

## Report

	uniq-contigs-contigs-contigs-contigs-contigs
# contigs (>= 0 bp)	13
# contigs (>= 1000 bp)	5
# contigs (>= 5000 bp)	5
# contigs (>= 10000 bp)	5
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	4
Total length (>= 0 bp)	544177
Total length (>= 1000 bp)	539607
Total length (>= 5000 bp)	539607
Total length (>= 10000 bp)	539607
Total length (>= 25000 bp)	539607
Total length (>= 50000 bp)	507195
# contigs	13
Largest contig	201112
Total length	544177
Reference length	599940
GC (%)	51.15
Reference GC (%)	51.01
N50	138705
NG50	138705
N75	108090
NG75	59288
L50	2
LG50	2
L75	3
LG75	4
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	89.945
Duplication ratio	1.008
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.56
Largest alignment	201112
Total aligned length	544177
NA50	138705
NGA50	138705
NA75	108090
NGA75	59288
LA50	2
LGA50	2
LA75	3
LGA75	4

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	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	0
# indels	3
# indels ( $\leq 5$ bp)	2
# indels ( $> 5$ bp)	1
Indels length	40

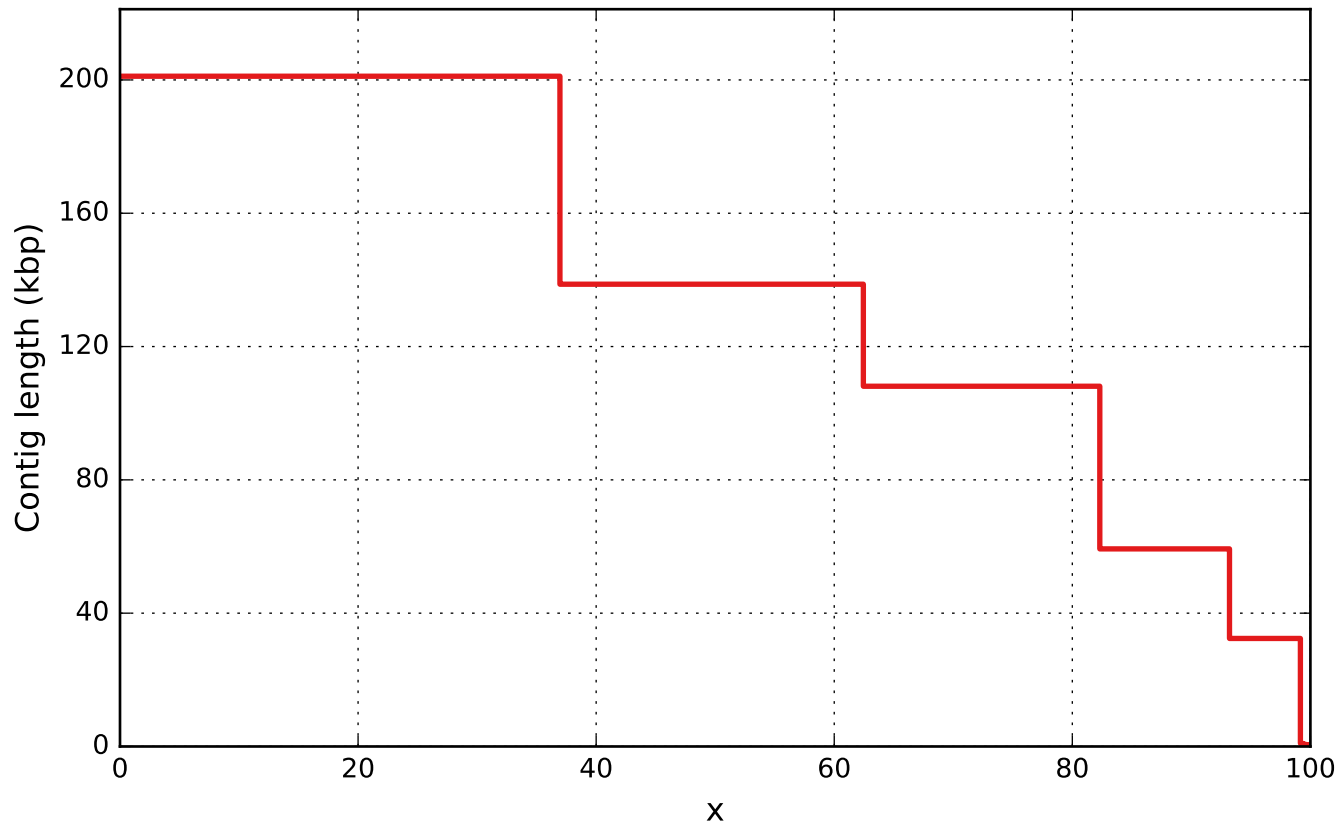
All statistics are based on contigs of size  $\geq 400$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	uniq-contigs-contigs-contigs-contigs-contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

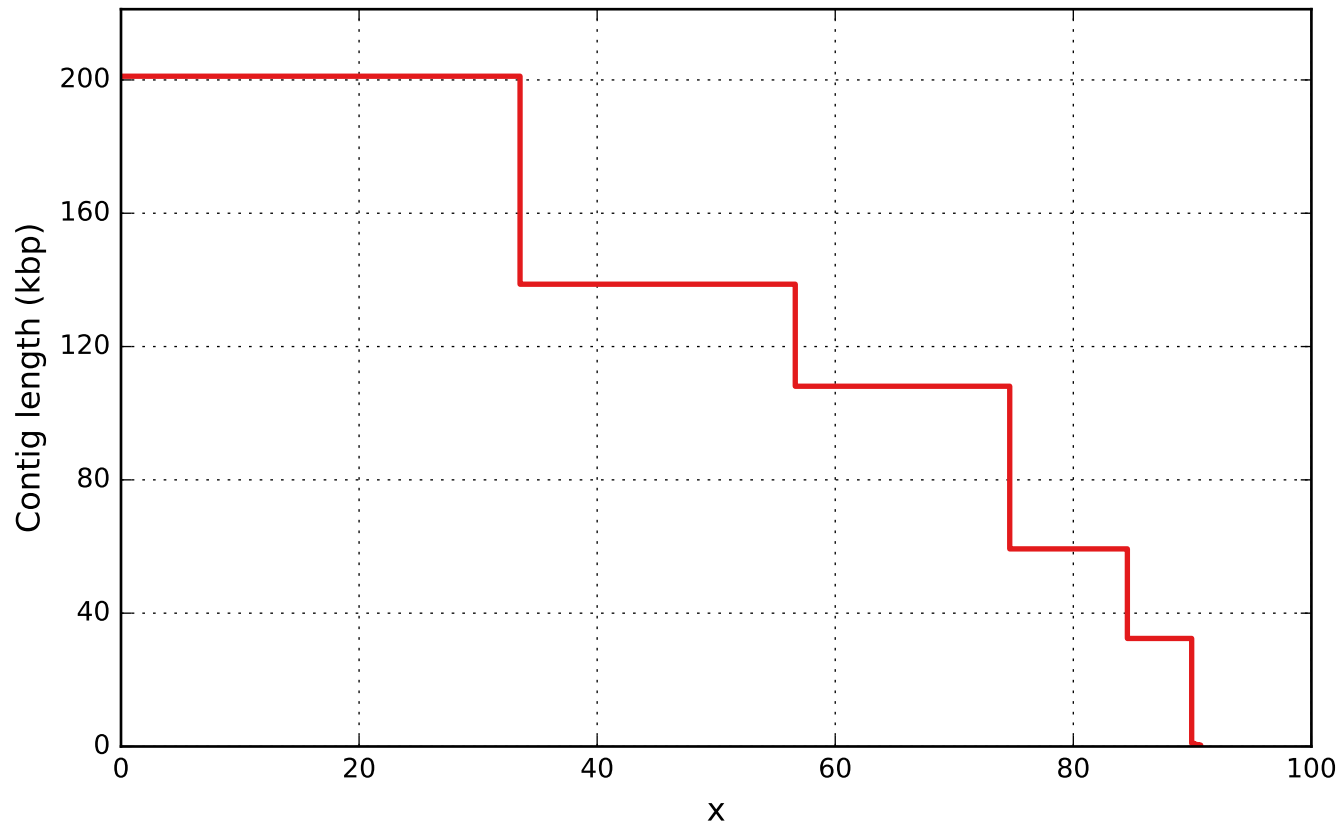
All statistics are based on contigs of size  $\geq 400$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



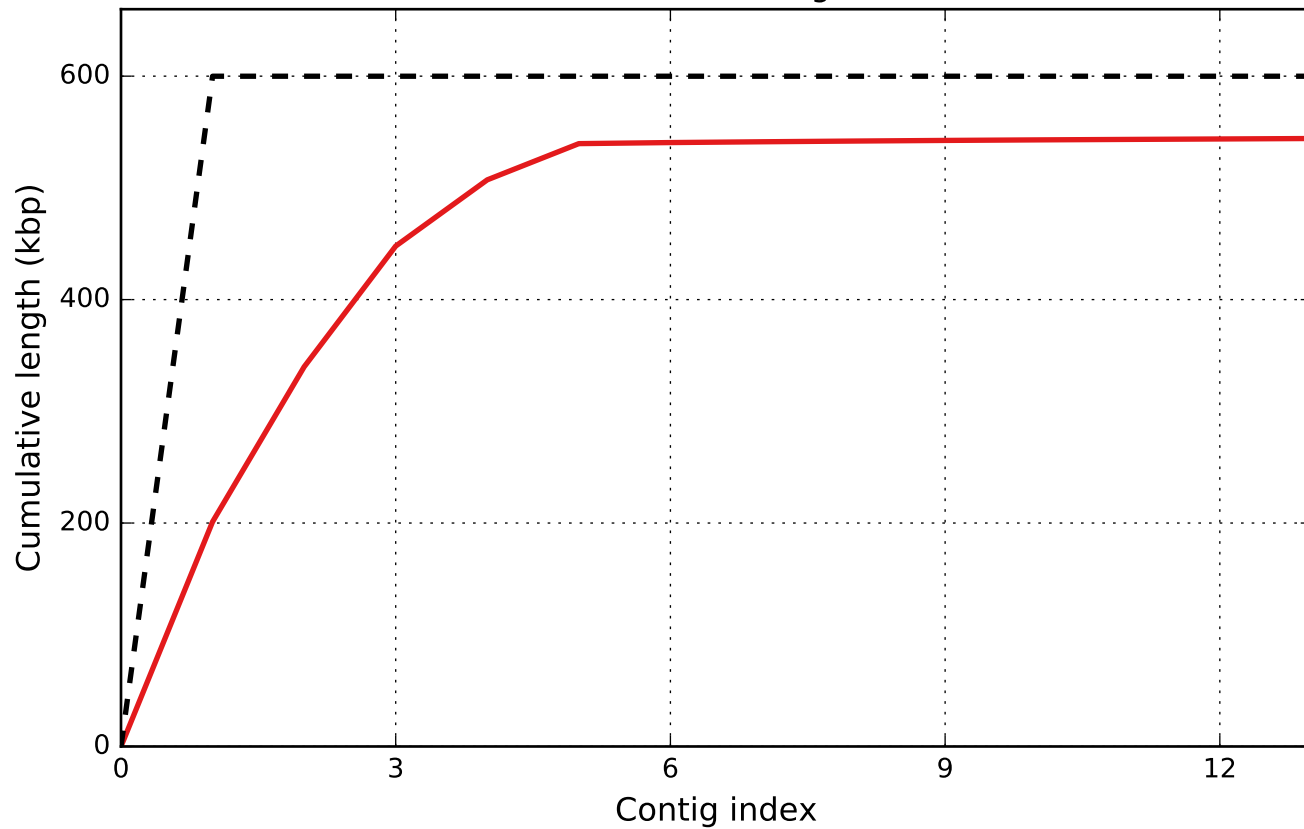
— uniq-contigs-contigs-contigs-contigs-contigs

NGx



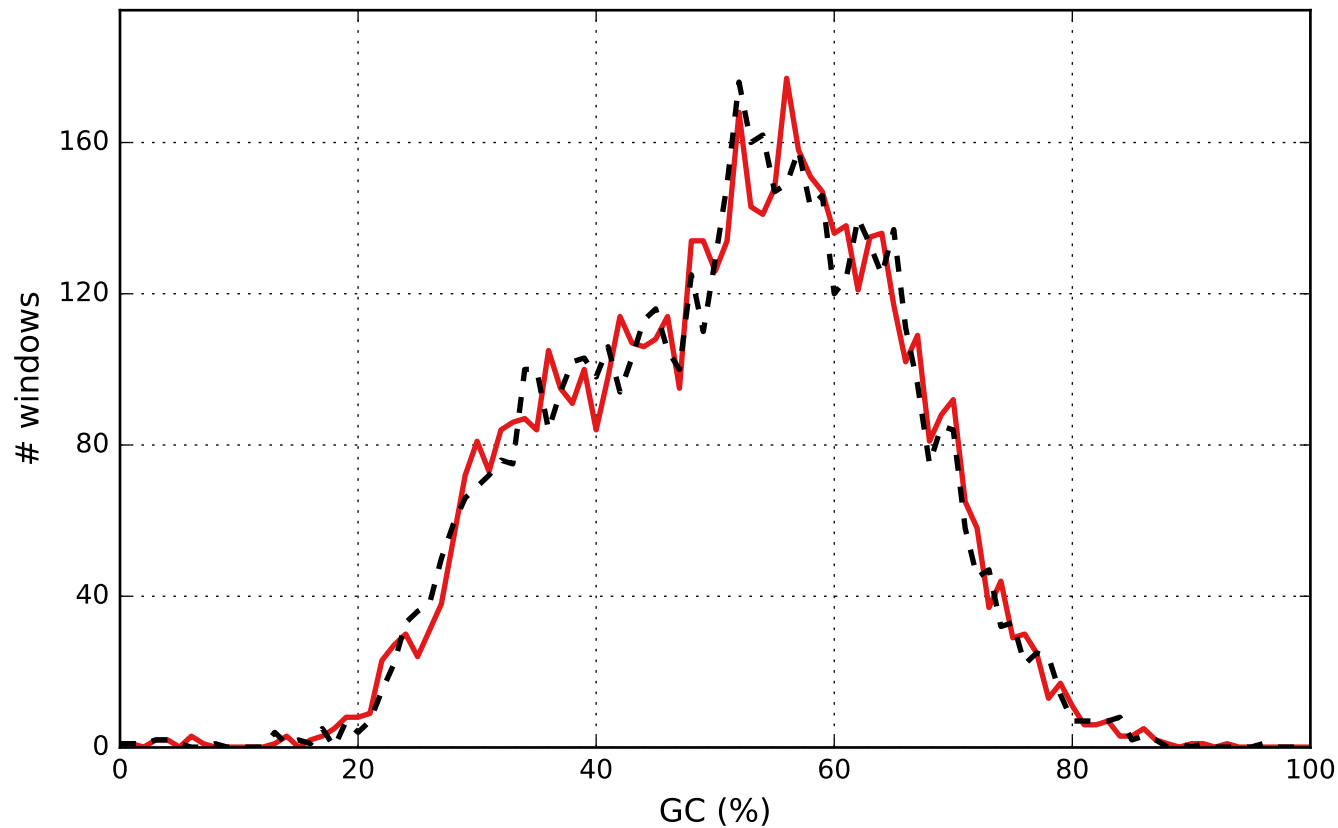
— uniq-contigs-contigs-contigs-contigs-contigs

Cumulative length

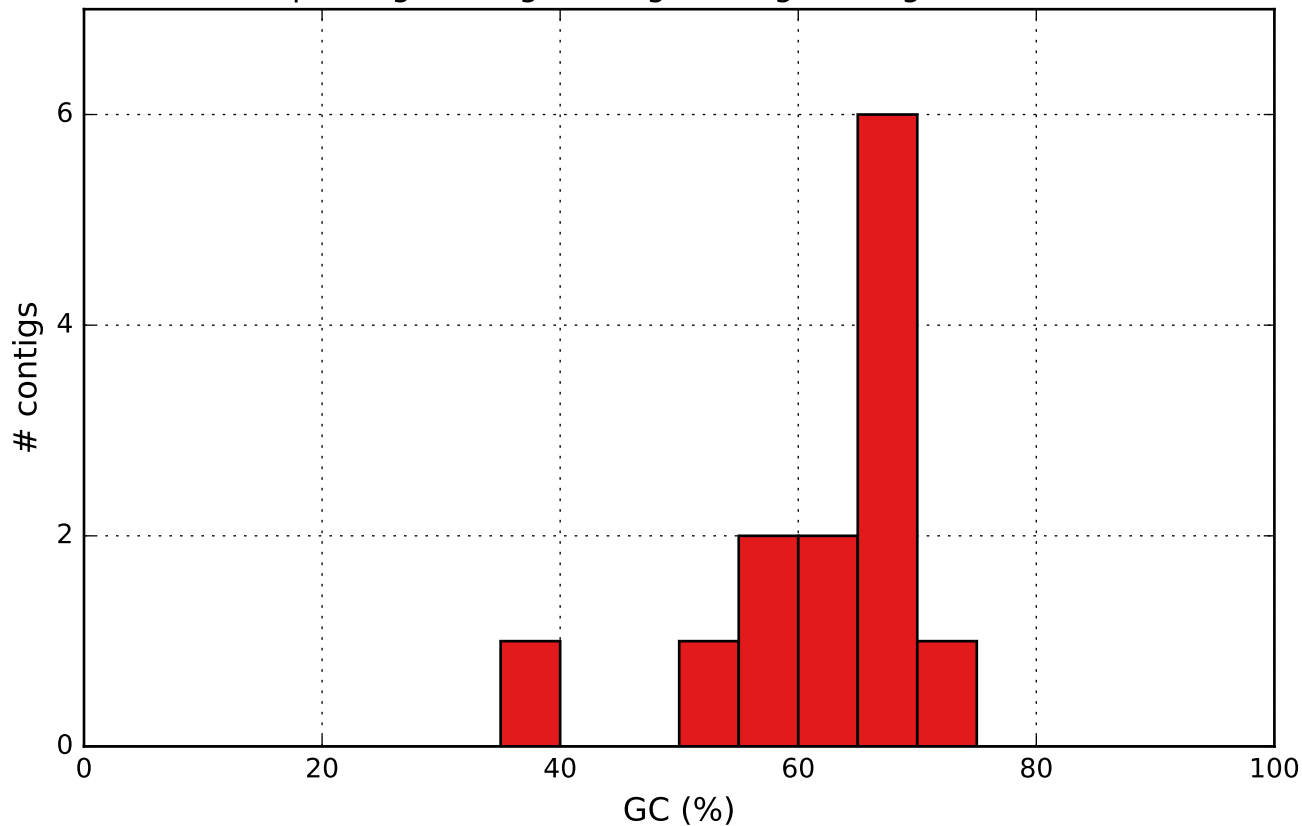


— uniq-contigs-contigs-contigs-contigs-contigs      - - Reference

GC content

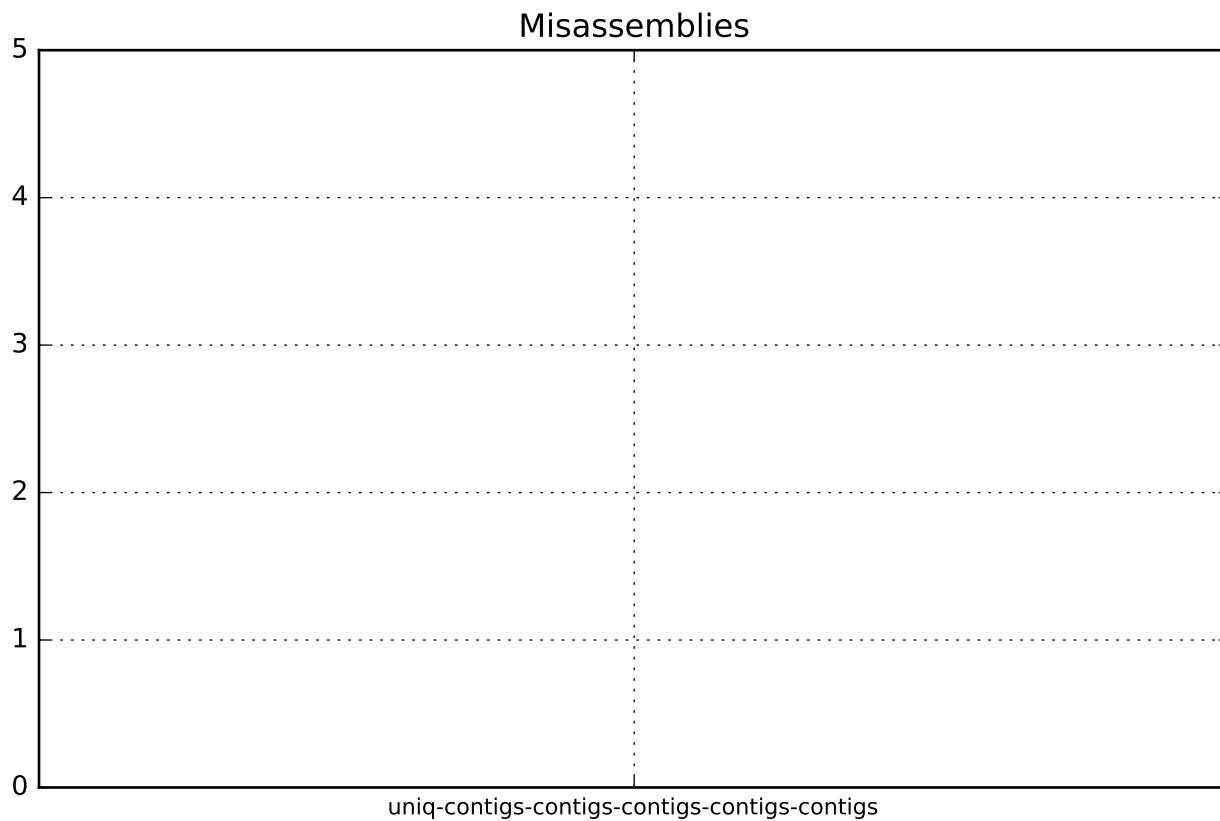


uniq-contigs-contigs-contigs-contigs-contigs GC content

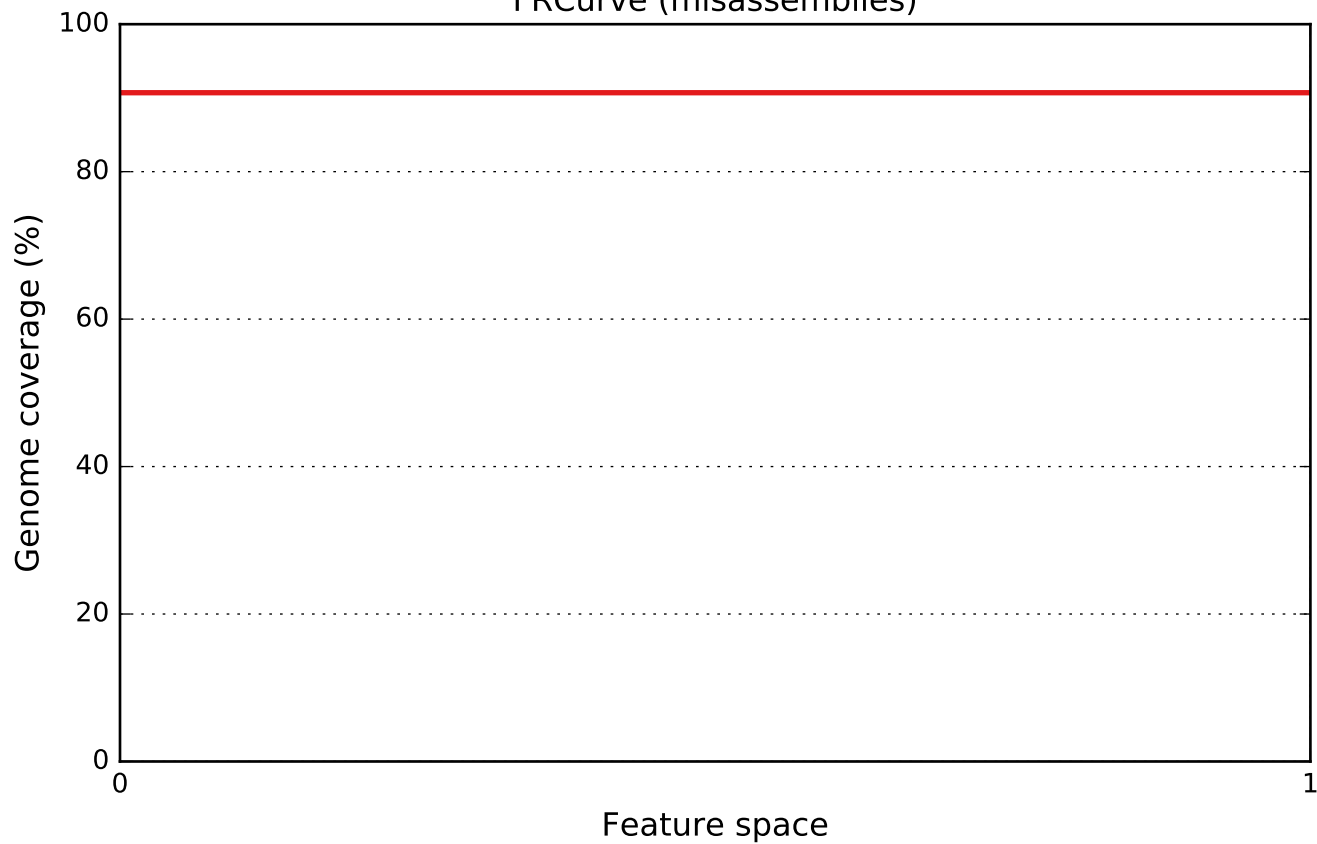


uniq-contigs-contigs-contigs-contigs-contigs

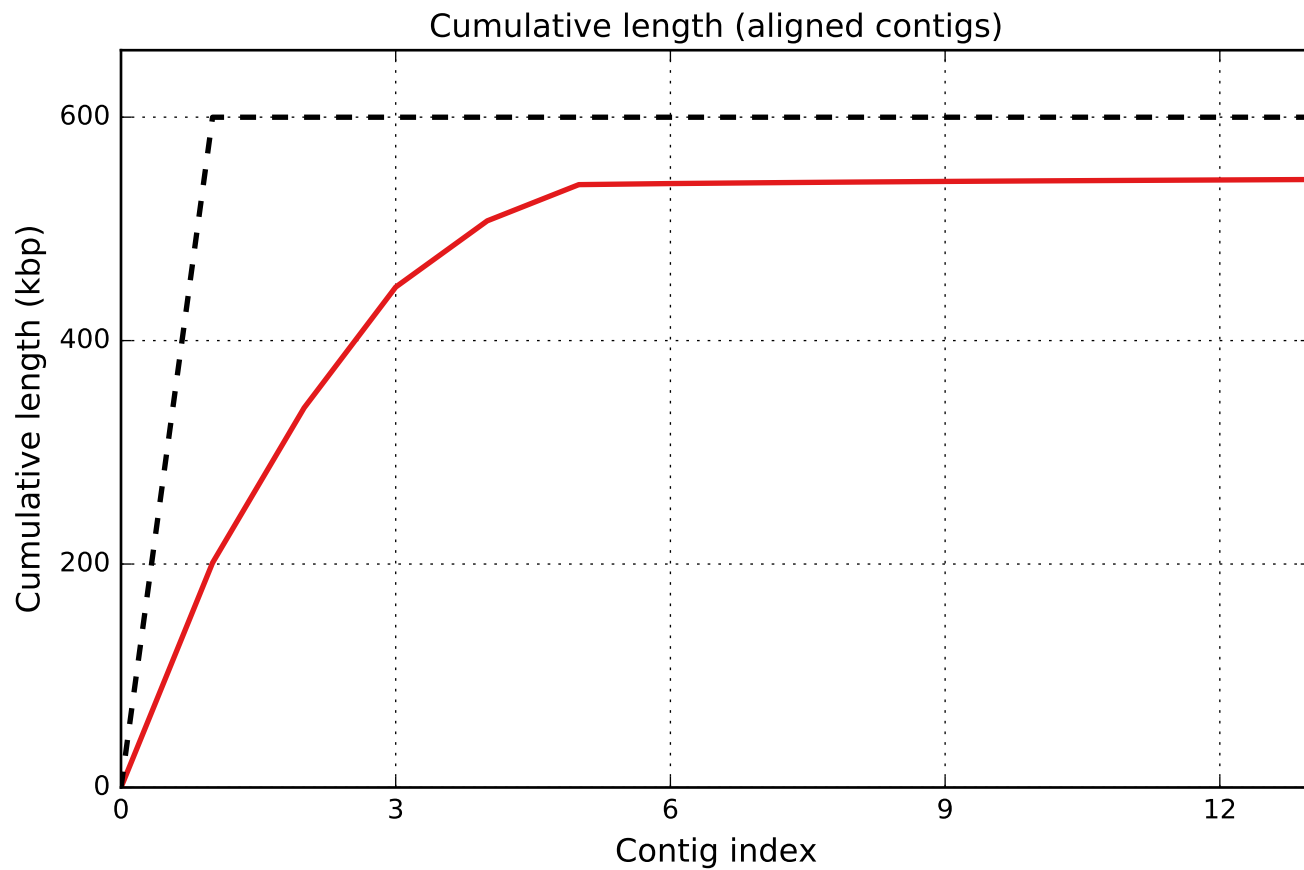




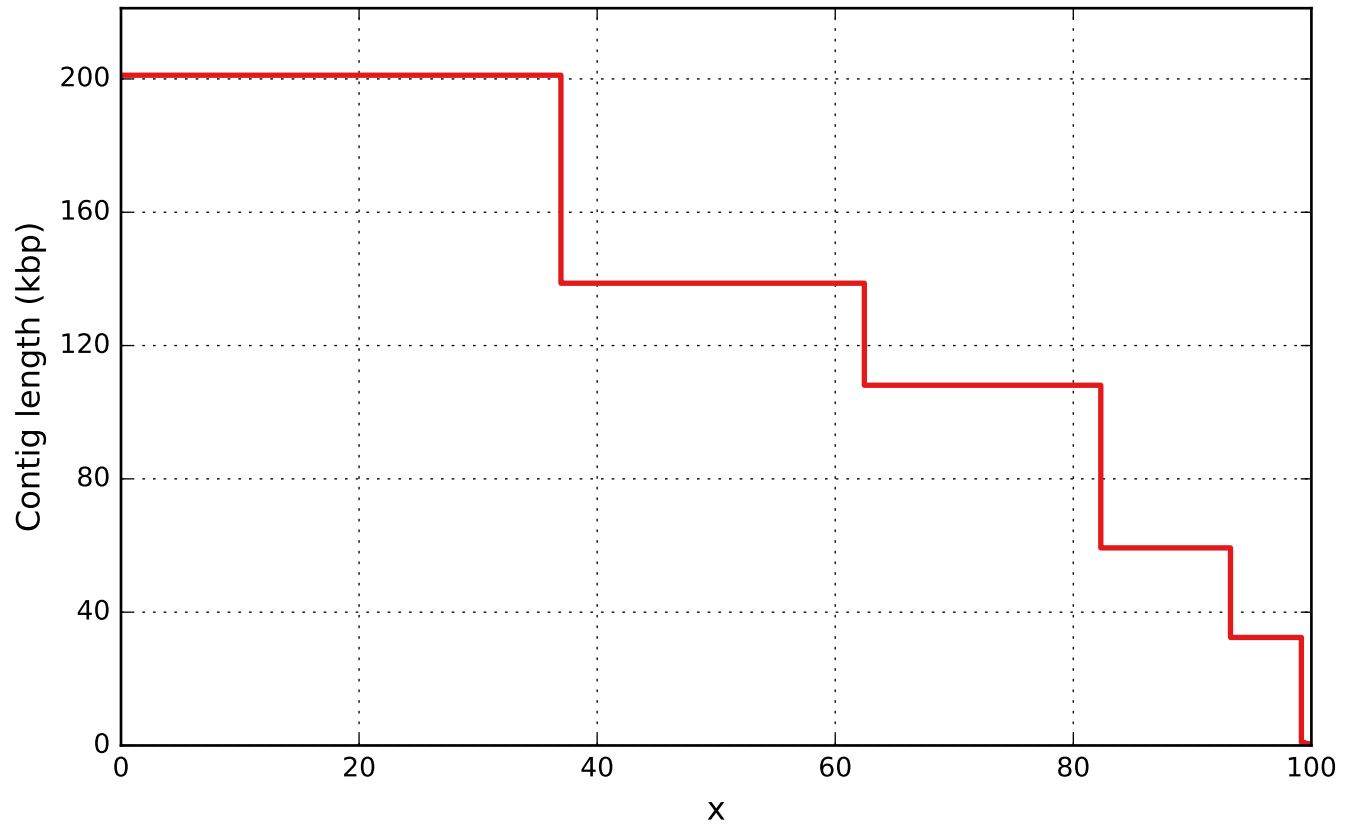
FRCurve (misassemblies)



— uniq-contigs-contigs-contigs-contigs-contigs

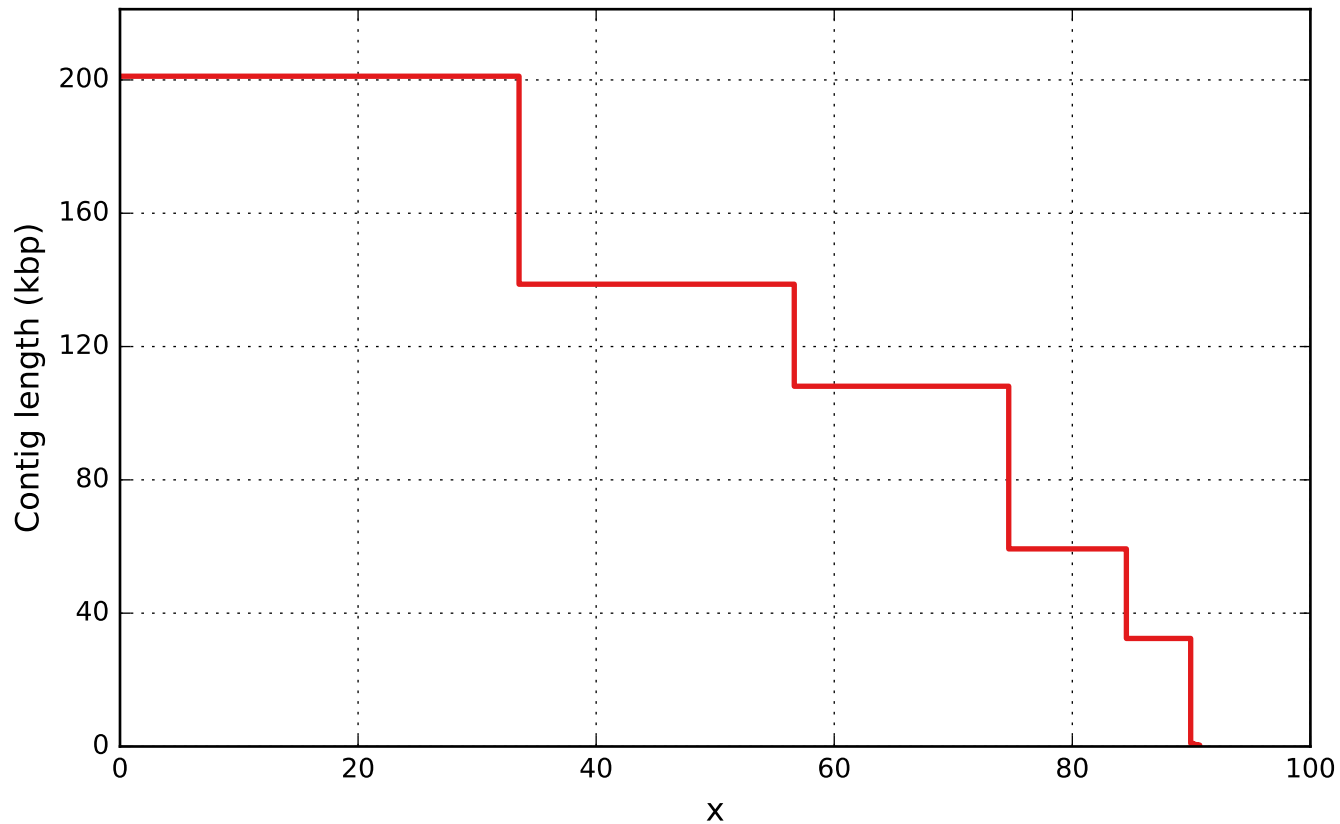


NAx



— uniq-contigs-contigs-contigs-contigs-contigs

NGAx



— uniq-contigs-contigs-contigs-contigs-contigs