

# Report

	final.contigs
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	8219
Total length (>= 5000 bp)	5303
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	5
Largest contig	5303
Total length	9469
Reference length	4305801
GC (%)	34.55
Reference GC (%)	34.36
N50	5303
N75	1444
L50	1
L75	3
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	1
# unaligned contigs	0 + 3 part
Unaligned length	7819
Genome fraction (%)	0.019
Duplication ratio	1.990
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2774.43
# indels per 100 kbp	120.63
Largest alignment	353
Total aligned length	830
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

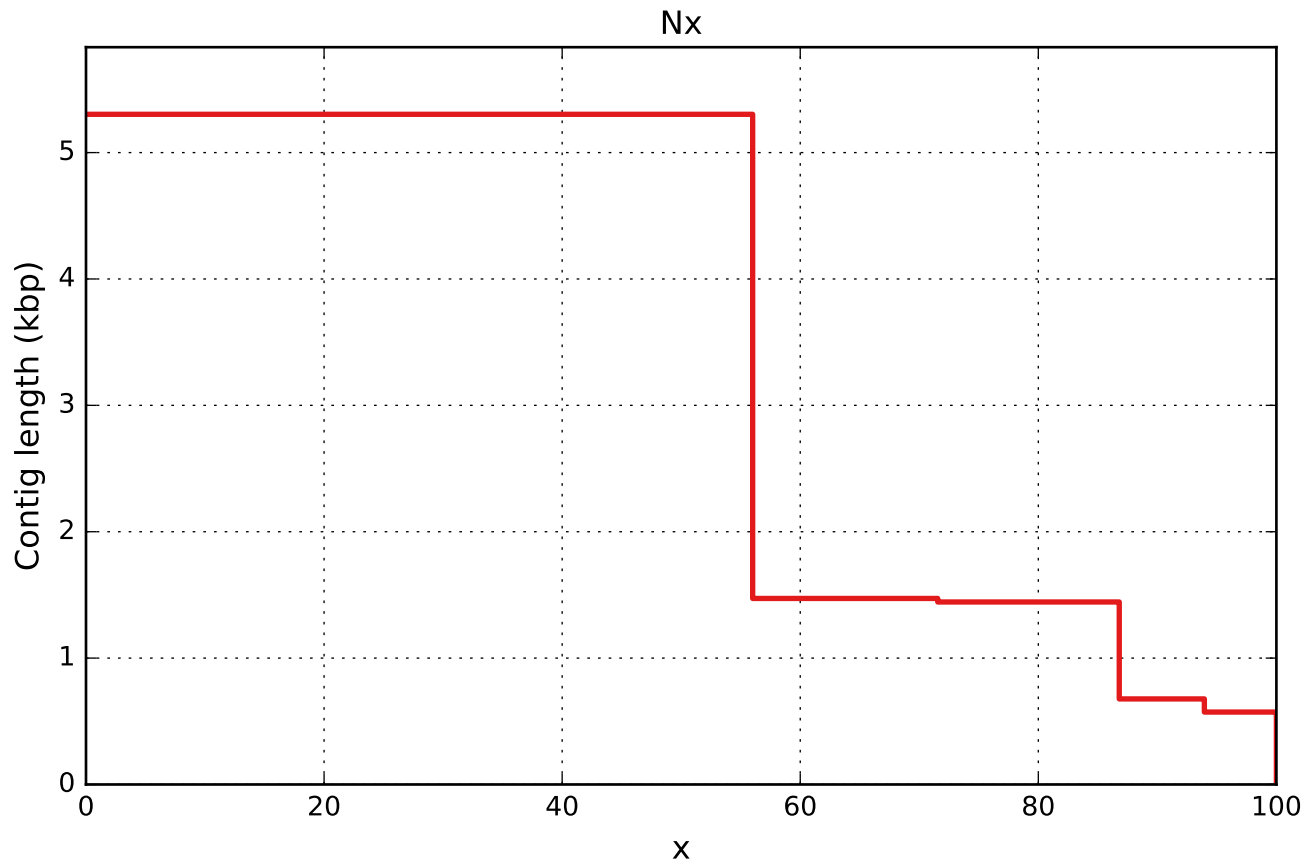
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	1
# mismatches	23
# indels	1
# indels ( $\leq 5$ bp)	1
# indels ( $> 5$ bp)	0
Indels length	1

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

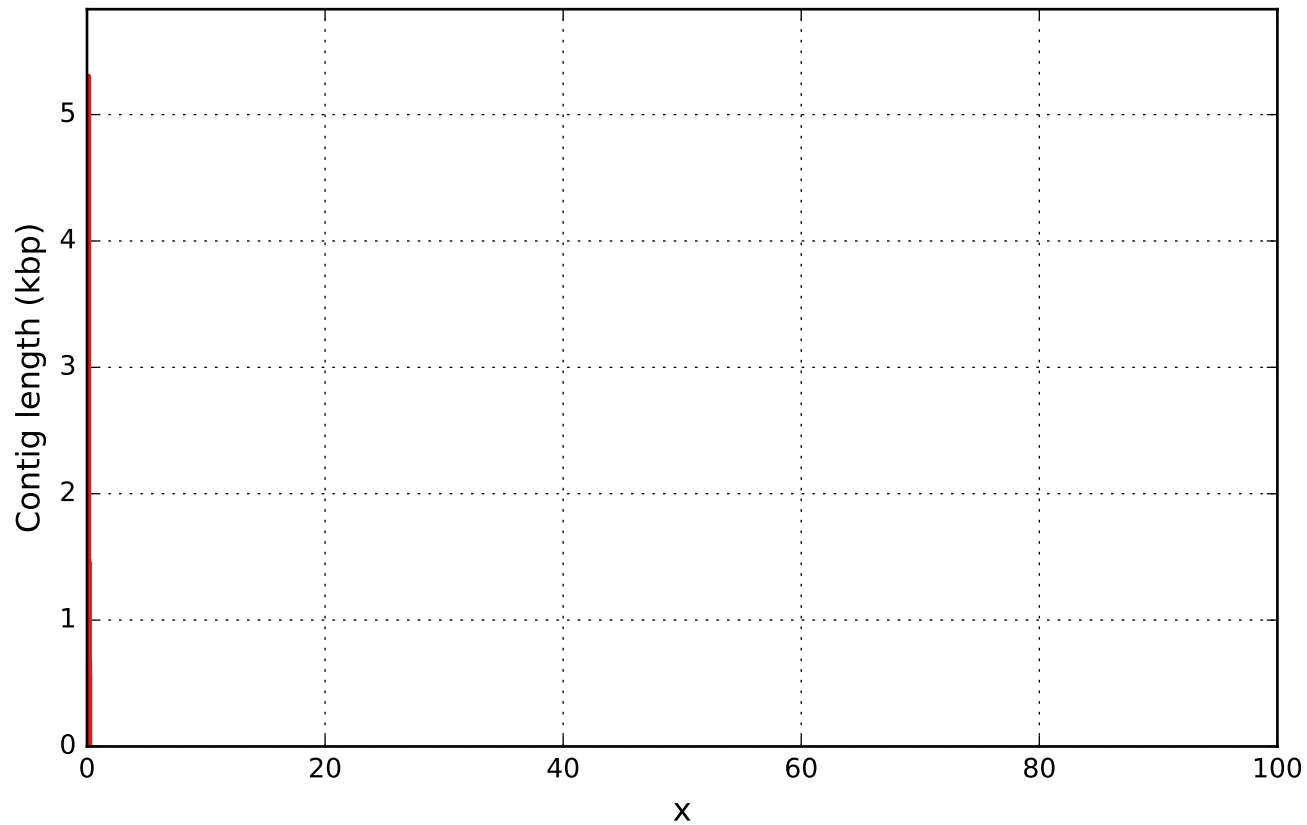
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
Partially unaligned length	7819
# N's	0

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).

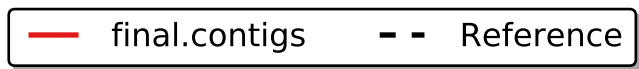
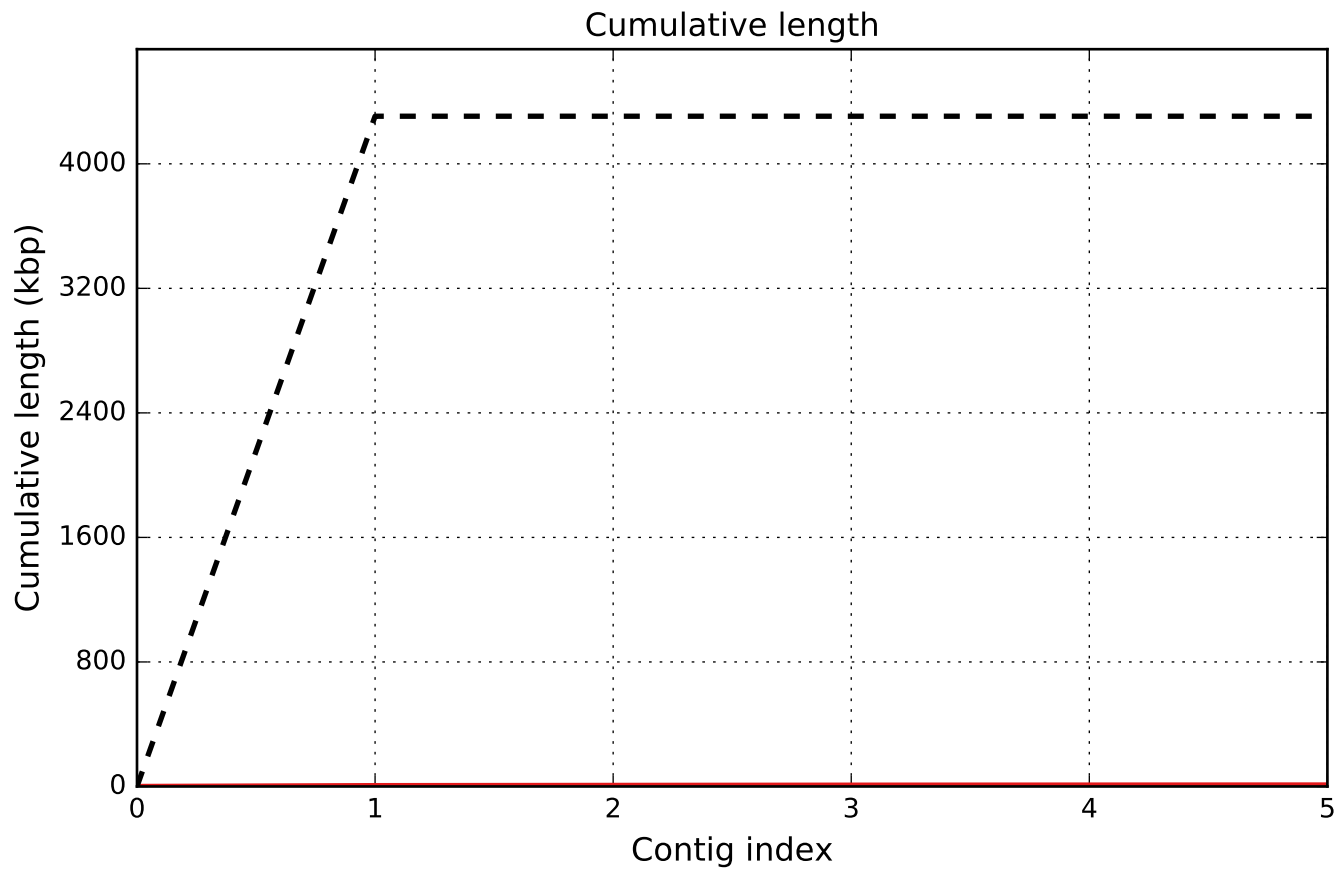


— final.contigs

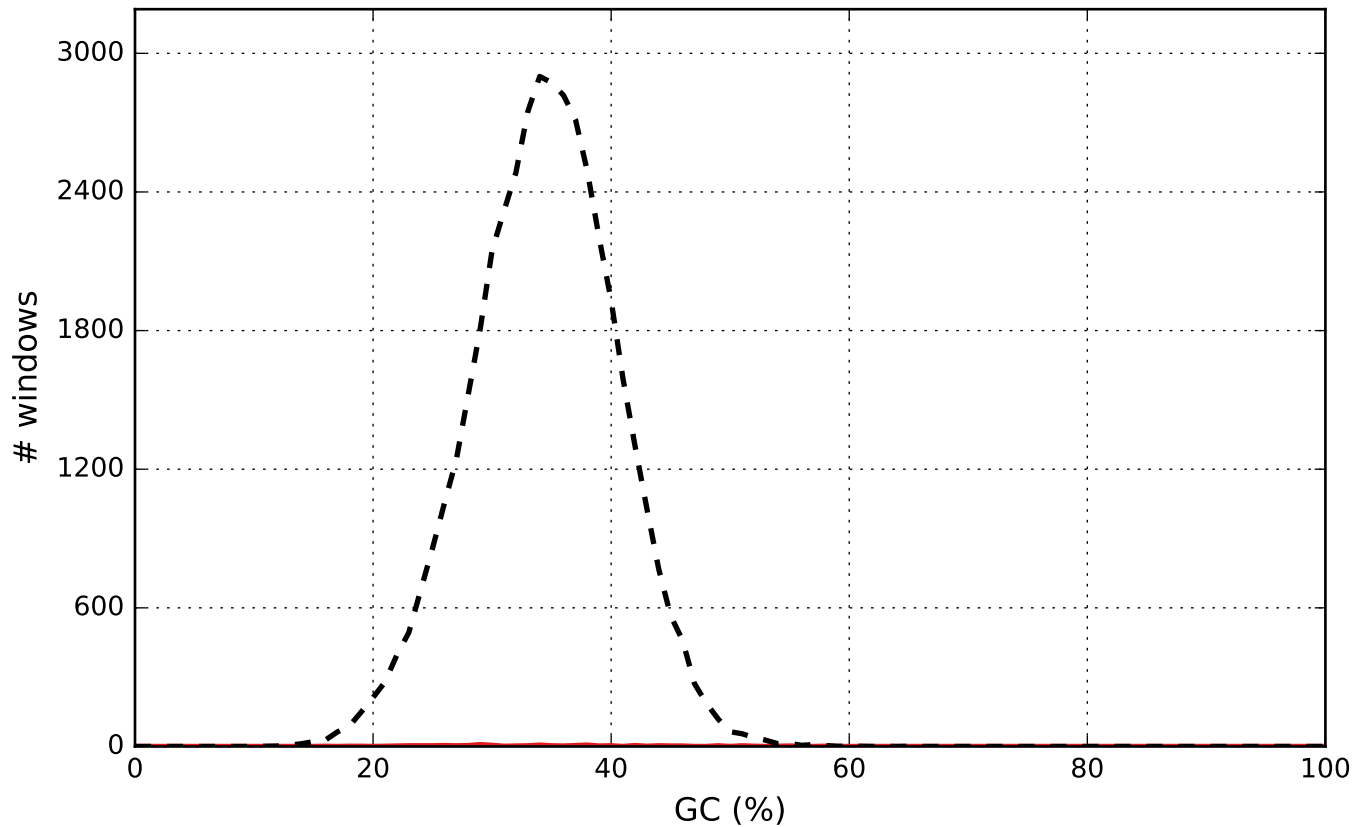
NGx



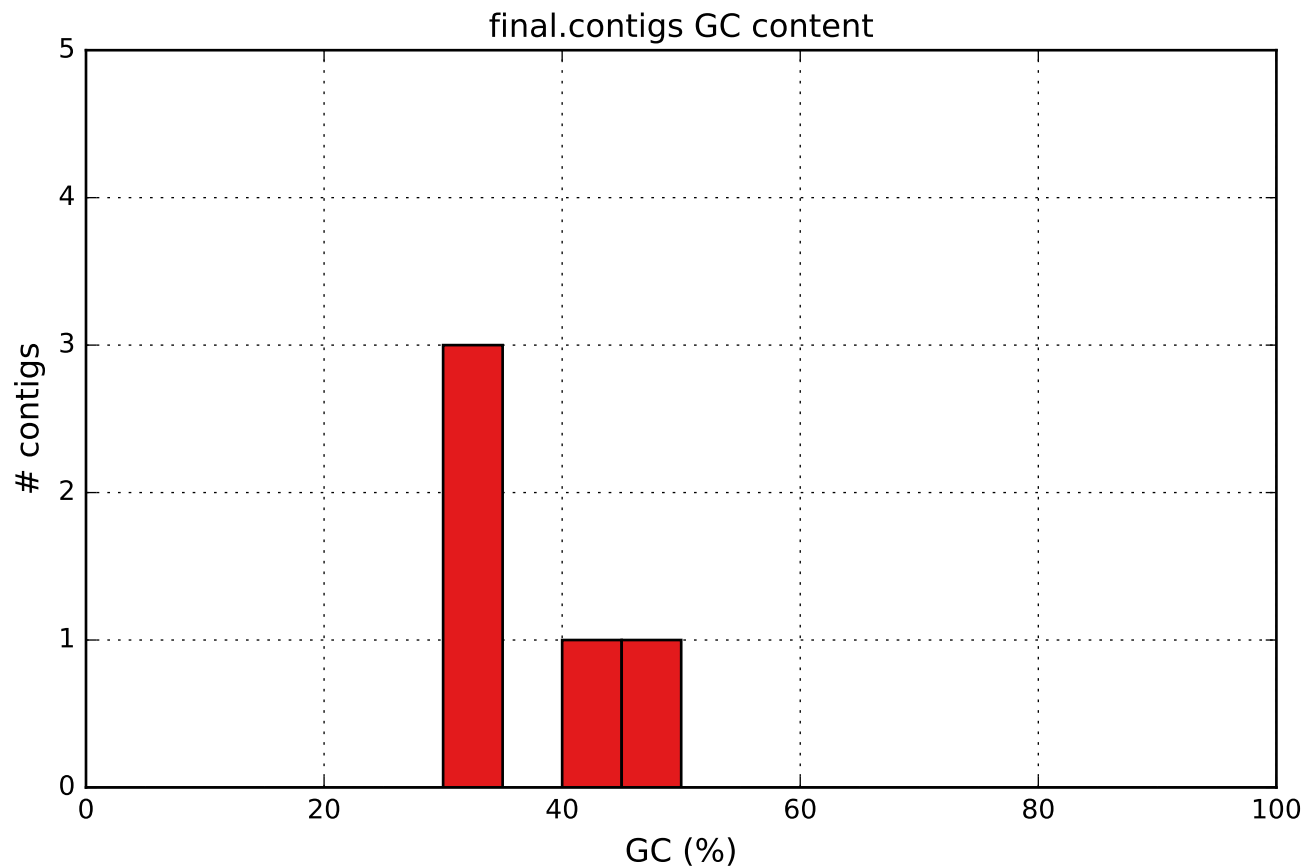
— final.contigs



GC content

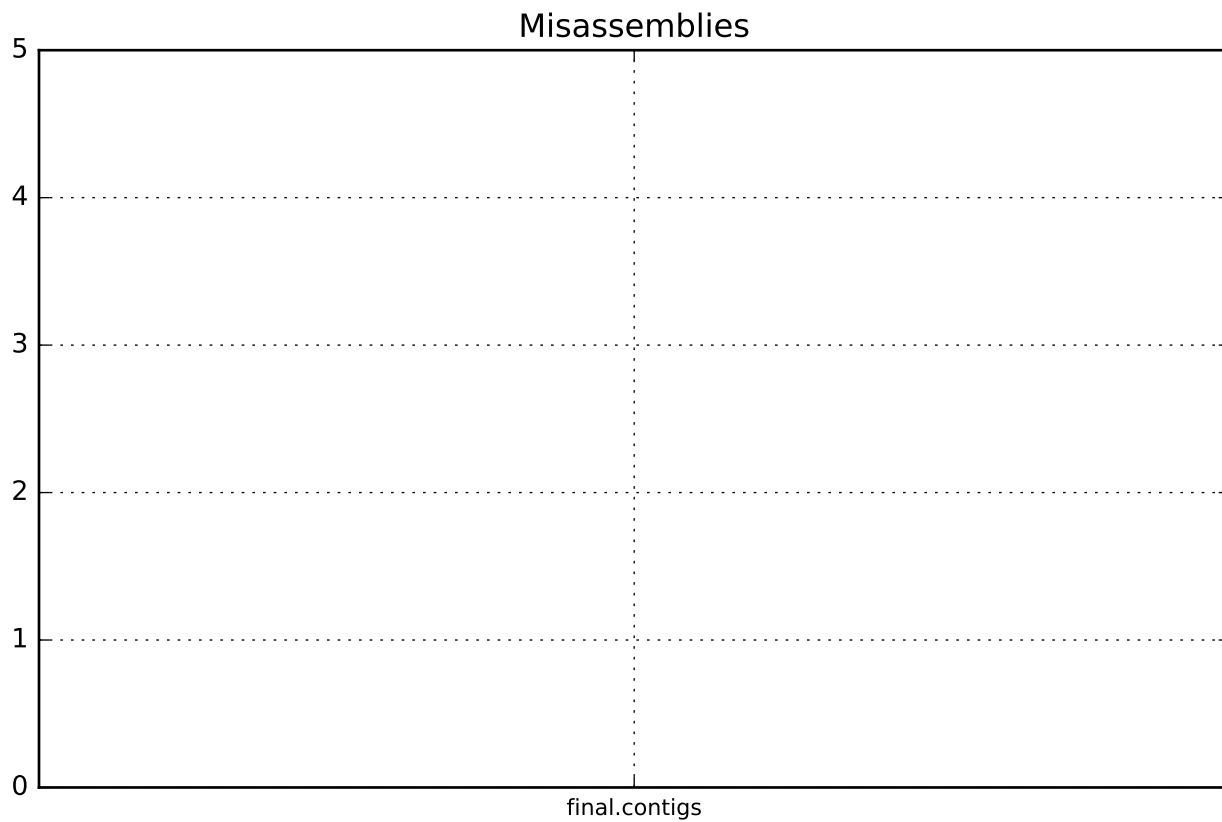


— final.contigs    - - Reference

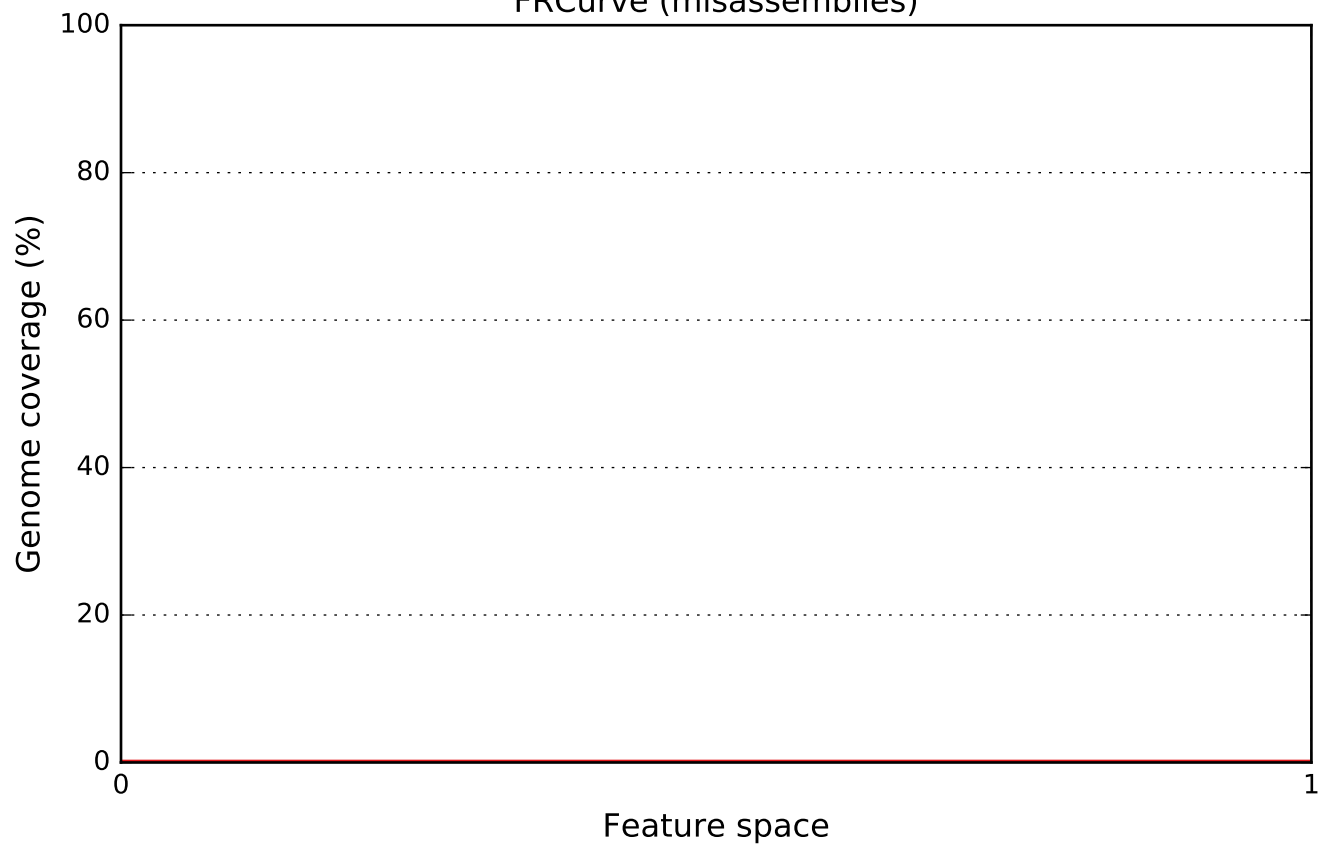


final.contigs



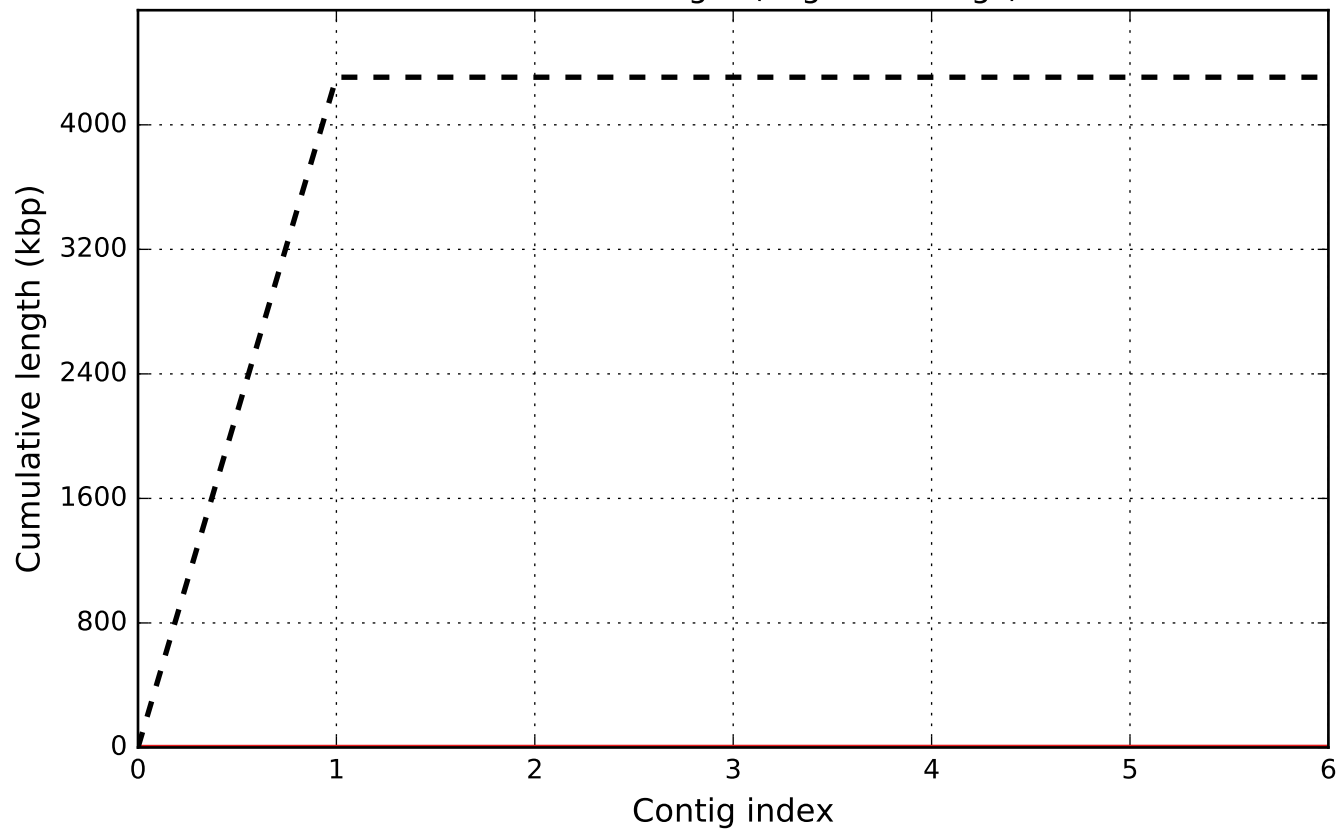


FRCurve (misassemblies)

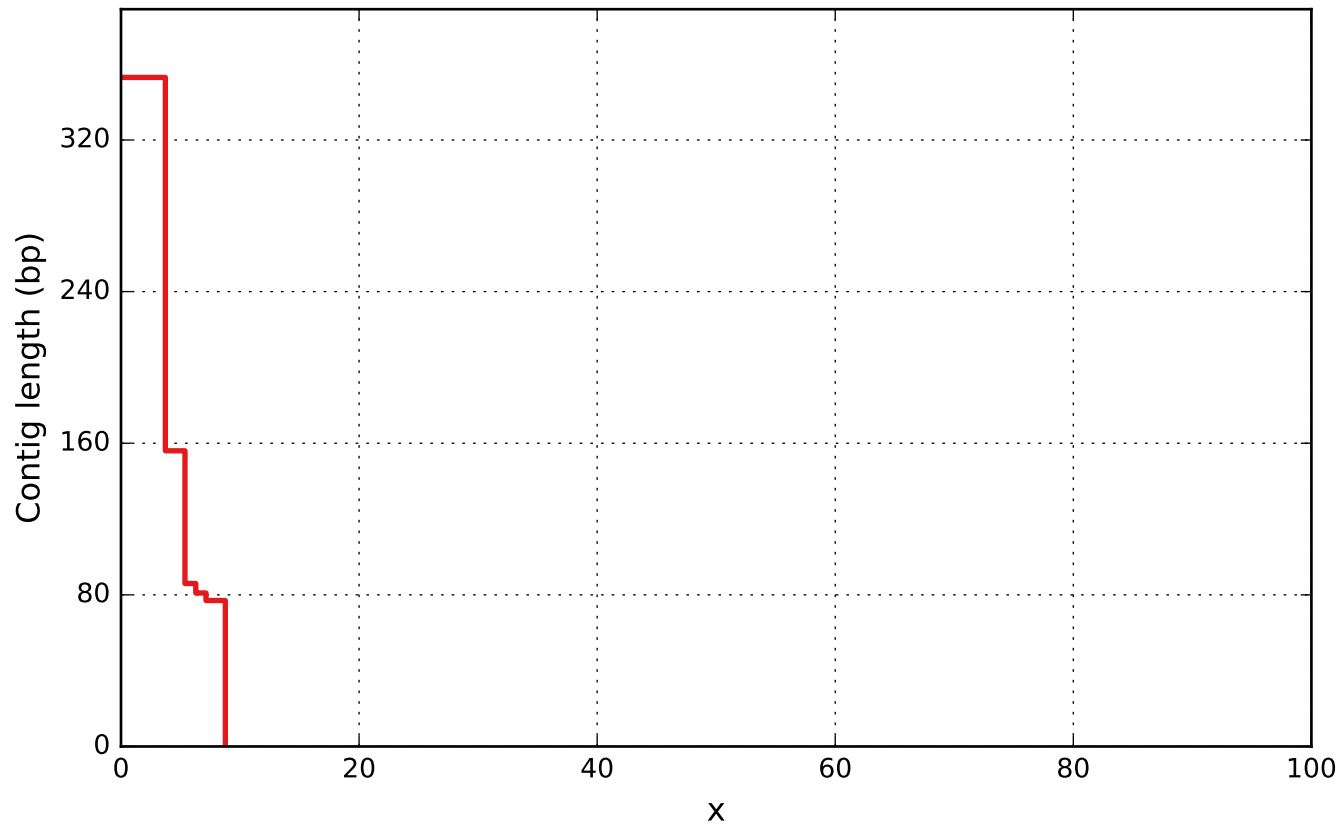


— final.contigs

Cumulative length (aligned contigs)

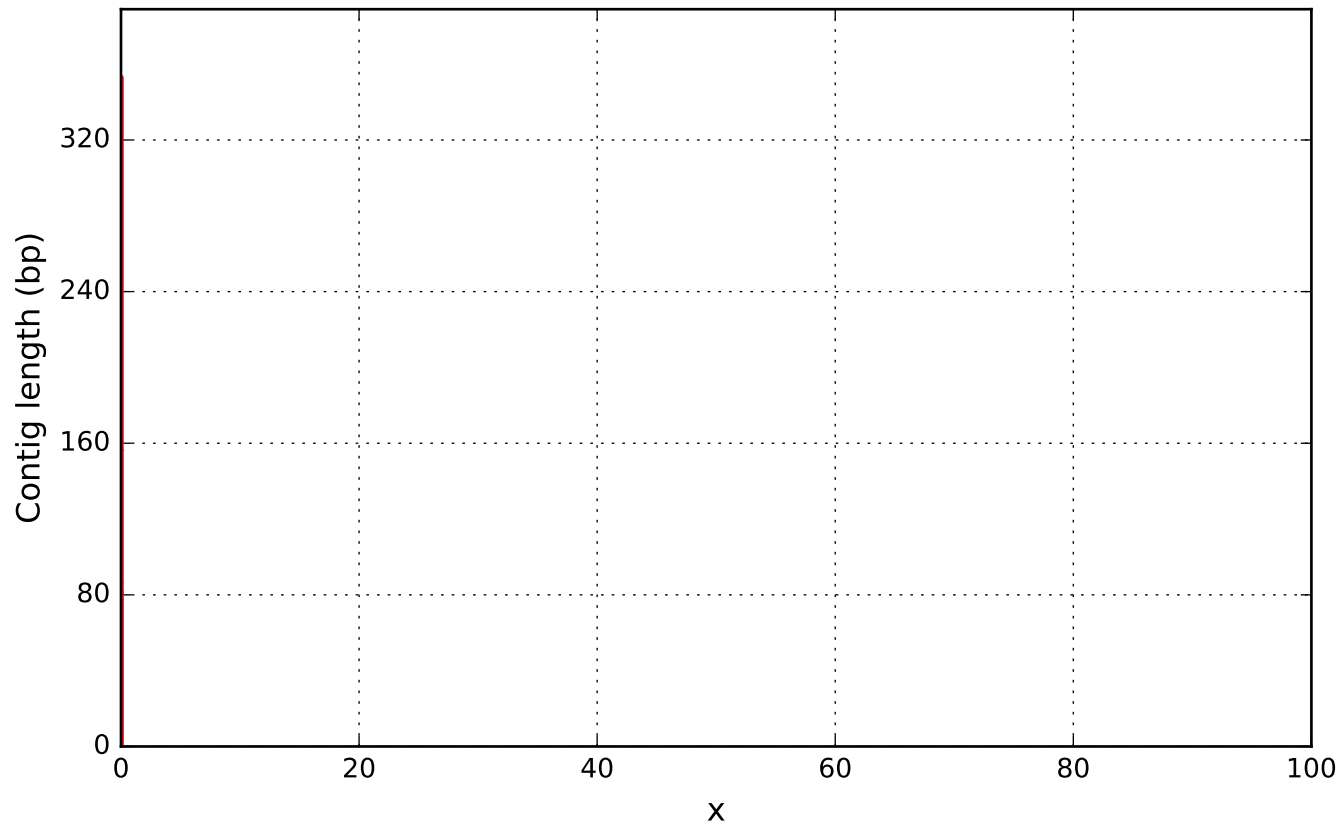


NAx



— final.contigs

NGAx



— final.contigs