

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	3817
# contigs ( $\geq 1000$ bp)	119
# contigs ( $\geq 5000$ bp)	0
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	1910447
Total length ( $\geq 1000$ bp)	147351
Total length ( $\geq 5000$ bp)	0
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	1401
Largest contig	2634
Total length	971818
Reference length	4641652
GC (%)	50.67
Reference GC (%)	50.79
N50	671
N75	569
L50	549
L75	944
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	7880
# local misassemblies	0
# unaligned contigs	817 + 5 part
Unaligned length	561890
Genome fraction (%)	8.813
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	652.97
# indels per 100 kbp	1.71
Largest alignment	2463
NGA50	-

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

	final.contigs
# misassemblies	4
# relocations	4
# translocations	0
# inversions	0
# misassembled contigs	4
Misassembled contigs length	7880
# local misassemblies	0
# mismatches	2671
# indels	7
# short indels	7
# long indels	0
Indels length	7

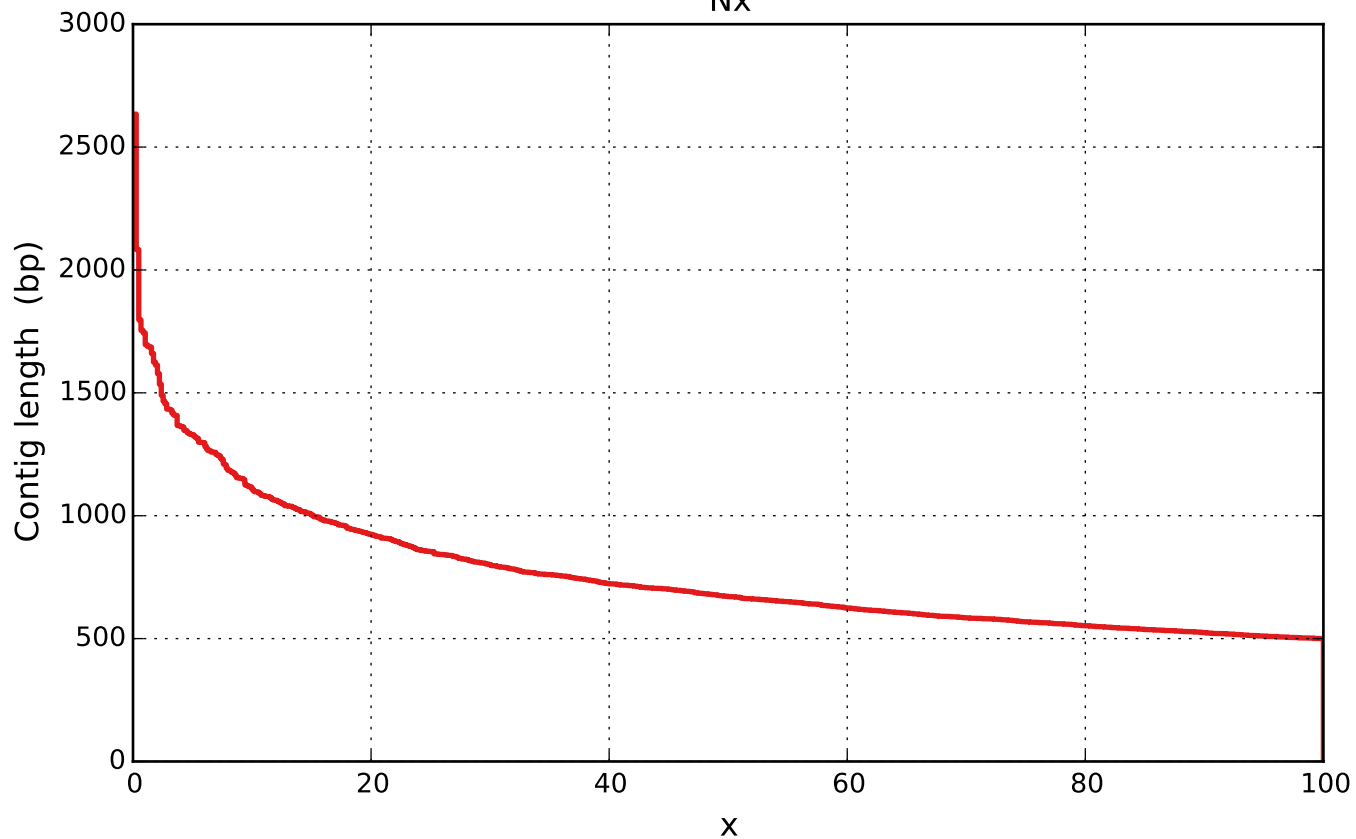
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	final.contigs
# fully unaligned contigs	817
Fully unaligned length	559707
# partially unaligned contigs	5
# with misassembly	0
# both parts are significant	0
Partially unaligned length	2183
# N's	0

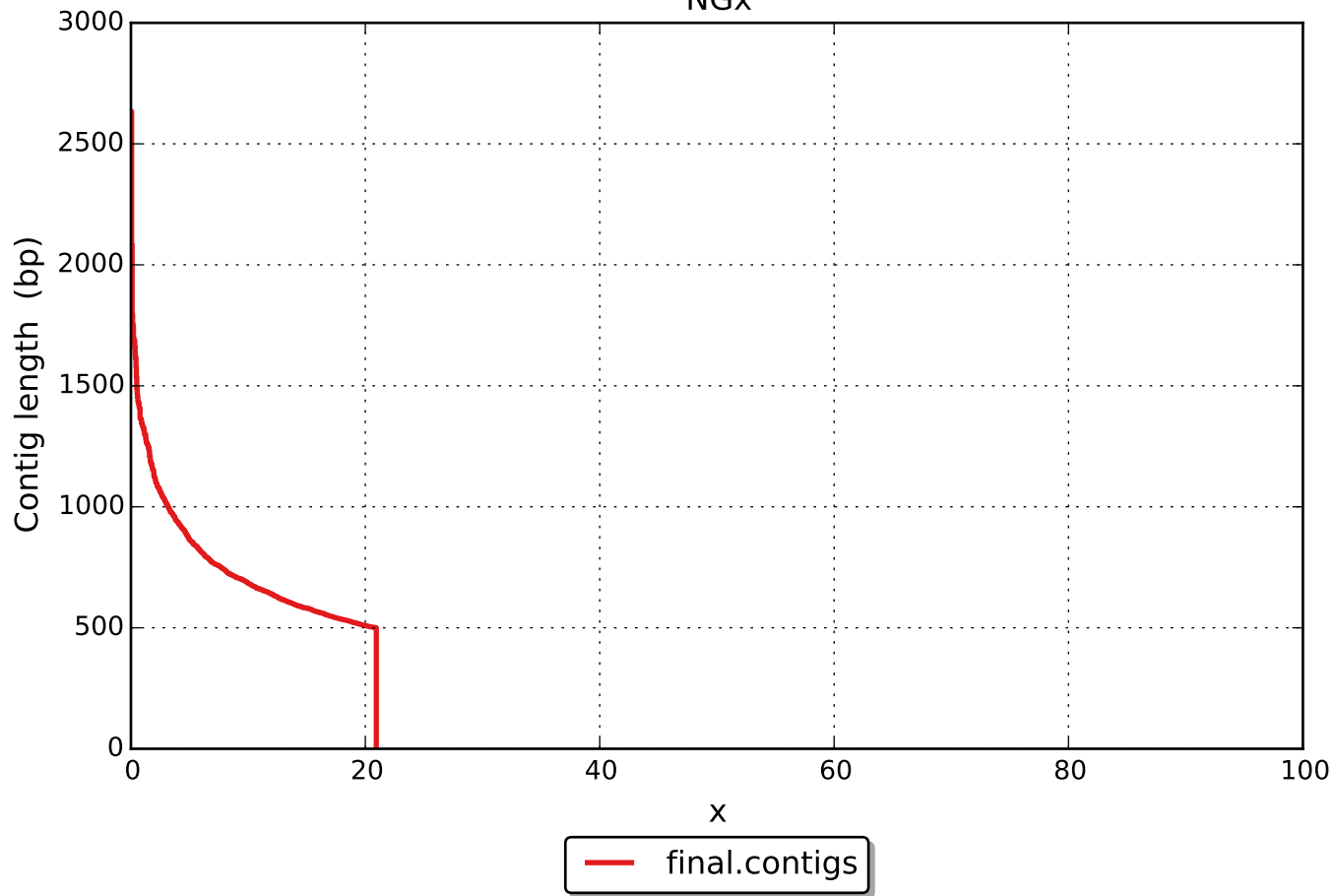
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

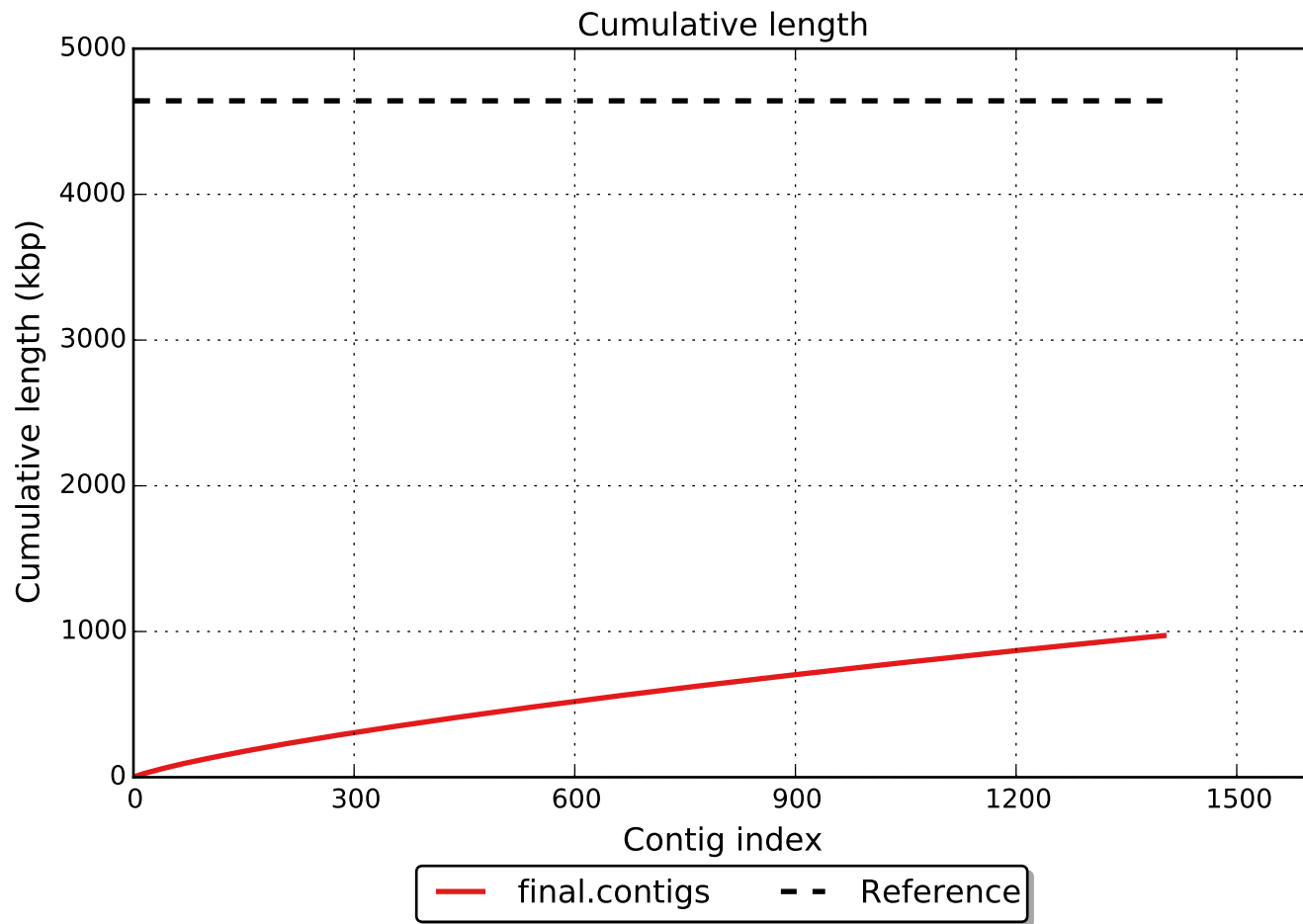
Nx



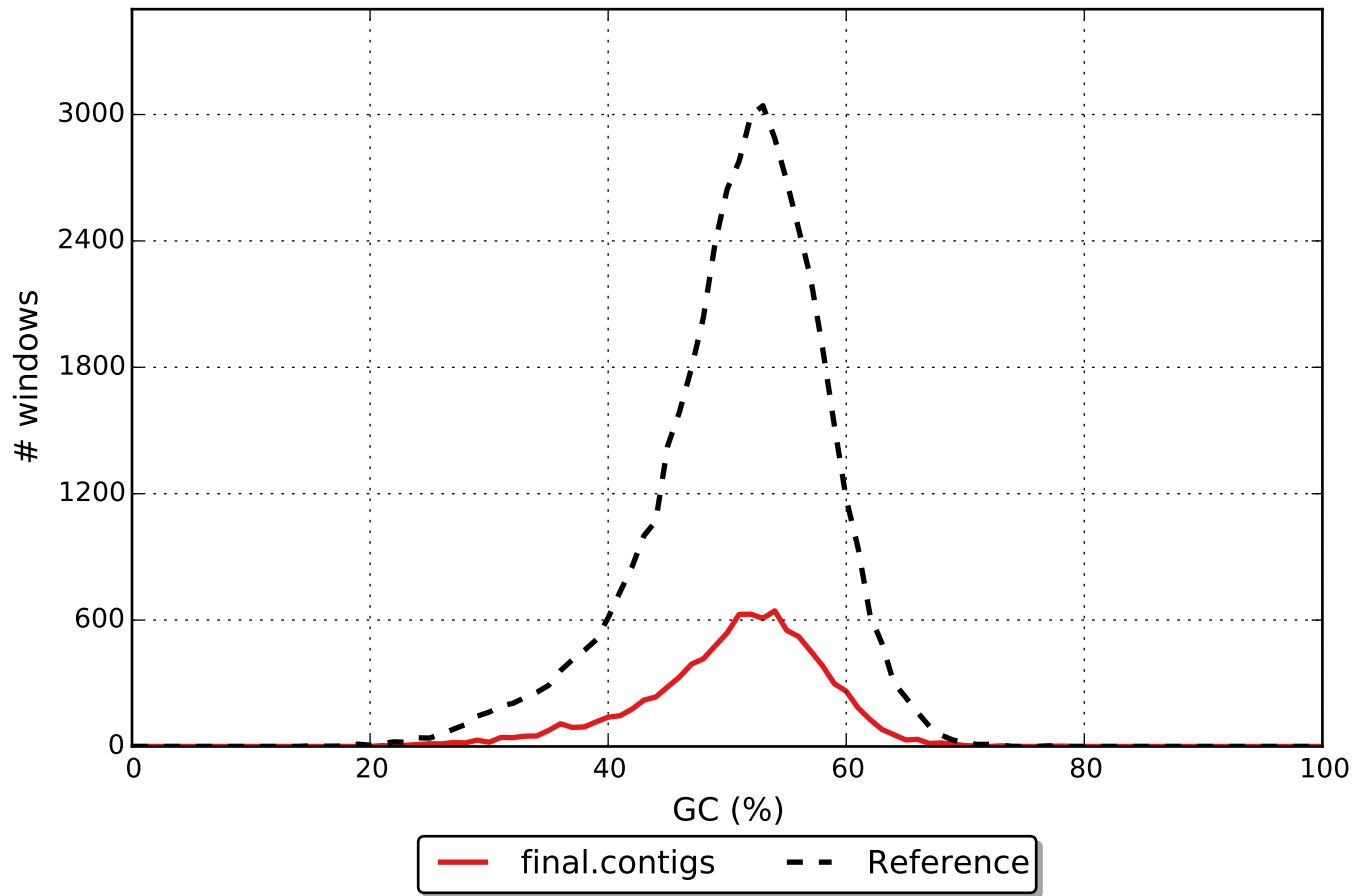
— final.contigs

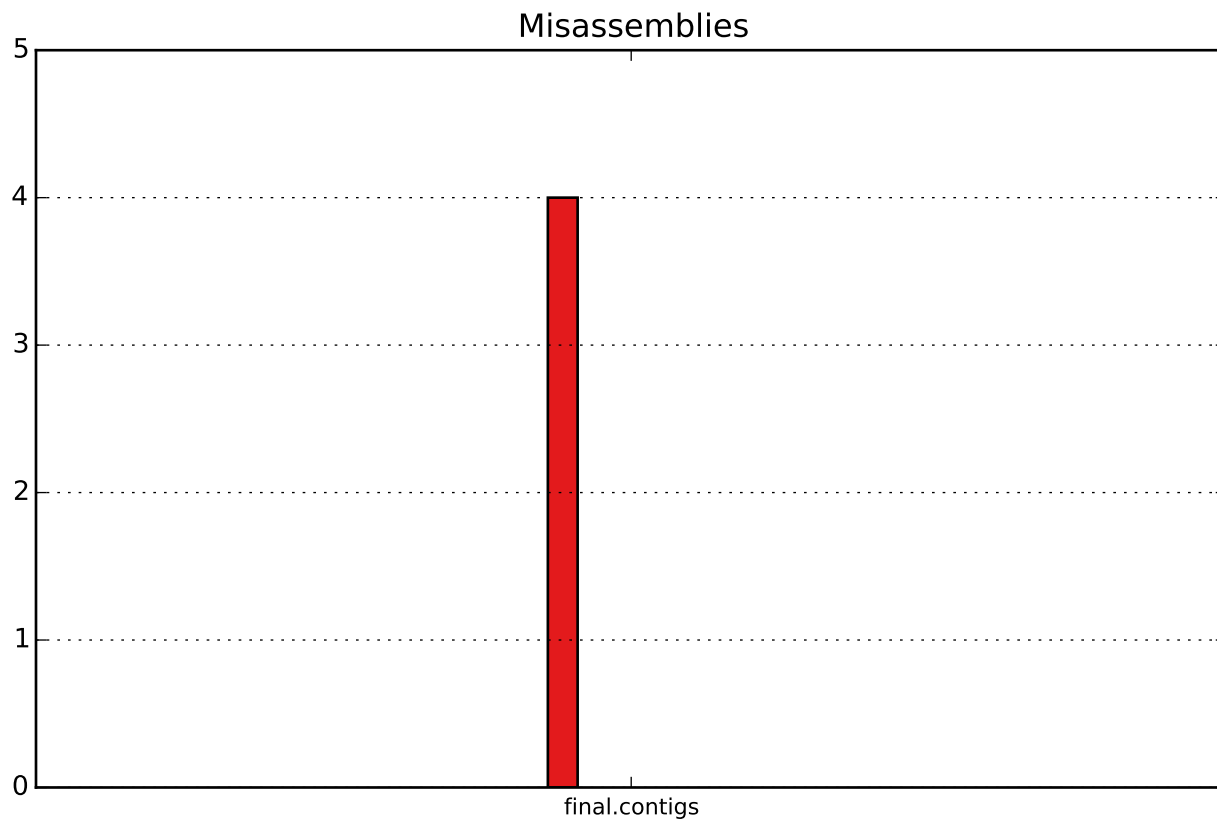
NGx





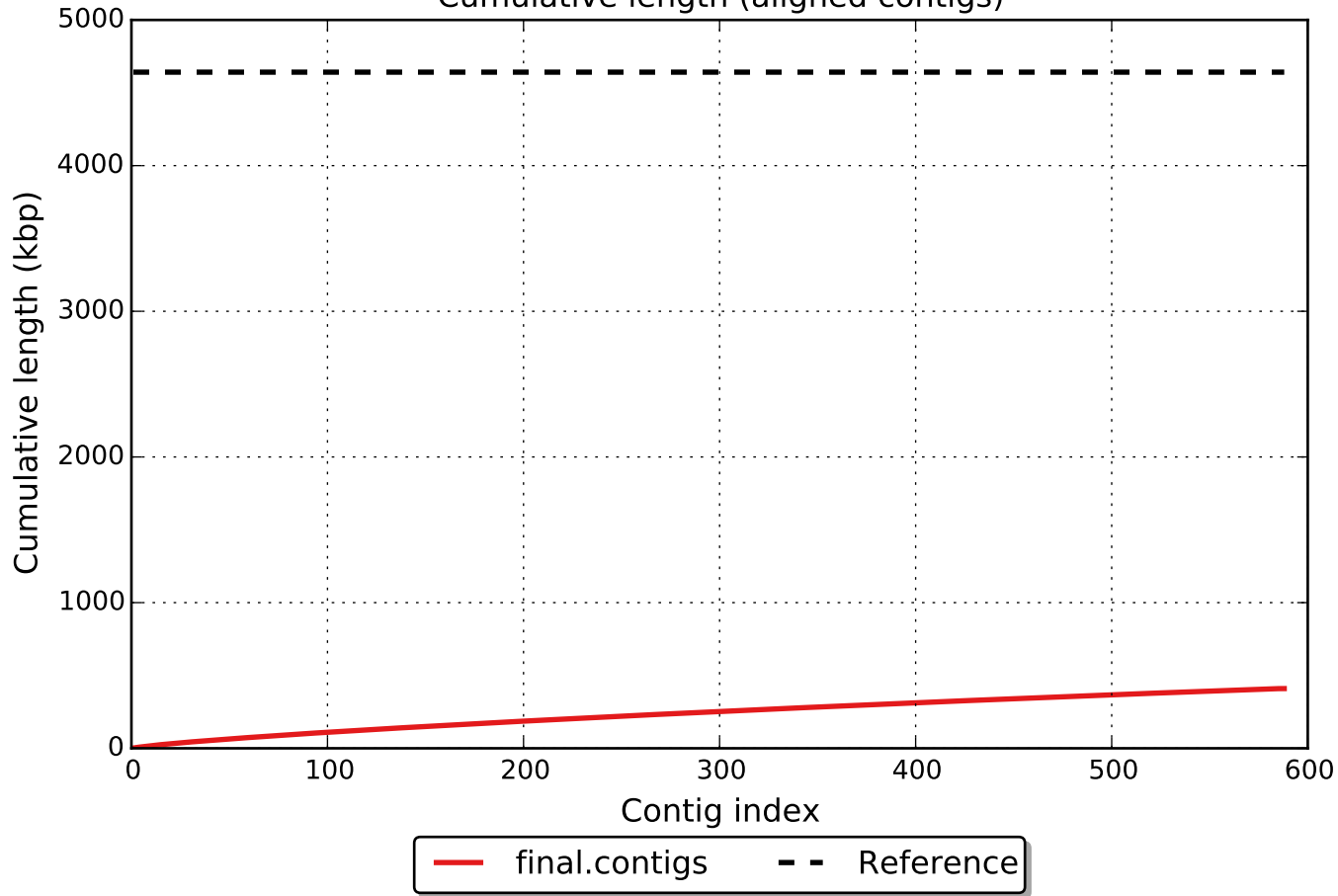
GC content



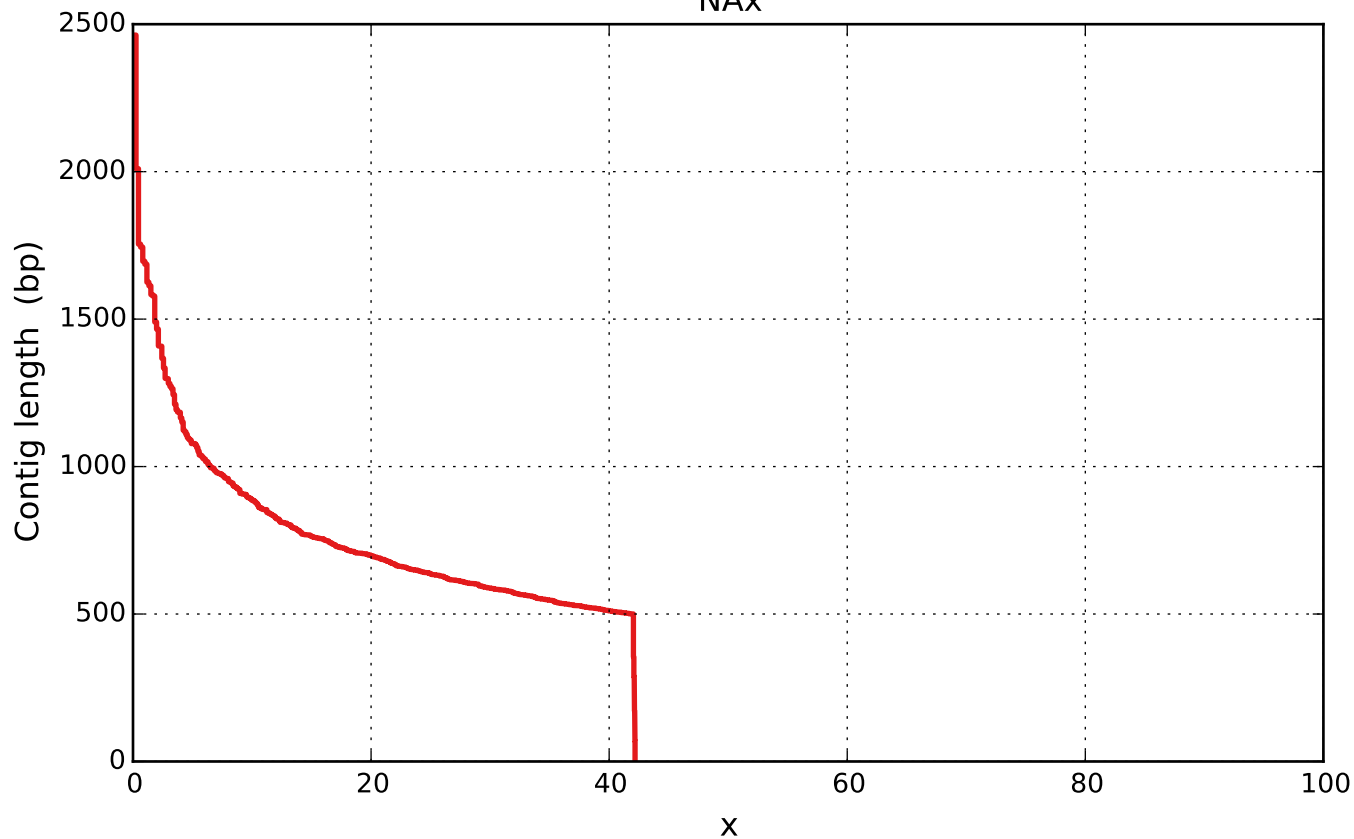




Cumulative length (aligned contigs)



NAx



— final.contigs

NGAx

