

Report

	final.contigs
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	10832
Total length (>= 5000 bp)	6602
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	6
Largest contig	6602
Total length	12206
Reference length	3825707
GC (%)	35.00
Reference GC (%)	32.40
N50	6602
N75	1307
L50	1
L75	3
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 5 part
Unaligned length	11141
Genome fraction (%)	0.020
Duplication ratio	1.409
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2248.68
# indels per 100 kbp	0.00
Largest alignment	377
Total aligned length	756
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

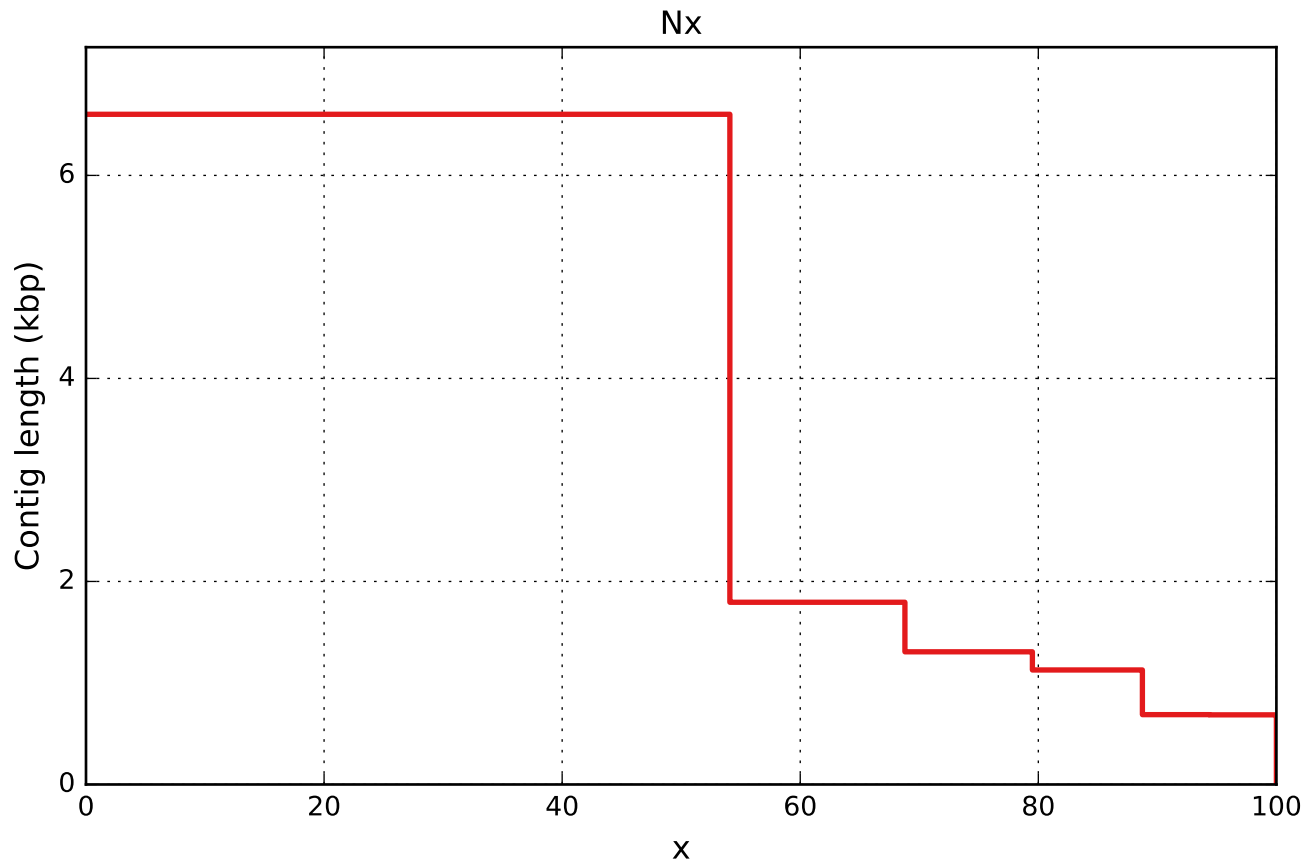
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	17
# indels	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

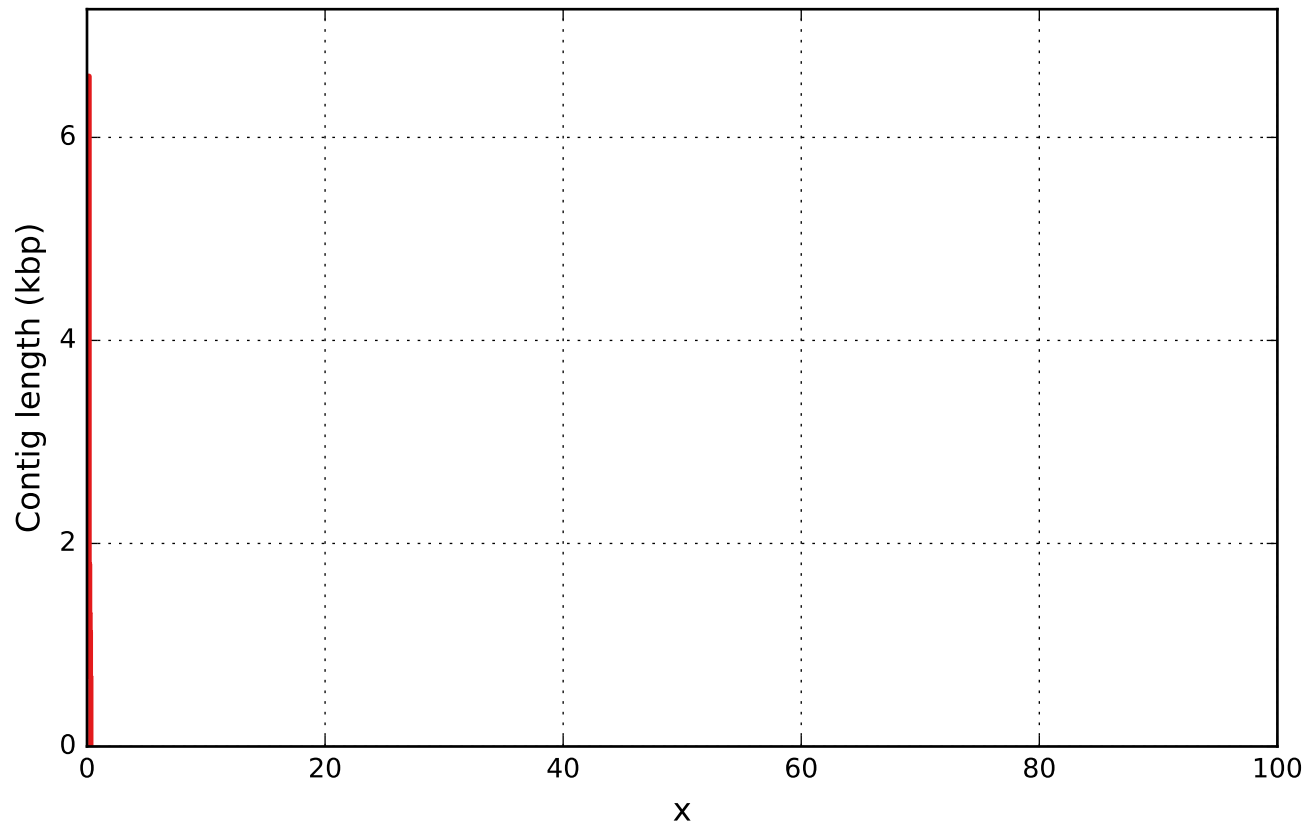
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	5
Partially unaligned length	11141
# N's	0

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).

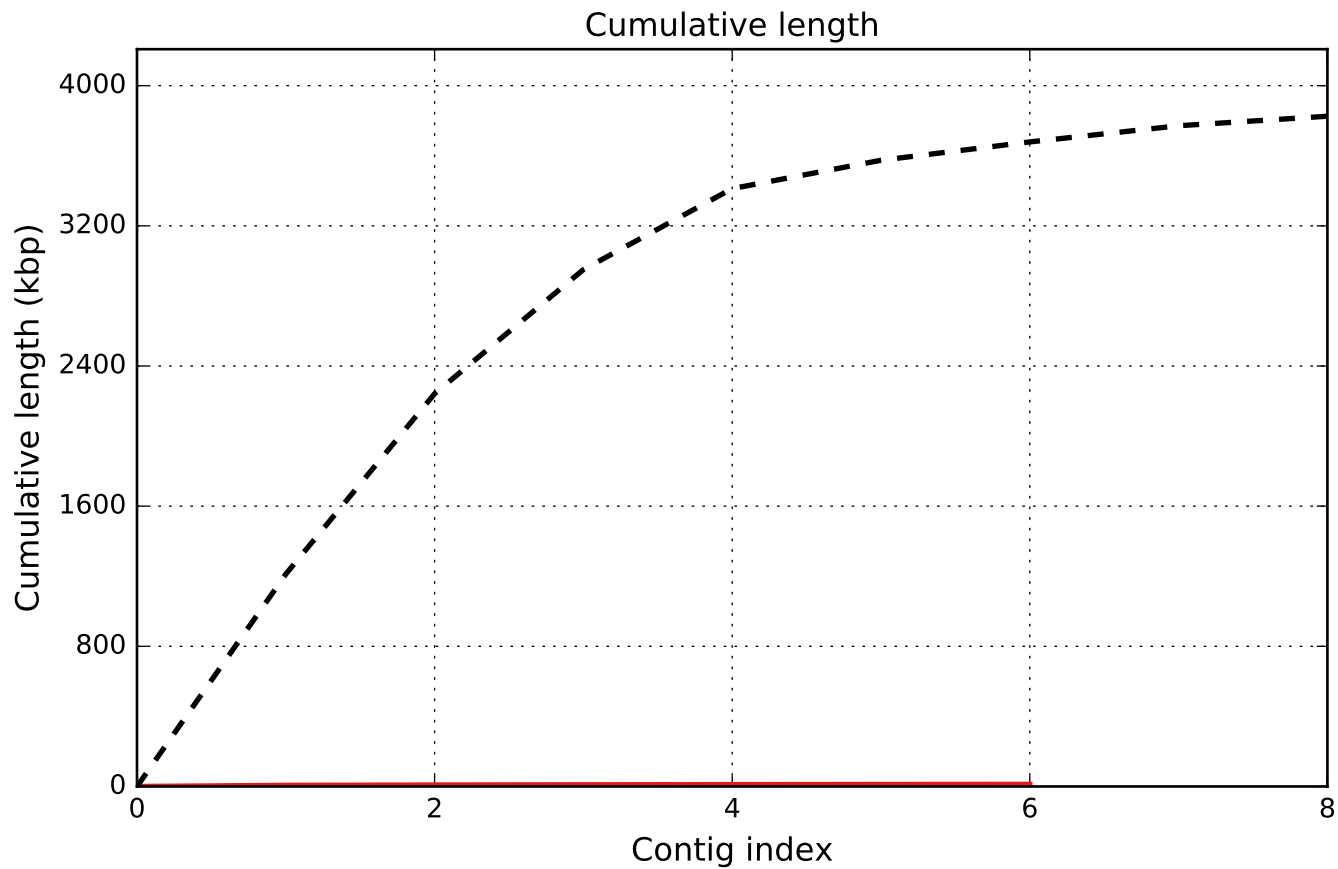


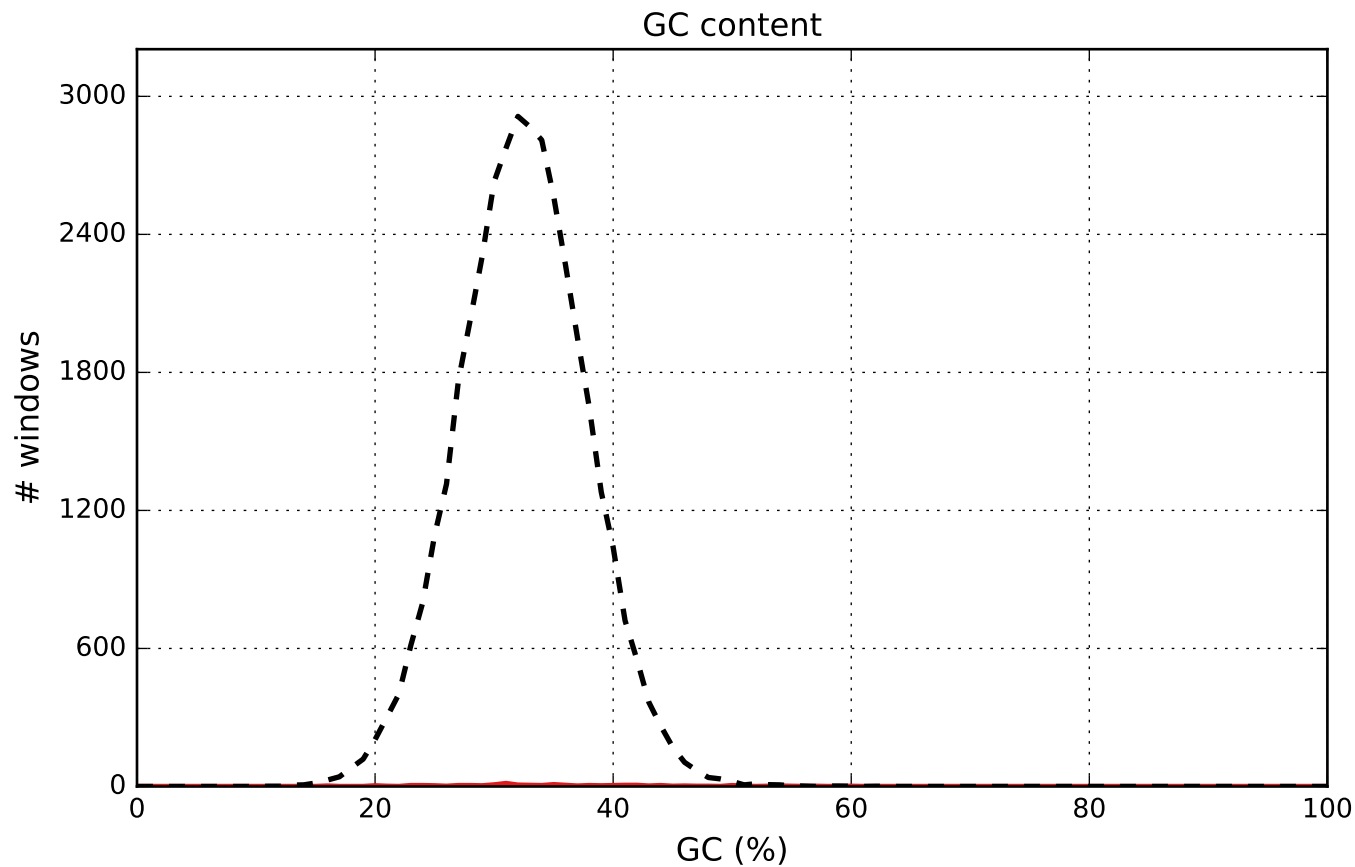
— final.contigs

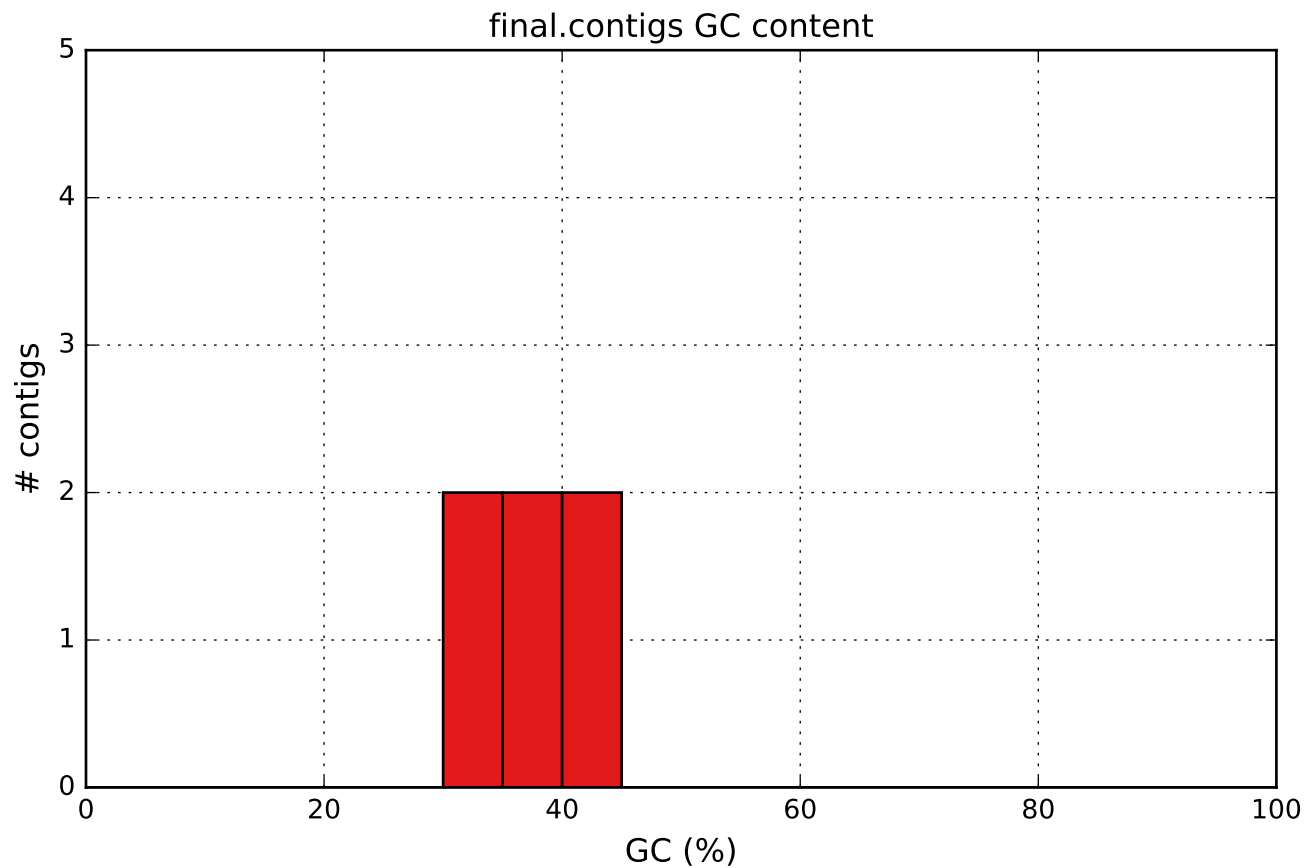
NGx



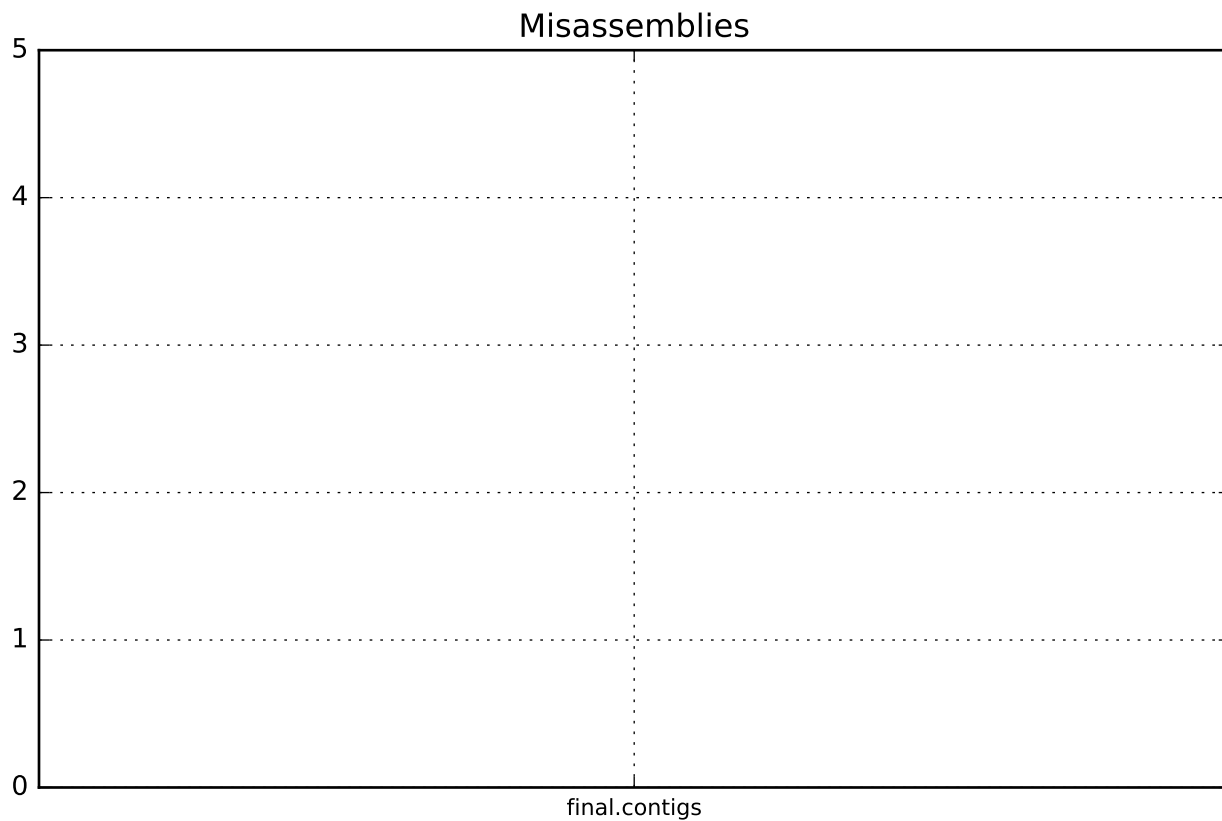
— final.contigs



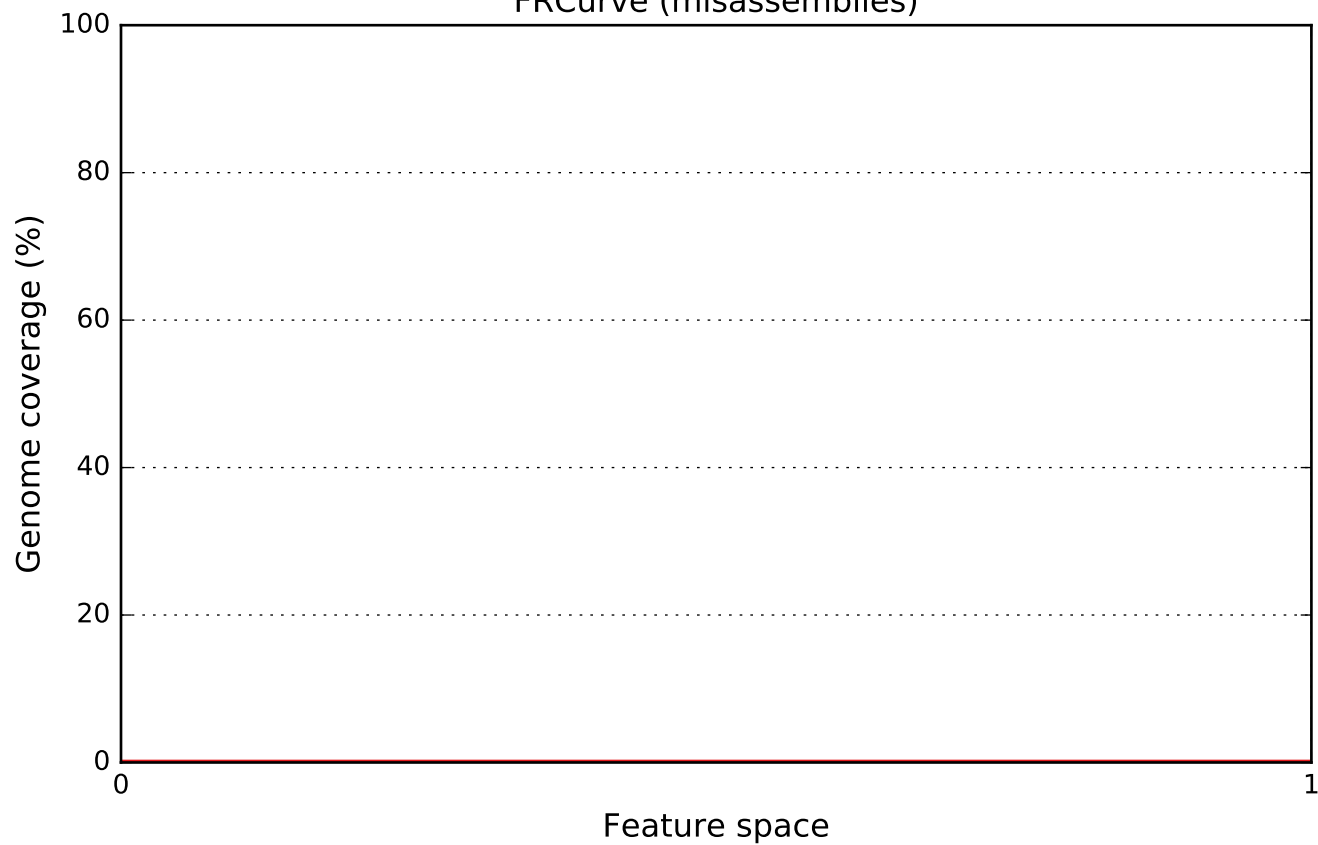




final.contigs

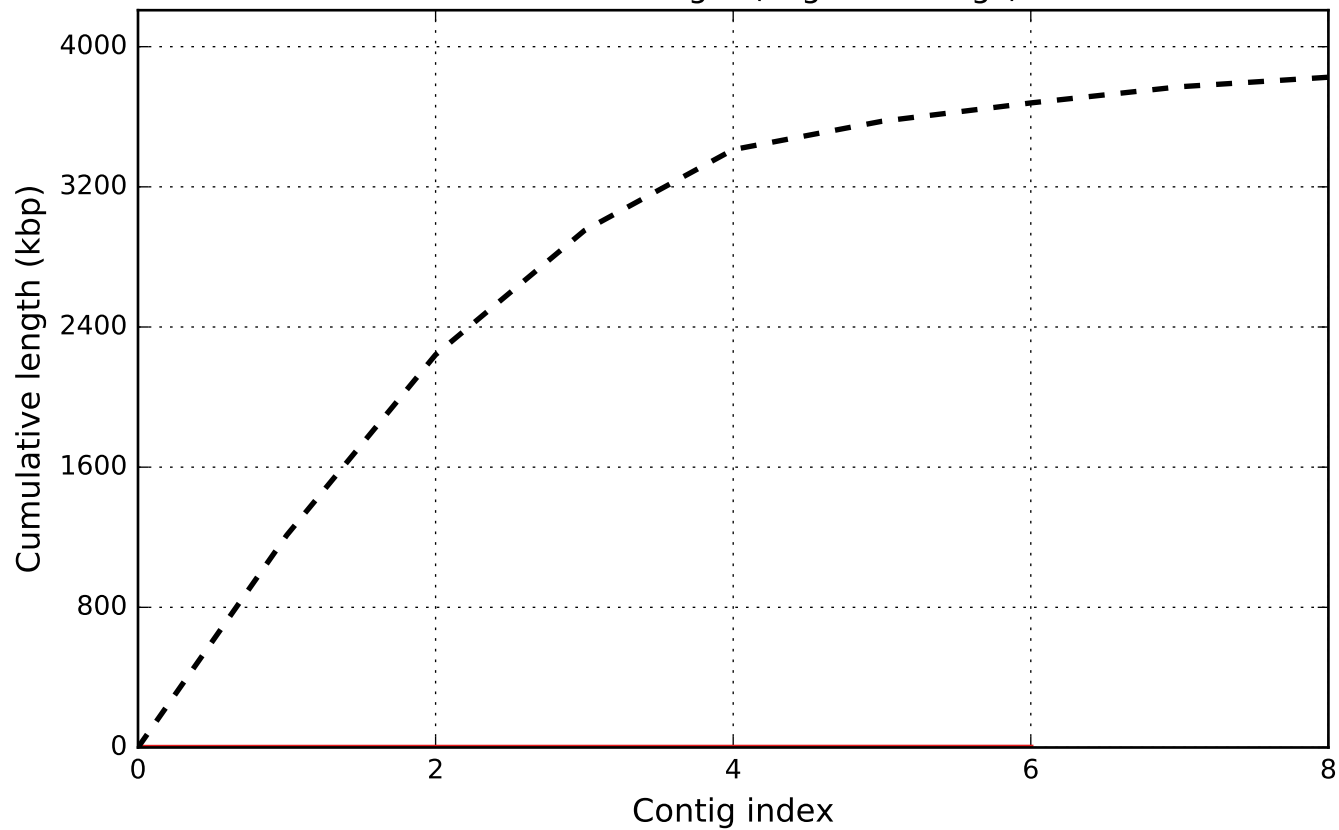


FRCurve (misassemblies)

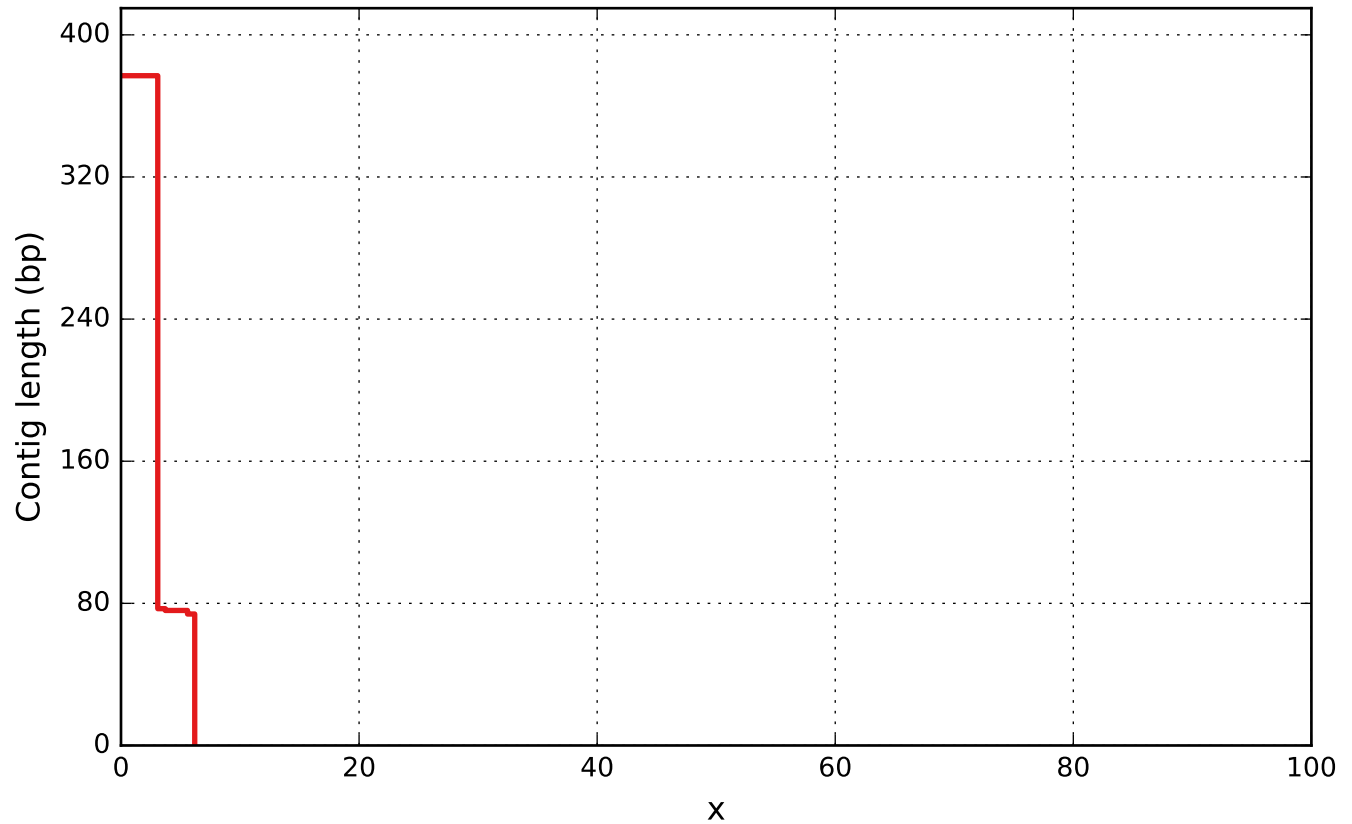


— final.contigs

Cumulative length (aligned contigs)

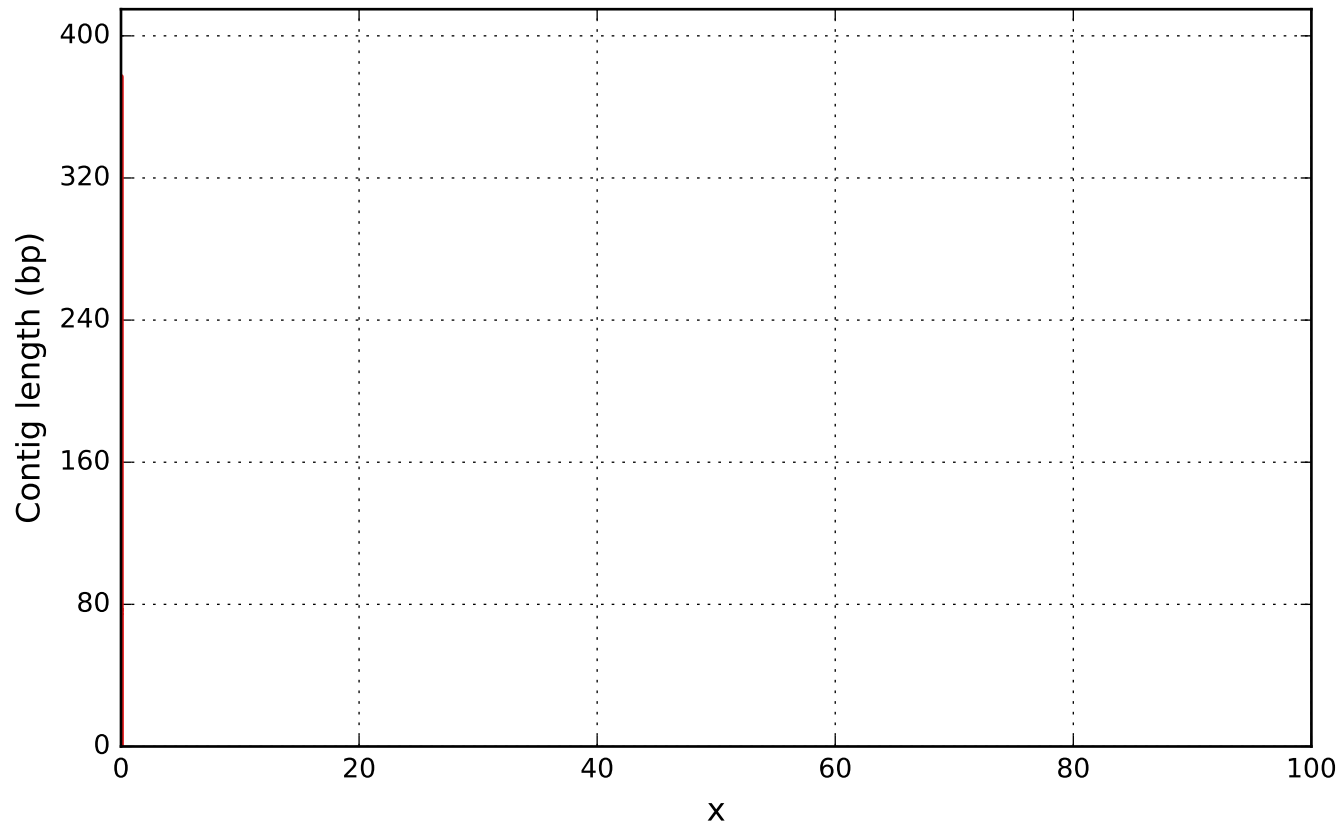


NAx



— final.contigs

NGAx



— final.contigs