

Report

	combined.final.contigs
# contigs (≥ 1000 bp)	6
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 1000 bp)	13777
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	13
Largest contig	3511
Total length	18367
Reference length	4053139
GC (%)	49.95
Reference GC (%)	70.41
N50	1835
N75	1566
L50	4
L75	6
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 8 part
Unaligned length	14868
Genome fraction (%)	0.025
Duplication ratio	3.434
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1472.03
# indels per 100 kbp	98.14
Largest alignment	259
Total aligned length	1265
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

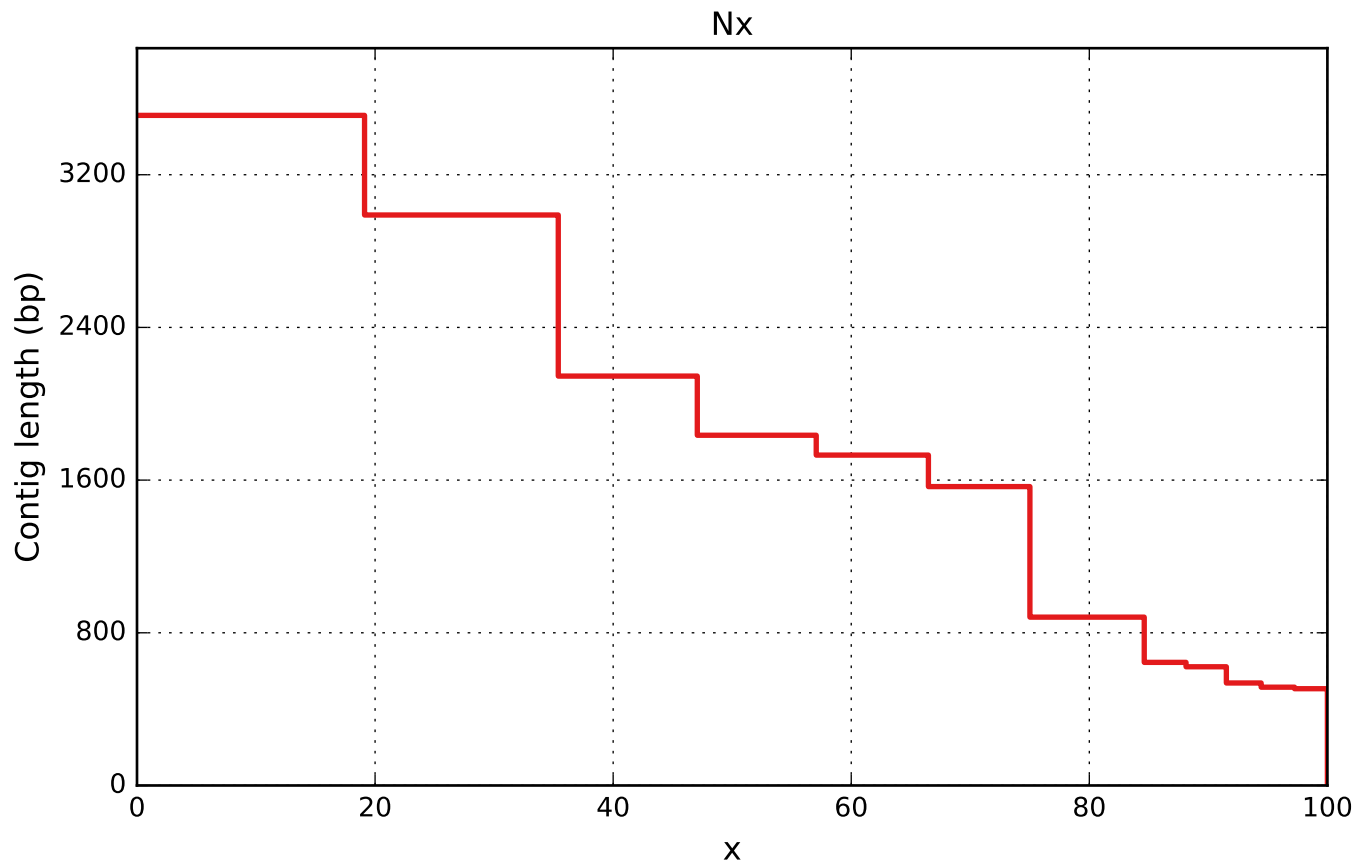
	combined.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	15
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	2

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).

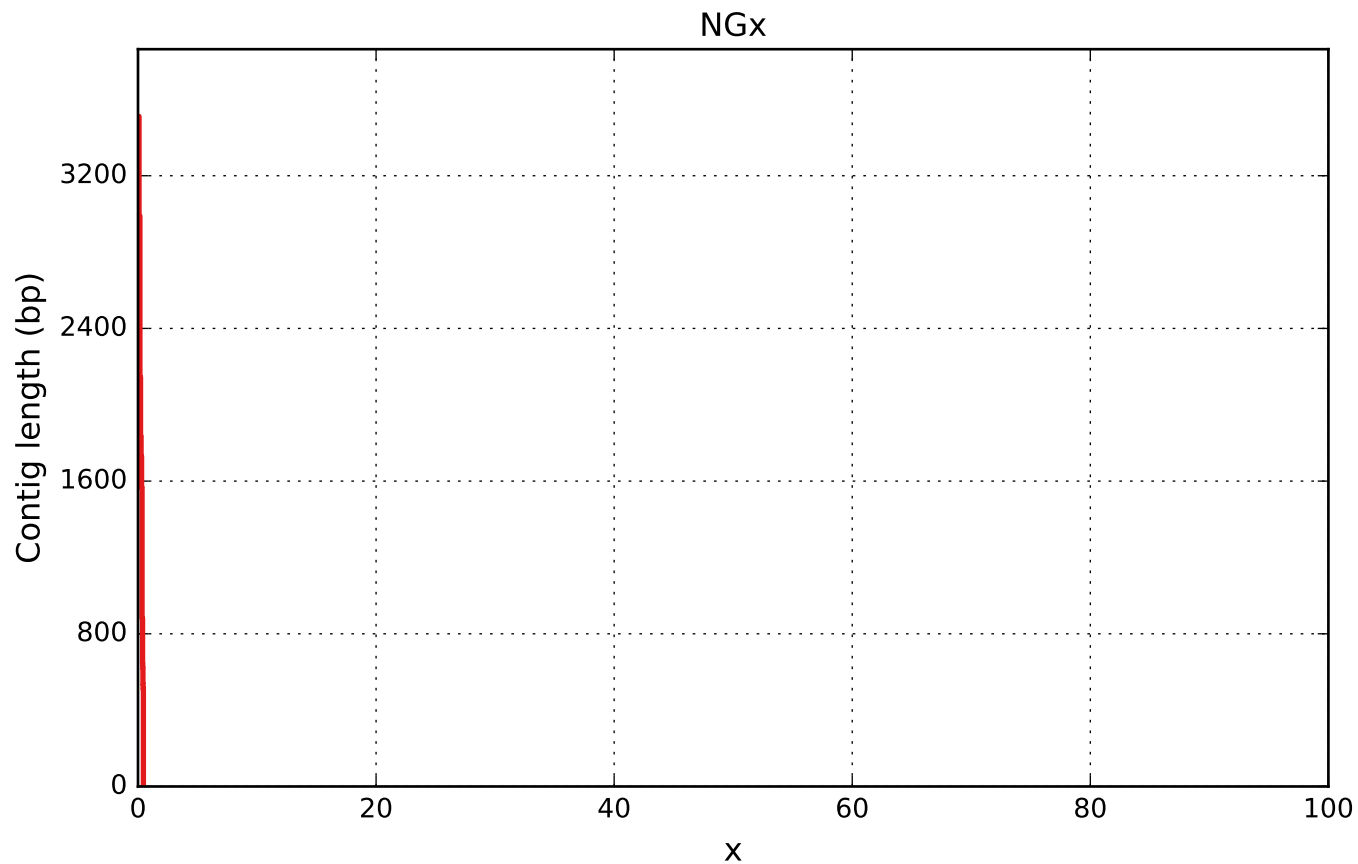
Unaligned report

	combined.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	8
Partially unaligned length	14868
# N's	0

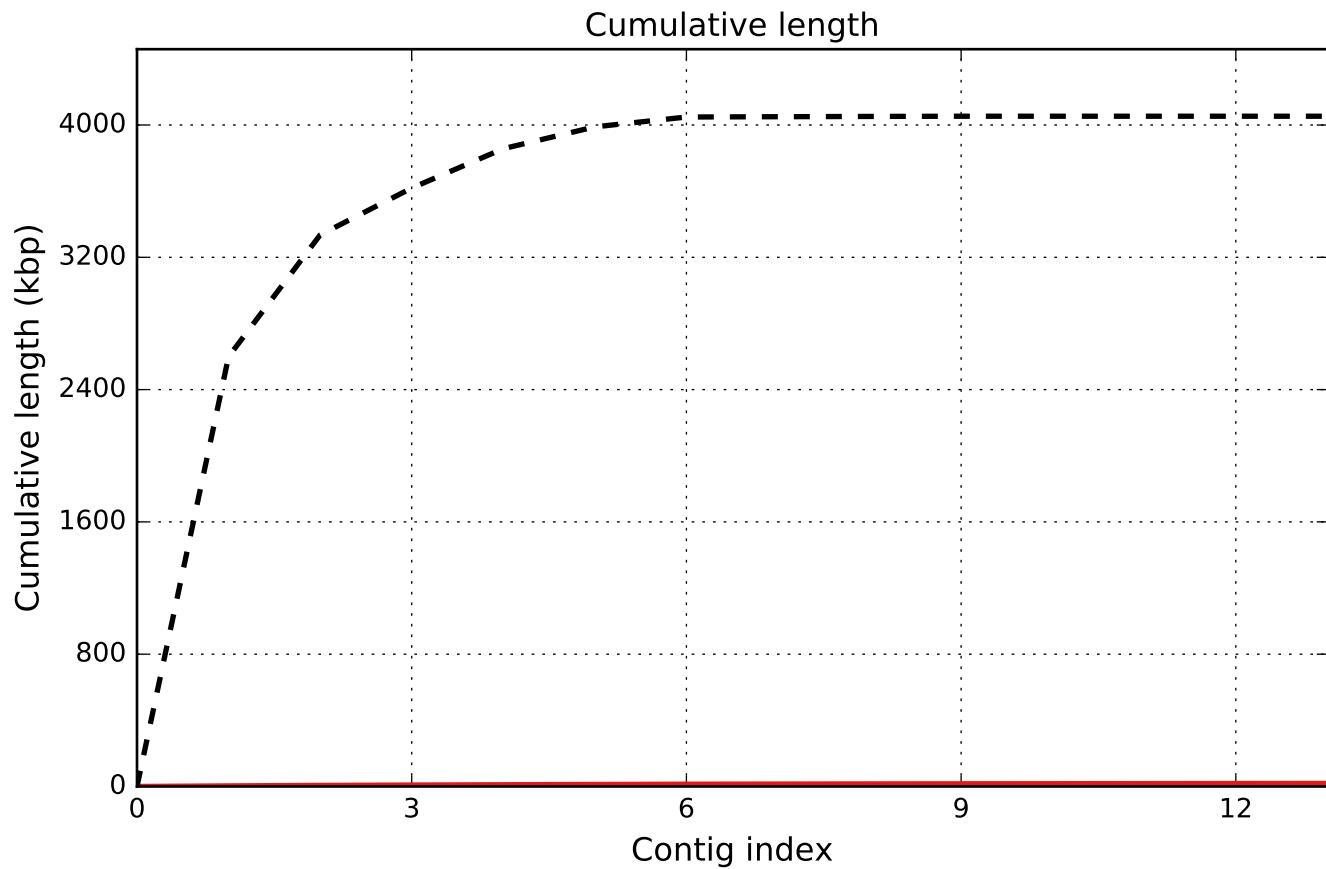
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

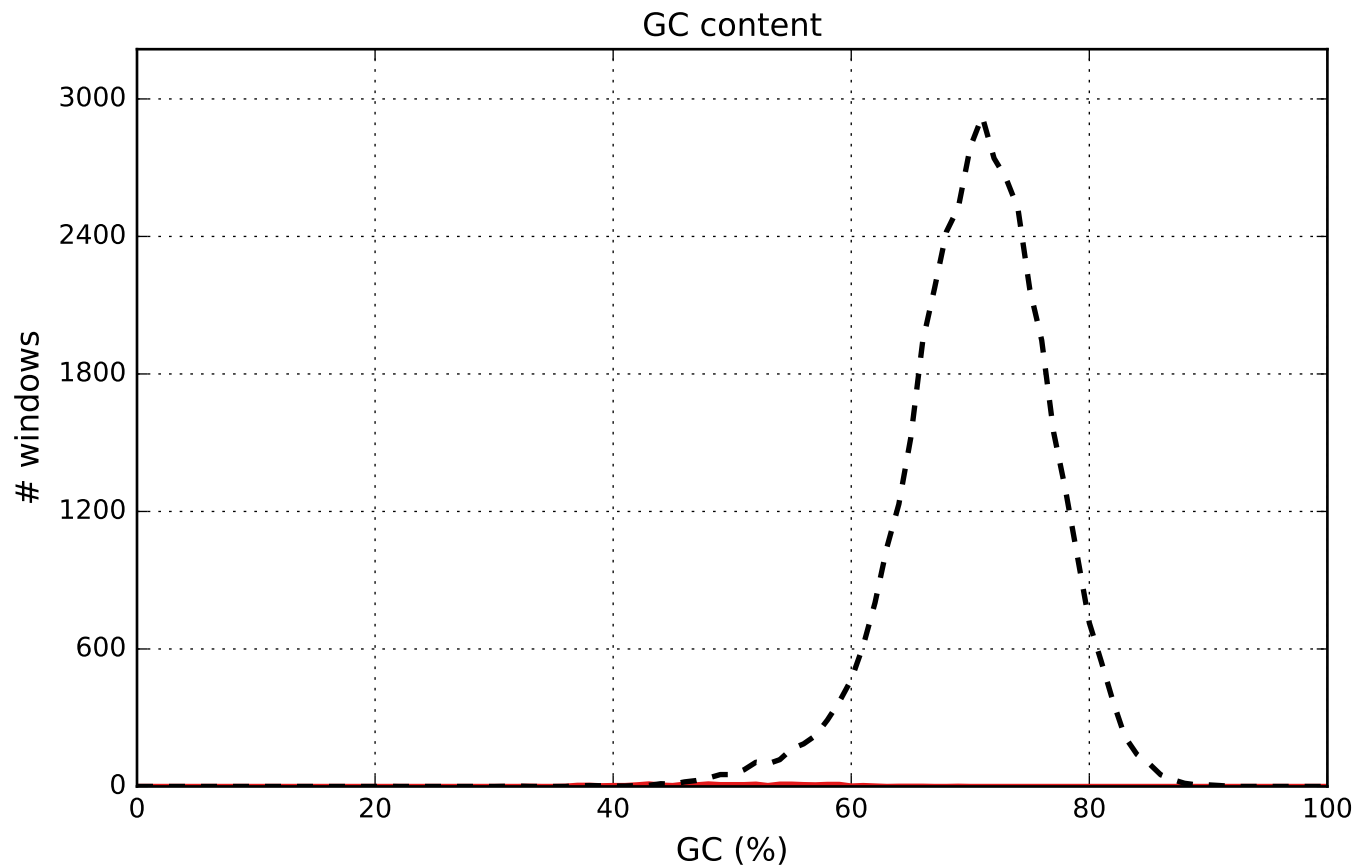


— combined.final.contigs

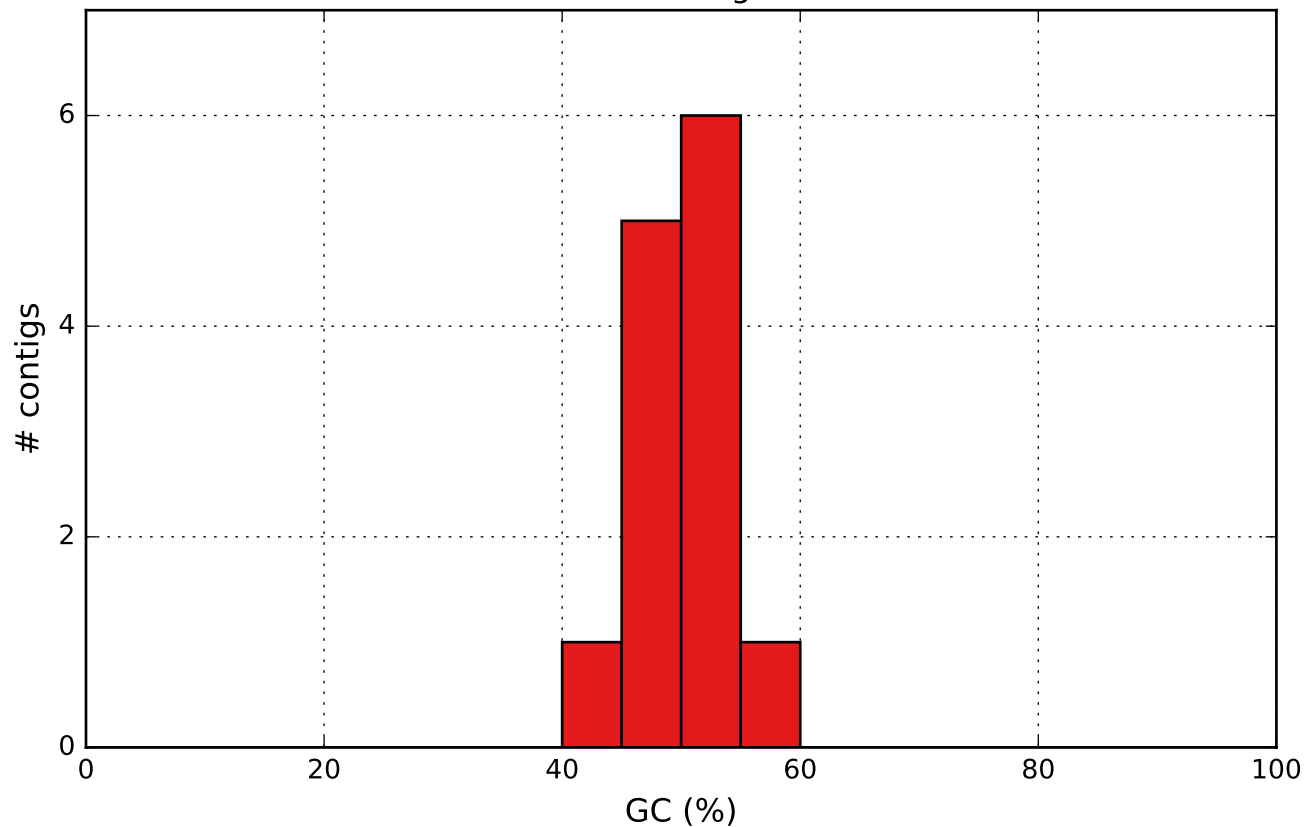



— combined.final.contigs

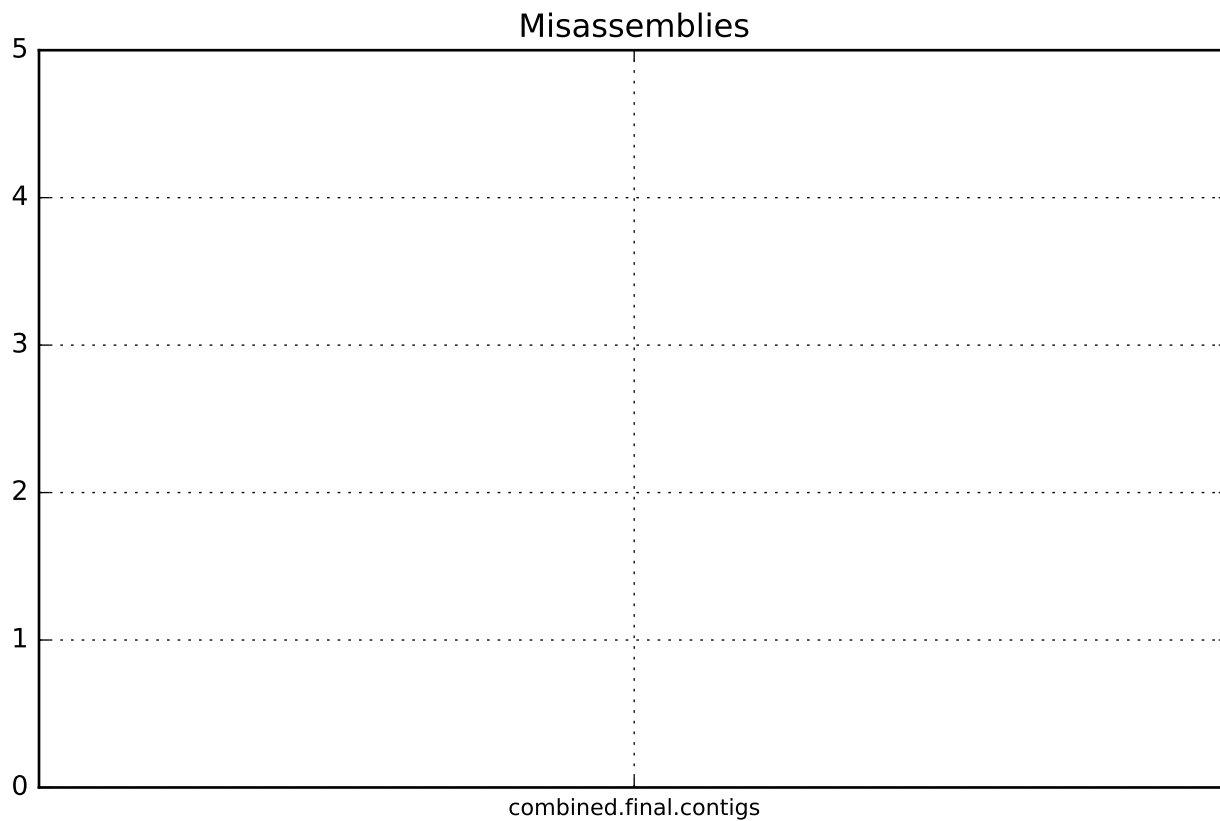




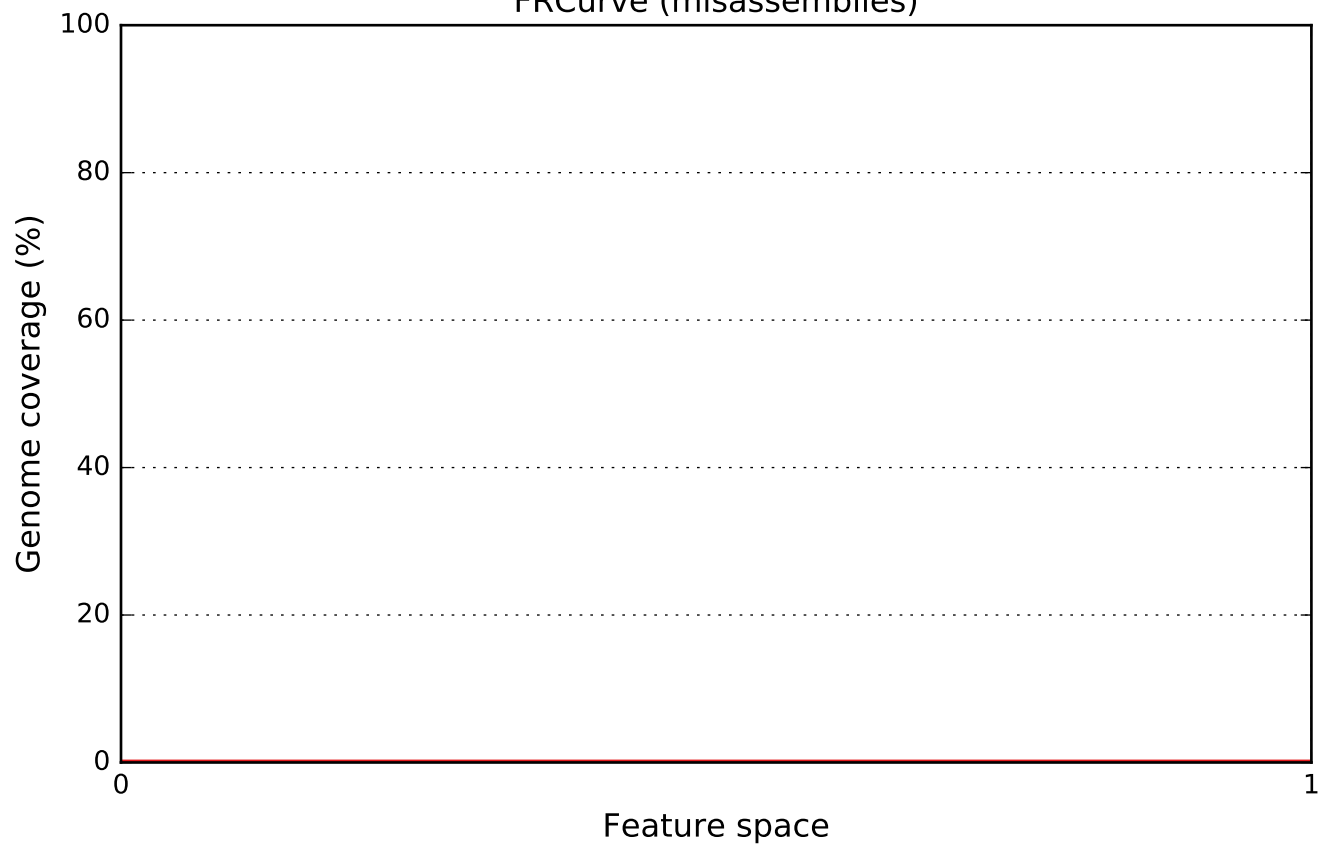
combined.final.contigs GC content



 combined.final.contigs

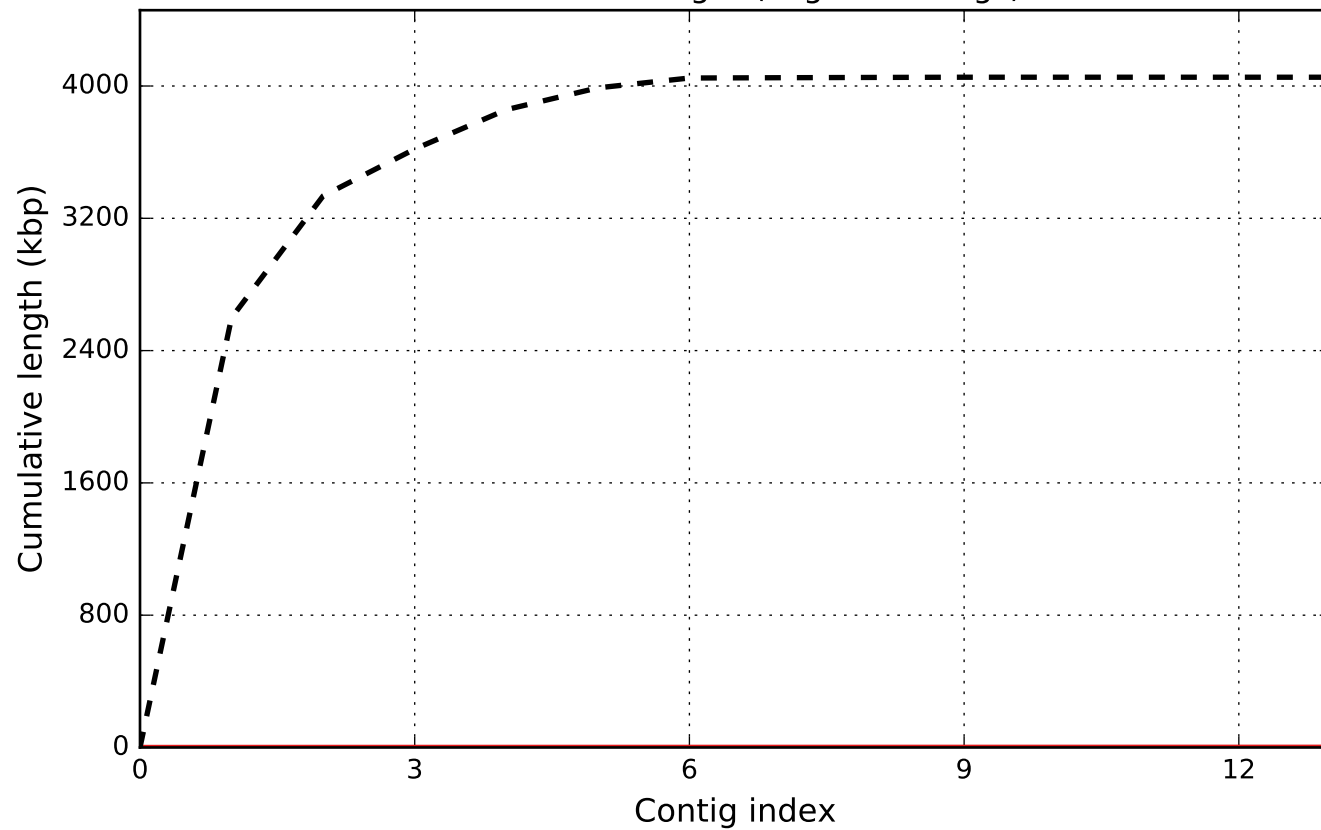


FRCurve (misassemblies)



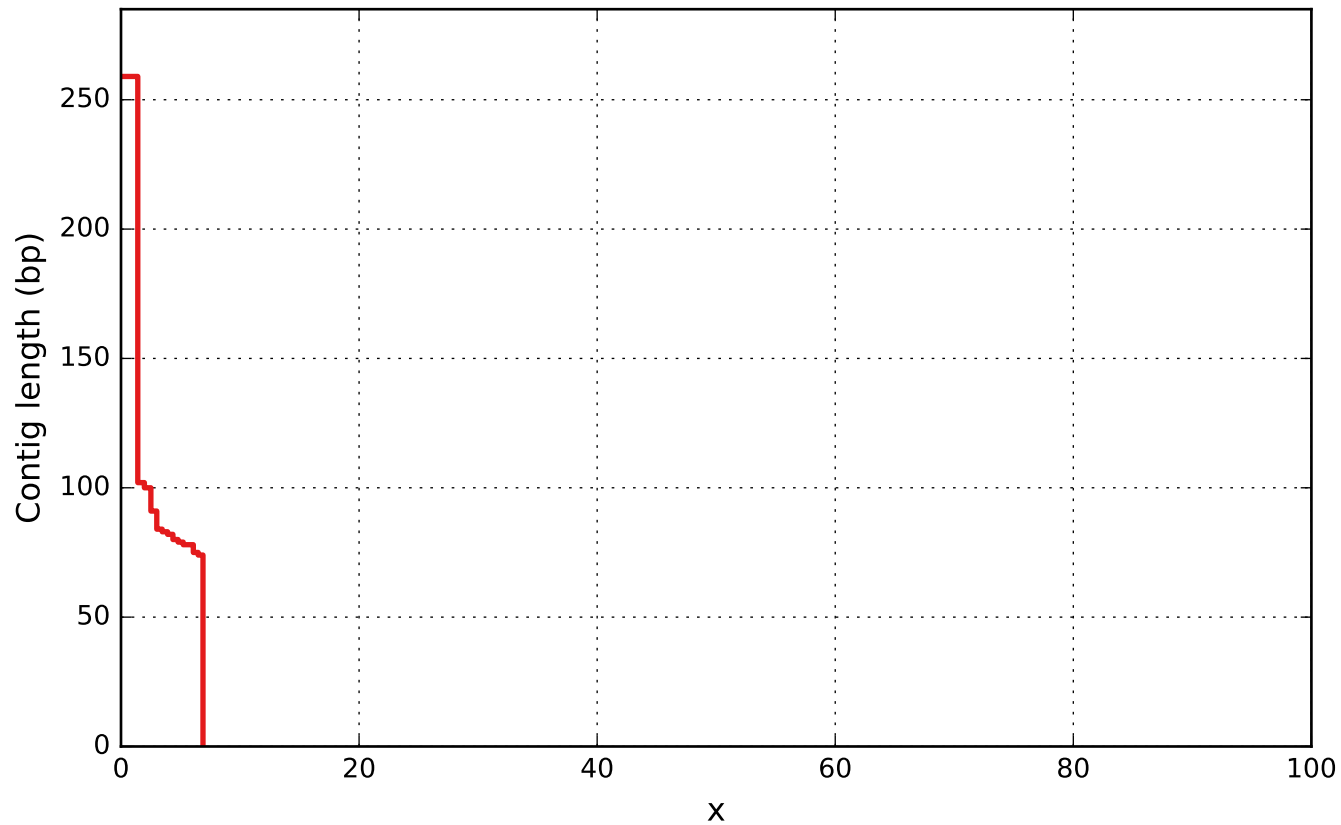
— combined.final.contigs

Cumulative length (aligned contigs)



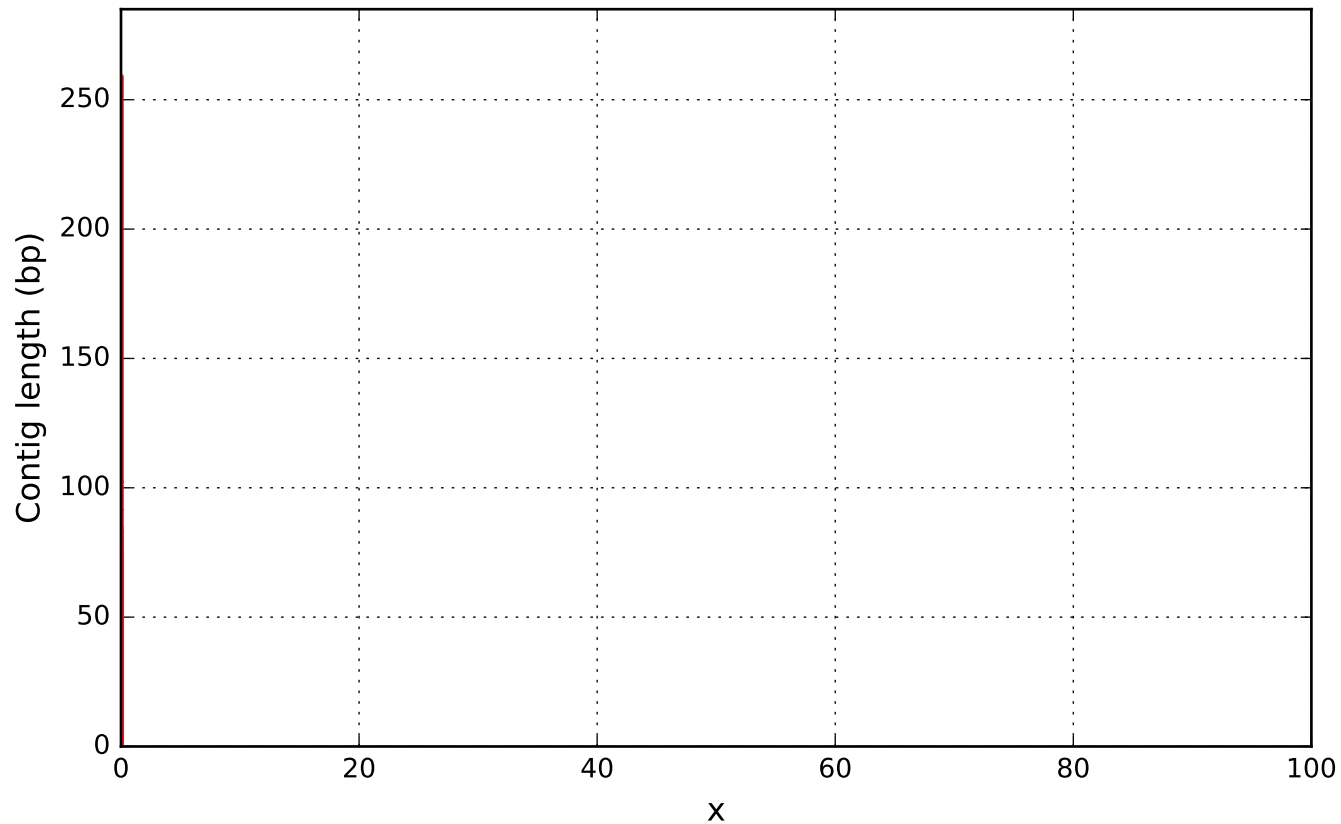
— combined.final.contigs - - Reference

NAx



— combined.final.contigs

NGAx



— combined.final.contigs