

## Report

	contigs
# contigs ( $\geq 0$ bp)	92
# contigs ( $\geq 1000$ bp)	70
# contigs ( $\geq 5000$ bp)	51
# contigs ( $\geq 10000$ bp)	46
# contigs ( $\geq 25000$ bp)	40
# contigs ( $\geq 50000$ bp)	27
Total length ( $\geq 0$ bp)	4572180
Total length ( $\geq 1000$ bp)	4567341
Total length ( $\geq 5000$ bp)	4523224
Total length ( $\geq 10000$ bp)	4483317
Total length ( $\geq 25000$ bp)	4392129
Total length ( $\geq 50000$ bp)	3940881
# contigs	72
Largest contig	327064
Total length	4568765
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	173977
NG50	173977
N75	80764
NG75	80764
L50	10
LG50	10
L75	20
LG75	20
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	40143
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.345
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6.97
# indels per 100 kbp	0.35
Largest alignment	327064
NA50	173977
NGA50	173977
NA75	80764
NGA75	80764
LA50	10
LGA50	10
LA75	20
LGA75	20

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	40143
# local misassemblies	4
# mismatches	318
# indels	16
# short indels	16
# long indels	0
Indels length	22

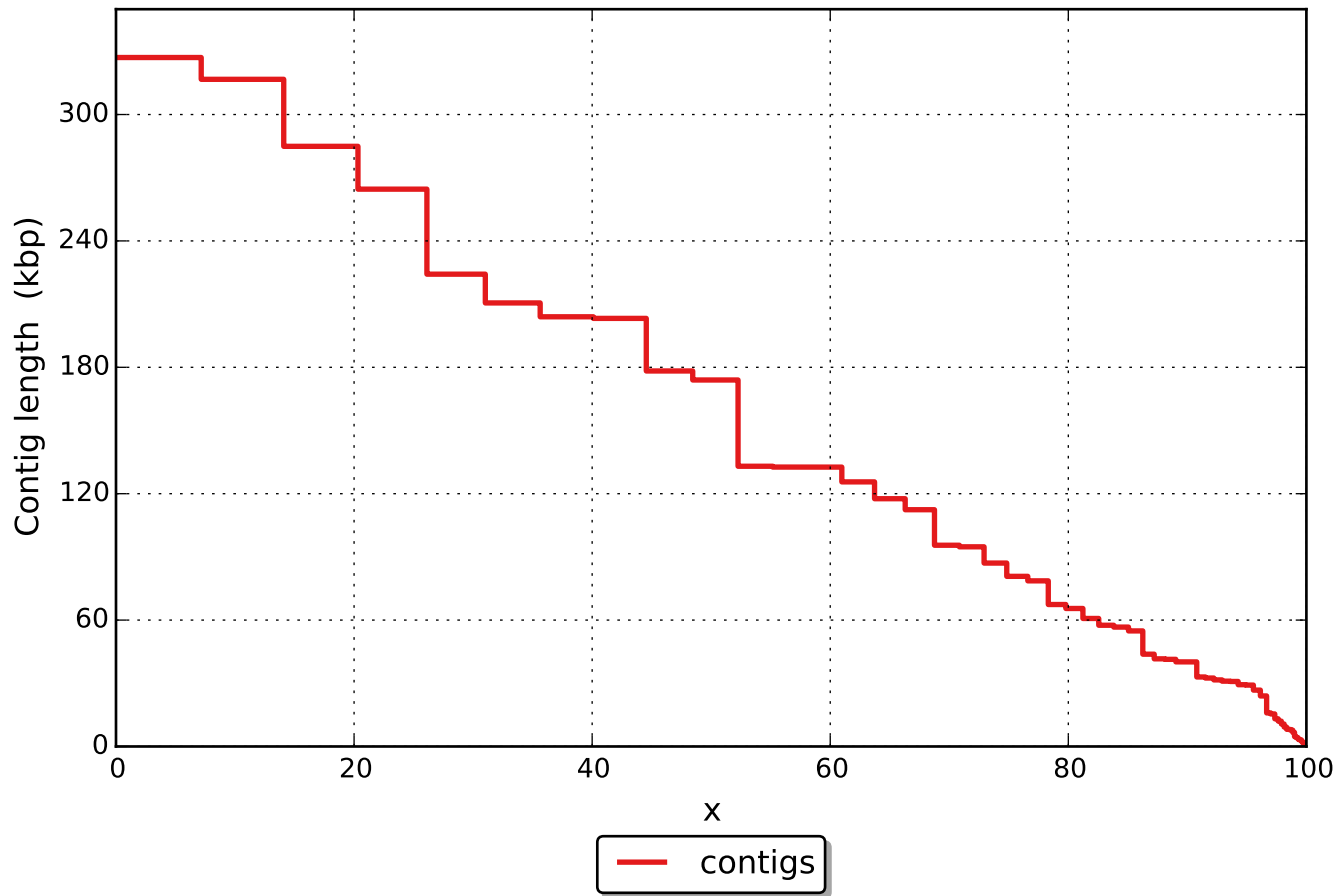
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

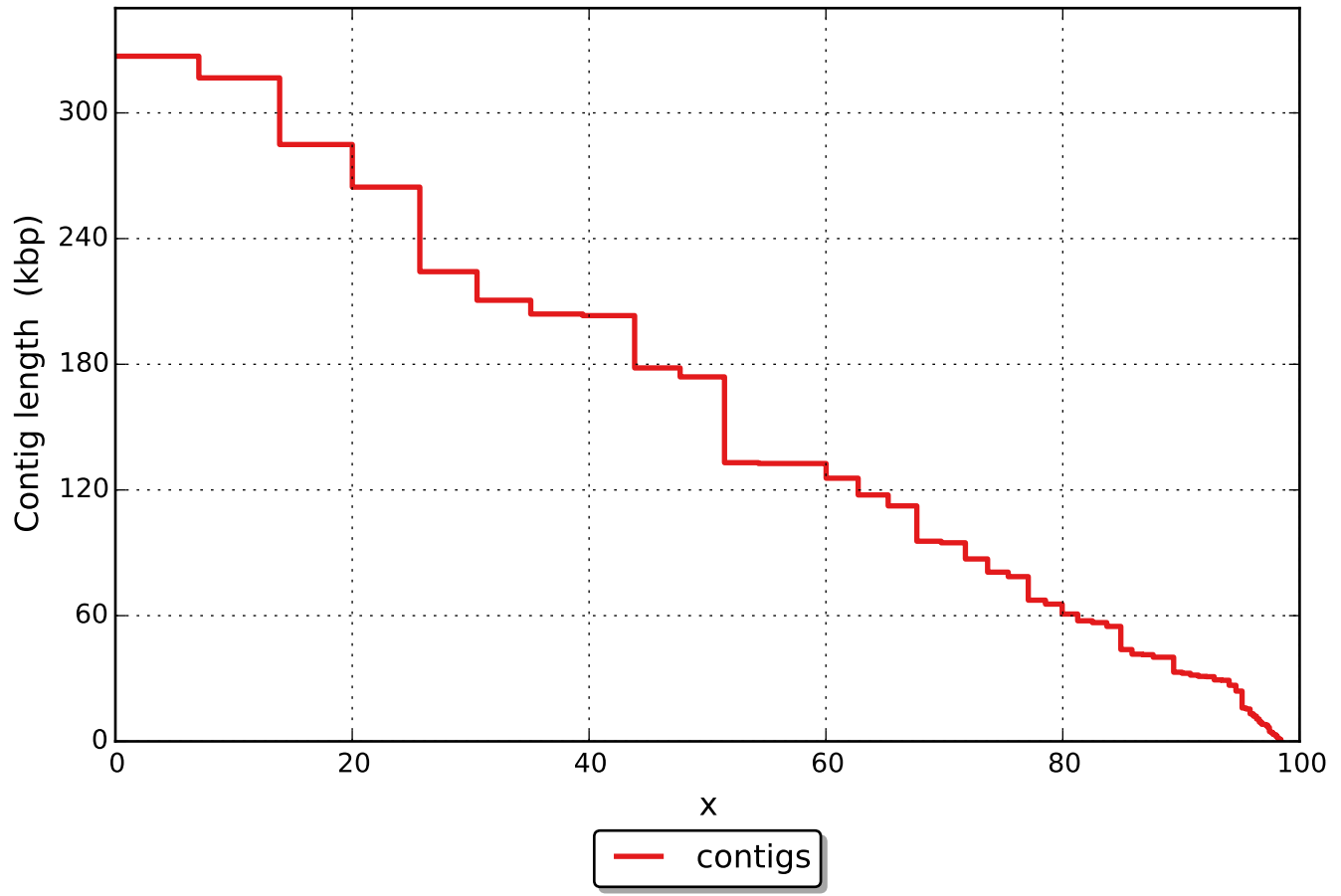
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

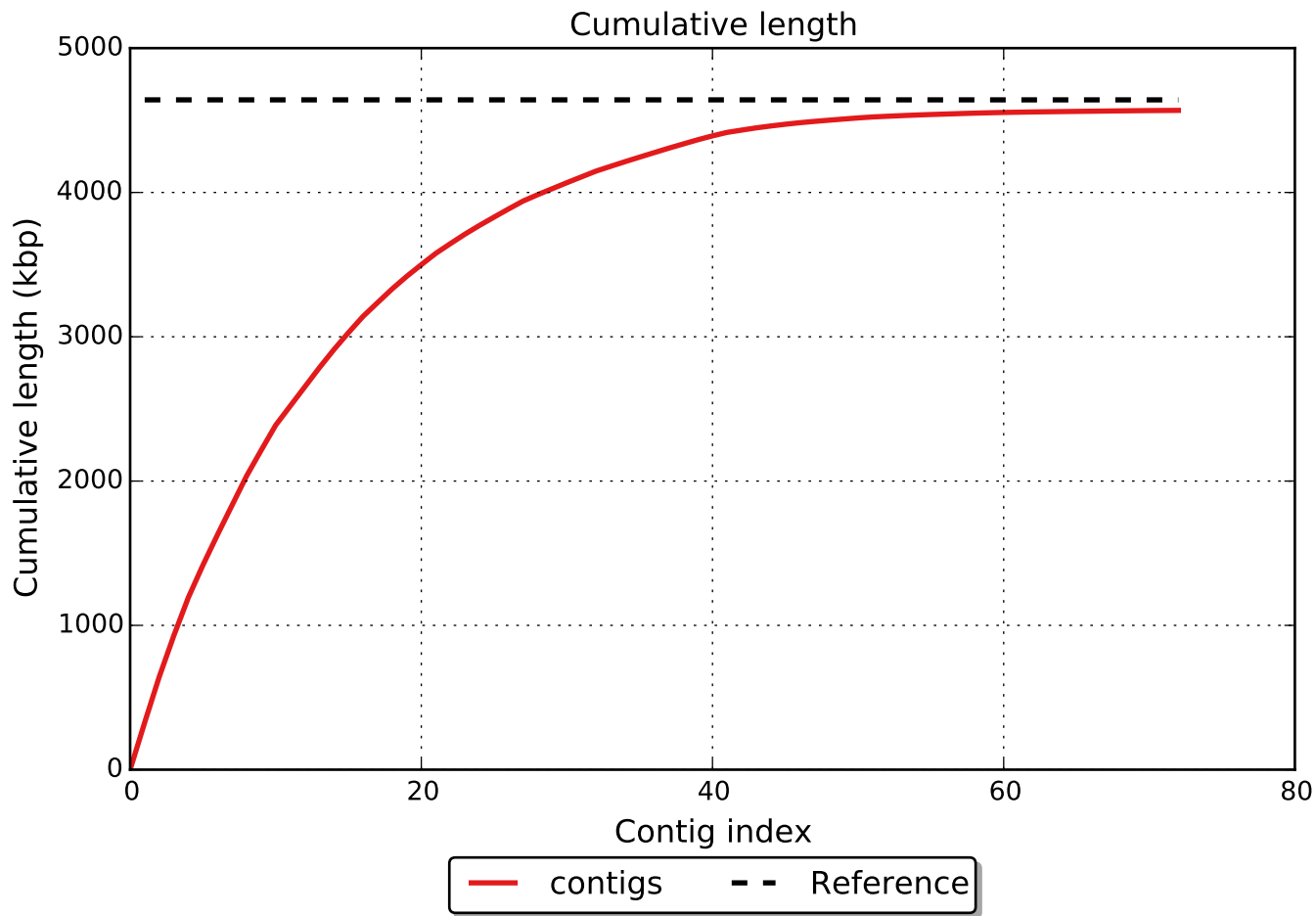
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

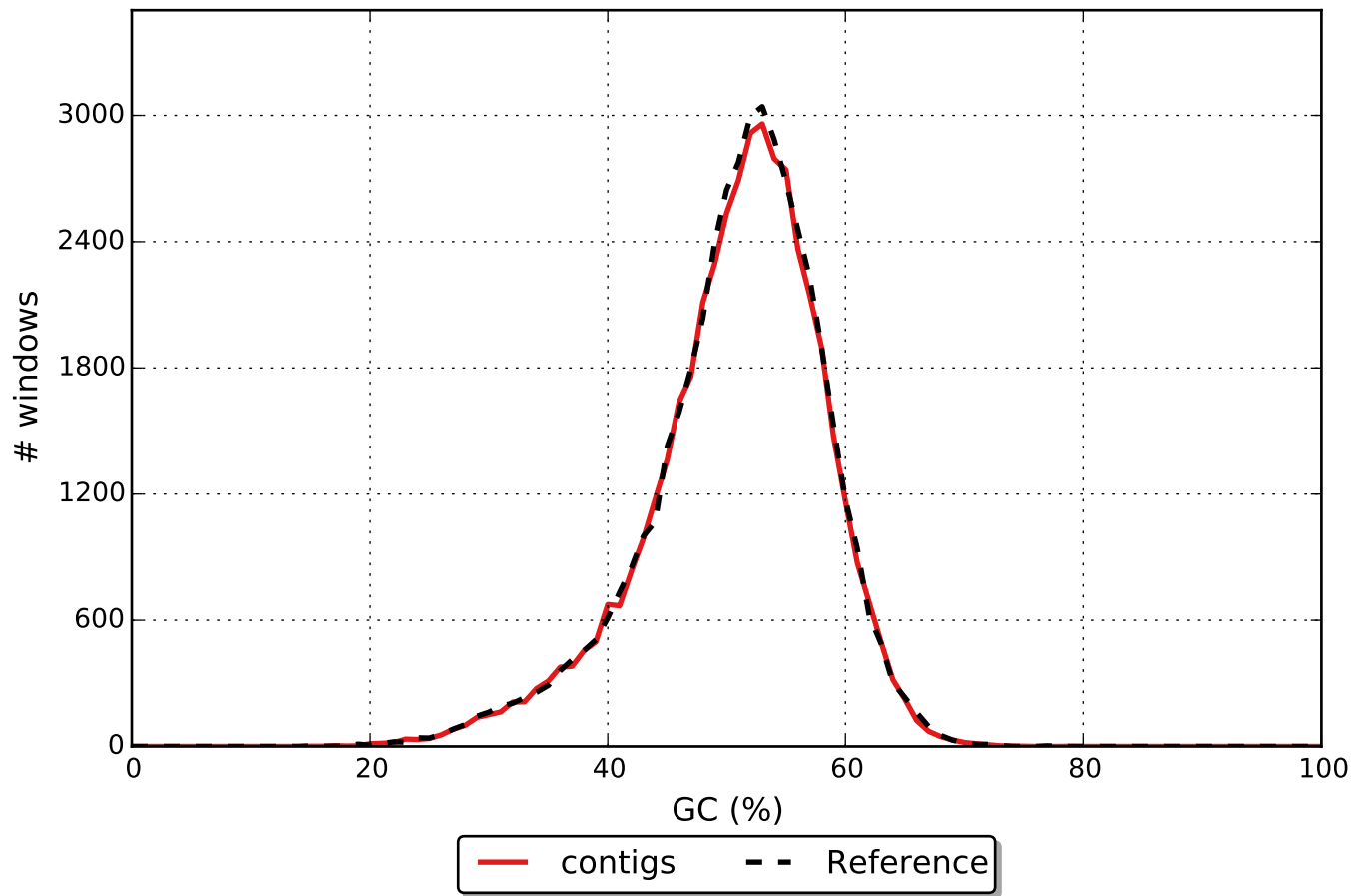


NGx





GC content



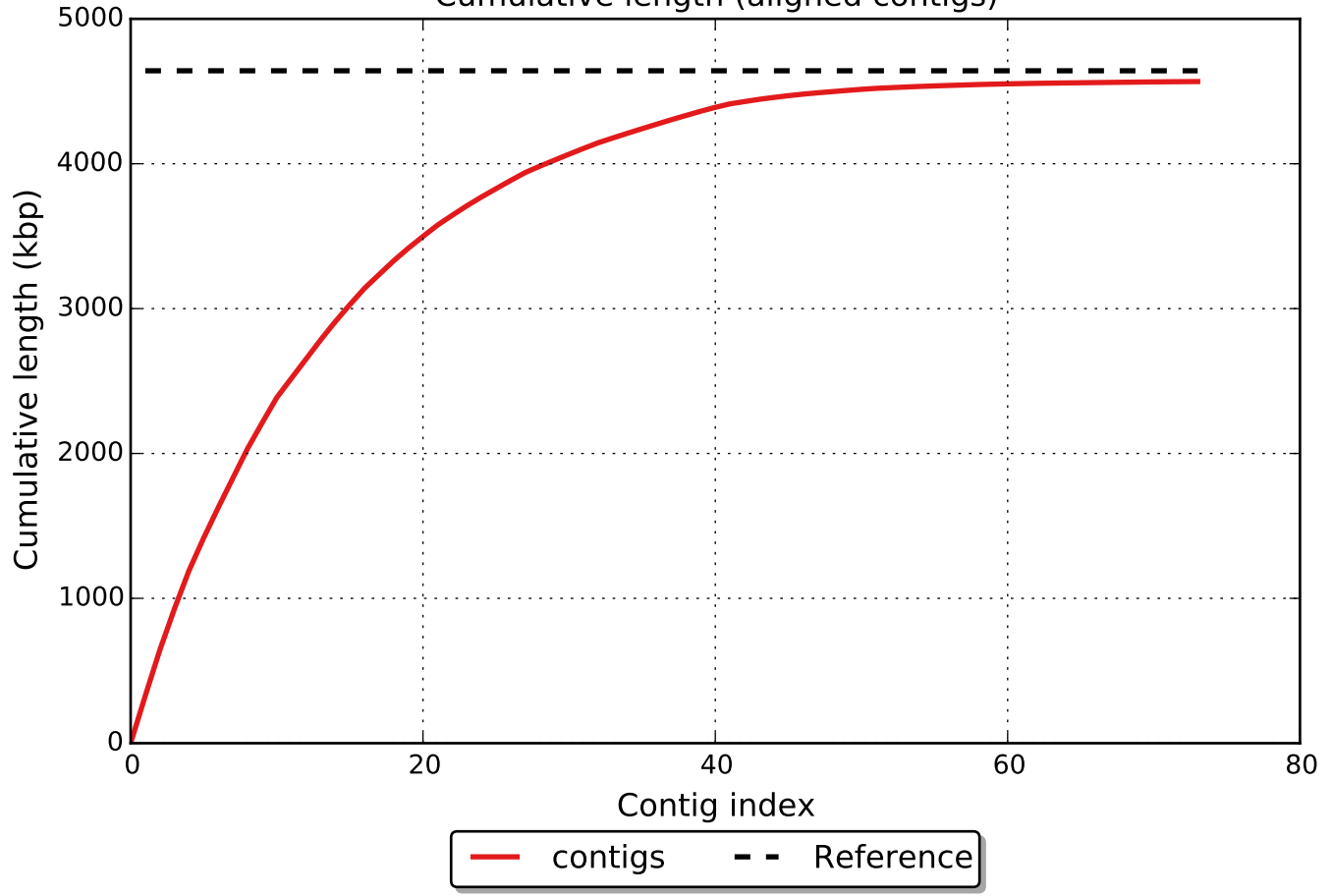
# Misassemblies



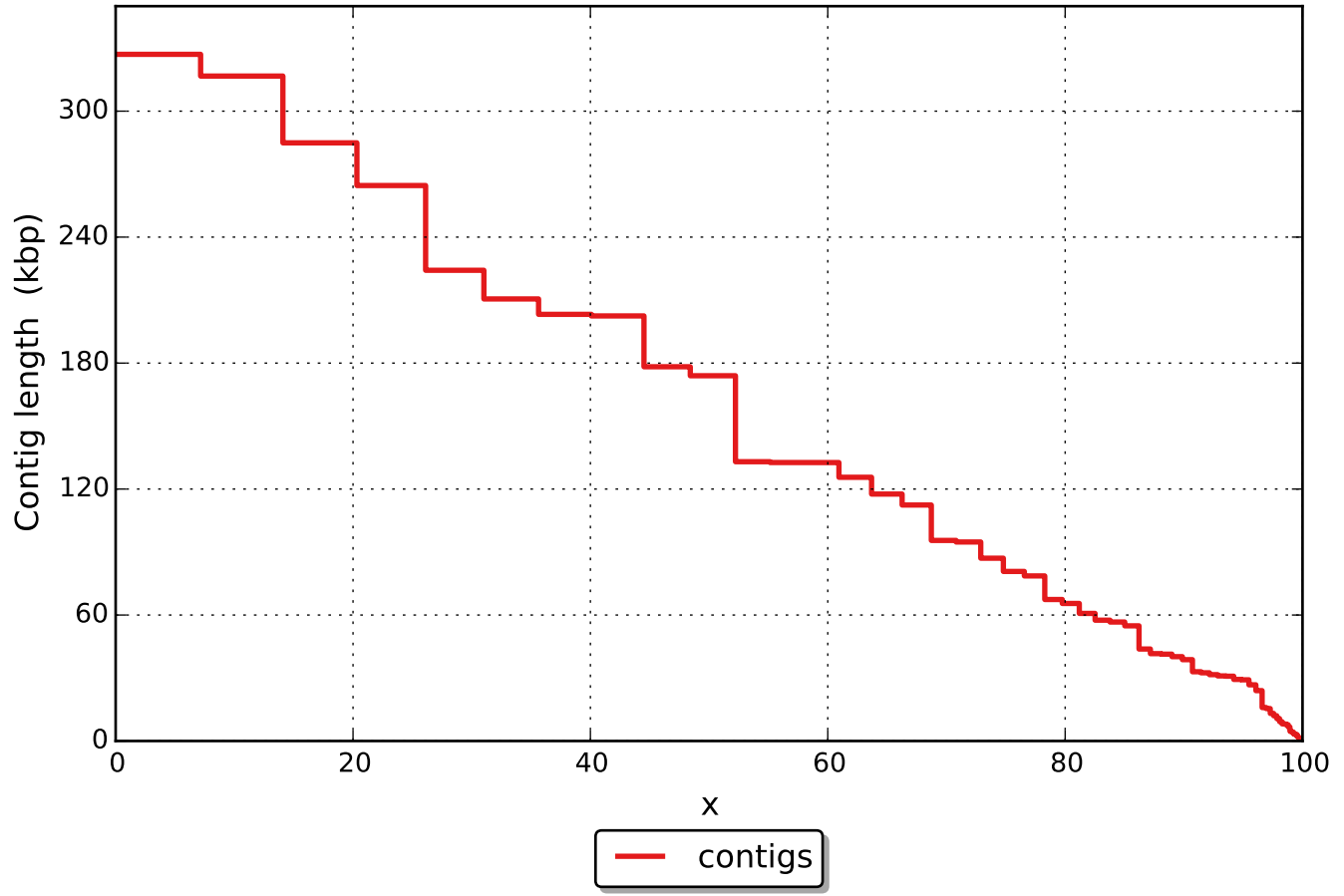
 # relocations



Cumulative length (aligned contigs)



NAx



# NGAx

