

## Report

	contigs
# contigs ( $\geq 1000$ bp)	79
# contigs ( $\geq 5000$ bp)	45
# contigs ( $\geq 10000$ bp)	43
# contigs ( $\geq 25000$ bp)	36
# contigs ( $\geq 50000$ bp)	26
Total length ( $\geq 1000$ bp)	4504662
Total length ( $\geq 5000$ bp)	4434662
Total length ( $\geq 10000$ bp)	4420192
Total length ( $\geq 25000$ bp)	4319073
Total length ( $\geq 50000$ bp)	3973751
# contigs	101
Largest contig	475325
Total length	4519847
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	186479
NG50	173165
N75	85499
NG75	78915
L50	8
LG50	9
L75	18
LG75	19
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.229
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	862.39
# indels per 100 kbp	0.78
Largest alignment	475325
NA50	186479
NGA50	173164
NA75	85499
NGA75	78915
LA50	8
LGA50	9
LA75	18
LGA75	19

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	1
# mismatches	38920
# indels	35
# short indels	33
# long indels	2
Indels length	48

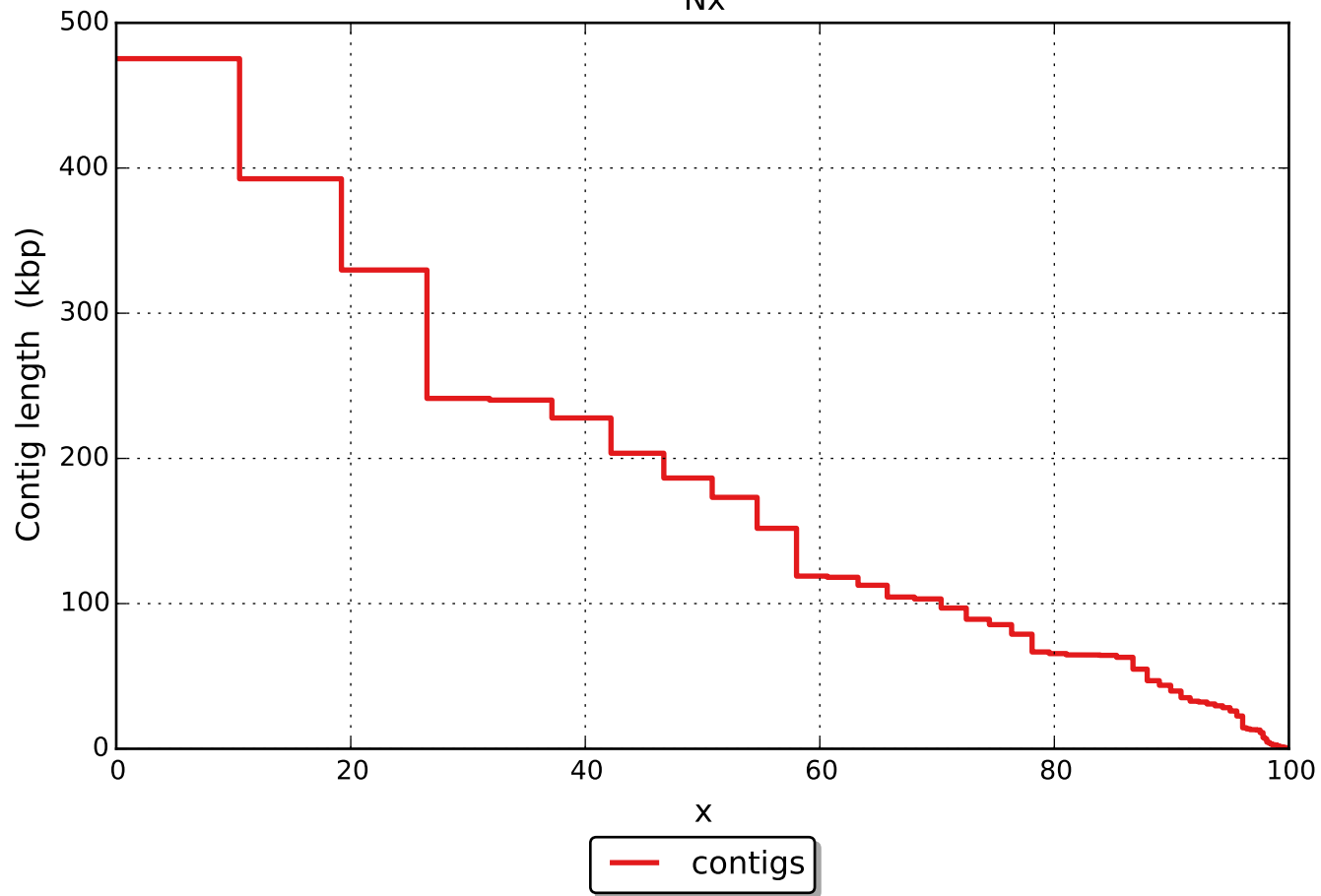
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

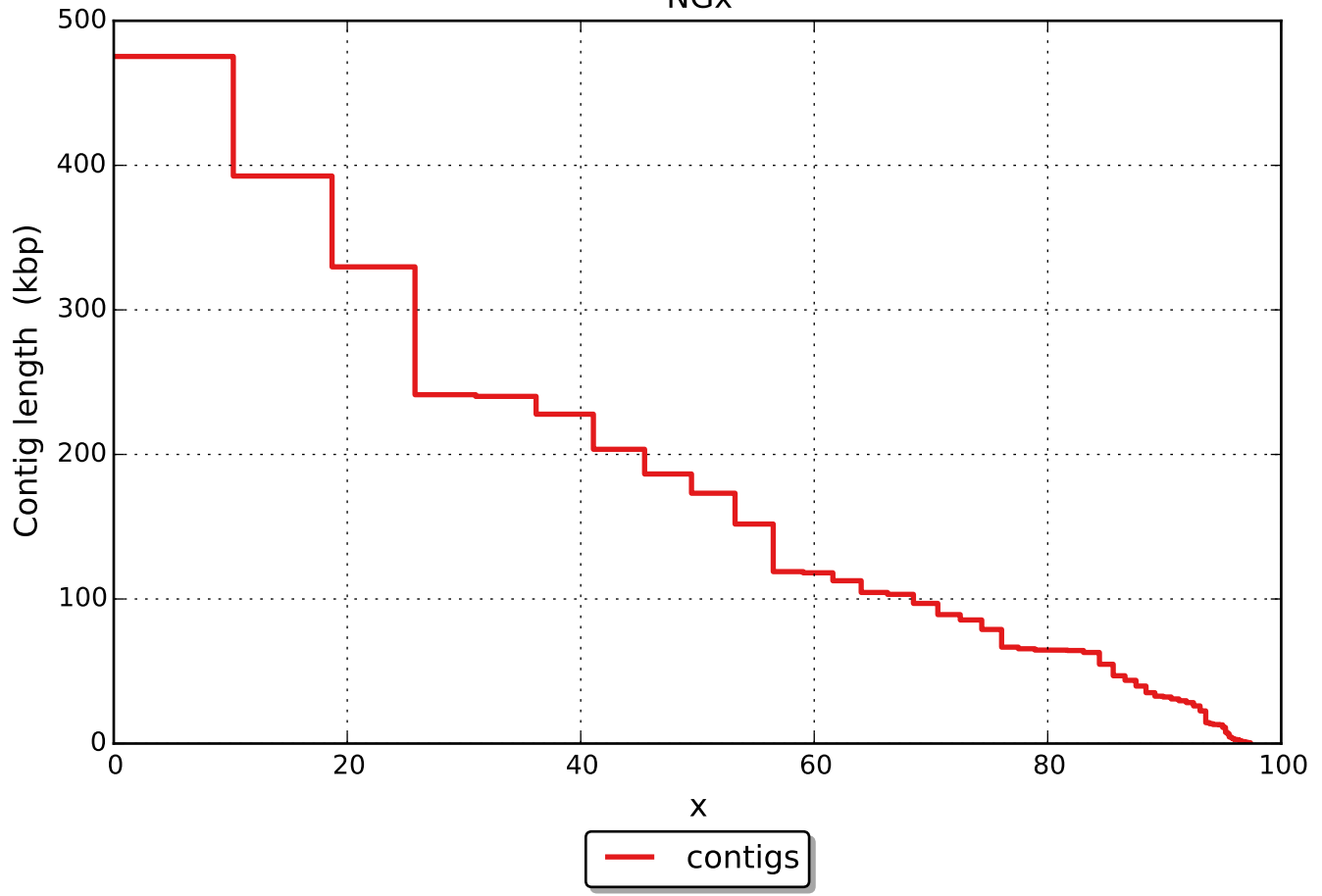
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

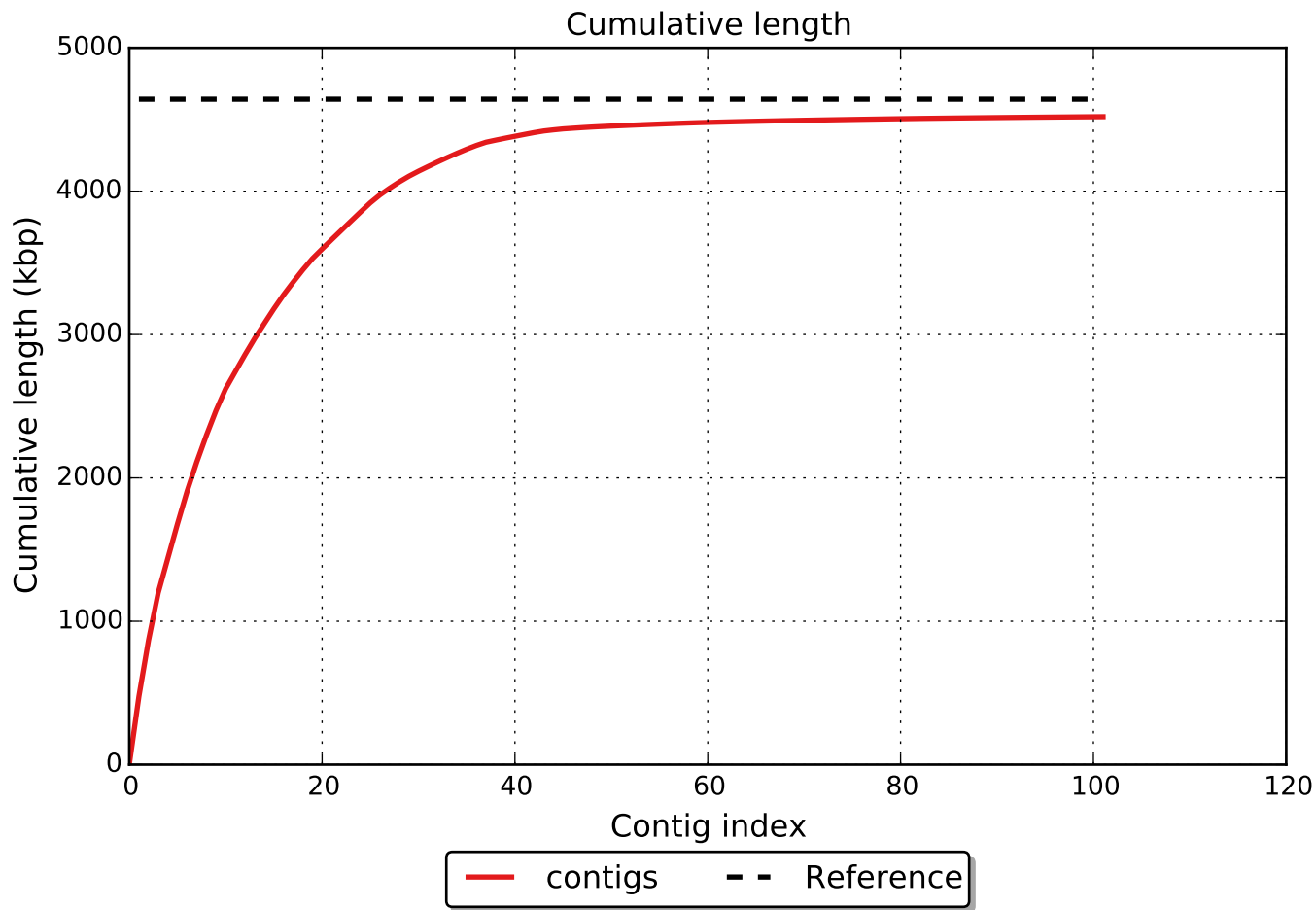
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

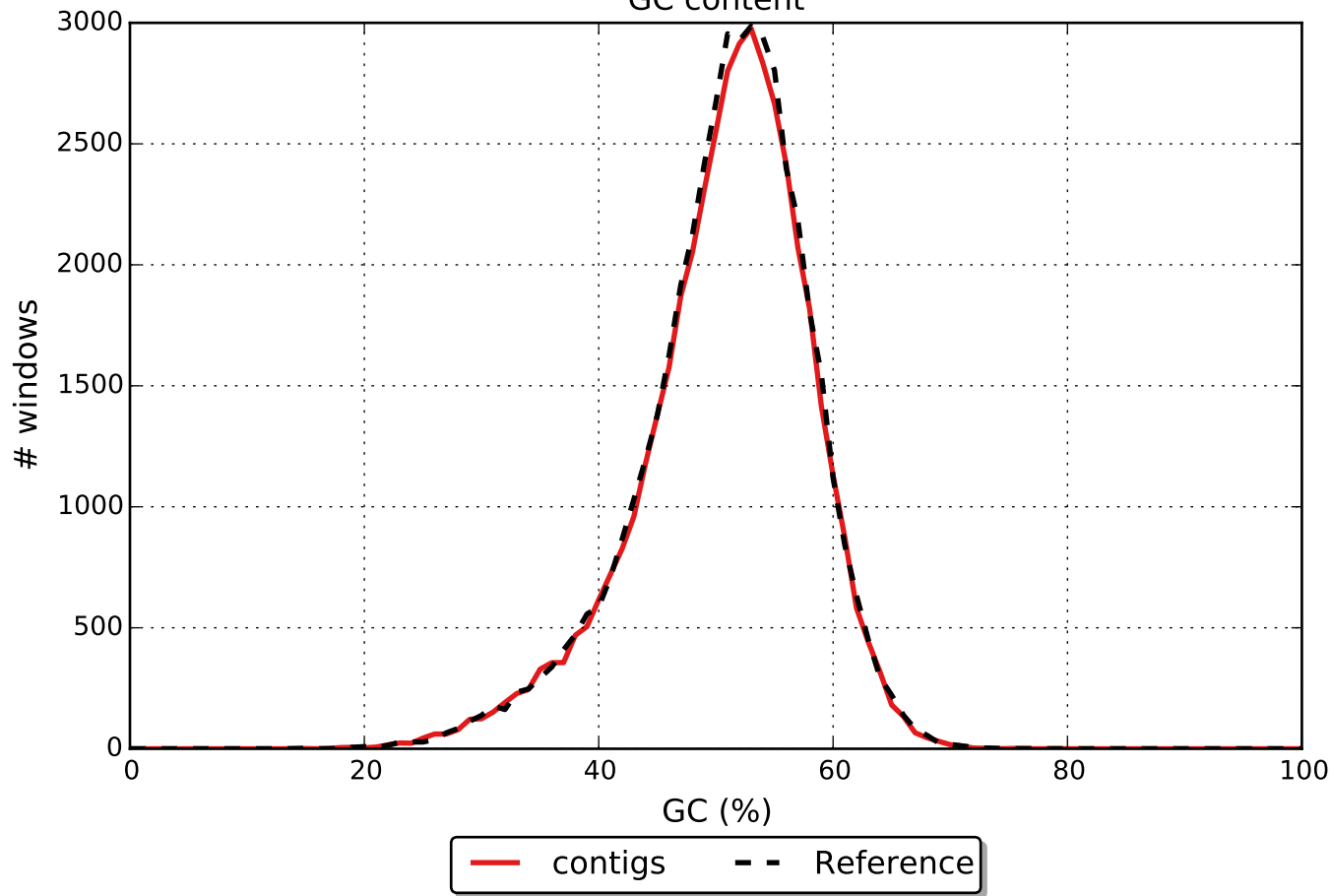


NGx





GC content

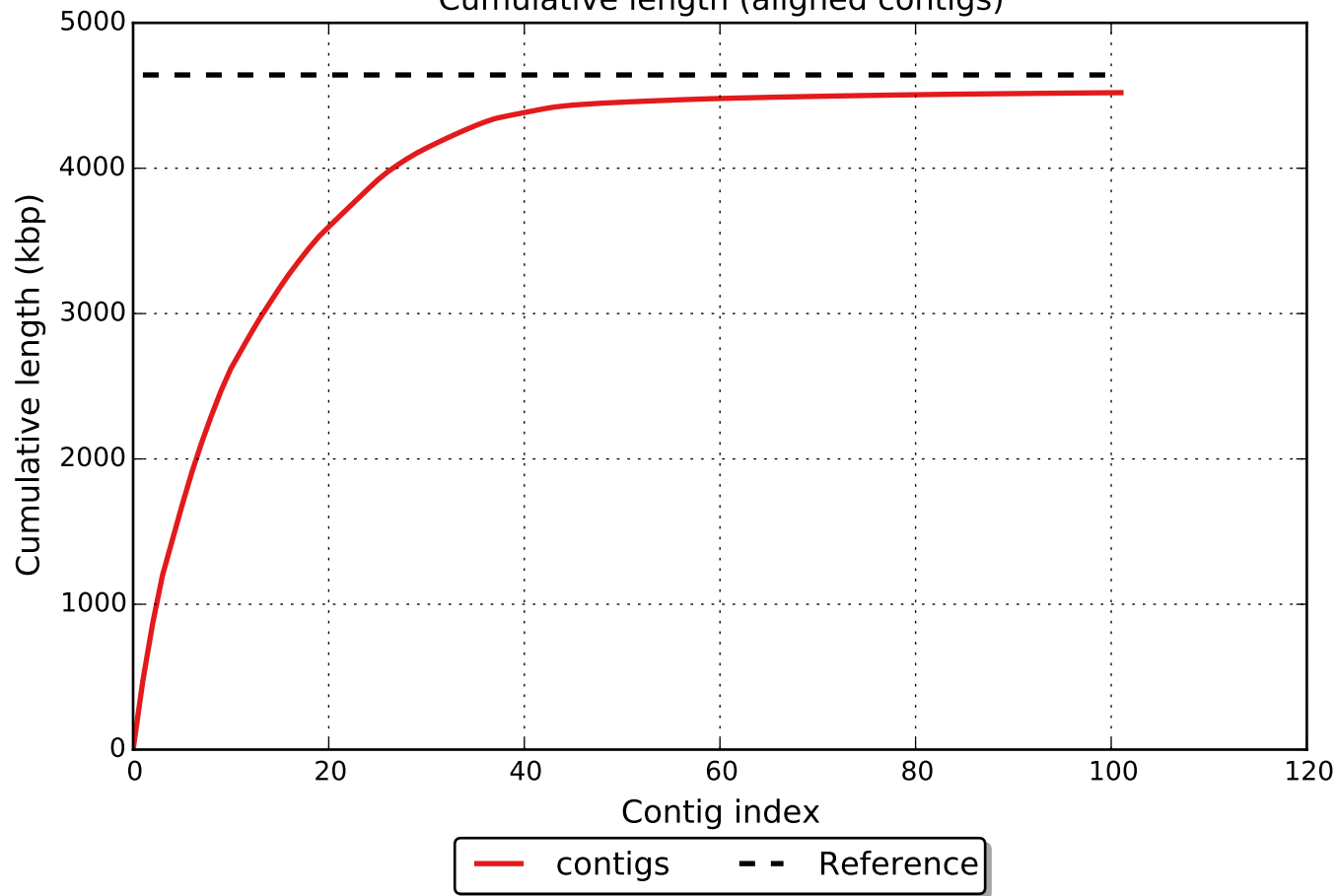


# Misassemblies

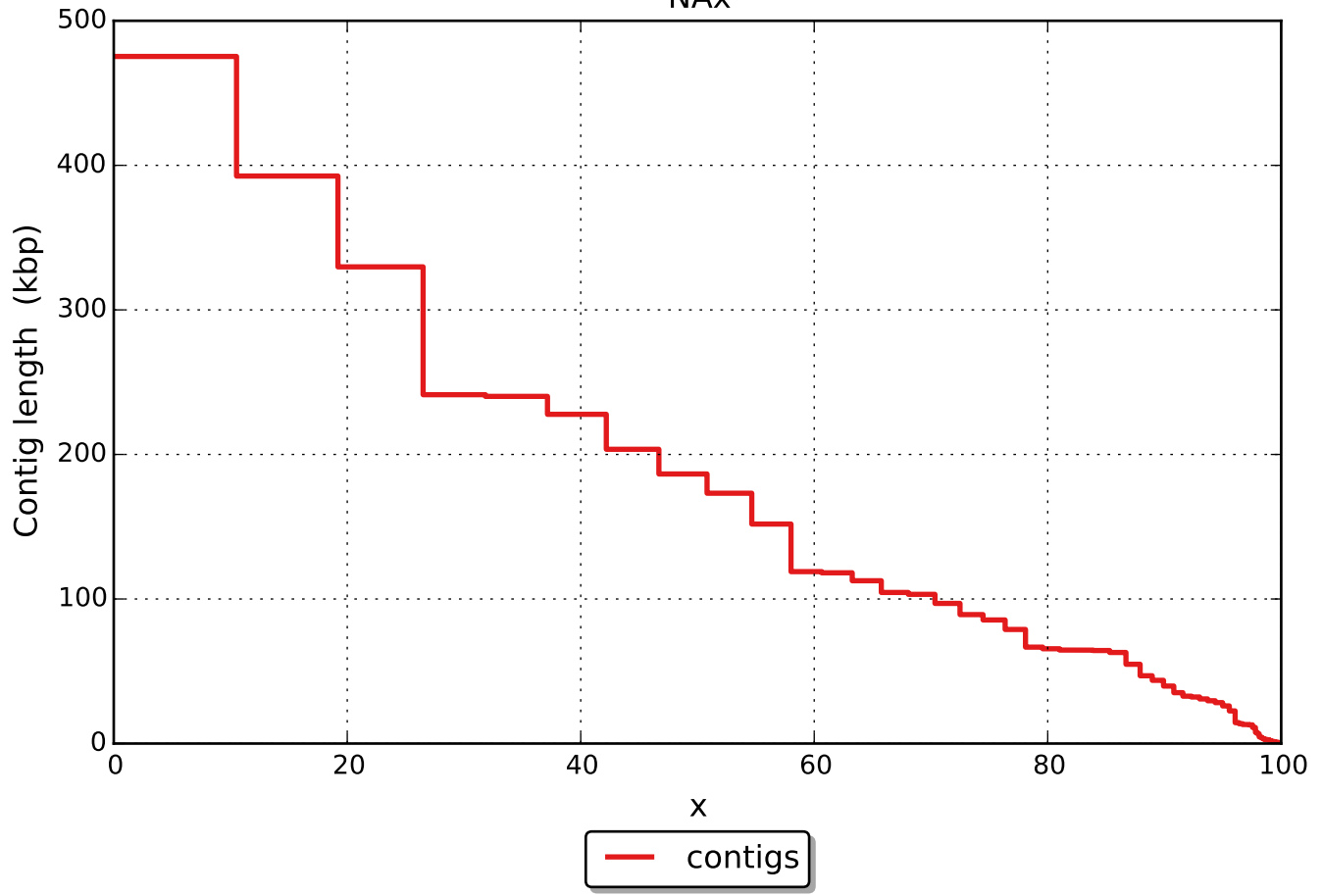




Cumulative length (aligned contigs)



NAx



NGAx

