

## Report

	scaffolds
# contigs ( $\geq 1000$ bp)	31
# contigs ( $\geq 5000$ bp)	28
# contigs ( $\geq 10000$ bp)	28
# contigs ( $\geq 25000$ bp)	27
# contigs ( $\geq 50000$ bp)	24
Total length ( $\geq 1000$ bp)	6000633
Total length ( $\geq 5000$ bp)	5996107
Total length ( $\geq 10000$ bp)	5996107
Total length ( $\geq 25000$ bp)	5985304
Total length ( $\geq 50000$ bp)	5873027
# contigs	34
Largest contig	700824
Total length	6003325
Reference length	4641652
GC (%)	50.71
Reference GC (%)	50.78
N50	333124
NG50	373445
N75	184667
NG75	330294
L50	7
LG50	5
L75	12
LG75	8
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	349059
# local misassemblies	1
# unaligned contigs	0 + 8 part
Unaligned length	1194117
Genome fraction (%)	99.582
Duplication ratio	1.040
# N's per 100 kbp	0.00
# mismatches per 100 kbp	352.62
# indels per 100 kbp	1.10
Largest alignment	700544
NA50	325448
NGA50	373445
NA75	54773
NGA75	188536
LA50	7
LGA50	5
LA75	18
LGA75	9

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	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	8
# misassembled contigs	1
Misassembled contigs length	349059
# local misassemblies	1
# mismatches	16299
# indels	51
# short indels	51
# long indels	0
Indels length	51

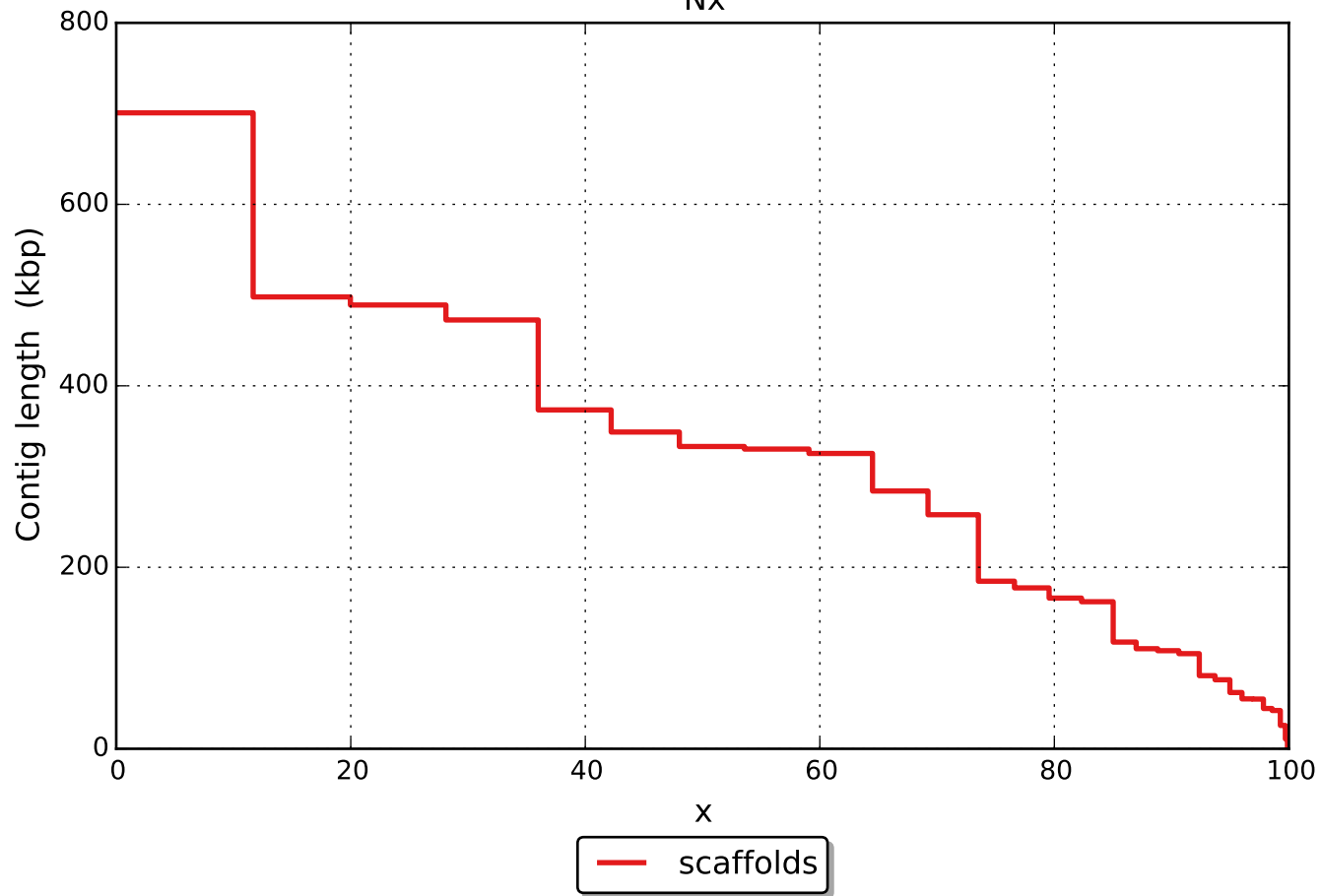
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

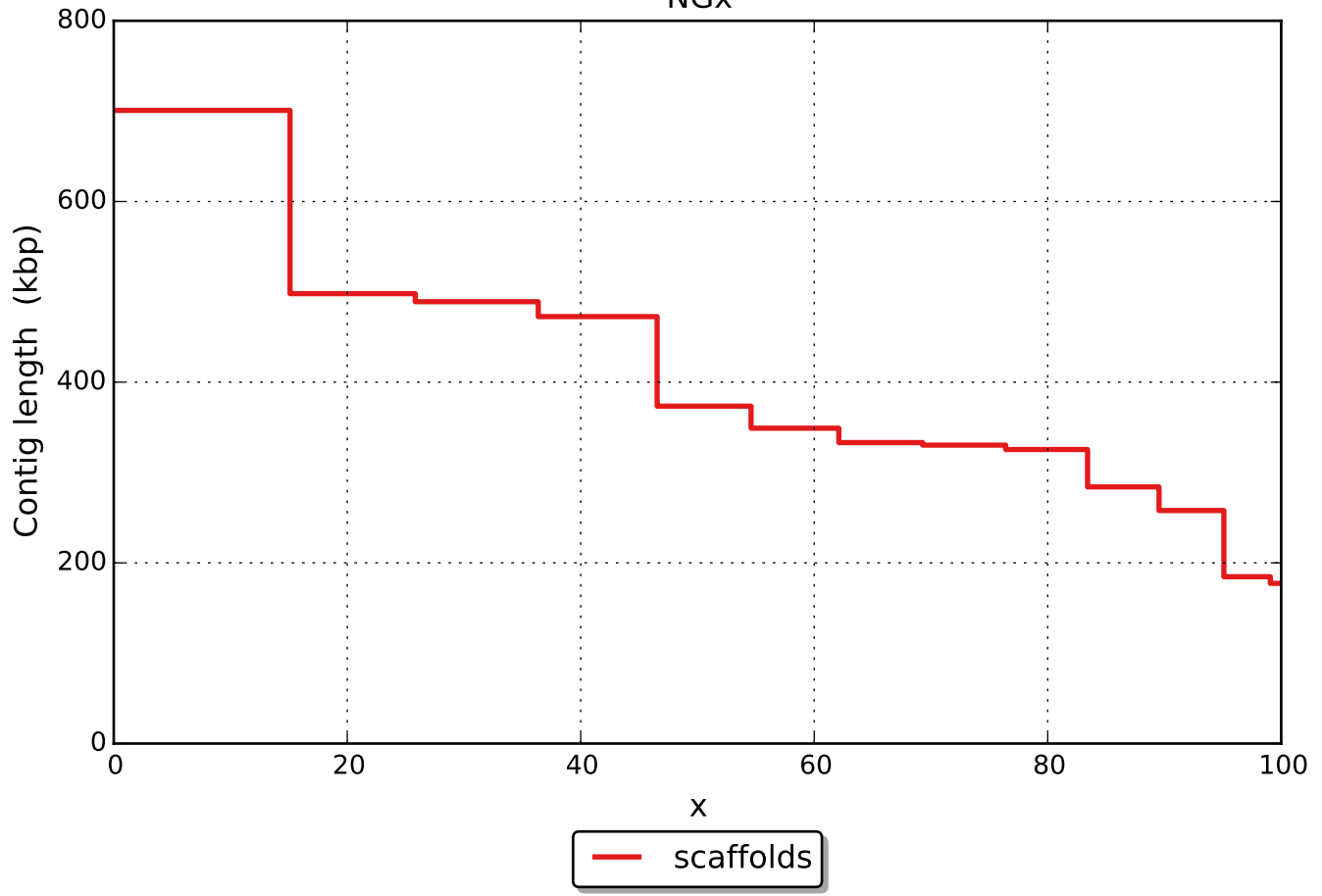
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	8
# with misassembly	3
# both parts are significant	7
Partially unaligned length	1194117
# N's	0

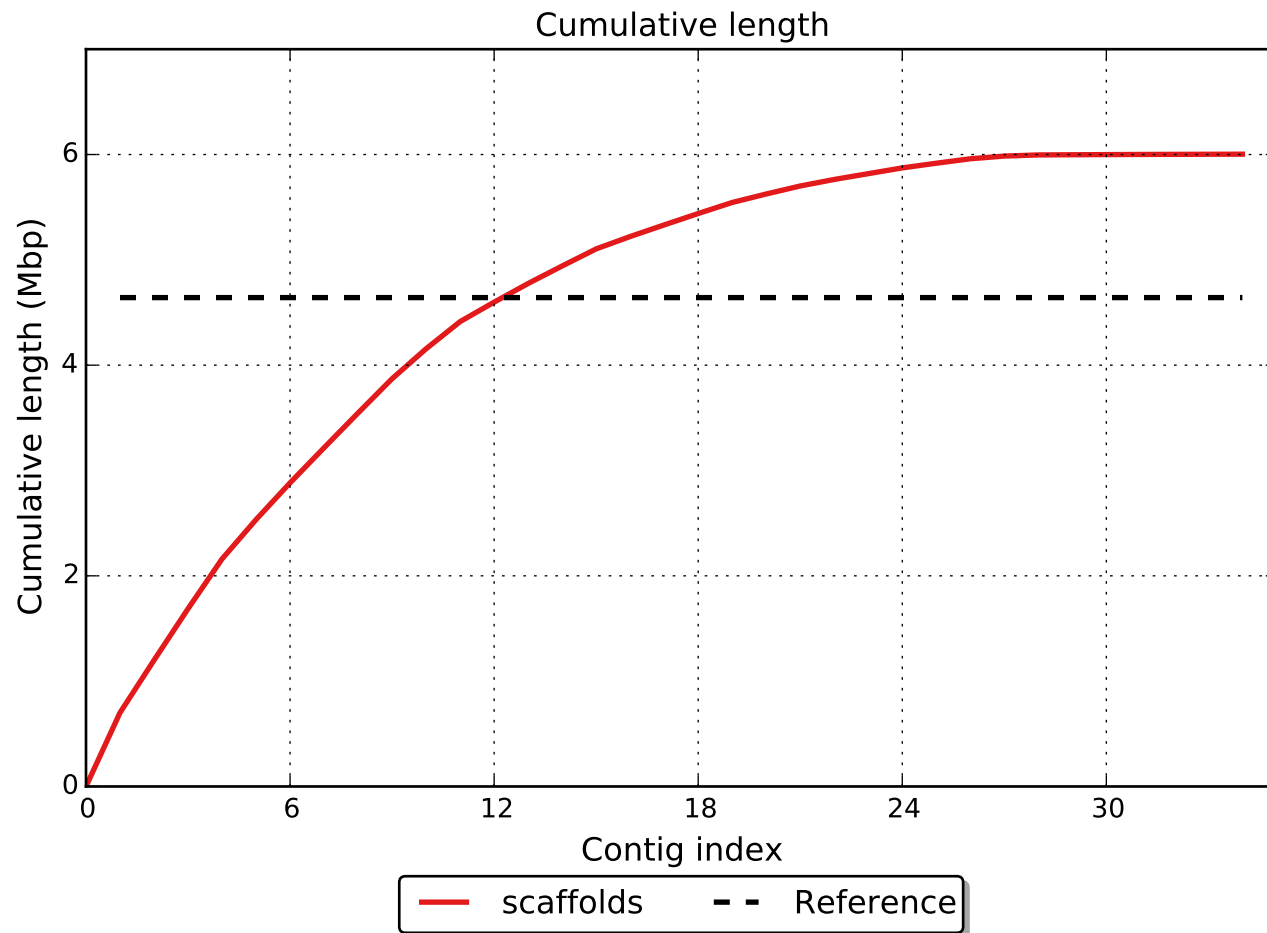
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

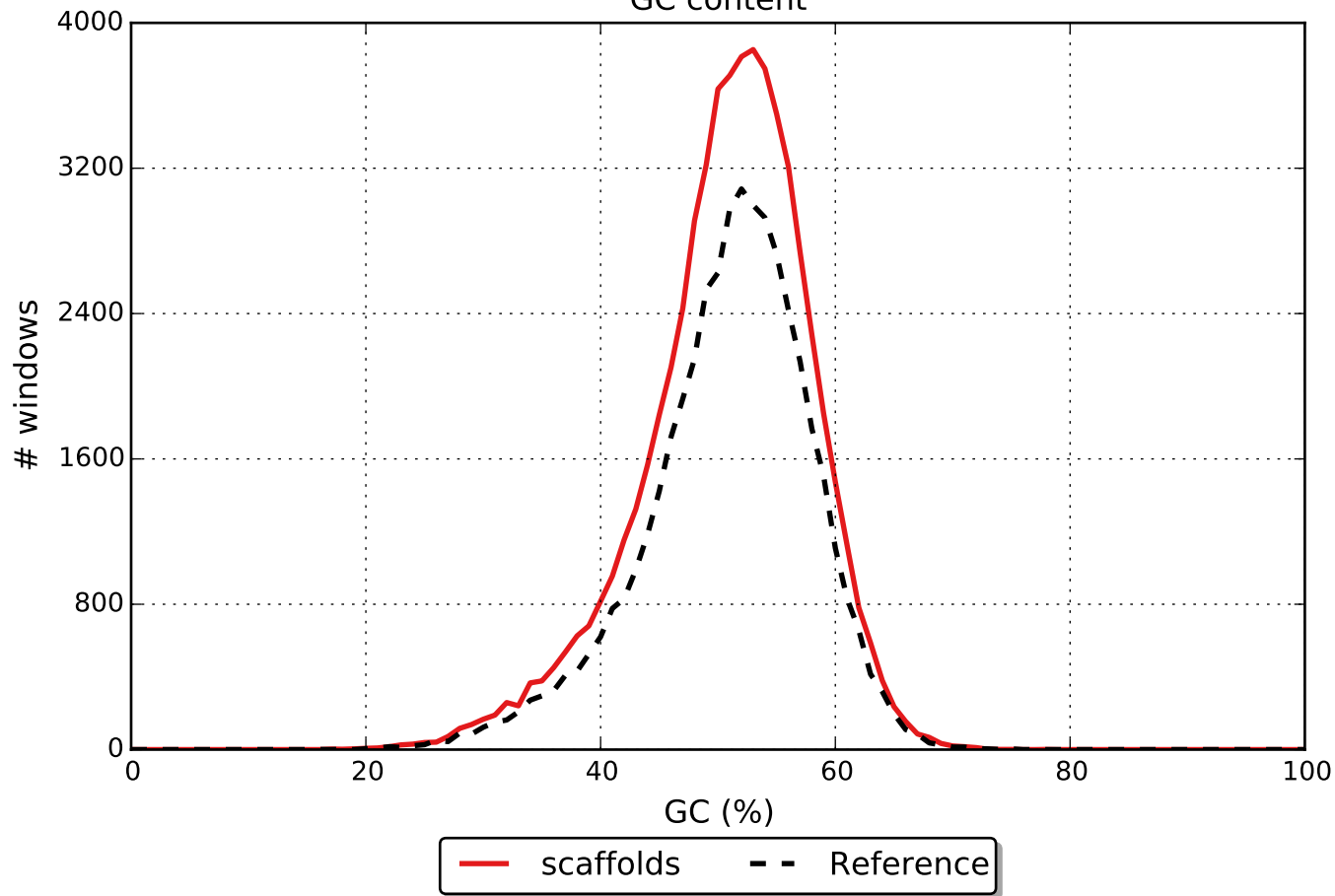


NGx





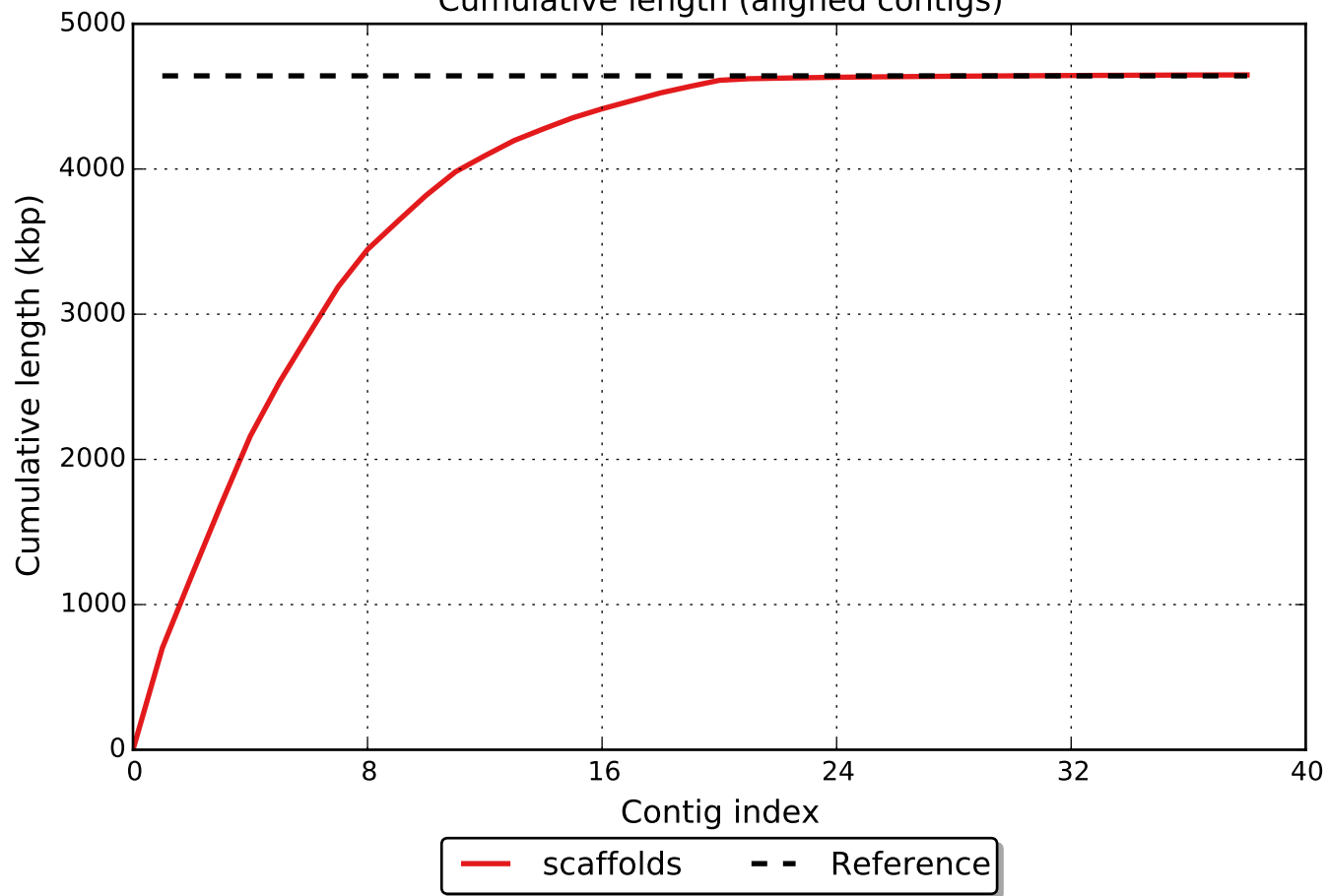
GC content



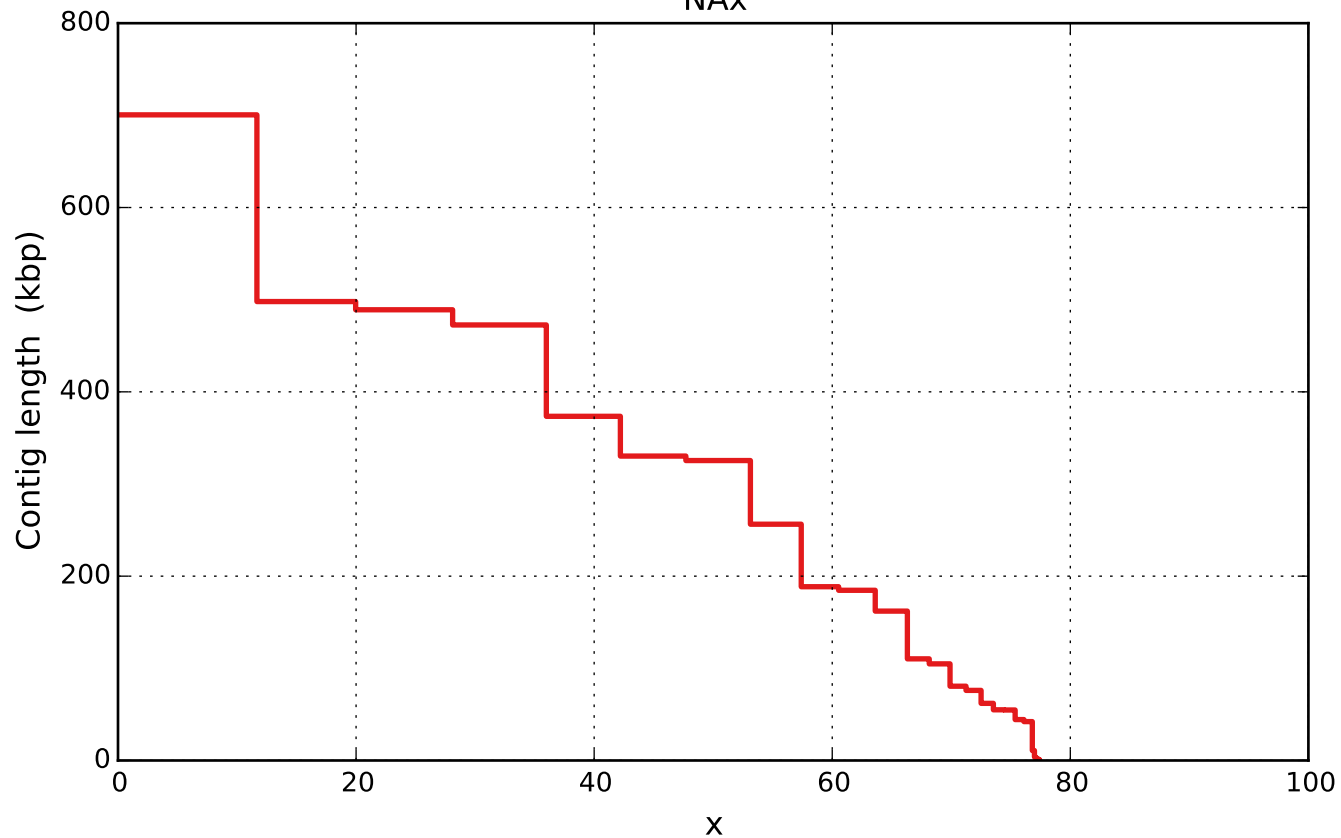




Cumulative length (aligned contigs)



NAx



— scaffolds

# NGAx

