

# Report

	scaffolds
# contigs ( $\geq 1000$ bp)	10
# contigs ( $\geq 5000$ bp)	1
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 1000$ bp)	18699
Total length ( $\geq 5000$ bp)	5443
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	71
Largest contig	5443
Total length	56195
Reference length	4641652
GC (▼)	51.08
Reference GC (▼)	50.79
N50	674
N75	562
L50	22
L75	45
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	7077
# local misassemblies	1
# unaligned contigs	0 + 8 part
Unaligned length	795
Genome fraction (▼)	1.186
Duplication ratio	1.007
# N's per 100 kbp	676.22
# mismatches per 100 kbp	694.15
# indels per 100 kbp	70.87
Largest alignment	5372
NA50	649
NGA50	-
NA75	556
LA50	24
LA75	48

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

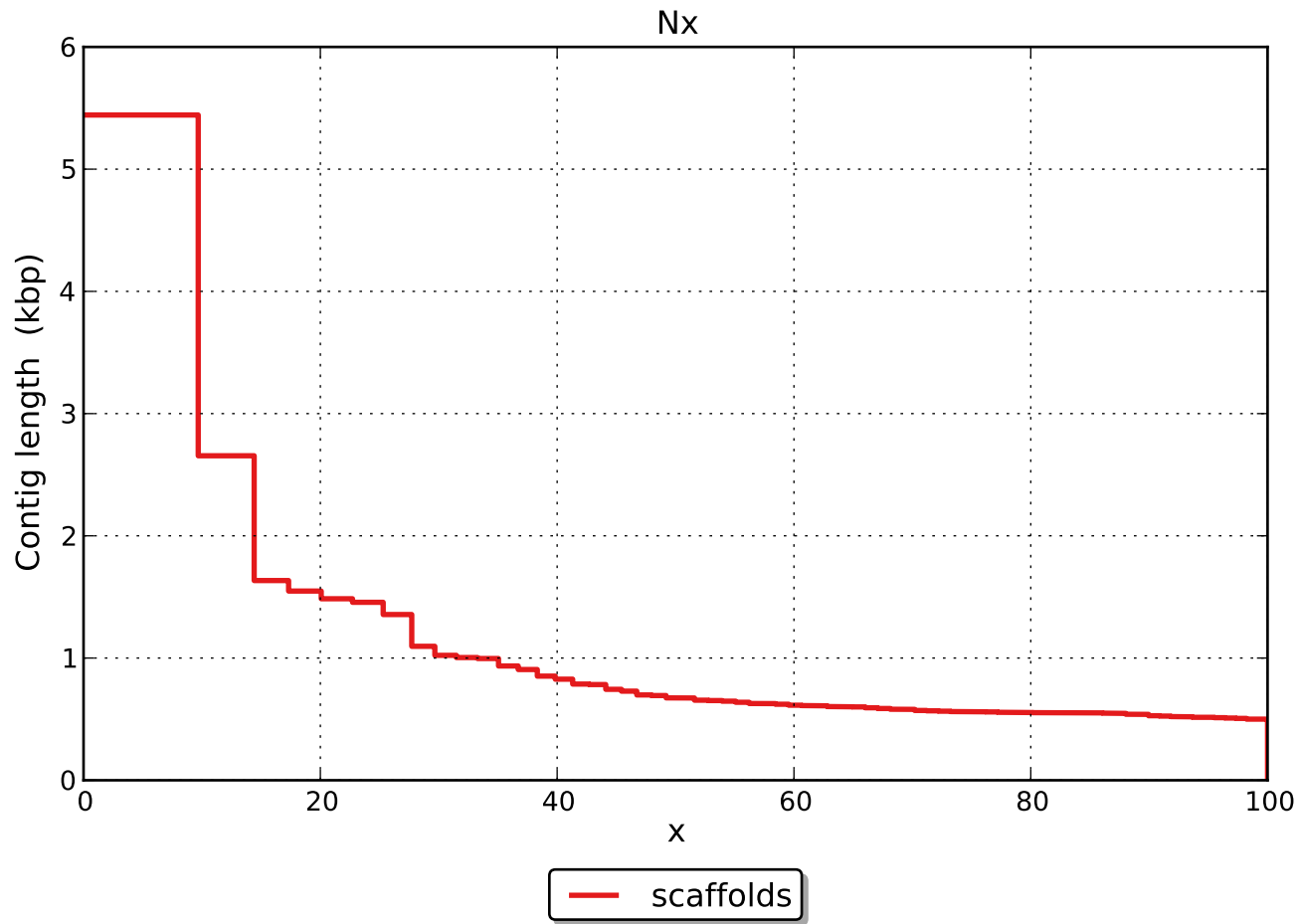
	scaffolds
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	7077
# local misassemblies	1
# mismatches	382
# indels	39
# short indels	24
# long indels	15
Indels length	218

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).

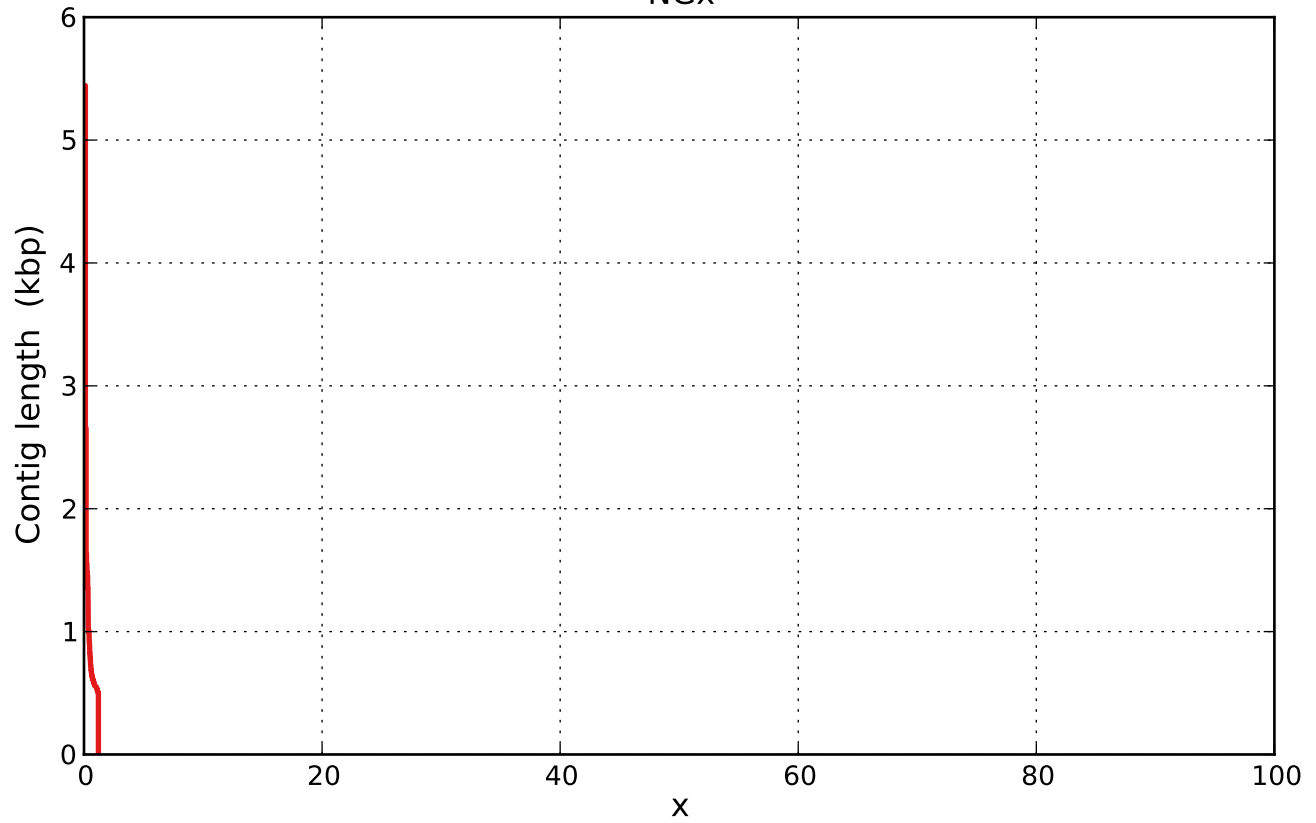
## Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	8
# with misassembly	0
# both parts are significant	0
Partially unaligned length	795
# N's	380

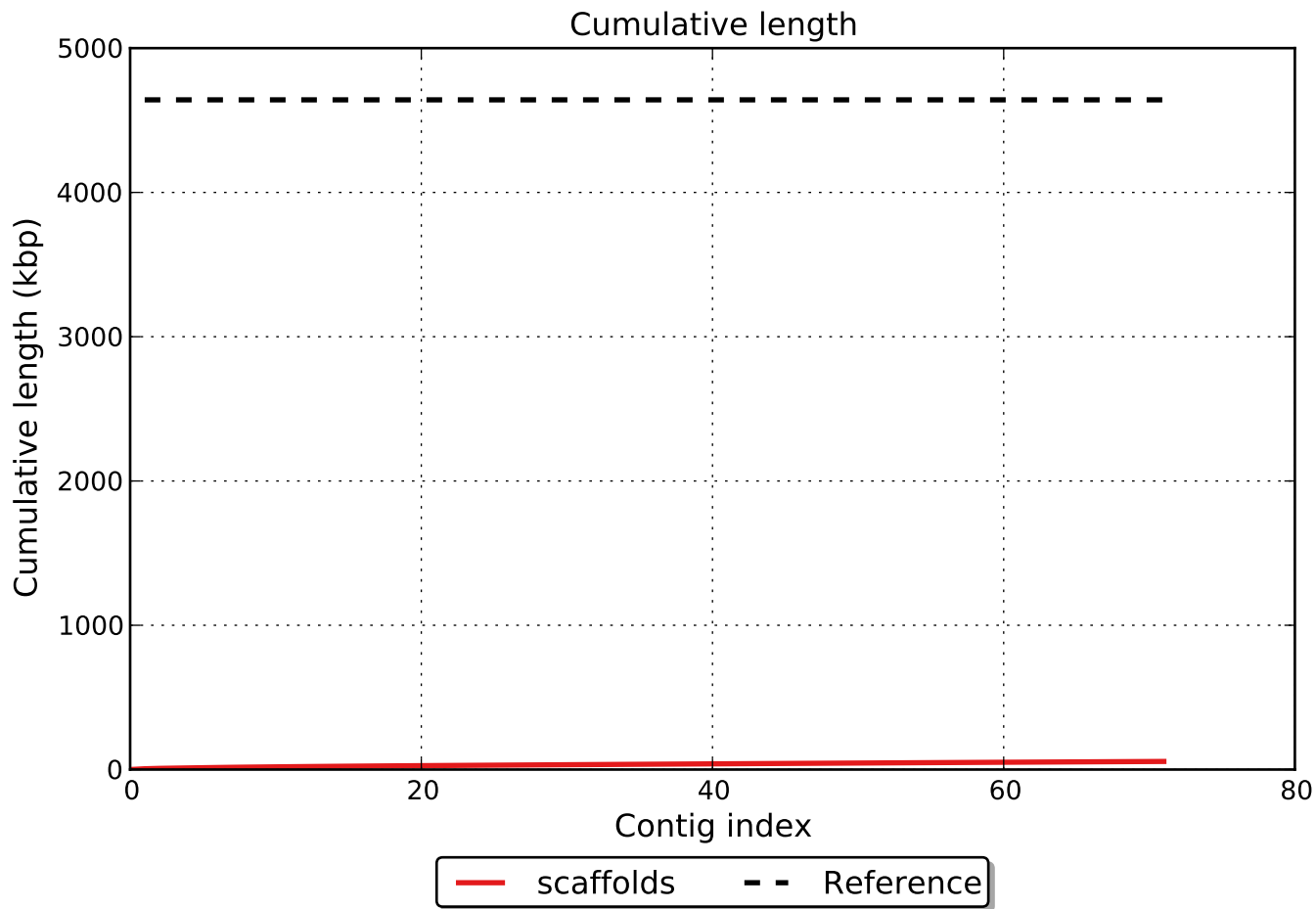
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



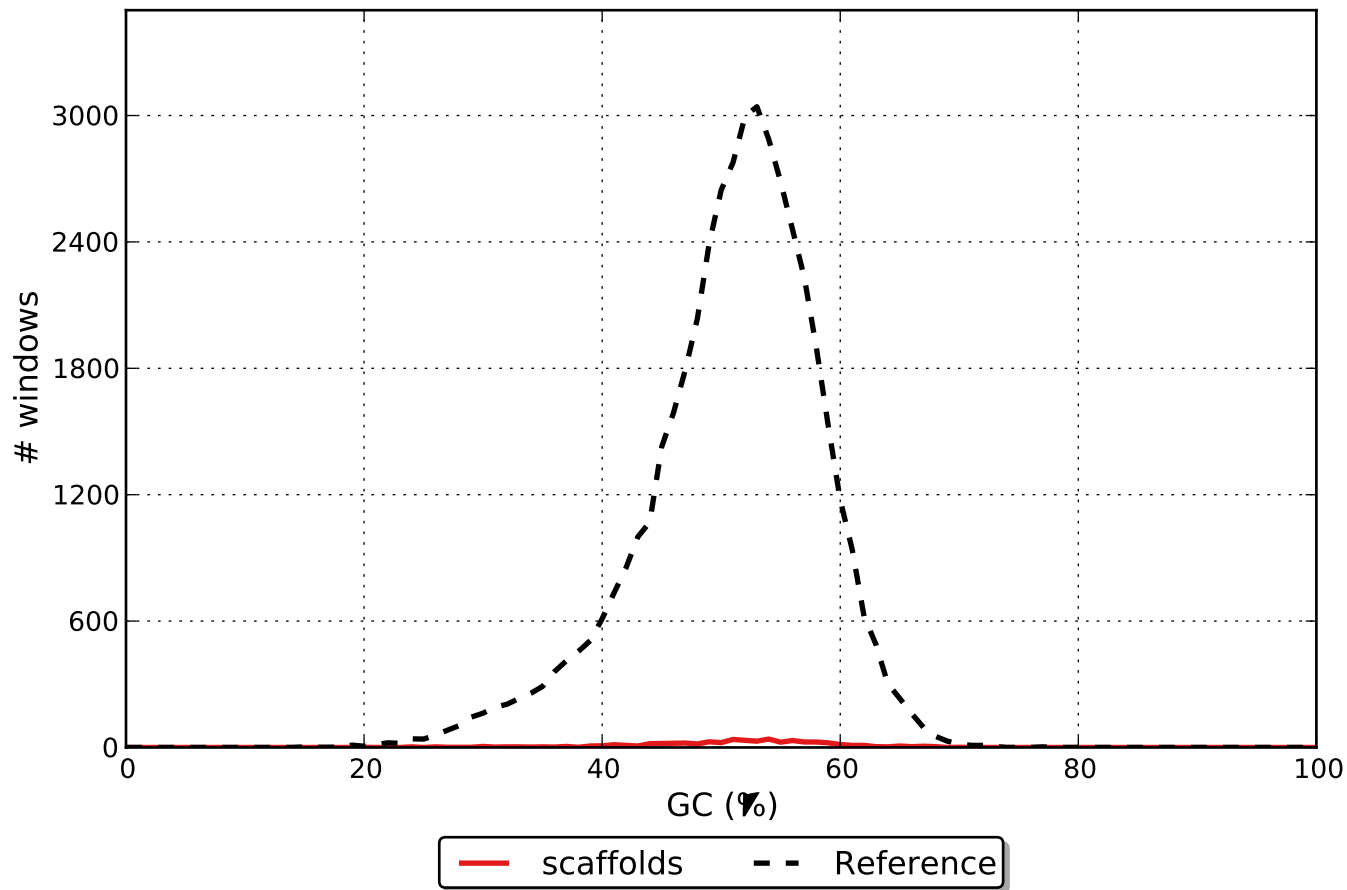
NGx

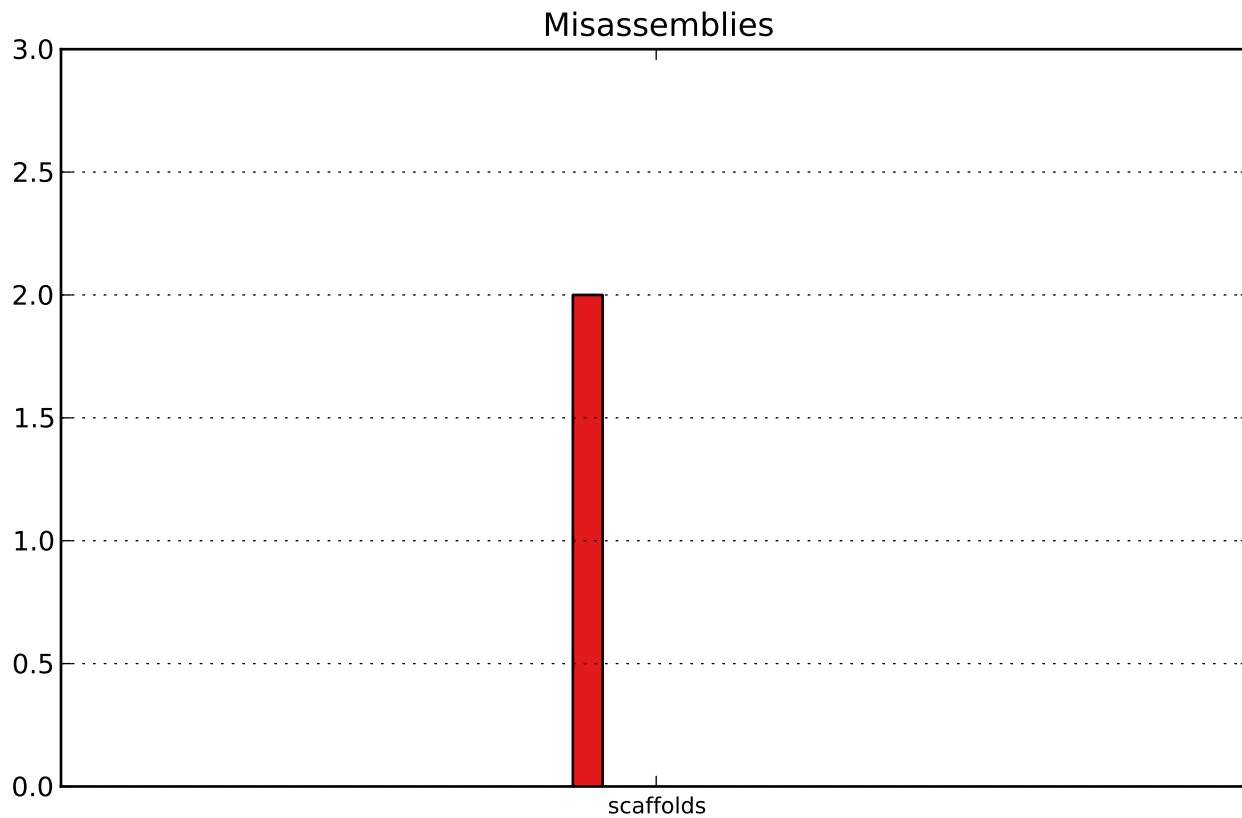


— scaffolds



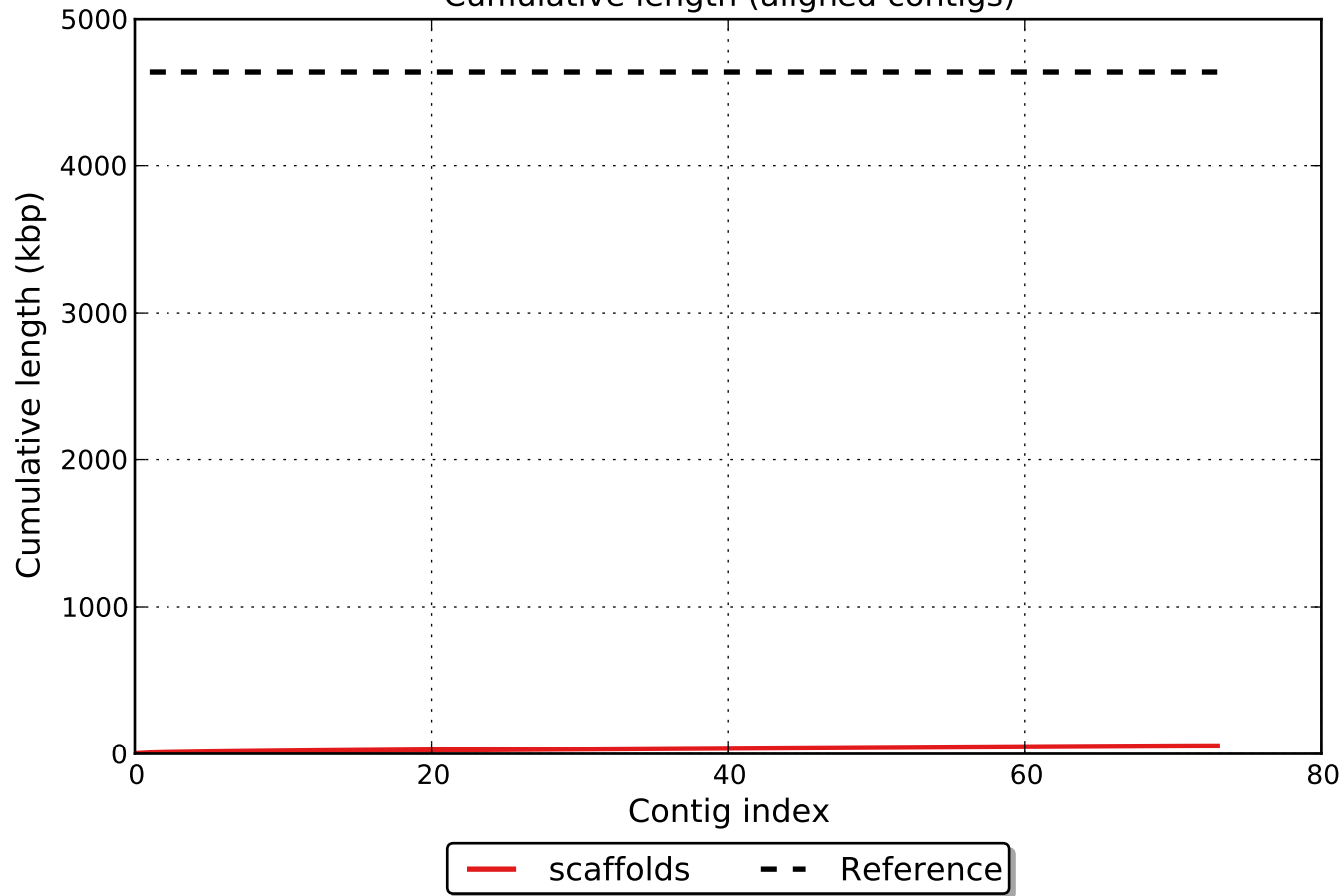
# GC content



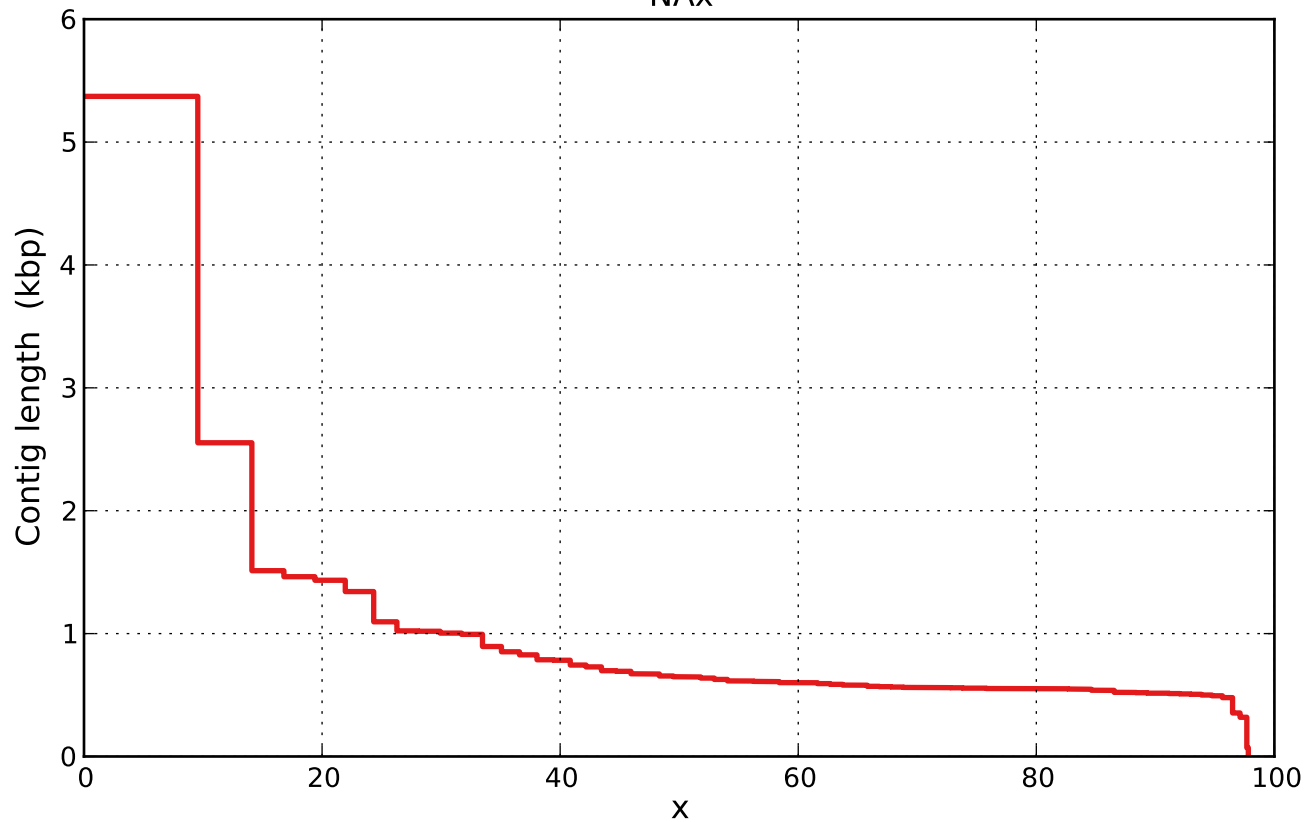




Cumulative length (aligned contigs)



NAx



— scaffolds

