

## Report

	final.contigs
# contigs (>= 1000 bp)	8
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	23078
Total length (>= 5000 bp)	13190
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	14
Largest contig	8046
Total length	26911
Reference length	4282232
GC (%)	60.94
Reference GC (%)	66.99
N50	4046
N75	1109
L50	3
L75	6
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 9 part
Unaligned length	22596
Genome fraction (%)	0.061
Duplication ratio	1.655
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3297.55
# indels per 100 kbp	268.40
Largest alignment	1270
Total aligned length	2929
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

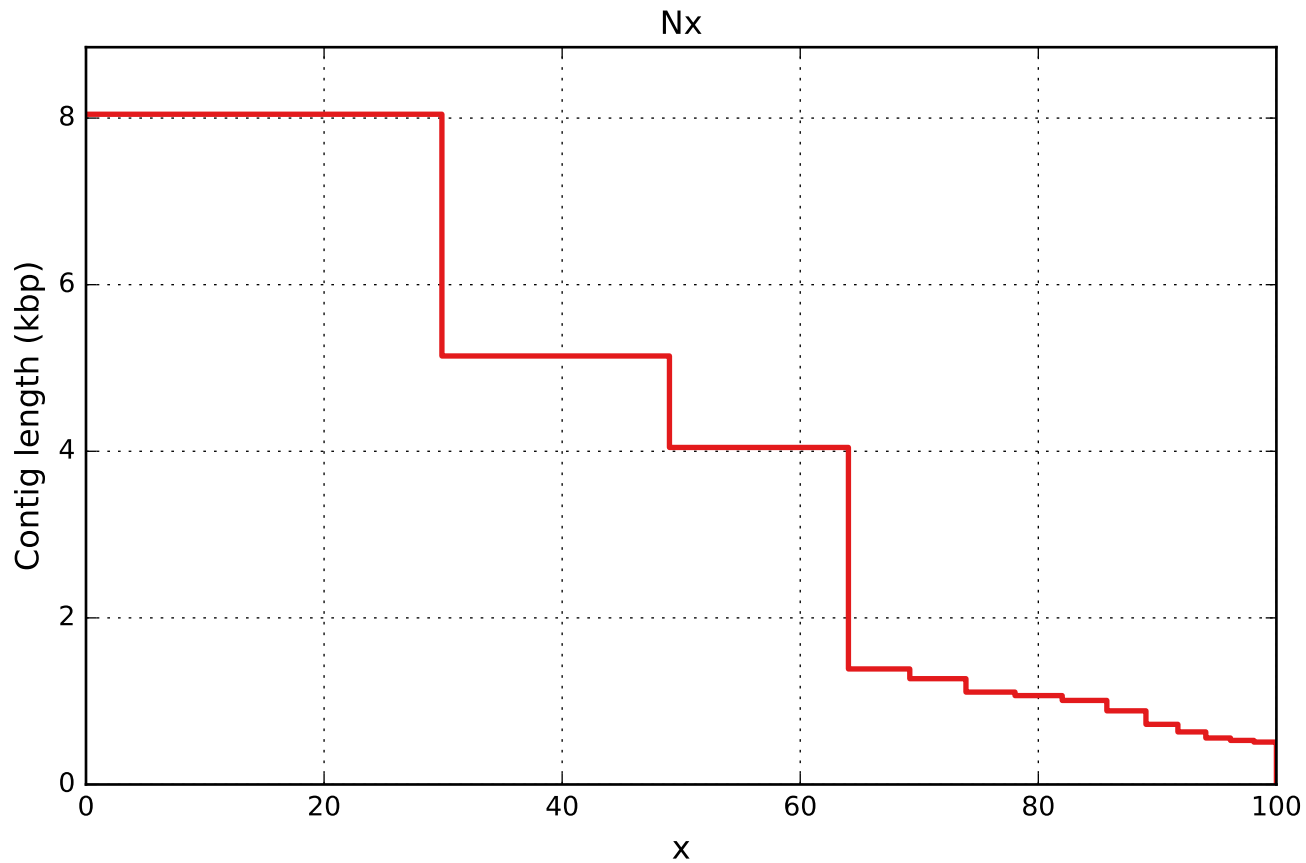
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	86
# indels	7
# indels (<= 5 bp)	7
# indels (> 5 bp)	0
Indels length	7

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

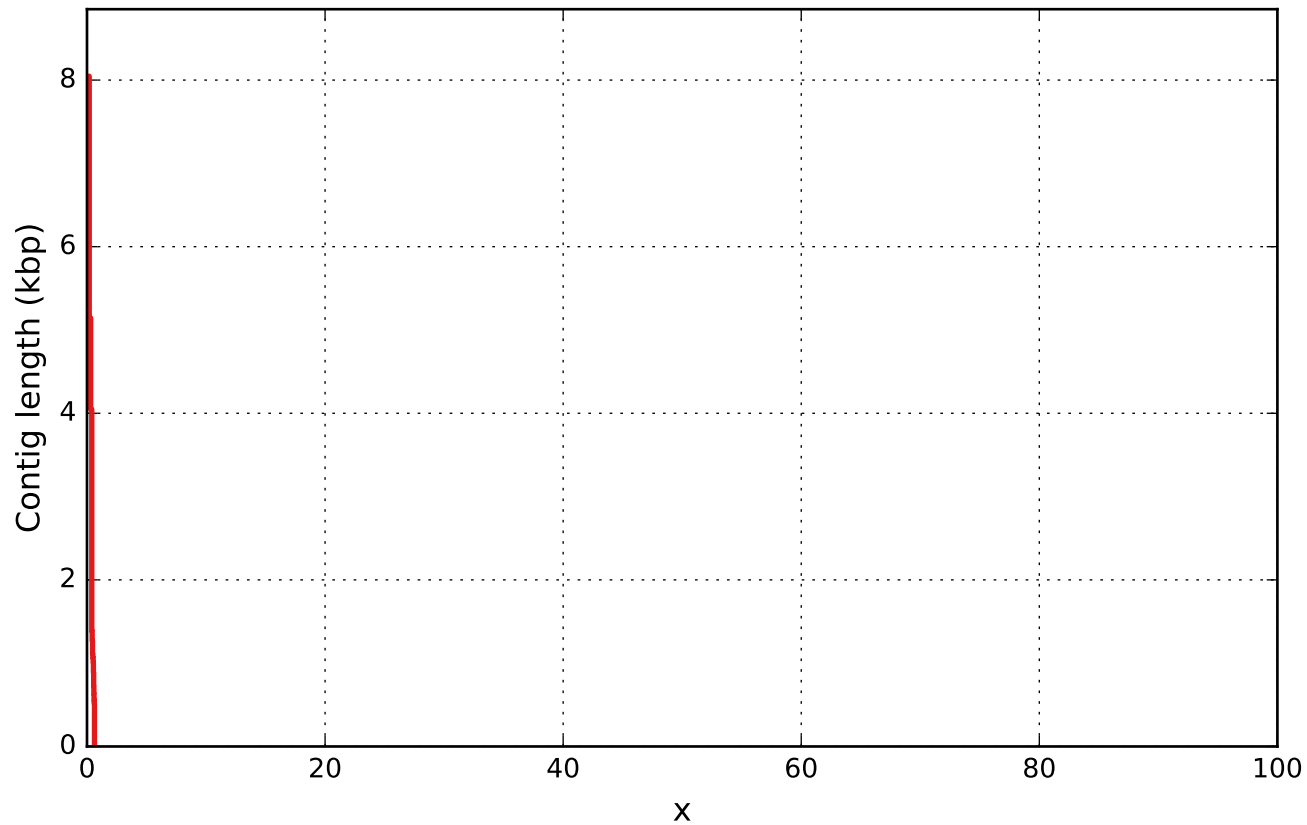
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	9
Partially unaligned length	22596
# N's	0

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).

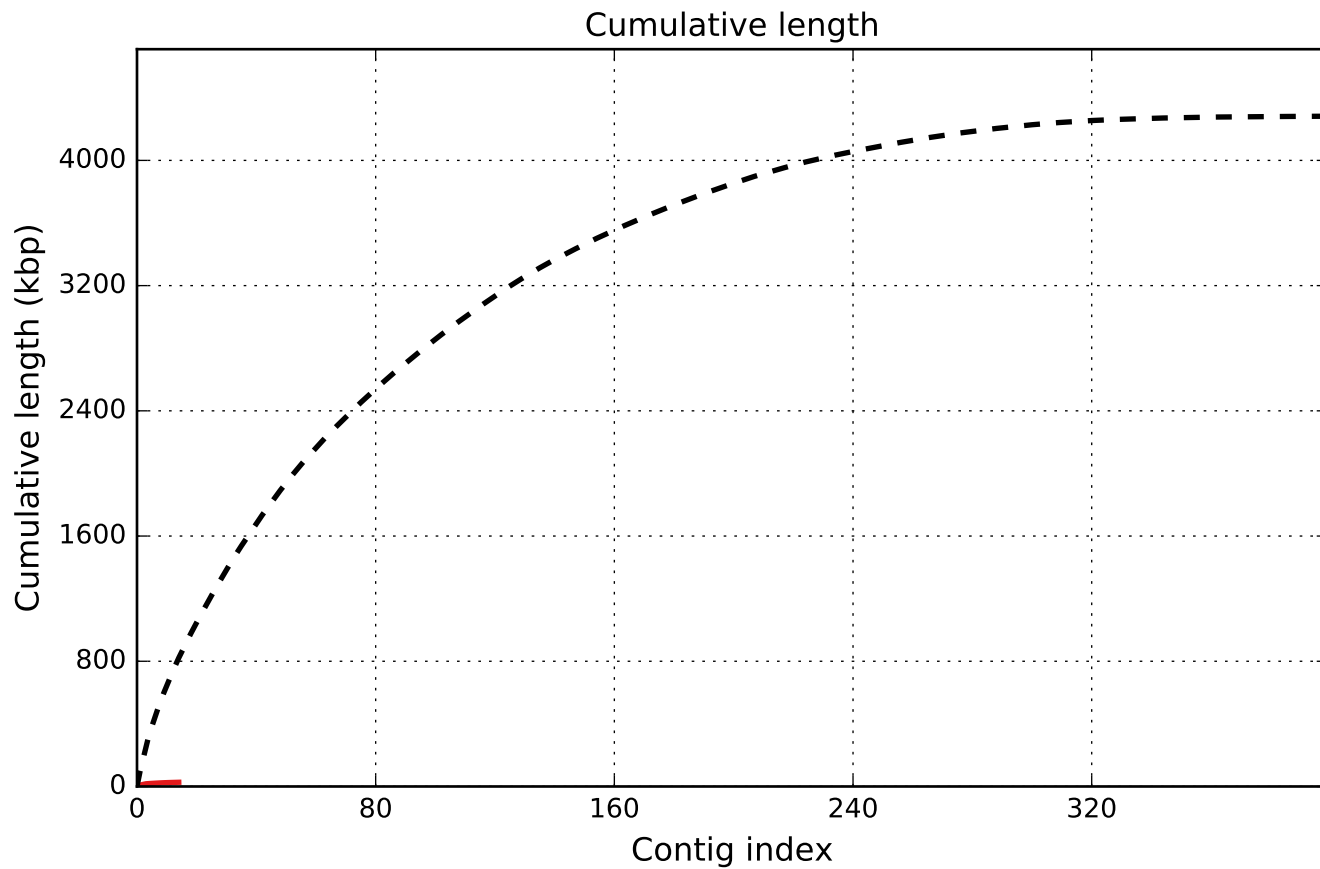


— final.contigs

NGx

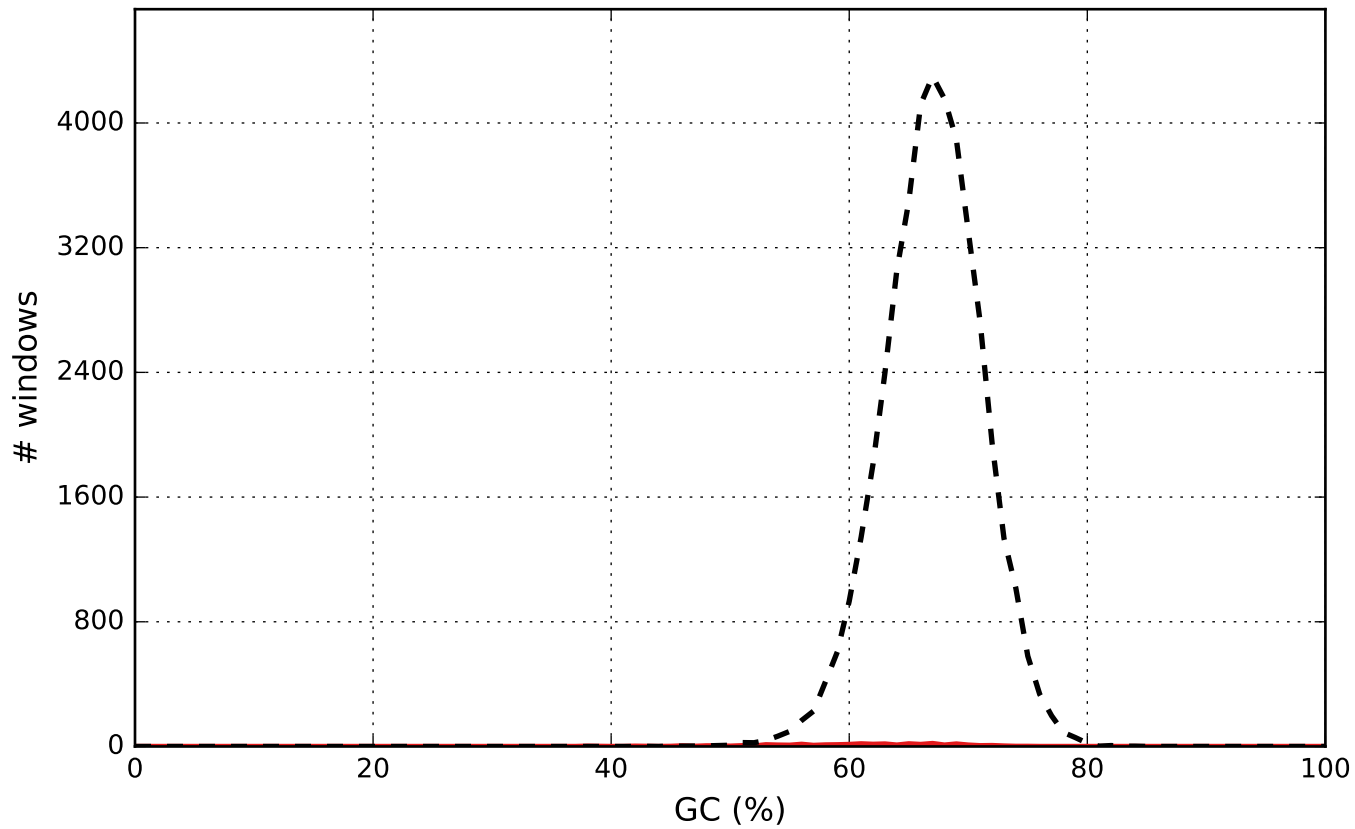


— final.contigs

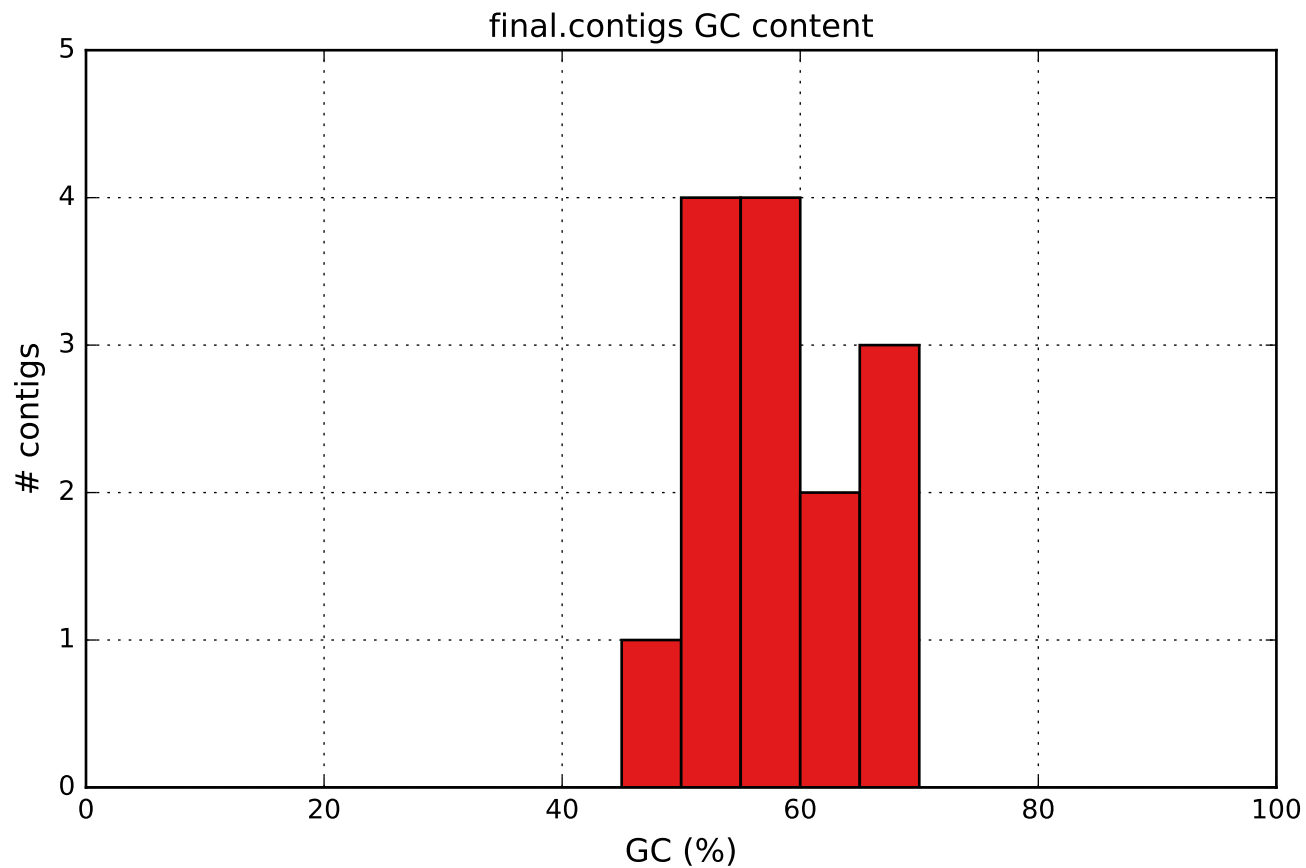


— final.contigs    - - Reference

# GC content



— final.contigs    - - Reference

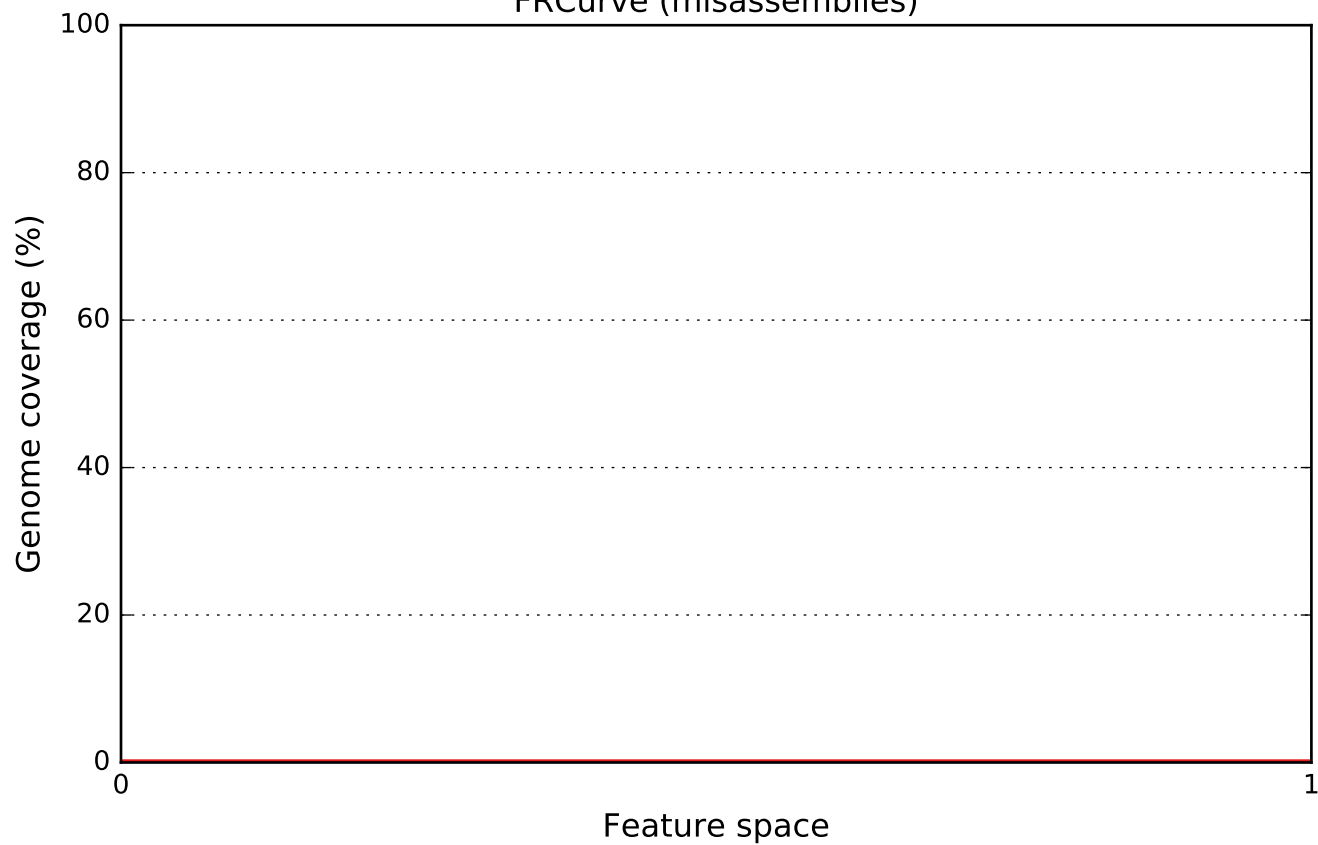


final.contigs



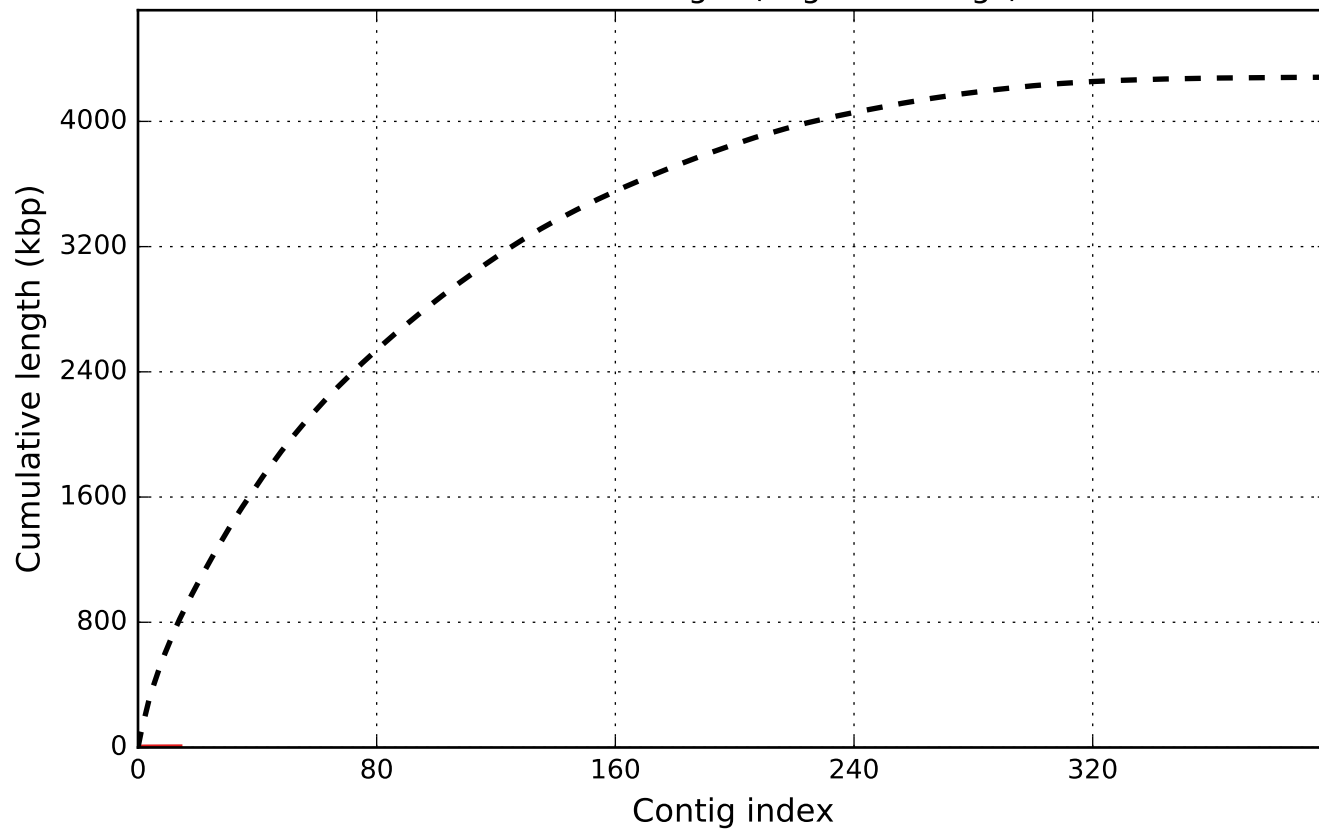


FRCurve (misassemblies)

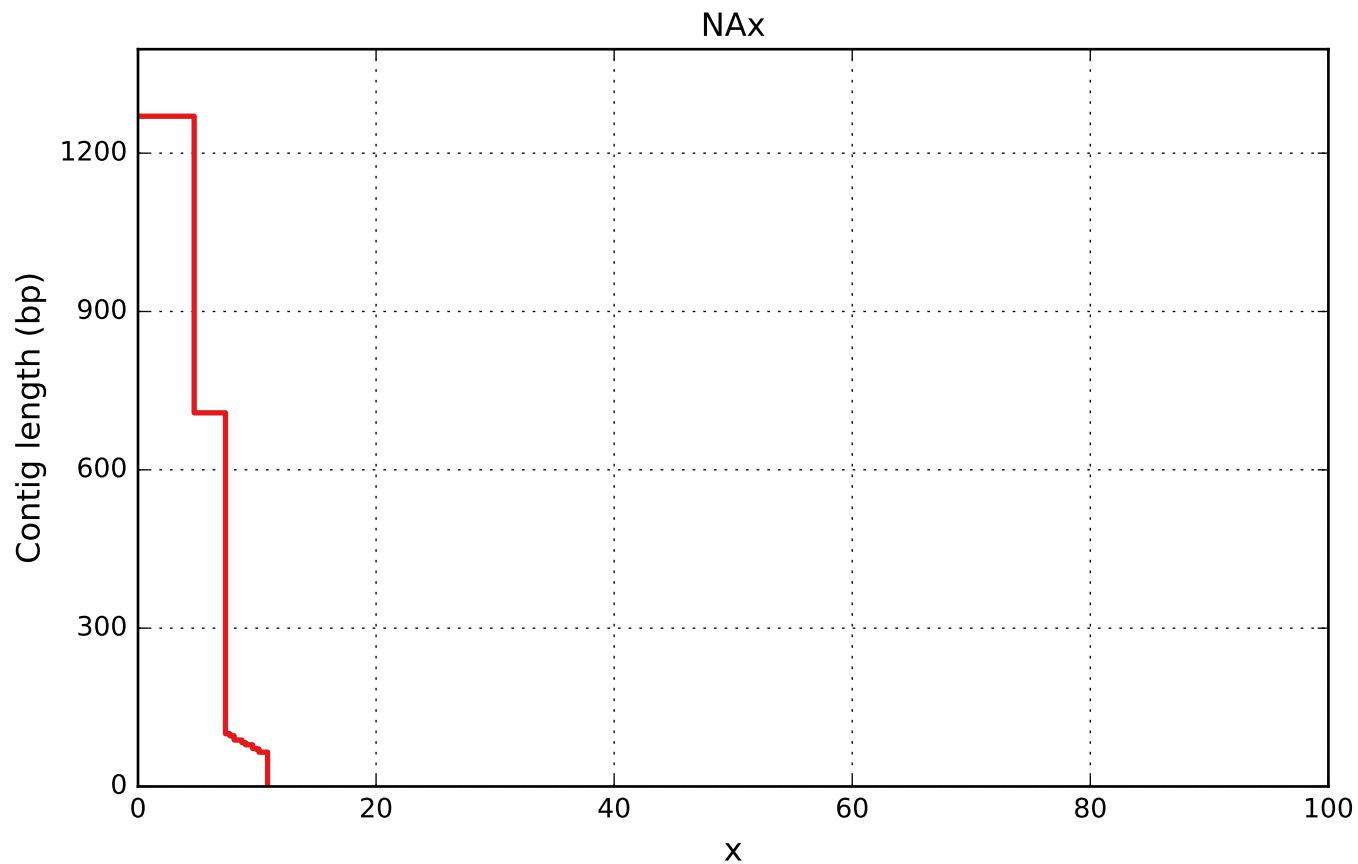


— final.contigs

Cumulative length (aligned contigs)

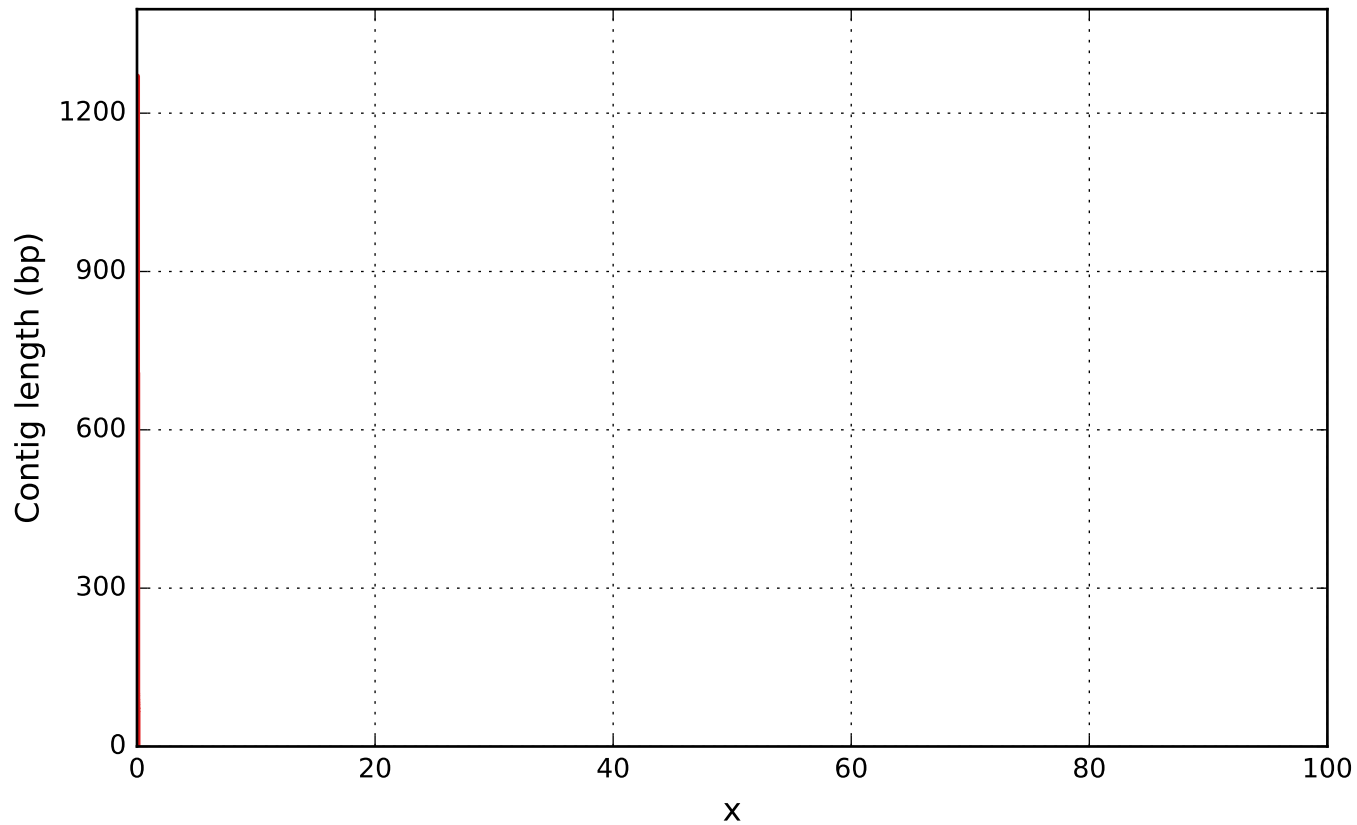


— final.contigs    - - Reference



— final.contigs

NGAx



— final.contigs