

# Report

	final.contigs
# contigs ( $\geq 1000$ bp)	4
# 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)	5986
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	6
Largest contig	2387
Total length	7651
Reference length	4282232
GC (%)	58.79
Reference GC (%)	66.99
N50	1190
N75	1054
L50	3
L75	4
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 3 part
Unaligned length	4662
Genome fraction (%)	0.045
Duplication ratio	1.567
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2515.72
# indels per 100 kbp	471.70
Largest alignment	977
Total aligned length	1894
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

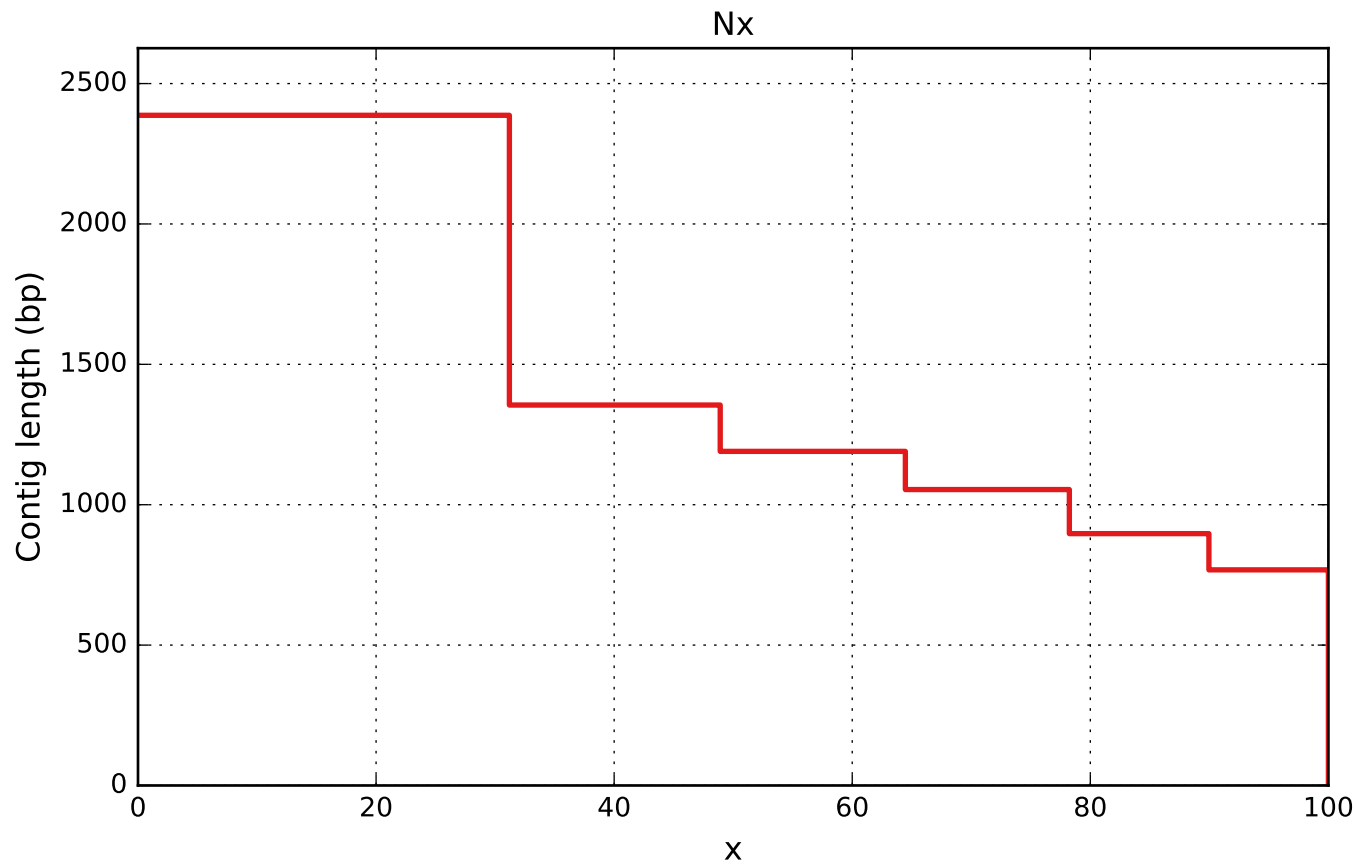
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# mismatches	48
# indels	9
# indels ( $\leq 5$ bp)	9
# indels ( $> 5$ bp)	0
Indels length	14

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).

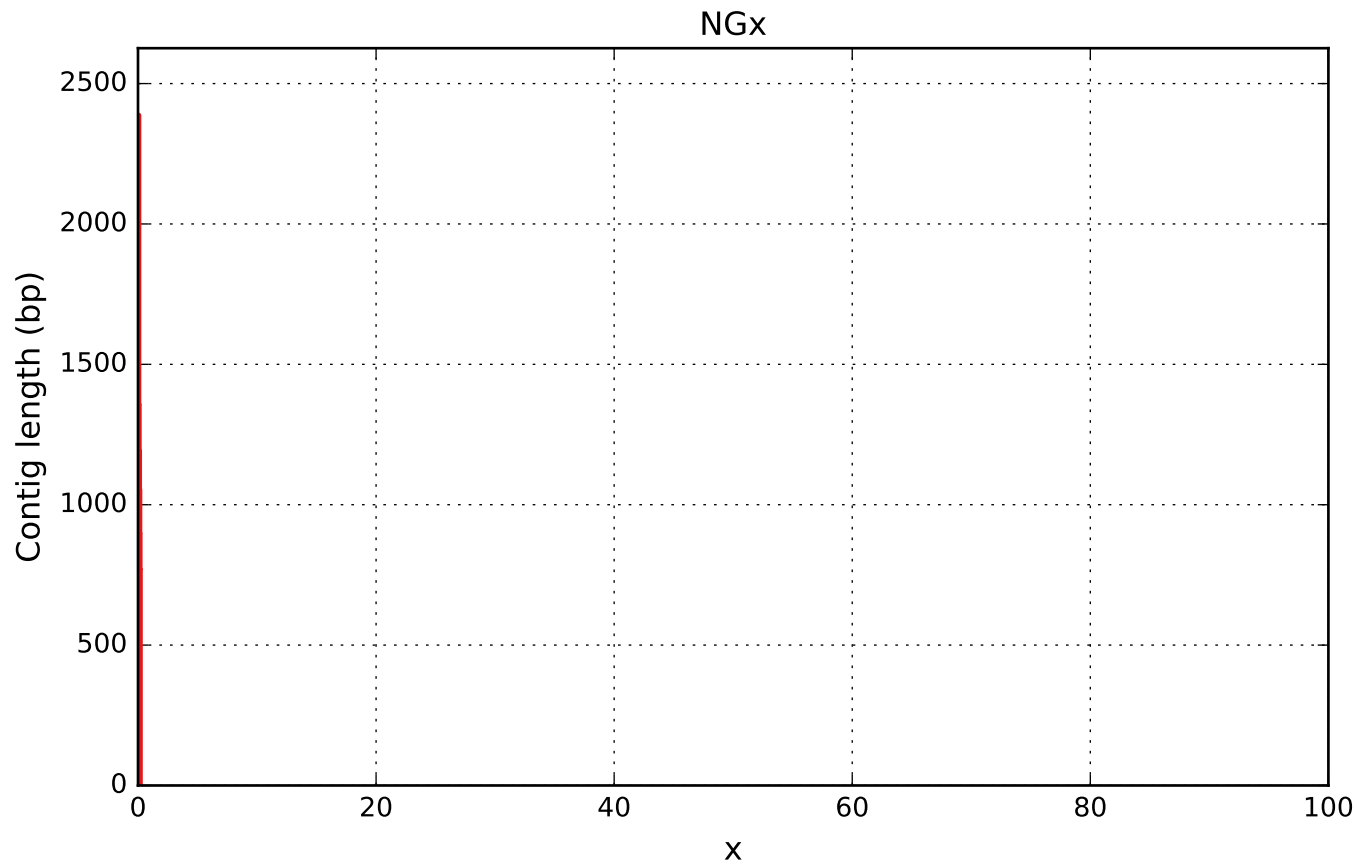
## Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
Partially unaligned length	4662
# N's	0

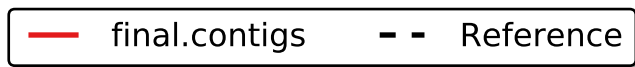
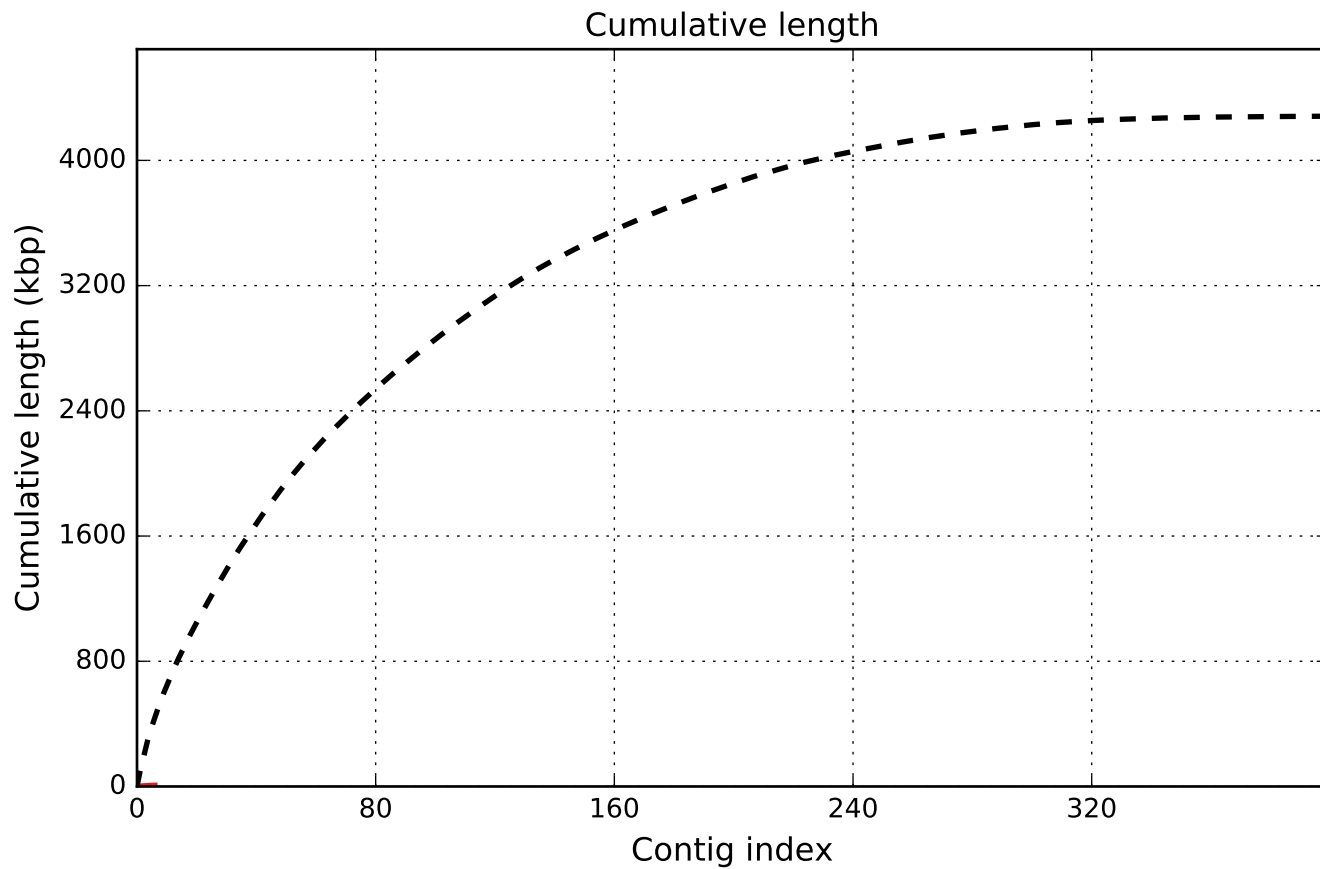
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



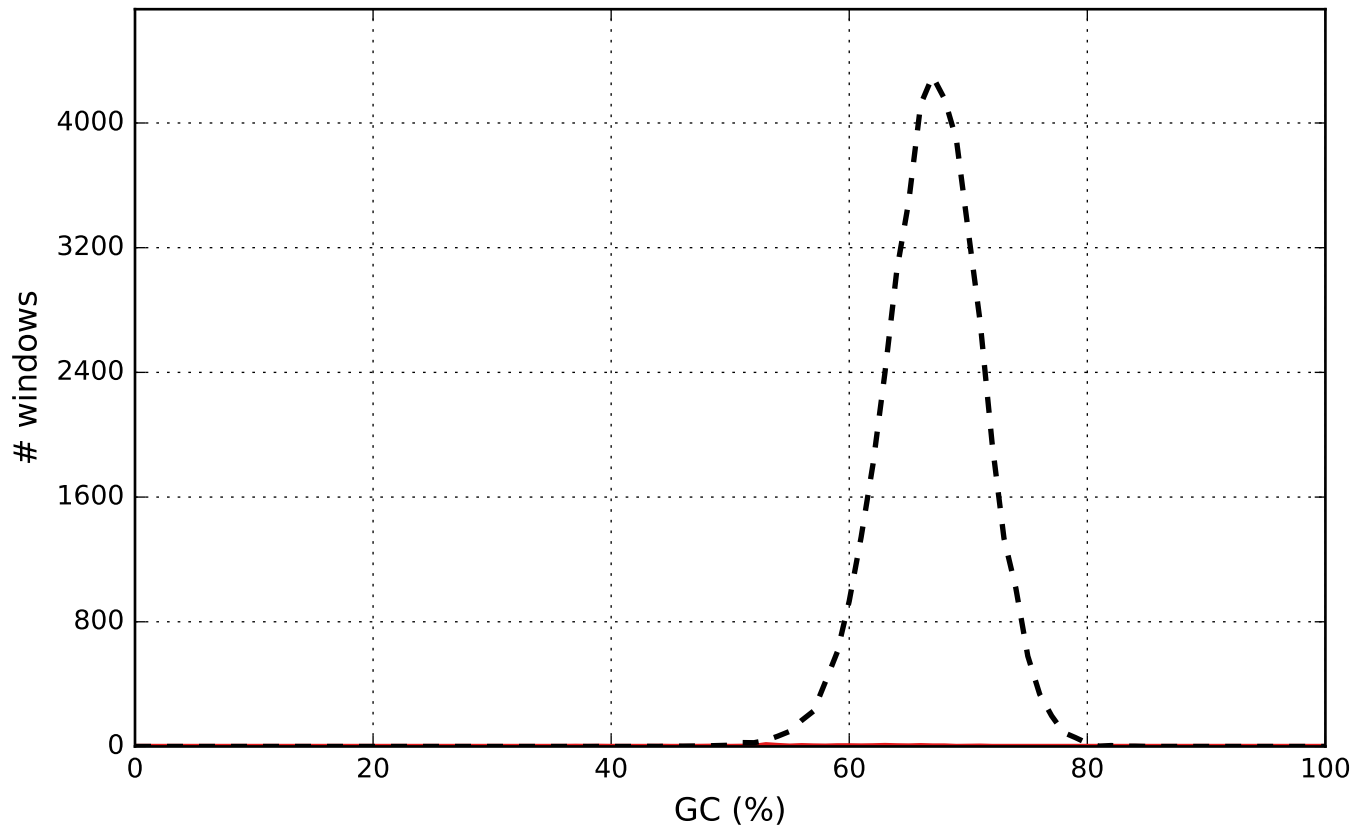
— final.contigs



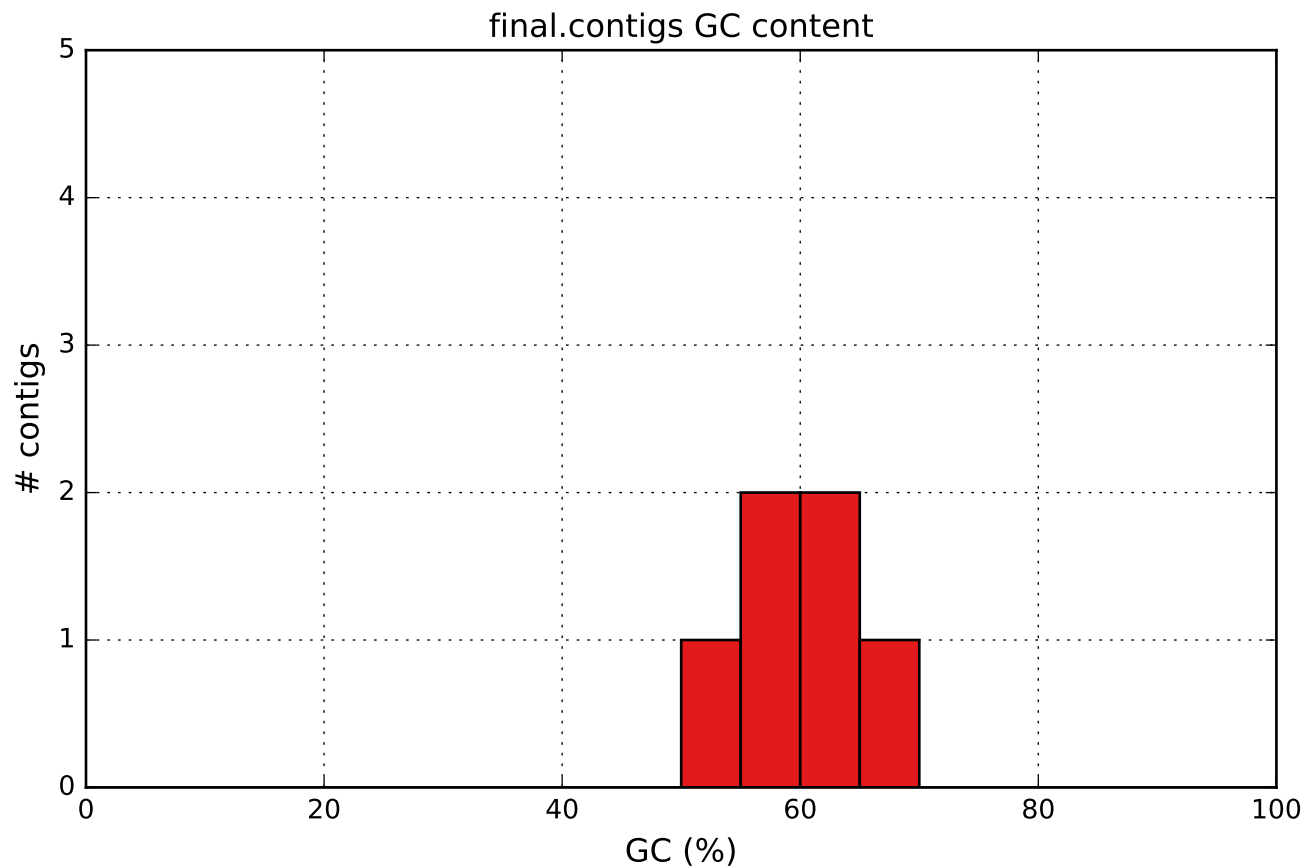
— final.contigs



# GC content



— final.contigs    - - Reference

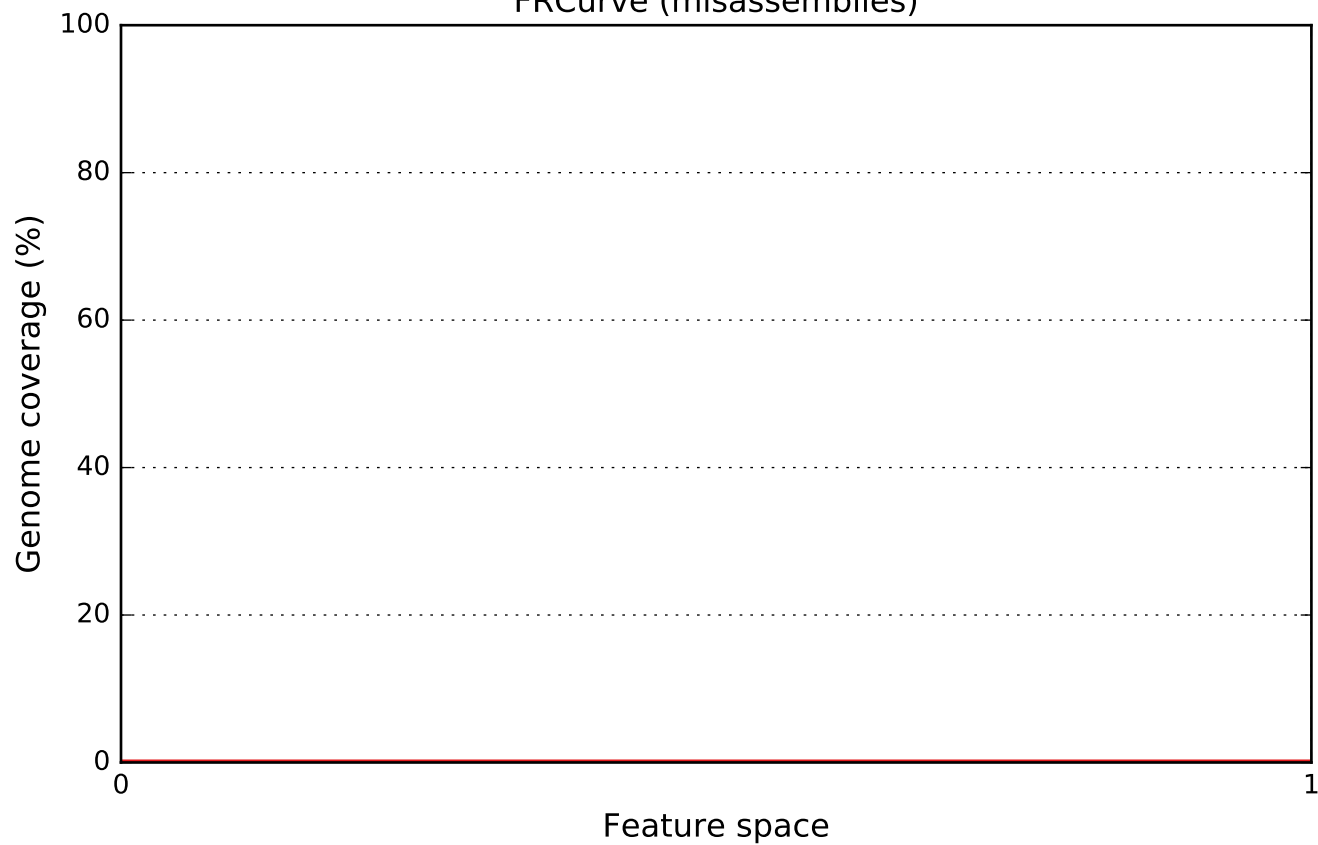


 final.contigs



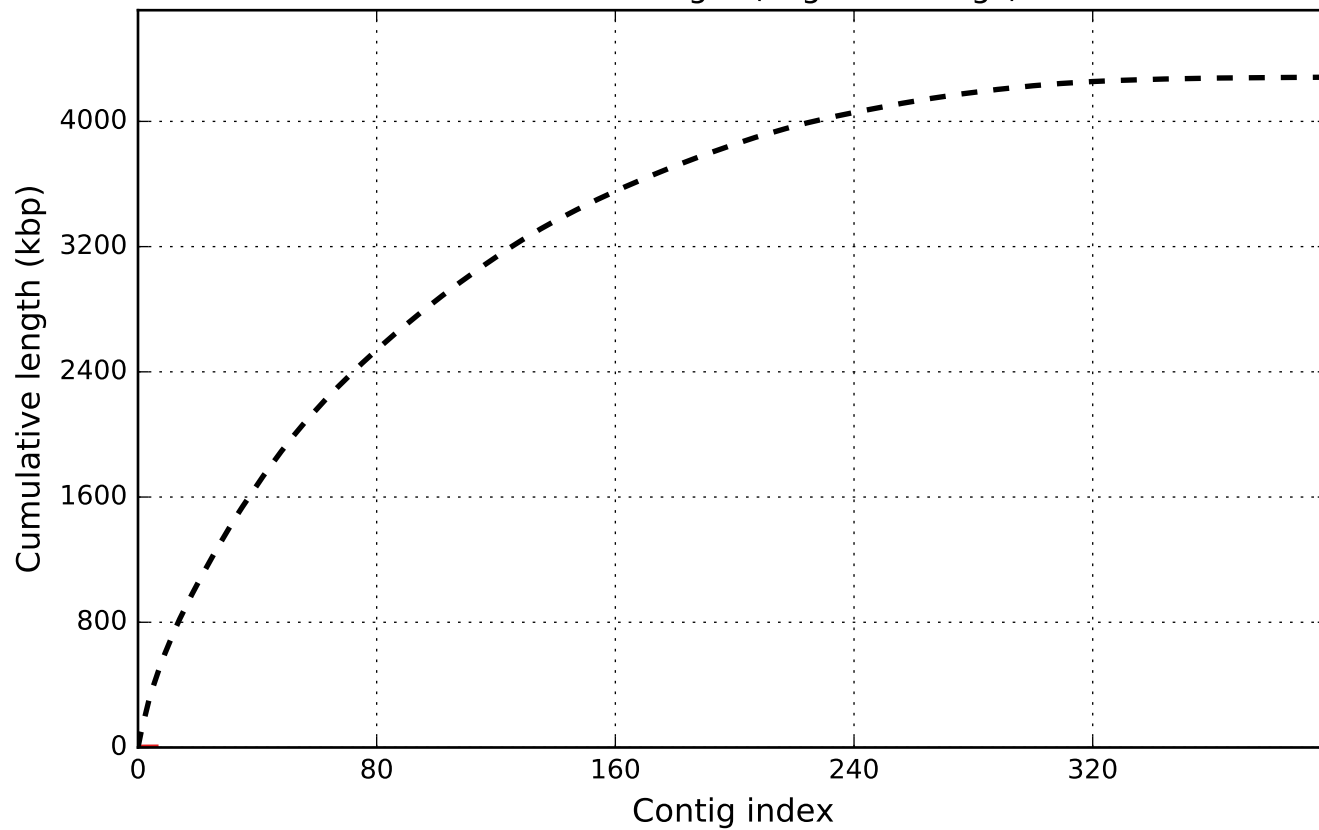


FRCurve (misassemblies)

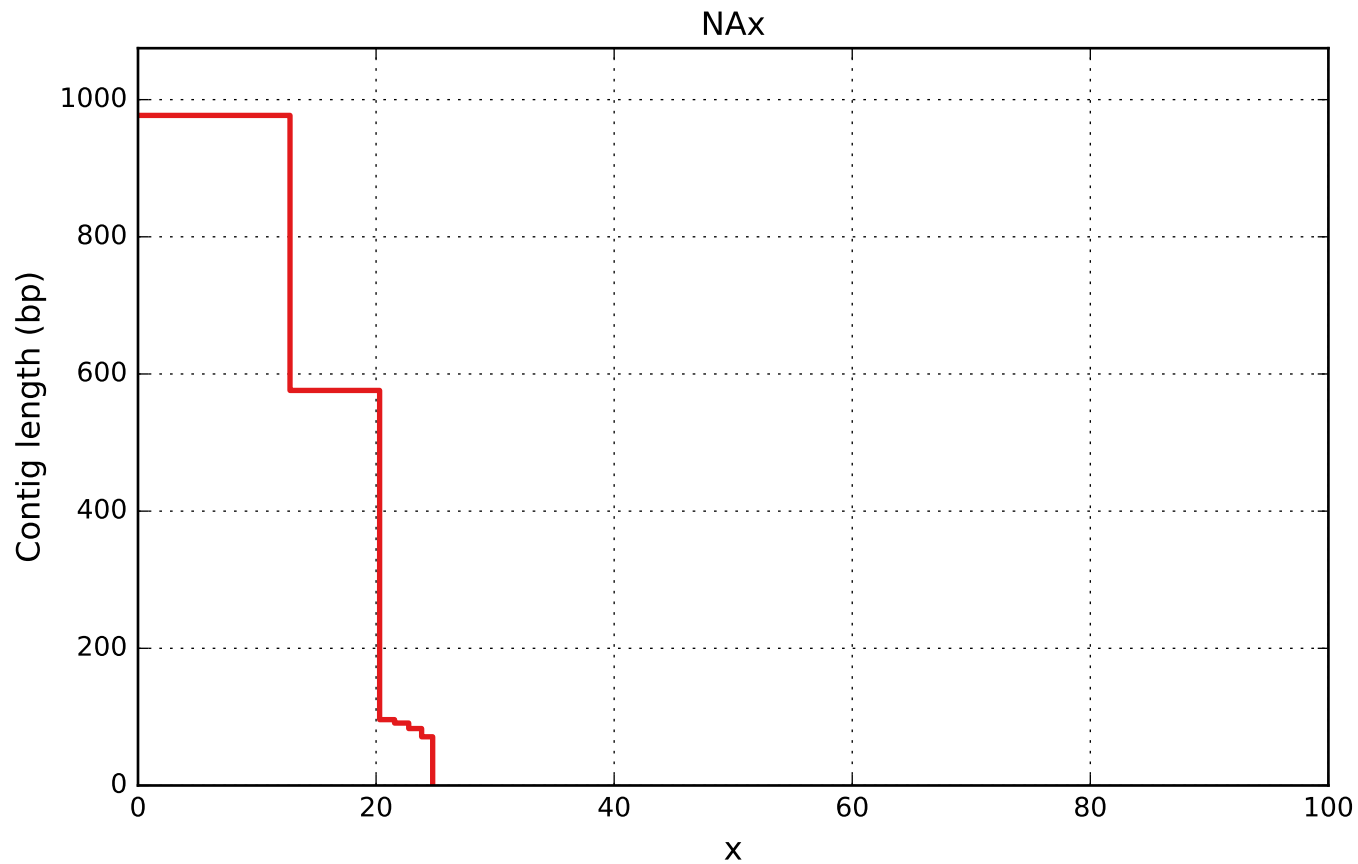


— final.contigs

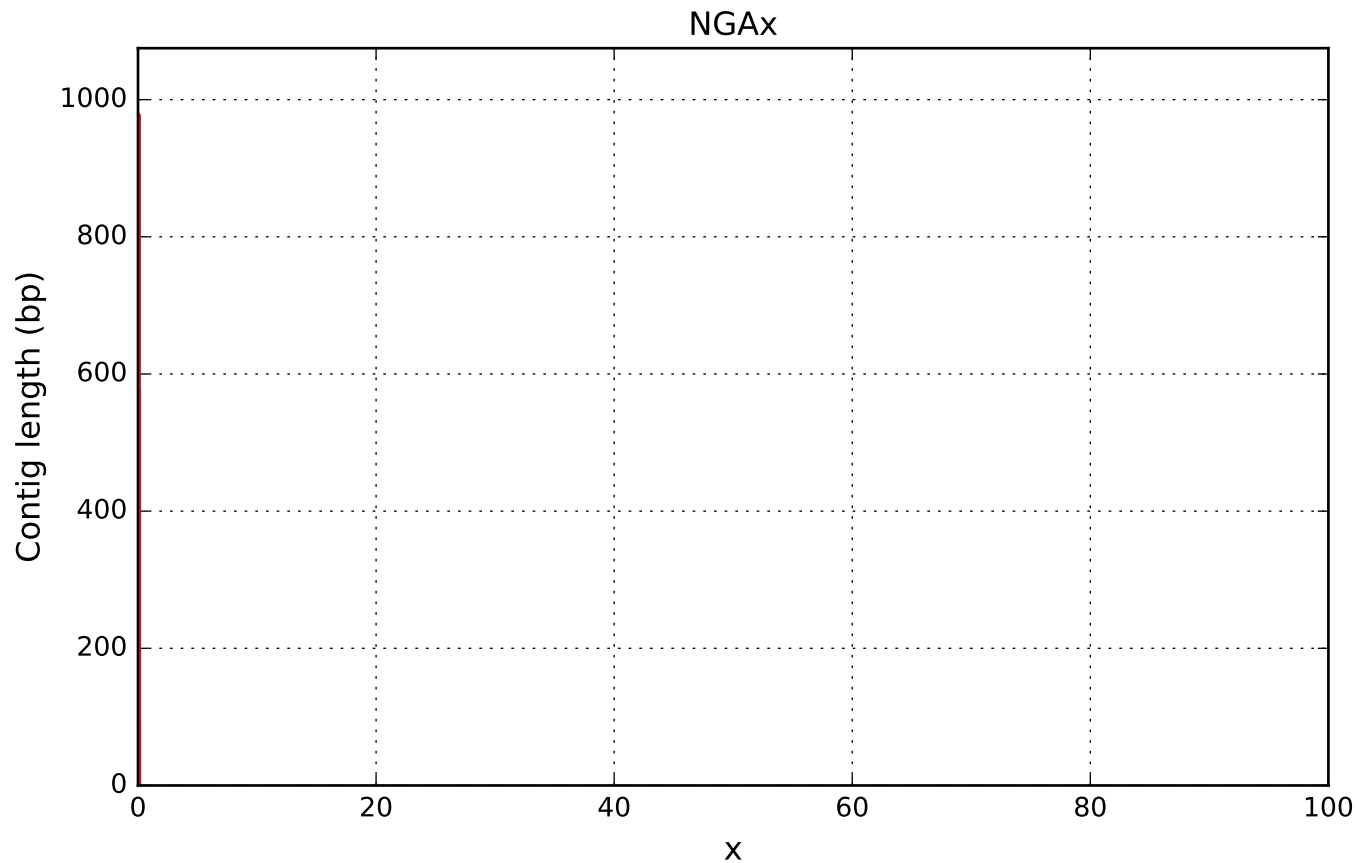
Cumulative length (aligned contigs)



— final.contigs    - - Reference



— final.contigs



— final.contigs