

## Report

	contigs
# contigs ( $\geq 0$ bp)	113
# contigs ( $\geq 1000$ bp)	70
# contigs ( $\geq 5000$ bp)	53
# contigs ( $\geq 10000$ bp)	49
# contigs ( $\geq 25000$ bp)	42
# contigs ( $\geq 50000$ bp)	27
Total length ( $\geq 0$ bp)	4573623
Total length ( $\geq 1000$ bp)	4557826
Total length ( $\geq 5000$ bp)	4521205
Total length ( $\geq 10000$ bp)	4491905
Total length ( $\geq 25000$ bp)	4378172
Total length ( $\geq 50000$ bp)	3840895
# contigs	84
Largest contig	327173
Total length	4567478
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	133063
NG50	133063
N75	86633
NG75	78670
L50	11
LG50	11
L75	21
LG75	22
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.360
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.82
# indels per 100 kbp	0.24
Largest alignment	327173
NA50	133063
NGA50	133063
NA75	86633
NGA75	78670
LA50	11
LGA50	11
LA75	21
LGA75	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).

## Misassemblies report

	contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# mismatches	83
# indels	11
# short indels	10
# long indels	1
Indels length	96

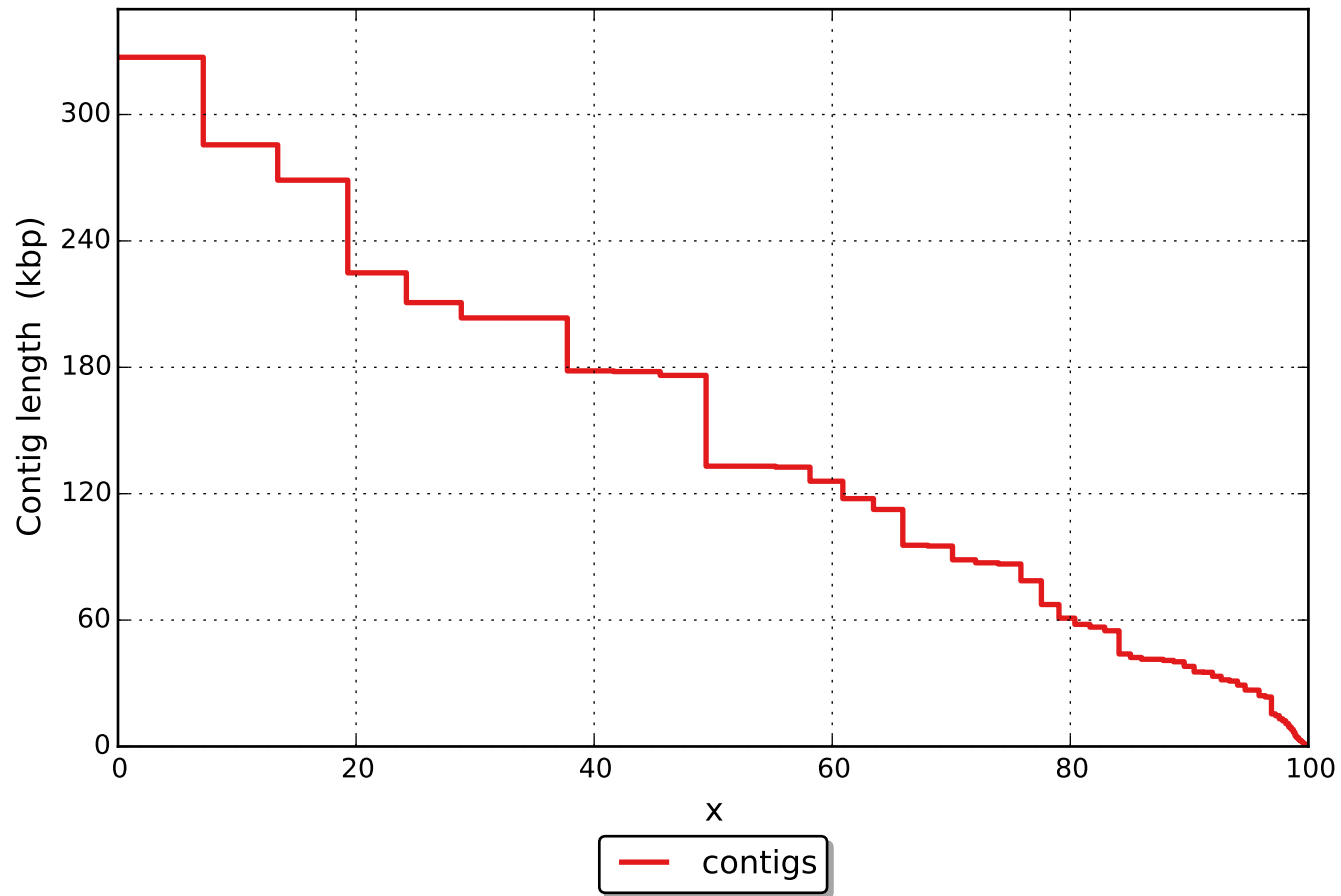
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

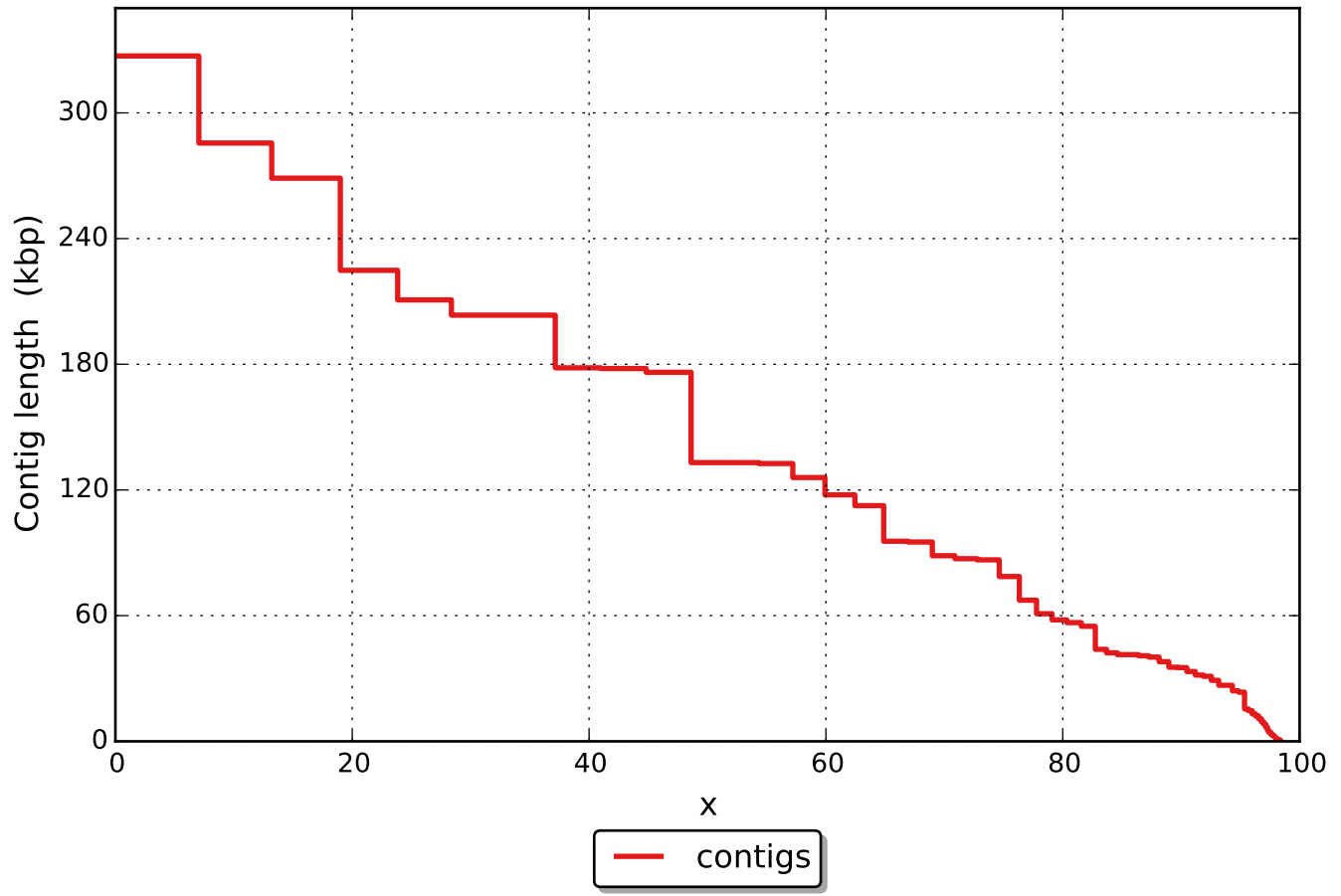
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

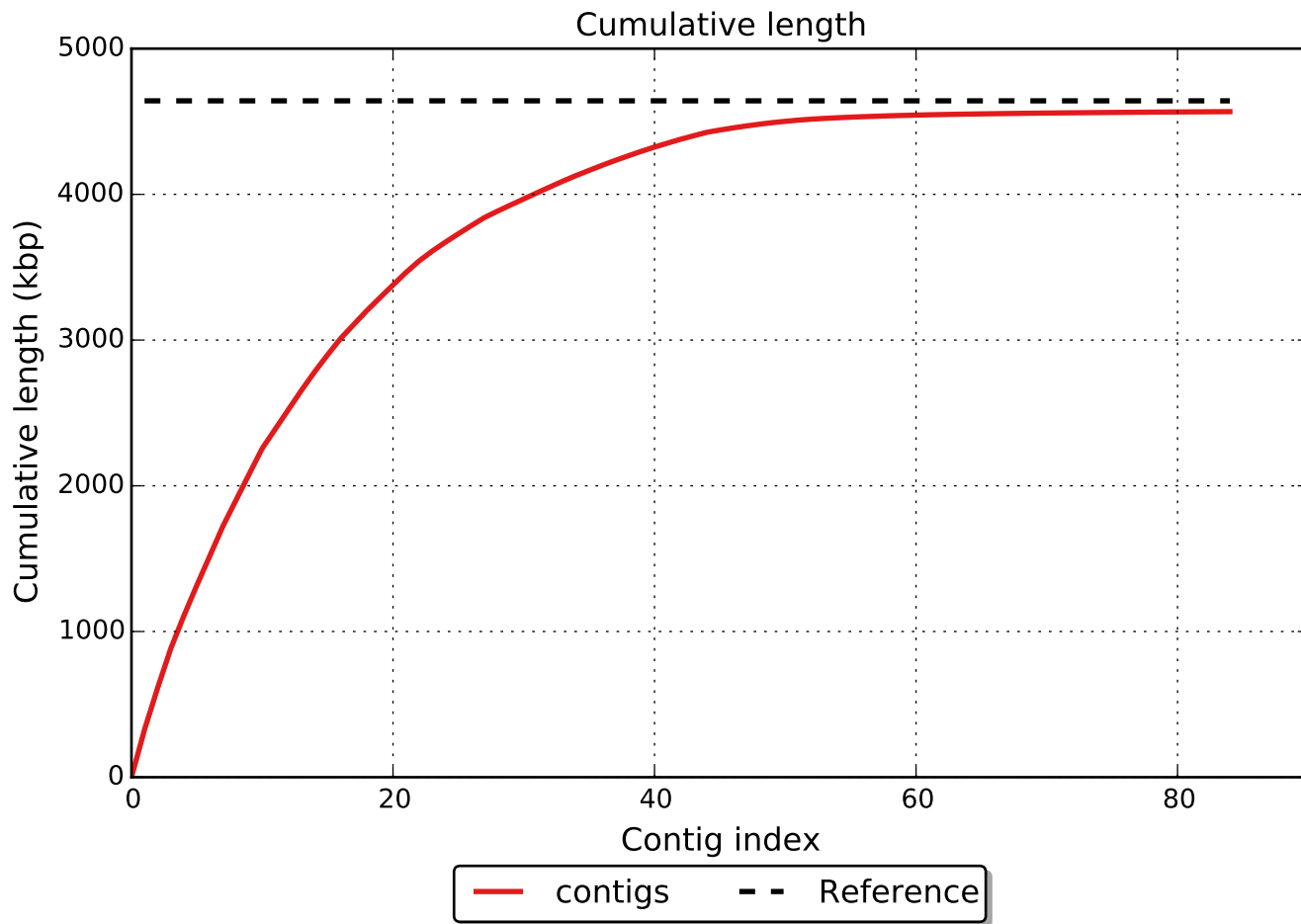
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

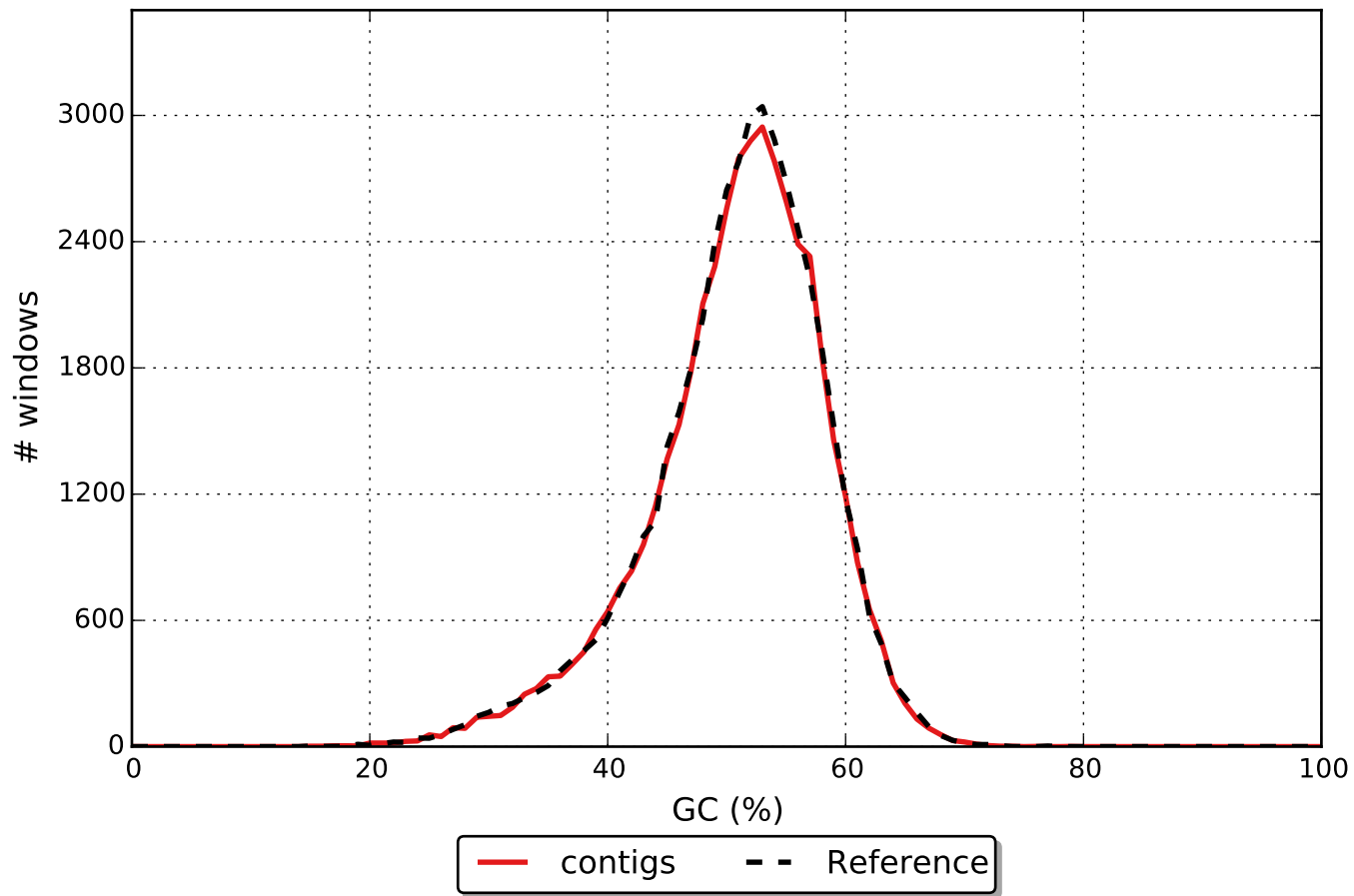


NGx





GC content

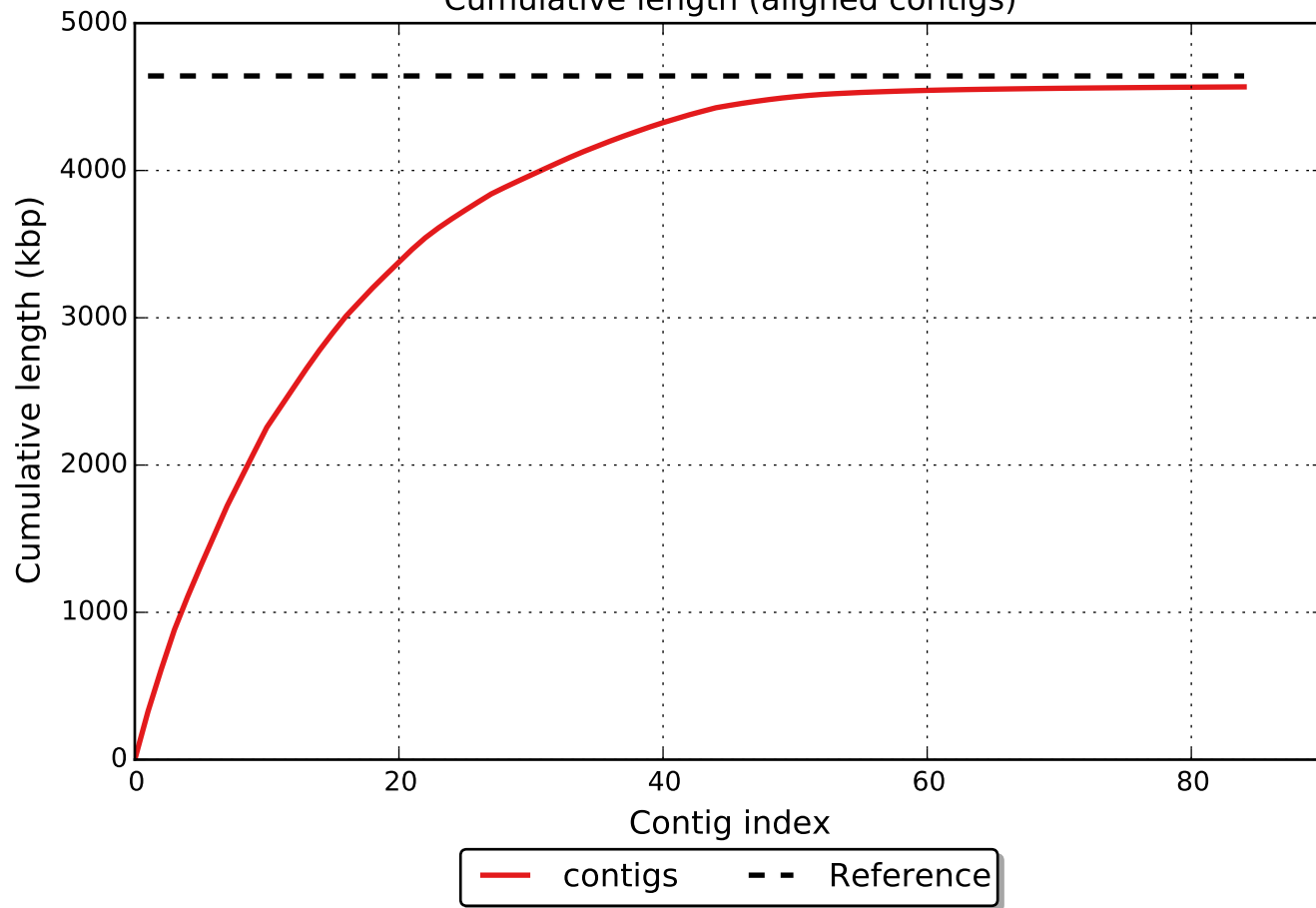


# Misassemblies

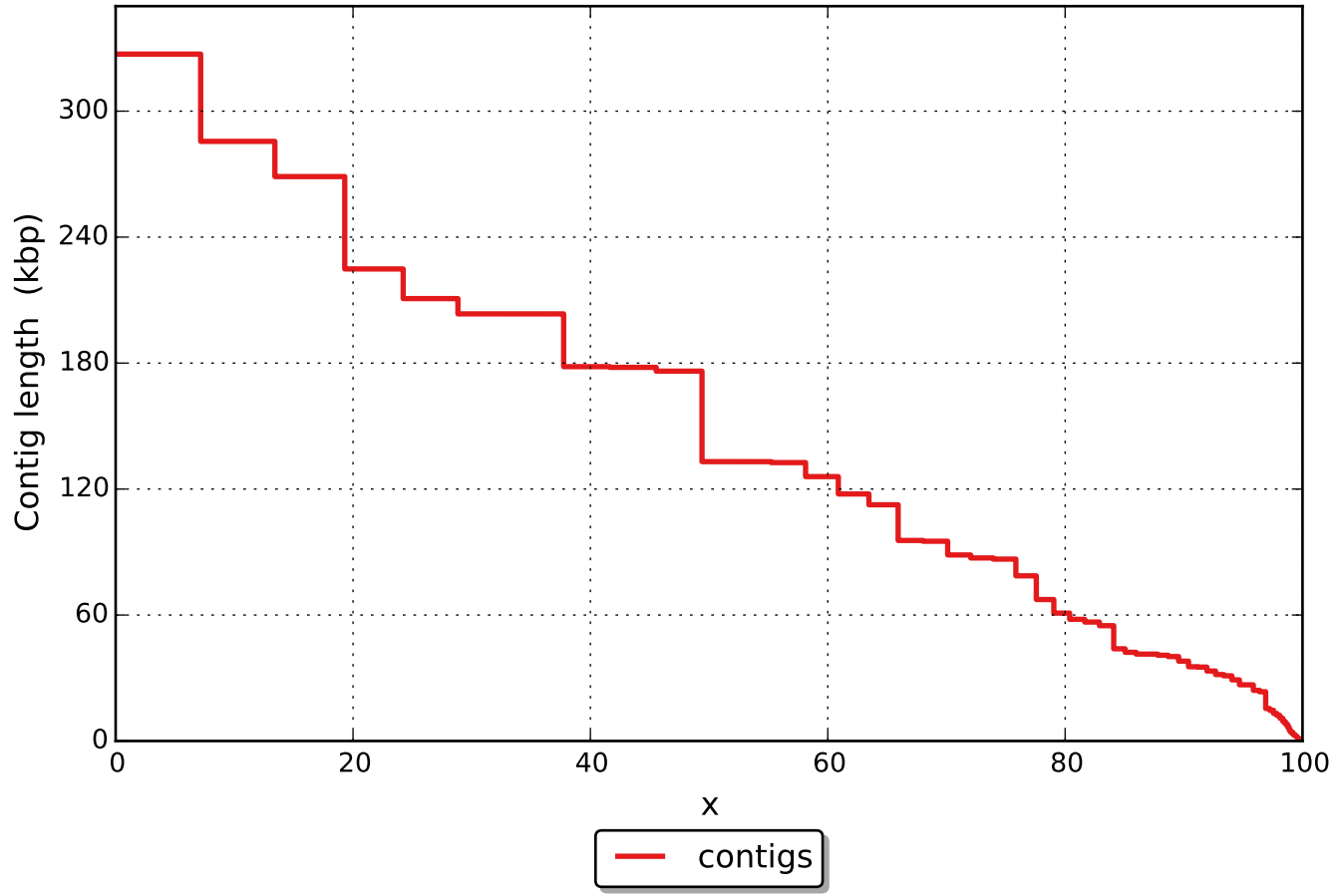




Cumulative length (aligned contigs)



NAx



# NGAx

