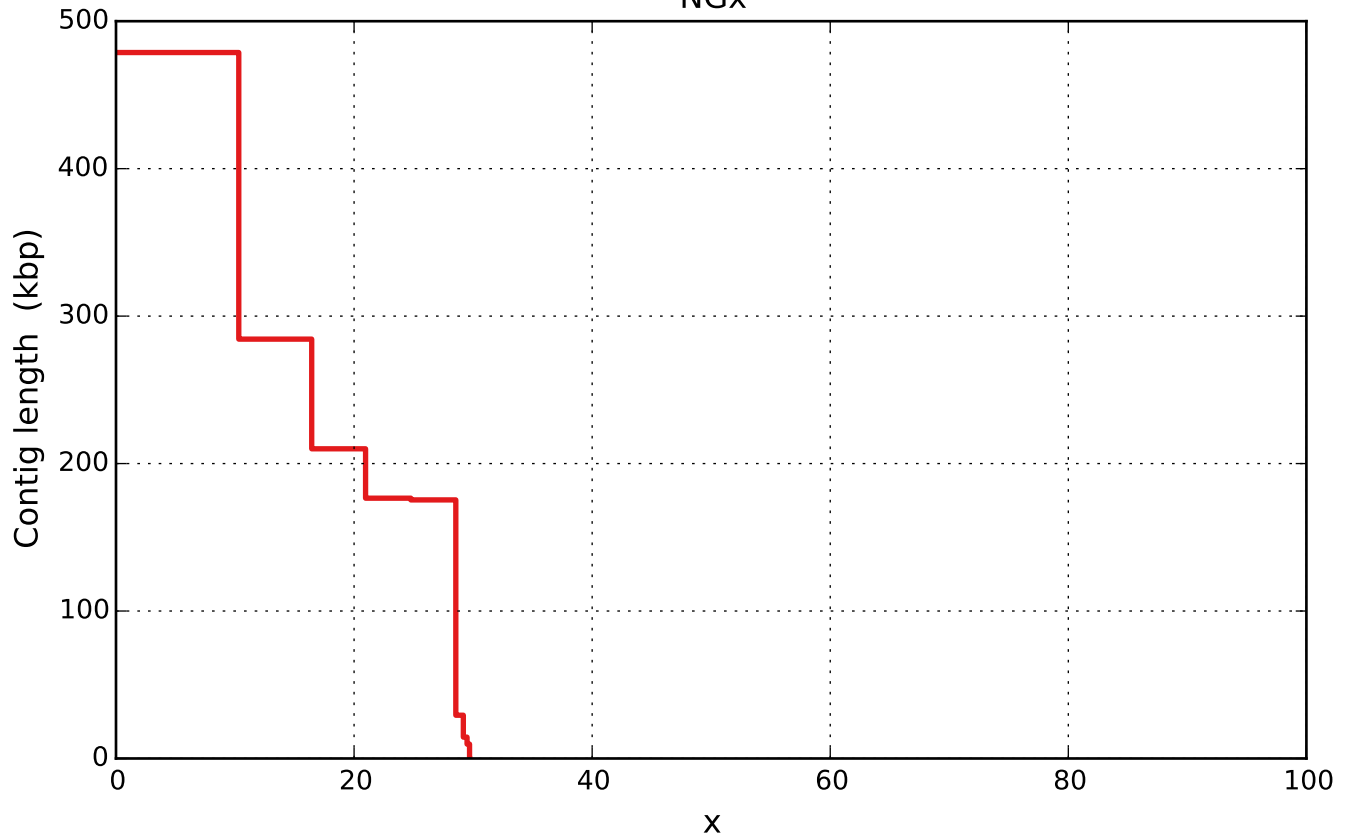
Nx



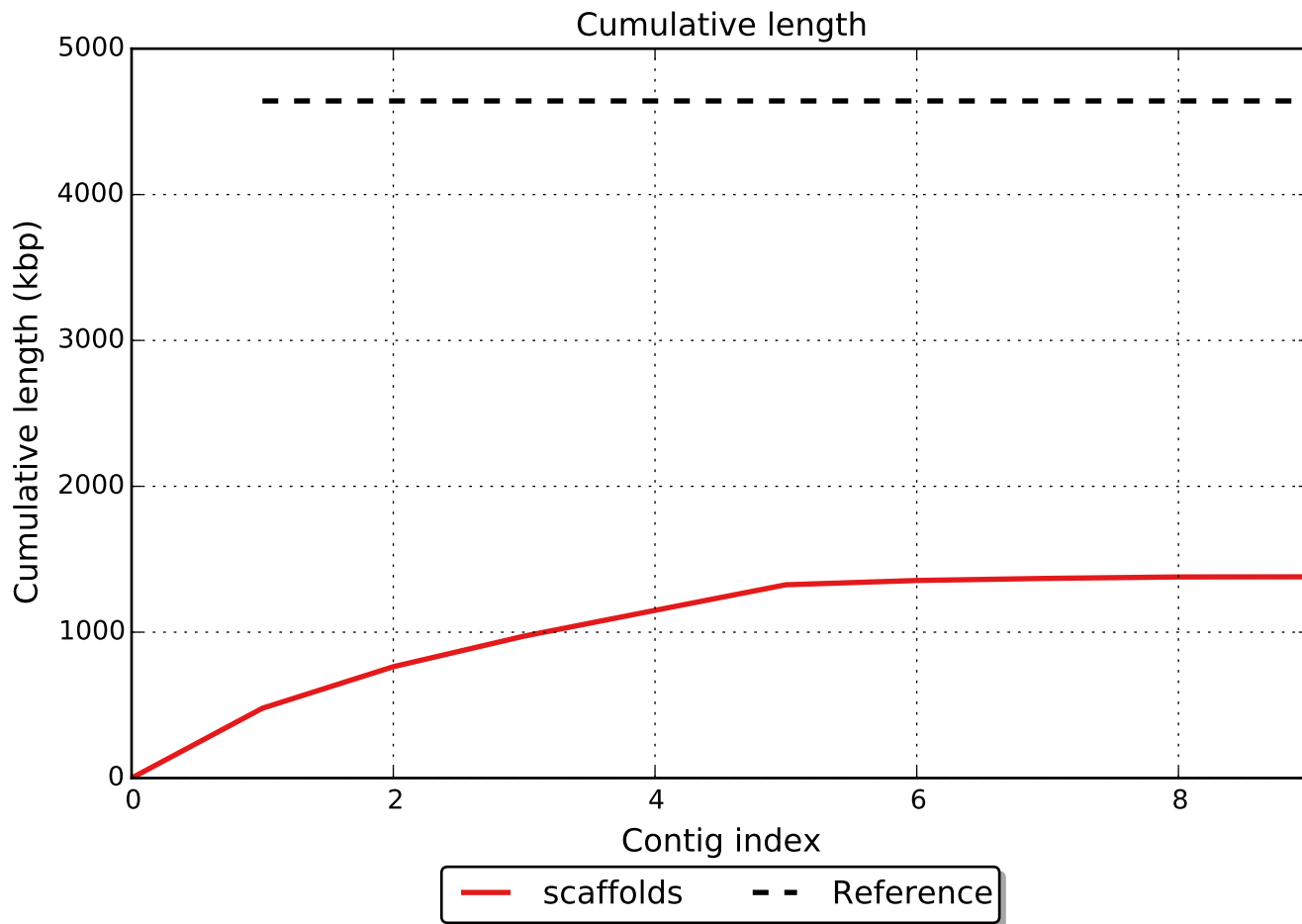
—

scaffolds

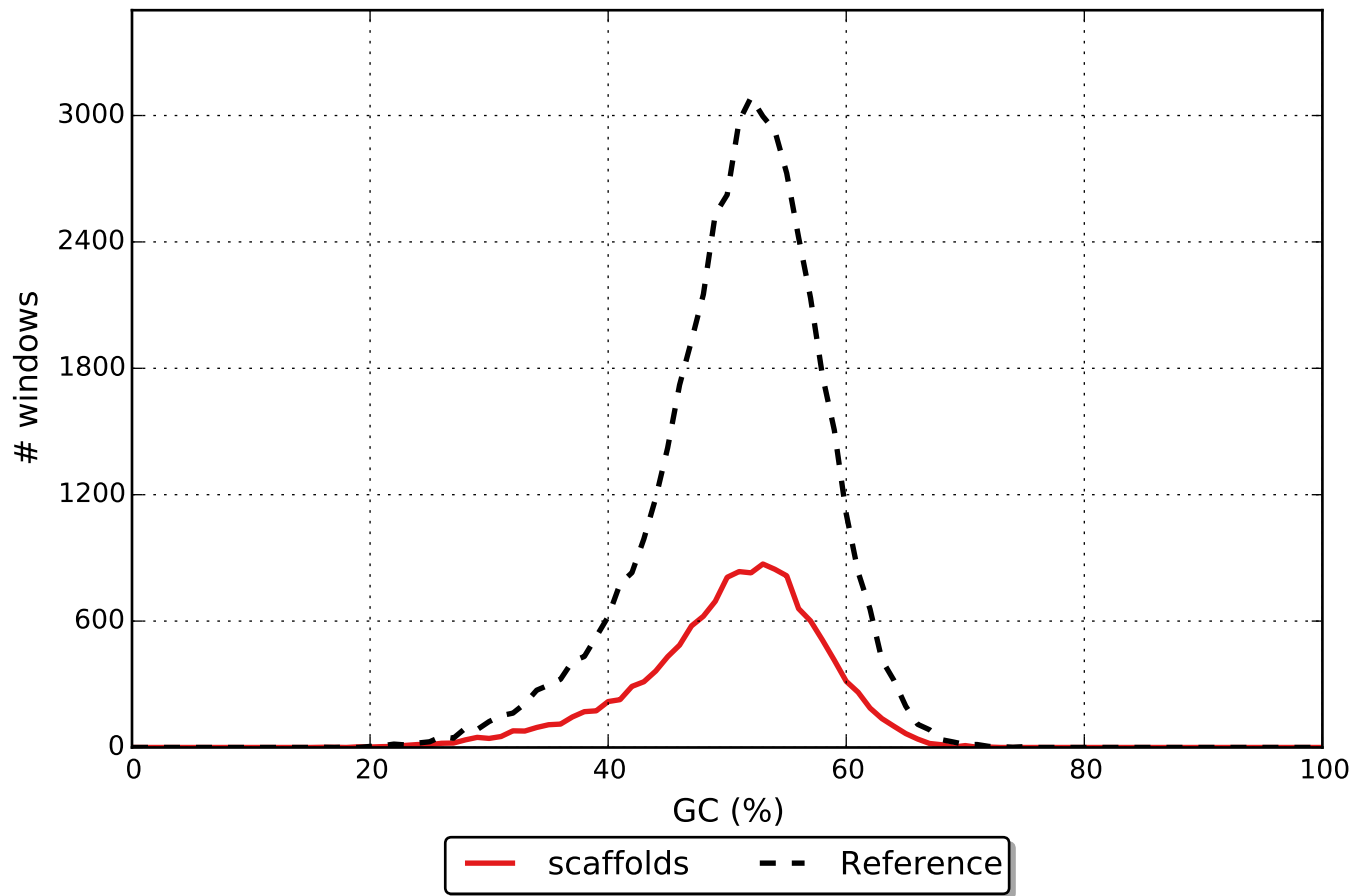
NGx

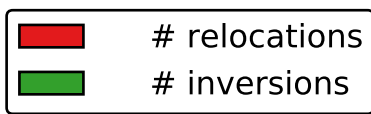
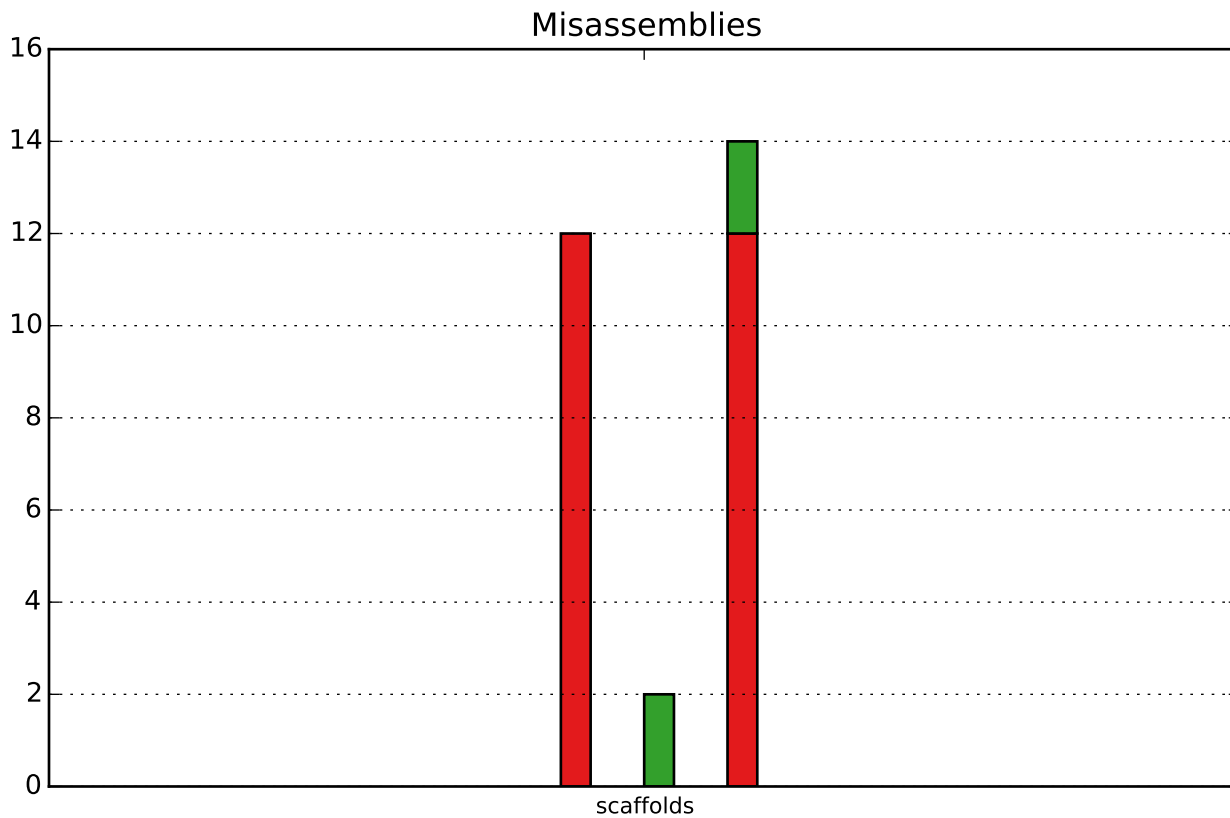


— scaffolds



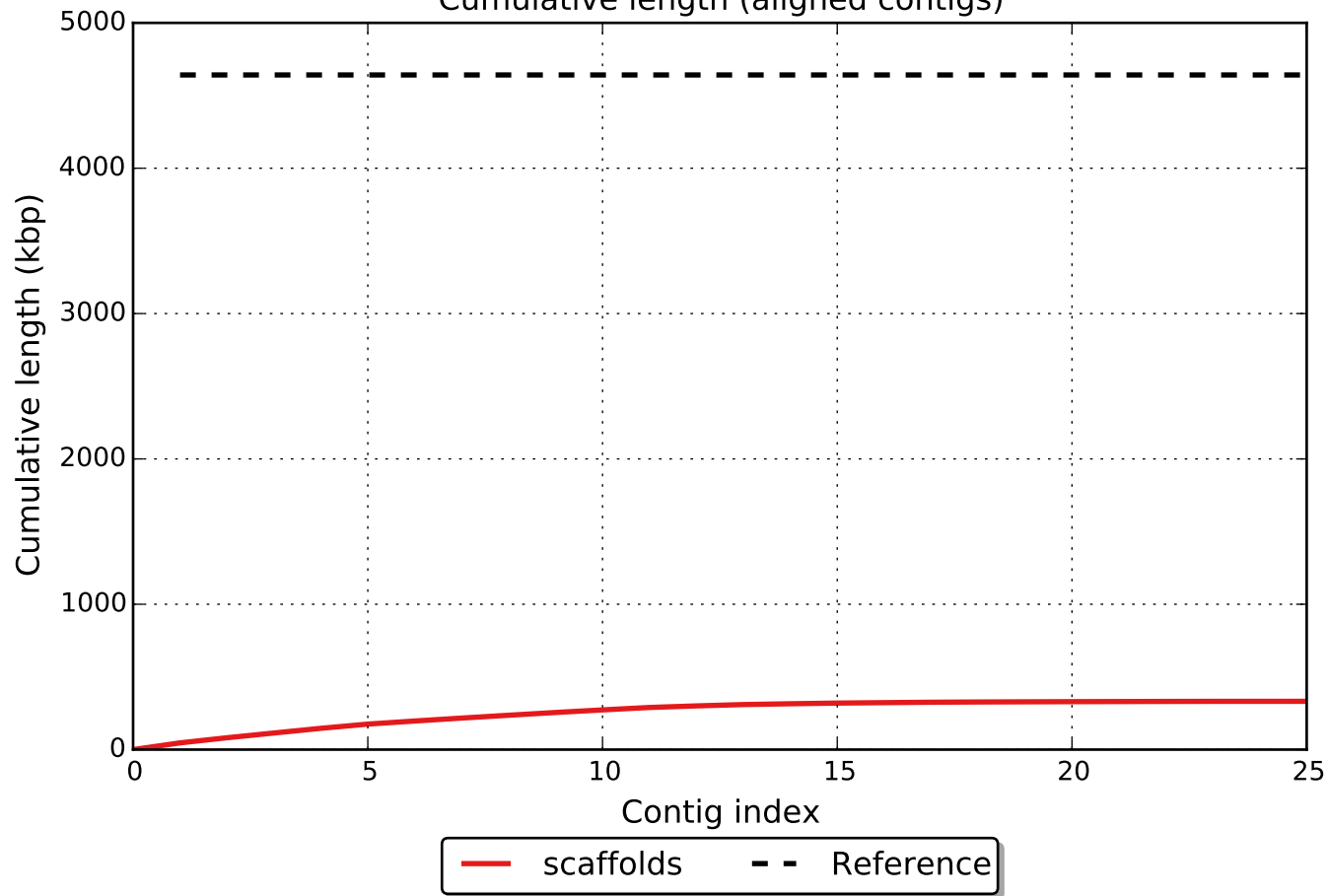
# GC content

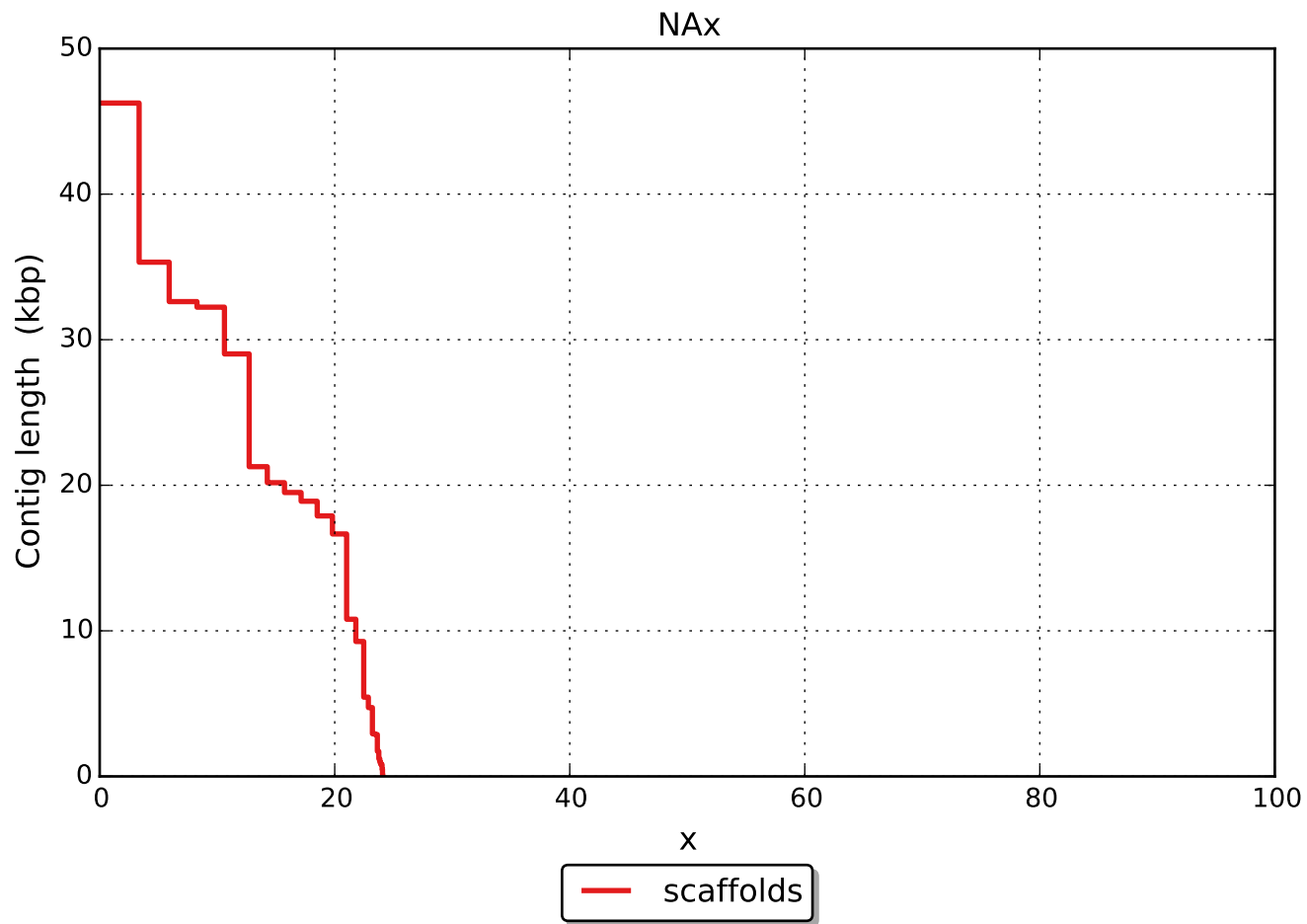






Cumulative length (aligned contigs)





NGAx

