

Report

	combined.final.contigs
# contigs (≥ 1000 bp)	5
# contigs (≥ 5000 bp)	3
# contigs (≥ 10000 bp)	2
# contigs (≥ 25000 bp)	1
# contigs (≥ 50000 bp)	1
Total length (≥ 1000 bp)	94270
Total length (≥ 5000 bp)	91828
Total length (≥ 10000 bp)	86009
Total length (≥ 25000 bp)	74564
Total length (≥ 50000 bp)	74564
# contigs	5
Largest contig	74564
Total length	94270
Reference length	3925629
GC (%)	56.66
Reference GC (%)	47.16
N50	74564
N75	74564
L50	1
L75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 5 part
Unaligned length	93498
Genome fraction (%)	0.018
Duplication ratio	1.097
# N's per 100 kbp	0.00
# mismatches per 100 kbp	994.32
# indels per 100 kbp	142.05
Largest alignment	452
Total aligned length	772
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

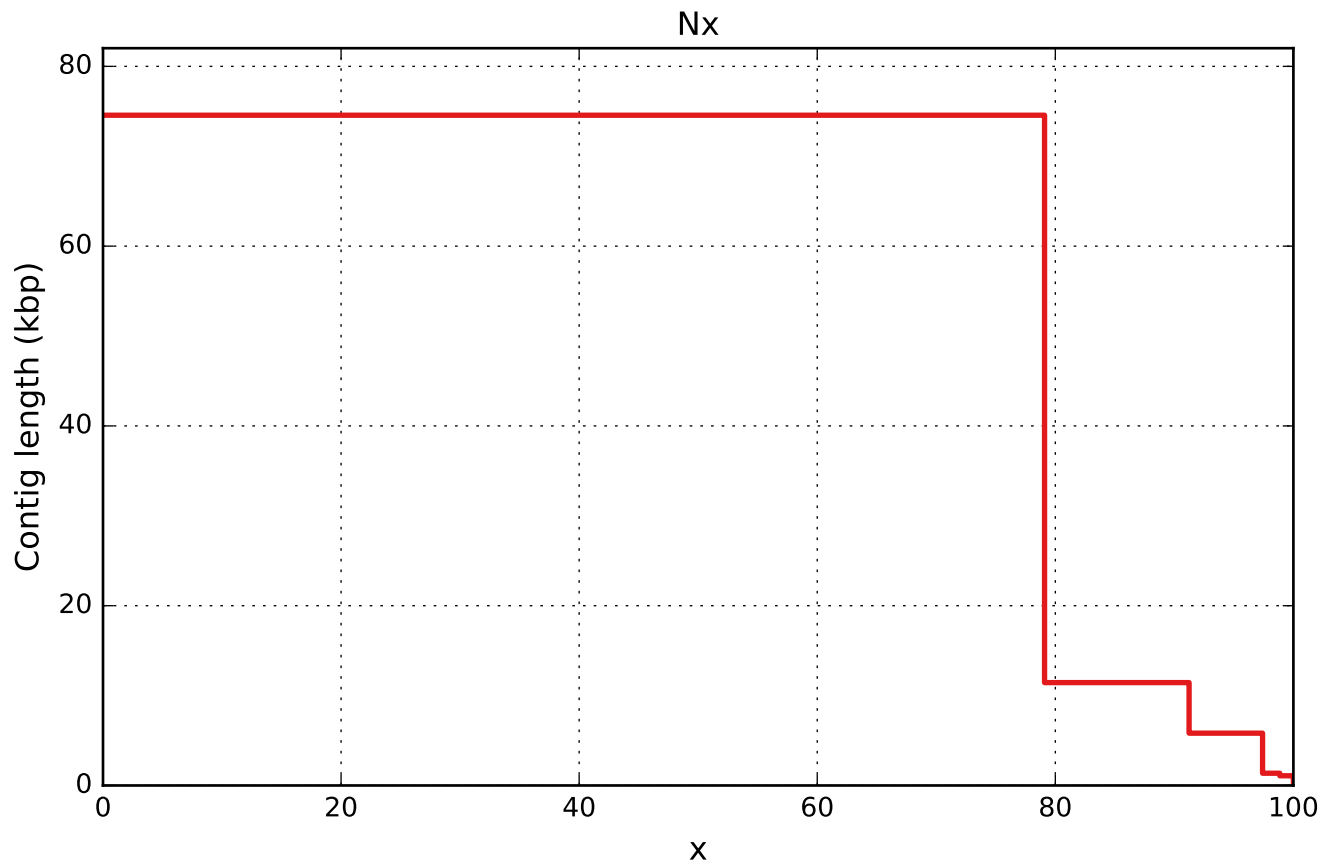
	combined.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	7
# indels	1
# indels (<= 5 bp)	0
# indels (> 5 bp)	1
Indels length	11

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

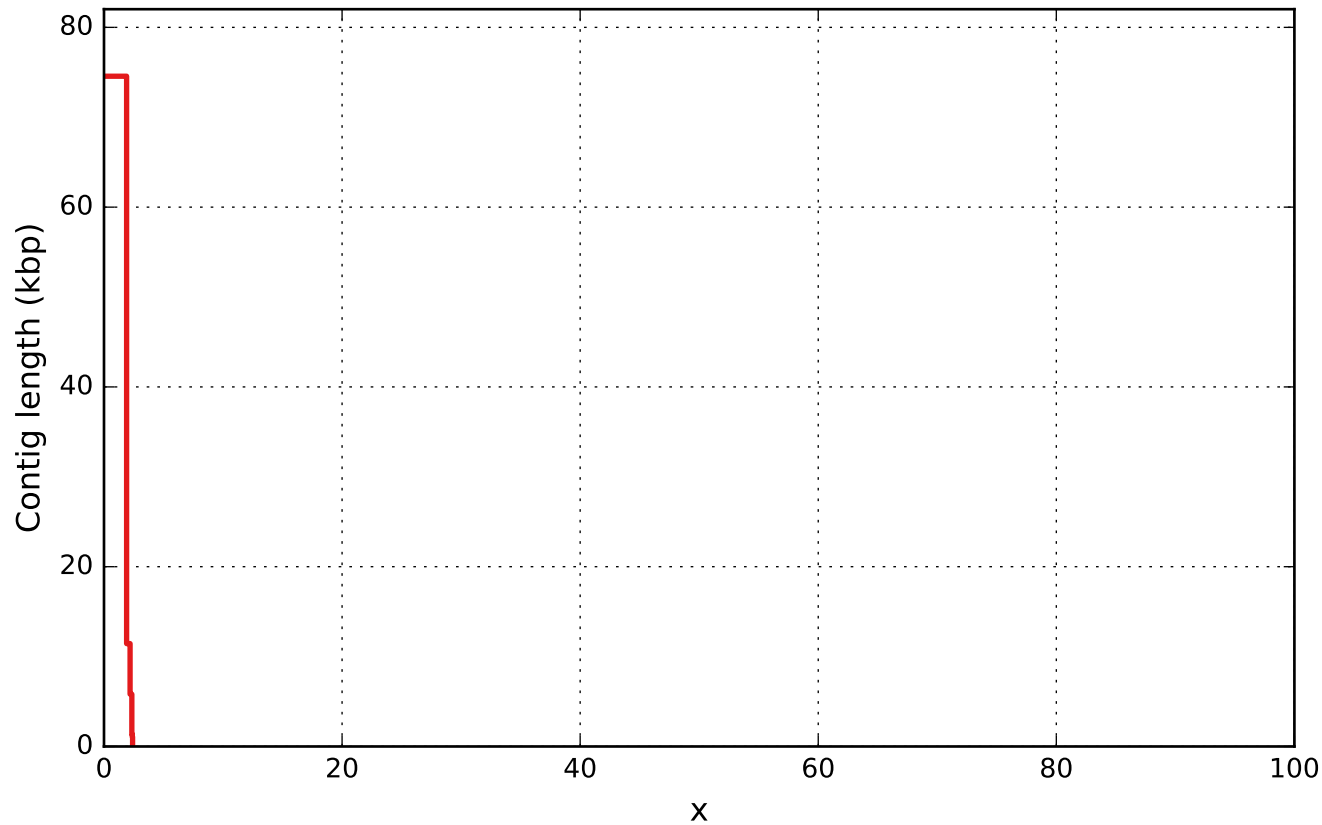
	combined.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	5
Partially unaligned length	93498
# N's	0

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).

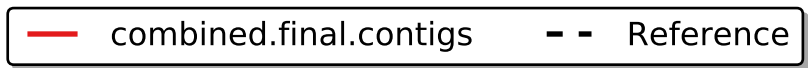
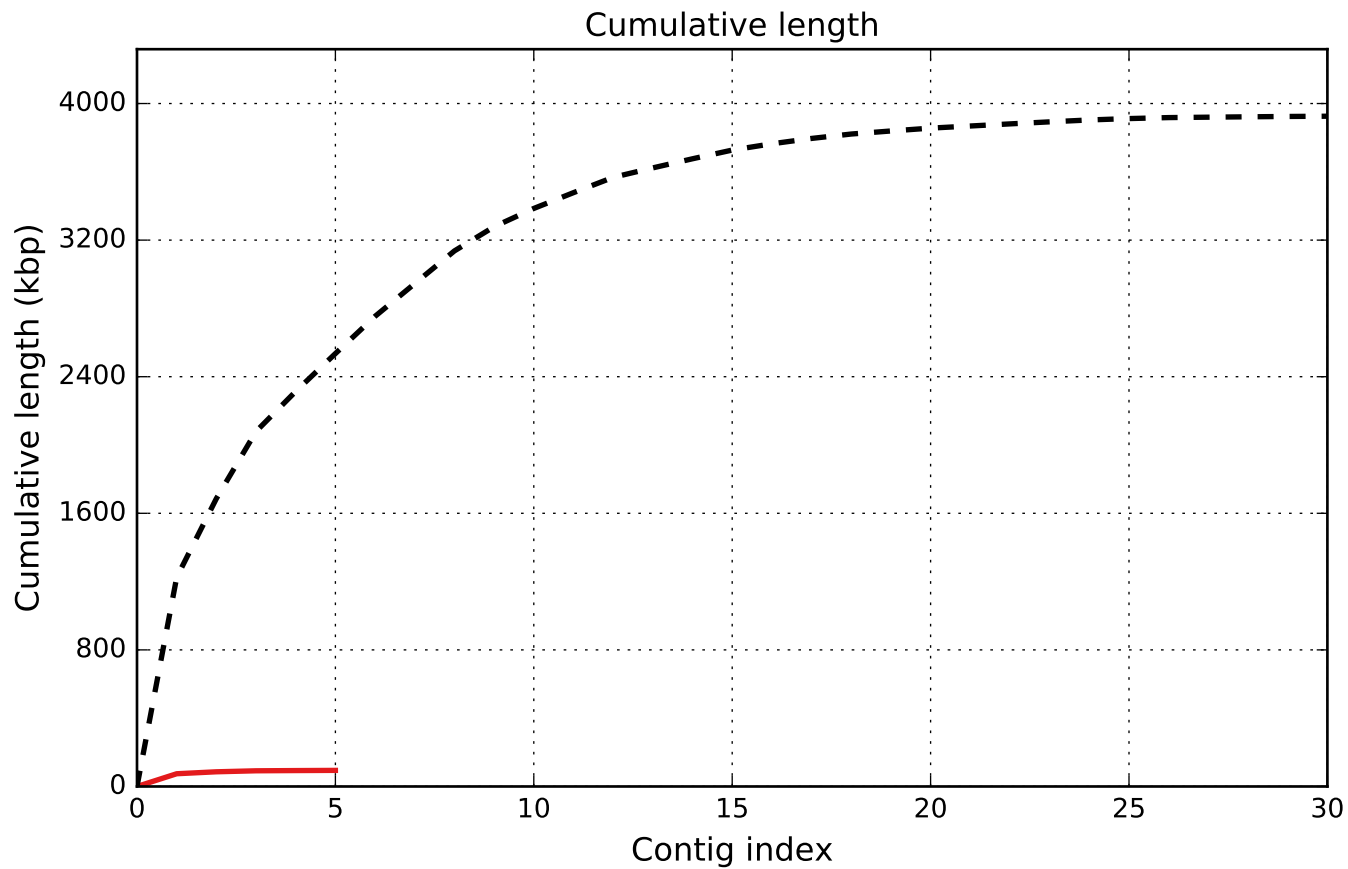


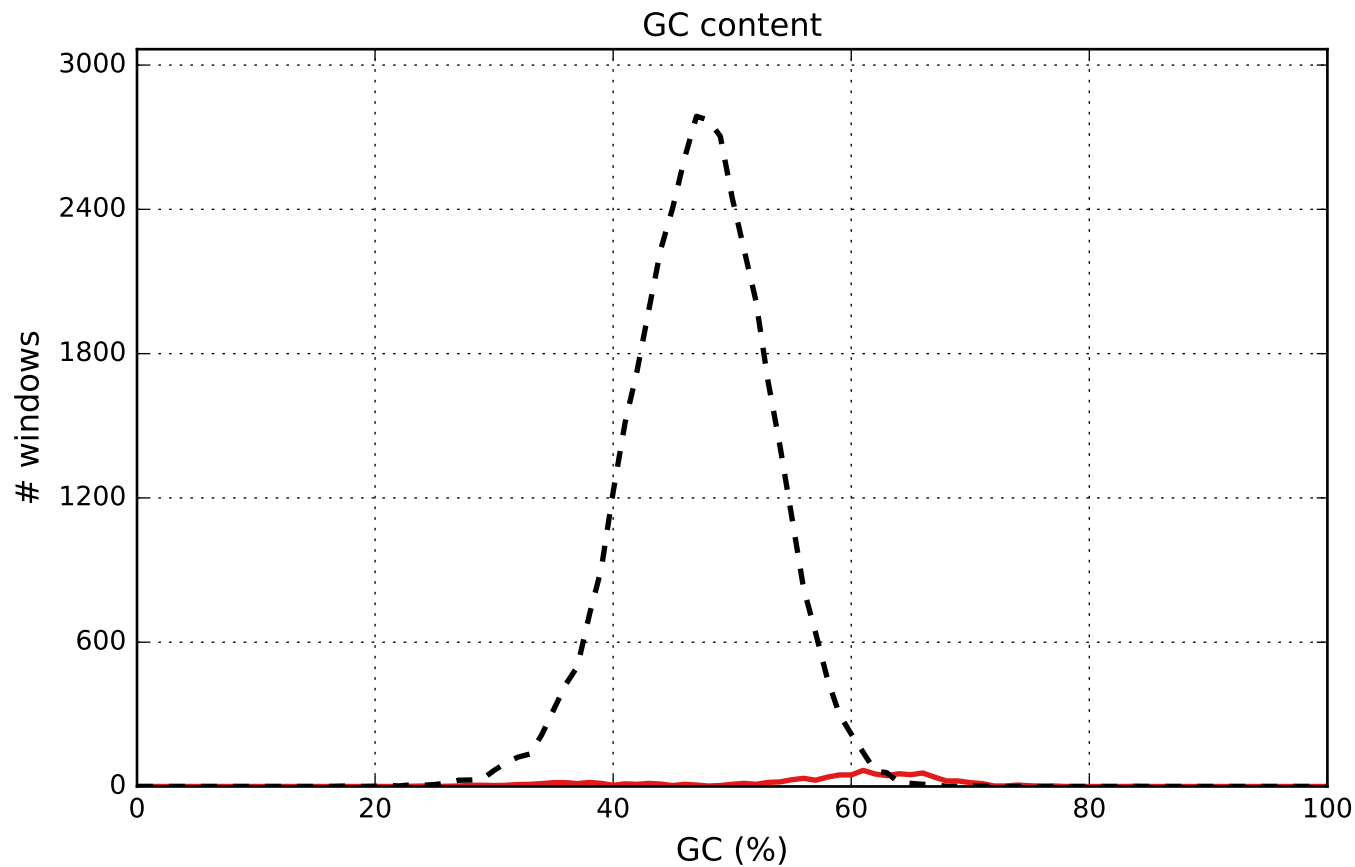
— combined.final.contigs

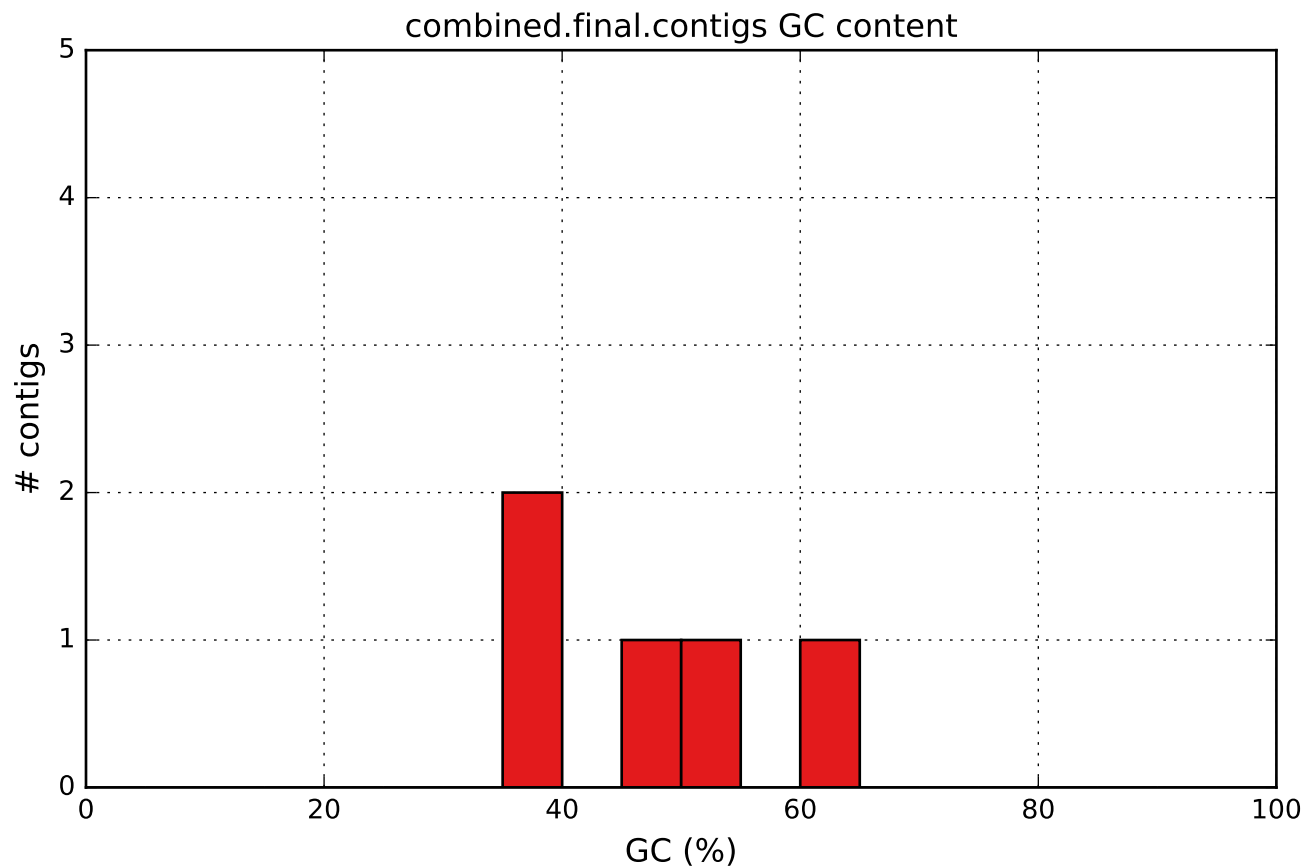
NGx



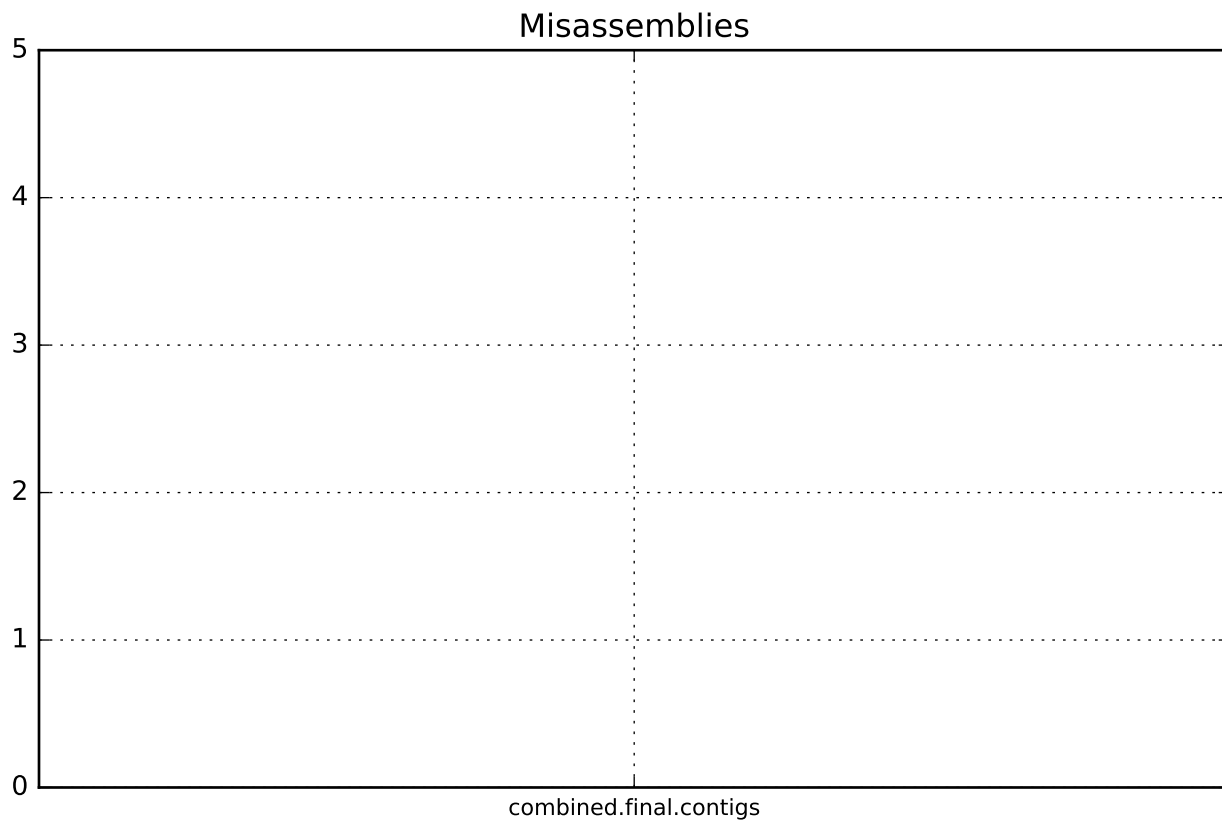
— combined.final.contigs



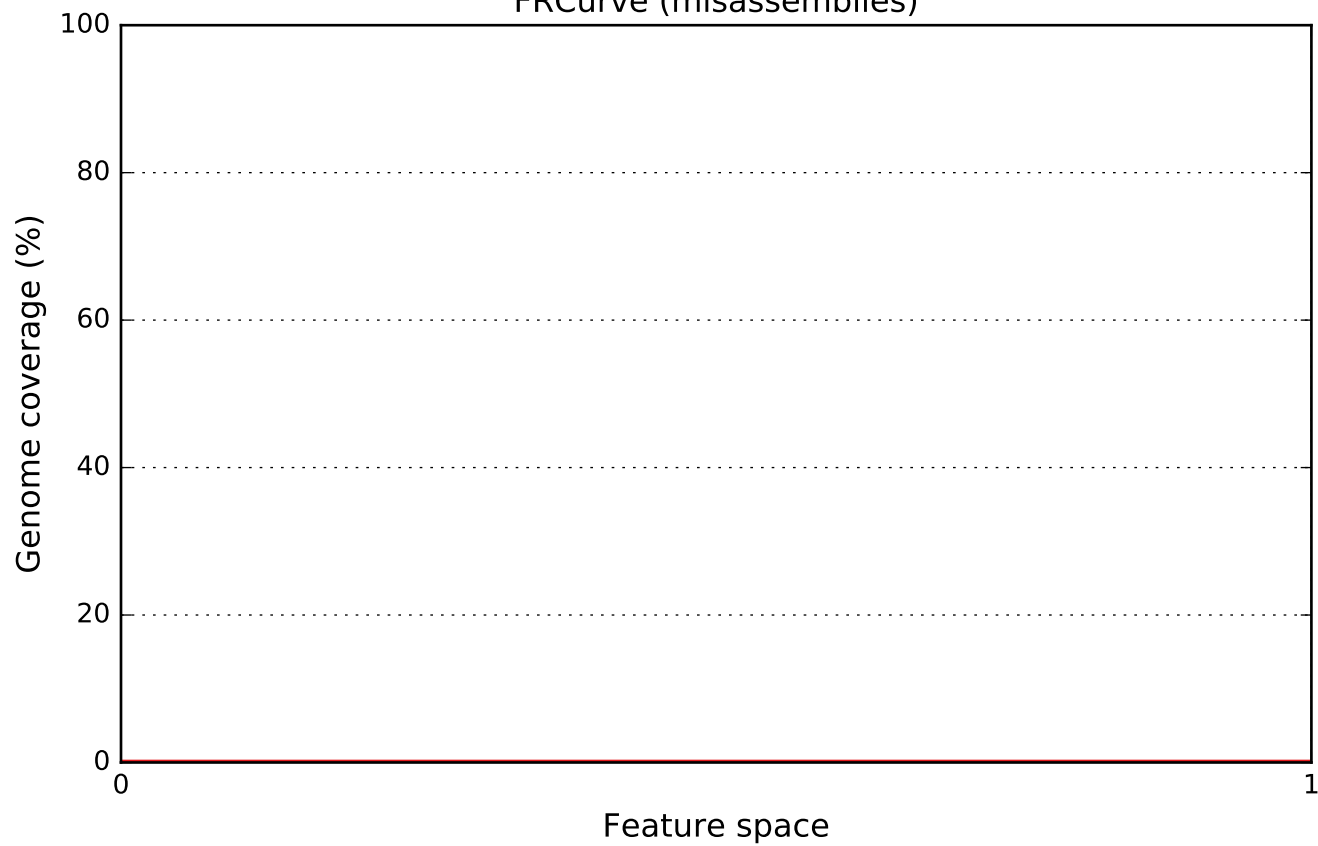




combined.final.contigs

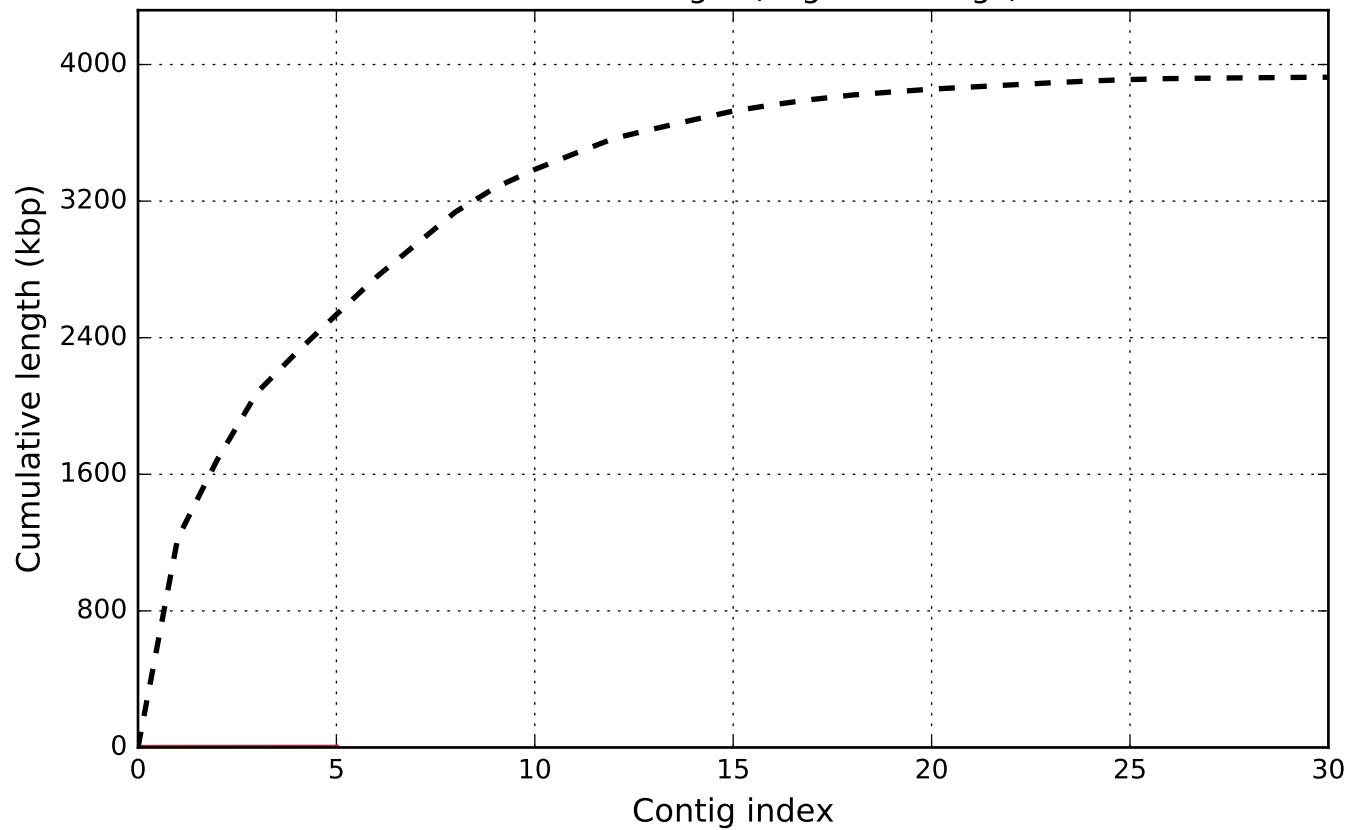


FRCurve (misassemblies)



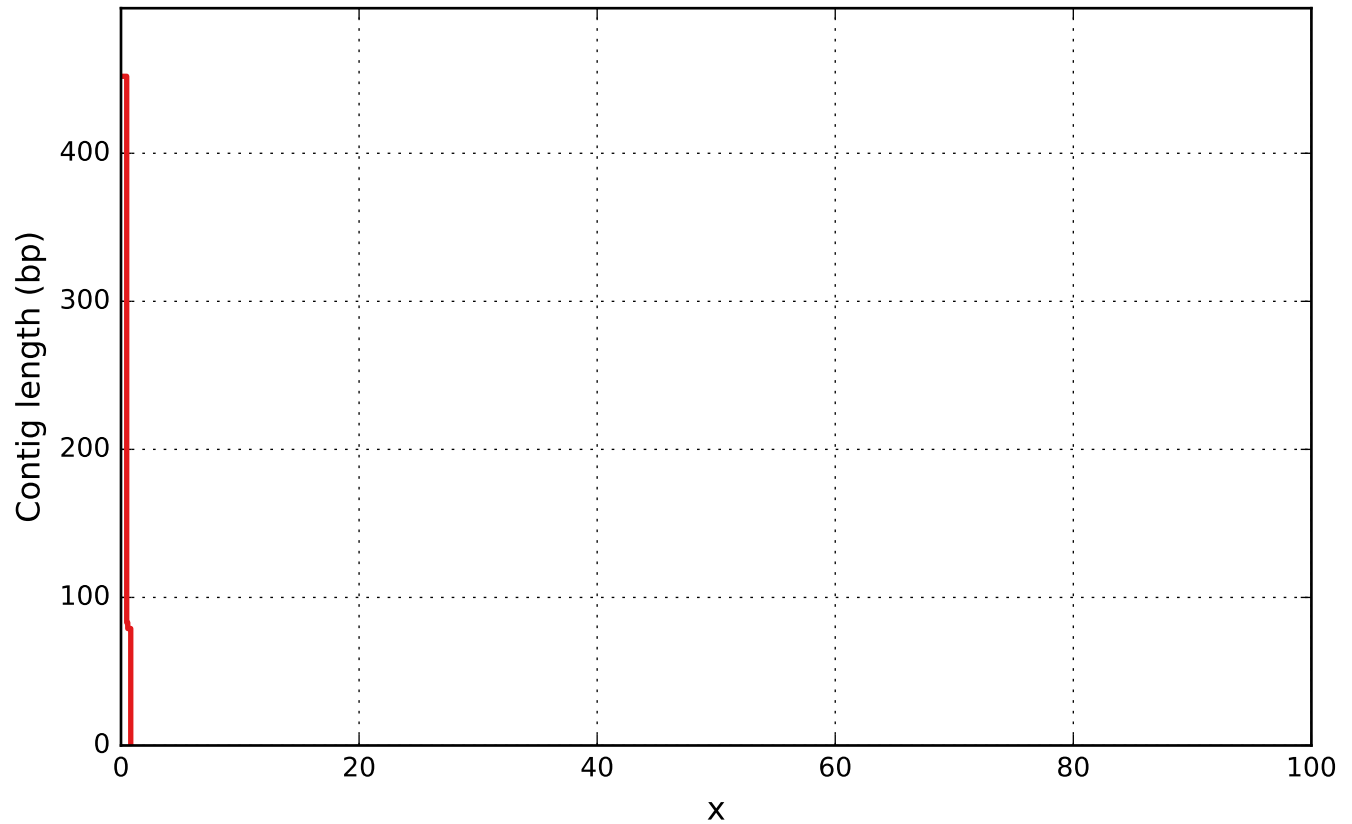
— combined.final.contigs

Cumulative length (aligned contigs)



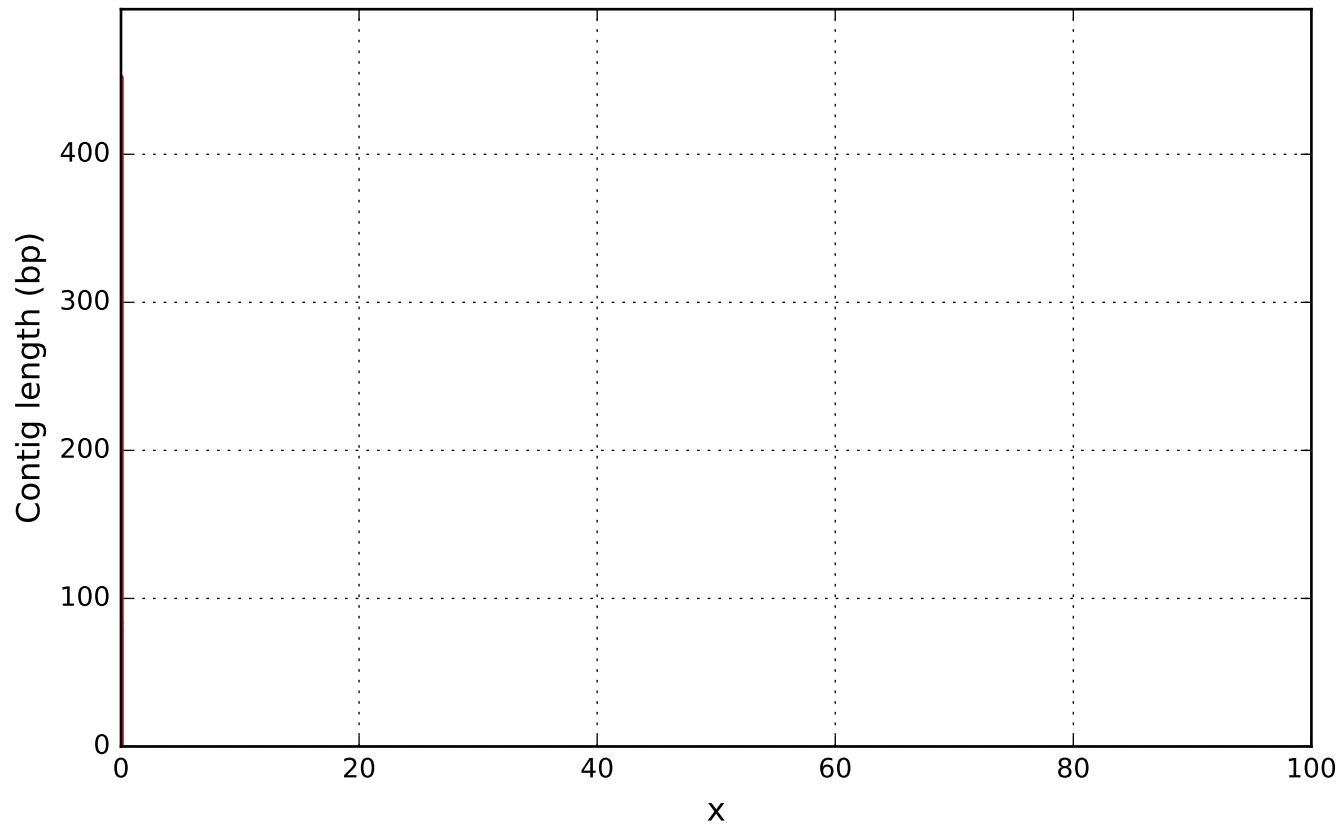
— combined.final.contigs - - Reference

NAx



— combined.final.contigs

NGAx



— combined.final.contigs