

## Report

	uniq_contigs_contigs_contigs_contigs_contigs
# contigs (>= 0 bp)	893
# contigs (>= 1000 bp)	141
# contigs (>= 5000 bp)	46
# contigs (>= 10000 bp)	43
# contigs (>= 25000 bp)	35
# contigs (>= 50000 bp)	34
Total length (>= 0 bp)	56040006
Total length (>= 1000 bp)	55603682
Total length (>= 5000 bp)	55455374
Total length (>= 10000 bp)	55432649
Total length (>= 25000 bp)	55304596
Total length (>= 50000 bp)	55273984
# contigs	893
Largest contig	6805451
Total length	56040006
Reference length	59128983
GC (%)	48.37
Reference GC (%)	48.36
N50	2707433
NG50	2648109
N75	1495452
NG75	1237545
L50	6
LG50	7
L75	12
LG75	14
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	6813834
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# possible TEs	0
# unaligned mis. contigs	0
# unaligned contigs	362 + 0 part
Unaligned length	157566
Genome fraction (%)	99.888
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.15
# indels per 100 kbp	0.07
Largest alignment	6805451
Total aligned length	55882408
NA50	2547739
NGA50	2547739
NA75	1495452
NGA75	1237545
LA50	7
LGA50	7
LA75	13
LGA75	15

All statistics are based on contigs of size >= 400 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

## Misassemblies report

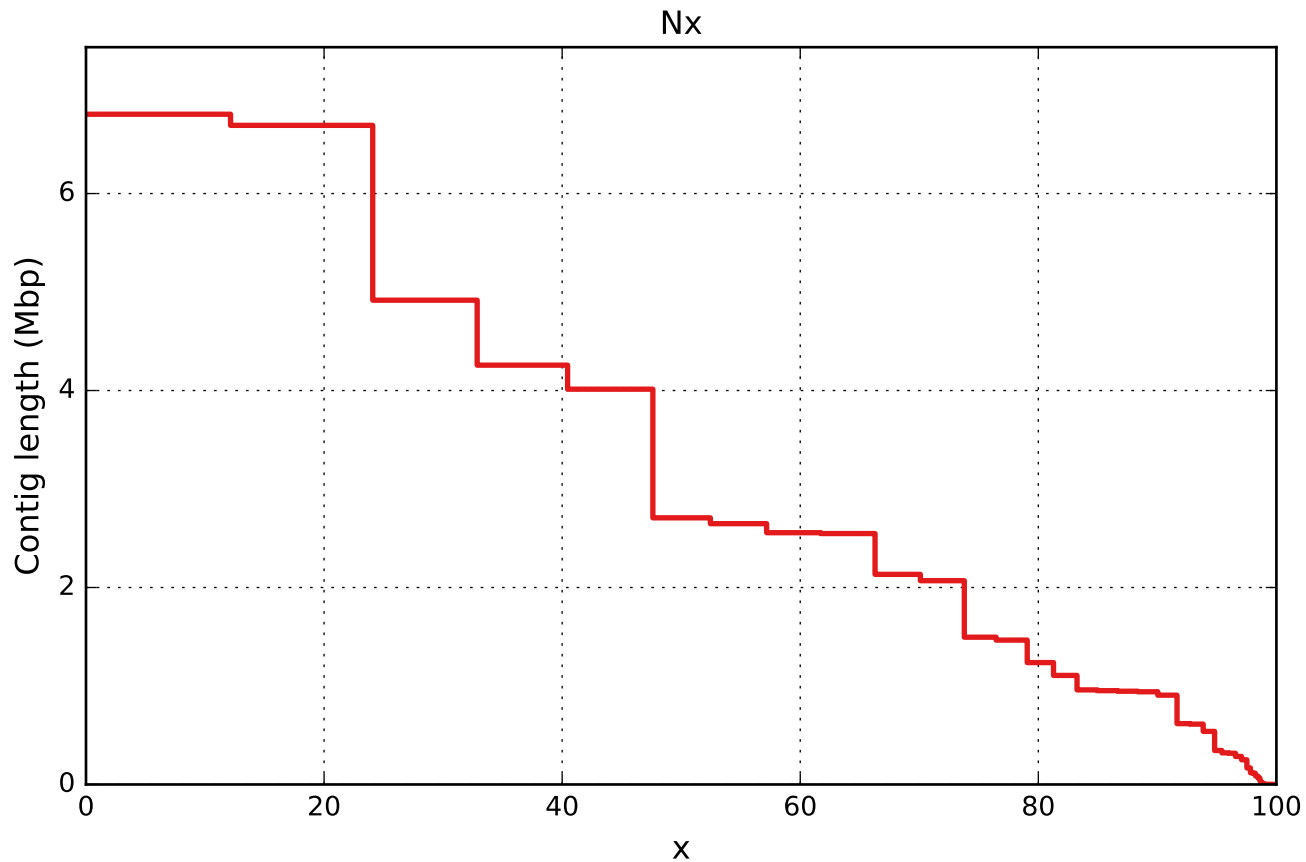
	uniq_contigs_contigs_contigs_contigs_contigs
# misassemblies	2
# contig misassemblies	2
# c. relocations	2
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	2
Misassembled contigs length	6813834
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# misassemblies caused by fragmented reference	0
# possible TEs	0
# unaligned mis. contigs	0
# mismatches	82
# indels	41
# indels (<= 5 bp)	36
# indels (> 5 bp)	5
Indels length	725

All statistics are based on contigs of size  $\geq 400$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

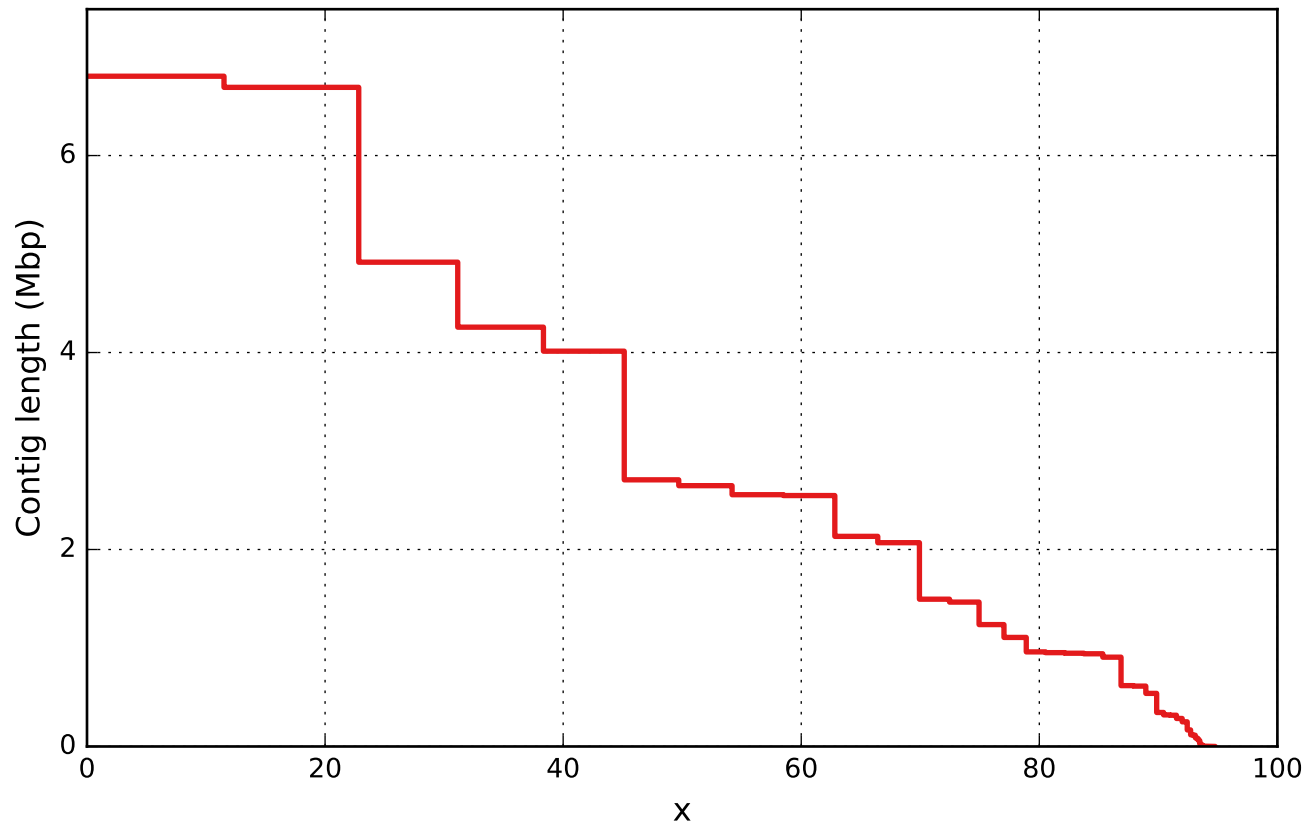
	uniq_contigs_contigs_contigs_contigs
# fully unaligned contigs	362
Fully unaligned length	157566
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

All statistics are based on contigs of size  $\geq 400$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

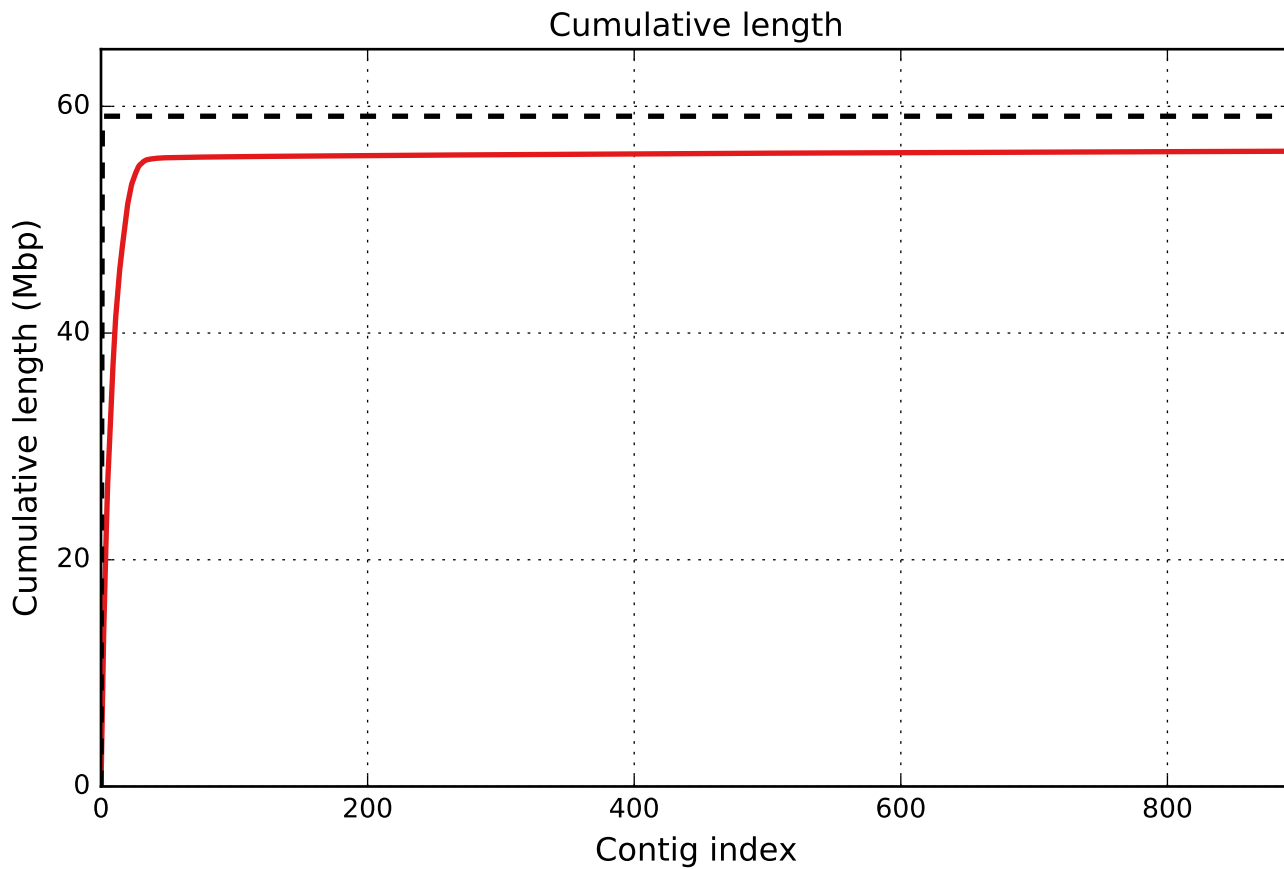


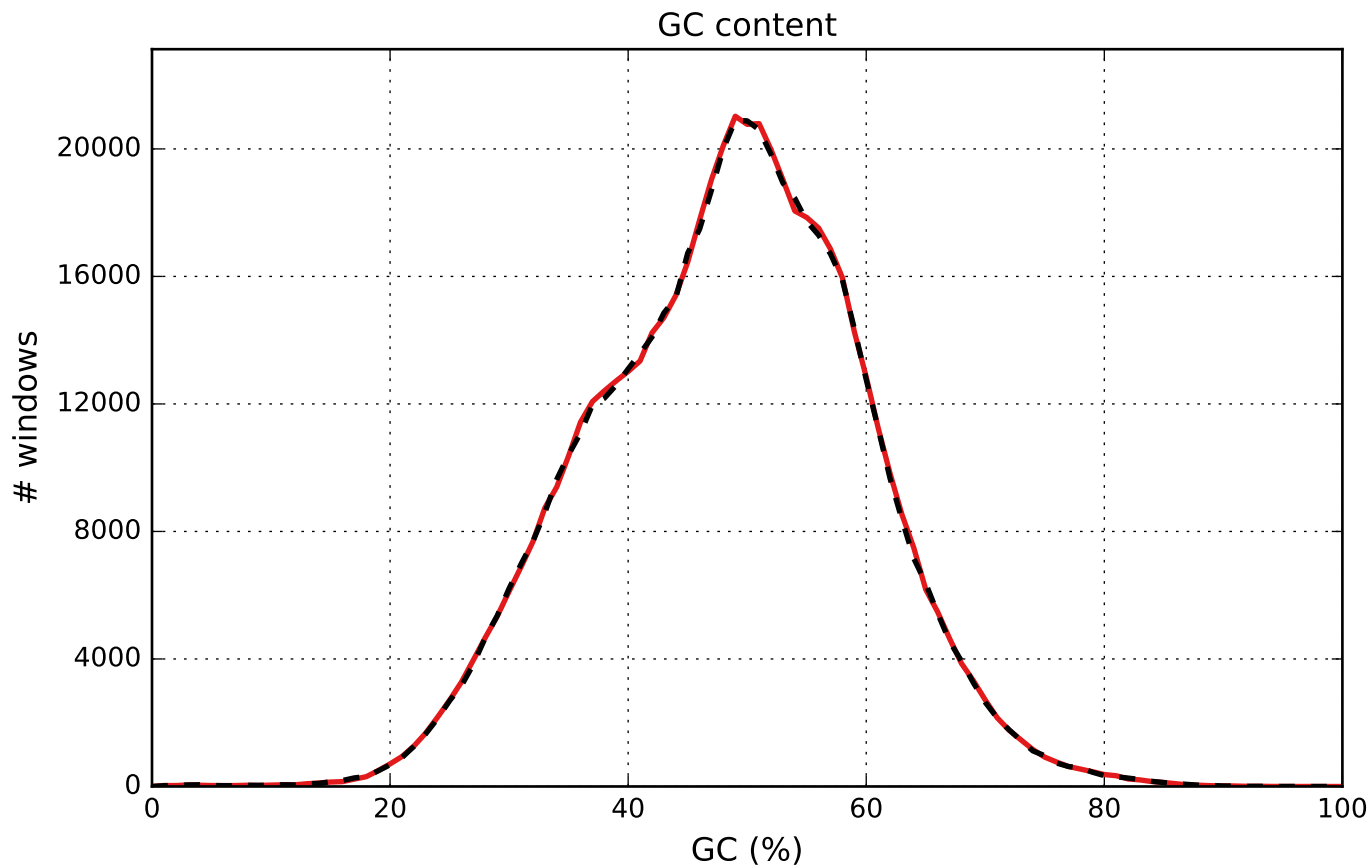
— uniq\_contigs\_contigs\_contigs\_contigs

NGx



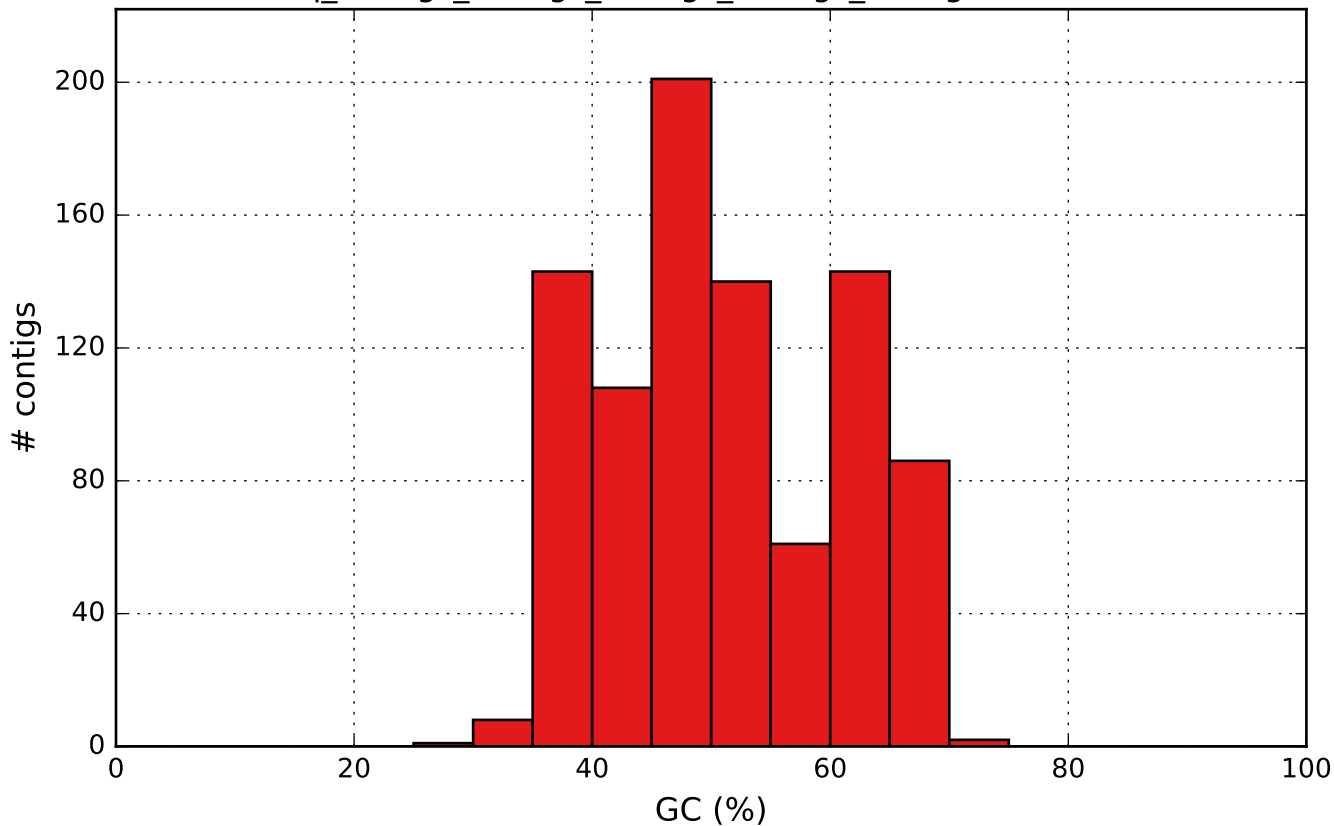
— uniq\_contigs\_contigs\_contigs\_contigs





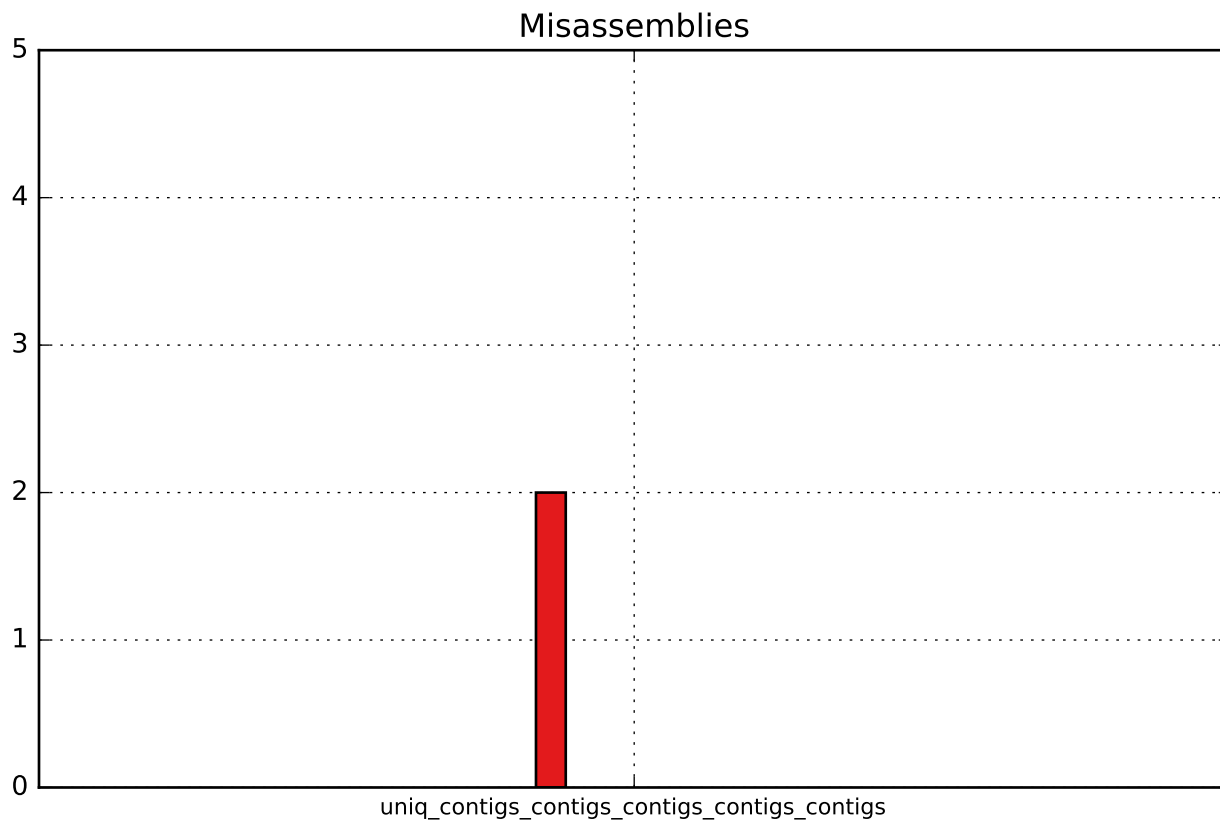
— uniq\_contigs\_contigs\_contigs\_contigs      - - Reference

uniq\_contigs\_contigs\_contigs\_contigs\_contigs GC content

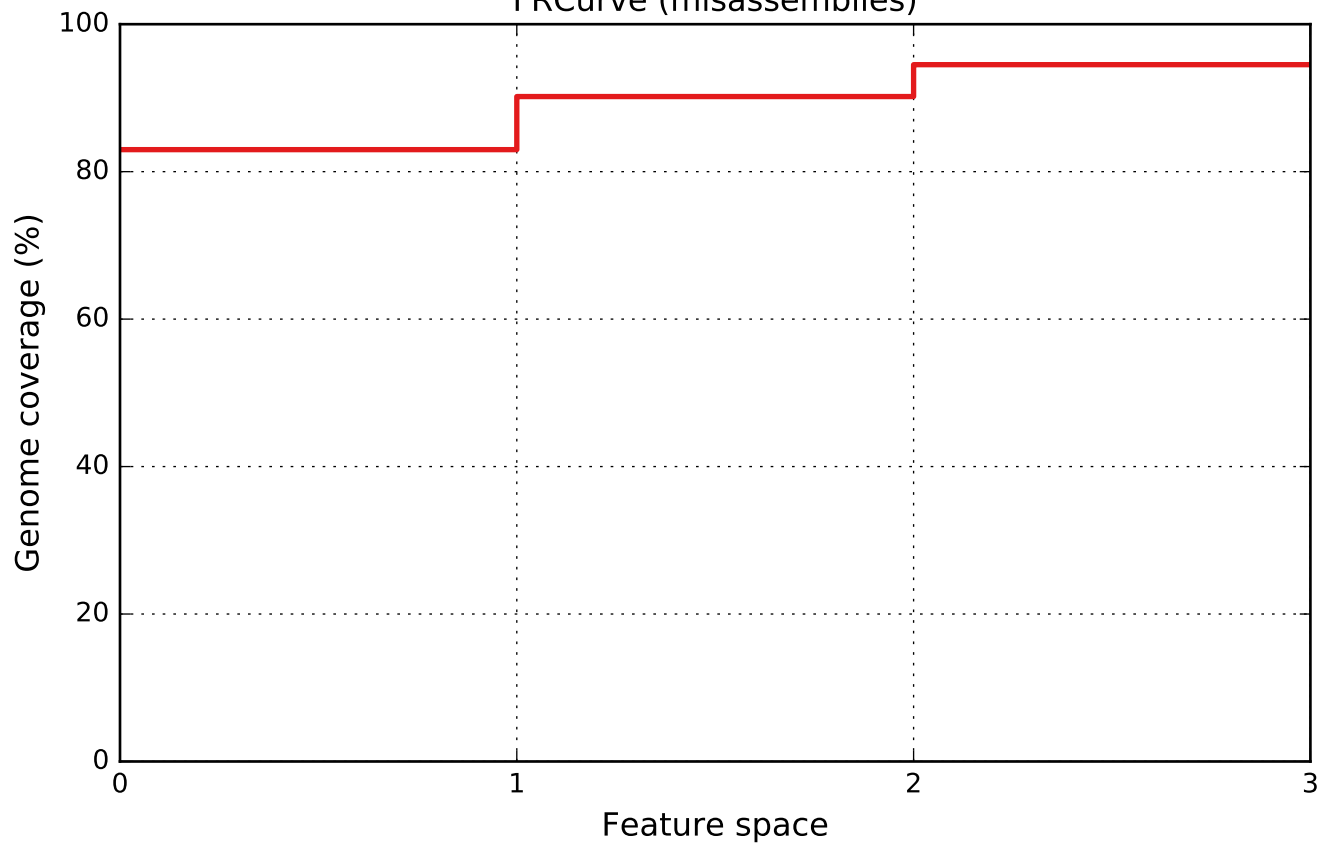


uniq\_contigs\_contigs\_contigs\_contigs\_contigs



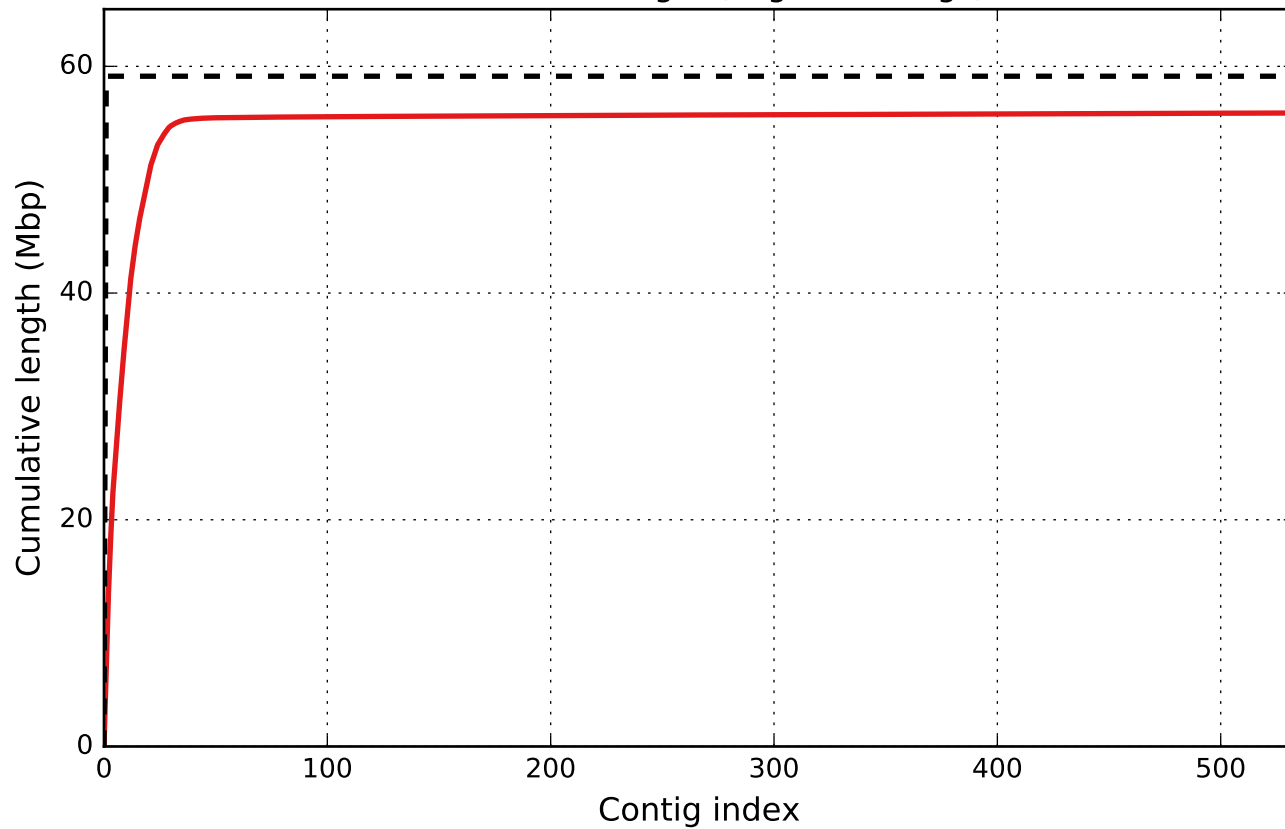


FRCurve (misassemblies)



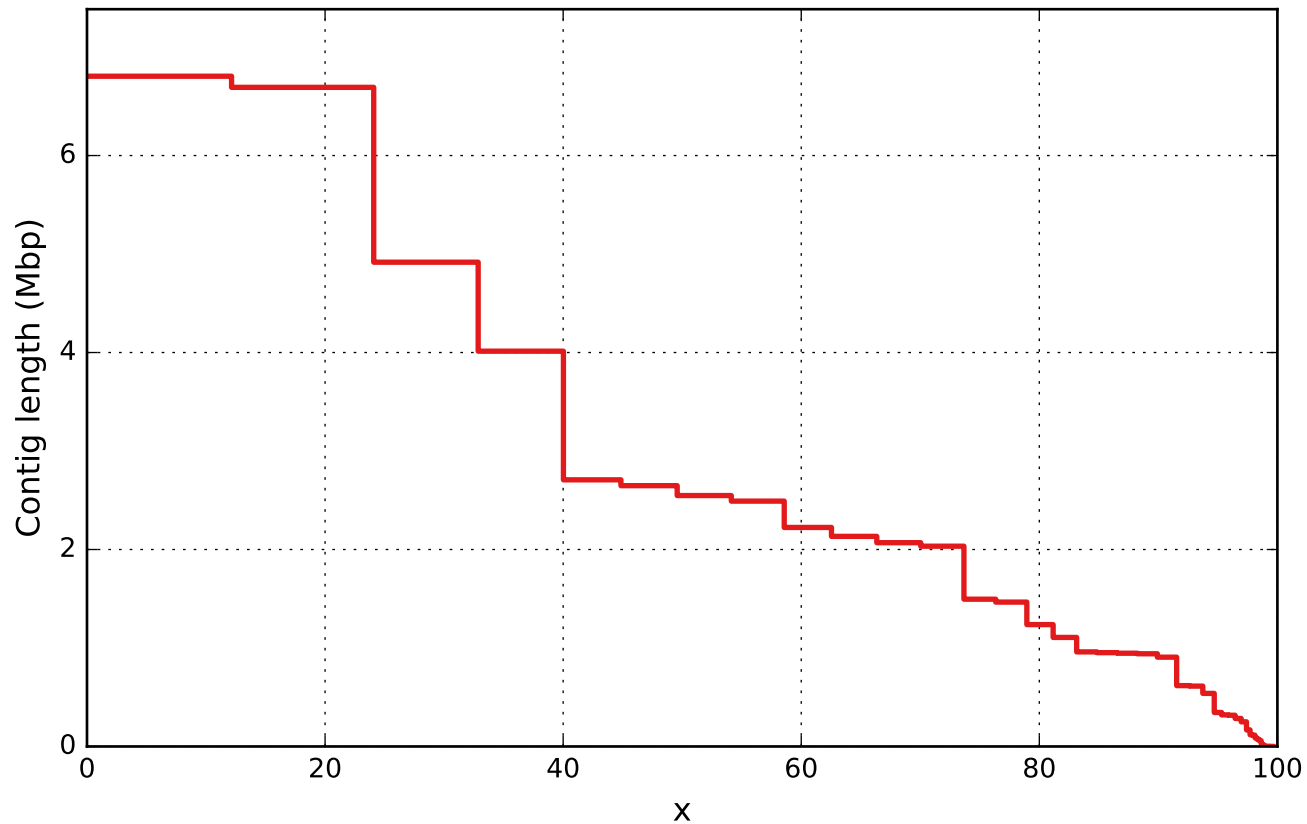
— uniq\_contigs\_contigs\_contigs\_contigs\_contigs

Cumulative length (aligned contigs)



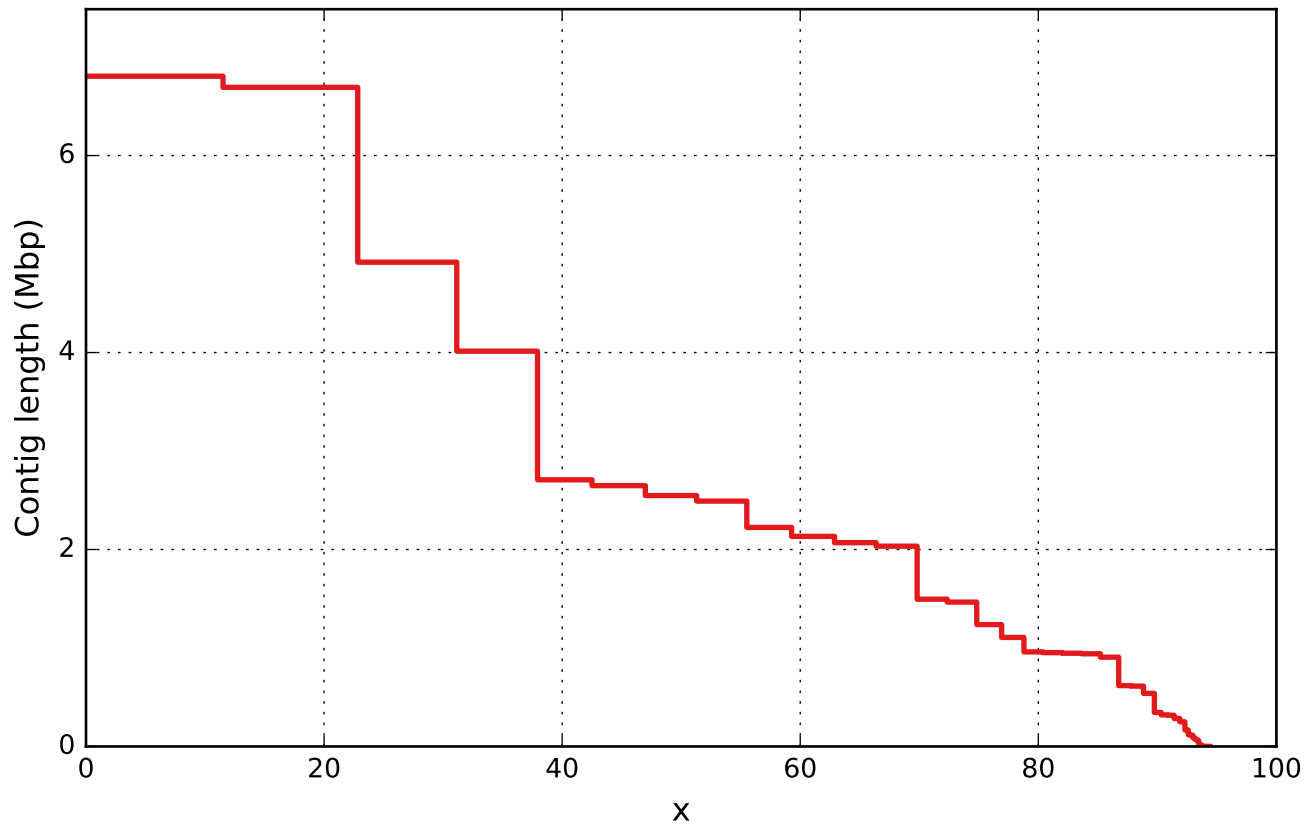
— uniq\_contigs\_contigs\_contigs\_contigs      - - Reference

NAx



— uniq\_contigs\_contigs\_contigs\_contigs

# NGAx



— uniq\_contigs\_contigs\_contigs\_contigs