

# 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	9
# misassembled contigs	9
Misassembled contigs length	11359
# local misassemblies	2
# unaligned contigs	0 + 4 part
Unaligned length	156
Genome fraction (%)	20.793
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1141.61
# indels per 100 kbp	1.97
Largest alignment	2463
NA50	670
NGA50	-
NA75	568
LA50	551
LA75	946

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	9
# relocations	8
# translocations	0
# inversions	1
# misassembled contigs	9
Misassembled contigs length	11359
# local misassemblies	2
# mismatches	11018
# indels	19
# short indels	19
# long indels	0
Indels length	20

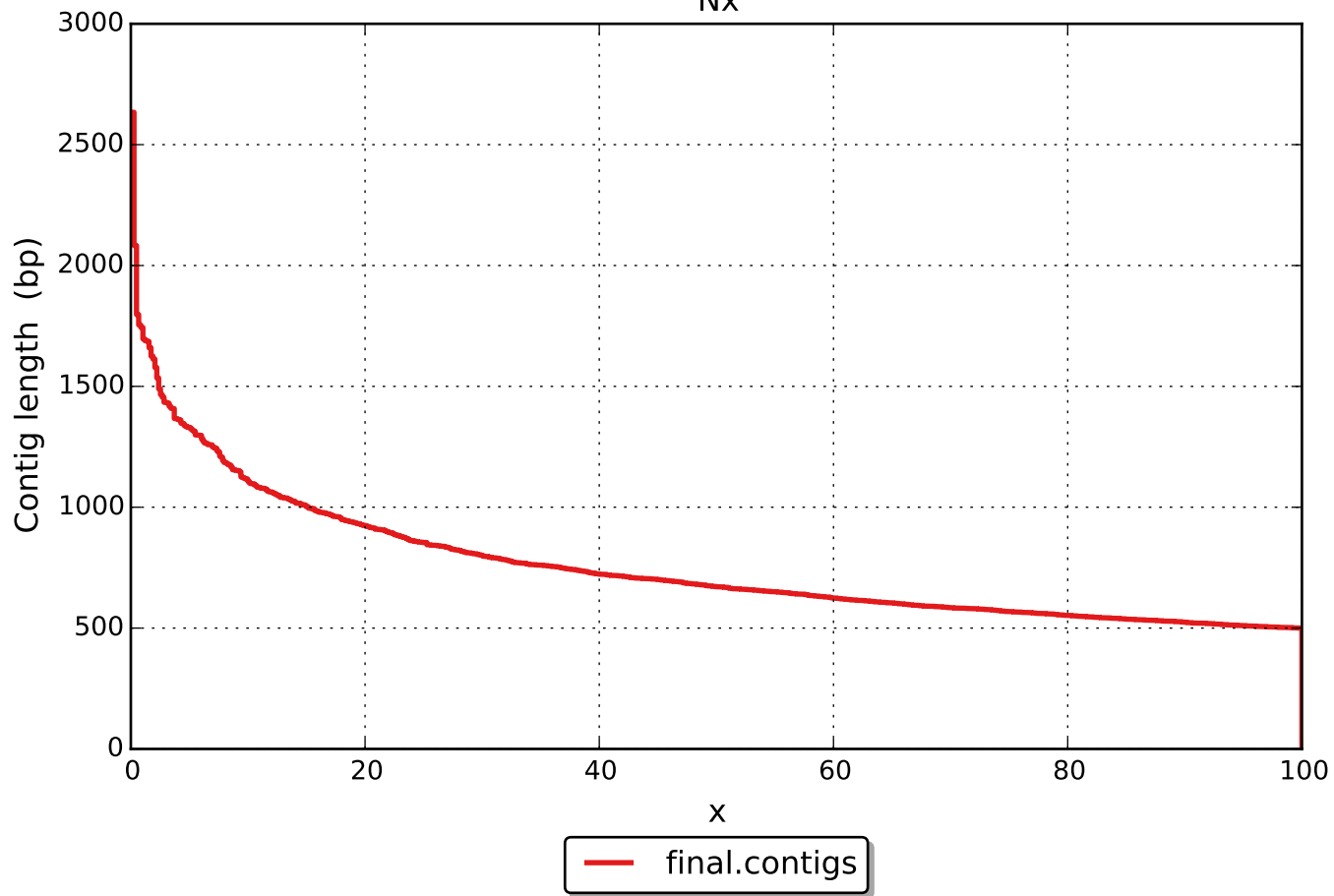
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

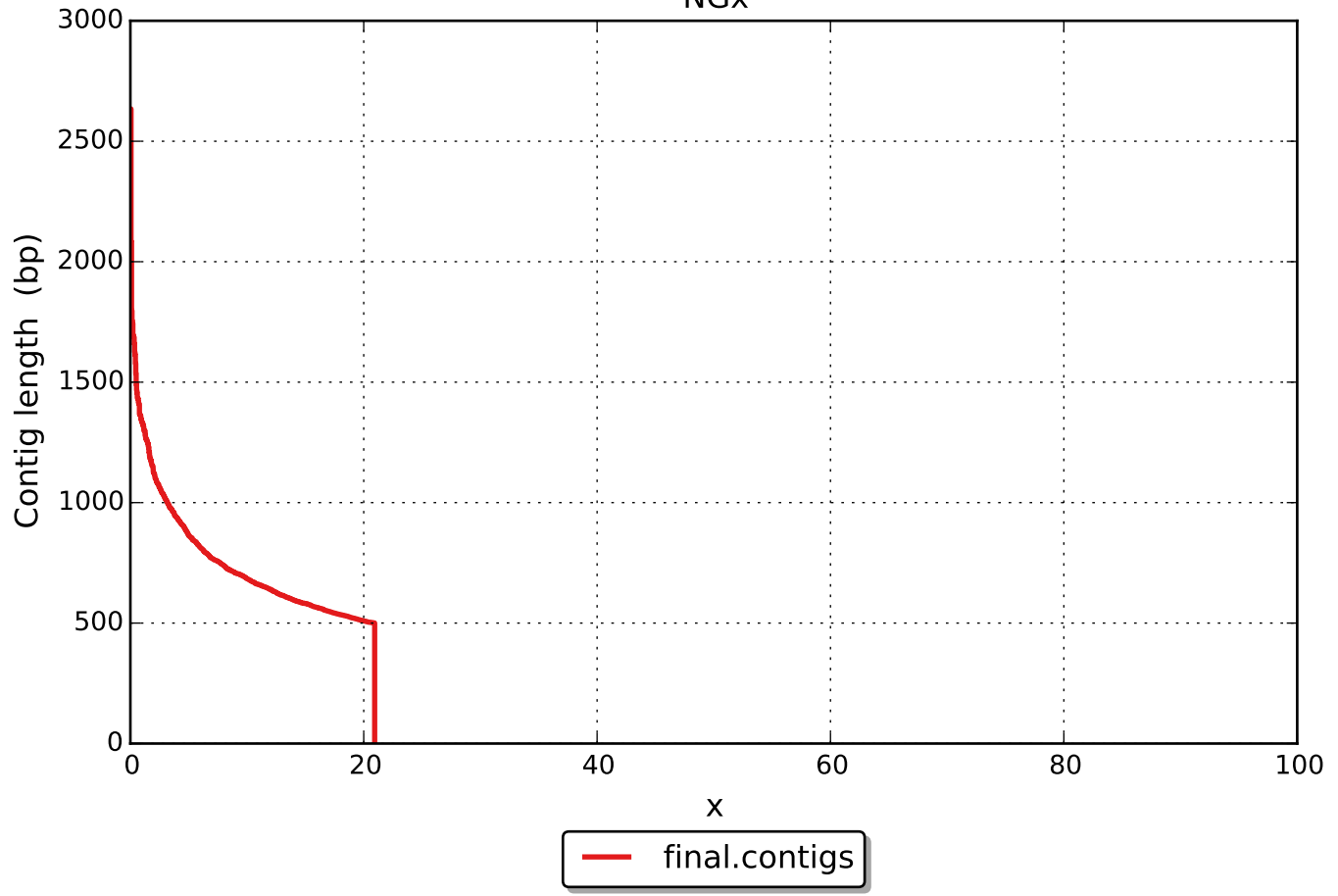
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	4
# with misassembly	0
# both parts are significant	0
Partially unaligned length	156
# N's	0

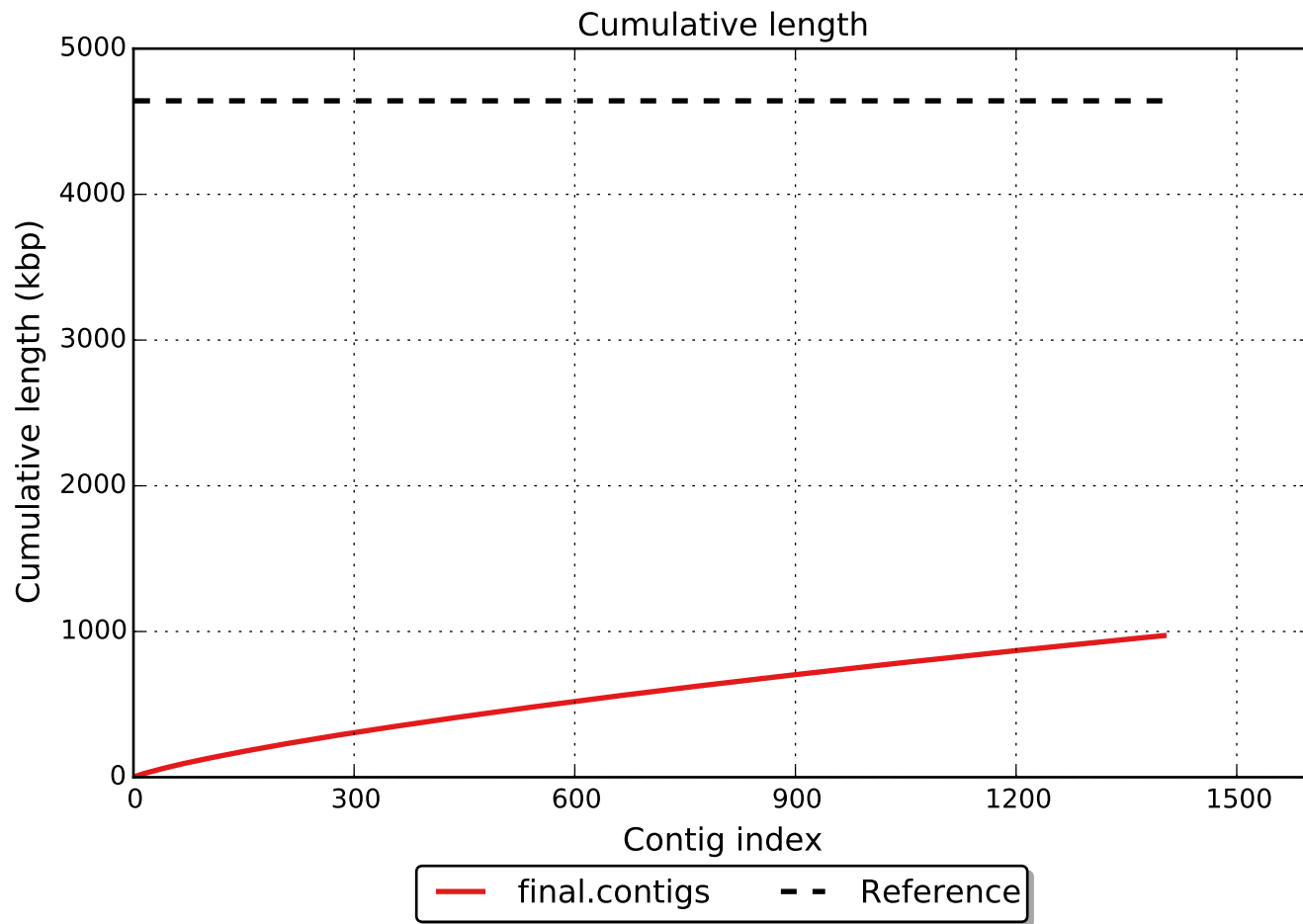
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

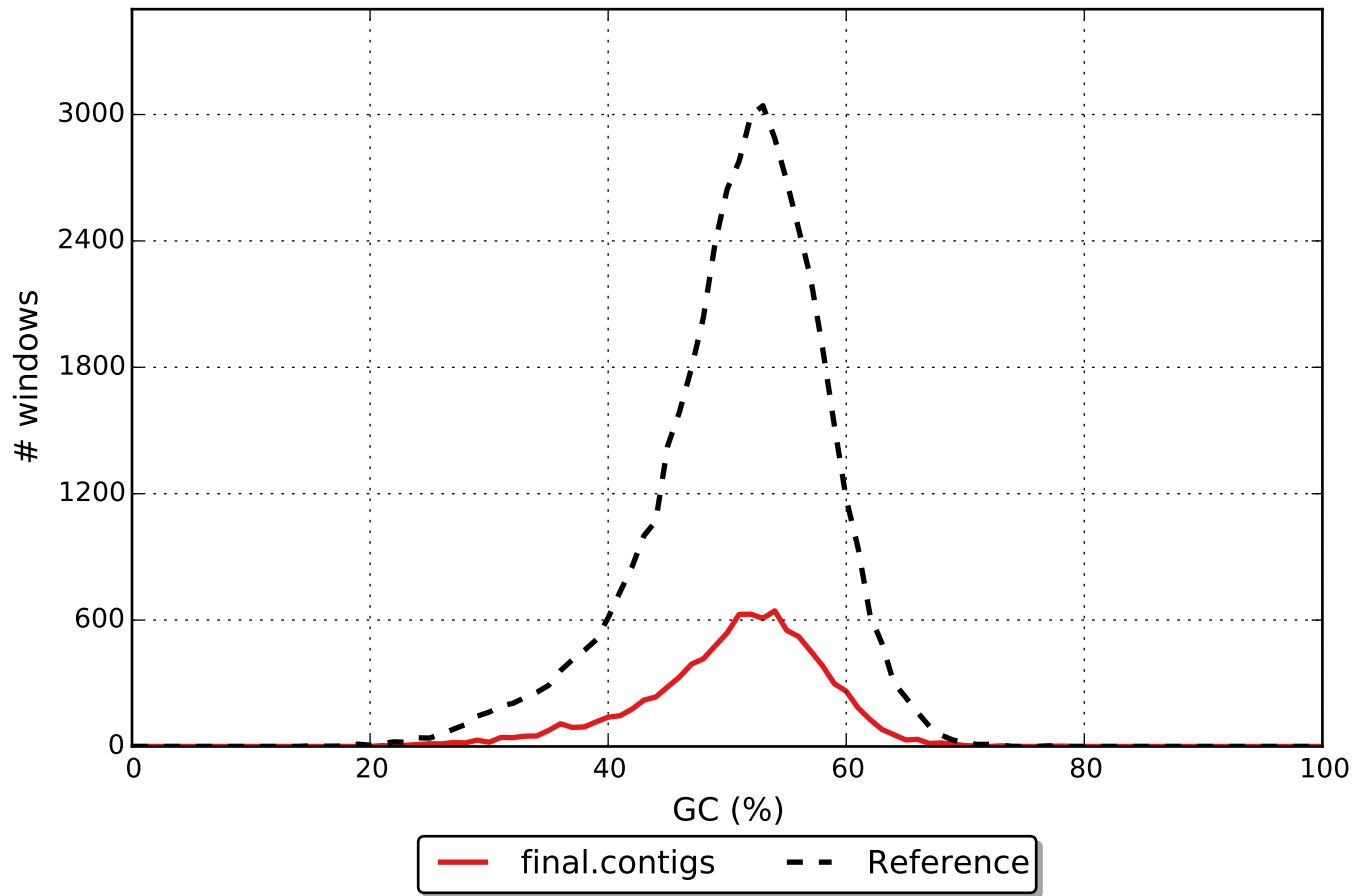


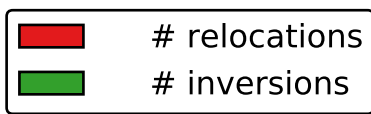
NGx





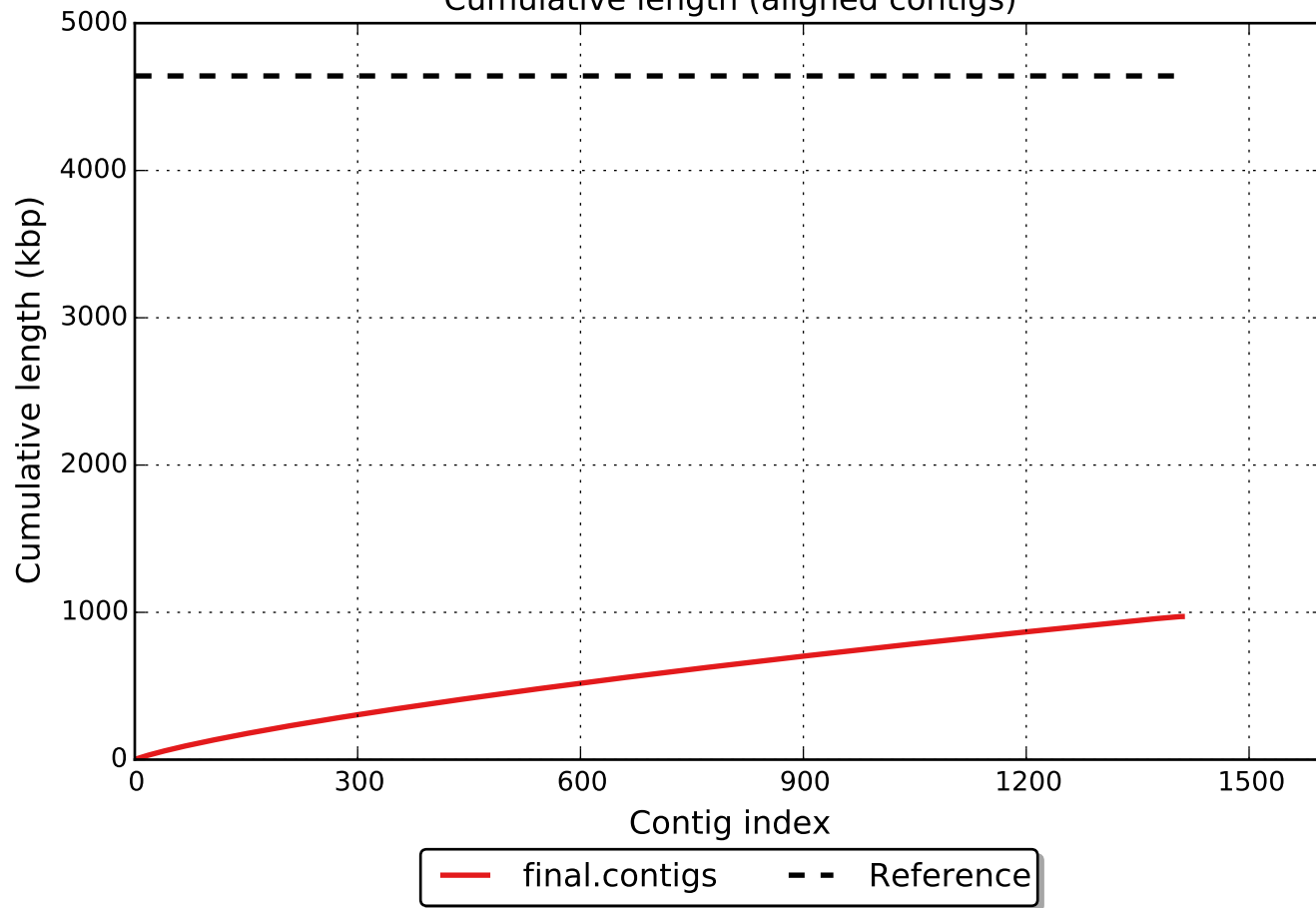
GC content



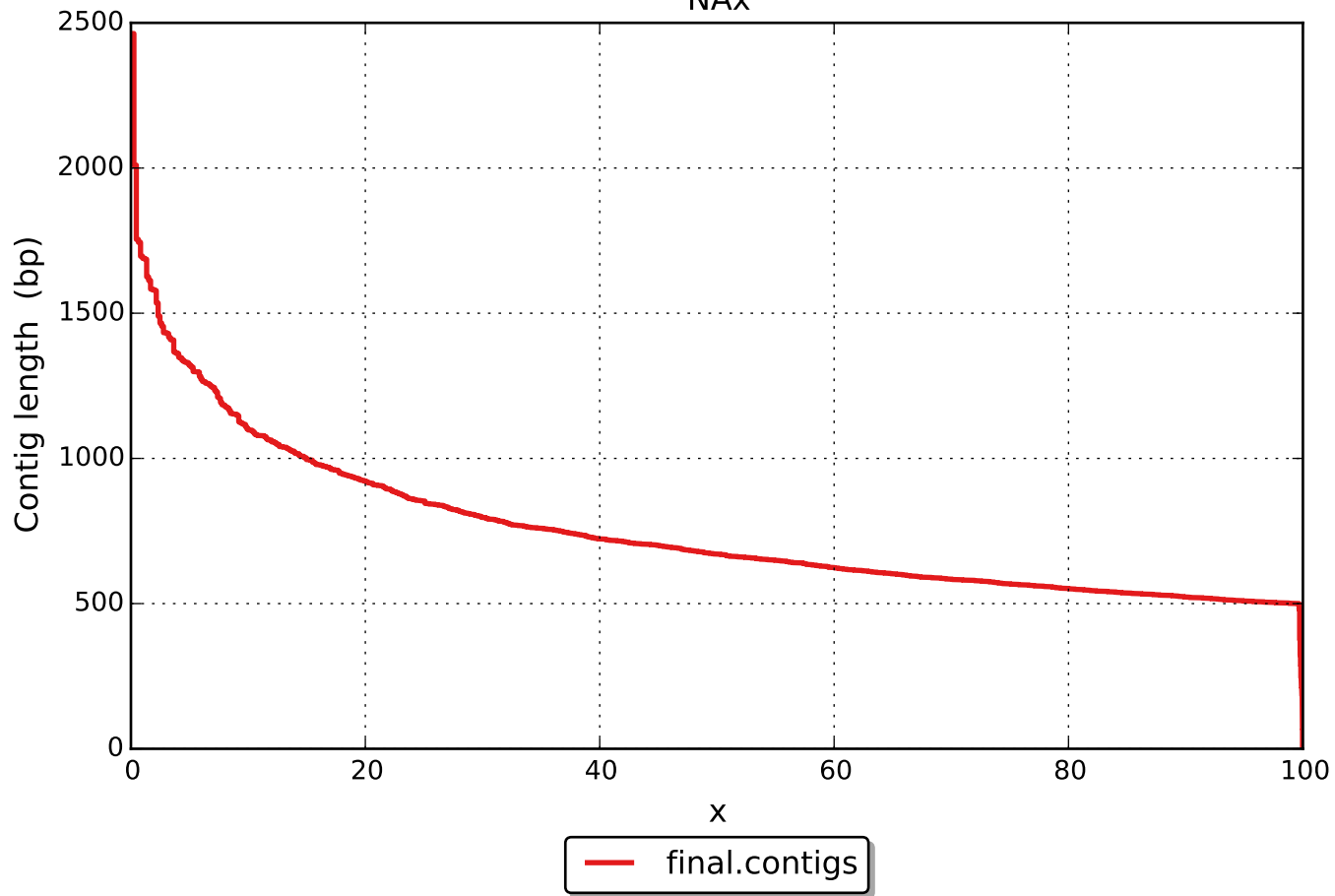




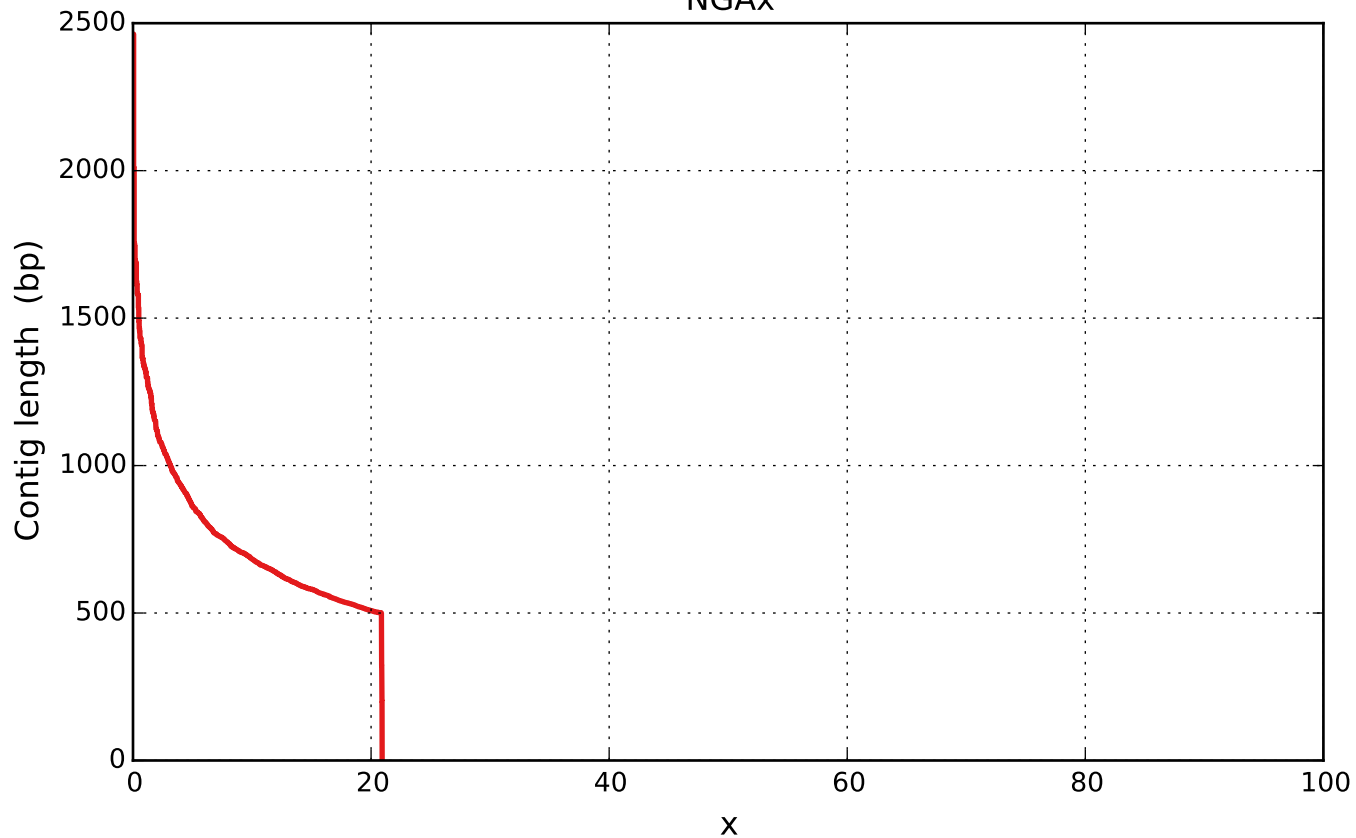
Cumulative length (aligned contigs)



NAx



NGAx



— final.contigs