

## Report

	final.contigs
# contigs ( $\geq 1000$ bp)	6
# contigs ( $\geq 5000$ bp)	3
# contigs ( $\geq 10000$ bp)	2
# contigs ( $\geq 25000$ bp)	1
# contigs ( $\geq 50000$ bp)	1
Total length ( $\geq 1000$ bp)	130792
Total length ( $\geq 5000$ bp)	126947
Total length ( $\geq 10000$ bp)	121128
Total length ( $\geq 25000$ bp)	109683
Total length ( $\geq 50000$ bp)	109683
# contigs	7
Largest contig	109683
Total length	131501
Reference length	2995049
GC (%)	56.15
Reference GC (%)	44.84
N50	109683
N75	109683
L50	1
L75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 7 part
Unaligned length	130863
Genome fraction (%)	0.013
Duplication ratio	1.636
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1282.05
# indels per 100 kbp	0.00
Largest alignment	144
Total aligned length	638
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

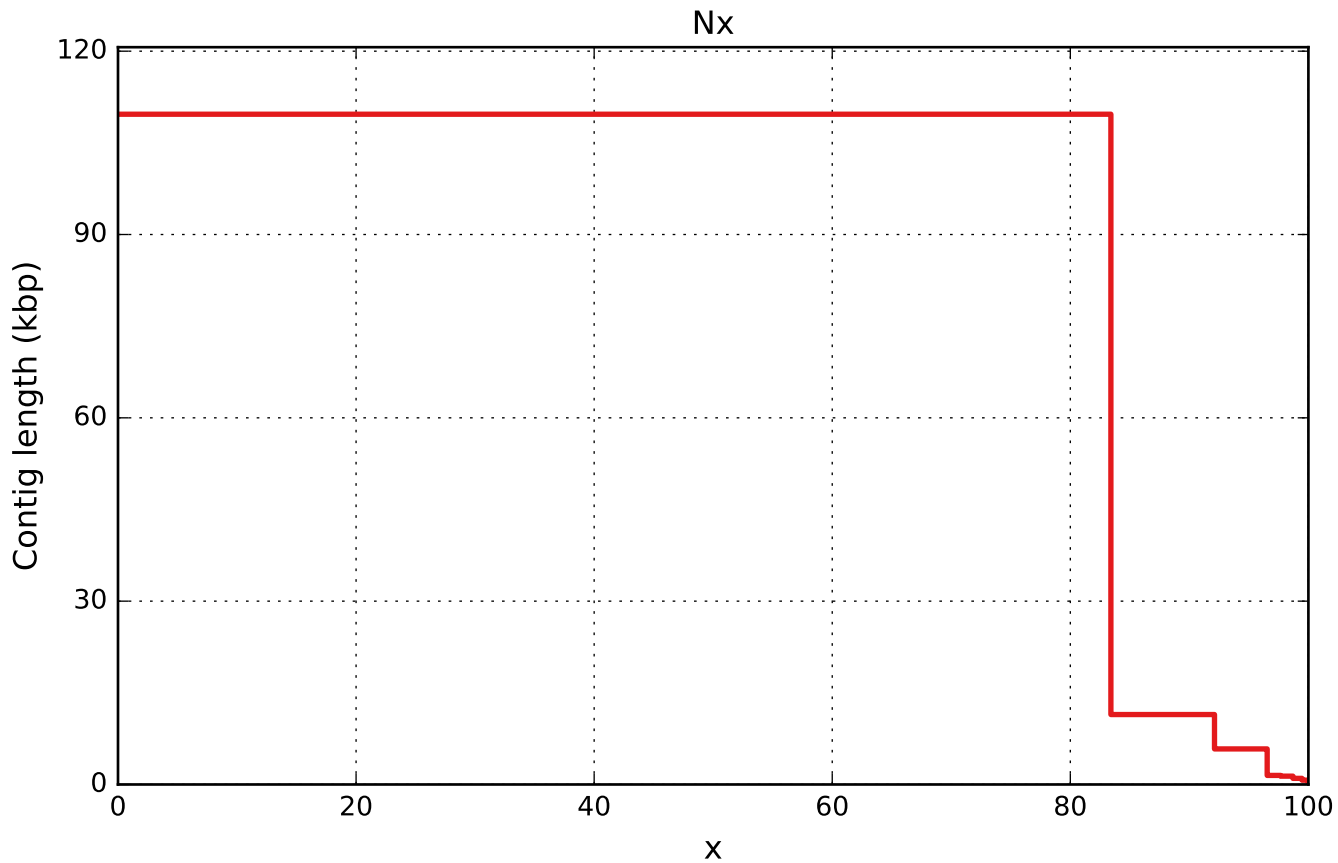
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	5
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	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

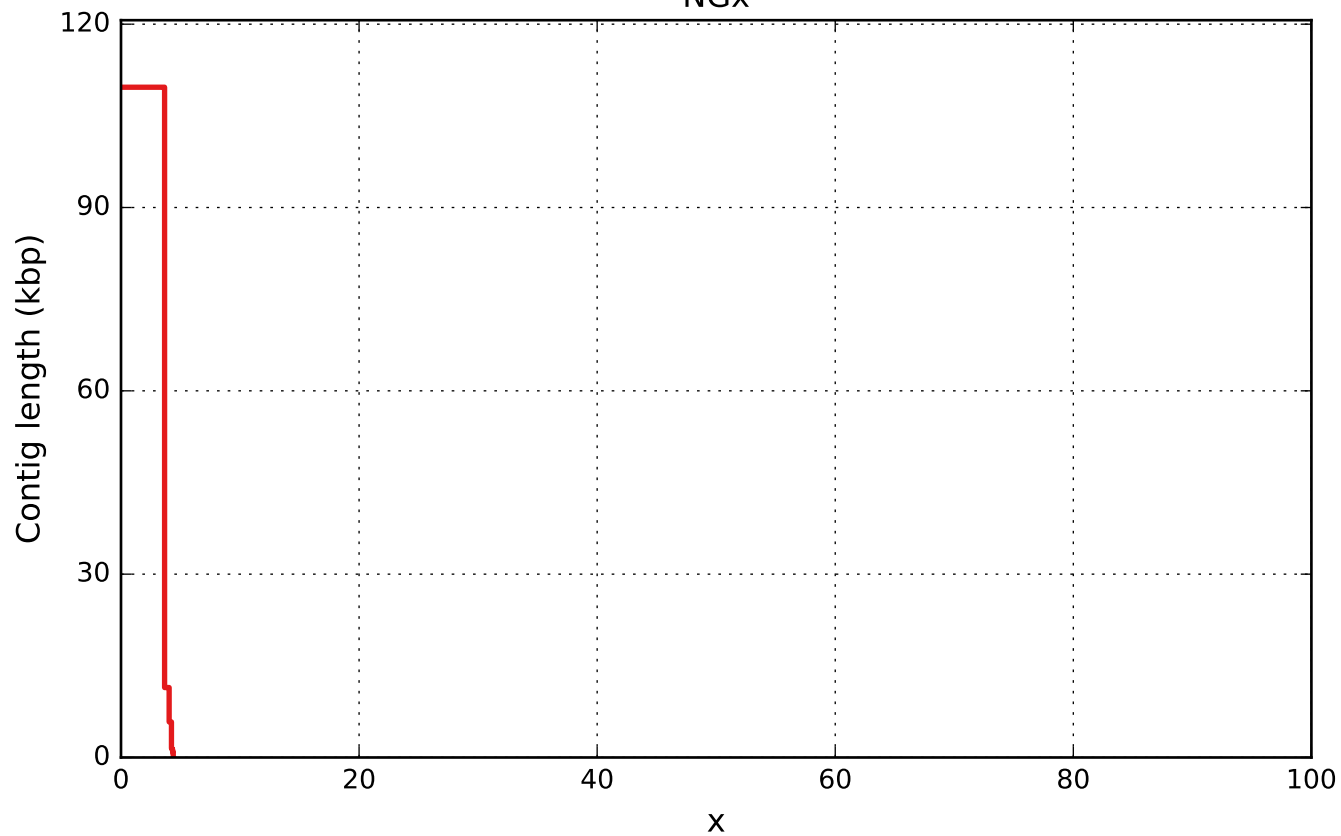
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	7
Partially unaligned length	130863
# N's	0

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).

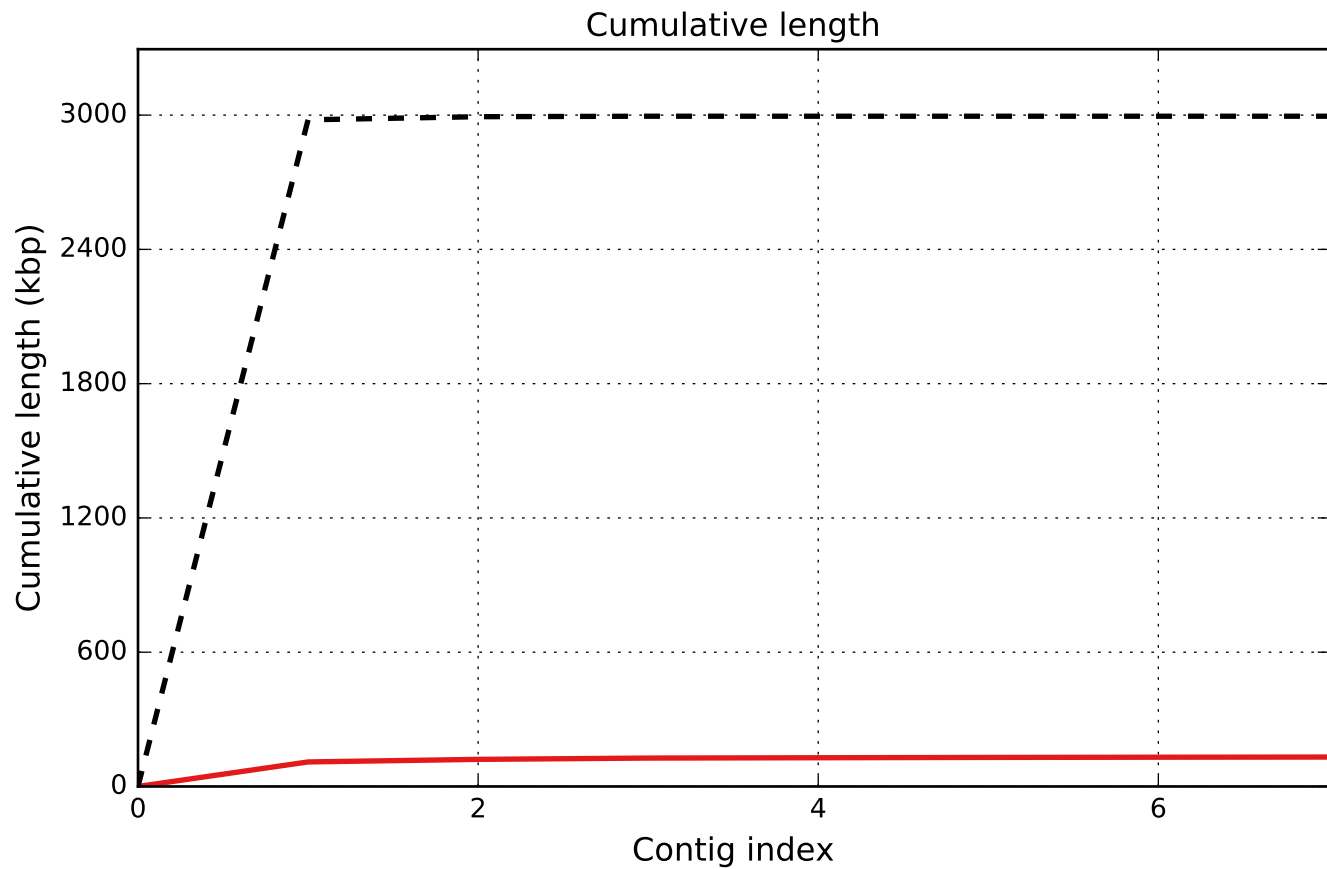


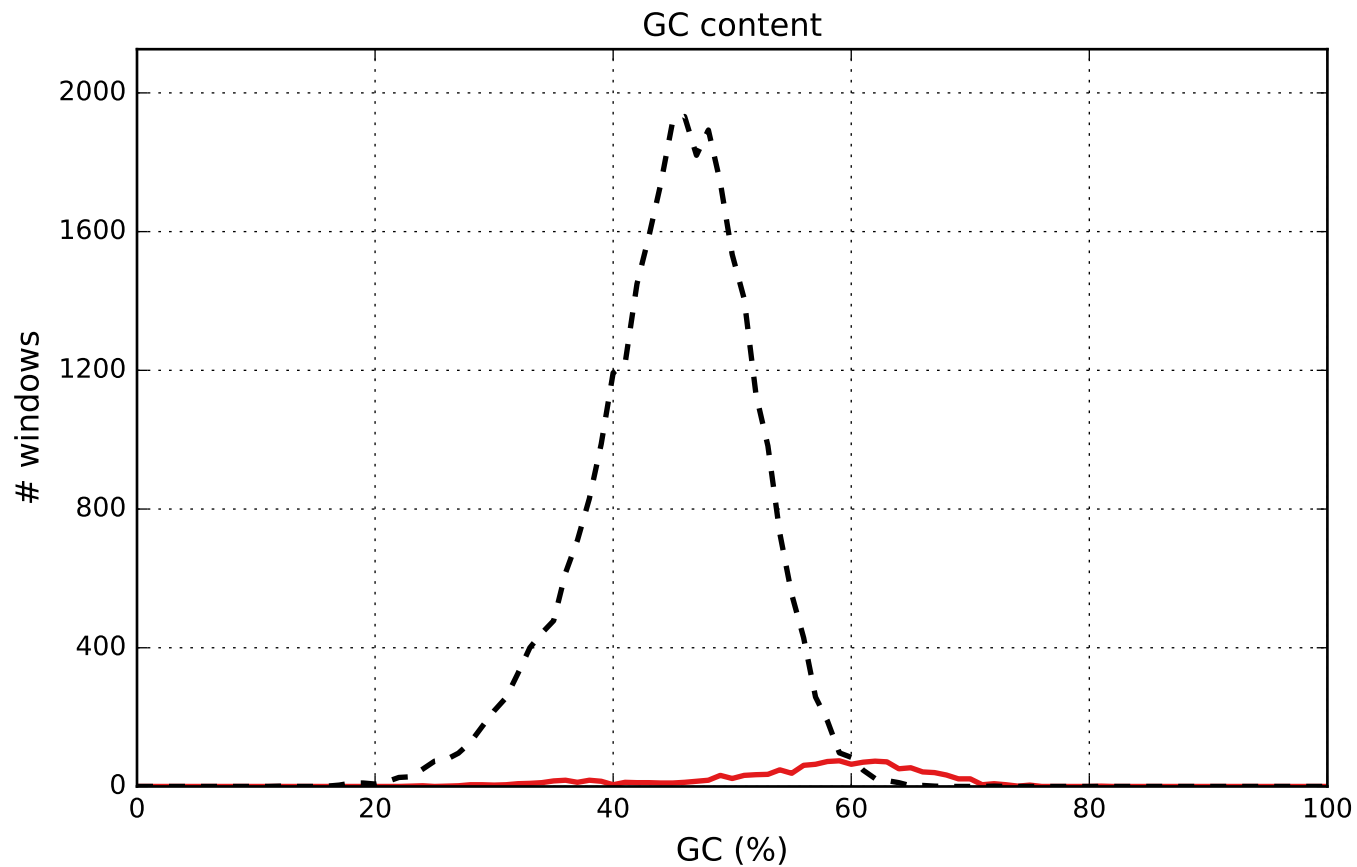
— final.contigs

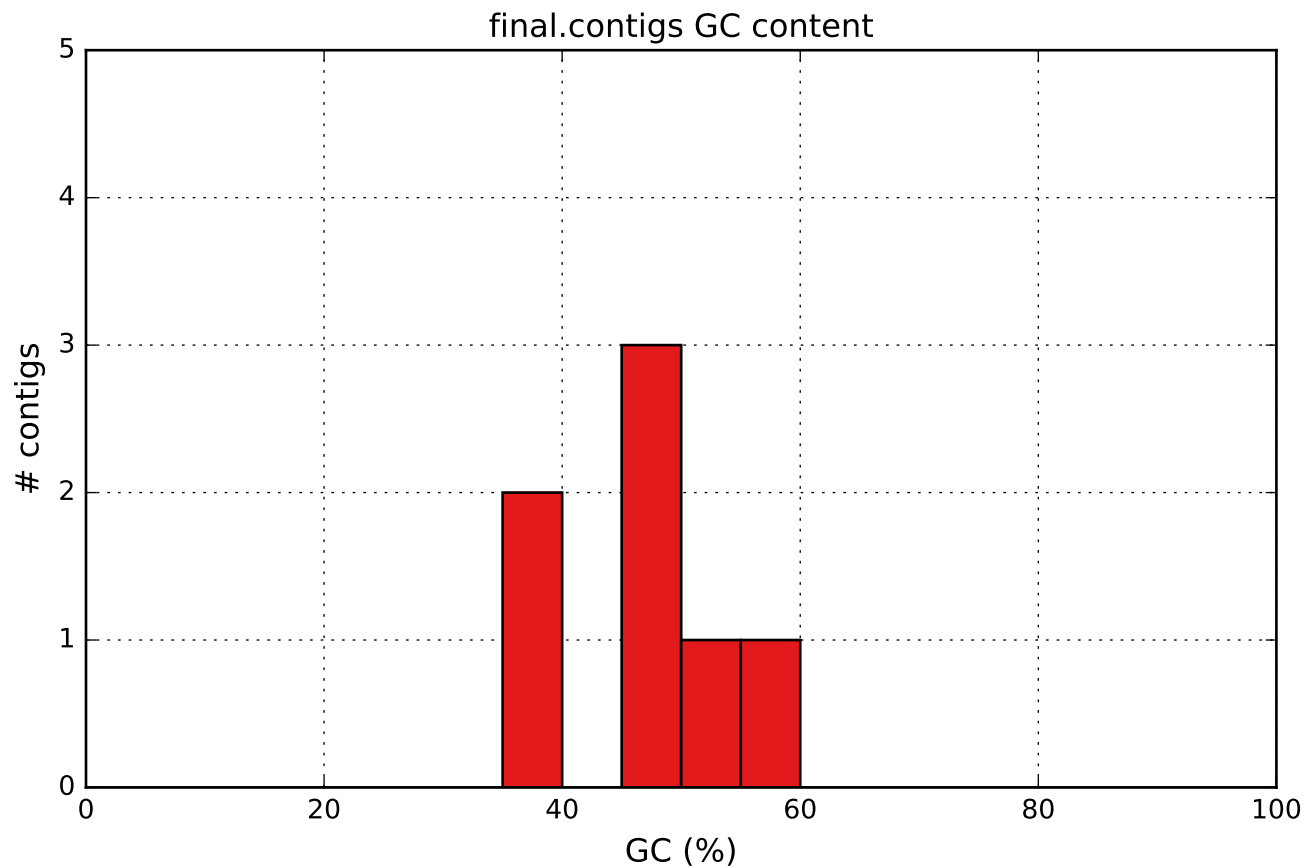
NGx



— final.contigs





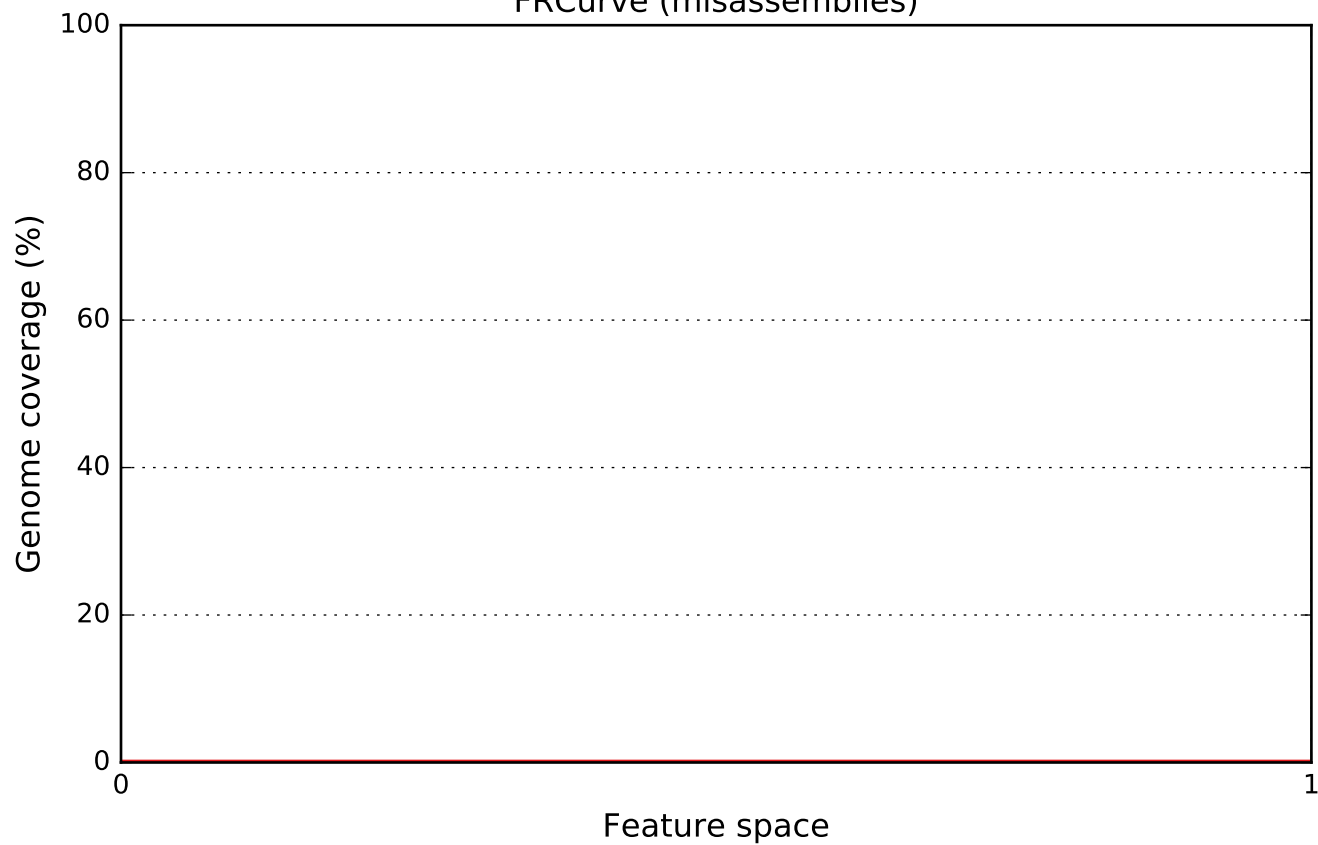


final.contigs



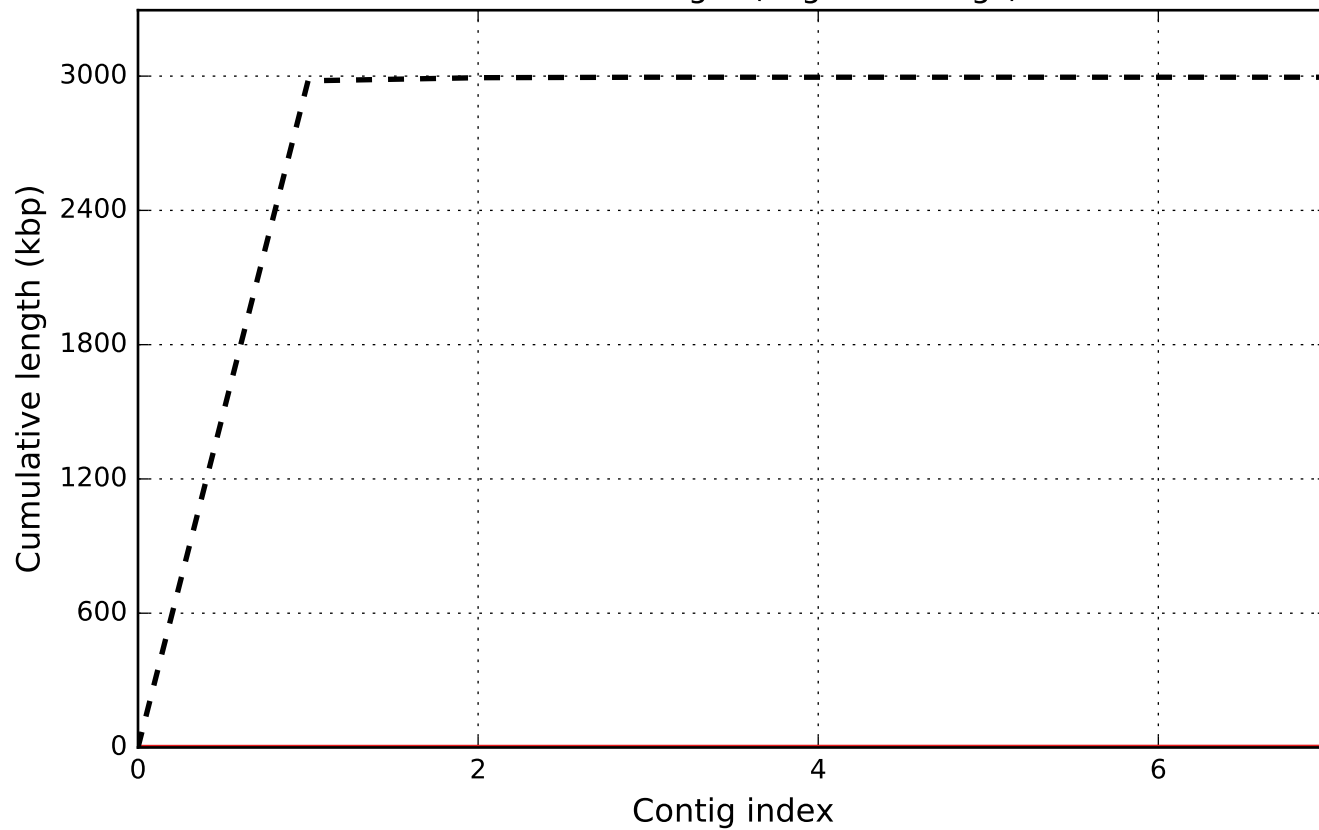


FRCurve (misassemblies)



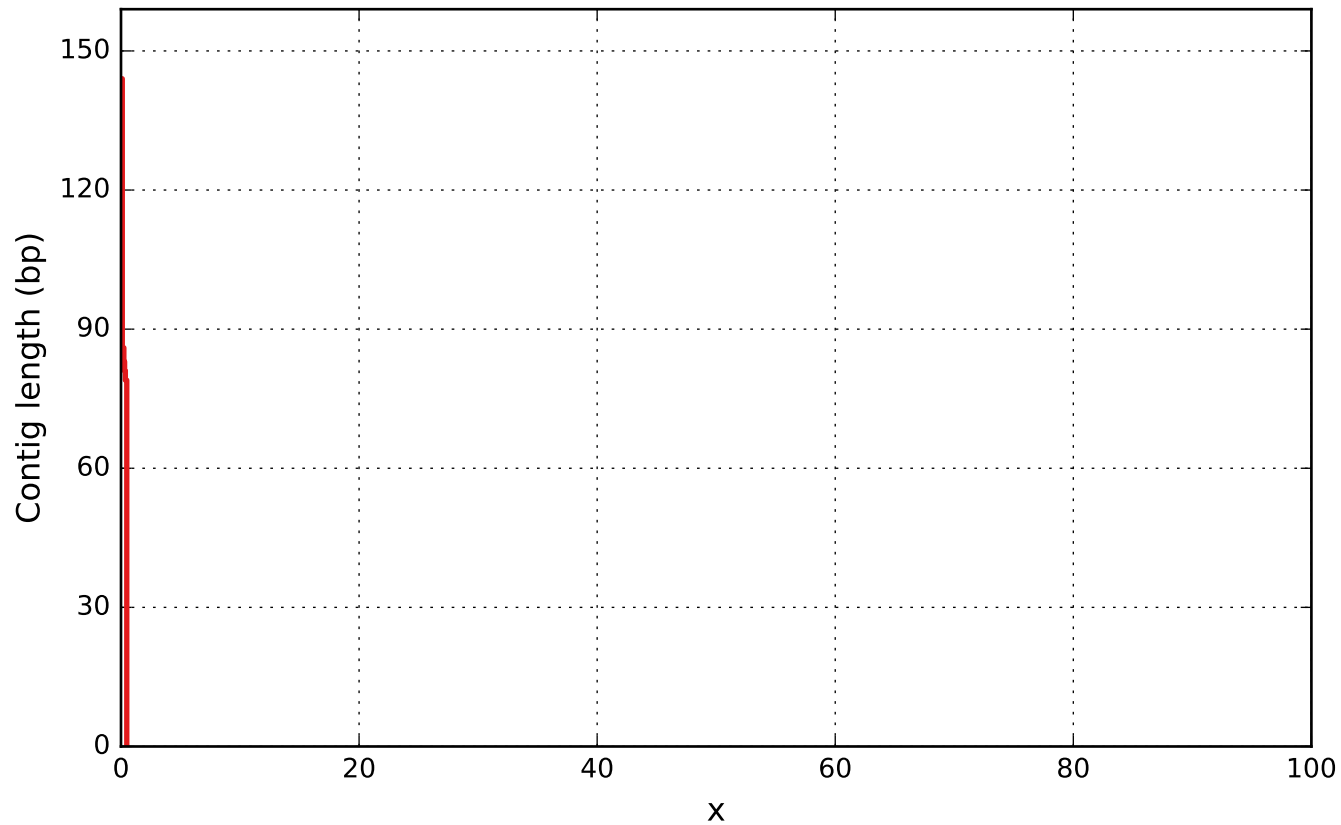
— final.contigs

Cumulative length (aligned contigs)



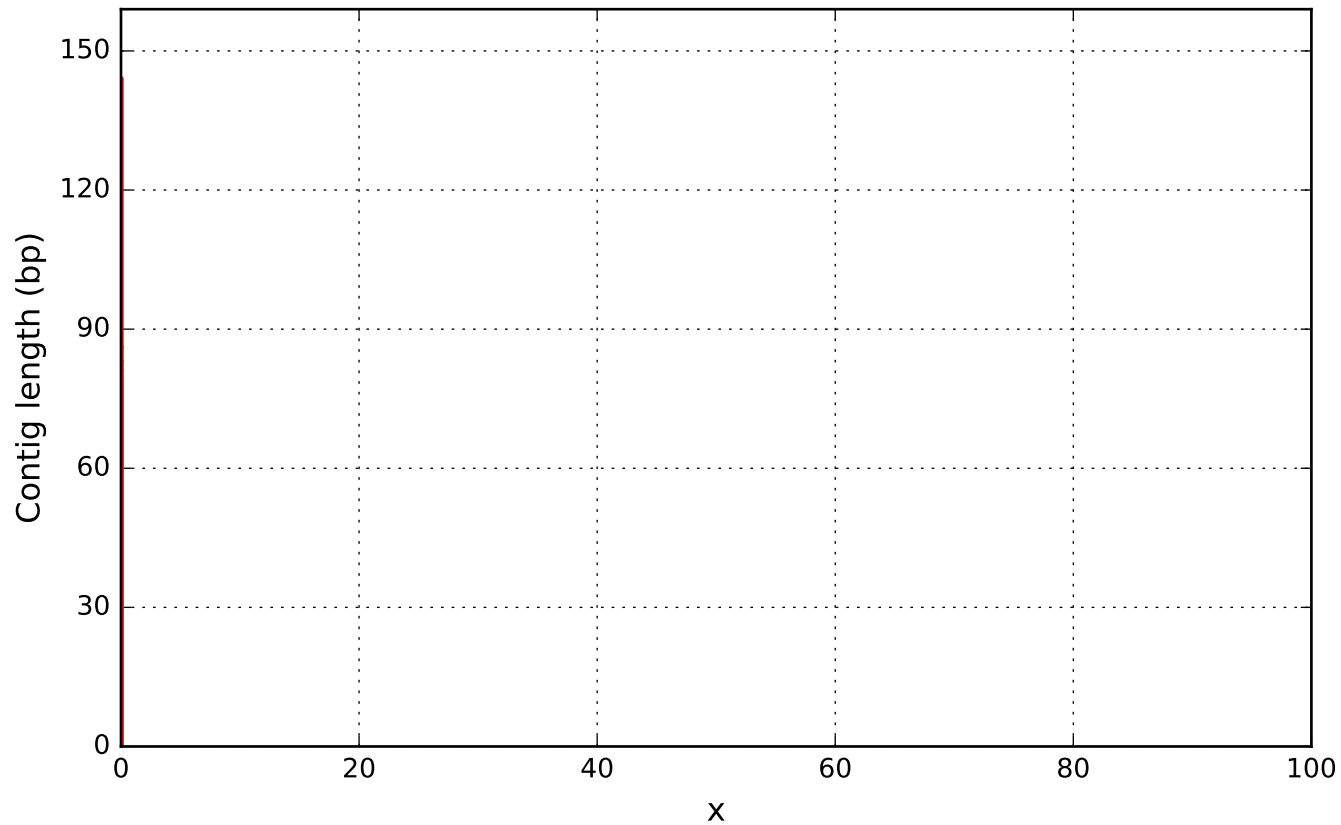
— final.contigs    - - Reference

NAx



— final.contigs

NGAx



— final.contigs