

# Report

	final.contigs
# contigs ( $\geq 1000$ bp)	5
# contigs ( $\geq 5000$ bp)	1
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 1000$ bp)	11545
Total length ( $\geq 5000$ bp)	5333
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	16
Largest contig	5333
Total length	19435
Reference length	3576081
GC (%)	56.92
Reference GC (%)	51.82
N50	1231
N75	805
L50	4
L75	9
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 11 part
Unaligned length	15474
Genome fraction (%)	0.038
Duplication ratio	2.941
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1855.98
# indels per 100 kbp	222.72
Largest alignment	394
Total aligned length	1752
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

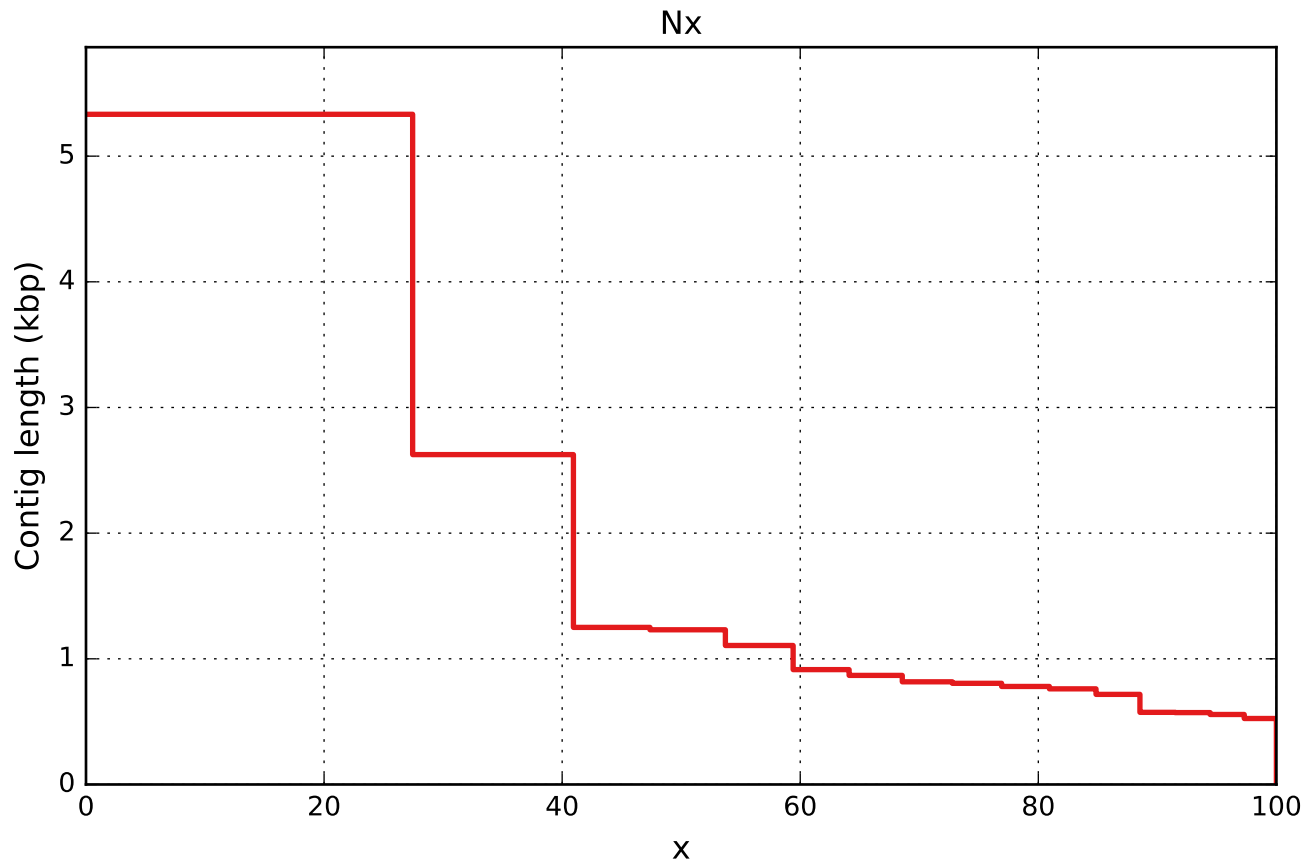
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	25
# indels	3
# indels (<= 5 bp)	3
# indels (> 5 bp)	0
Indels length	3

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## Unaligned report

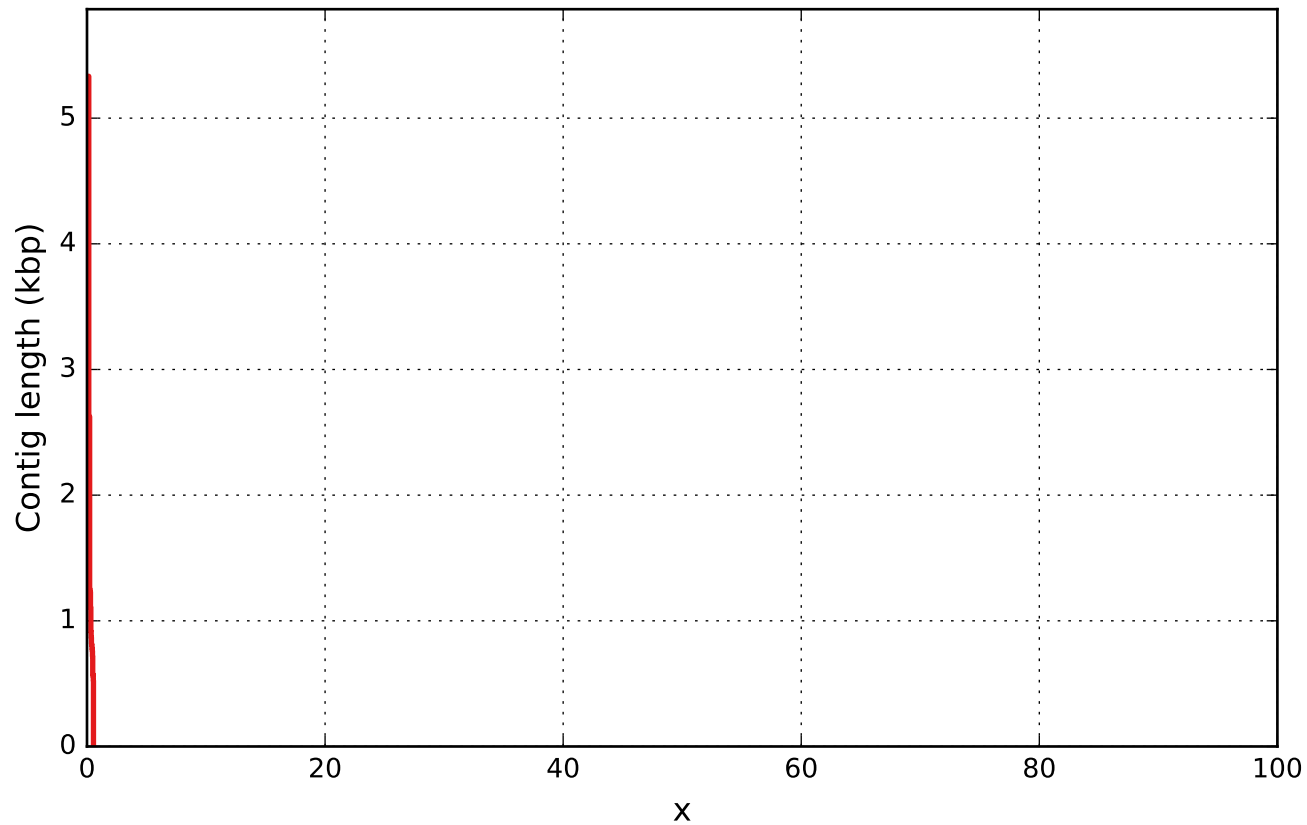
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	11
Partially unaligned length	15474
# N's	0

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).

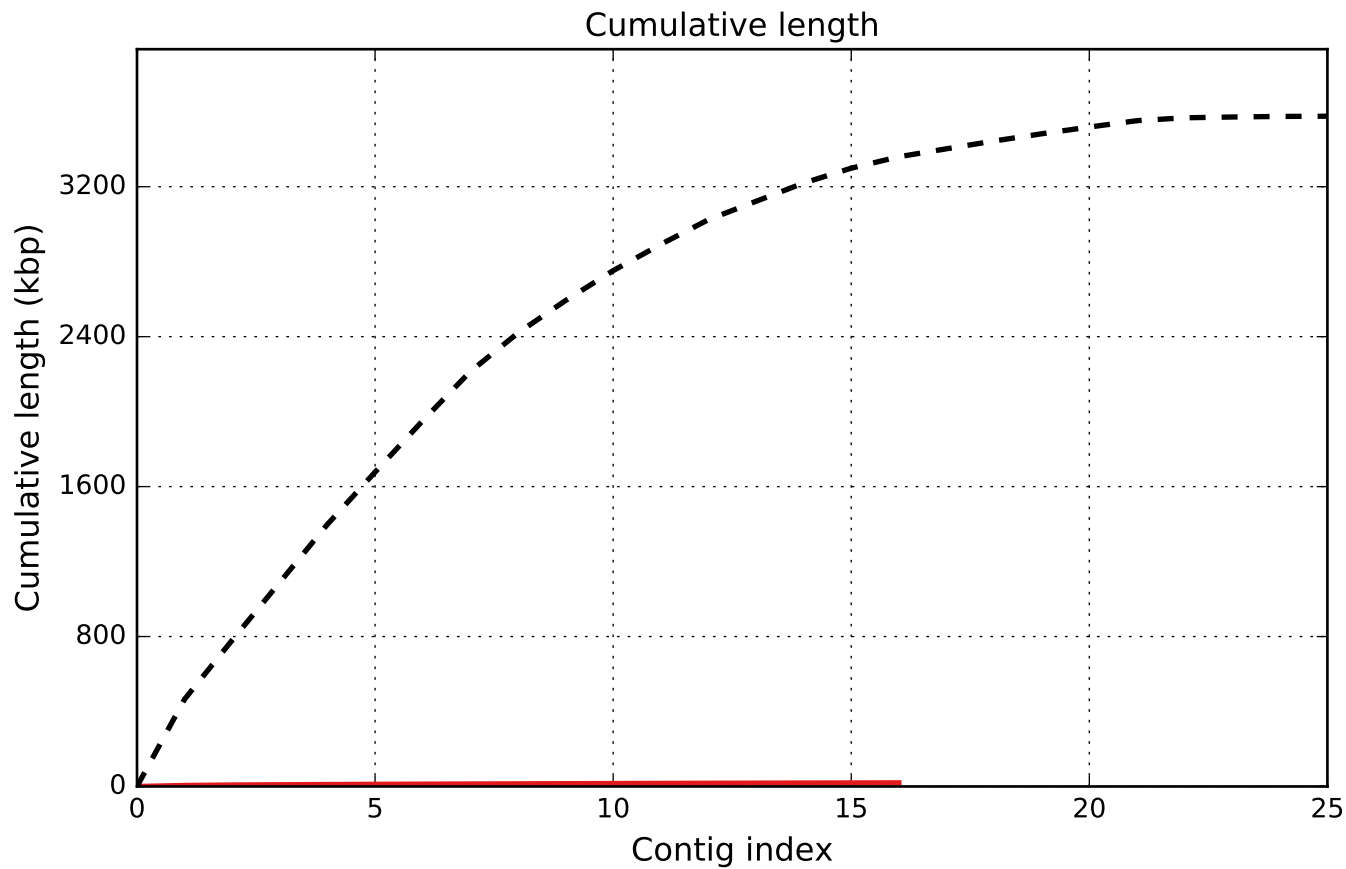


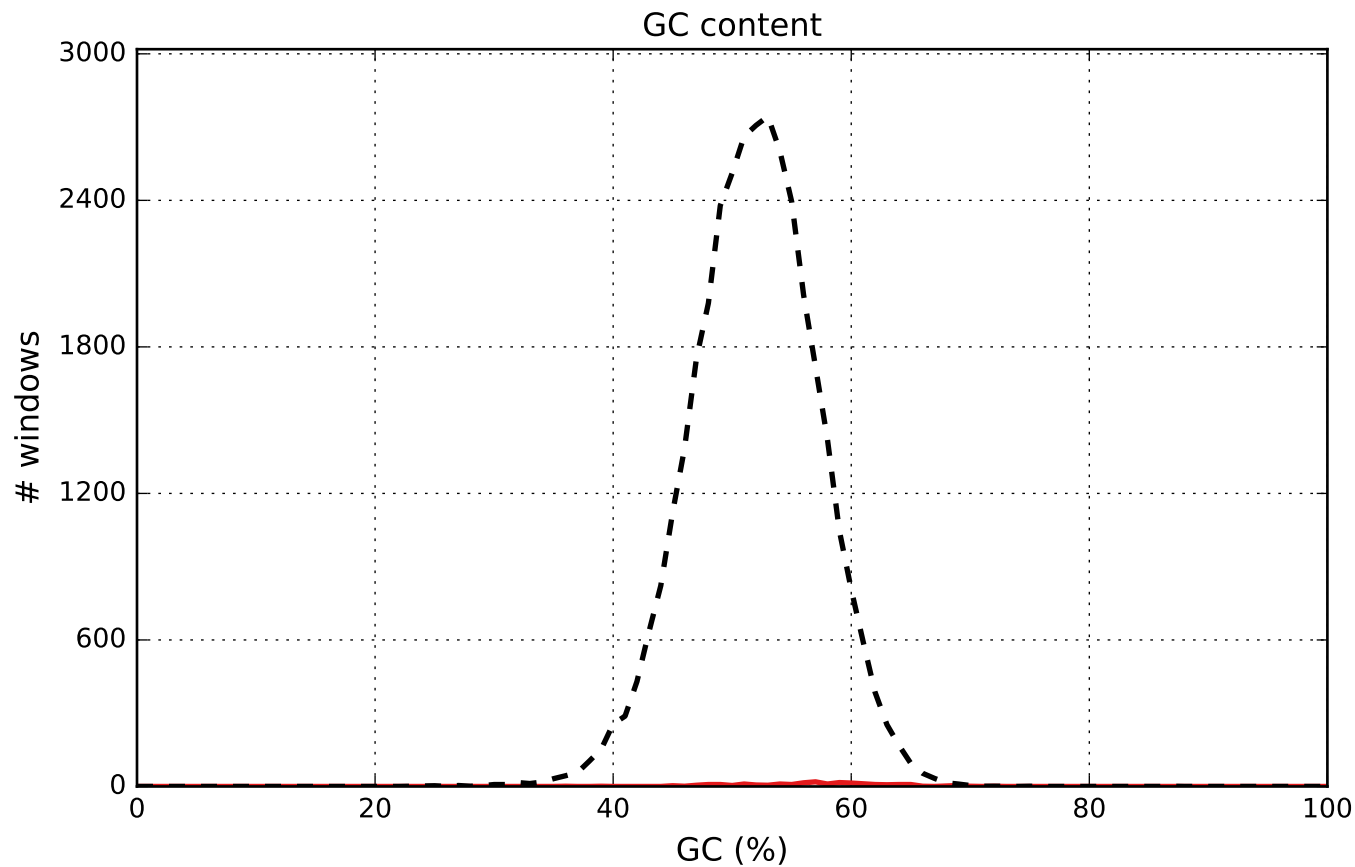
— final.contigs

NGx

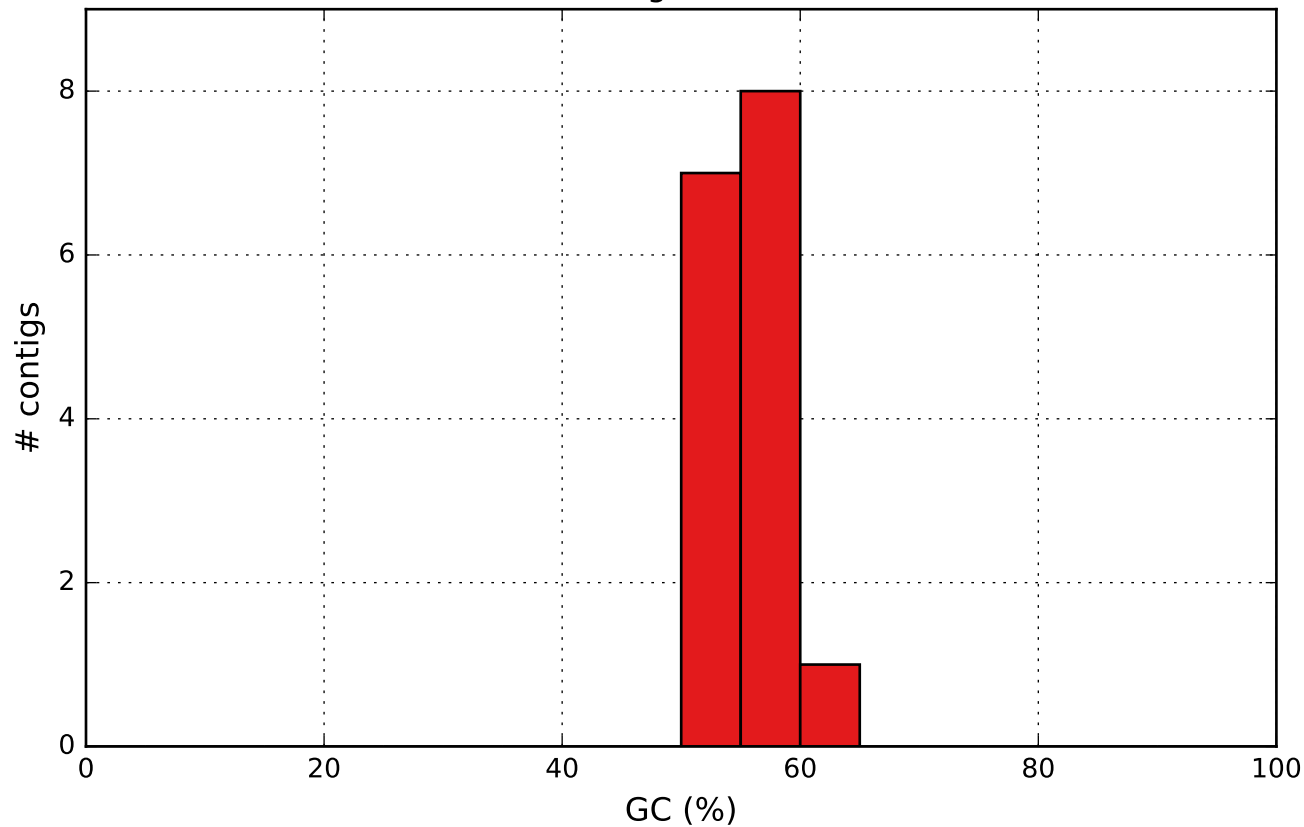


— final.contigs



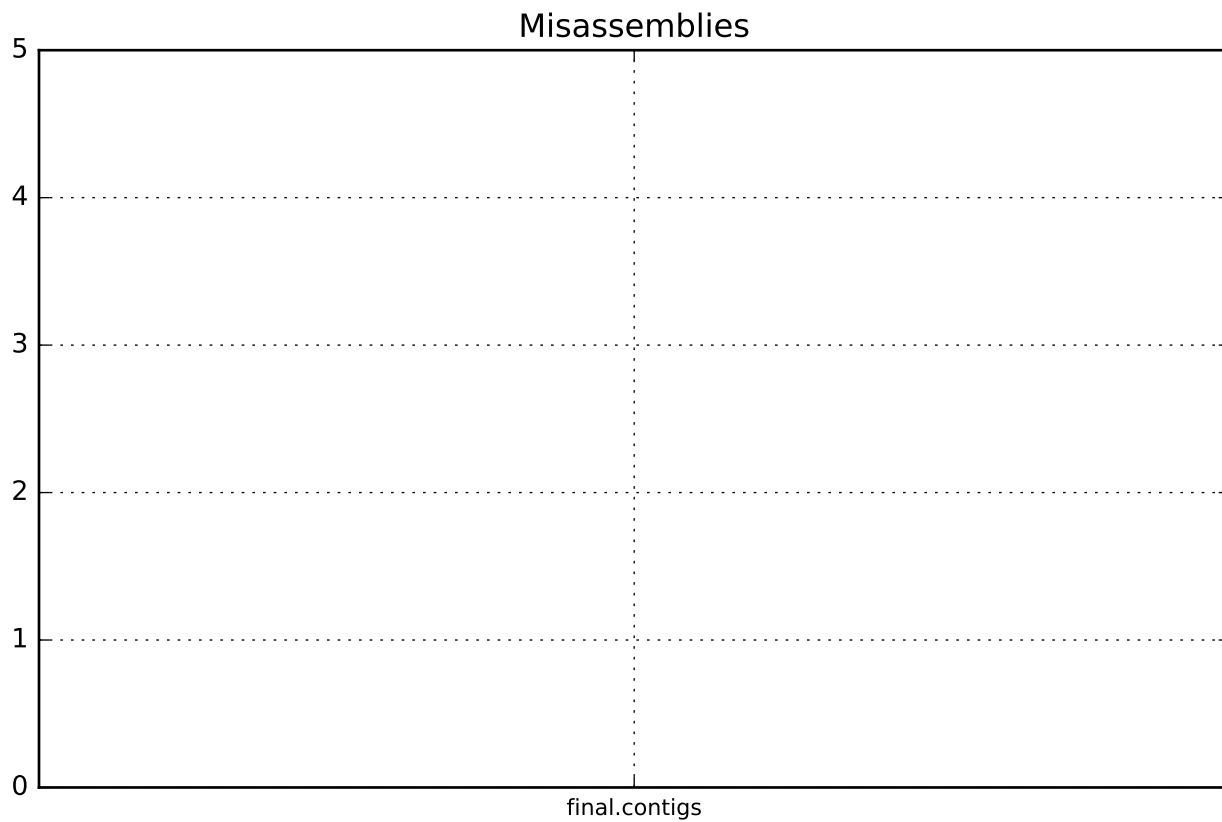


final.contigs GC content

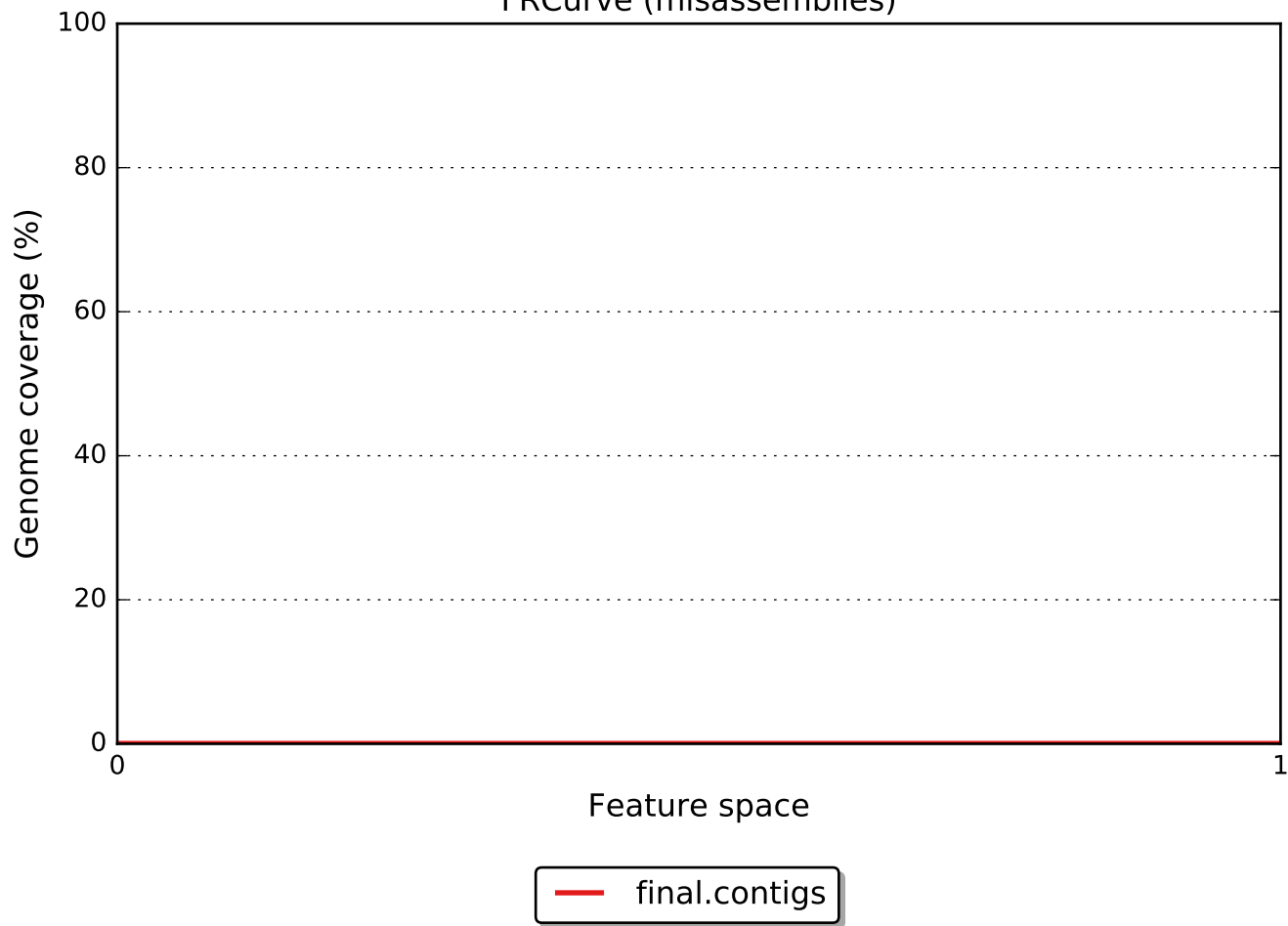


final.contigs

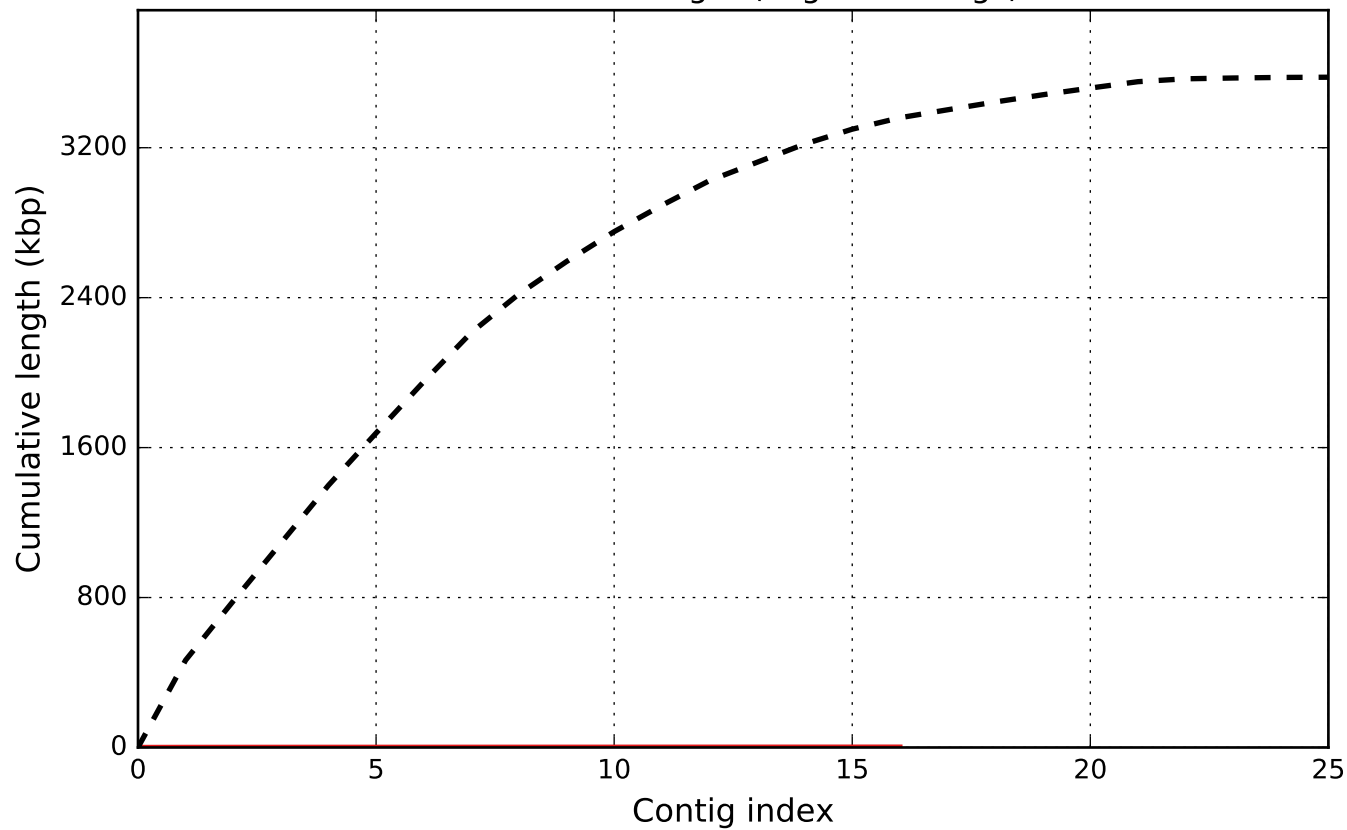




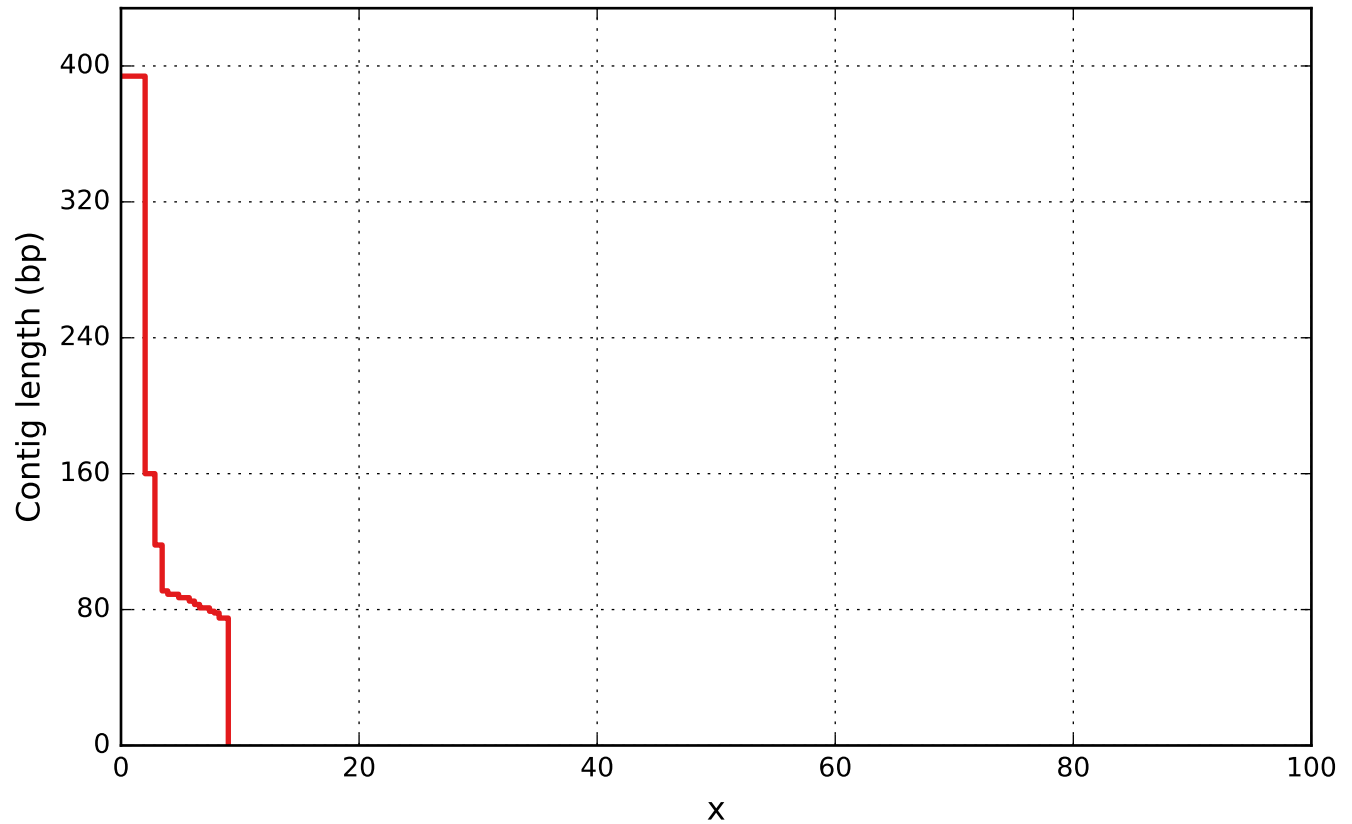
FRCurve (misassemblies)



Cumulative length (aligned contigs)

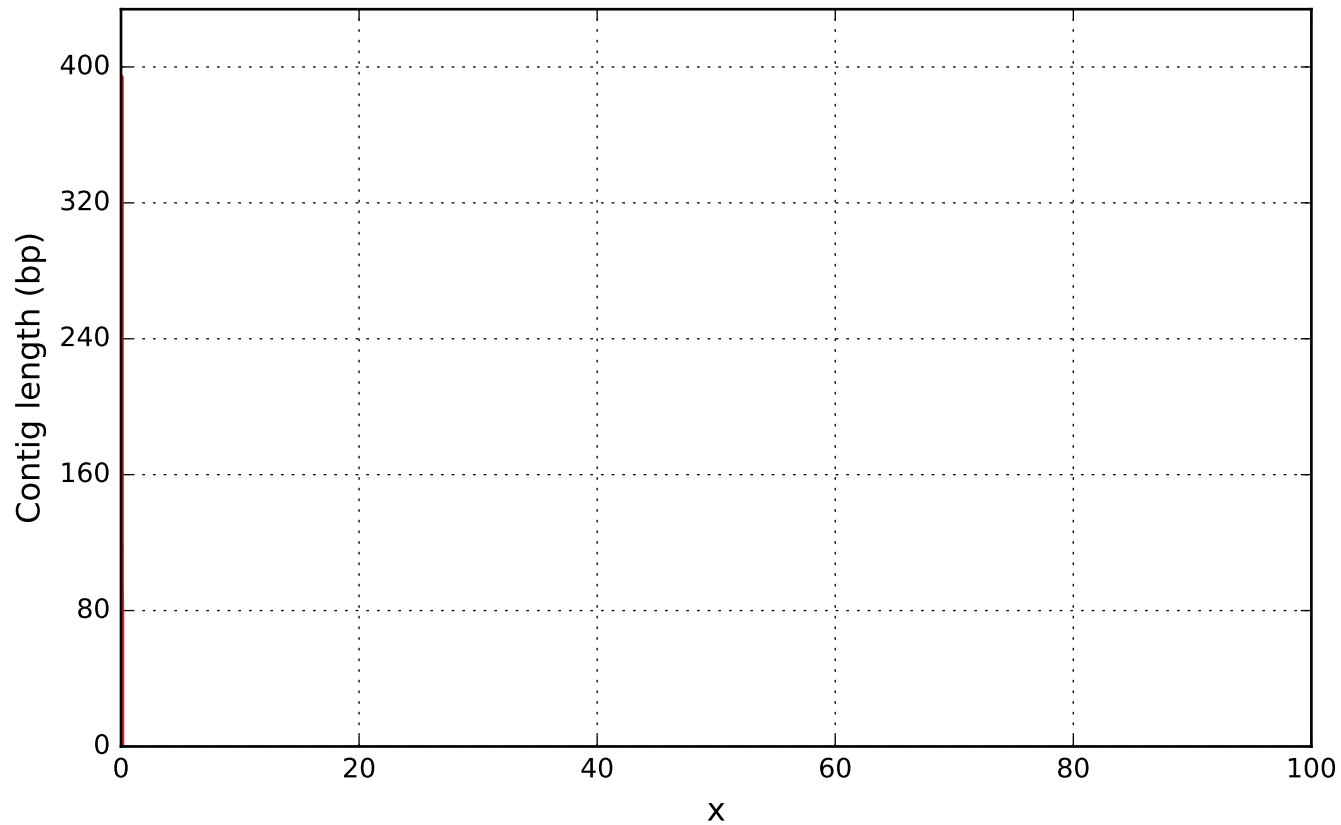


NAx



— final.contigs

NGAx



— final.contigs