

## Report

	contigs
# contigs ( $\geq 0$ bp)	858
# contigs ( $\geq 1000$ bp)	131
# contigs ( $\geq 5000$ bp)	84
# contigs ( $\geq 10000$ bp)	65
# contigs ( $\geq 25000$ bp)	45
# contigs ( $\geq 50000$ bp)	29
Total length ( $\geq 0$ bp)	4646713
Total length ( $\geq 1000$ bp)	4552003
Total length ( $\geq 5000$ bp)	4429052
Total length ( $\geq 10000$ bp)	4292835
Total length ( $\geq 25000$ bp)	3963006
Total length ( $\geq 50000$ bp)	3370591
# contigs	142
Largest contig	269551
Total length	4559641
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	97827
NG50	97827
N75	45320
NG75	45078
L50	15
LG50	15
L75	31
LG75	32
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	39208
# local misassemblies	6
# unaligned contigs	0 + 1 part
Unaligned length	21
Genome fraction (%)	98.132
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	22.50
# indels per 100 kbp	0.86
Largest alignment	269551
NA50	97825
NGA50	97825
NA75	45320
NGA75	45078
LA50	15
LGA50	15
LA75	31
LGA75	32

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

	contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	39208
# local misassemblies	6
# mismatches	1025
# indels	39
# short indels	39
# long indels	0
Indels length	47

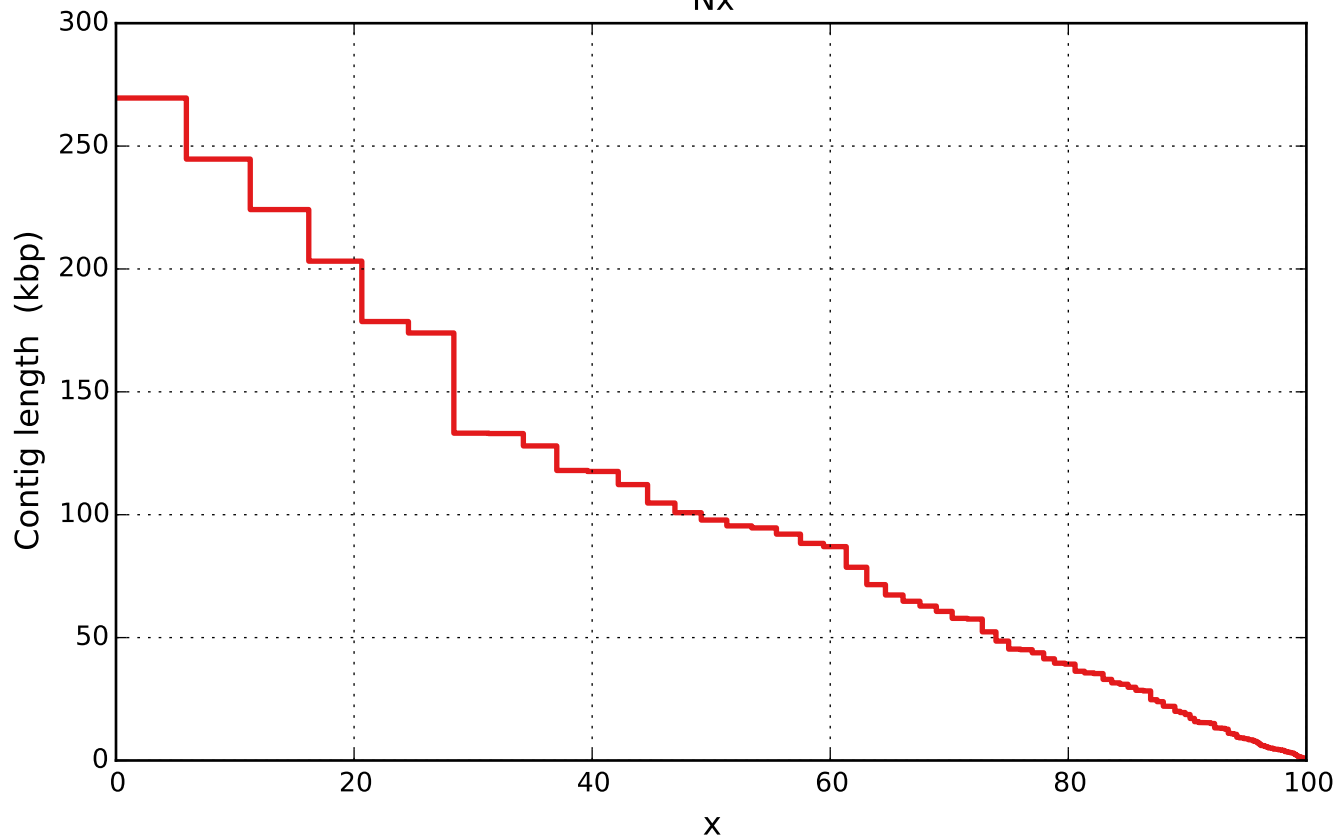
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	21
# N's	0

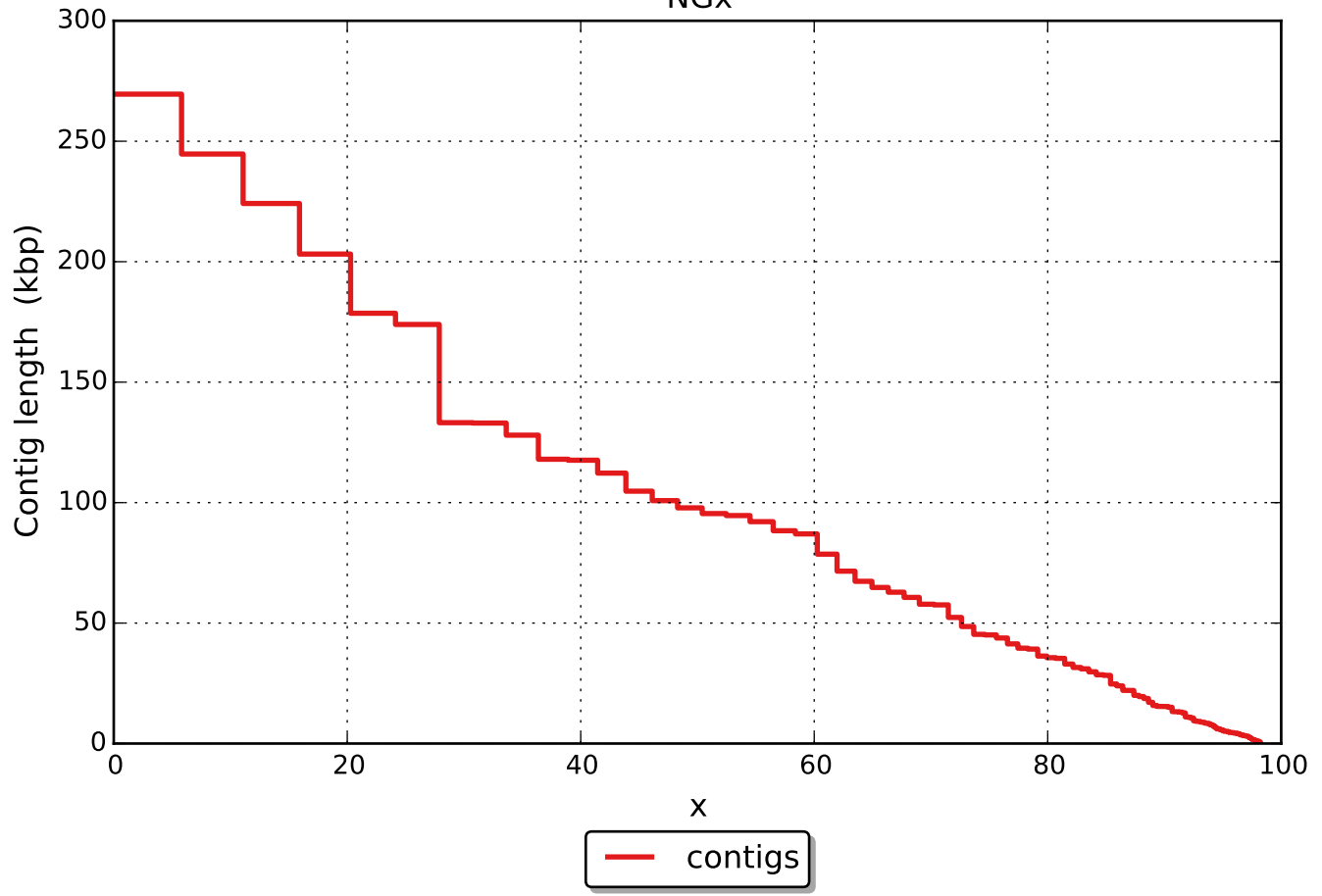
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

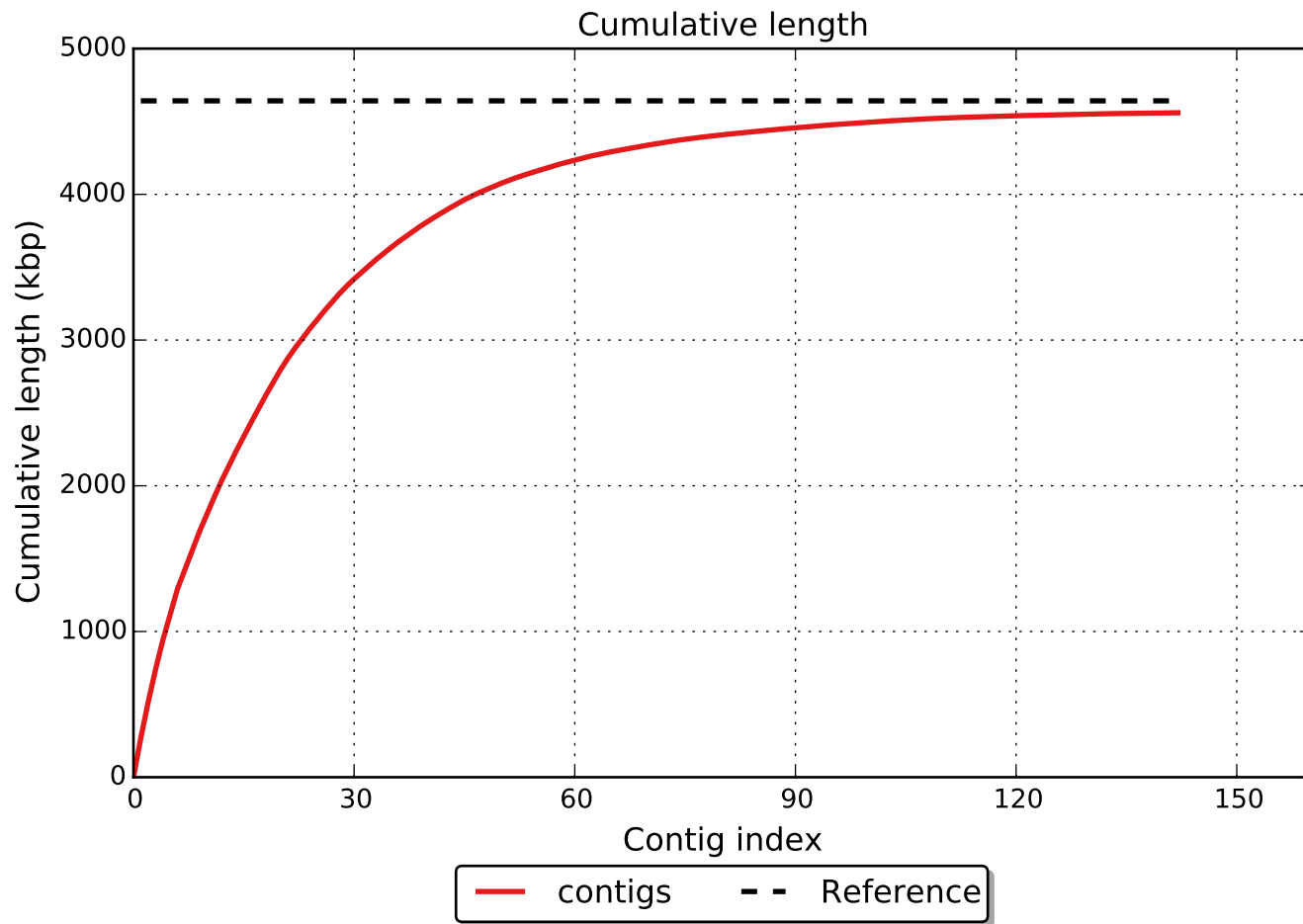
Nx



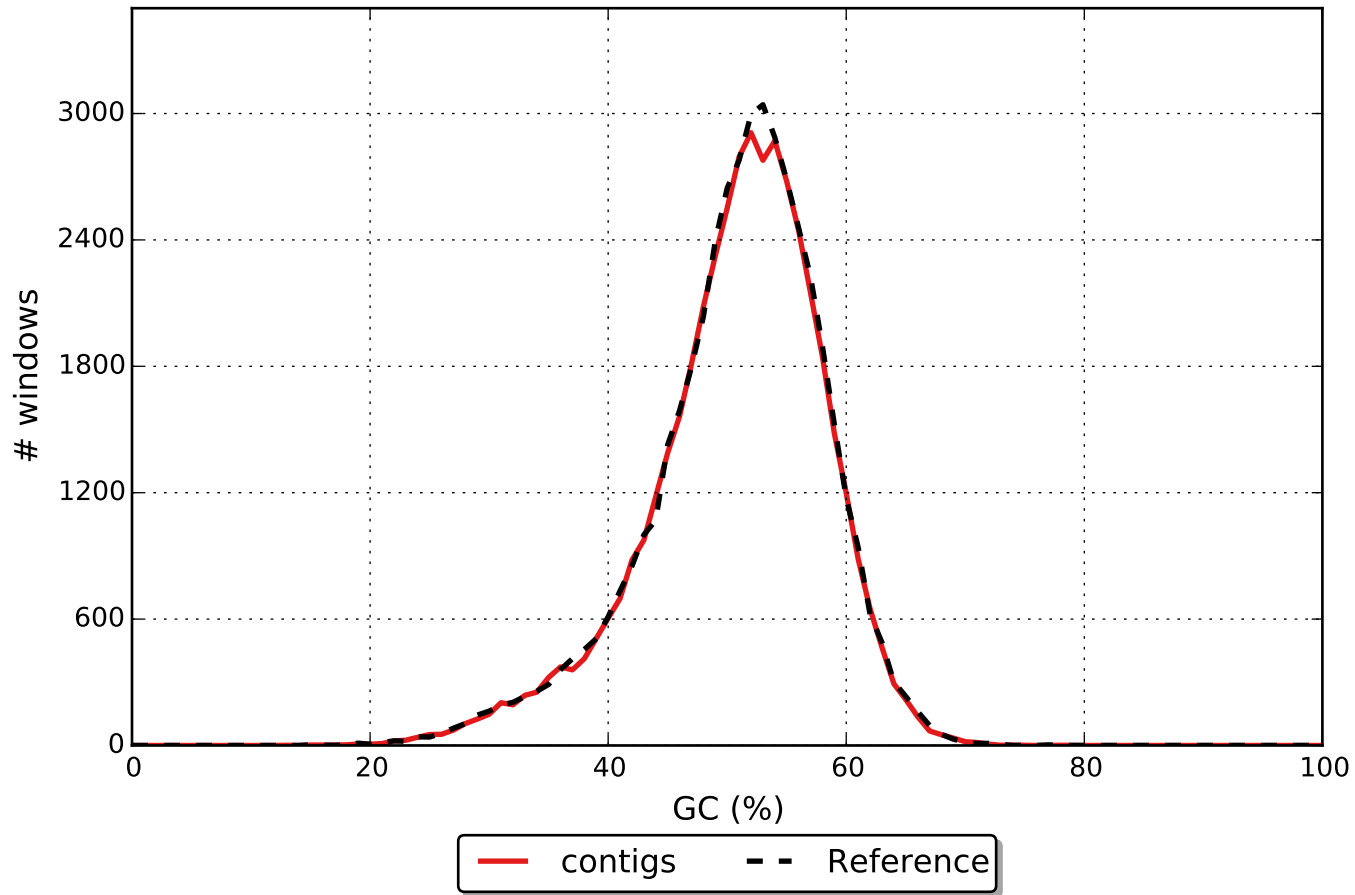
contigs

NGx





GC content

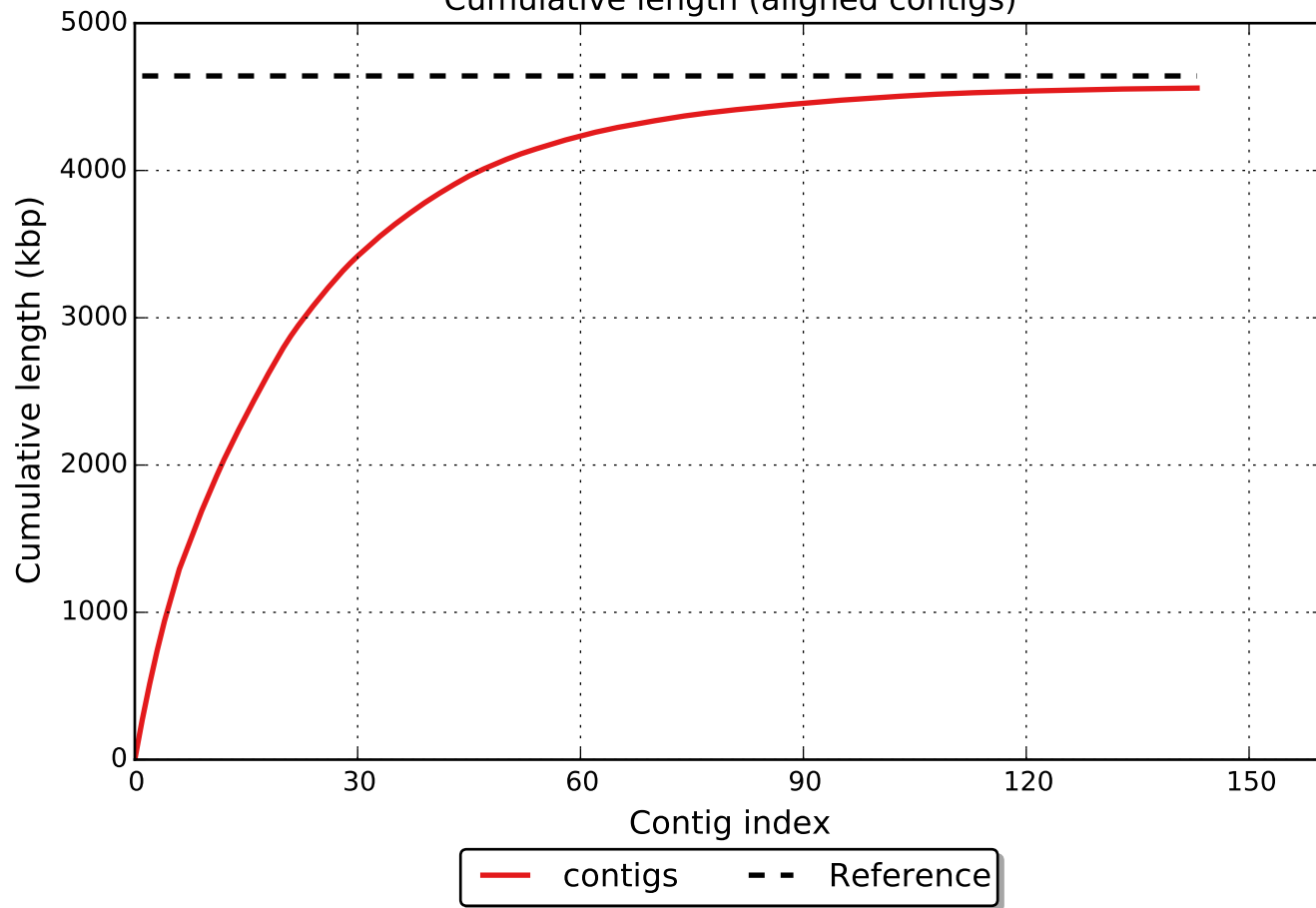


# Misassemblies

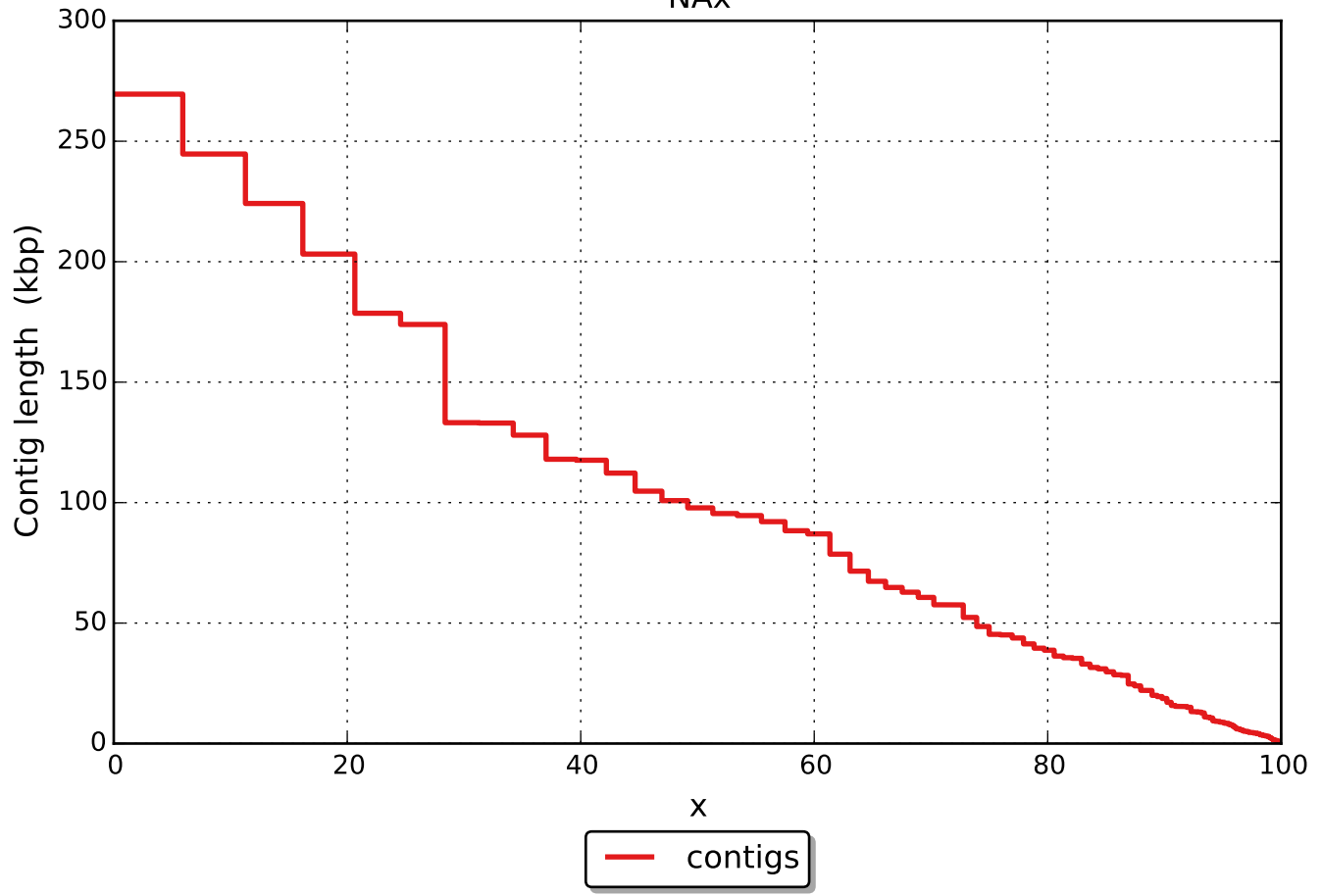




Cumulative length (aligned contigs)



NAx



# NGAx

