

Report

	combined.final.contigs
# contigs (>= 1000 bp)	5
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	11580
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	8
Largest contig	3836
Total length	13699
Reference length	3947342
GC (%)	38.71
Reference GC (%)	57.28
N50	2638
N75	1234
L50	3
L75	4
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 6 part
Unaligned length	11898
Genome fraction (%)	0.008
Duplication ratio	5.628
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1250.00
# indels per 100 kbp	0.00
Largest alignment	89
Total aligned length	637
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

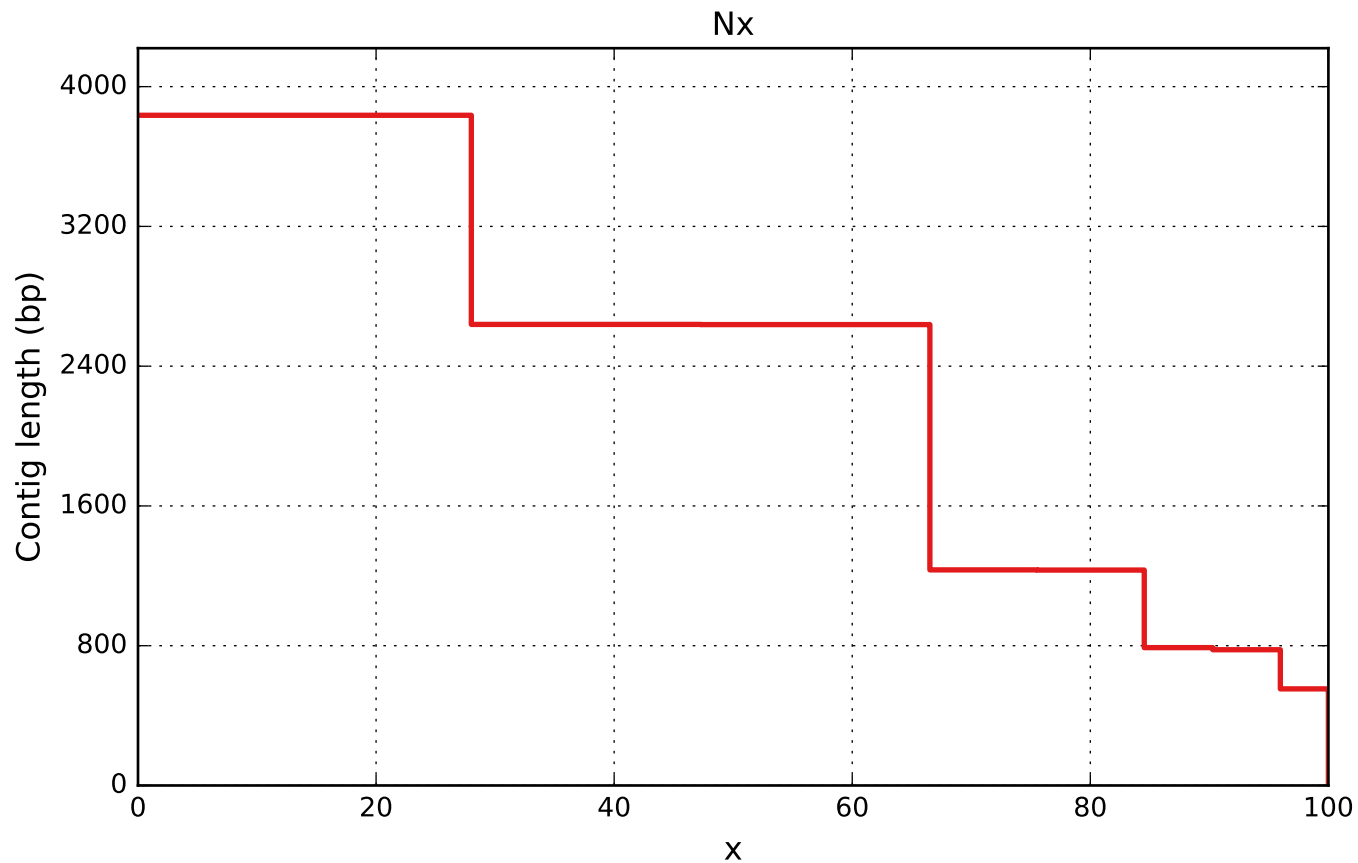
	combined.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	4
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	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).

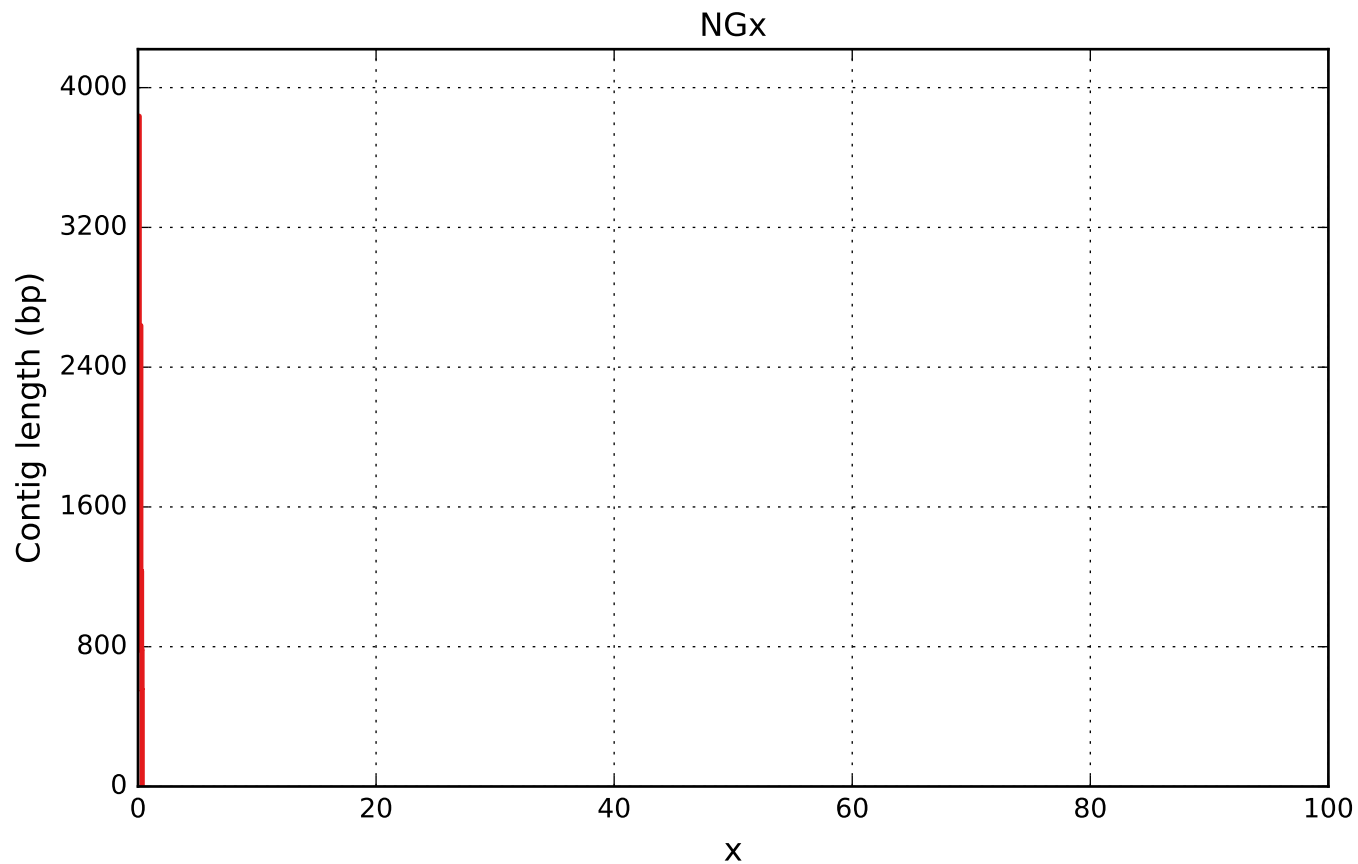
Unaligned report

	combined.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	6
Partially unaligned length	11898
# N's	0

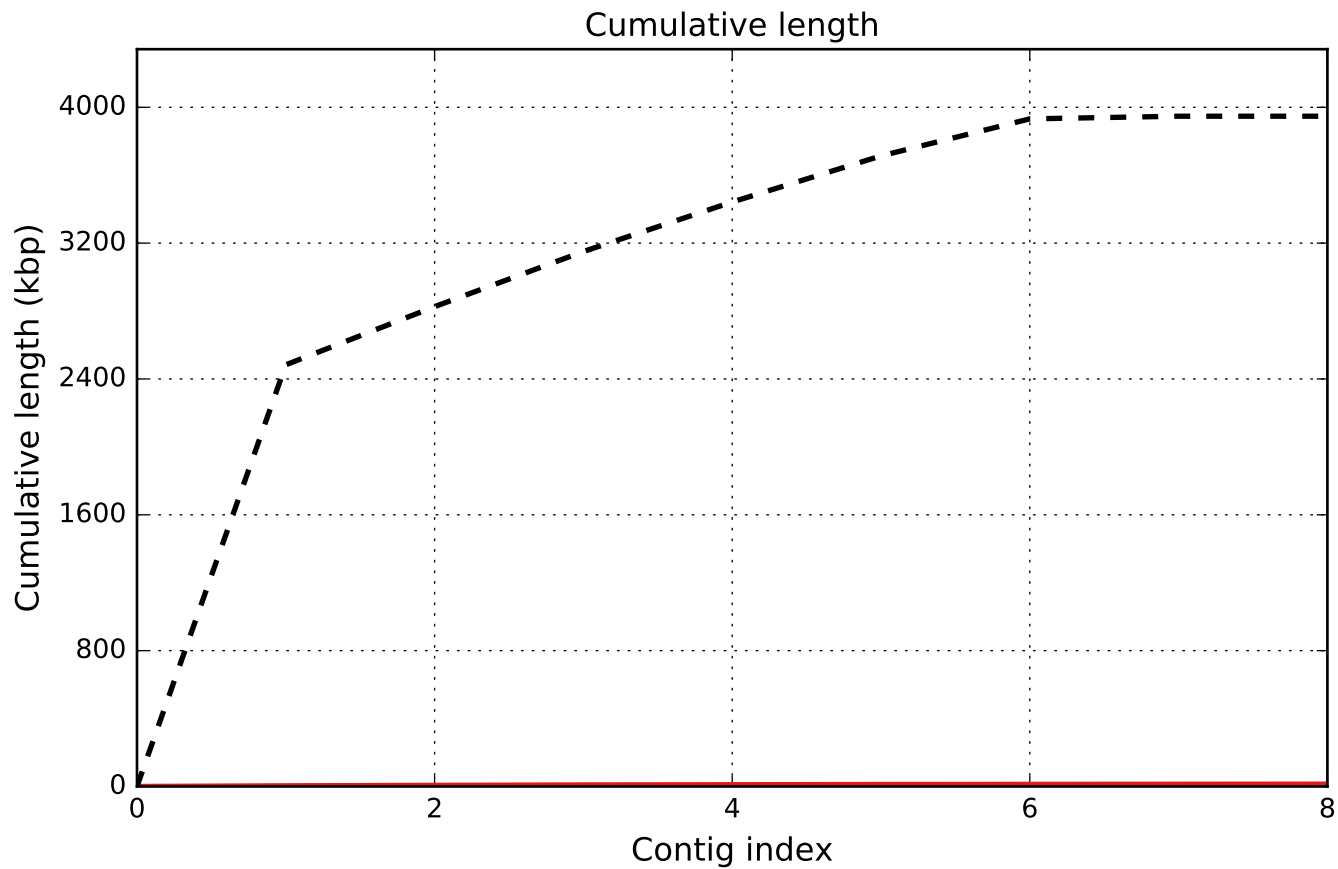
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

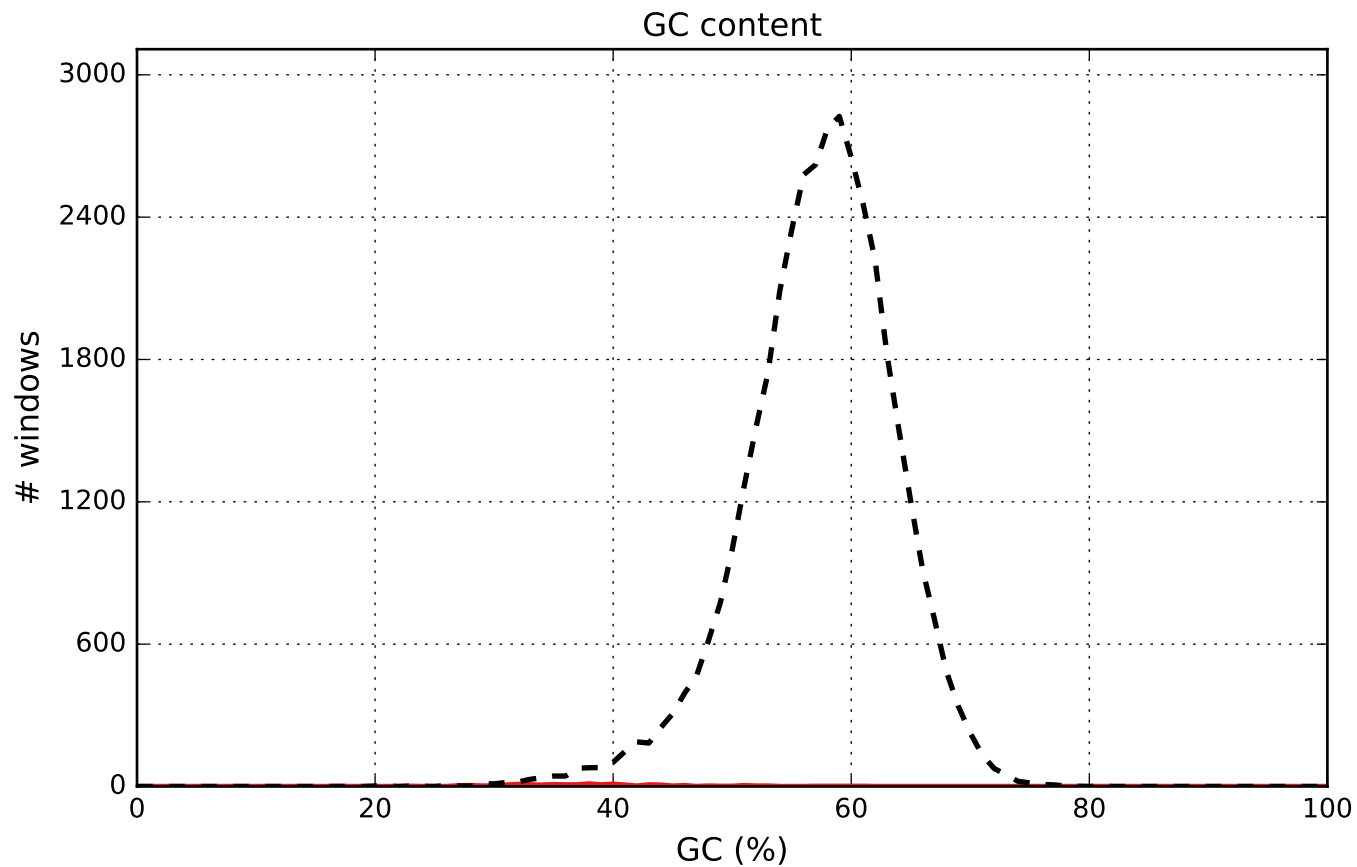


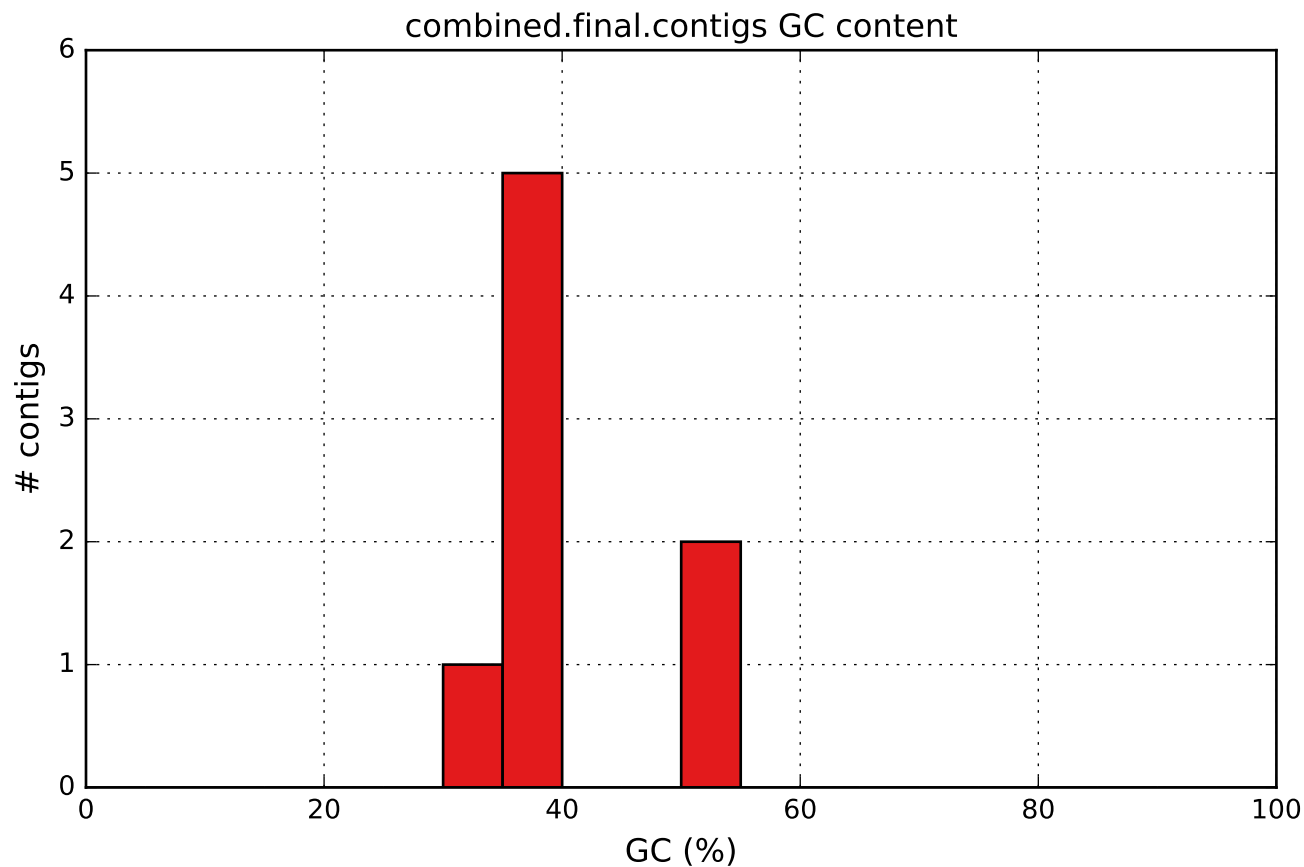
— combined.final.contigs



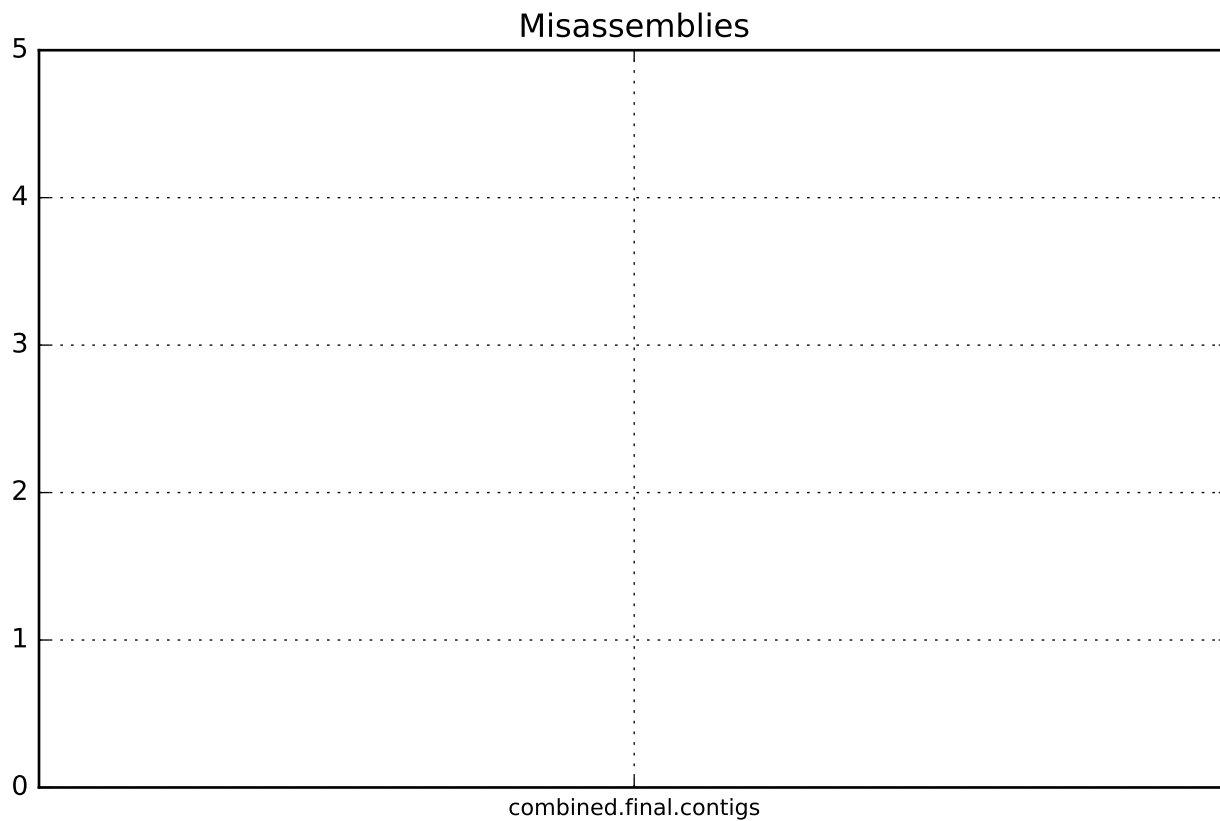
— combined.final.contigs



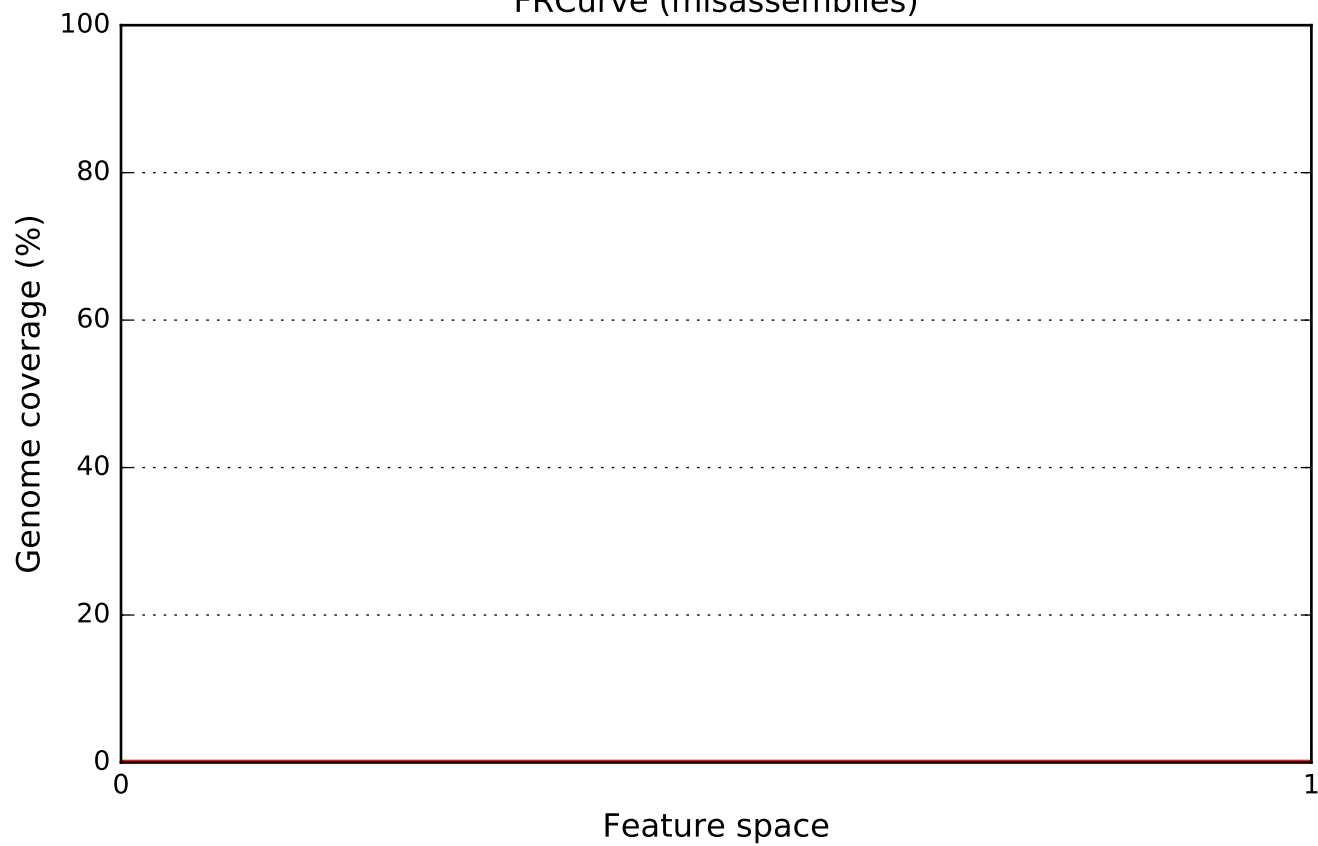




combined.final.contigs

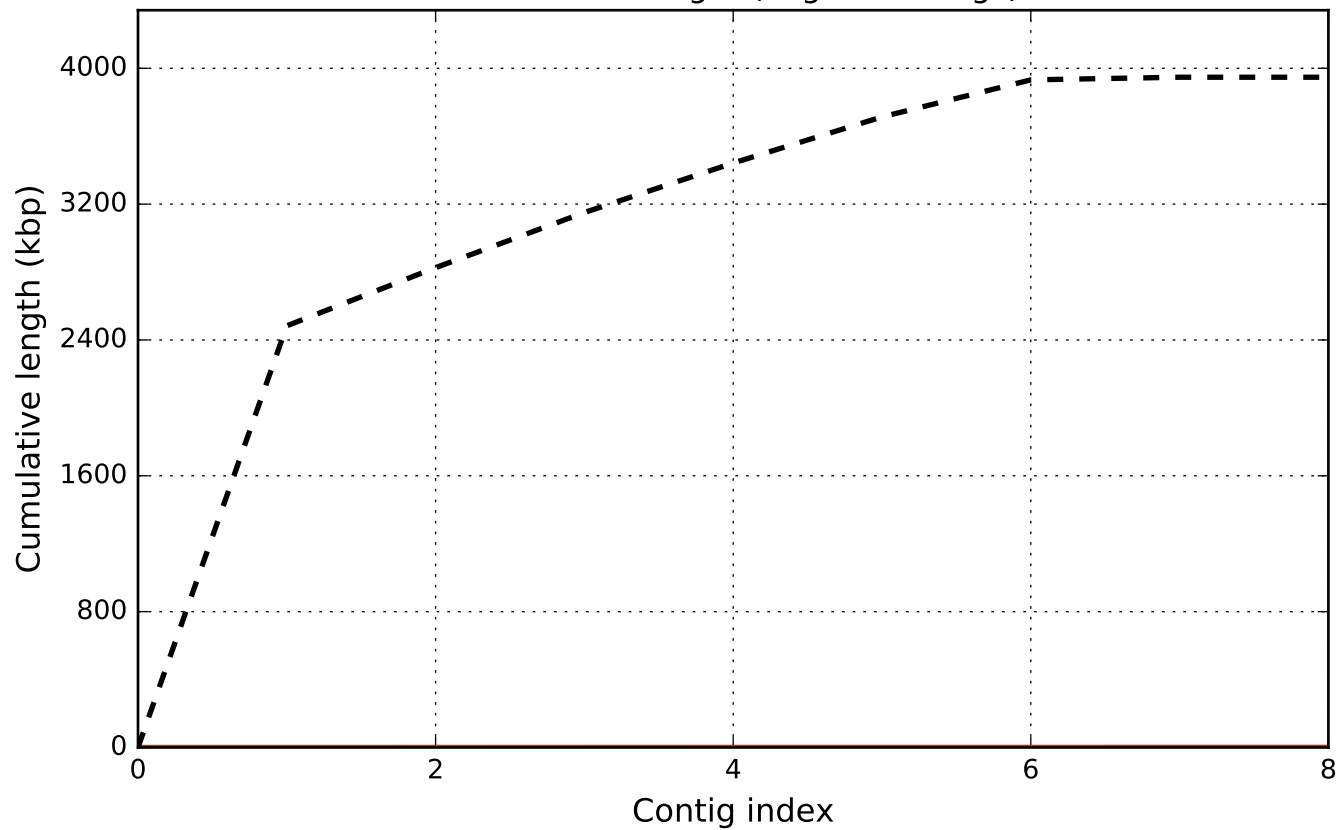


FRCurve (misassemblies)



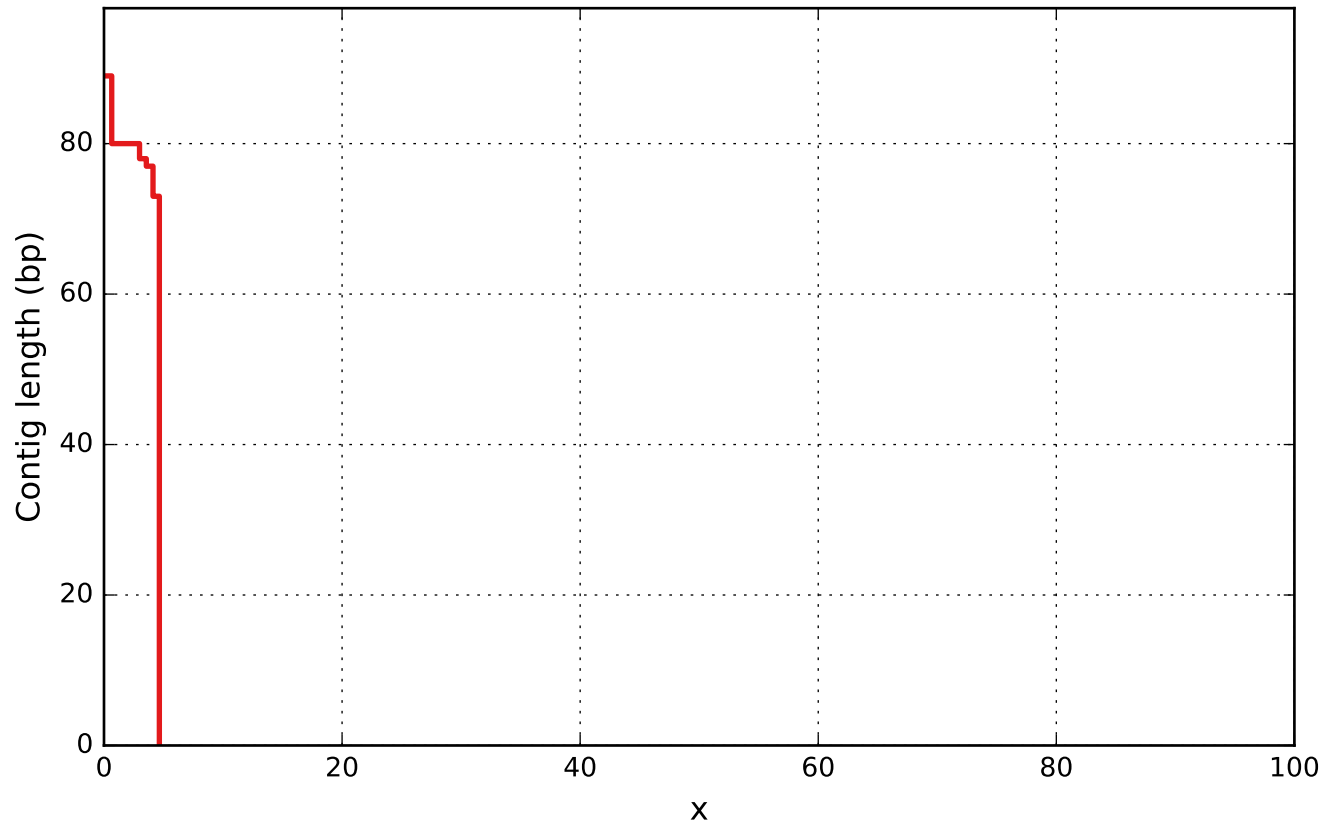
— combined.final.contigs

Cumulative length (aligned contigs)



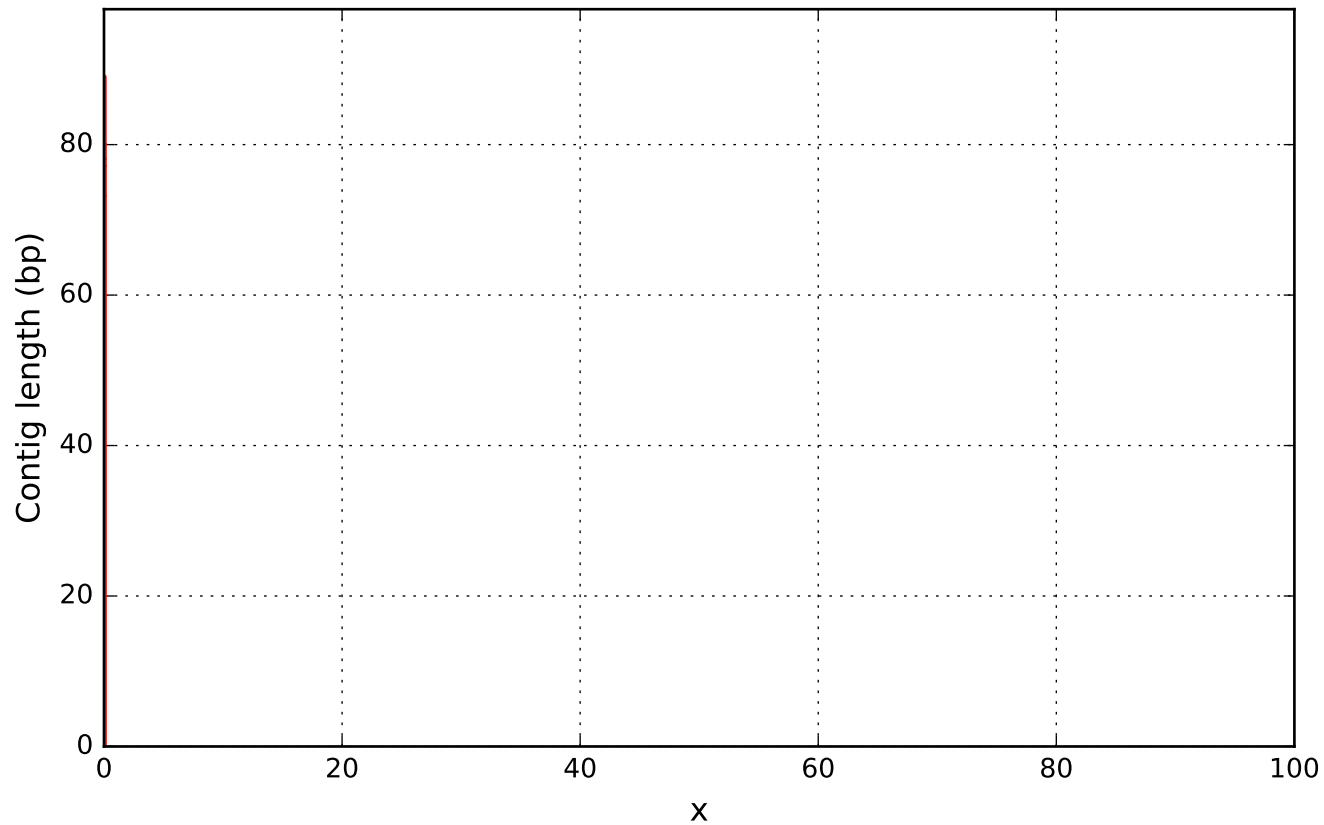
— combined.final.contigs - - Reference

NAx



— combined.final.contigs

NGAx



— combined.final.contigs