

## Report

	final.contigs
# contigs (>= 0 bp)	440
# contigs (>= 1000 bp)	146
# contigs (>= 5000 bp)	122
# contigs (>= 10000 bp)	103
# contigs (>= 25000 bp)	66
# contigs (>= 50000 bp)	28
Total length (>= 0 bp)	4638877
Total length (>= 1000 bp)	4540987
Total length (>= 5000 bp)	4477714
Total length (>= 10000 bp)	4338012
Total length (>= 25000 bp)	3772958
Total length (>= 50000 bp)	2406475
# contigs	166
Largest contig	169087
Total length	4554962
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	53827
NG50	53801
N75	31696
NG75	31480
L50	26
LG50	27
L75	54
LG75	56
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.014
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.48
# indels per 100 kbp	0.00
Largest alignment	169087
NA50	53827
NGA50	53801
NA75	31696
NGA75	31480
LA50	26
LGA50	27
LA75	54
LGA75	56

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

## Misassemblies report

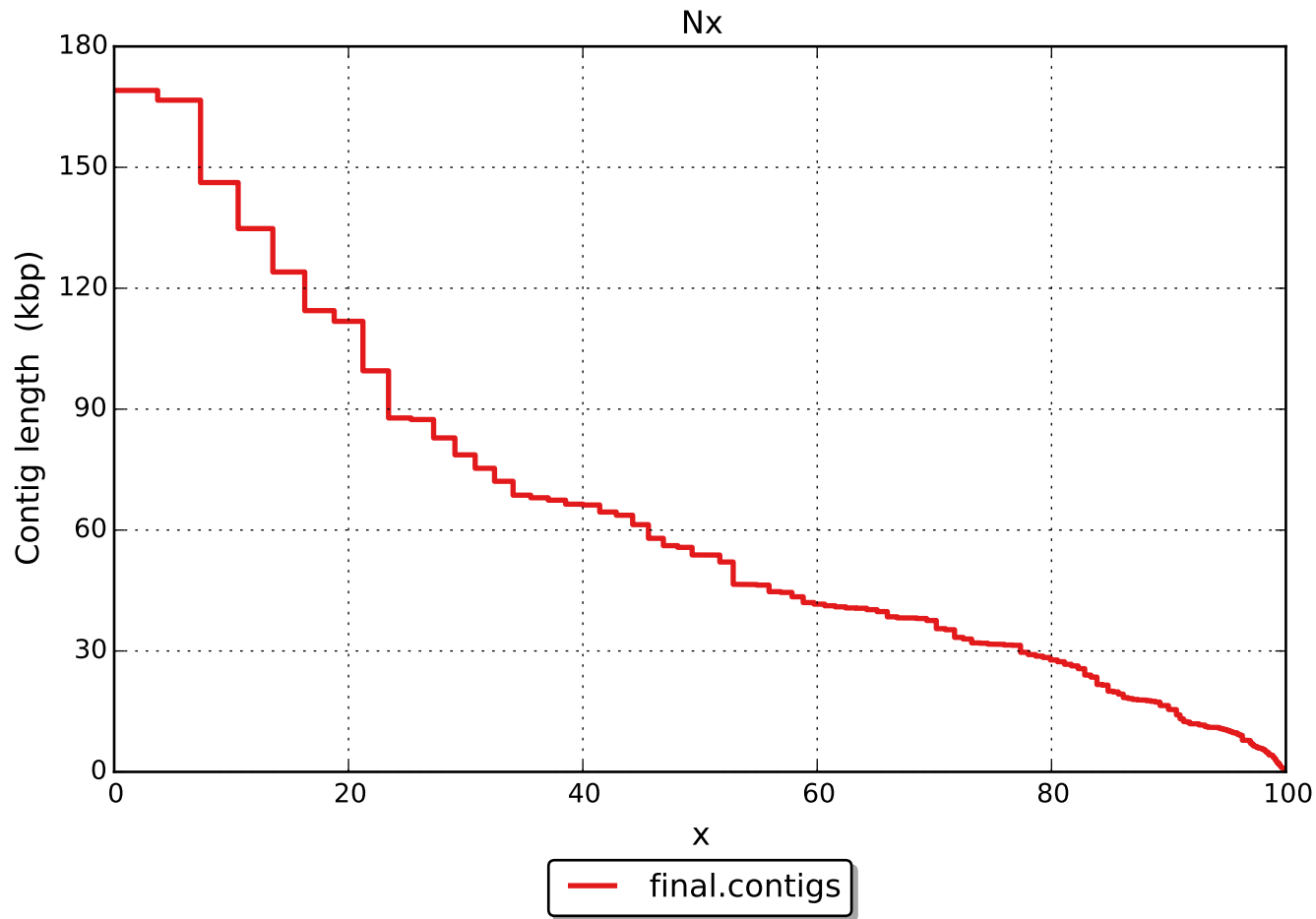
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	113
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

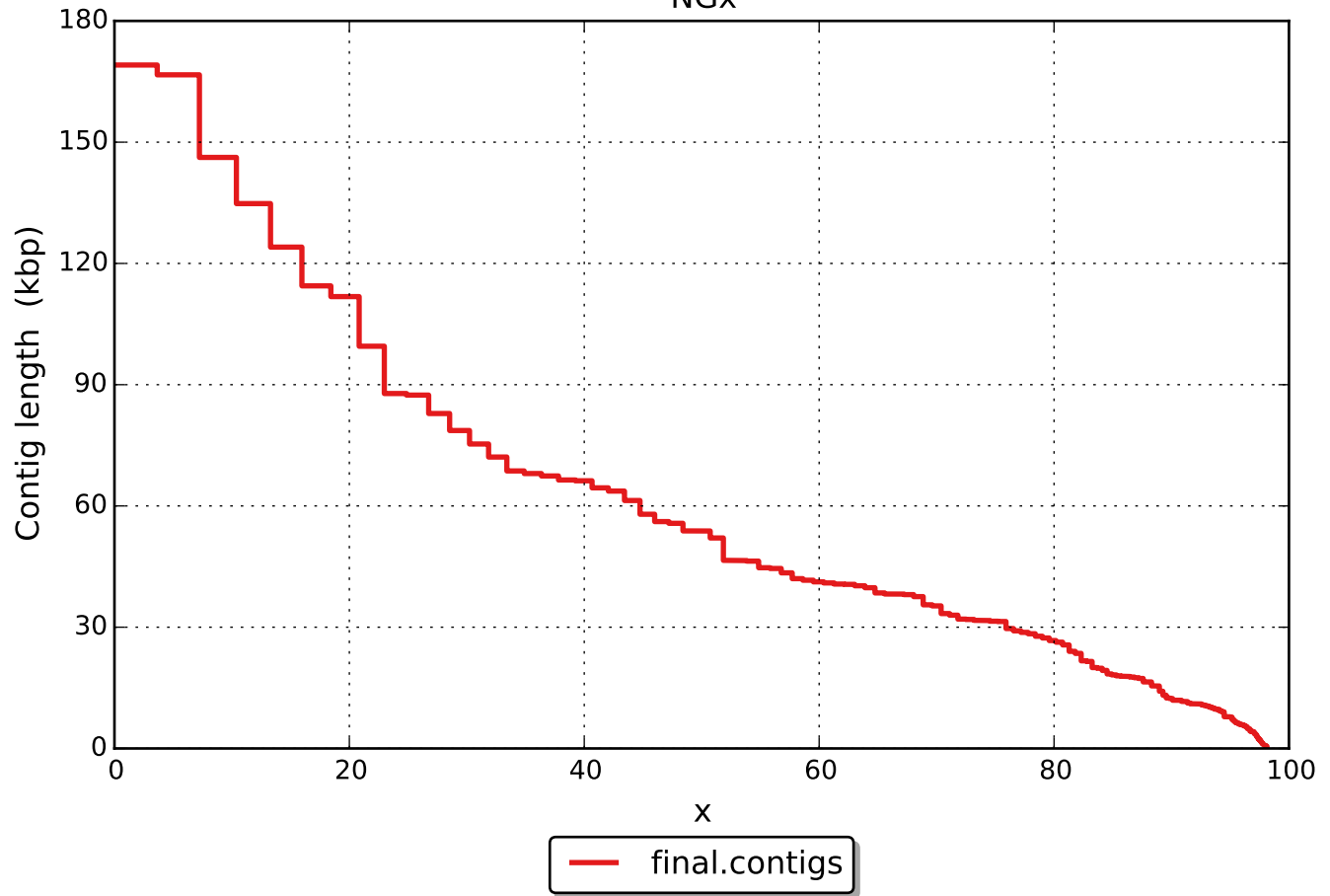
## Unaligned report

	final.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

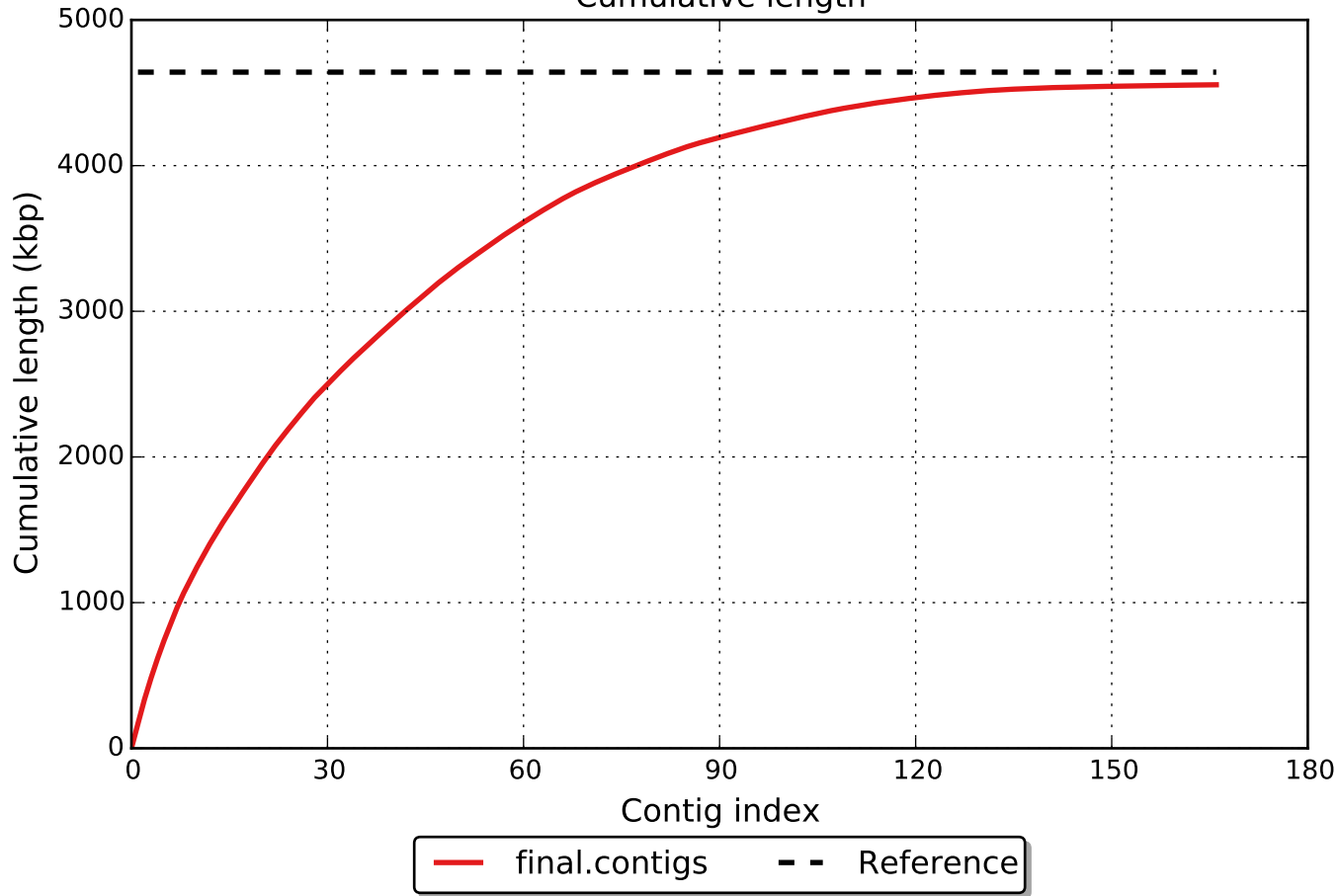
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



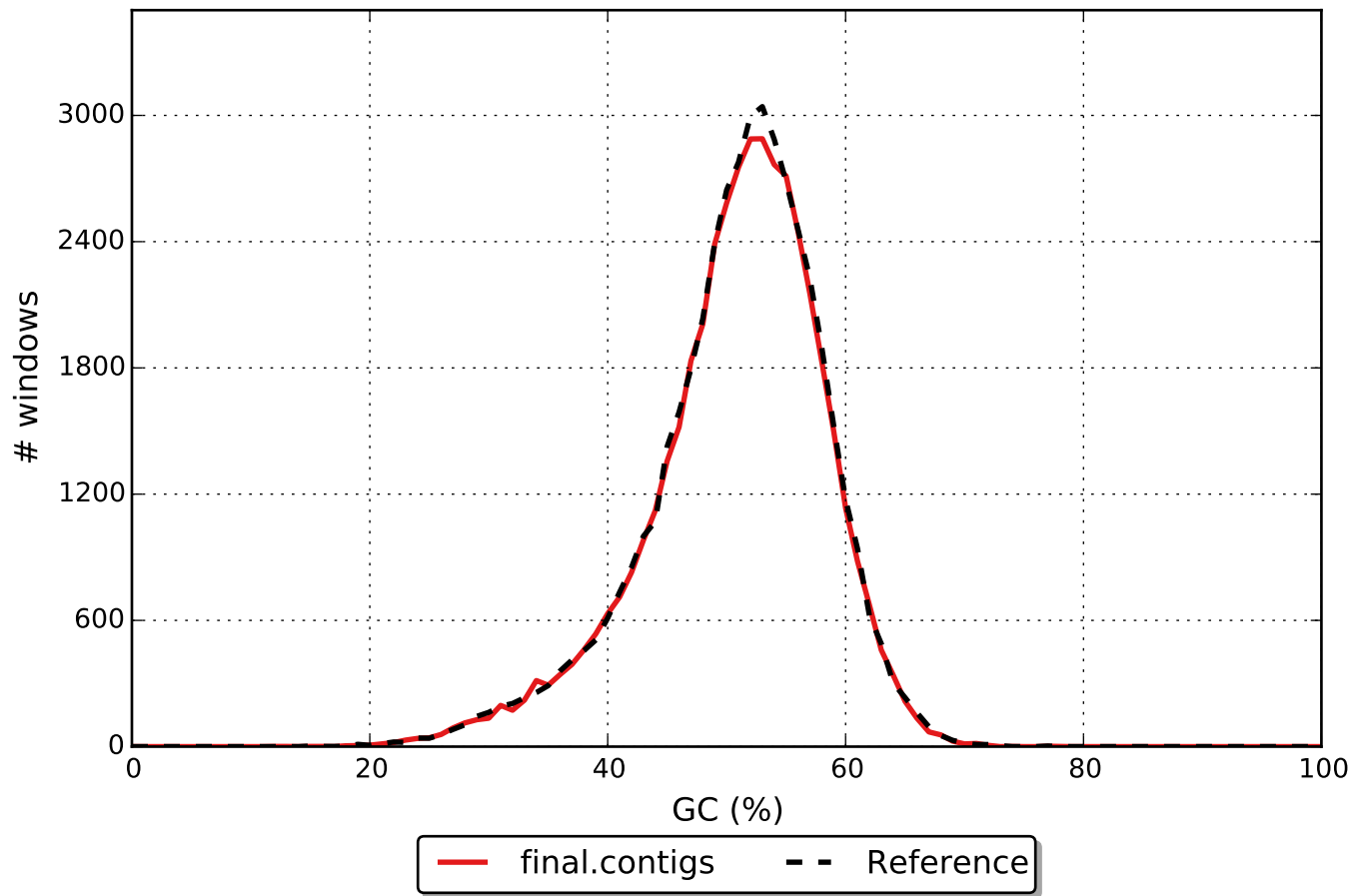
NGx



Cumulative length



# GC content

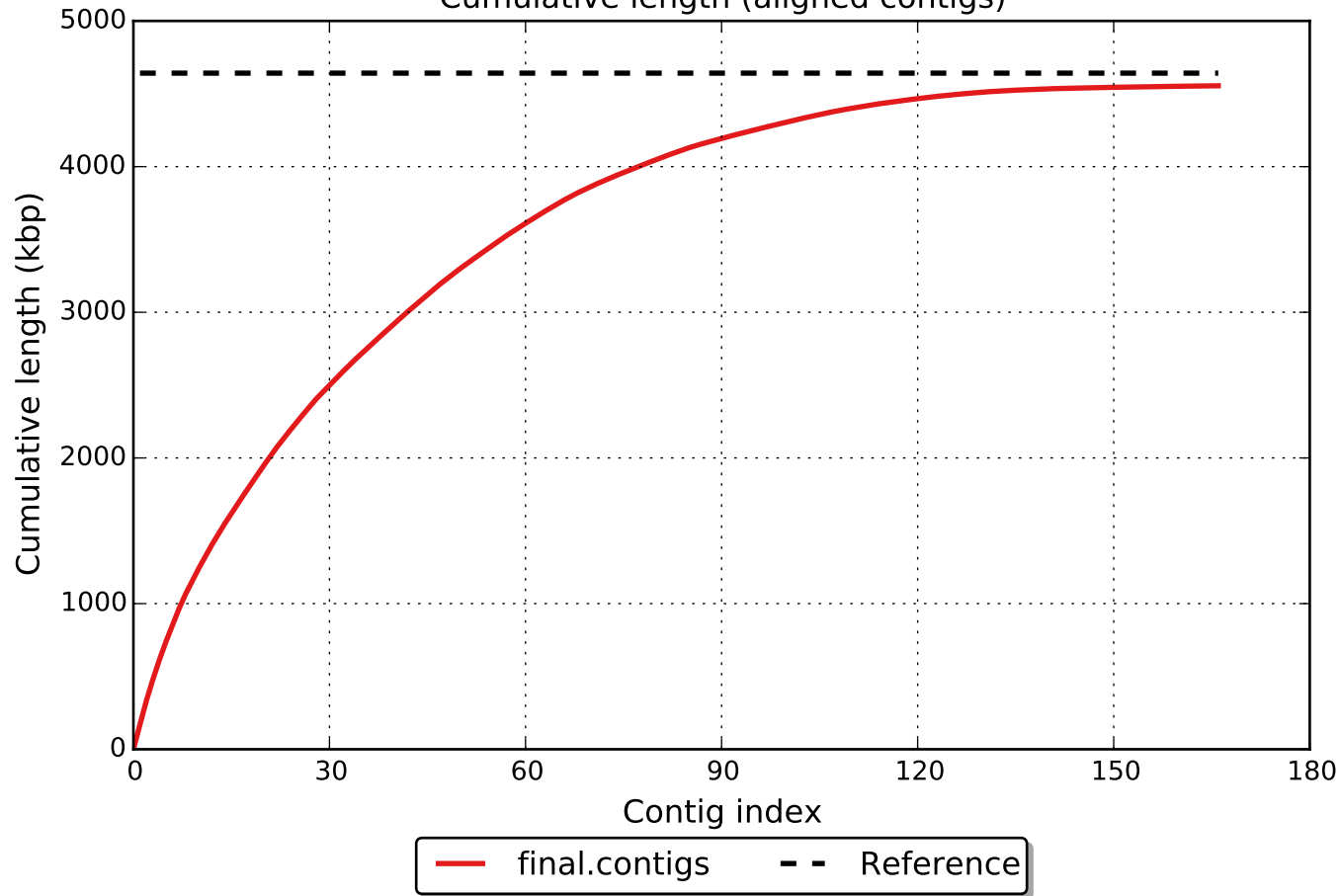


# Misassemblies

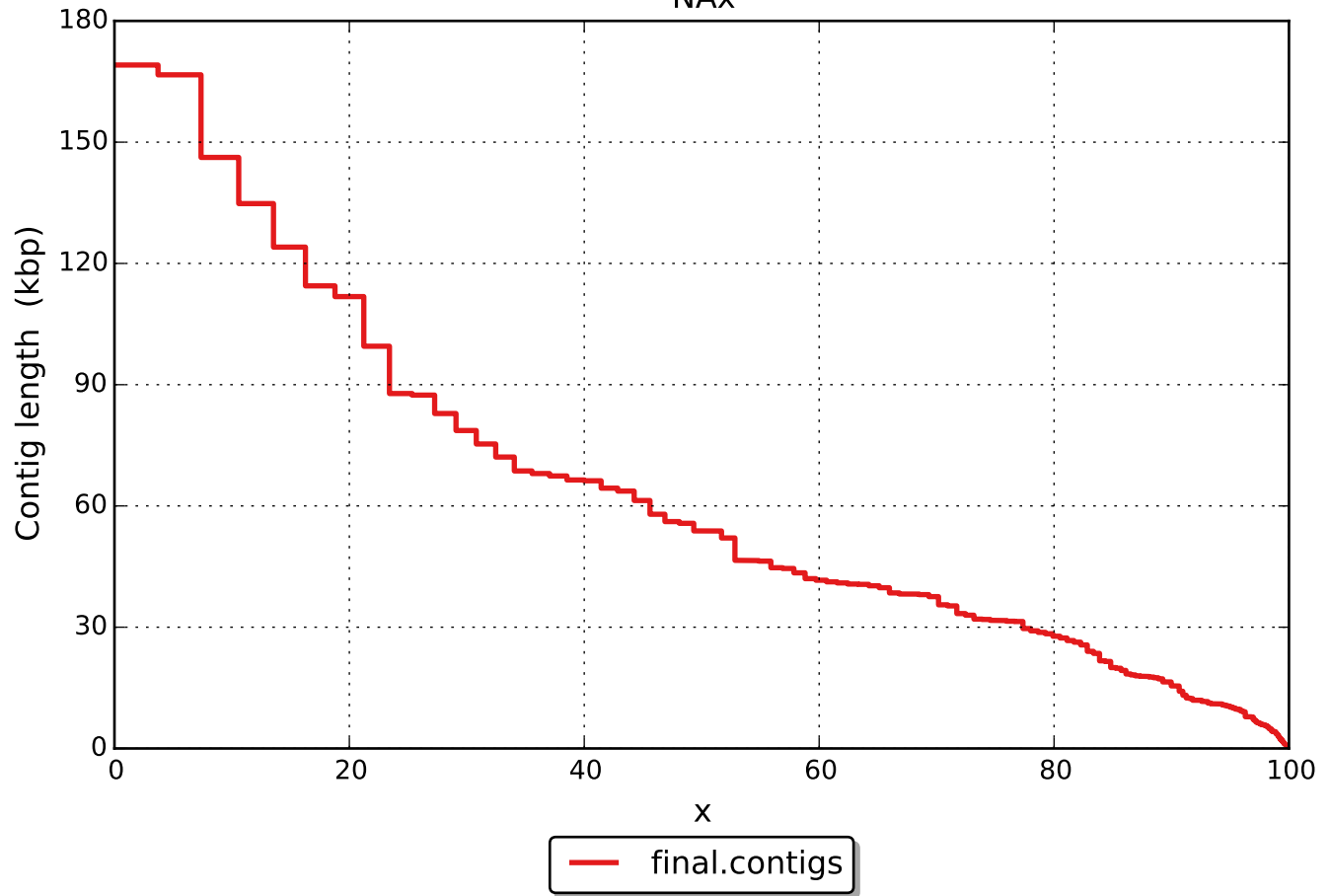




Cumulative length (aligned contigs)



NAx



# NGAx

