

## Report

	final.contigs
# contigs (>= 1000 bp)	24
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	55845
Total length (>= 5000 bp)	15341
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	55
Largest contig	8698
Total length	77662
Reference length	4830181
GC (%)	61.50
Reference GC (%)	67.29
N50	1501
N75	936
L50	11
L75	27
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	7
# unaligned contigs	8 + 28 part
Unaligned length	60580
Genome fraction (%)	0.138
Duplication ratio	2.555
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4771.16
# indels per 100 kbp	149.57
Largest alignment	1497
Total aligned length	9905
NGA50	-

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
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	26
# possible misassemblies	31
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	7
# mismatches	319
# indels	10
# indels (<= 5 bp)	10
# indels (> 5 bp)	0
Indels length	15

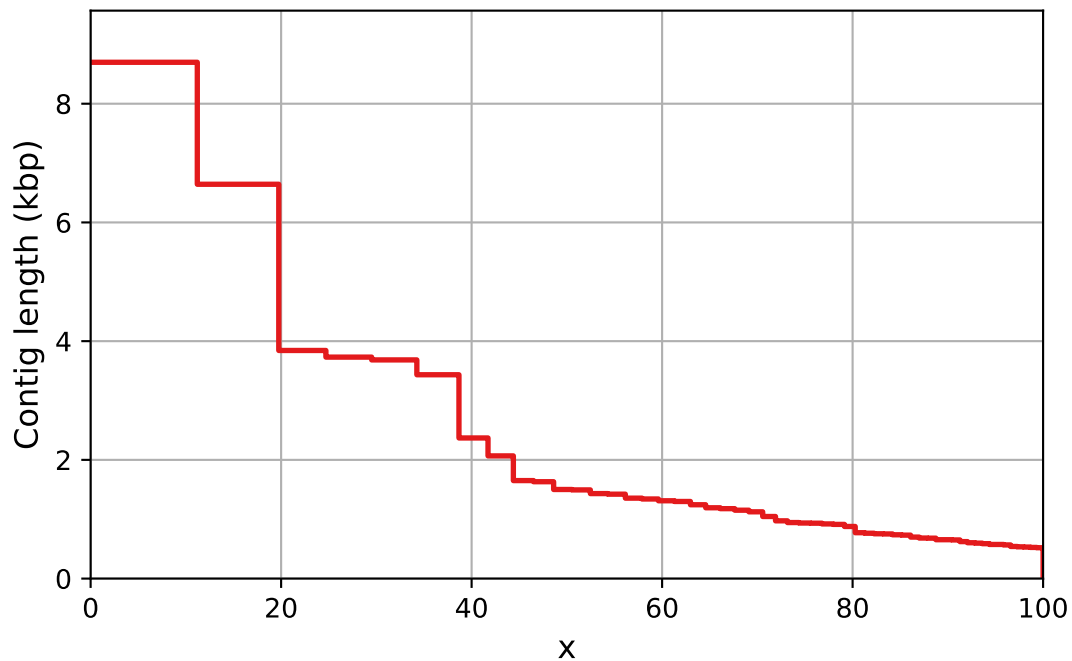
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	final.contigs
# fully unaligned contigs	8
Fully unaligned length	5863
# partially unaligned contigs	28
Partially unaligned length	54717
# N's	0

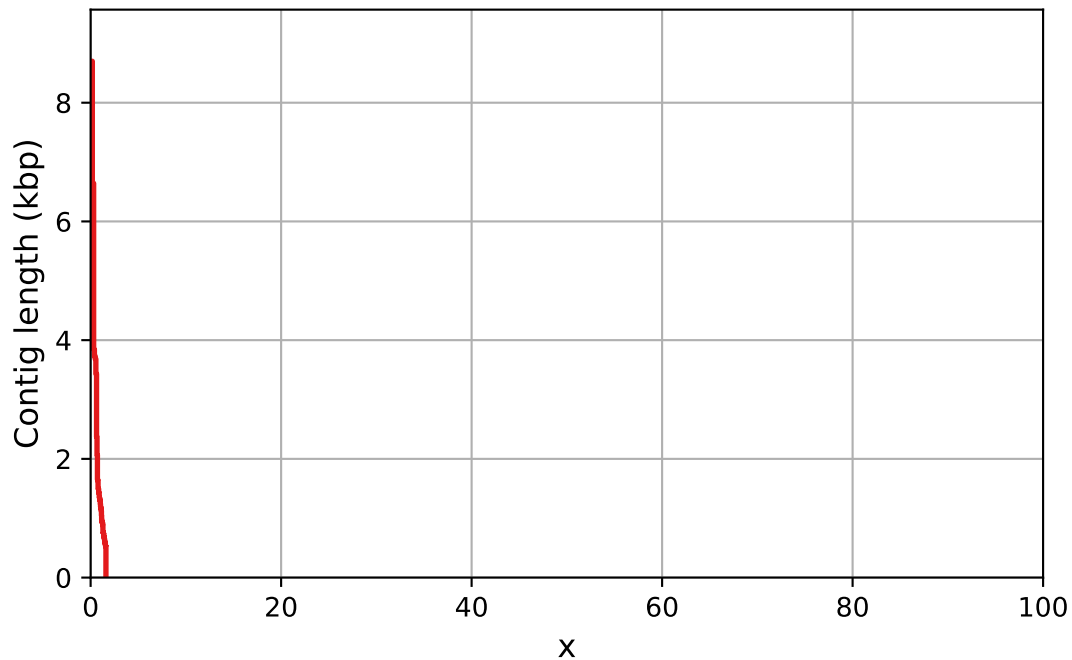
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

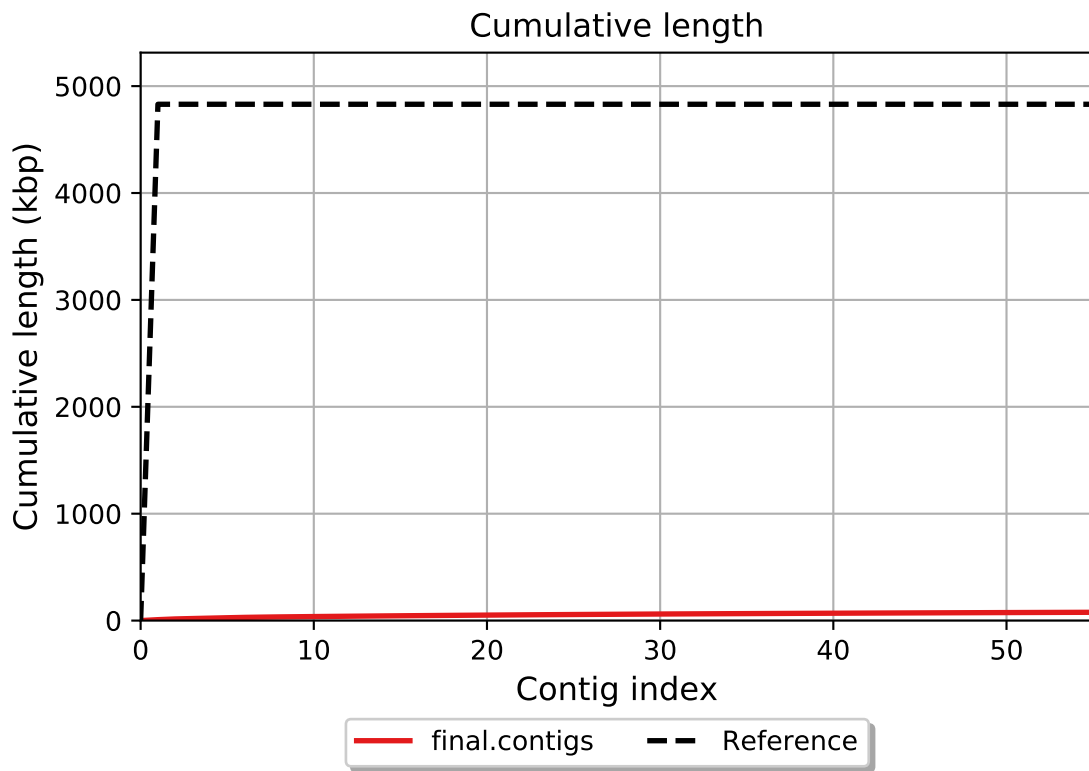


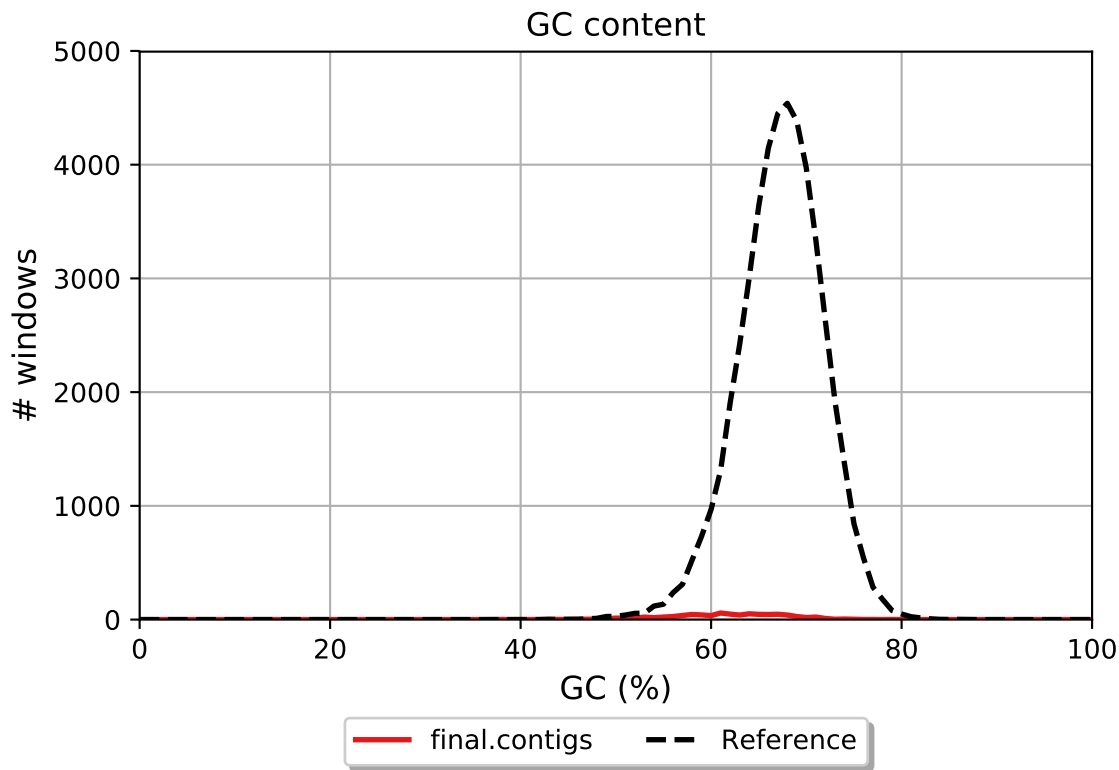
— final.contigs

NGx

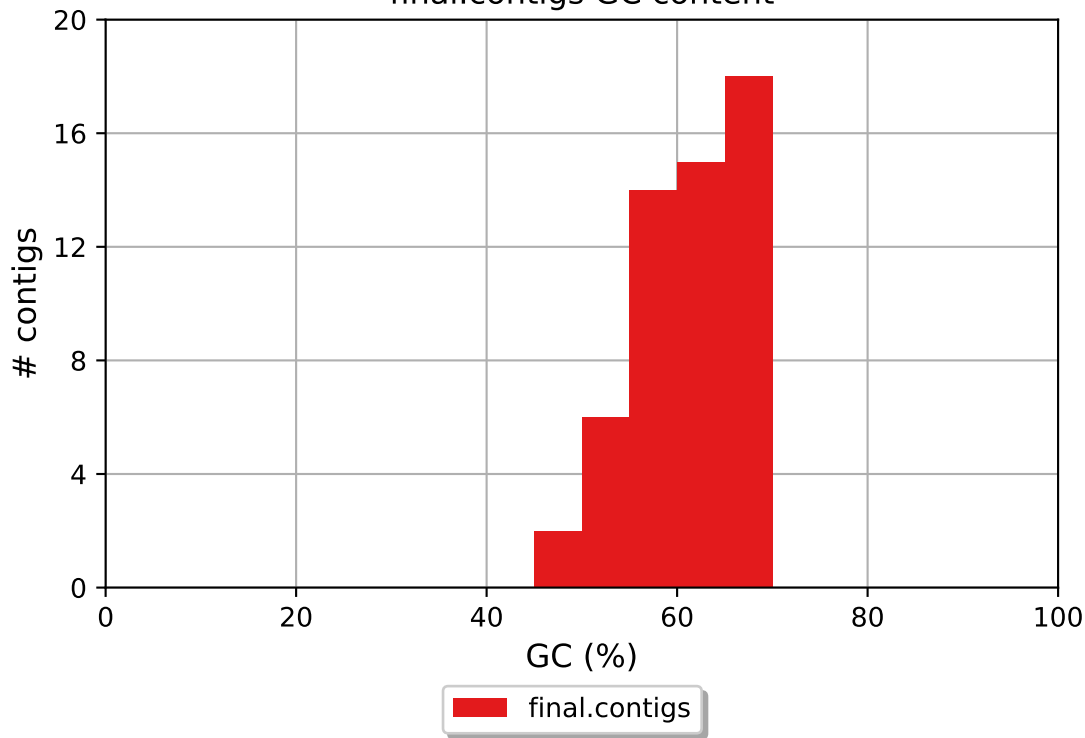


— final.contigs





final.contigs GC content

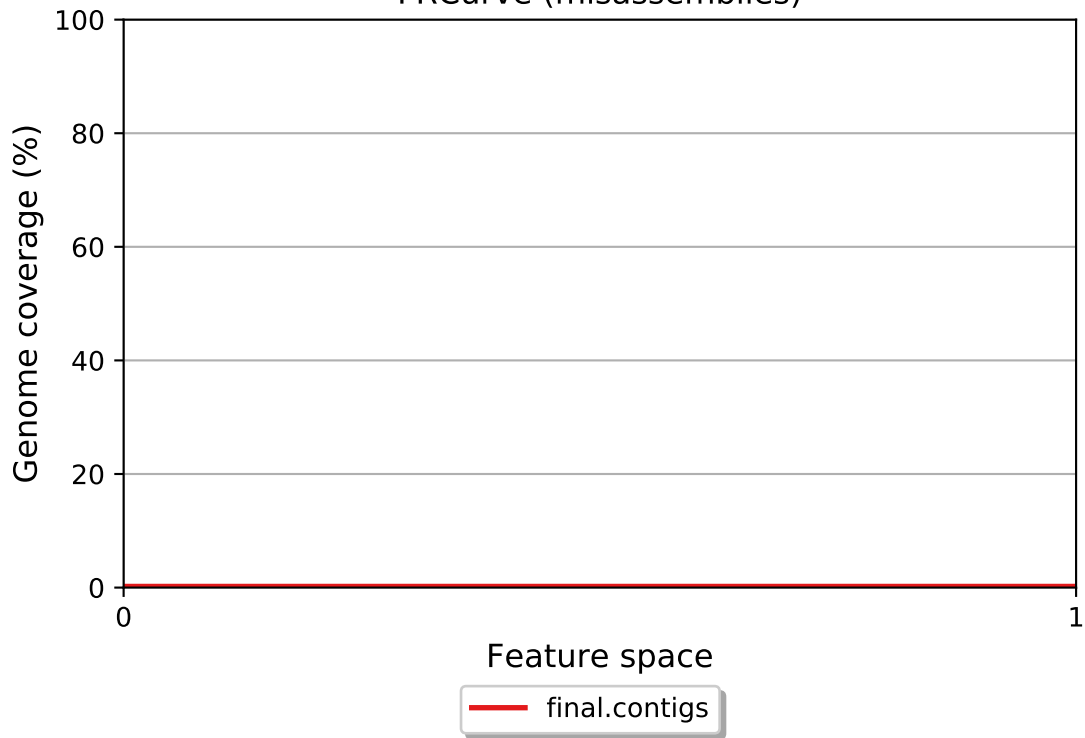




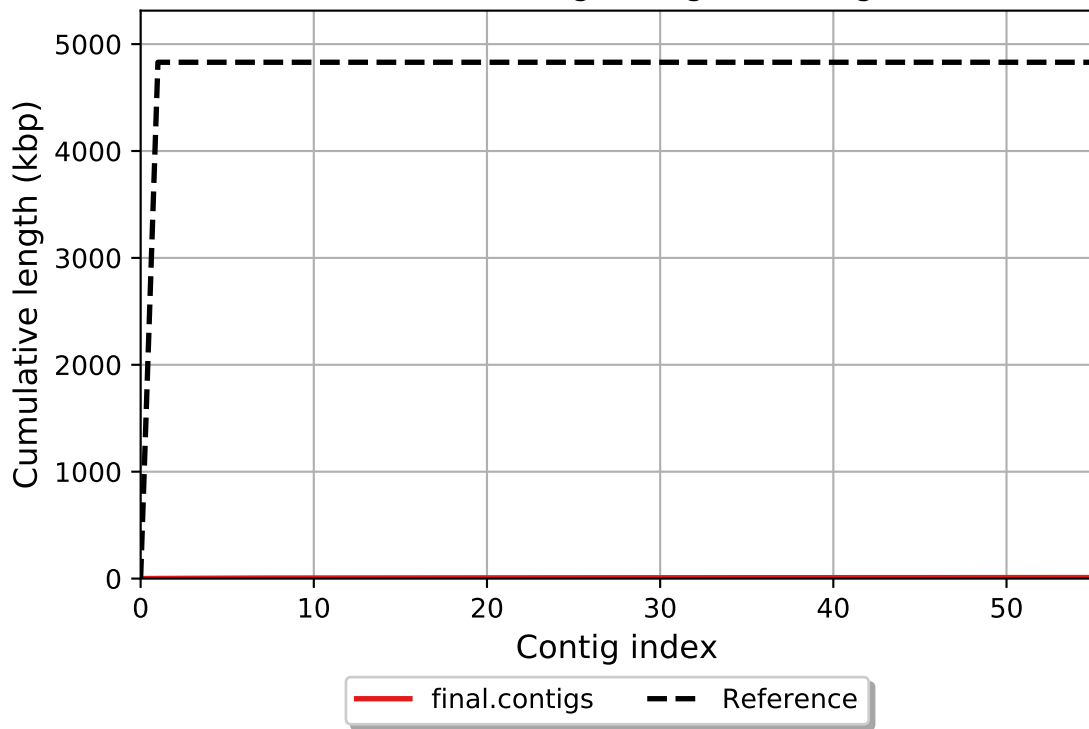
## Misassemblies



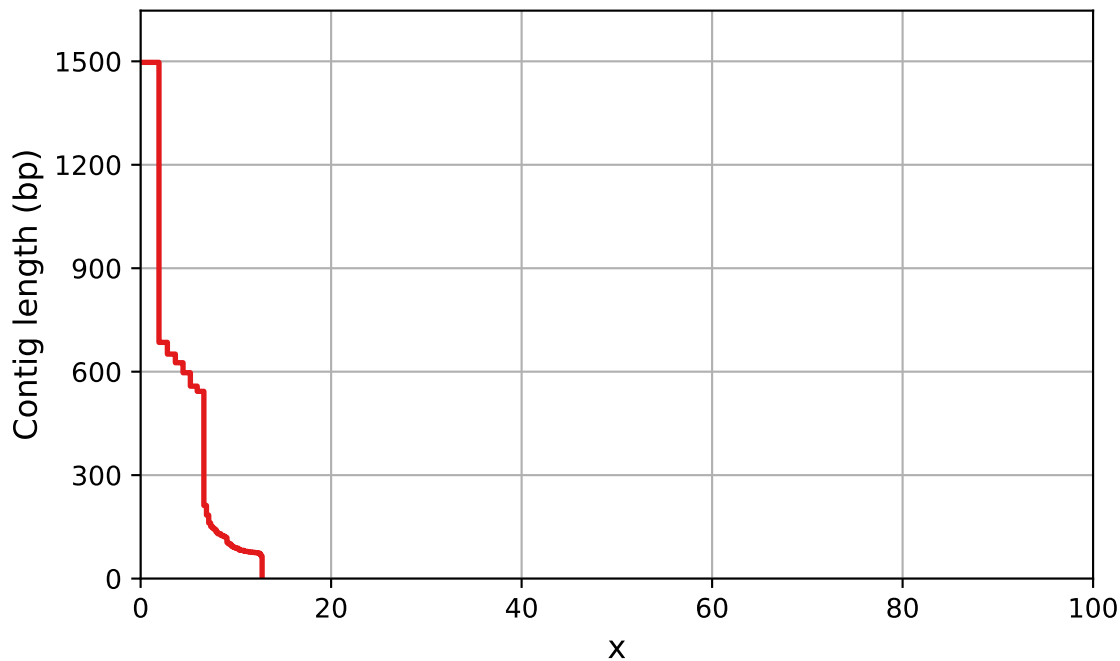
FRCurve (misassemblies)



Cumulative length (aligned contigs)

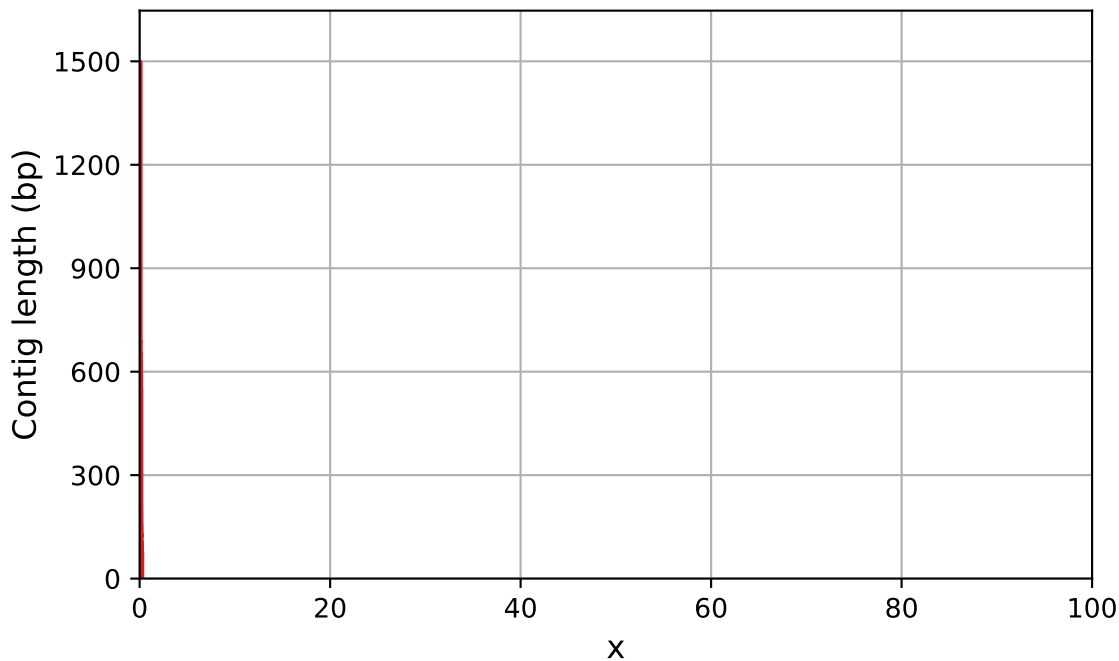


NAx



— final.contigs

# NGAx



— final.contigs