

## Report

	contigs
# contigs ( $\geq 1000$ bp)	31
# contigs ( $\geq 5000$ bp)	25
# contigs ( $\geq 10000$ bp)	25
# contigs ( $\geq 25000$ bp)	25
# contigs ( $\geq 50000$ bp)	23
Total length ( $\geq 1000$ bp)	4600624
Total length ( $\geq 5000$ bp)	4594006
Total length ( $\geq 10000$ bp)	4594006
Total length ( $\geq 25000$ bp)	4594006
Total length ( $\geq 50000$ bp)	4540210
# contigs	36
Largest contig	529642
Total length	4604027
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.79
N50	288372
NG50	288372
N75	158428
NG75	158428
L50	7
LG50	7
L75	11
LG75	11
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.144
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	447.23
# indels per 100 kbp	0.93
Largest alignment	529642
NA50	288372
NGA50	288372
NA75	158428
NGA75	158428
LA50	7
LGA50	7
LA75	11
LGA75	11

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
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	20581
# indels	43
# short indels	43
# long indels	0
Indels length	43

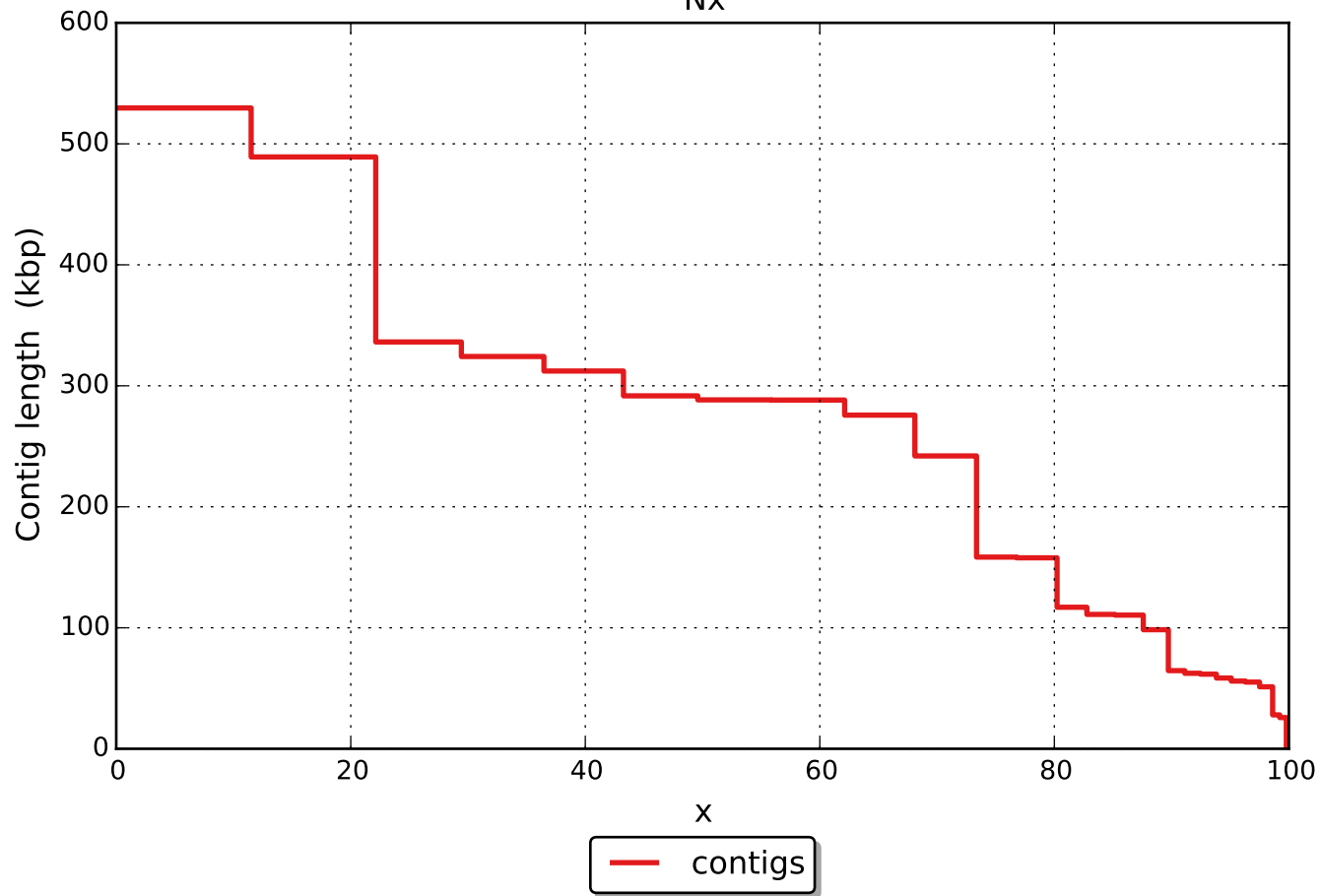
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

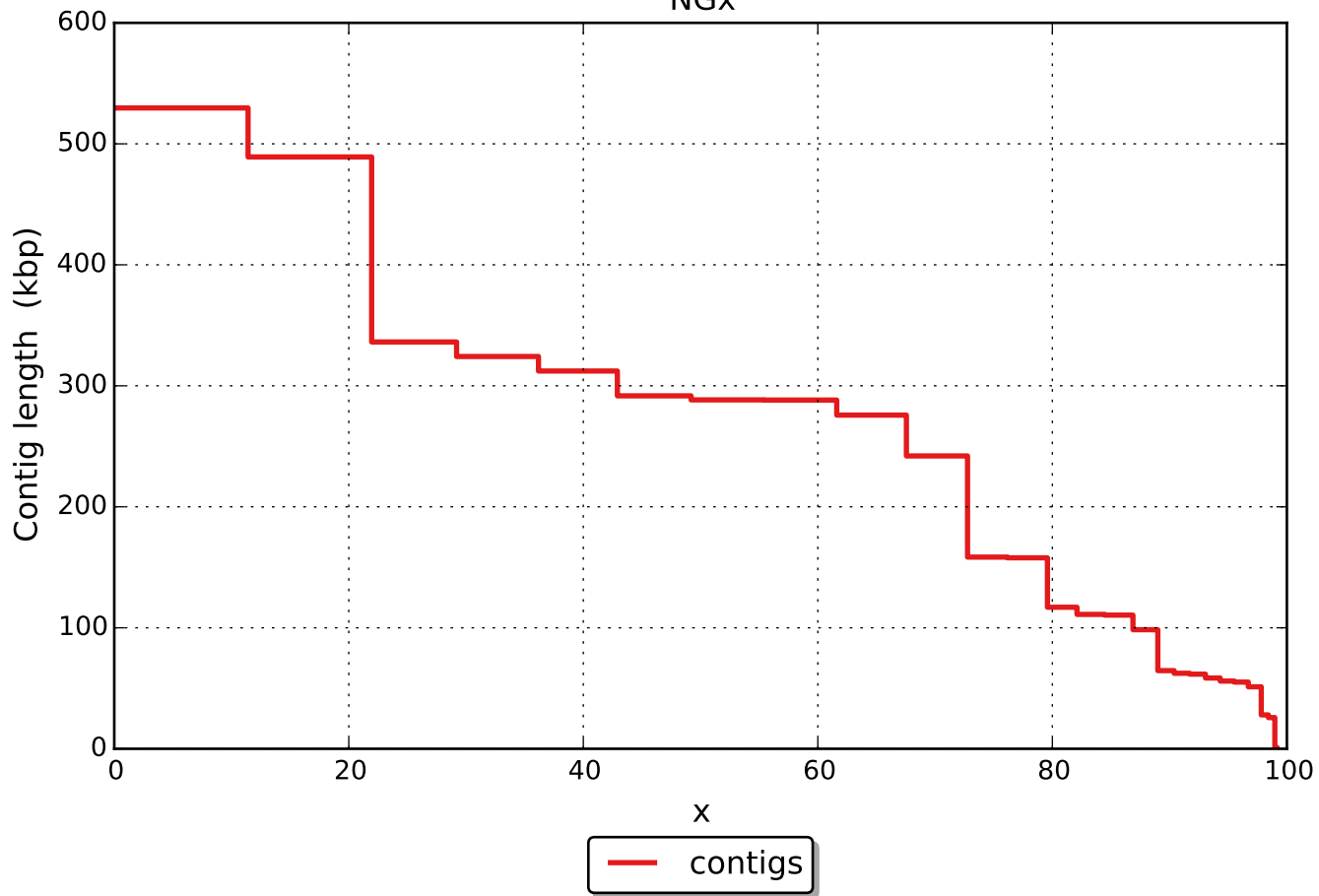
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

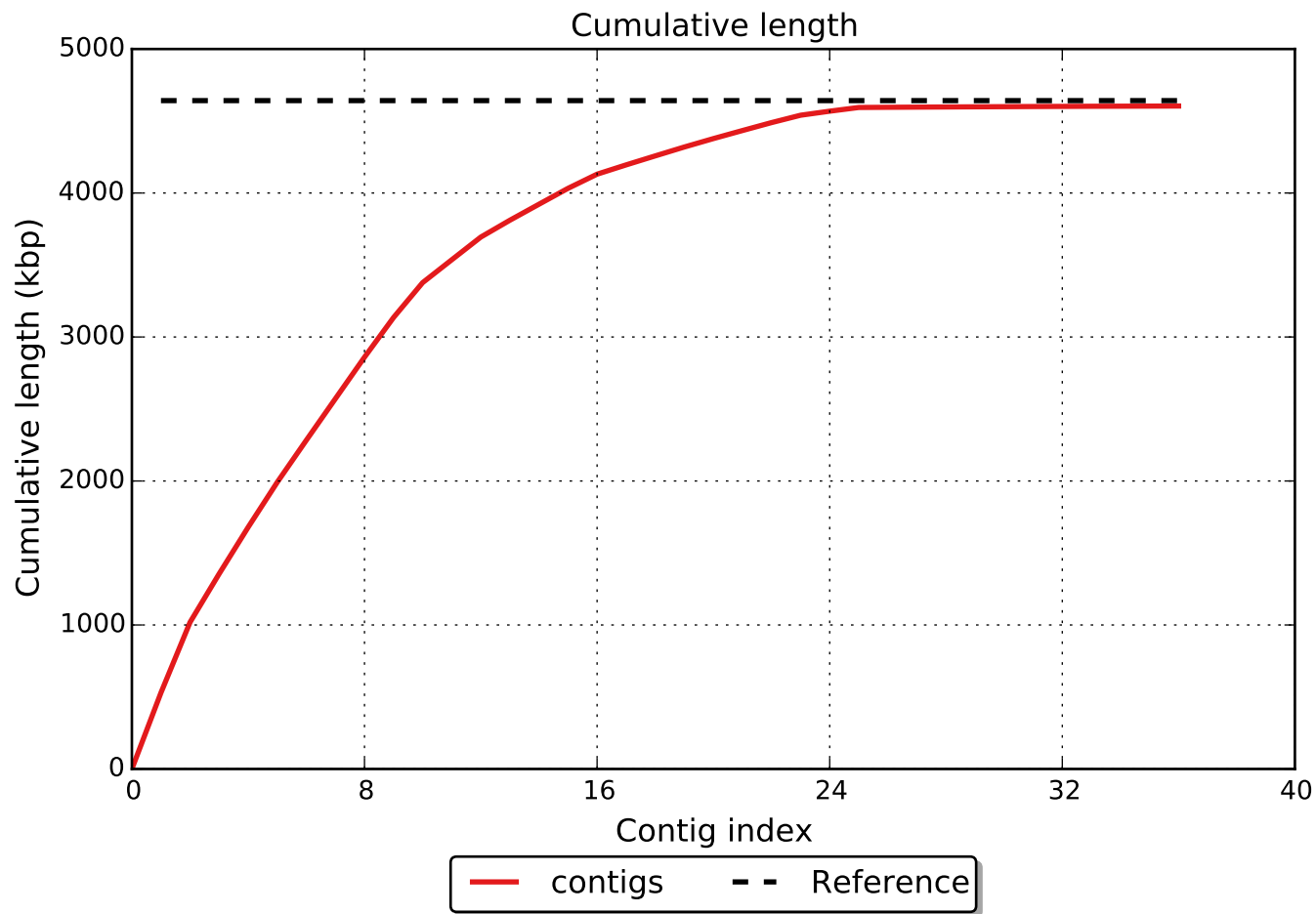
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

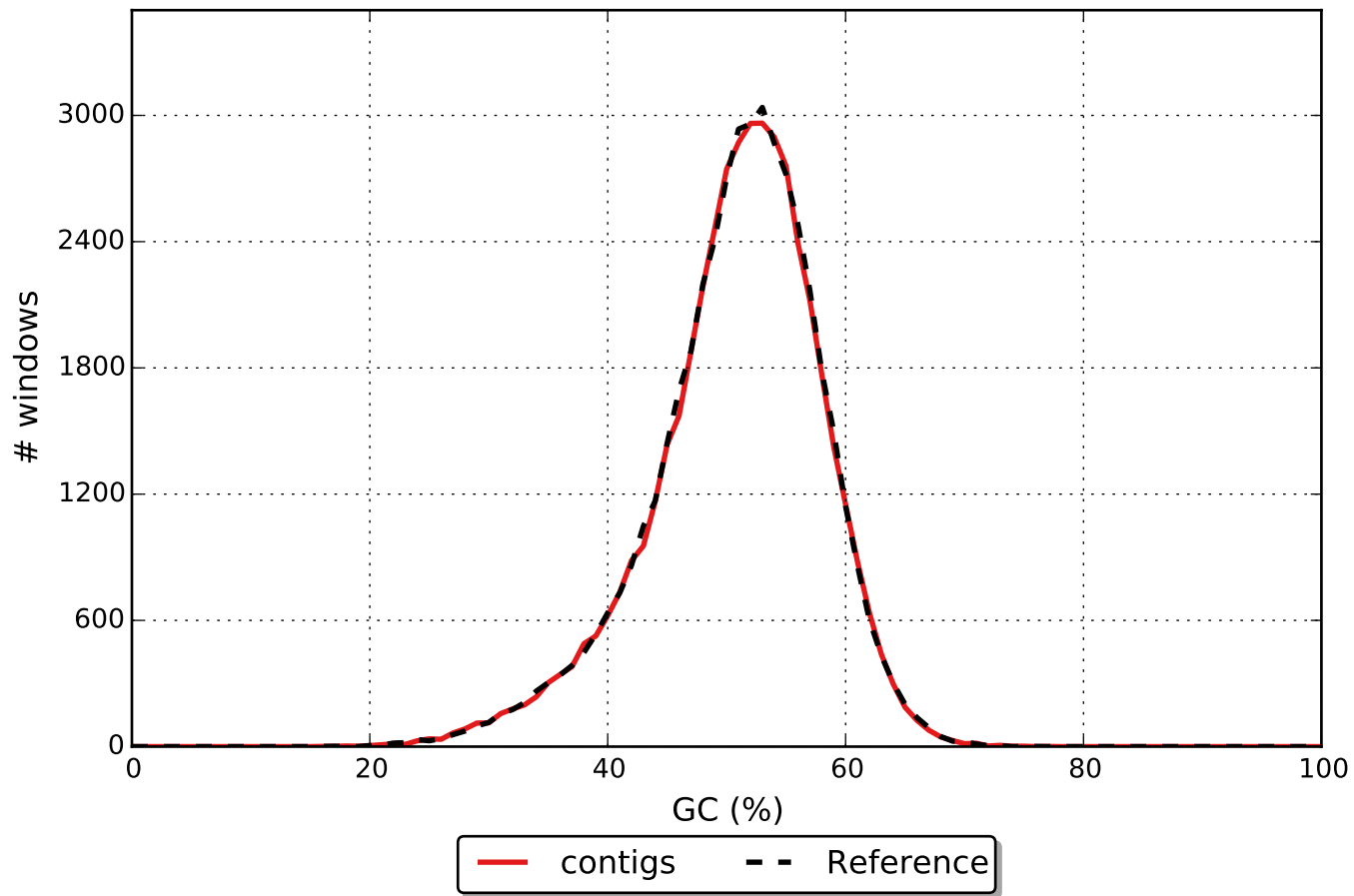


NGx





# GC content

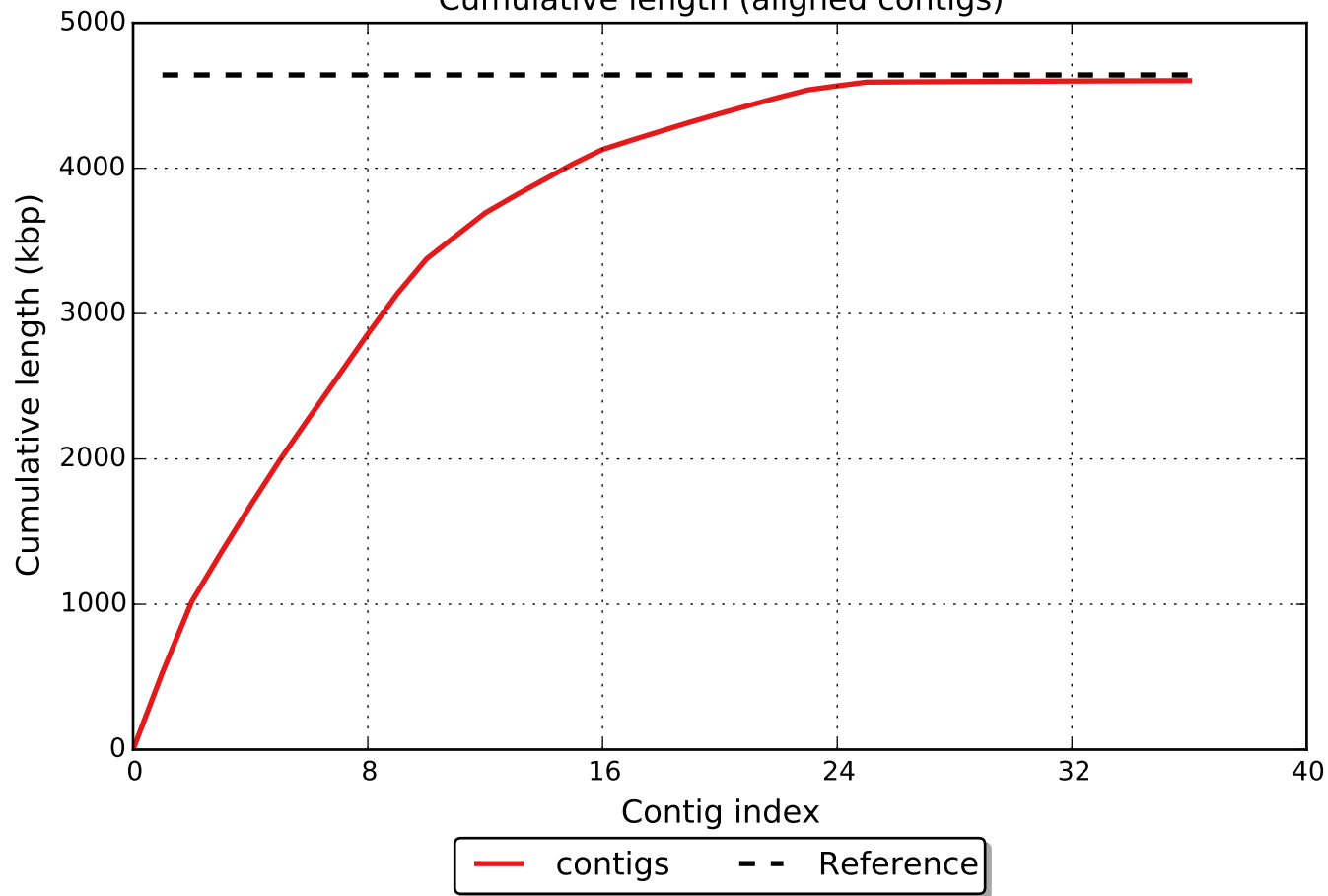


# Misassemblies

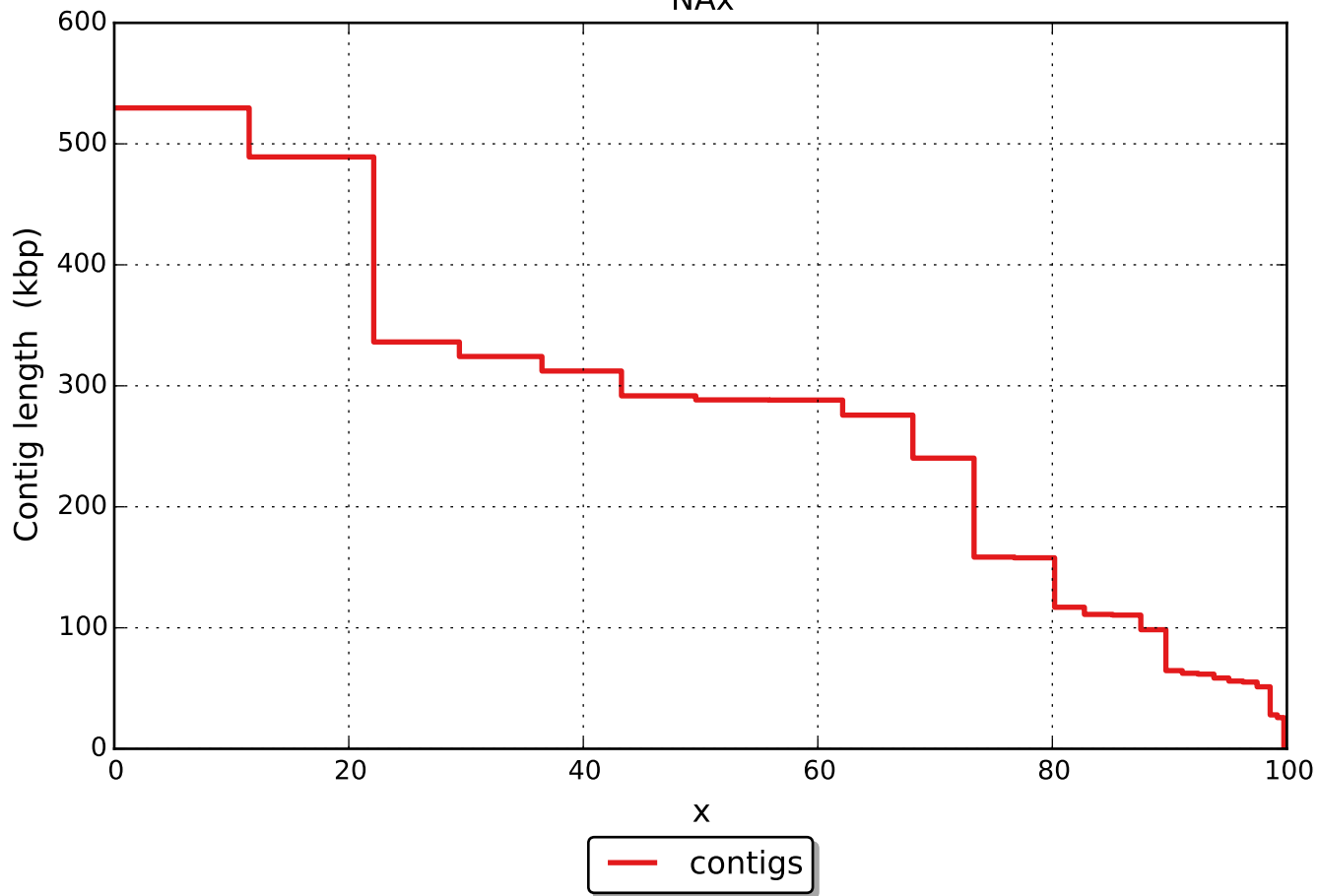




Cumulative length (aligned contigs)



NAx



NGAx

