

Report

	final.contigs
# contigs (>= 1000 bp)	8
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	18534
Total length (>= 5000 bp)	6389
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	26
Largest contig	6389
Total length	31115
Reference length	3261541
GC (%)	51.58
Reference GC (%)	56.74
N50	1071
N75	774
L50	6
L75	14
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	1
# unaligned contigs	0 + 13 part
Unaligned length	21581
Genome fraction (%)	0.078
Duplication ratio	3.755
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2520.68
# indels per 100 kbp	118.16
Largest alignment	538
Total aligned length	3250
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

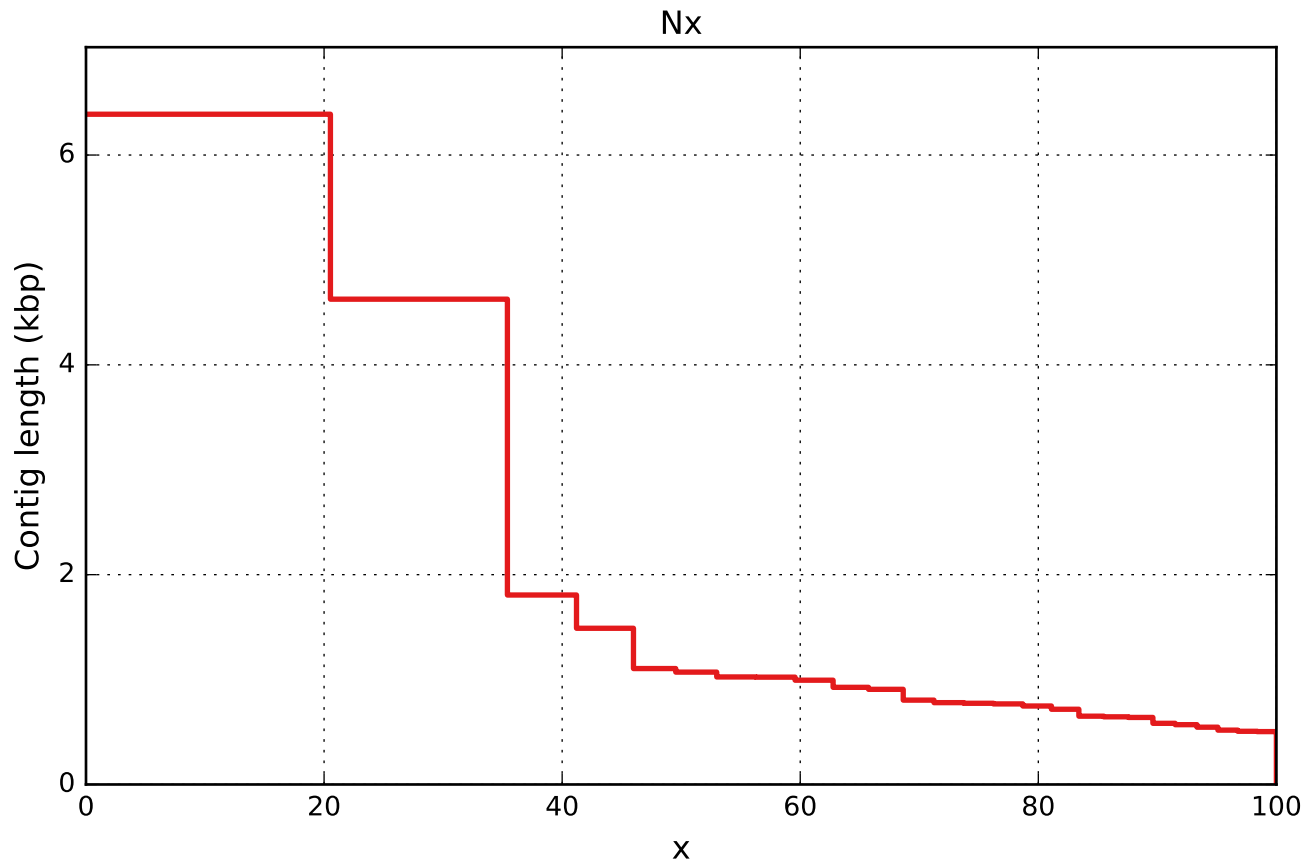
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	1
# mismatches	64
# indels	3
# indels (<= 5 bp)	3
# indels (> 5 bp)	0
Indels length	3

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).

Unaligned report

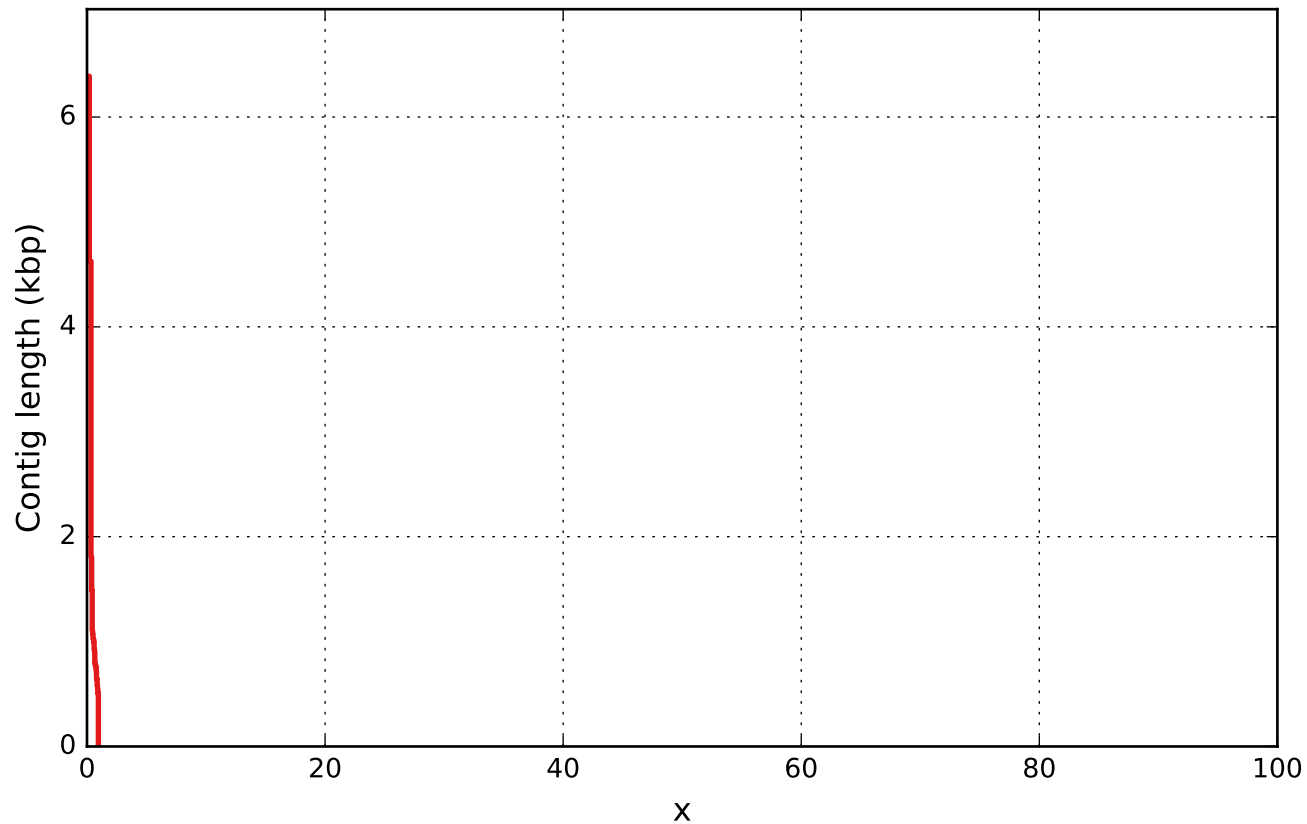
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	13
Partially unaligned length	21581
# N's	0

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).

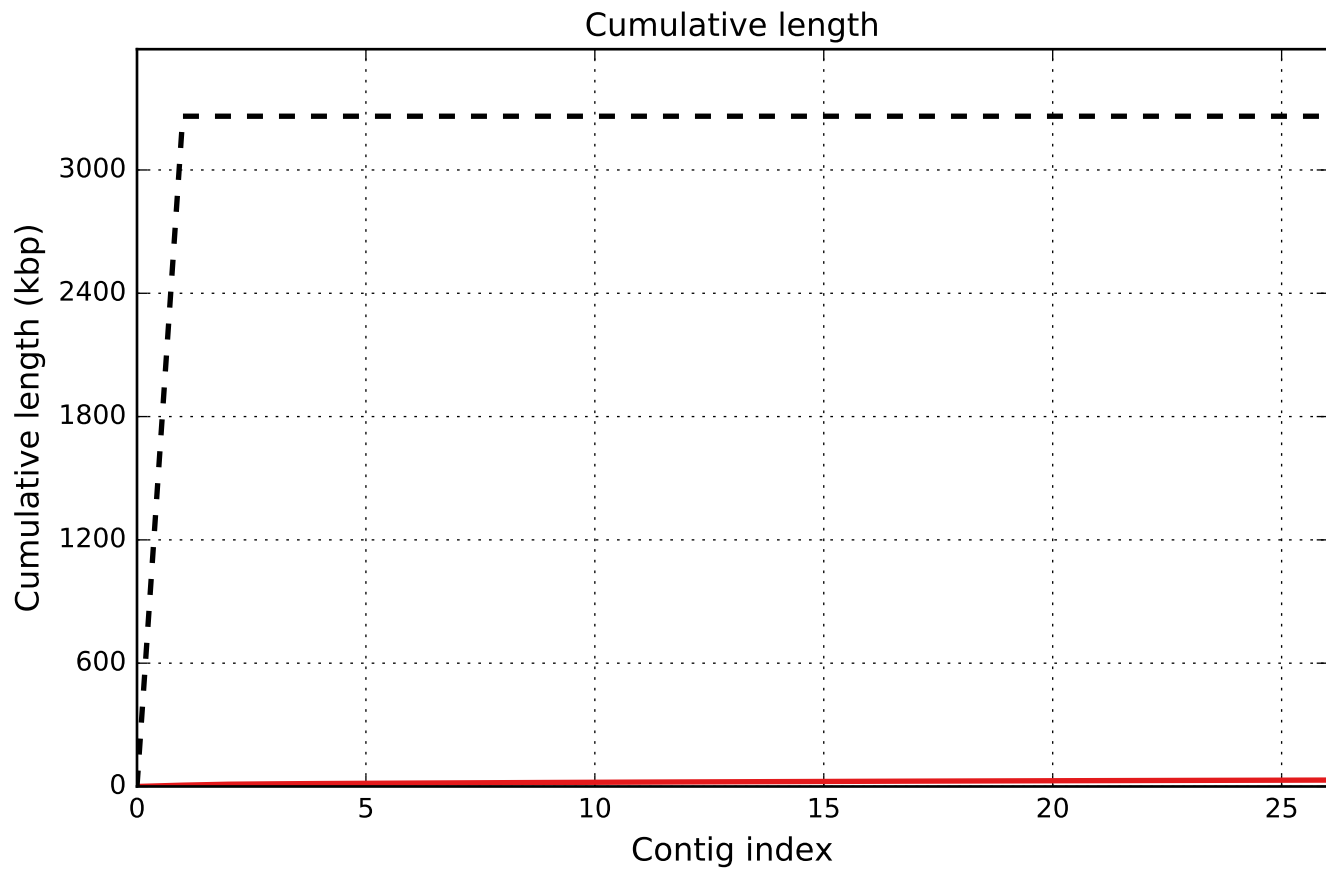


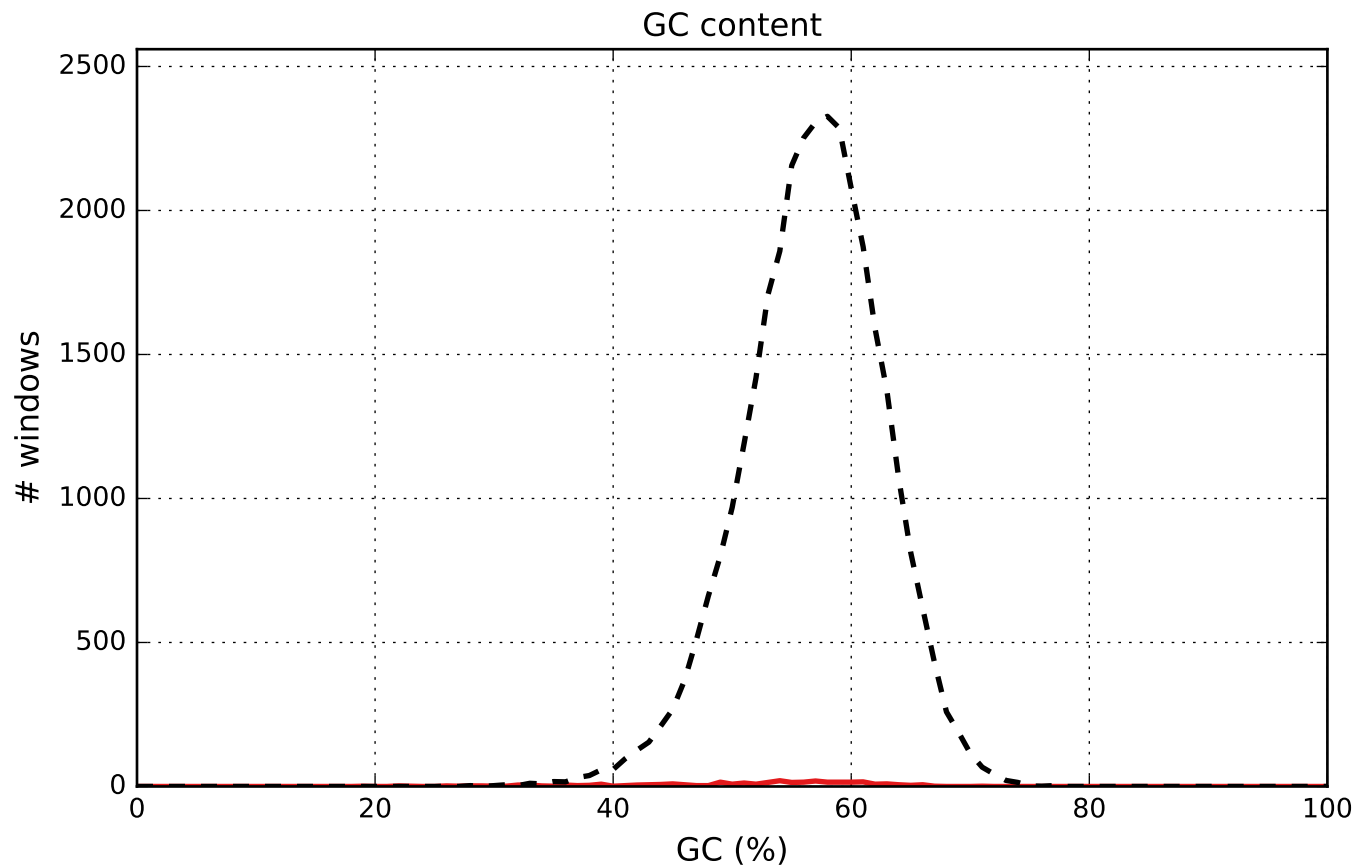
— final.contigs

NGx

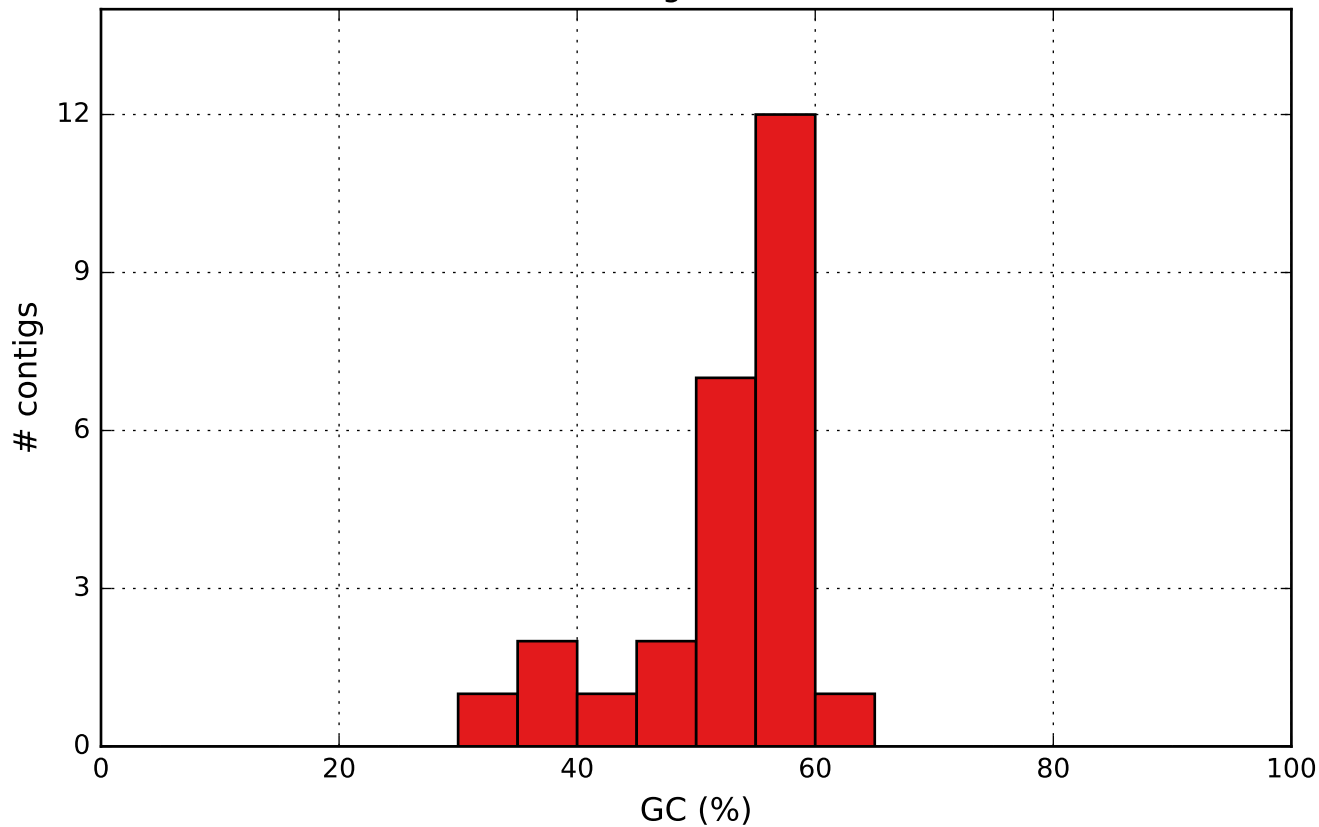


— final.contigs

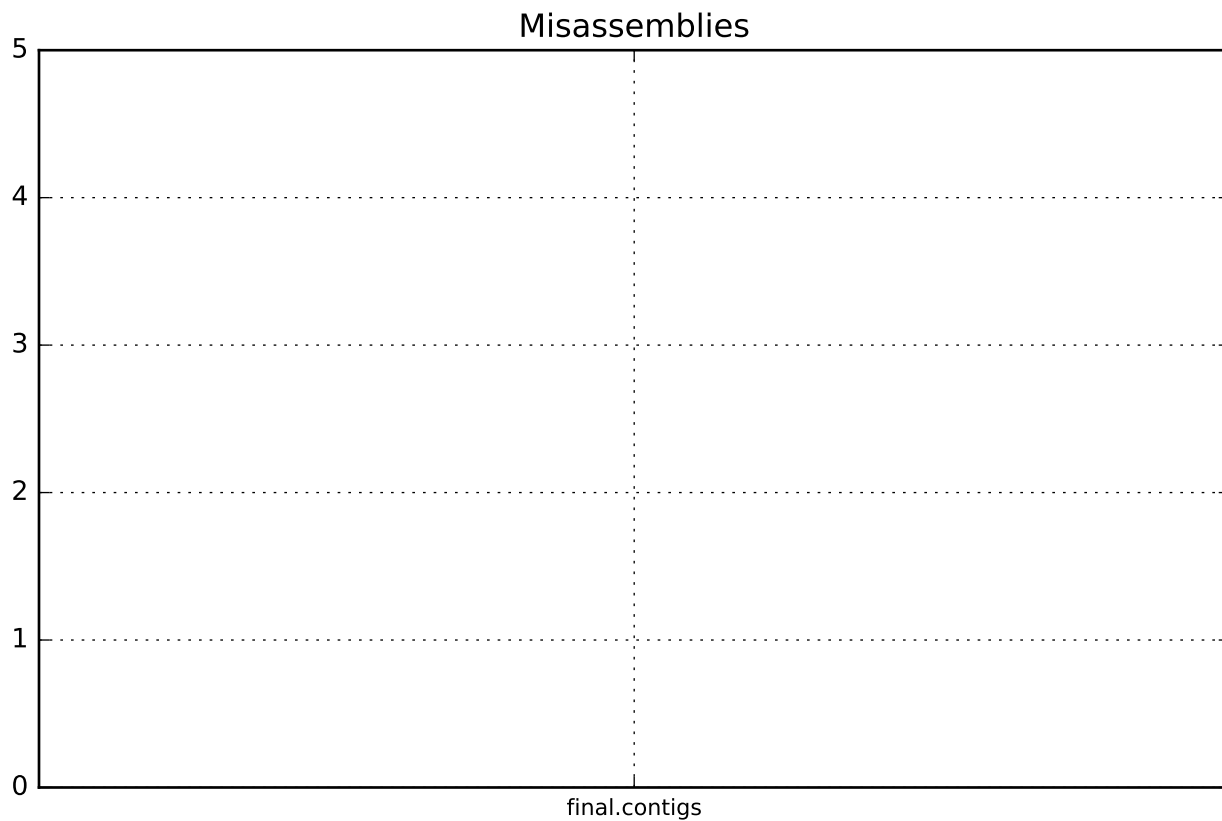




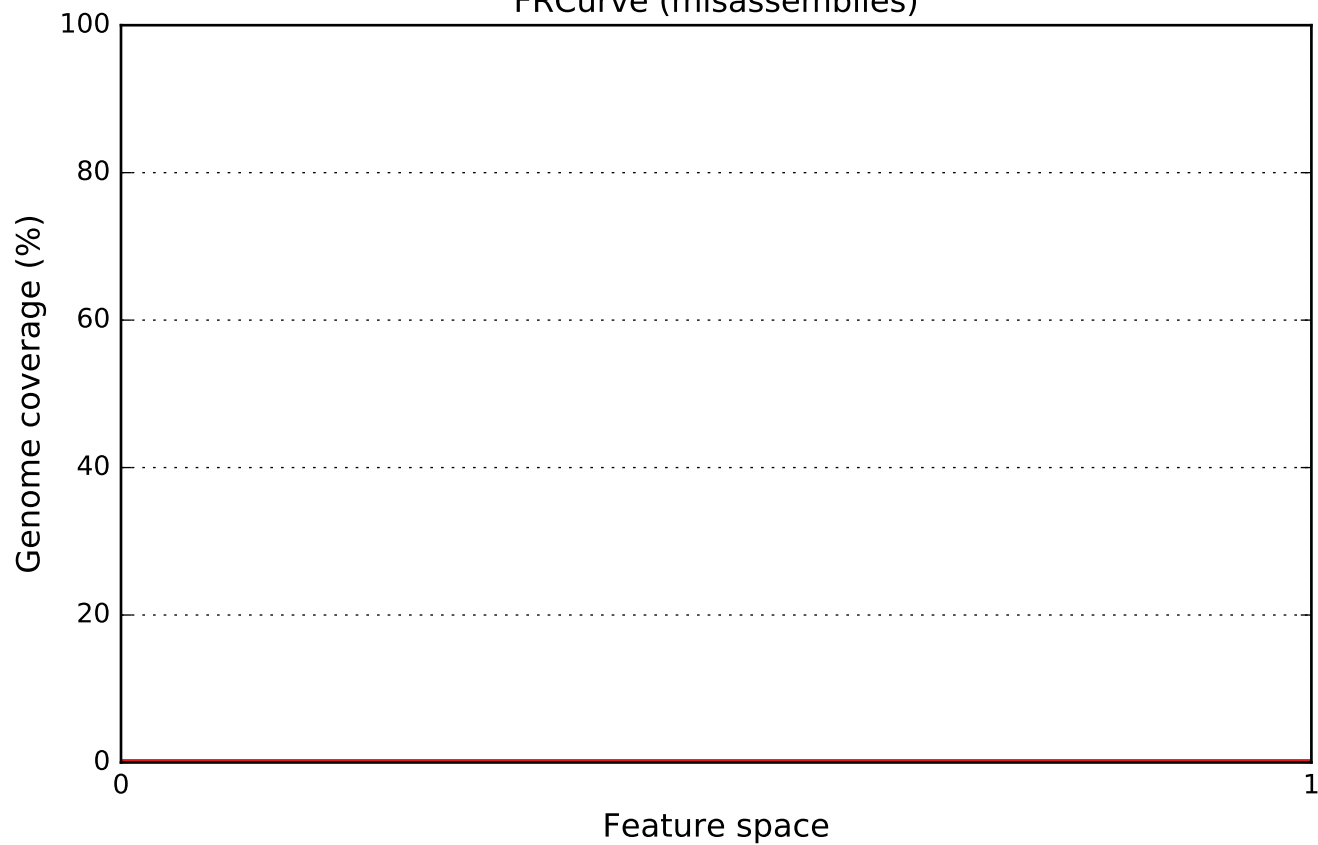
final.contigs GC content



final.contigs

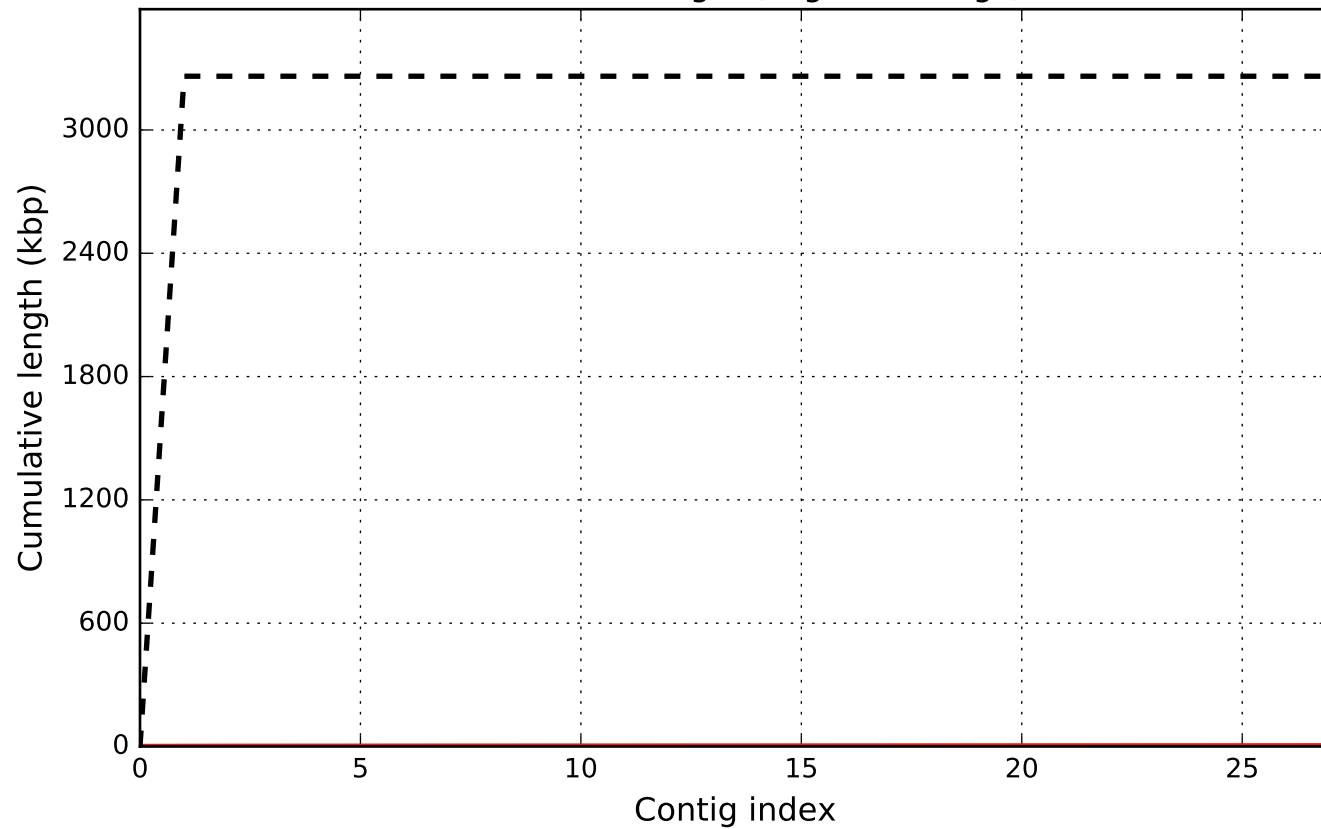


FRCurve (misassemblies)



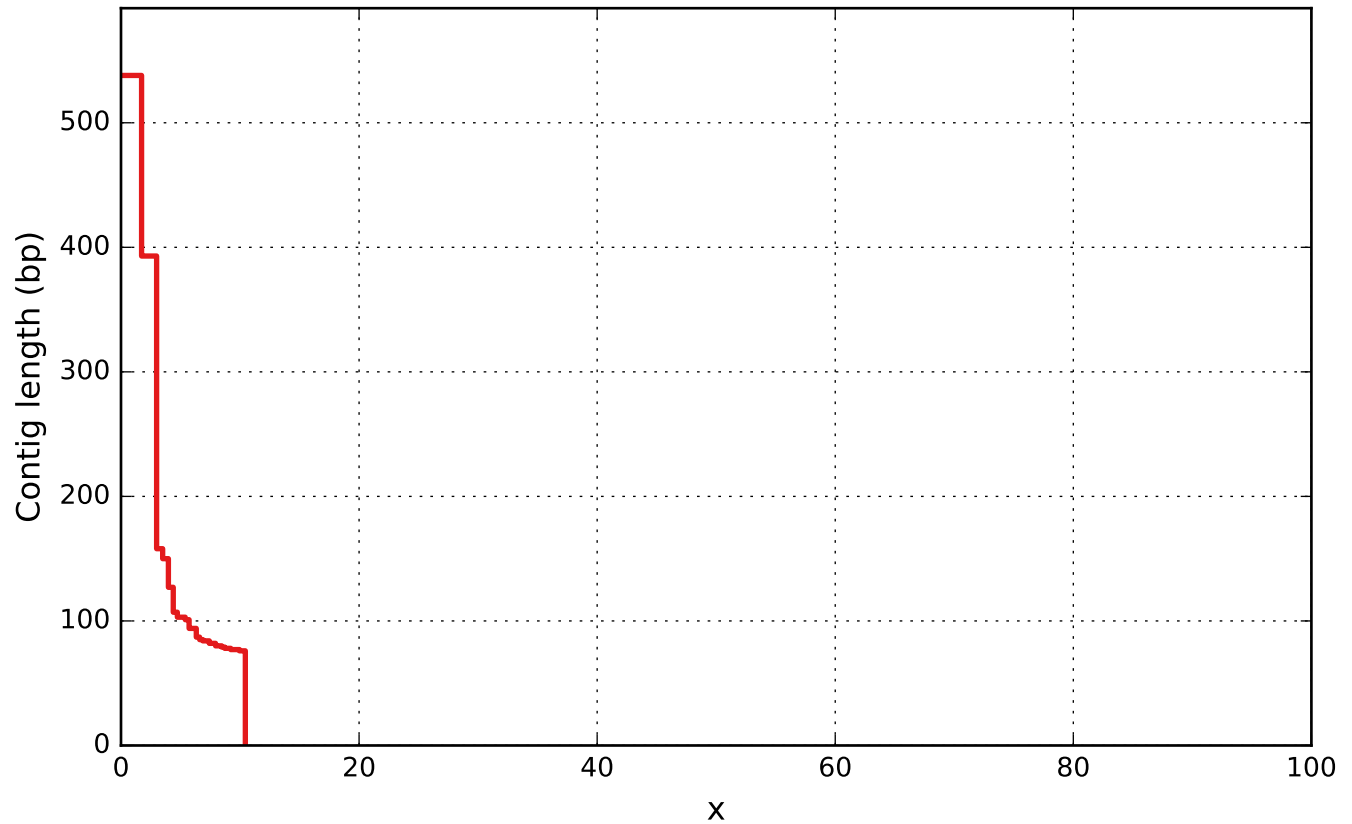
— final.contigs

Cumulative length (aligned contigs)



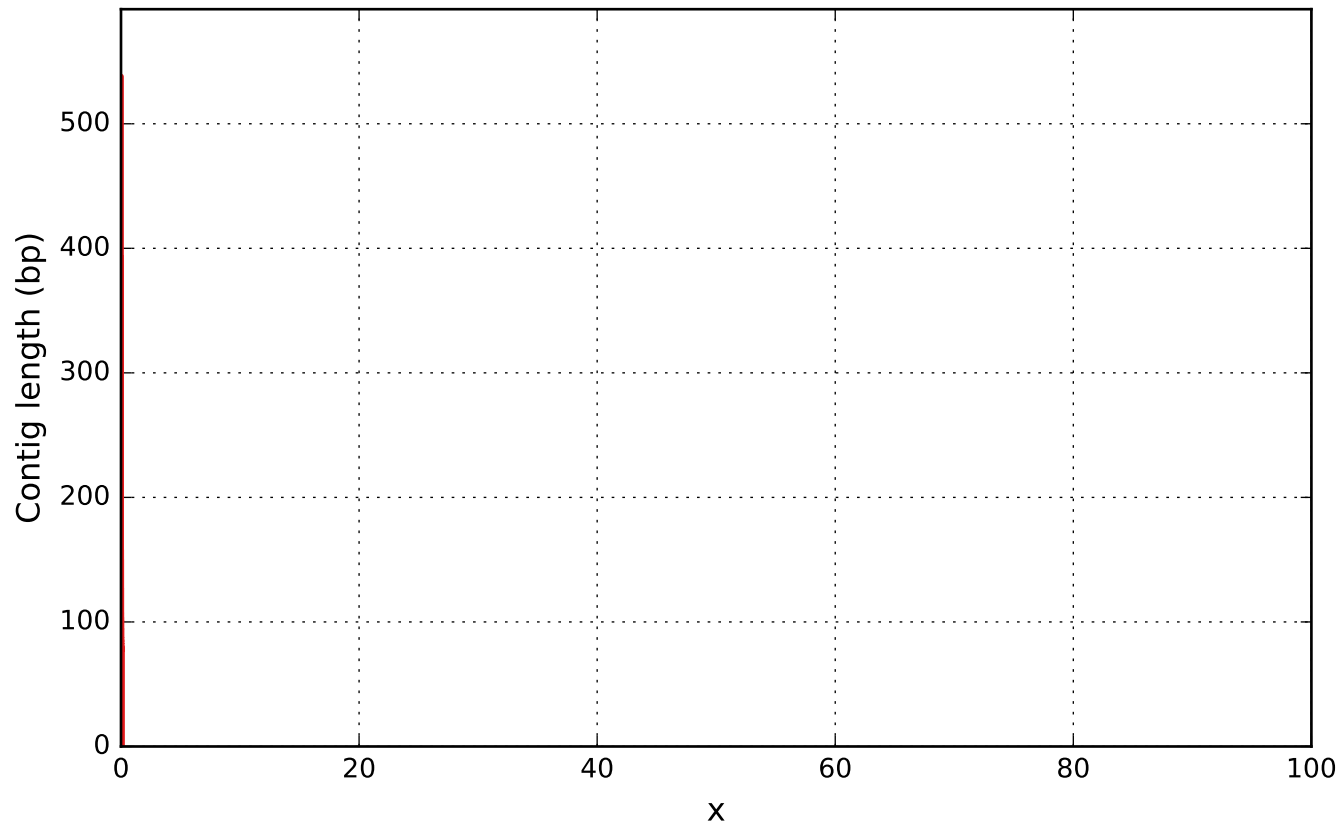
— final.contigs - - Reference

NAx



— final.contigs

NGAx



— final.contigs