

## Report

	contigs
# contigs ( $\geq 1000$ bp)	23
# contigs ( $\geq 5000$ bp)	21
# contigs ( $\geq 10000$ bp)	21
# contigs ( $\geq 25000$ bp)	20
# contigs ( $\geq 50000$ bp)	18
Total length ( $\geq 1000$ bp)	4787167
Total length ( $\geq 5000$ bp)	4784160
Total length ( $\geq 10000$ bp)	4784160
Total length ( $\geq 25000$ bp)	4773357
Total length ( $\geq 50000$ bp)	4686785
# contigs	25
Largest contig	700824
Total length	4789008
Reference length	4641652
GC (%)	50.70
Reference GC (%)	50.78
N50	373445
NG50	373445
N75	257933
NG75	325448
L50	5
LG50	5
L75	9
LG75	8
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	349059
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.565
Duplication ratio	1.036
# N's per 100 kbp	0.00
# mismatches per 100 kbp	351.90
# indels per 100 kbp	1.10
Largest alignment	700544
NA50	373445
NGA50	373445
NA75	188536
NGA75	188536
LA50	5
LGA50	5
LA75	9
LGA75	9

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
# possibly misassembled contigs	1
# misassembled contigs	1
Misassembled contigs length	349059
# local misassemblies	1
# mismatches	16263
# indels	51
# short indels	51
# long indels	0
Indels length	51

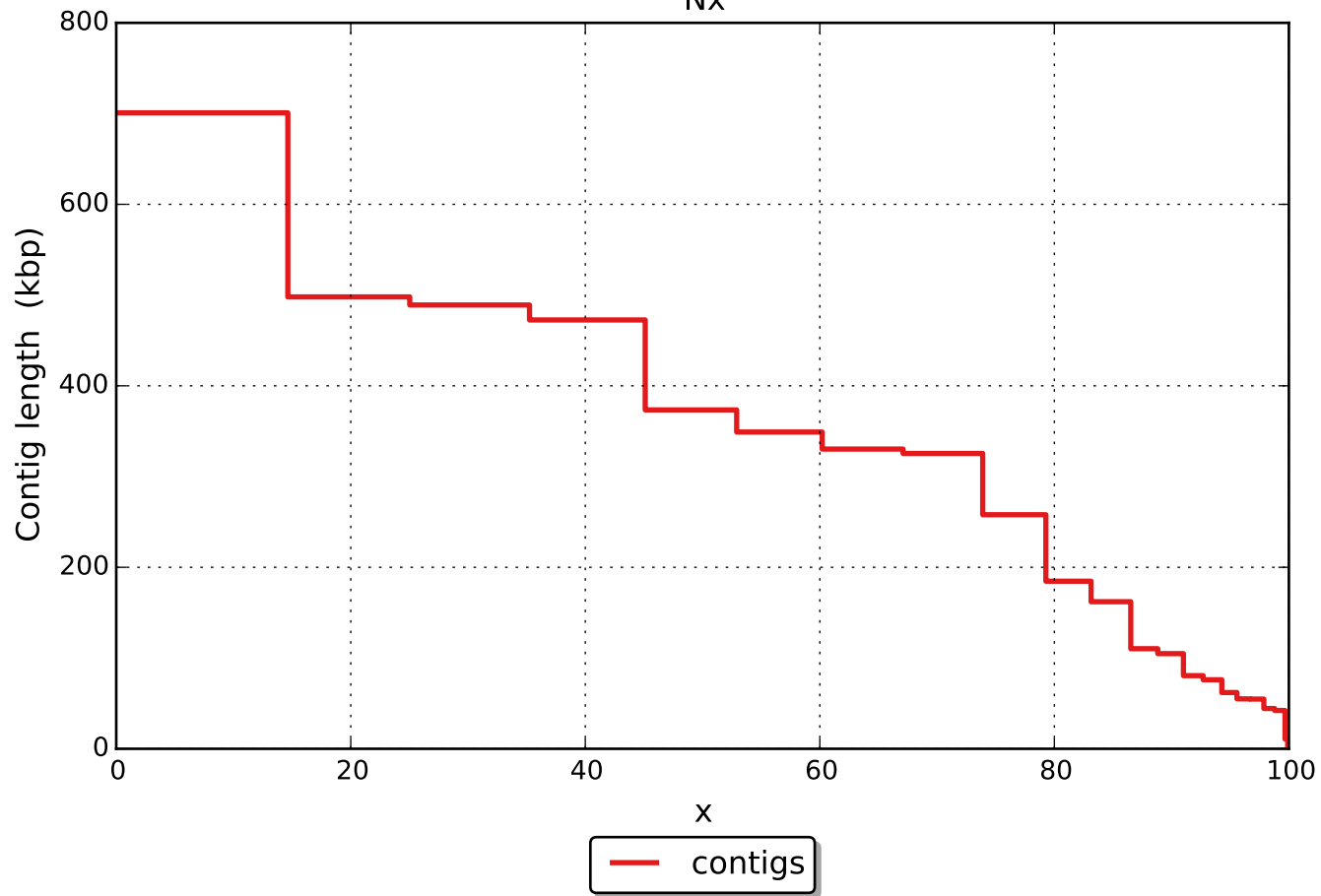
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

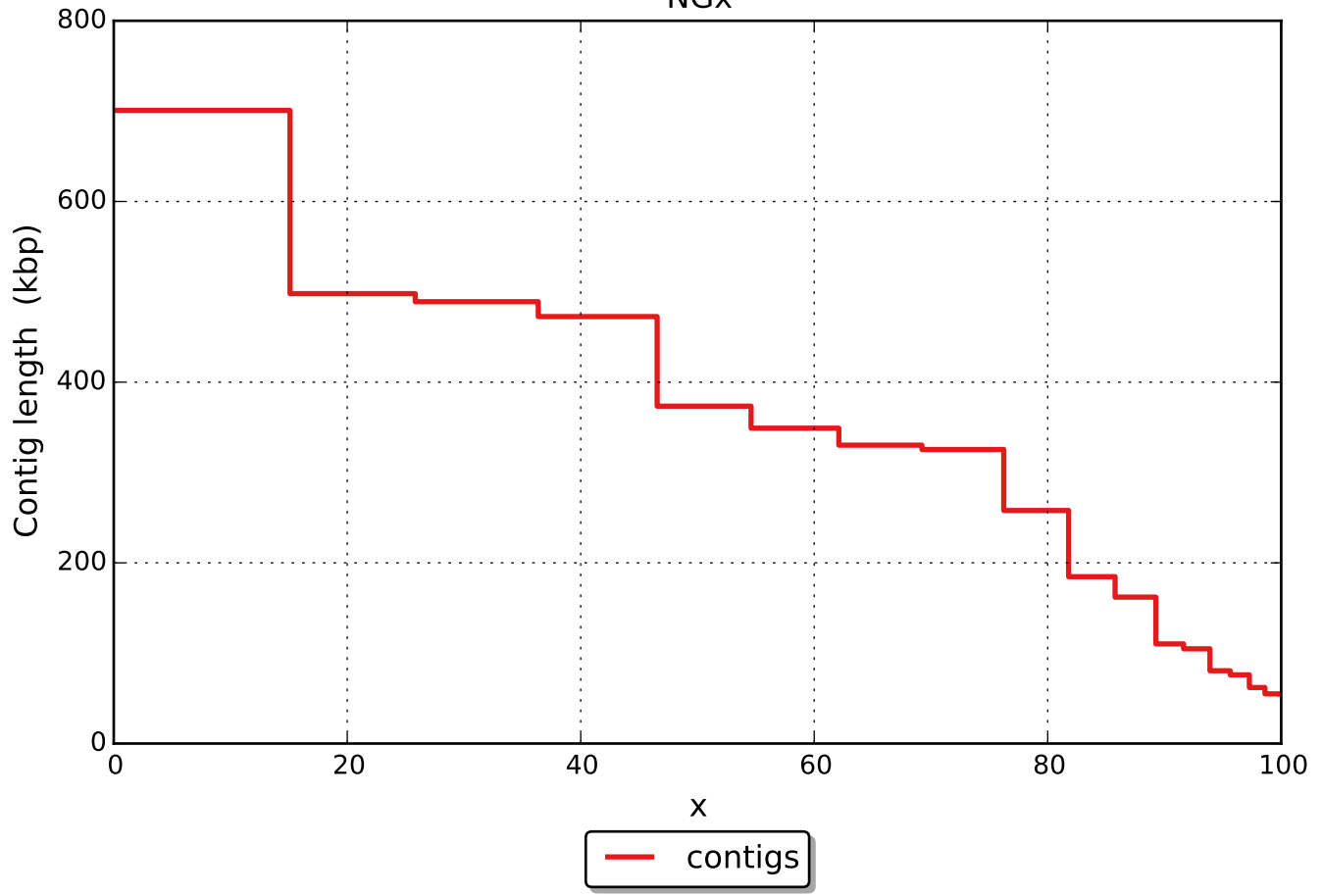
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

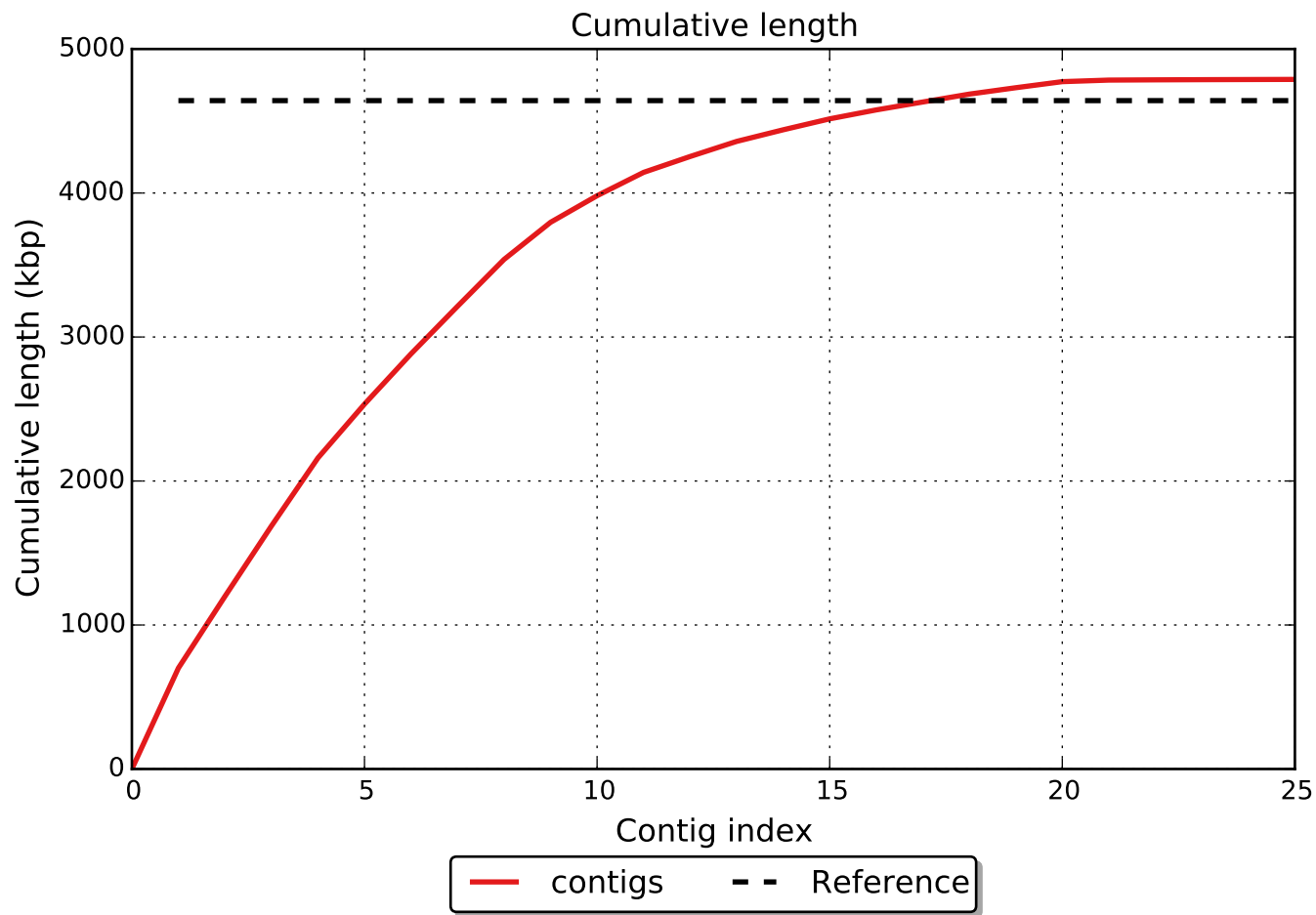
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

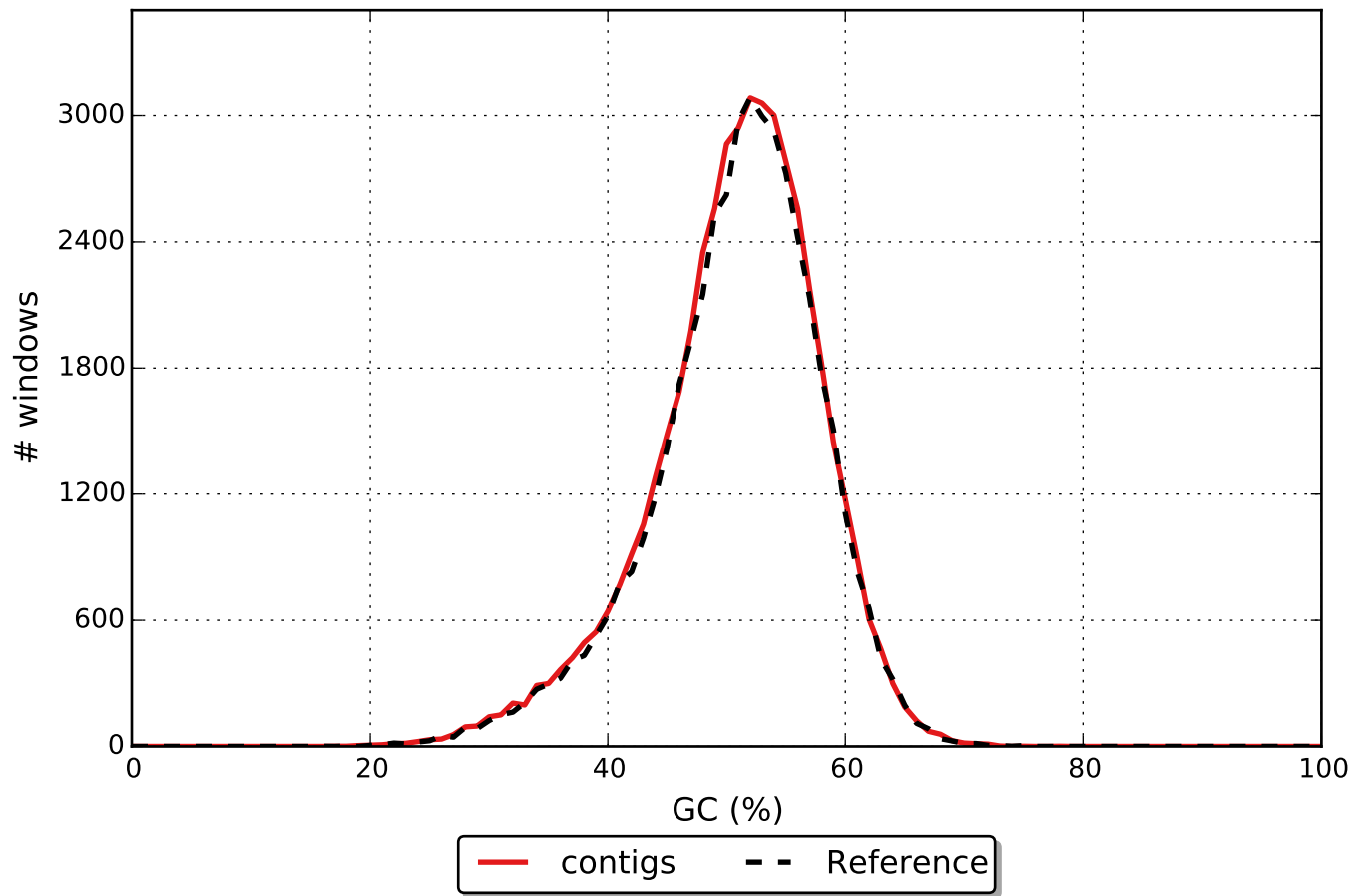


NGx





# GC content

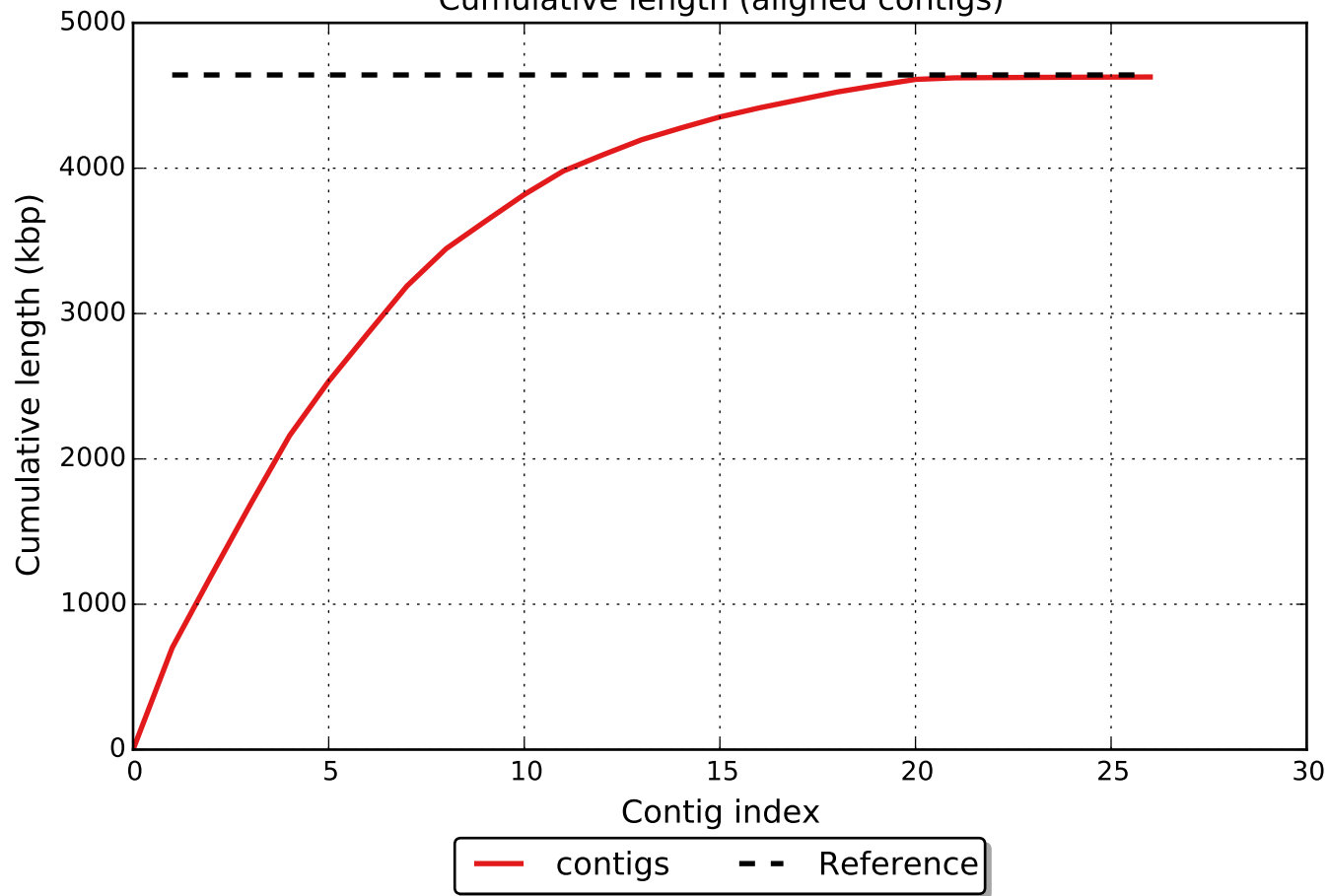


# Misassemblies

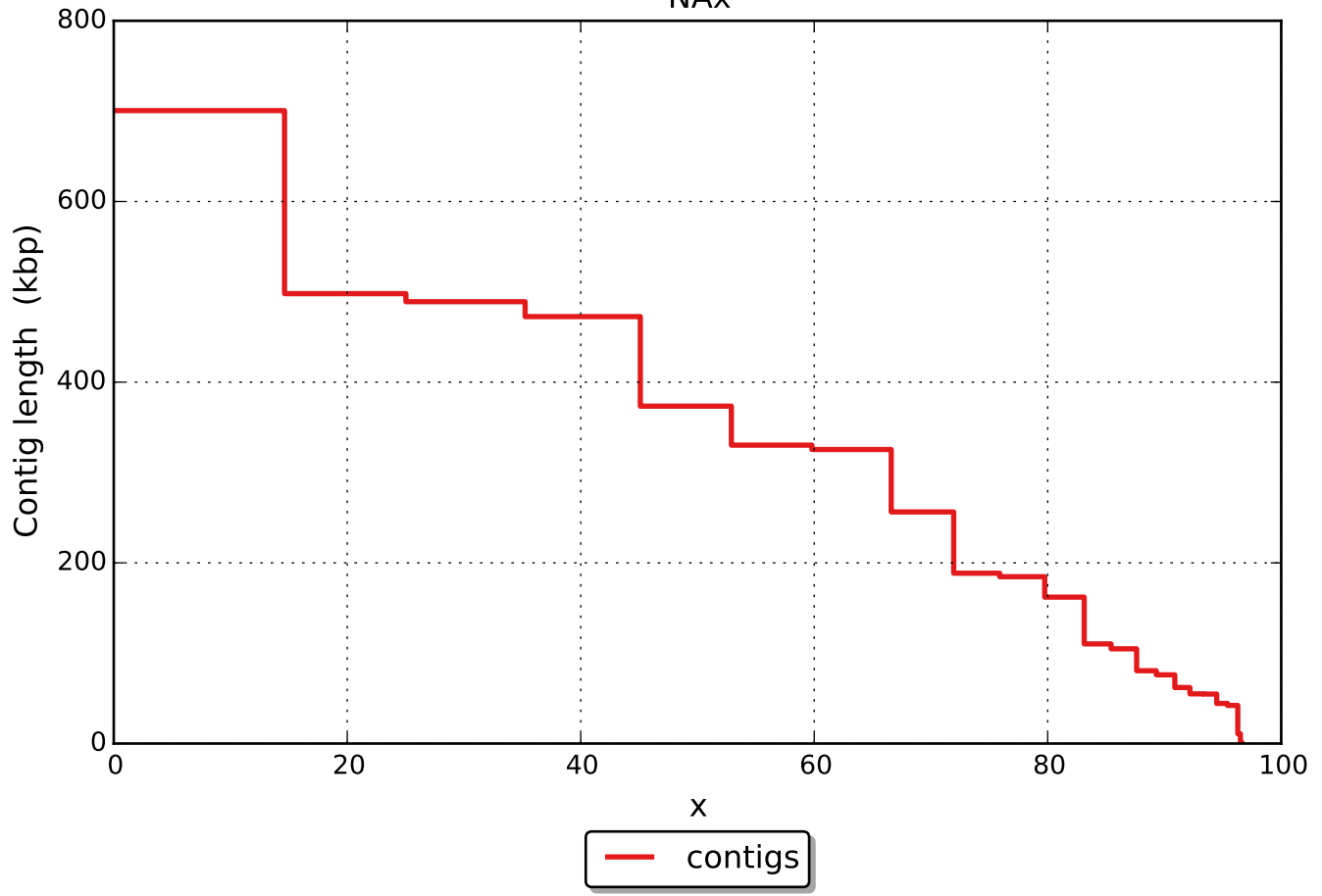




Cumulative length (aligned contigs)



NAx



NGAx

