

## Report

	scaffolds
# contigs ( $\geq 1000$ bp)	49
# contigs ( $\geq 5000$ bp)	42
# contigs ( $\geq 10000$ bp)	41
# contigs ( $\geq 25000$ bp)	40
# contigs ( $\geq 50000$ bp)	36
Total length ( $\geq 1000$ bp)	6660798
Total length ( $\geq 5000$ bp)	6651758
Total length ( $\geq 10000$ bp)	6646292
Total length ( $\geq 25000$ bp)	6633125
Total length ( $\geq 50000$ bp)	6495789
# contigs	59
Largest contig	529644
Total length	6667539
Reference length	4641652
GC (%)	50.88
Reference GC (%)	50.78
N50	210748
NG50	305443
N75	132907
NG75	210558
L50	10
LG50	6
L75	19
LG75	11
# misassemblies	3
# misassembled contigs	2
Misassembled contigs length	578950
# local misassemblies	1
# unaligned contigs	0 + 15 part
Unaligned length	1900420
Genome fraction (%)	99.233
Duplication ratio	1.035
# N's per 100 kbp	0.33
# mismatches per 100 kbp	379.11
# indels per 100 kbp	1.00
Largest alignment	529644
NA50	182223
NGA50	301763
NGA75	128117
LA50	11
LGA50	7
LGA75	12

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	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	15
# misassembled contigs	2
Misassembled contigs length	578950
# local misassemblies	1
# mismatches	17462
# indels	46
# short indels	45
# long indels	1
Indels length	67

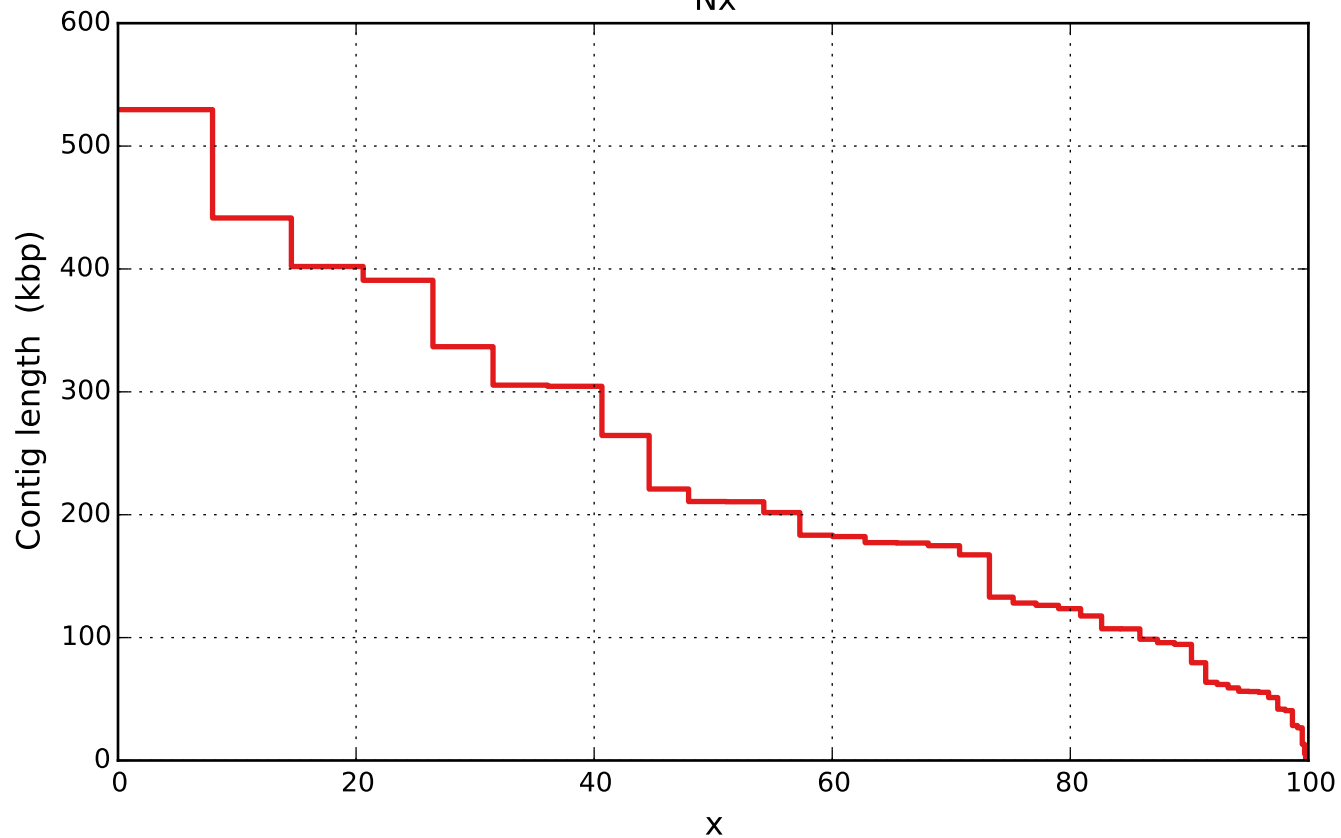
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	15
# with misassembly	6
# both parts are significant	14
Partially unaligned length	1900420
# N's	22

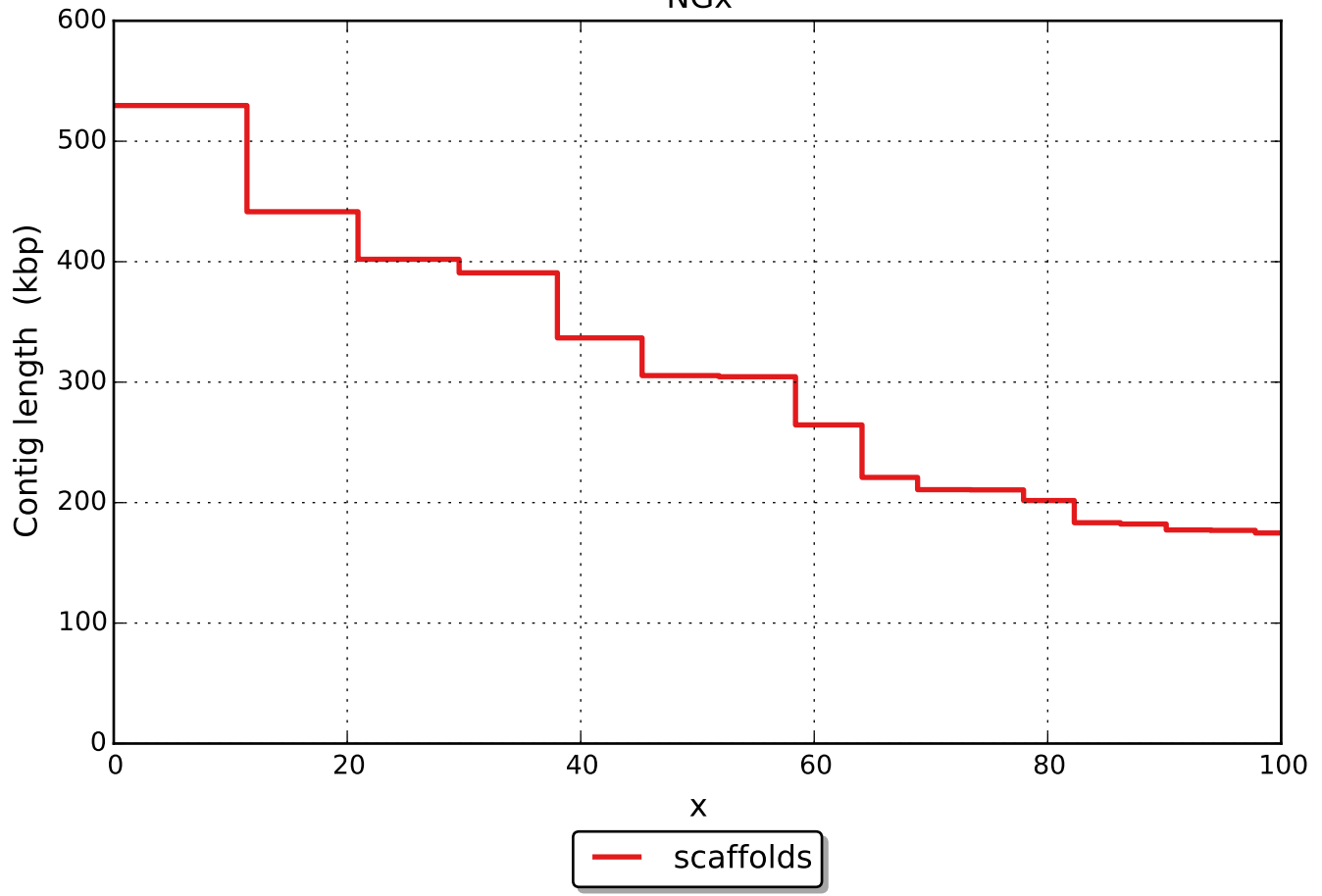
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

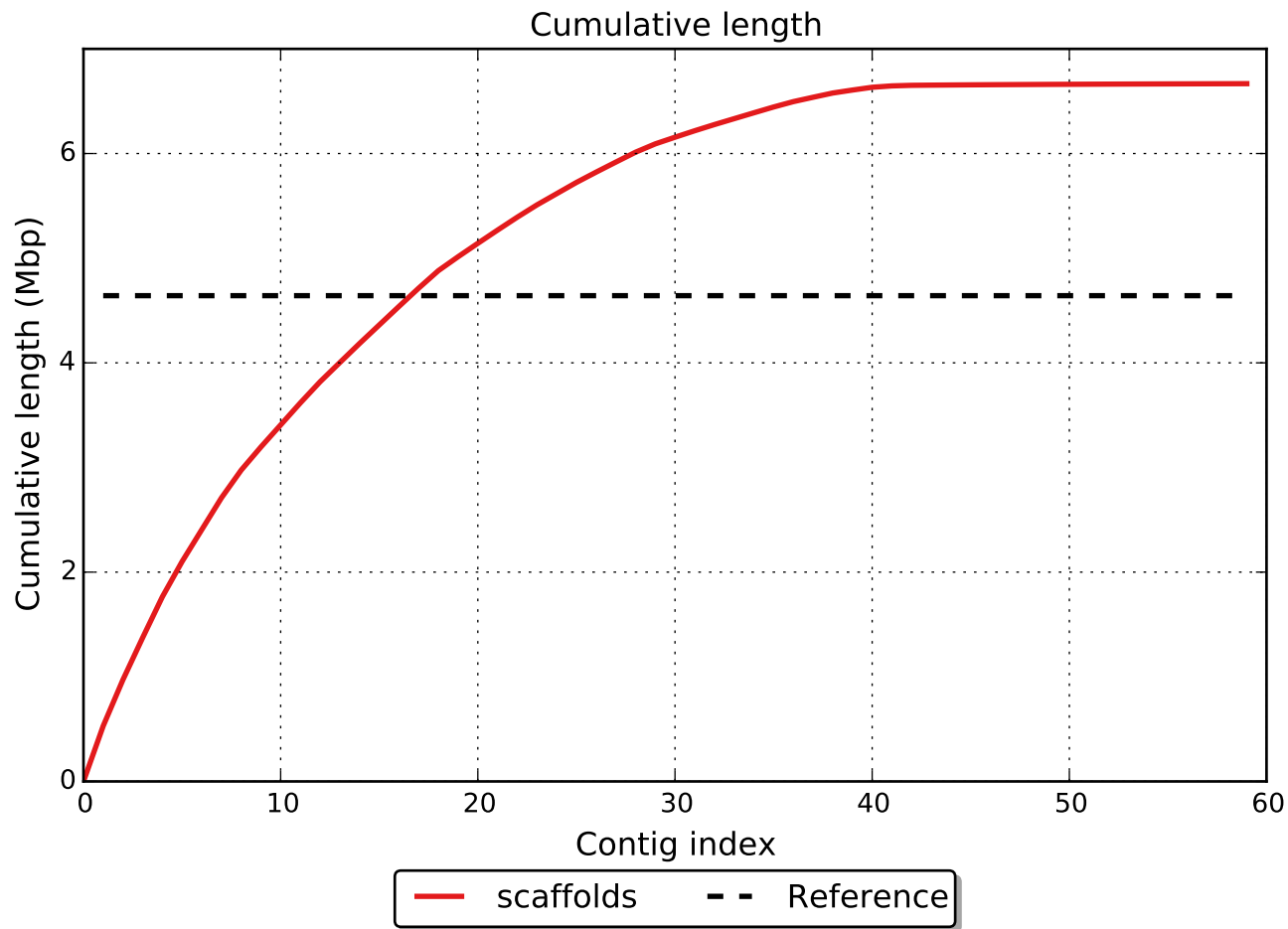
Nx



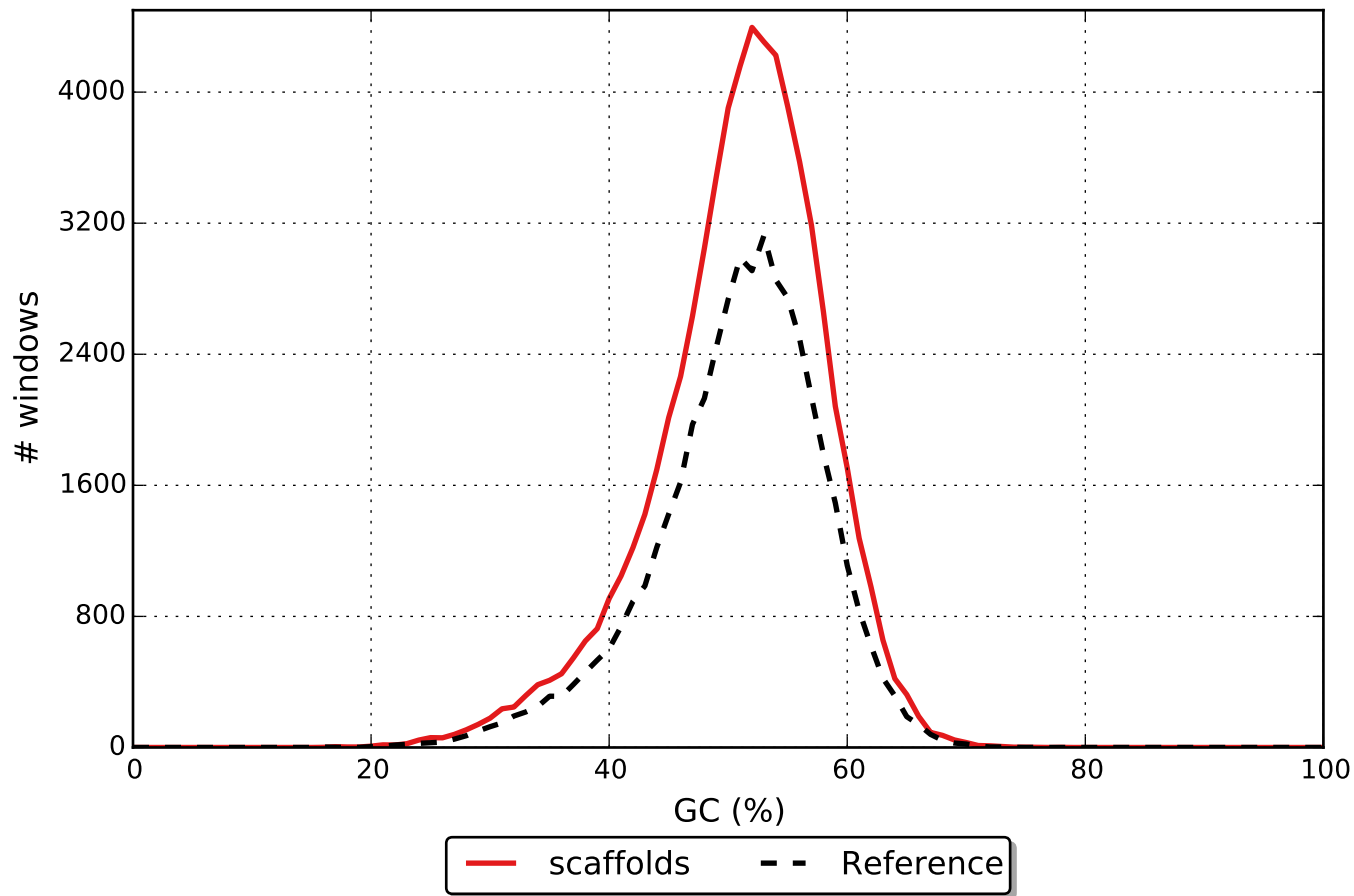
— scaffolds

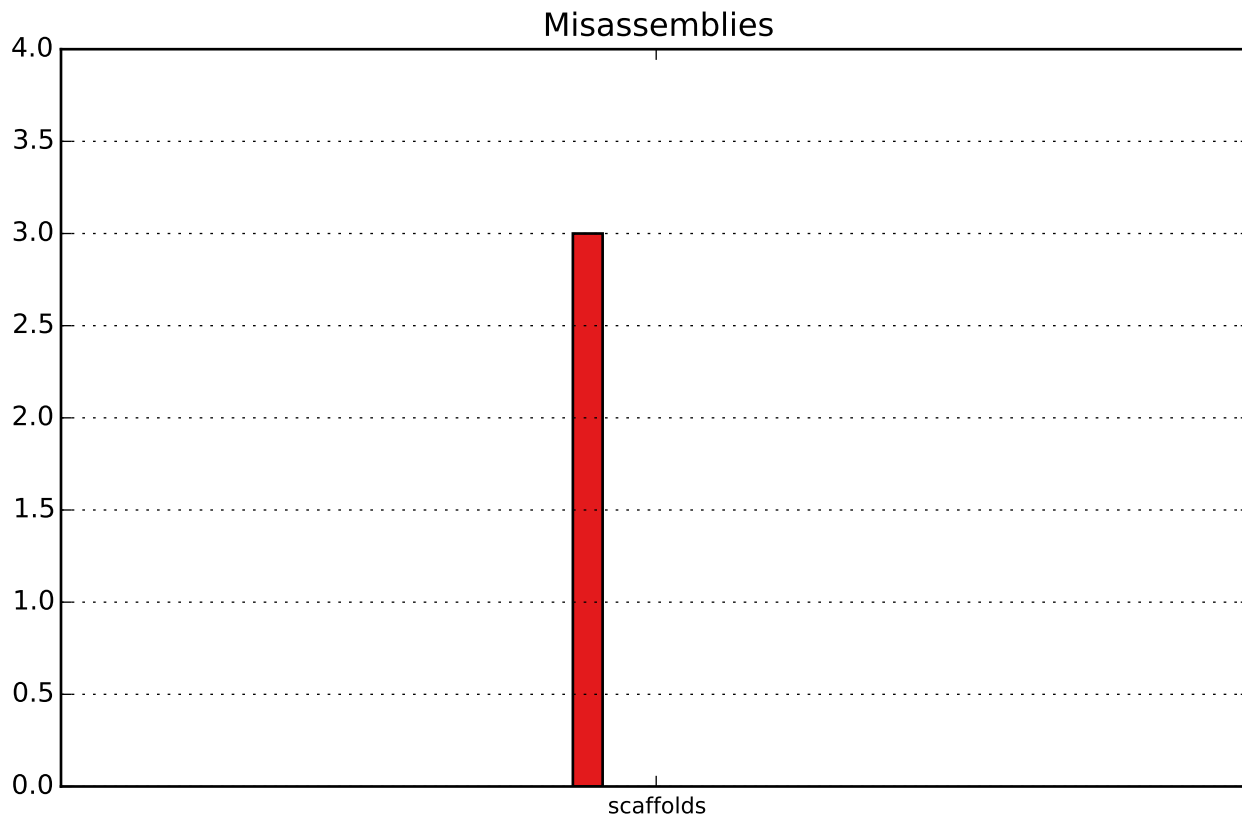
NGx





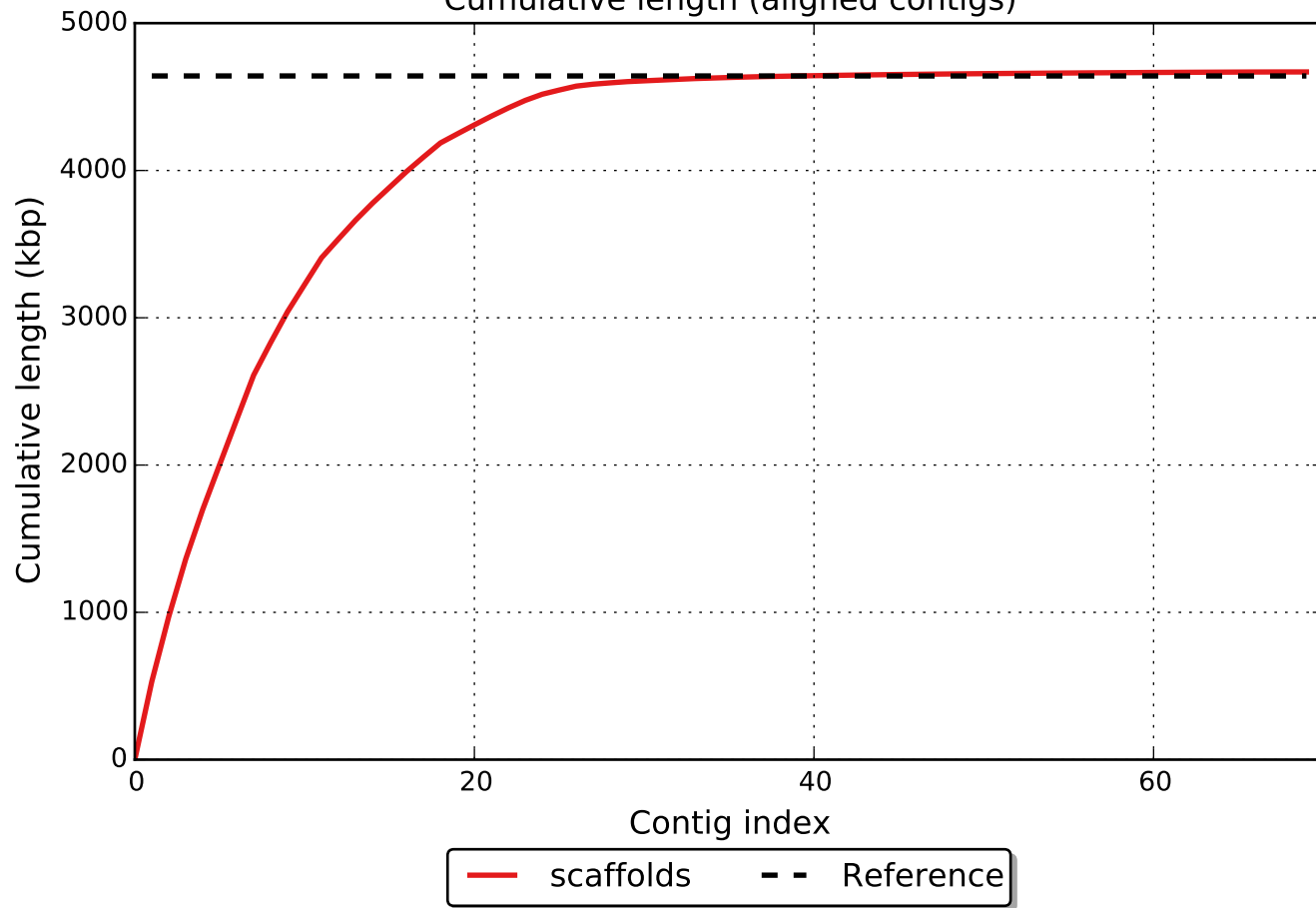
GC content



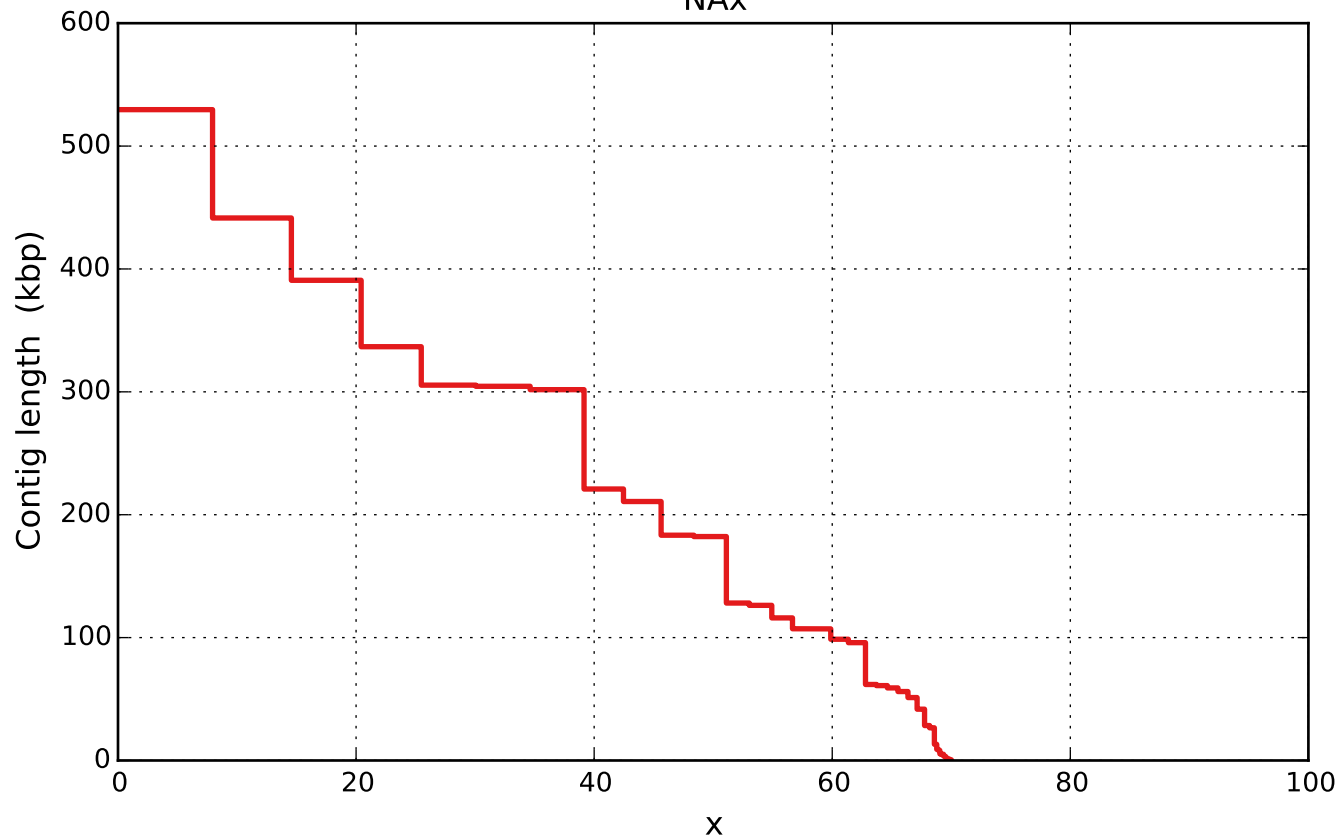




Cumulative length (aligned contigs)



NAx



— scaffolds

# NGAx

