

## Report

	contigs
# contigs ( $\geq 1000$ bp)	198
# contigs ( $\geq 5000$ bp)	124
# contigs ( $\geq 10000$ bp)	77
# contigs ( $\geq 25000$ bp)	36
# contigs ( $\geq 50000$ bp)	21
Total length ( $\geq 1000$ bp)	3679972
Total length ( $\geq 5000$ bp)	3465849
Total length ( $\geq 10000$ bp)	3129716
Total length ( $\geq 25000$ bp)	2482652
Total length ( $\geq 50000$ bp)	1943200
# contigs	231
Largest contig	189810
Total length	3701110
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.78
N50	54245
NG50	32009
N75	16218
NG75	4773
L50	20
LG50	31
L75	51
LG75	128
# misassemblies	3
# misassembled contigs	2
Misassembled contigs length	129141
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	76.466
Duplication ratio	1.043
# N's per 100 kbp	0.00
# mismatches per 100 kbp	989.44
# indels per 100 kbp	0.51
Largest alignment	189810
NA50	53403
NGA50	31790
NA75	15950
NGA75	4773
LA50	20
LGA50	32
LA75	53
LGA75	131

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	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	129141
# local misassemblies	3
# mismatches	35118
# indels	18
# short indels	18
# long indels	0
Indels length	18

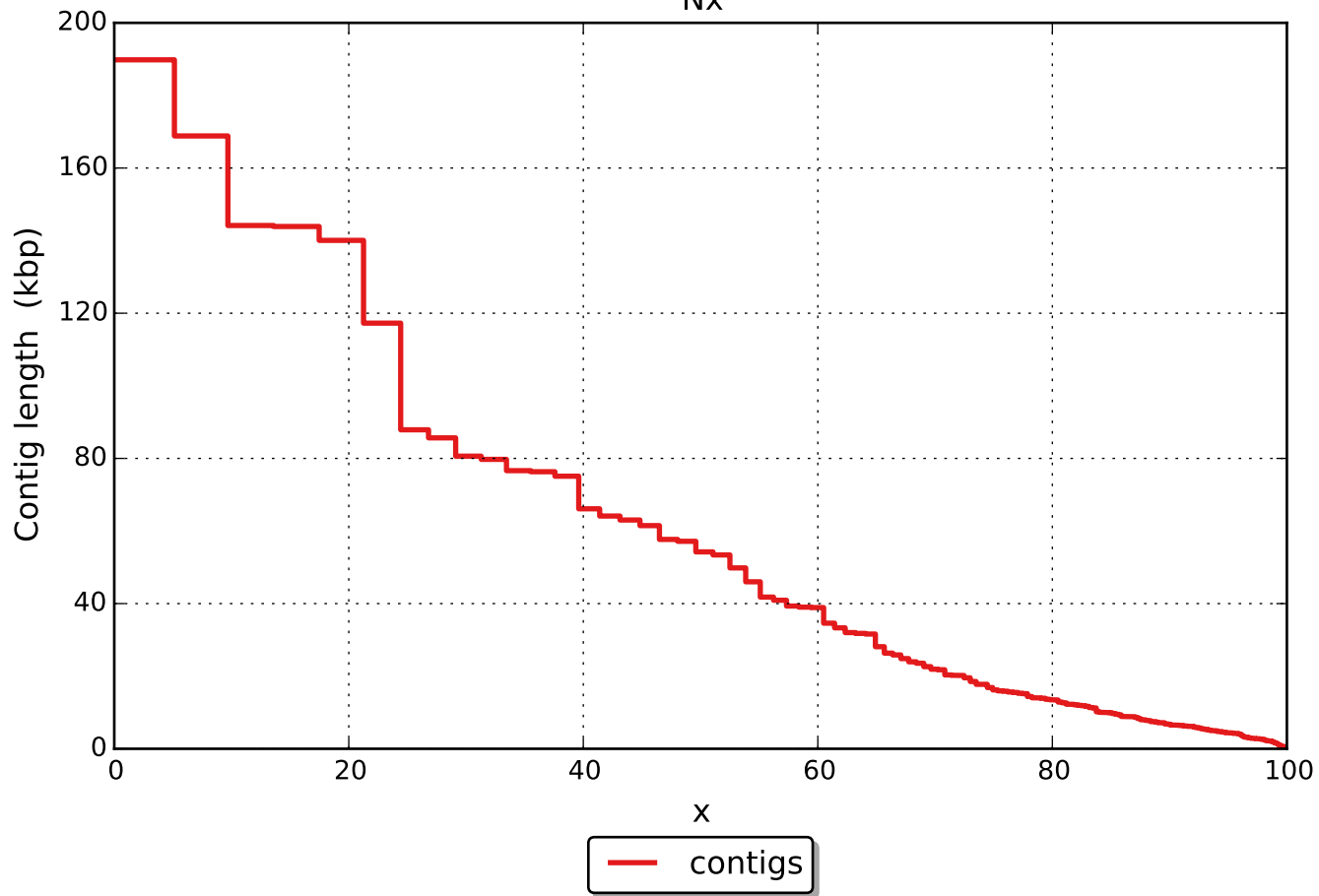
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

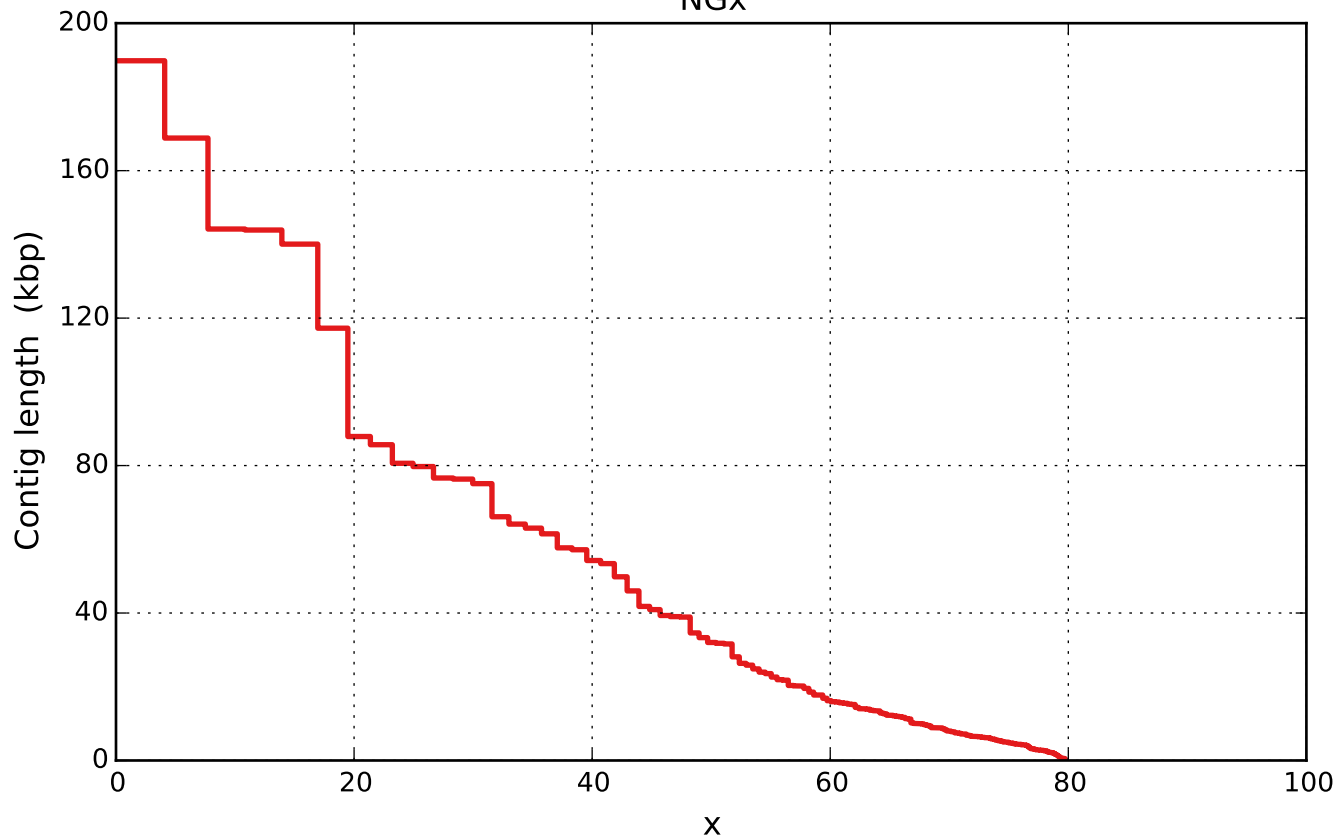
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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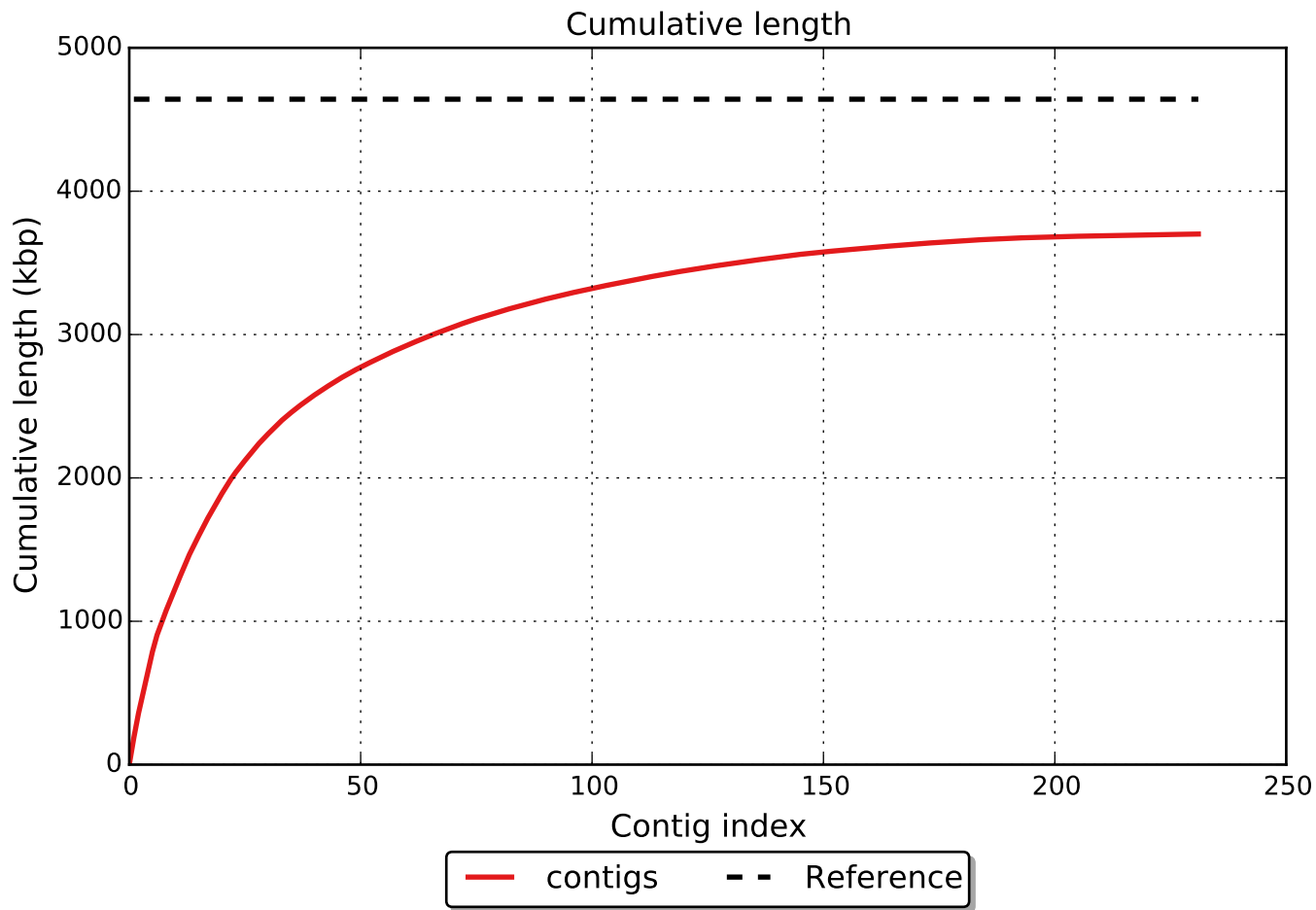
Nx



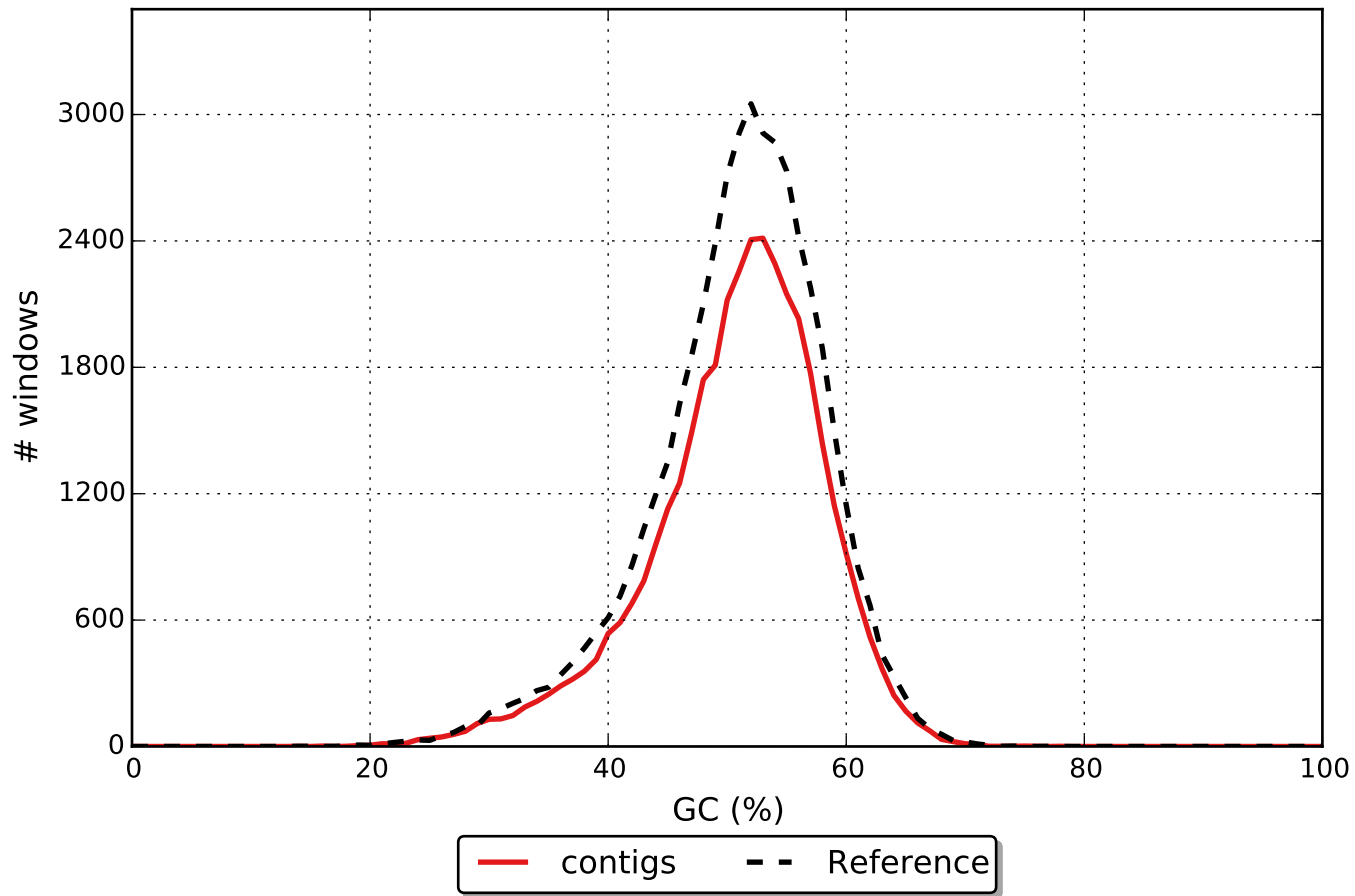
NGx

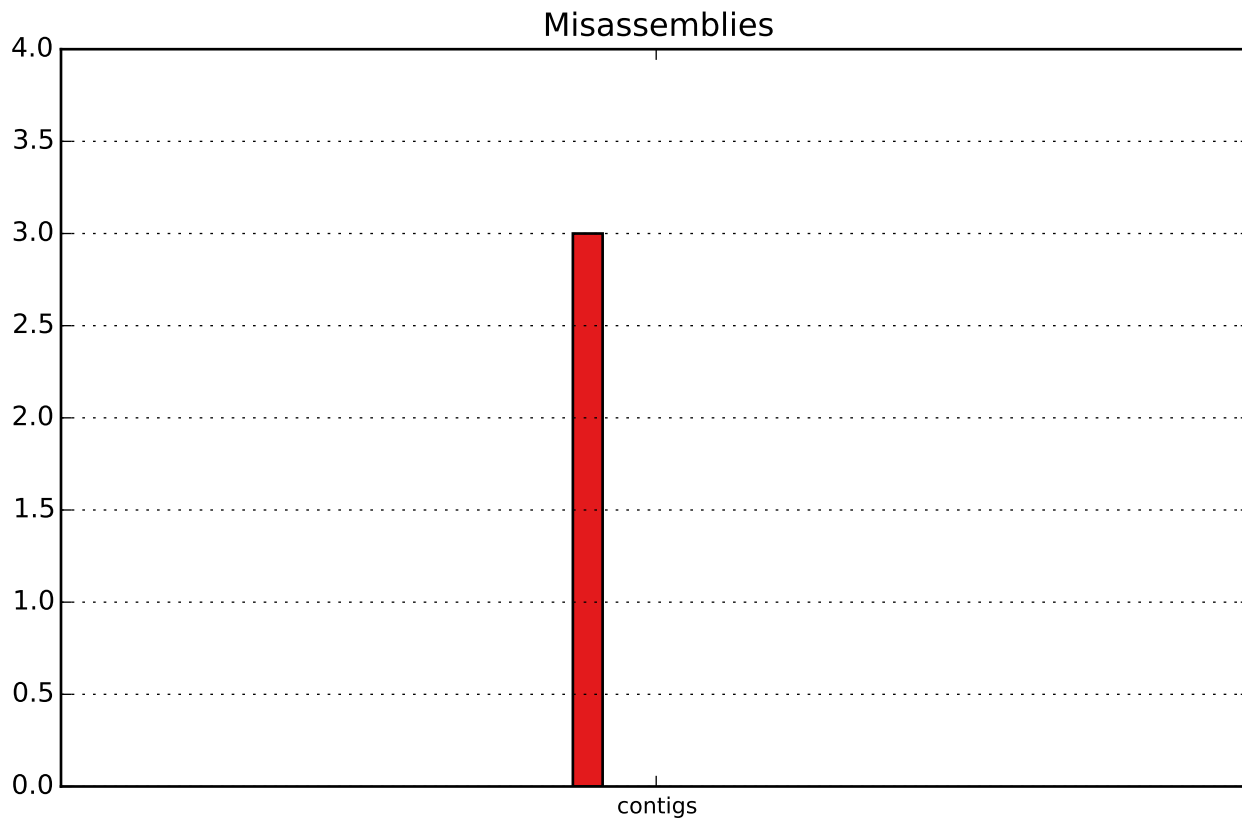


— contigs



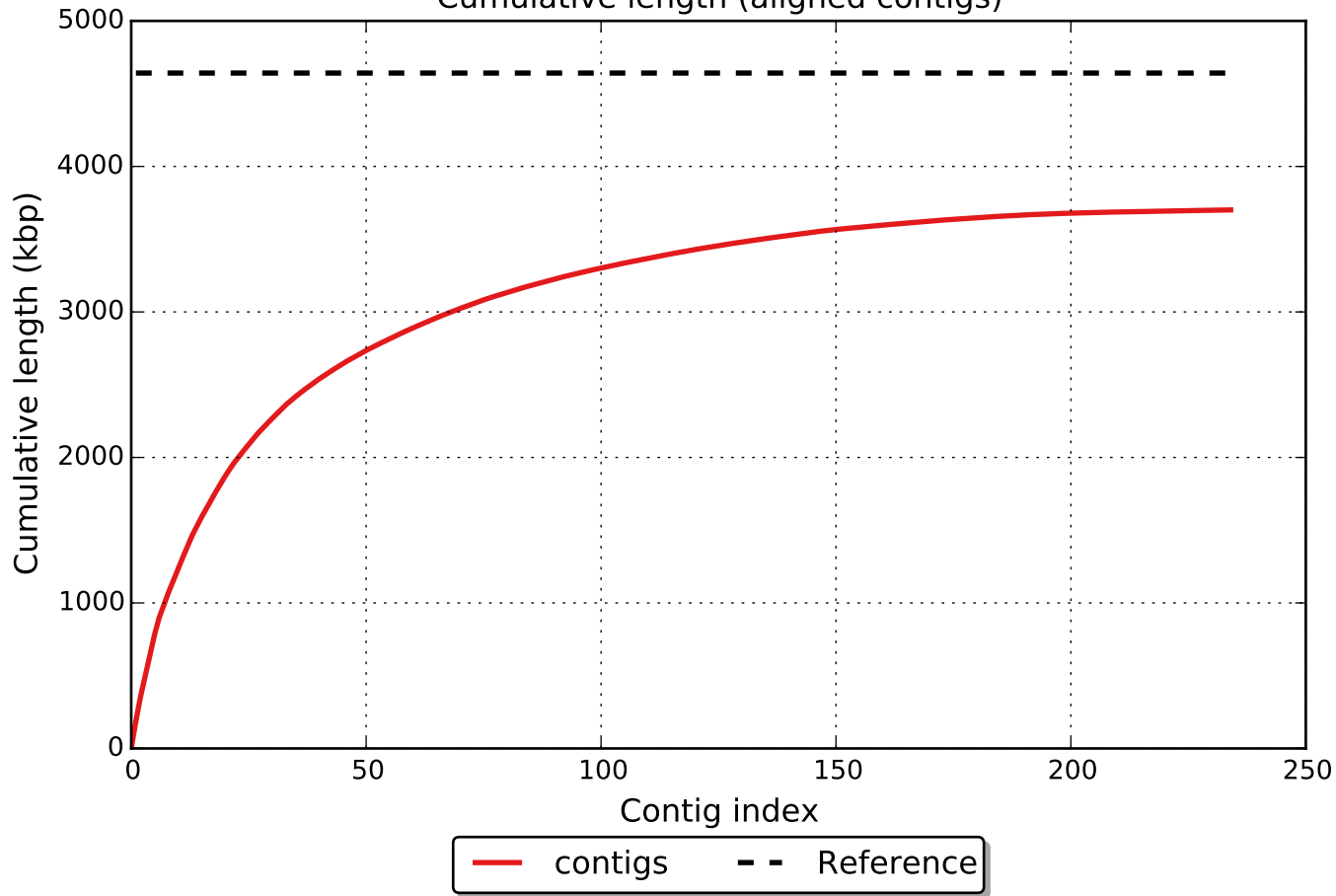
# GC content



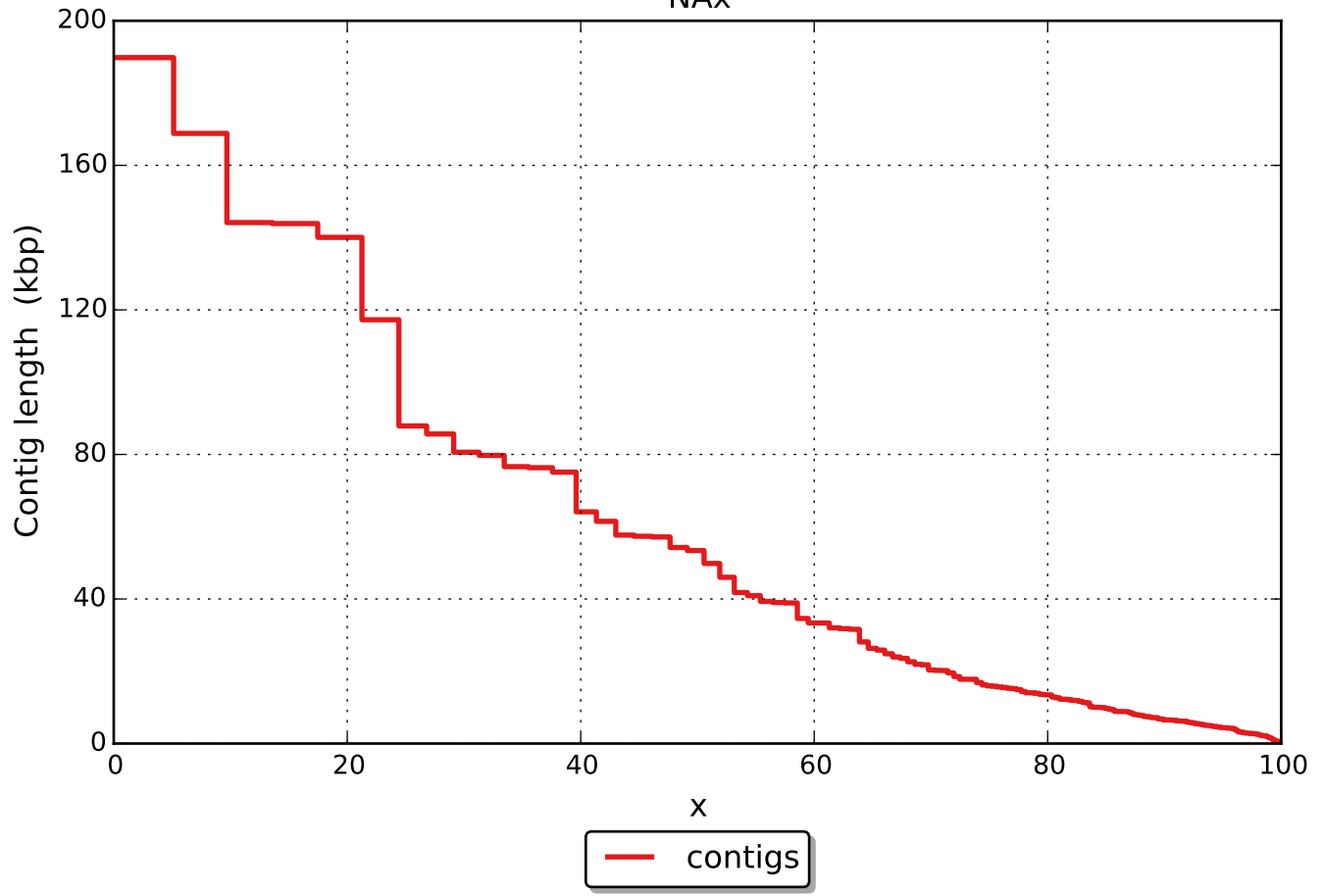




Cumulative length (aligned contigs)



NAx



NGAx

