

# Report

	final.contigs
# contigs ( $\geq 1000$ bp)	1
# contigs ( $\geq 5000$ bp)	0
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 1000$ bp)	1601
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	2
Largest contig	1601
Total length	2485
Reference length	4282232
GC (%)	50.50
Reference GC (%)	66.99
N50	1601
N75	884
L50	1
L75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 2 part
Unaligned length	2316
Genome fraction (%)	0.004
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4733.73
# indels per 100 kbp	0.00
Largest alignment	88
Total aligned length	169
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

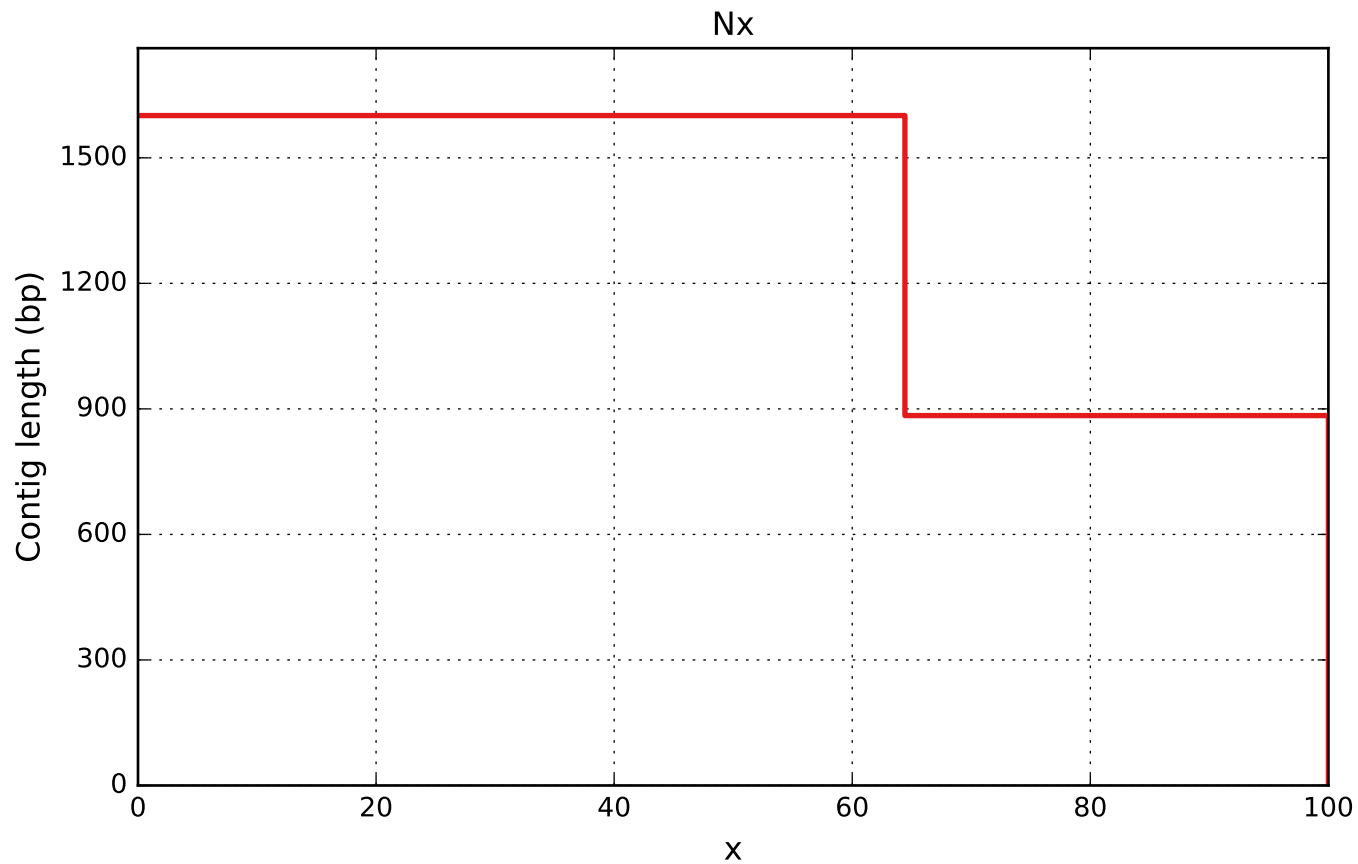
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# mismatches	8
# indels	0
# indels ( $\leq 5$ 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).

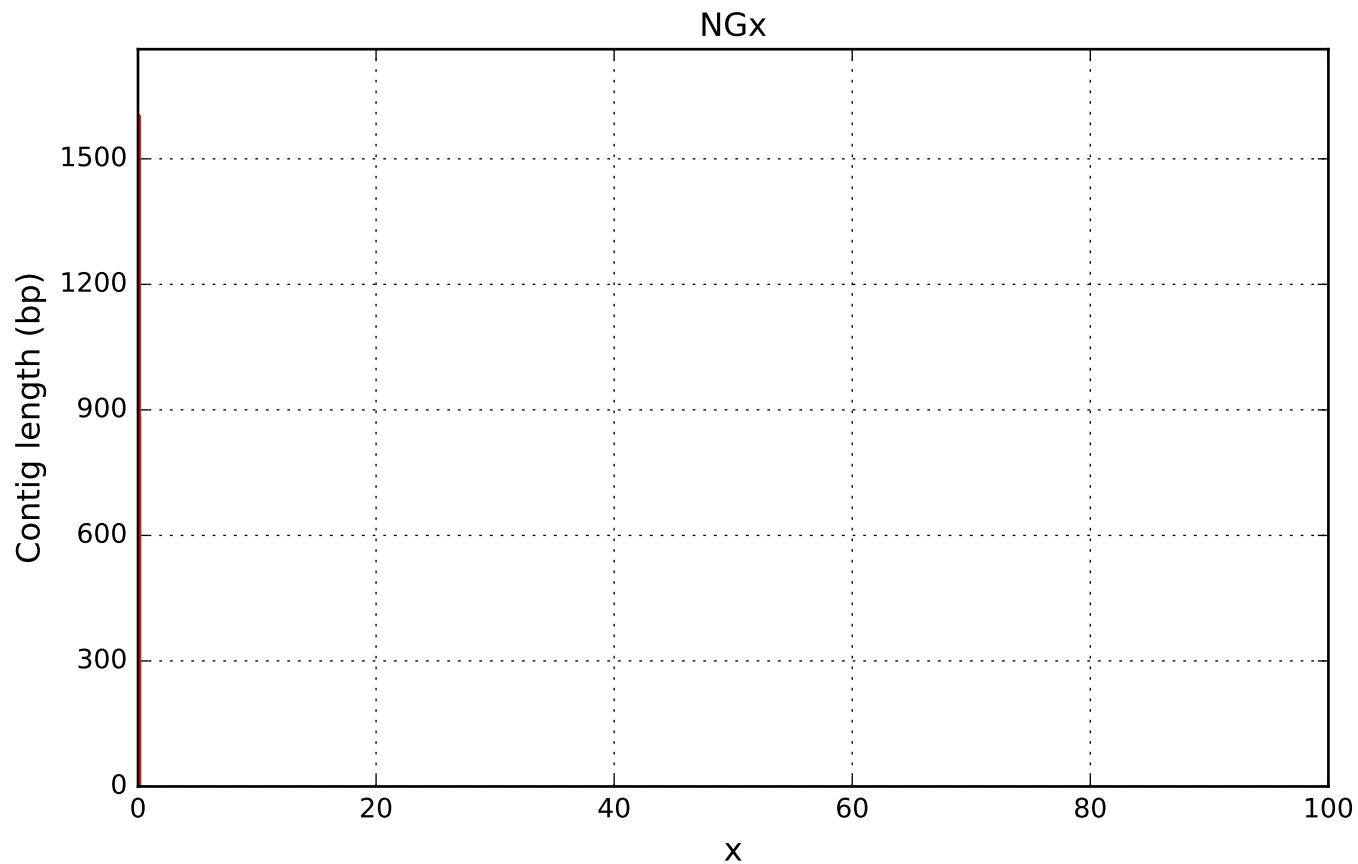
## Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
Partially unaligned length	2316
# N's	0

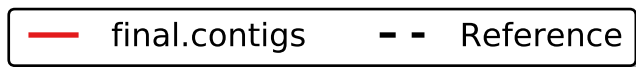
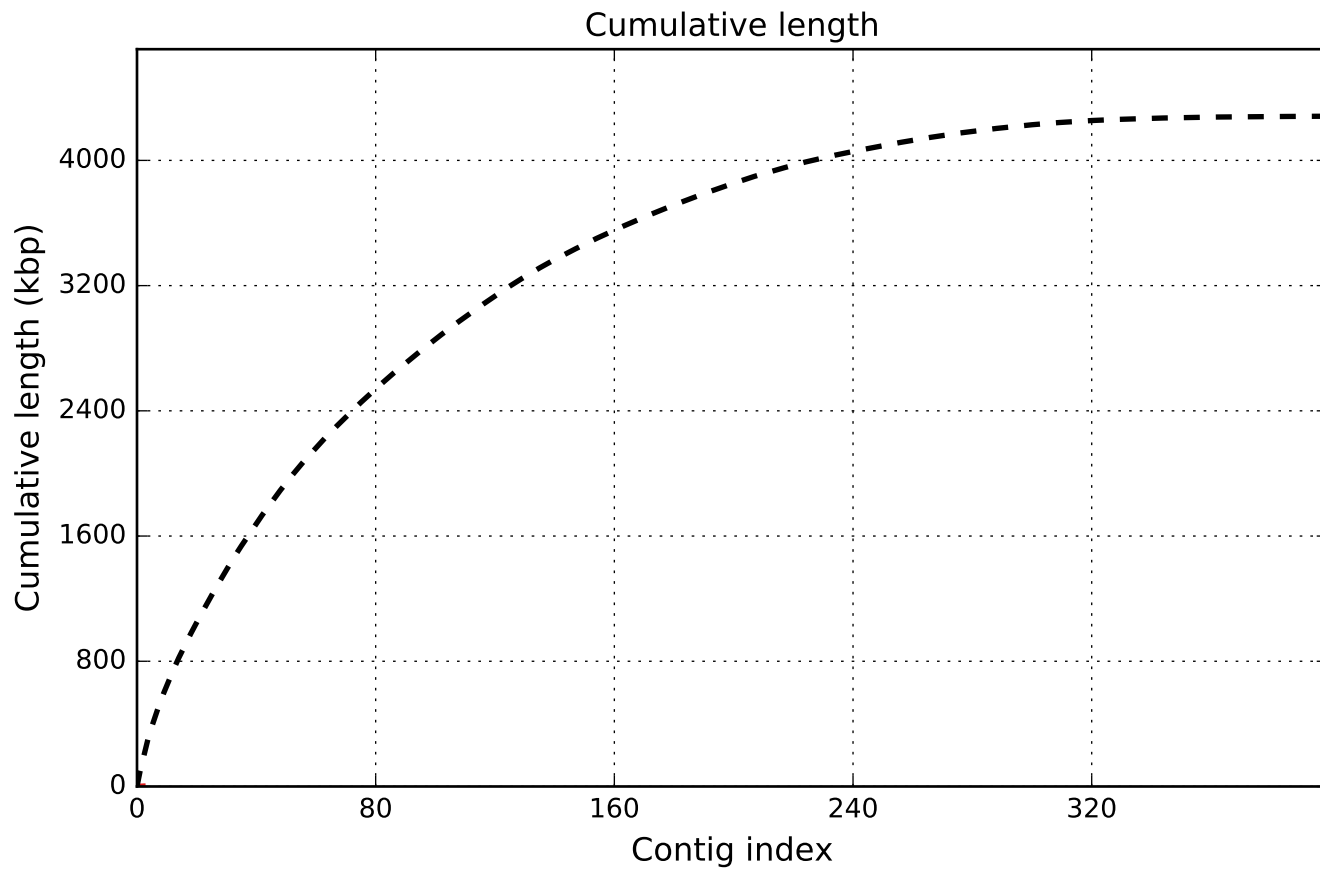
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



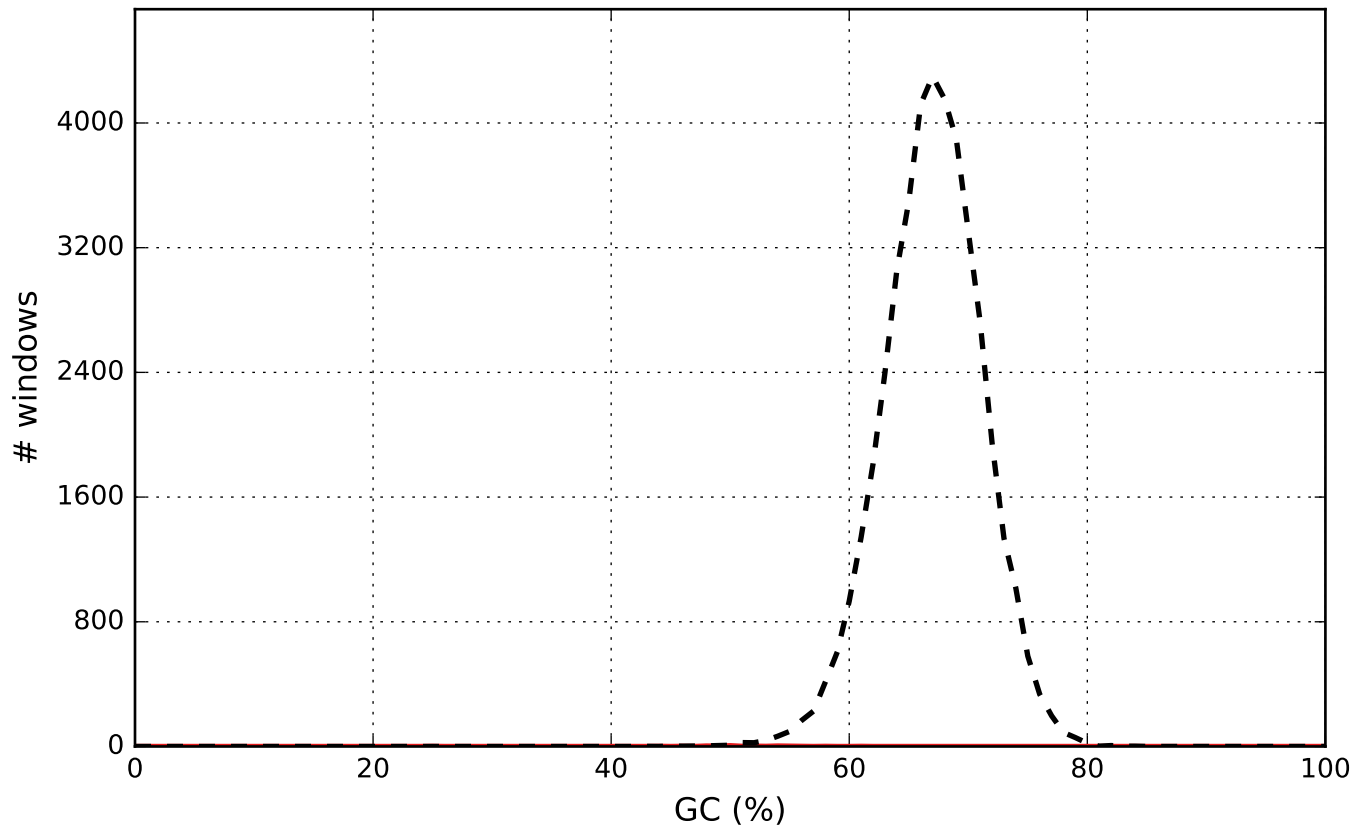
— final.contigs



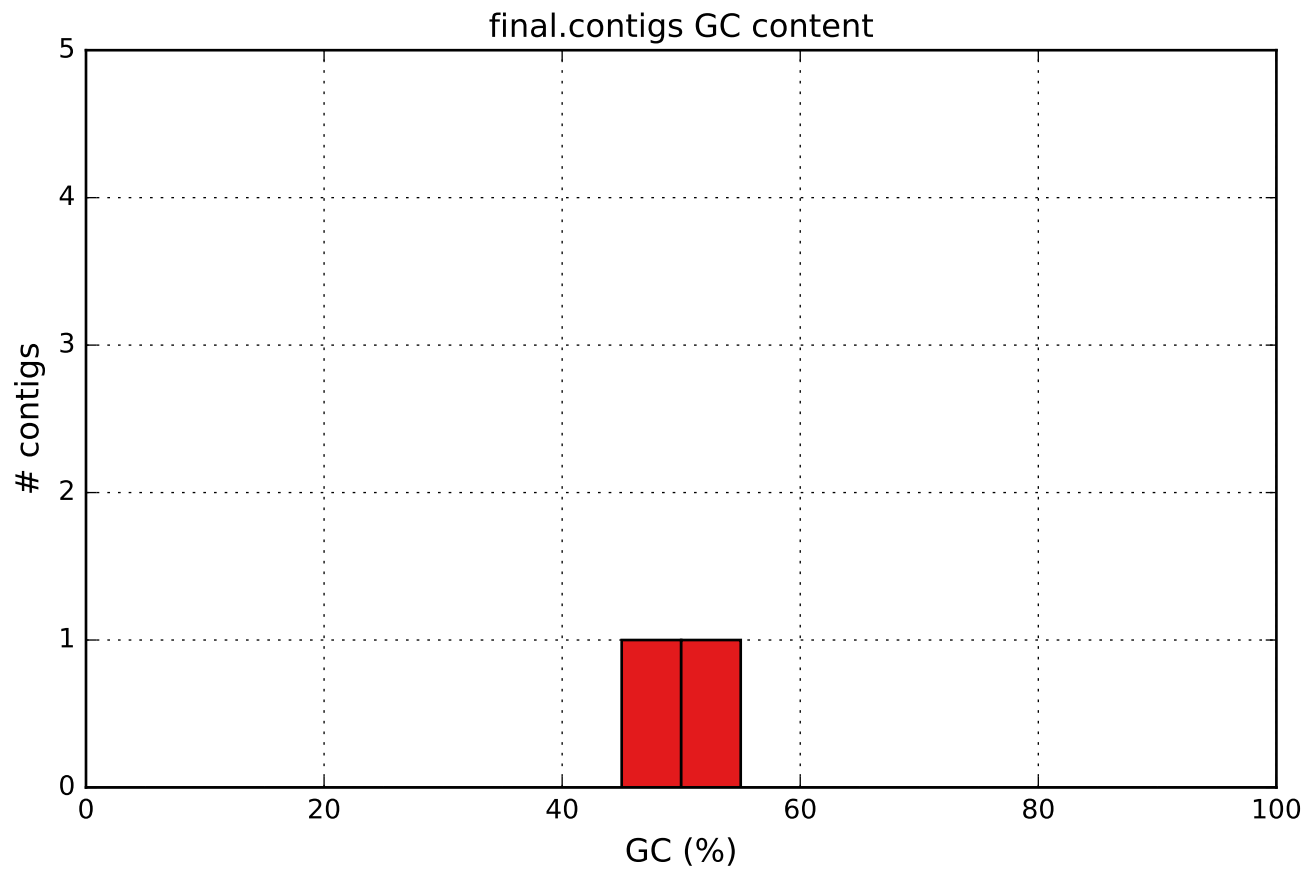
— final.contigs



# GC content



— final.contigs    - - Reference

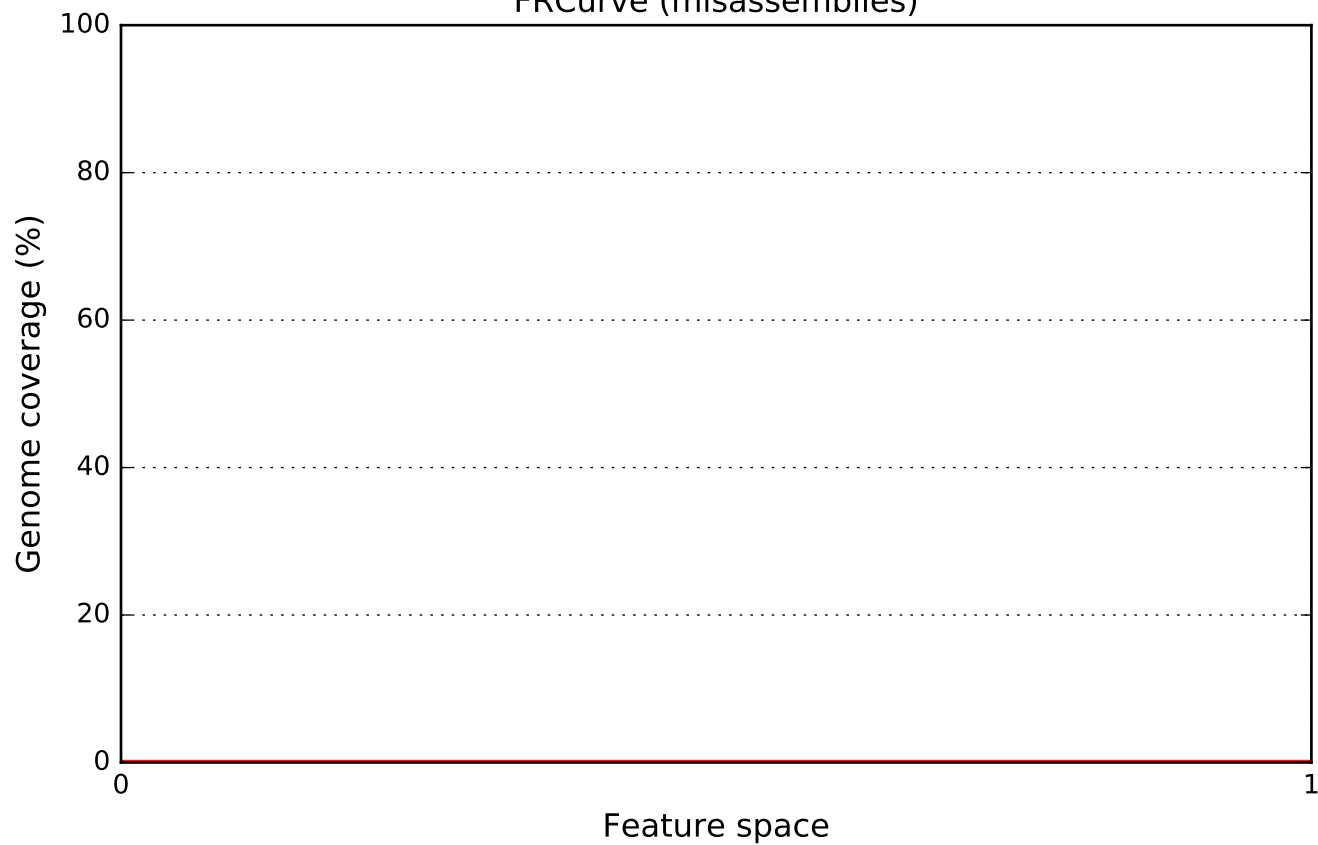


final.contigs



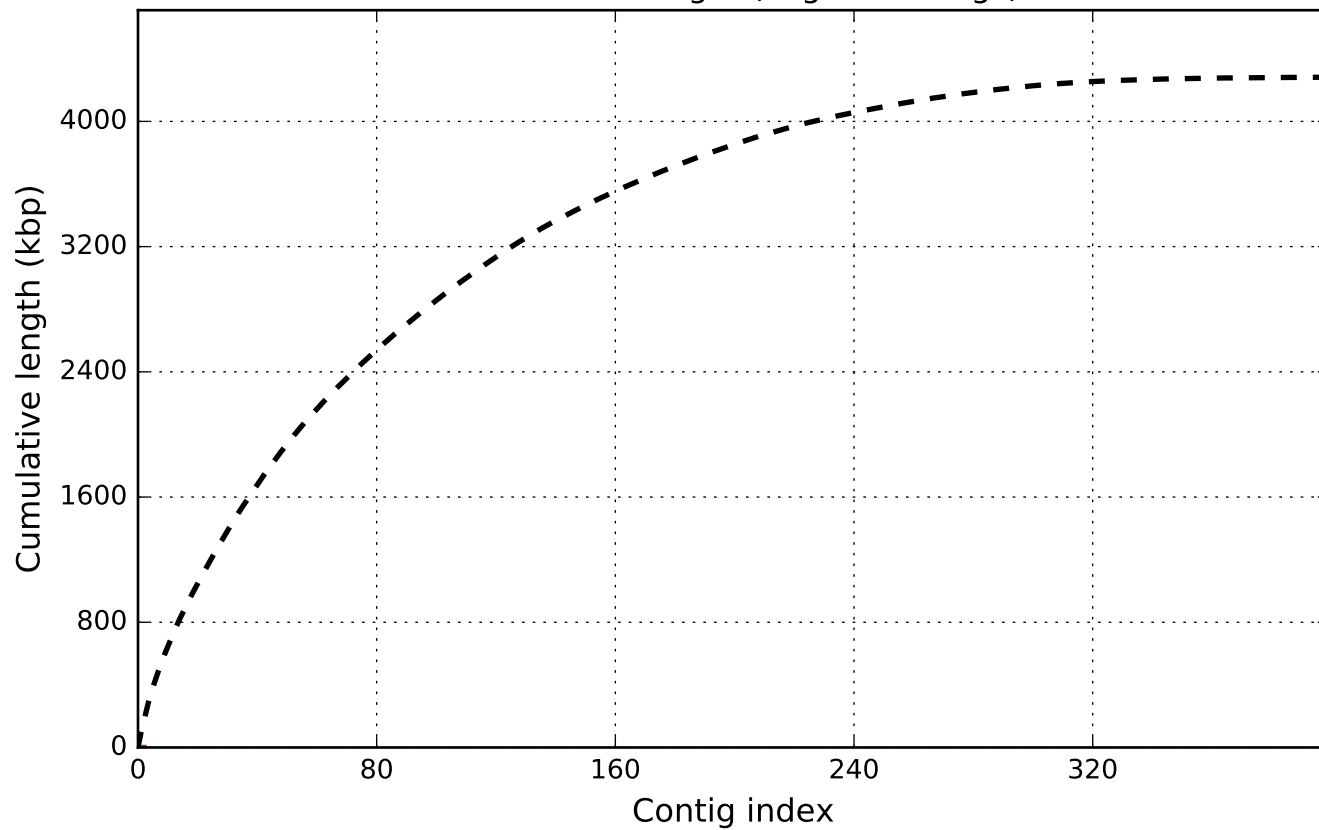


FRCurve (misassemblies)

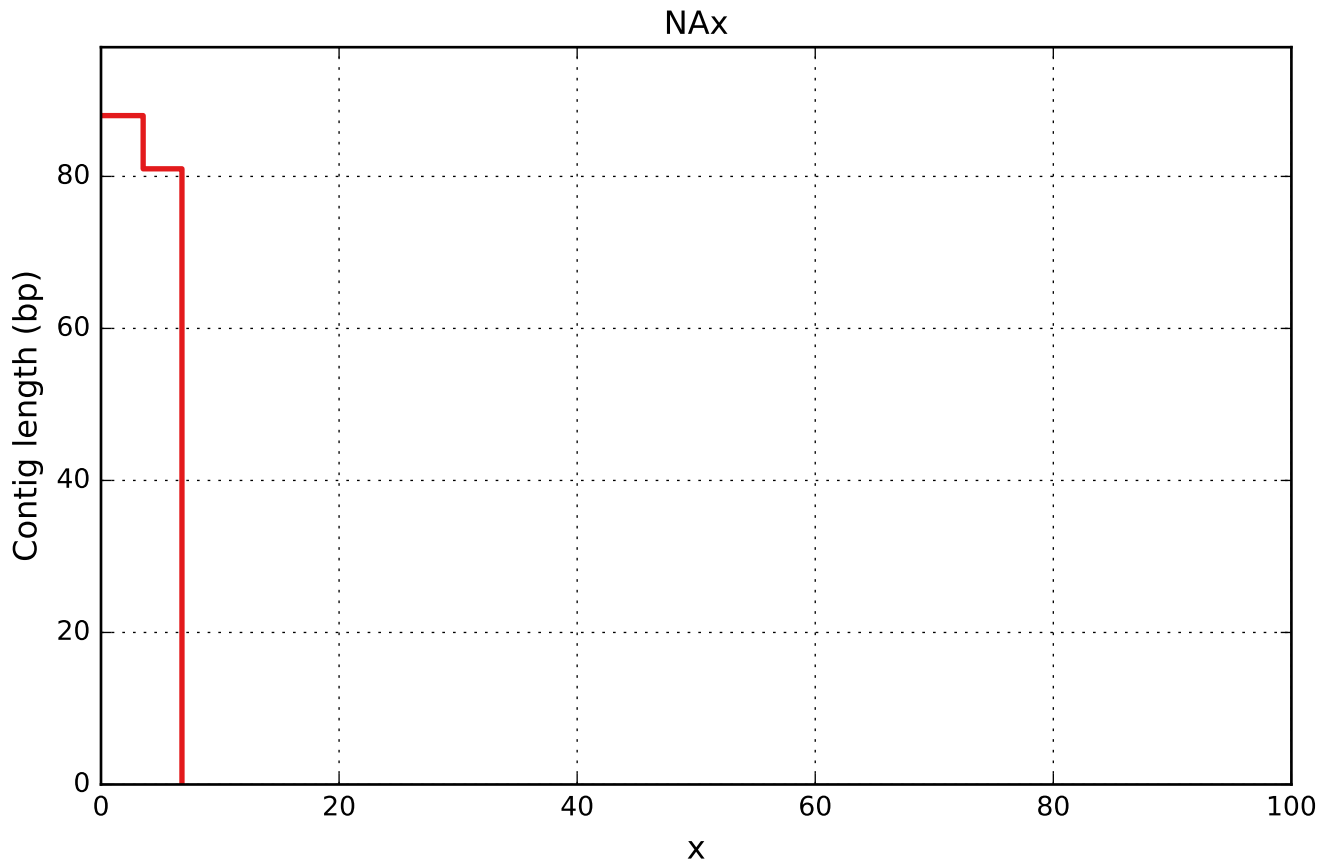


— final.contigs

Cumulative length (aligned contigs)

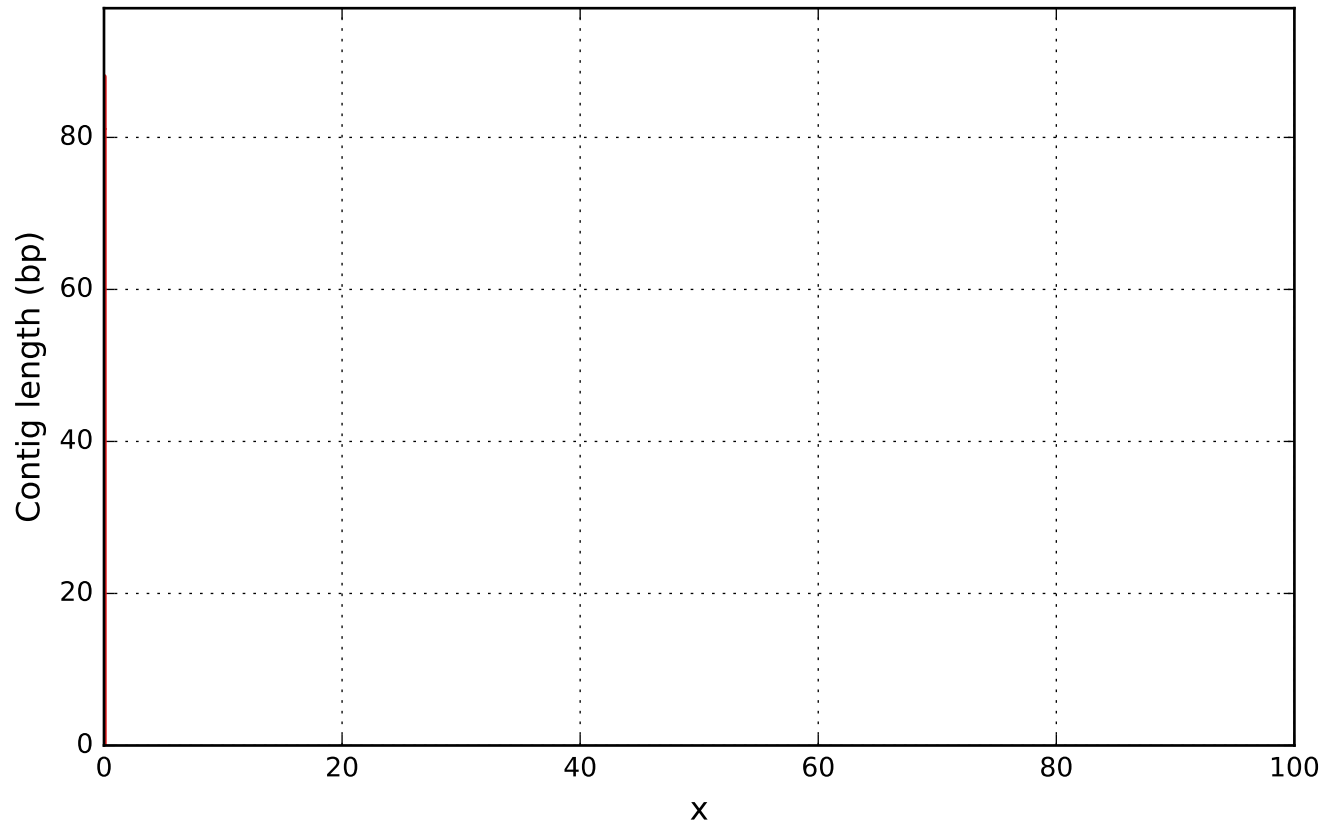


— final.contigs    - - Reference



— final.contigs

NGAx



— final.contigs