

Report

	combined.final.contigs
# contigs (≥ 1000 bp)	10
# contigs (≥ 5000 bp)	5
# contigs (≥ 10000 bp)	1
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 1000 bp)	59423
Total length (≥ 5000 bp)	45657
Total length (≥ 10000 bp)	17225
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	17
Largest contig	17225
Total length	64464
Reference length	4775416
GC (%)	60.74
Reference GC (%)	68.59
N50	6873
N75	3725
L50	4
L75	6
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned mis. contigs	0
# unaligned contigs	0 + 12 part
Unaligned length	60023
Genome fraction (%)	0.037
Duplication ratio	2.506
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2200.90
# indels per 100 kbp	338.60
Largest alignment	577
Total aligned length	2446
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

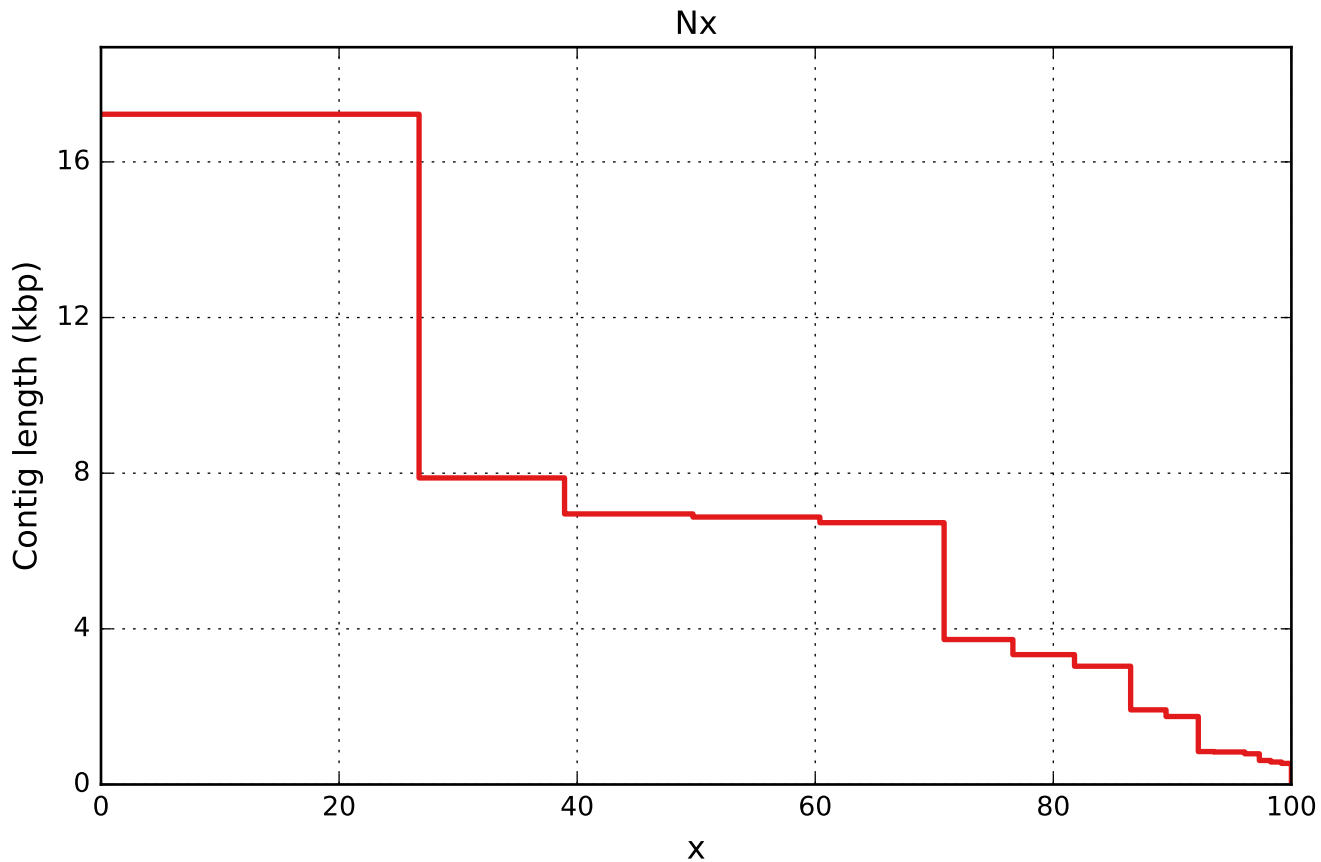
	combined.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	1
# unaligned mis. contigs	0
# mismatches	39
# indels	6
# indels (<= 5 bp)	6
# indels (> 5 bp)	0
Indels length	7

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

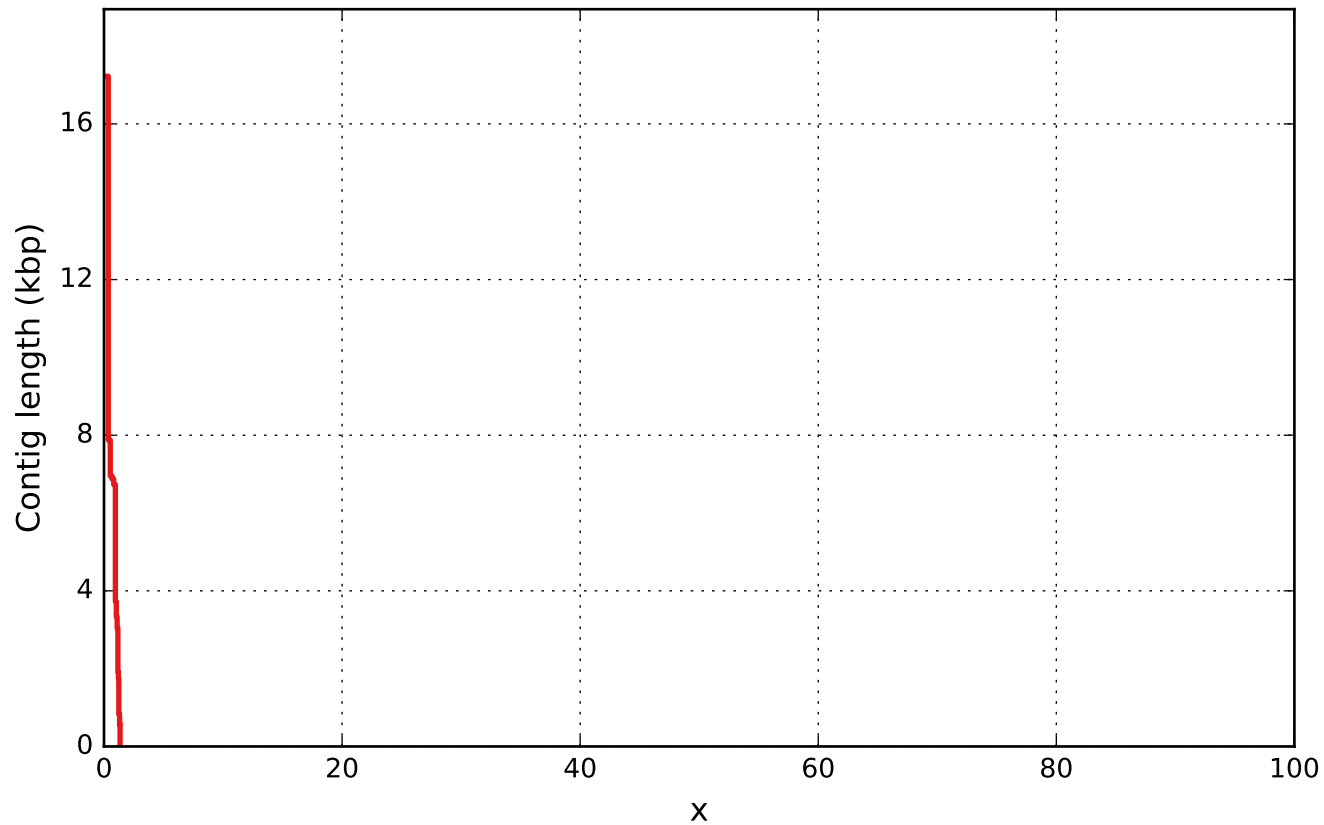
	combined.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	12
Partially unaligned length	60023
# N's	0

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).

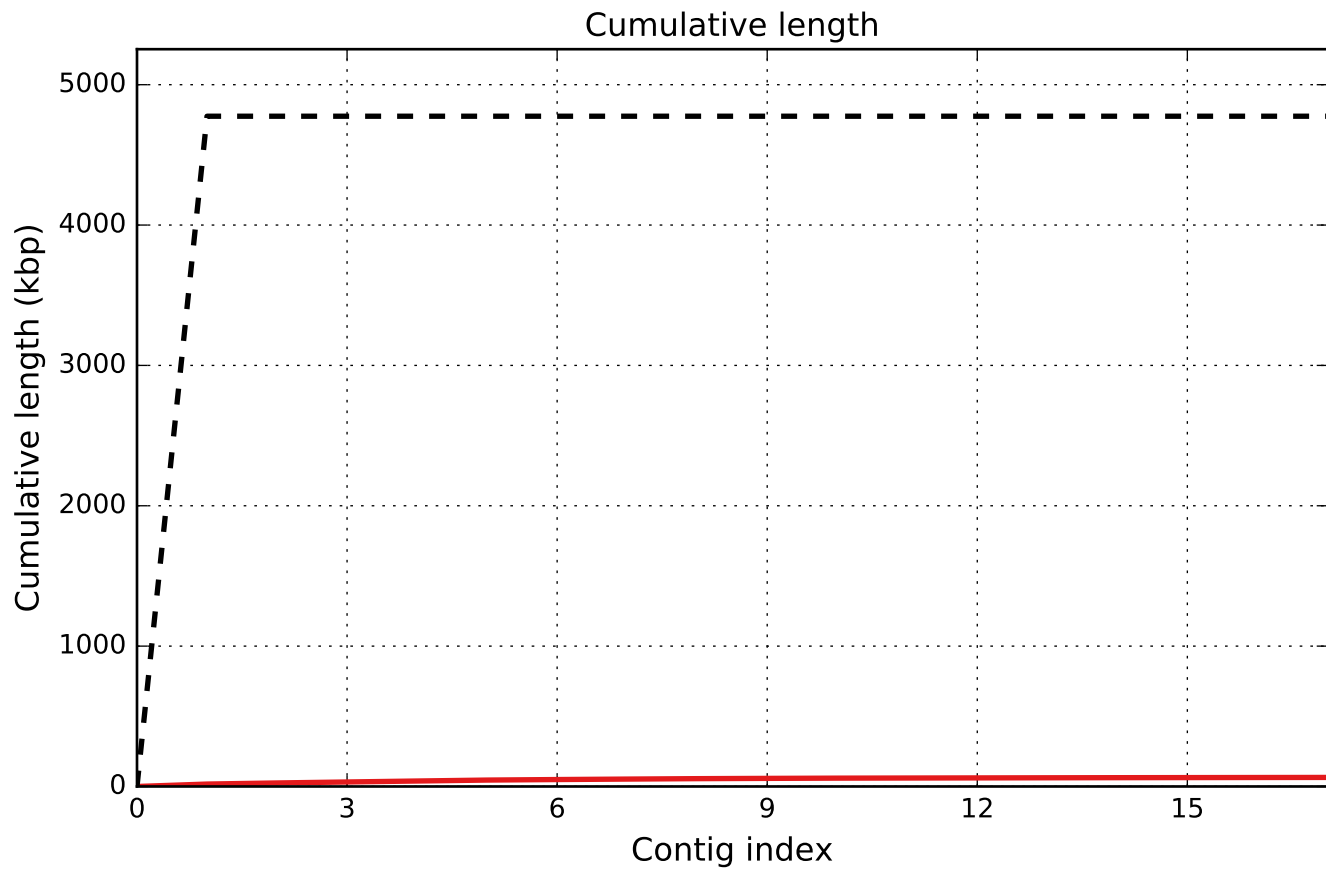


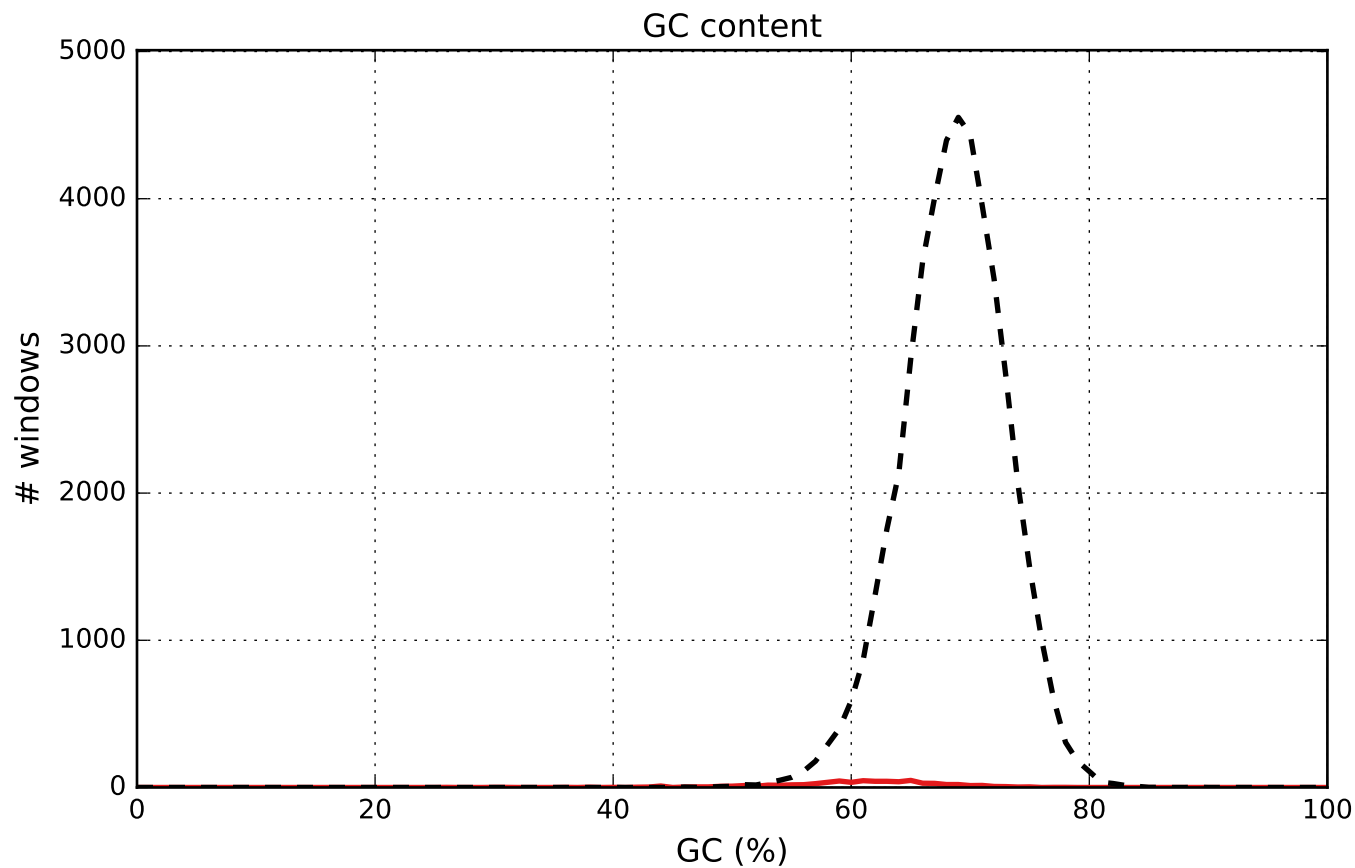
— combined.final.contigs

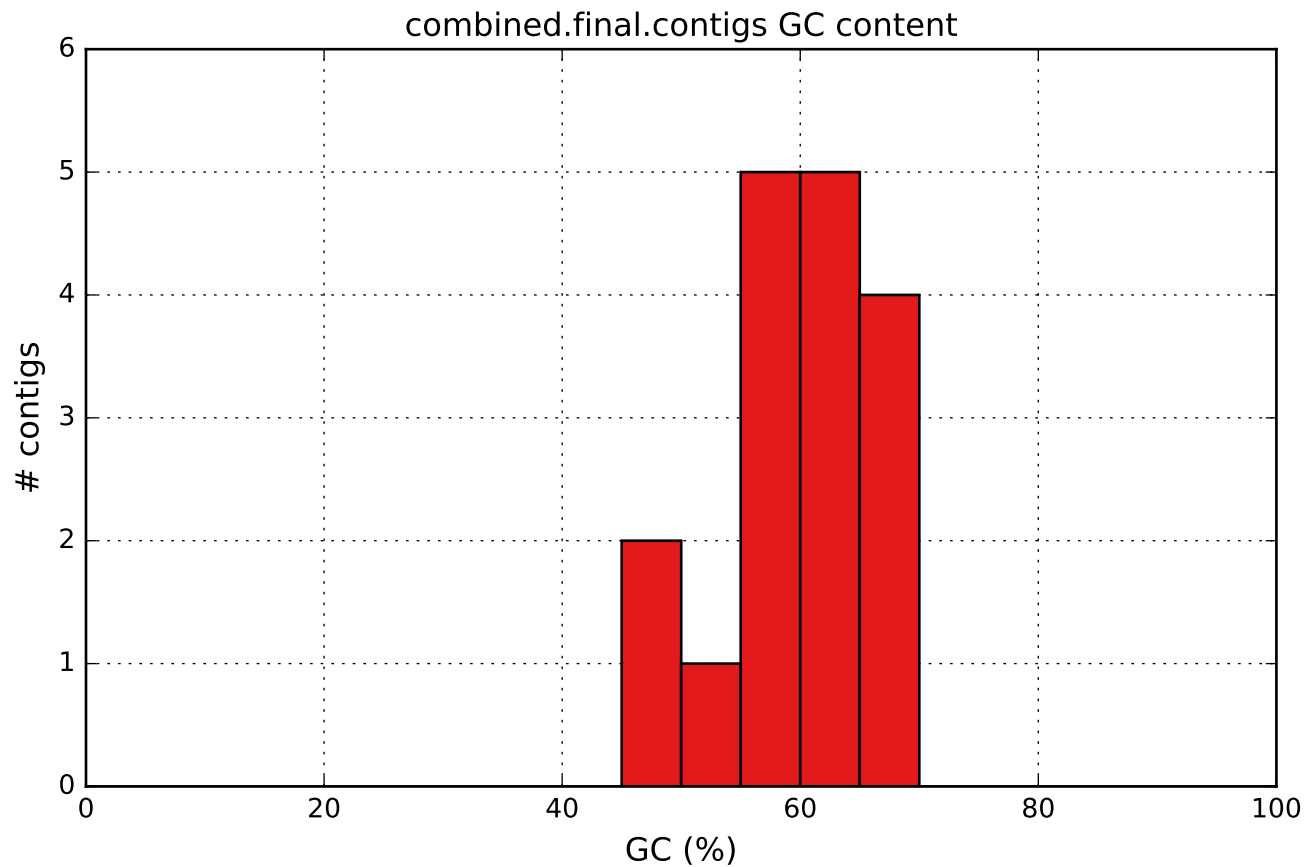
NGx



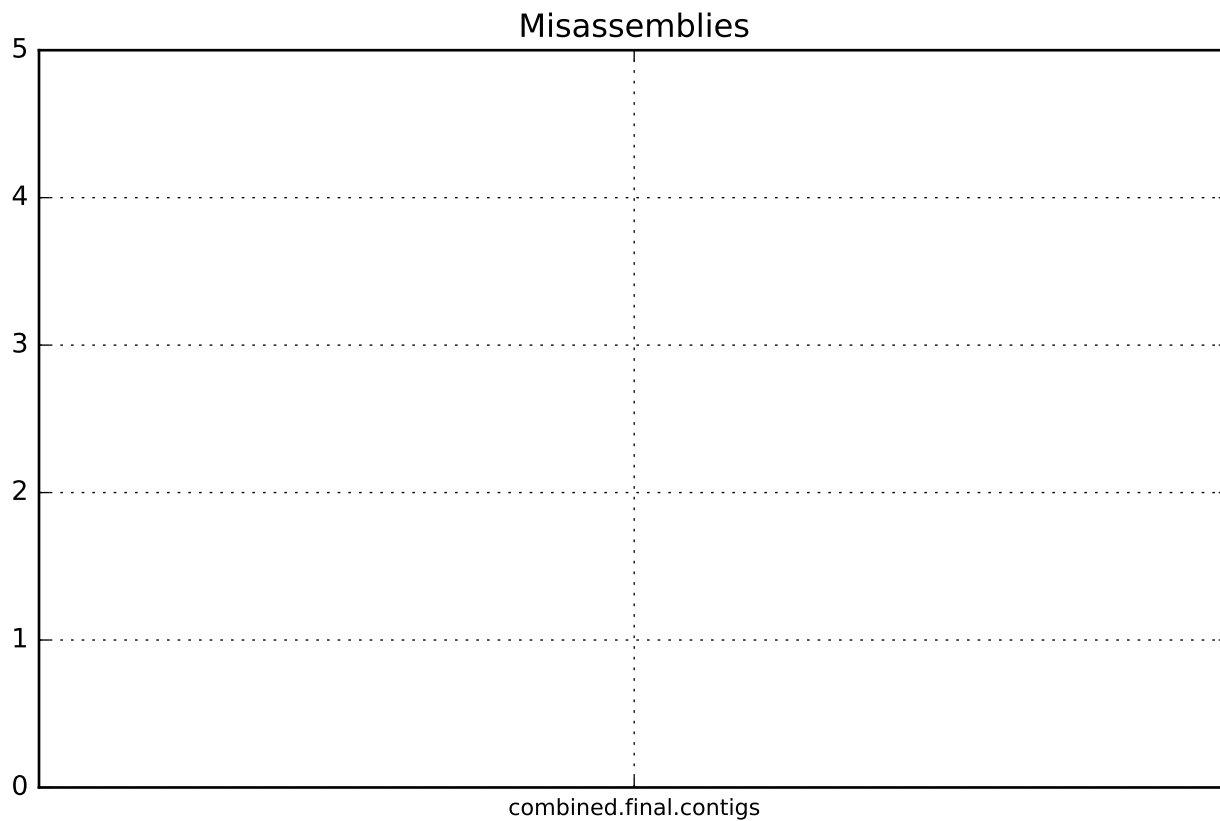
— combined.final.contigs



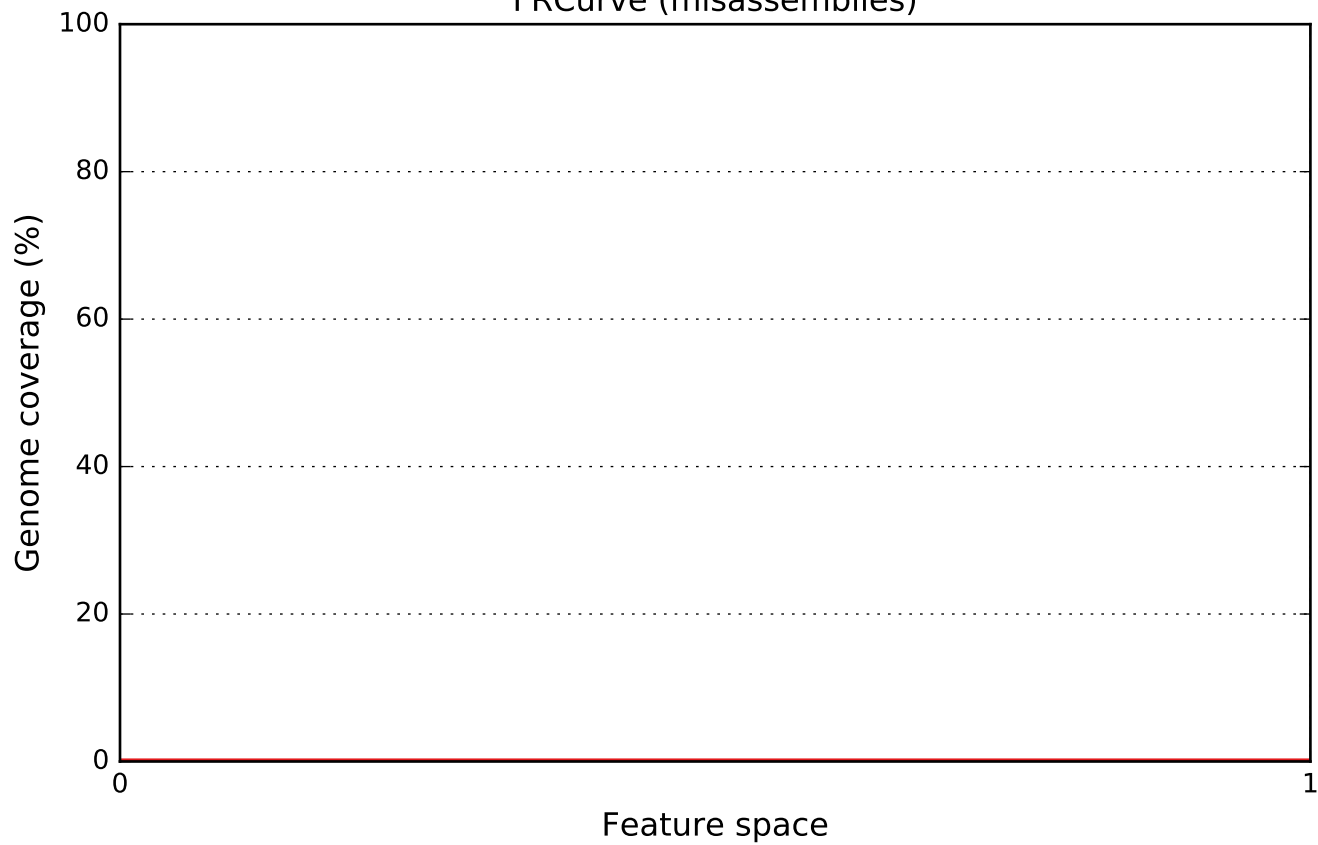




combined.final.contigs

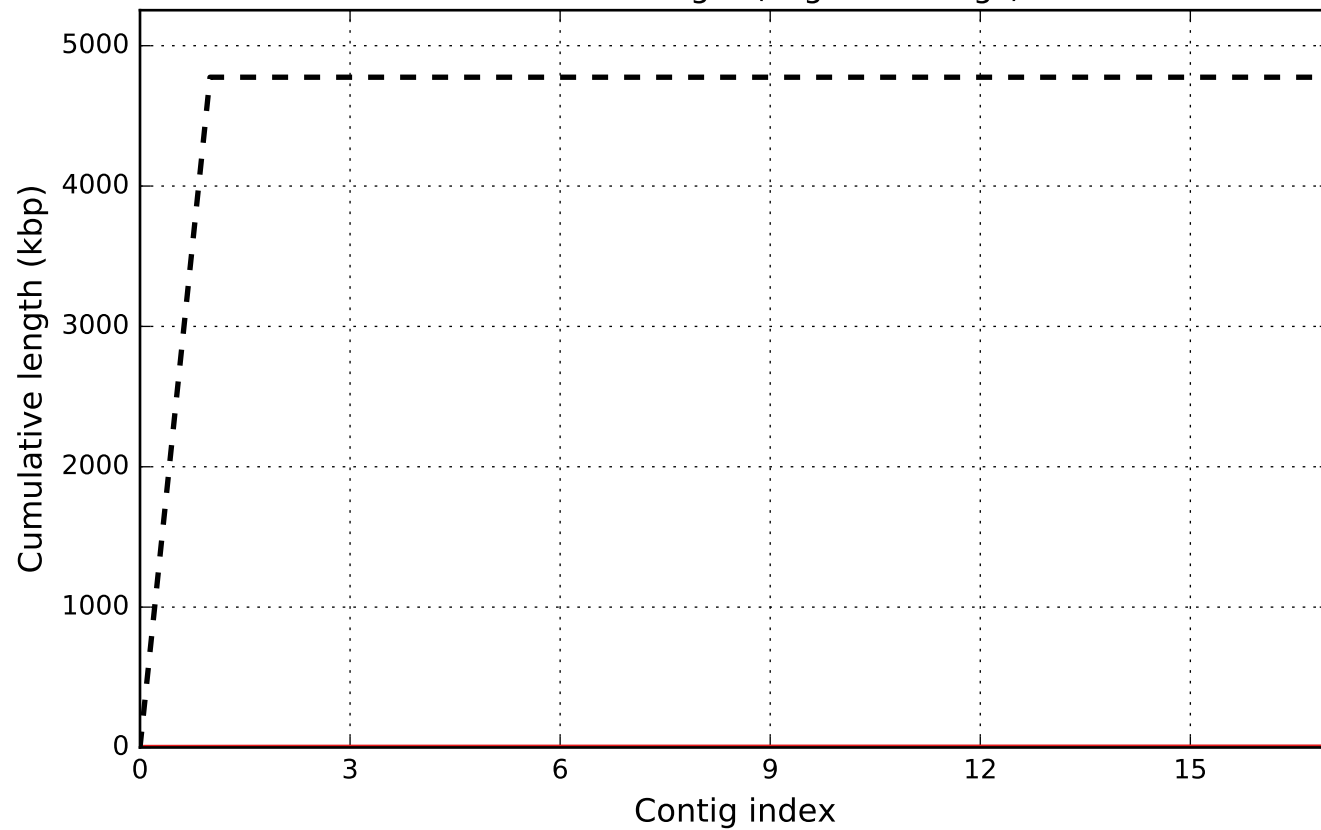


FRCurve (misassemblies)



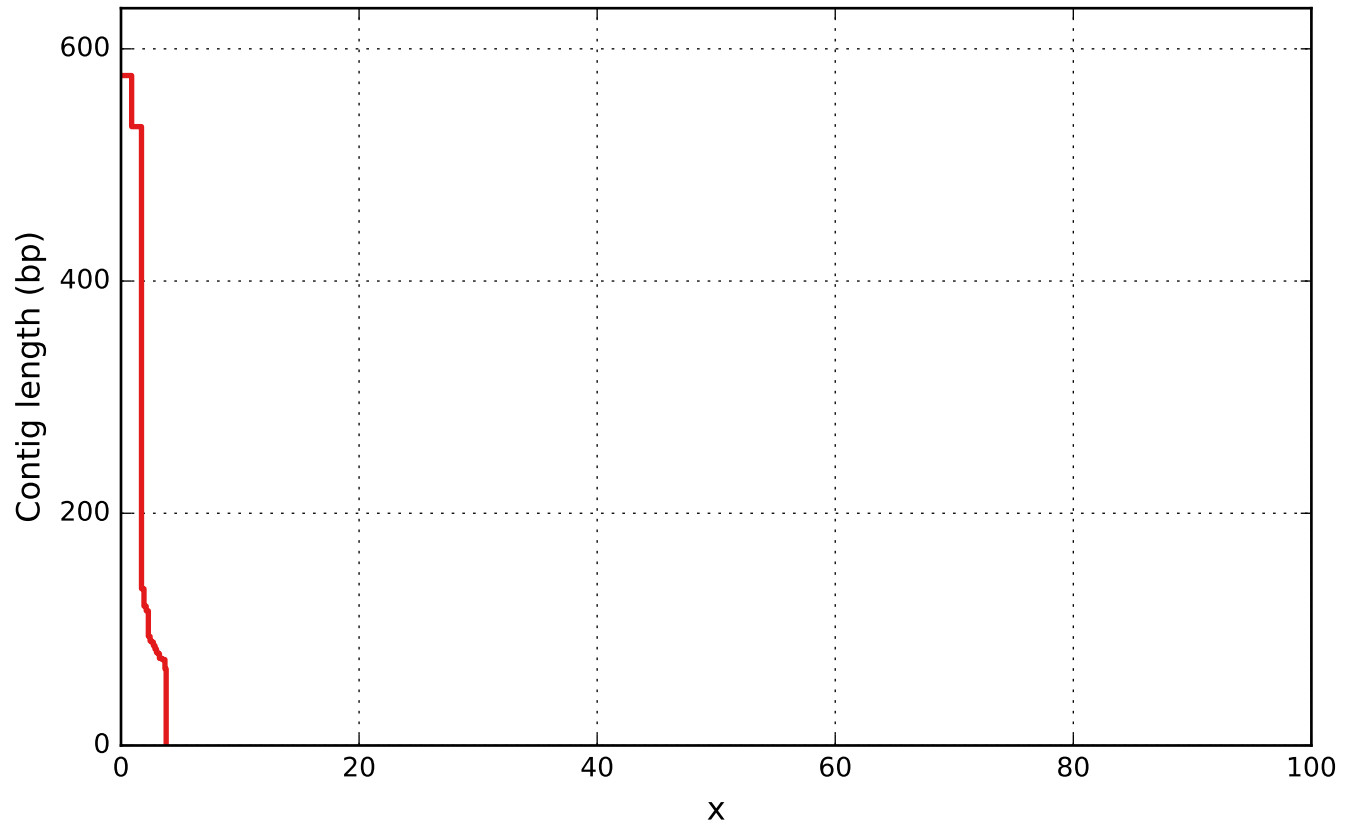
— combined.final.contigs

Cumulative length (aligned contigs)



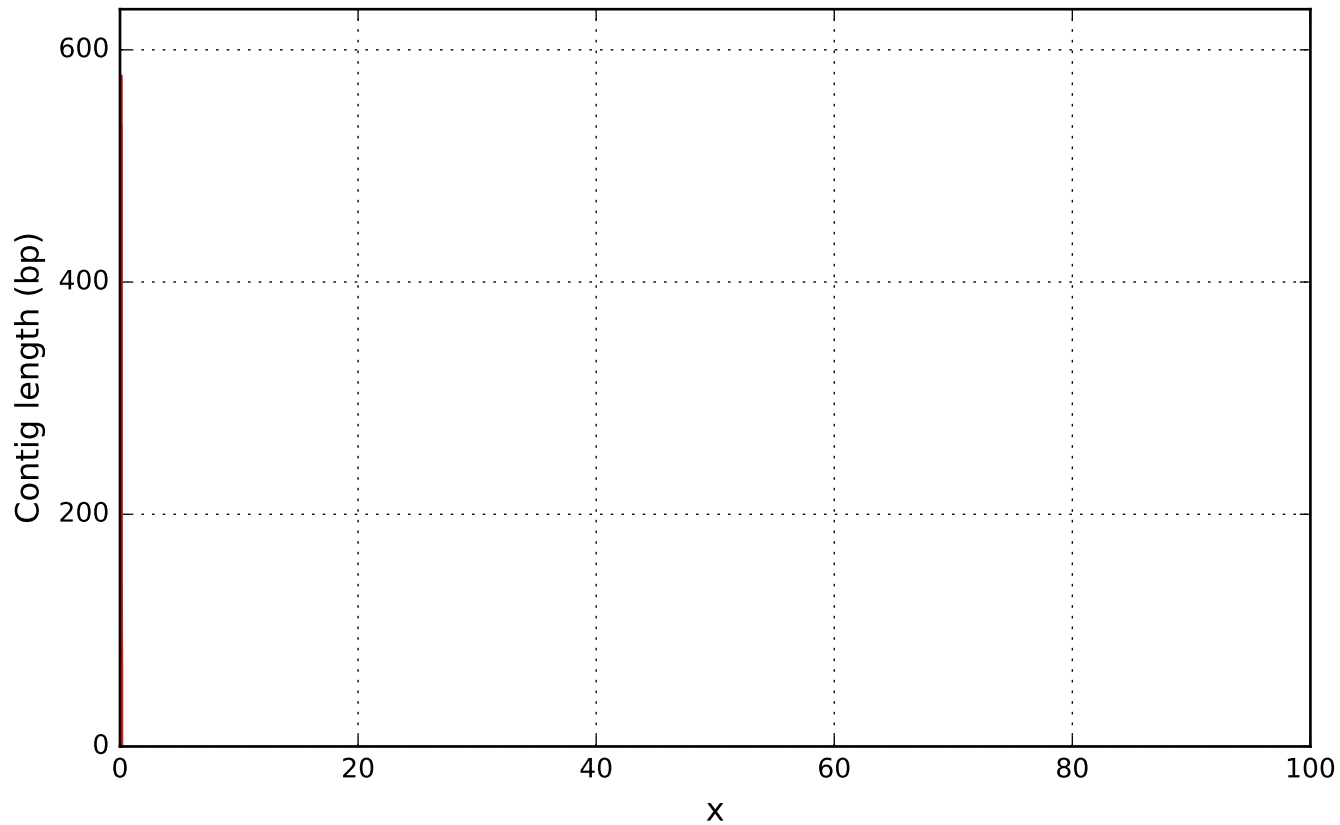
— combined.final.contigs - - Reference

NAx



— combined.final.contigs

NGAx



— combined.final.contigs