

Report

	Contigs
# contigs (>= 0 bp)	1014
# contigs (>= 1000 bp)	805
# contigs (>= 5000 bp)	389
# contigs (>= 10000 bp)	122
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4890536
Total length (>= 1000 bp)	4796447
Total length (>= 5000 bp)	3630483
Total length (>= 10000 bp)	1734053
Total length (>= 25000 bp)	27789
Total length (>= 50000 bp)	0
# contigs	876
Largest contig	27789
Total length	4851130
Reference length	4878012
GC (%)	52.08
Reference GC (%)	52.18
N50	8135
NG50	8084
N75	4992
NG75	4966
L50	199
LG50	201
L75	391
LG75	395
# misassemblies	77
# misassembled contigs	74
Misassembled contigs length	439620
# local misassemblies	7
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# unaligned contigs	28 + 11 part
Unaligned length	160259
Genome fraction (%)	89.904
Duplication ratio	1.070
# N's per 100 kbp	0.00
# mismatches per 100 kbp	26.02
# indels per 100 kbp	1.73
Largest alignment	27789
Total aligned length	4686264
NA50	7639
NGA50	7626
NA75	4435
NGA75	4379
LA50	207
LGA50	208
LA75	413
LGA75	418

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

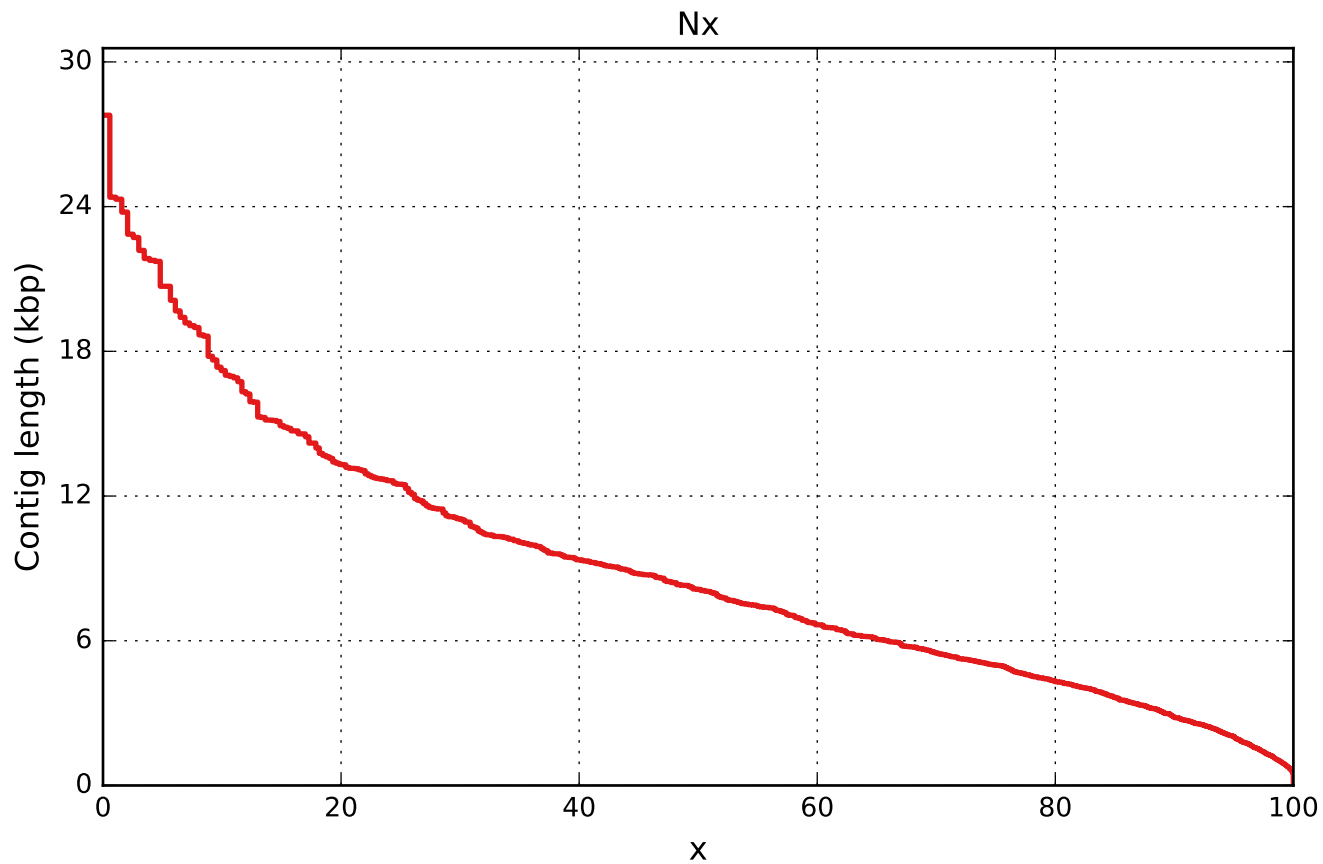
	Contigs
# misassemblies	77
# contig misassemblies	77
# c. relocations	37
# c. translocations	0
# c. inversions	40
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	74
Misassembled contigs length	439620
# local misassemblies	7
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	1141
# indels	76
# indels (<= 5 bp)	56
# indels (> 5 bp)	20
Indels length	482

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

## Unaligned report

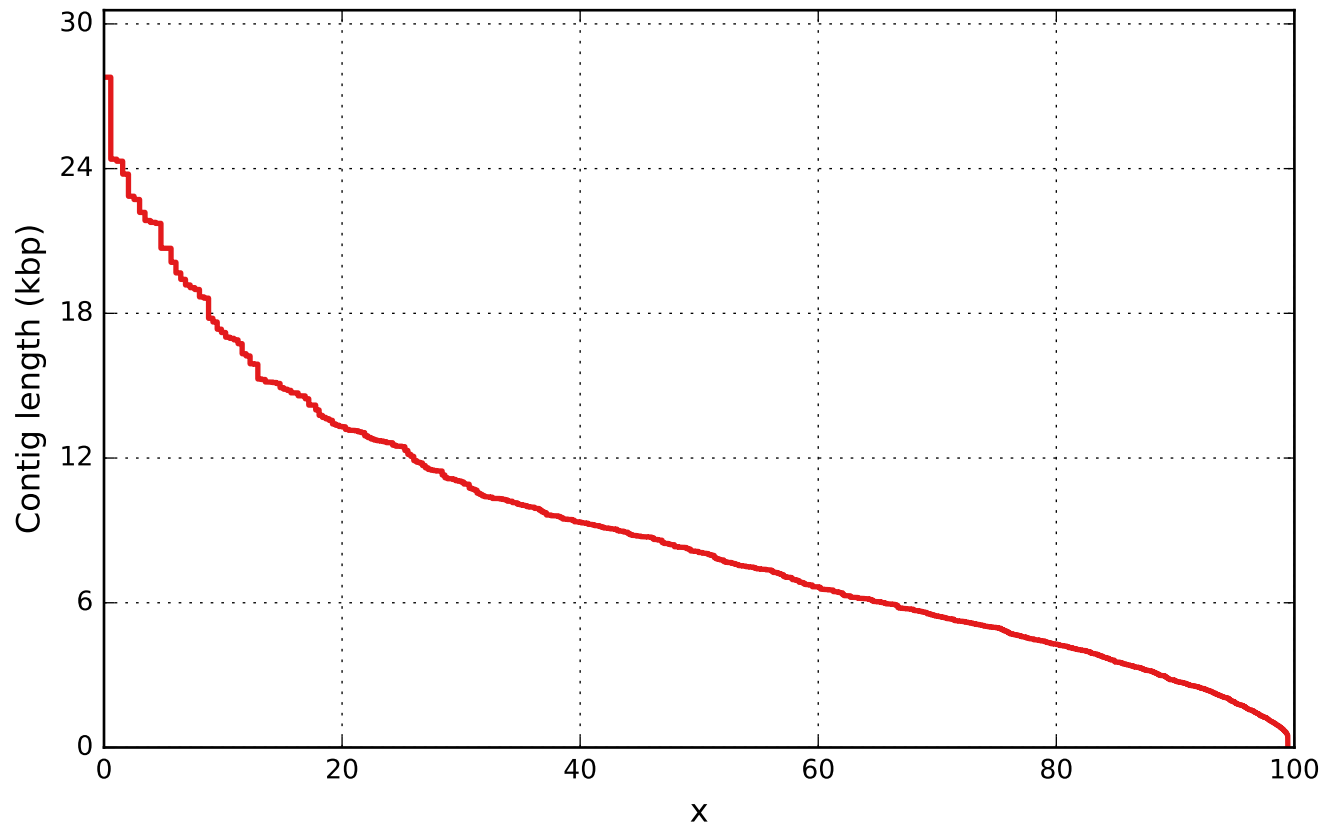
	Contigs
# fully unaligned contigs	28
Fully unaligned length	138796
# partially unaligned contigs	11
Partially unaligned length	21463
# N's	0

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

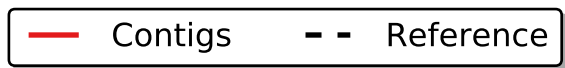
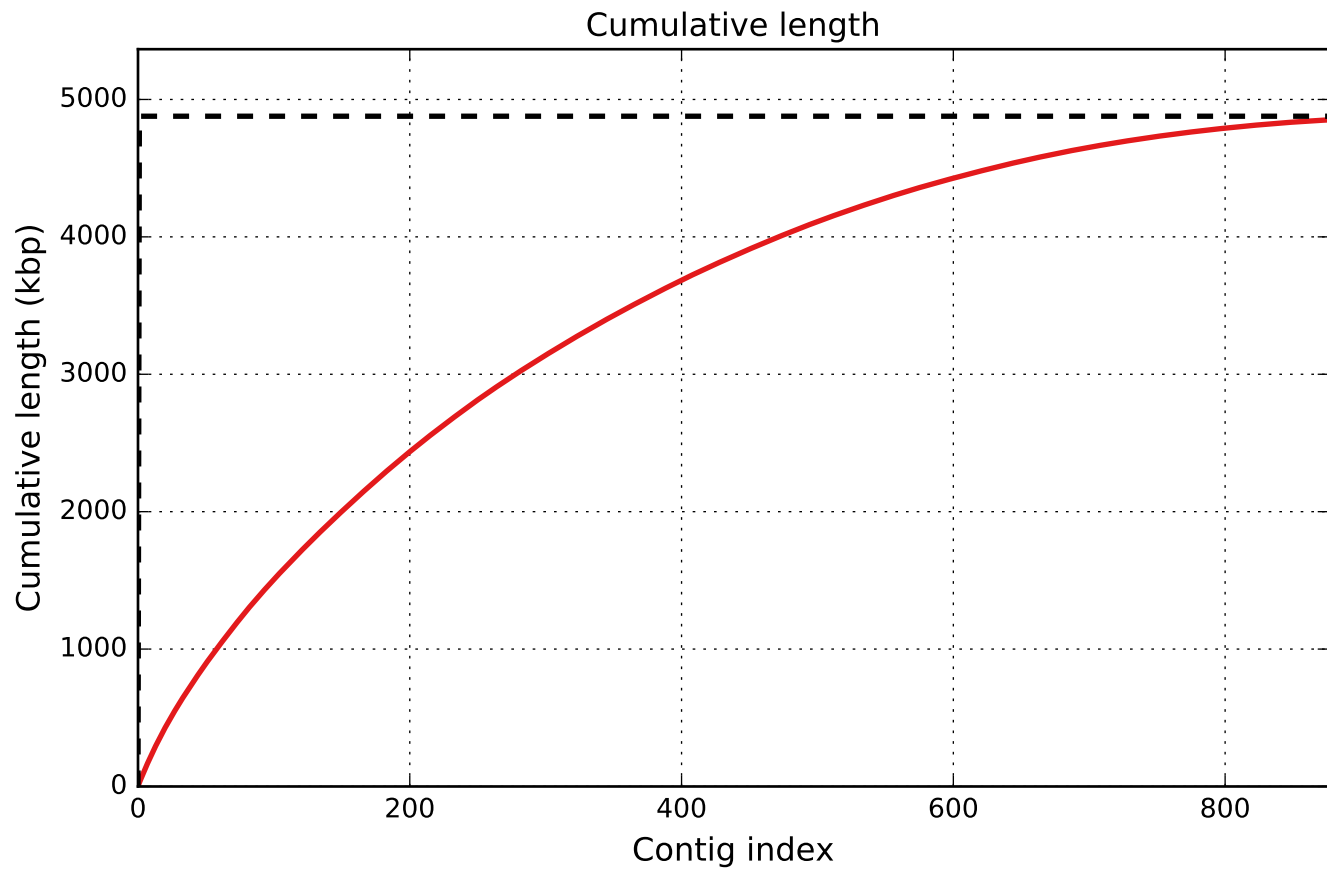


— Contigs

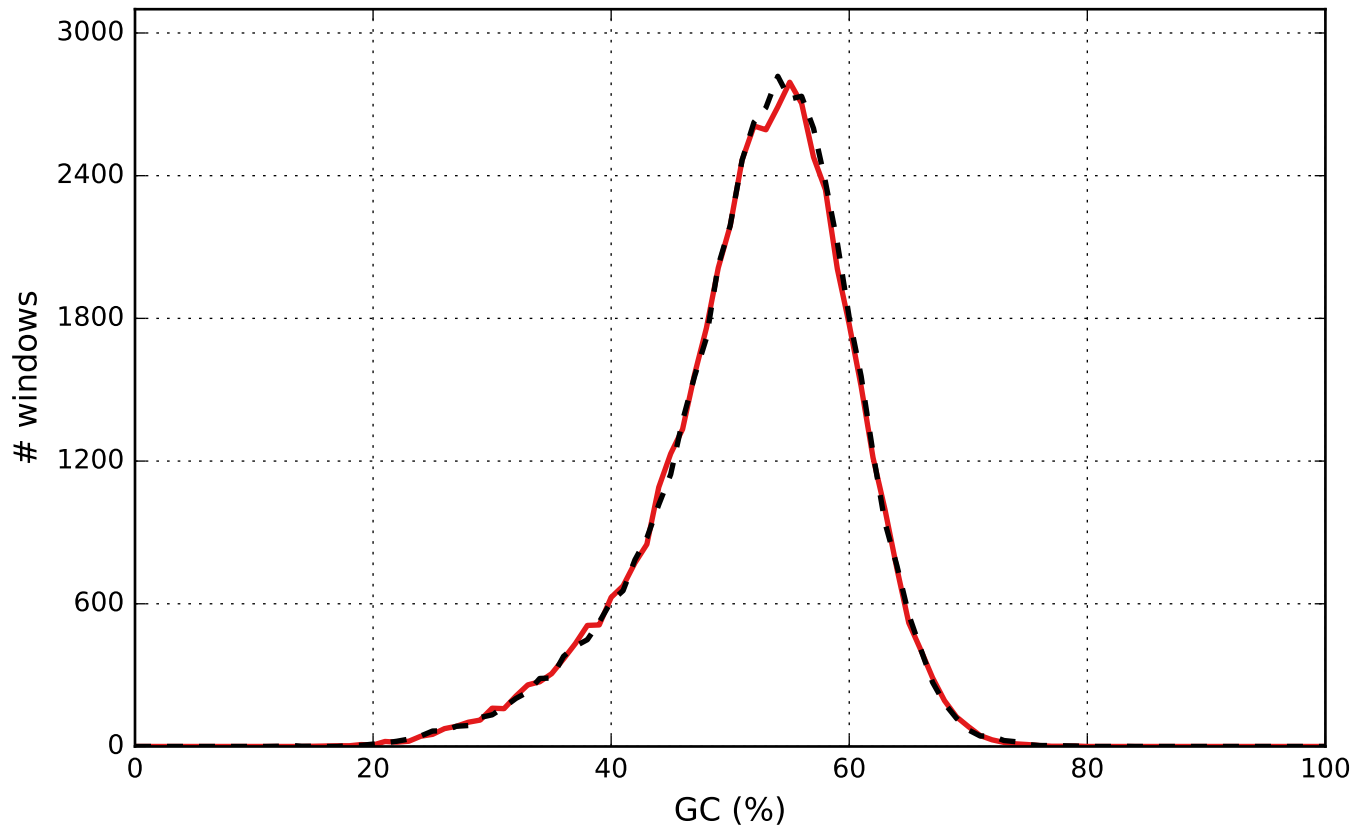
NGx



— Contigs

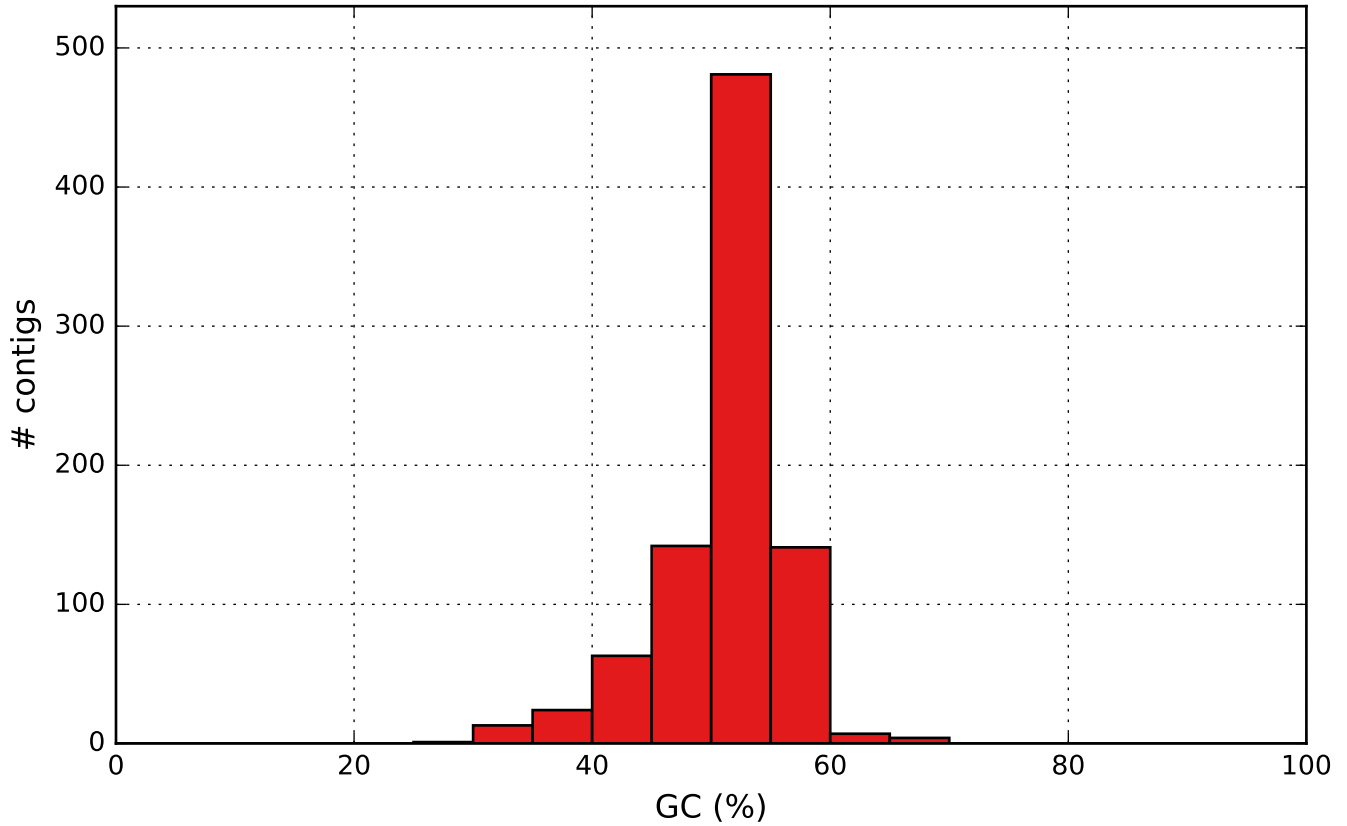


# GC content



— Contigs    - - Reference

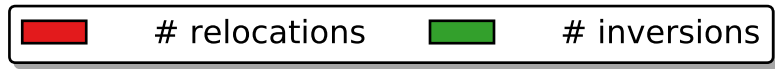
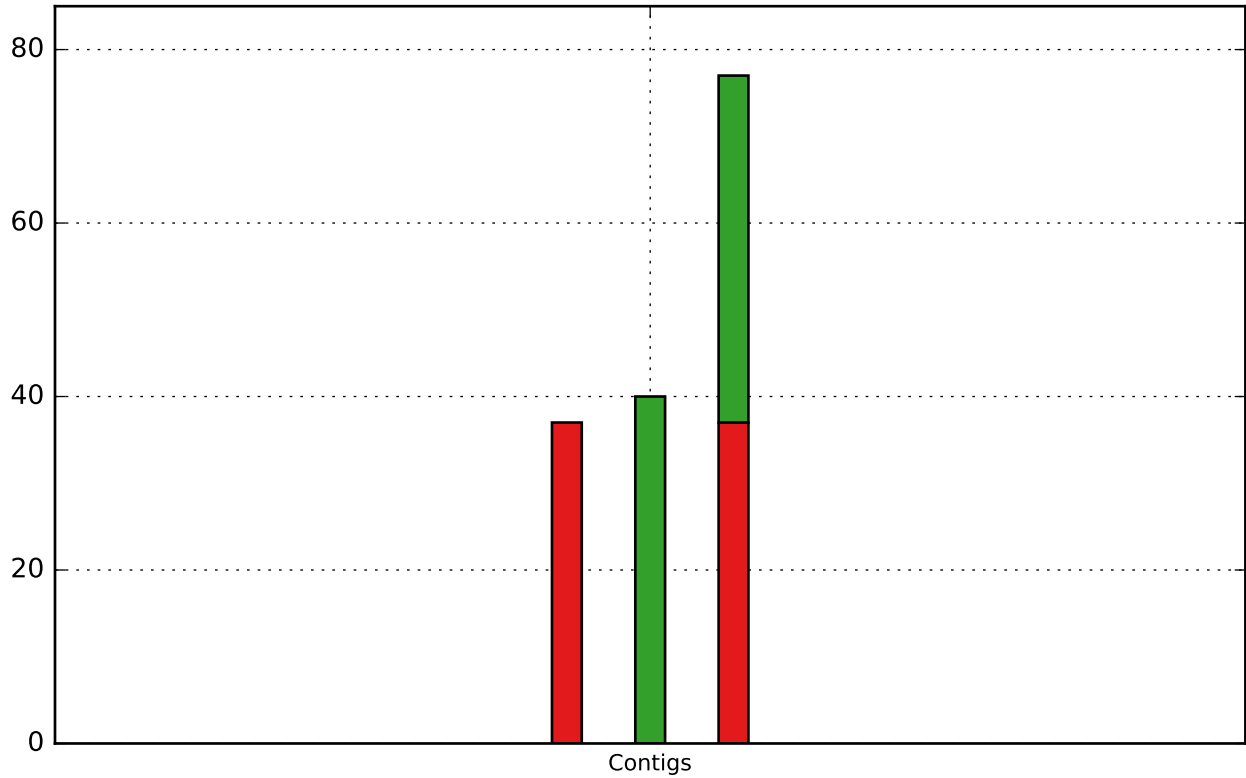
Contigs GC content



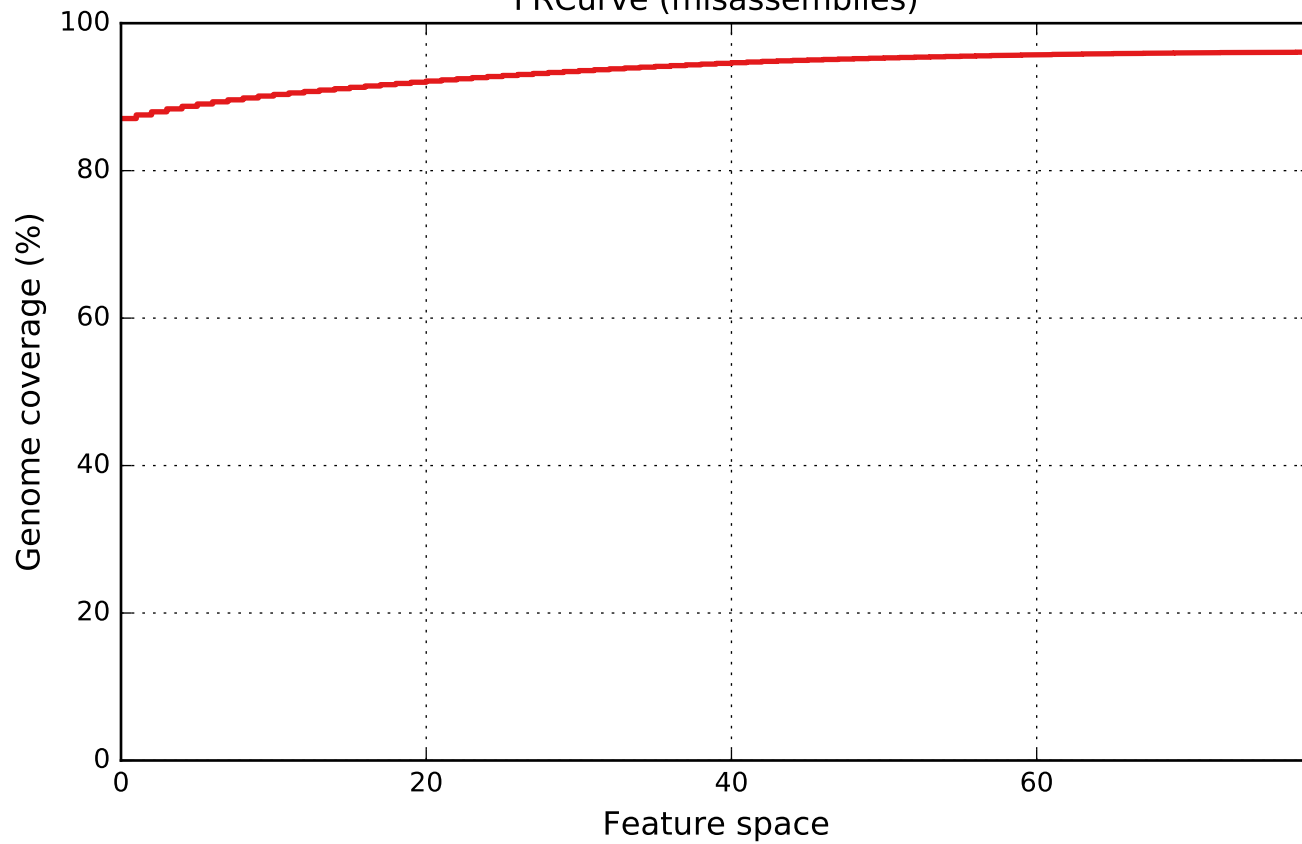
Contigs



# Misassemblies

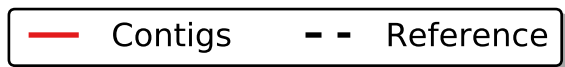
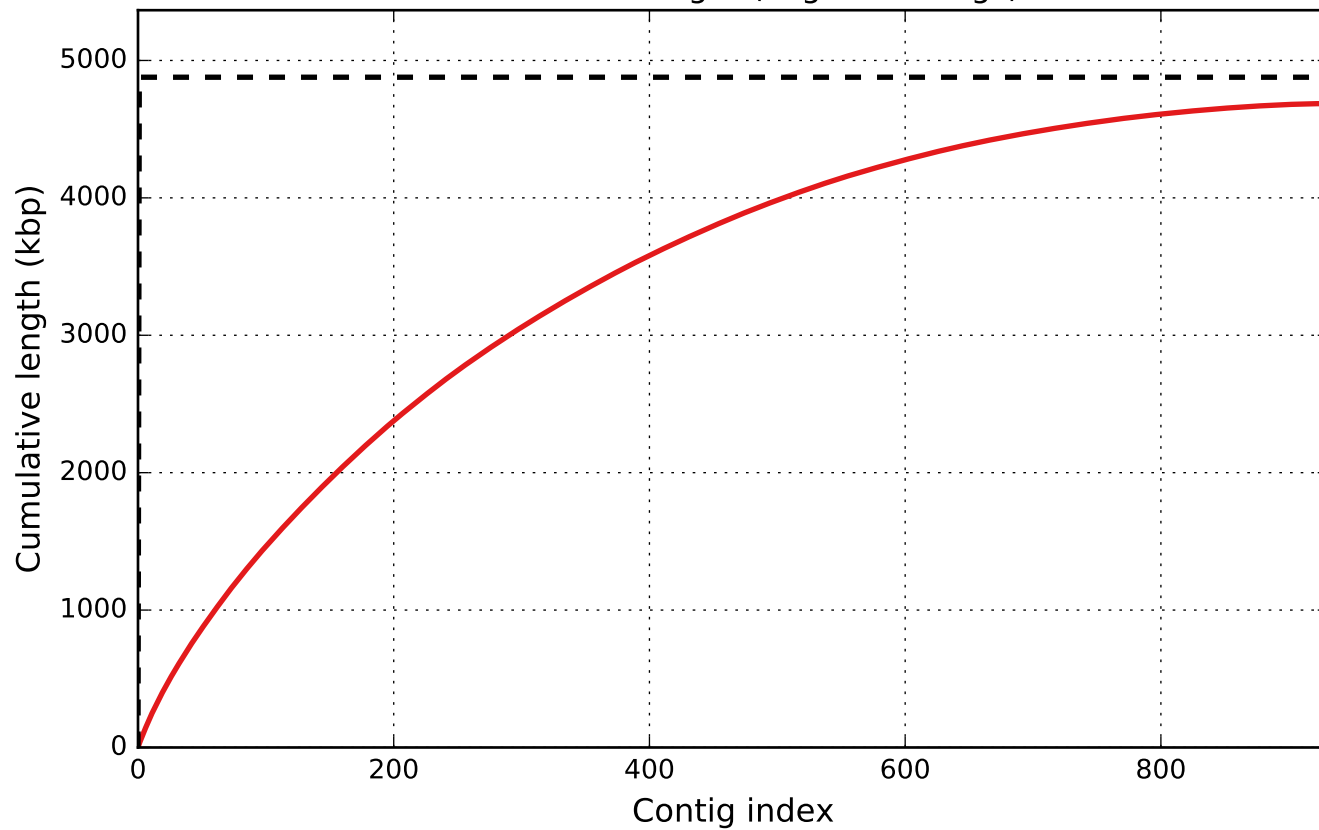


FRCurve (misassemblies)

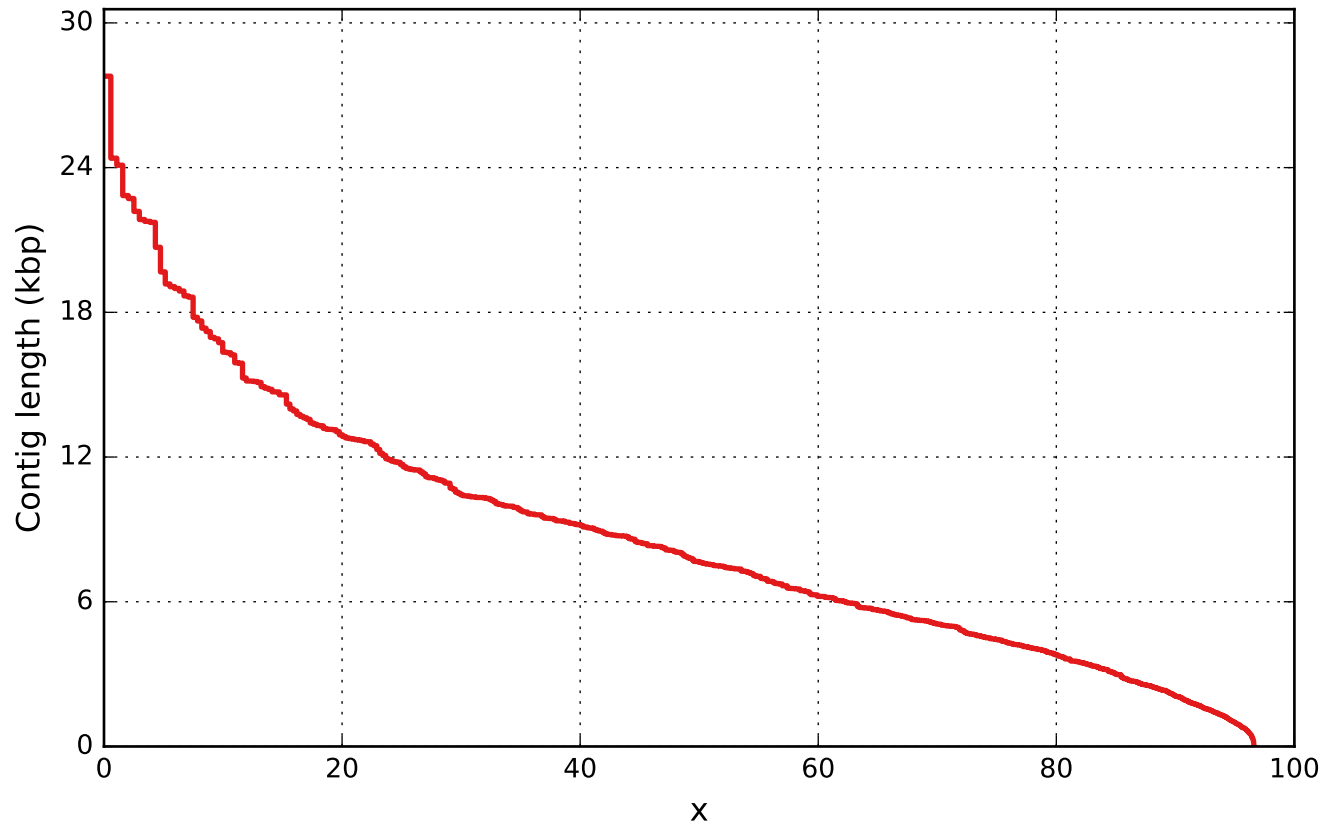


— Contigs

Cumulative length (aligned contigs)

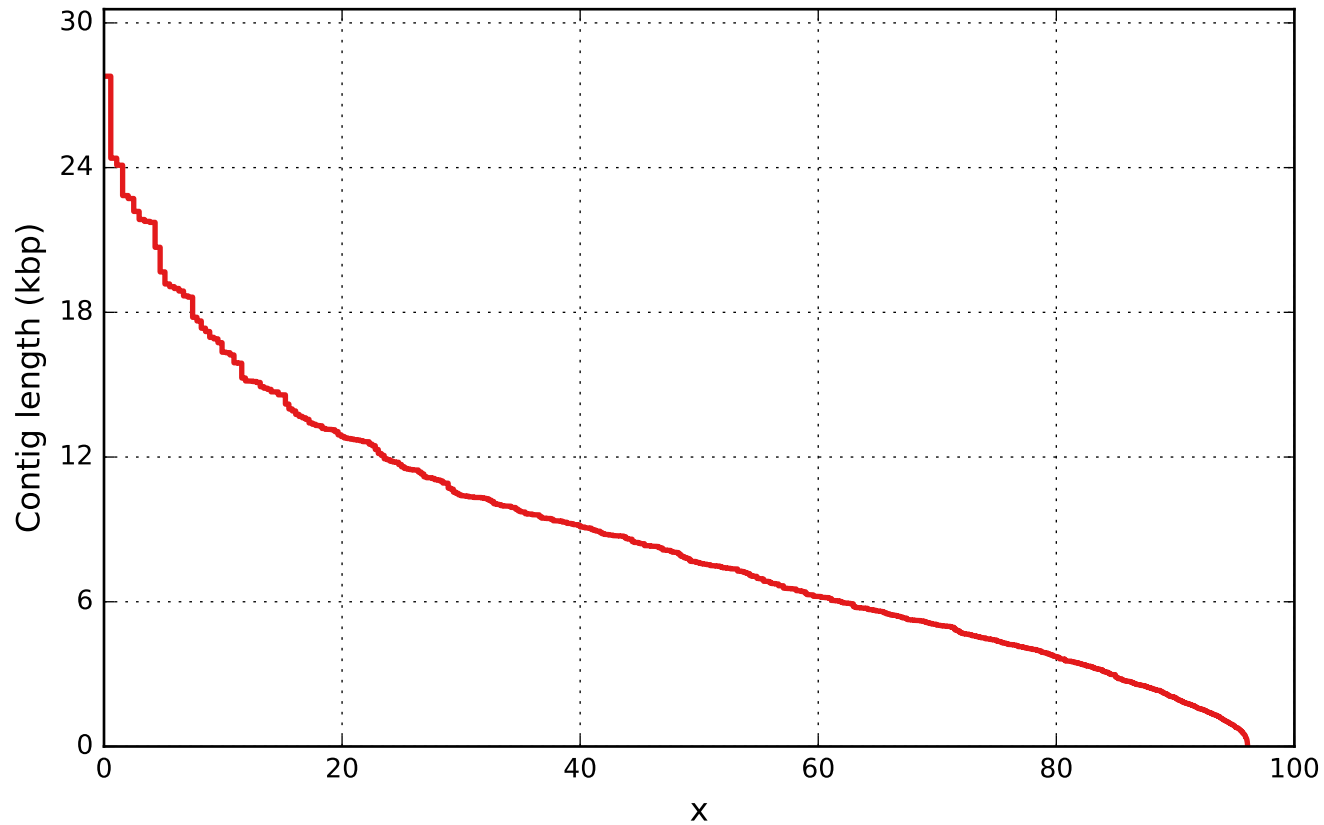


NAx



— Contigs

# NGAx



— Contigs