

## Report

	uniq-contigs-contigs-contigs-contigs-contigs
# contigs (>= 0 bp)	2
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	540315
Total length (>= 1000 bp)	539833
Total length (>= 5000 bp)	539833
Total length (>= 10000 bp)	539833
Total length (>= 25000 bp)	539833
Total length (>= 50000 bp)	539833
# contigs	2
Largest contig	539833
Total length	540315
Reference length	599940
GC (%)	51.04
Reference GC (%)	51.01
N50	539833
NG50	539833
N75	539833
NG75	539833
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	89.933
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.22
# indels per 100 kbp	0.56
Largest alignment	539833
Total aligned length	540315
NA50	539833
NGA50	539833
NA75	539833
NGA75	539833
LA50	1
LGA50	1
LA75	1
LGA75	1

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	1
# unaligned mis. contigs	0
# mismatches	12
# indels	3
# indels ( $\leq 5$ bp)	2
# indels ( $> 5$ bp)	1
Indels length	75

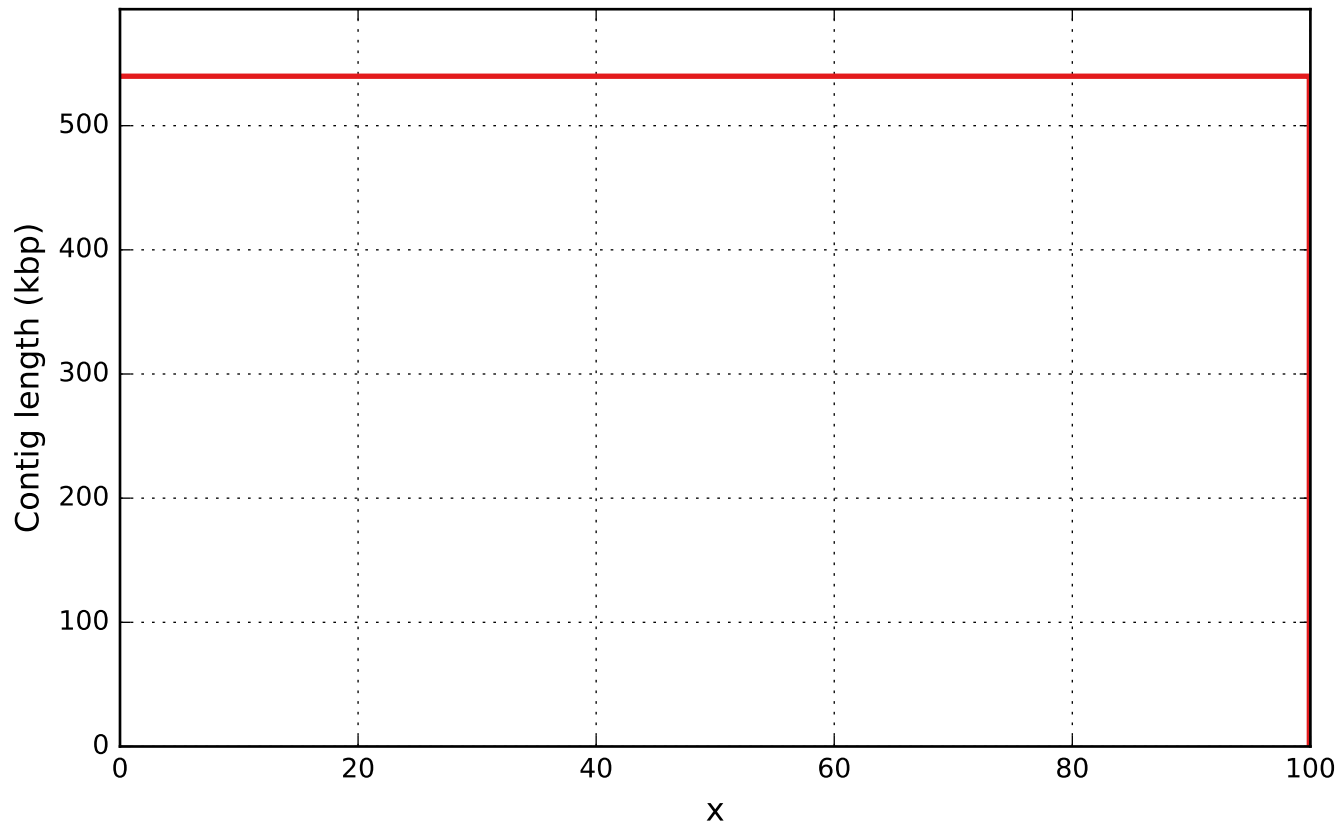
All statistics are based on contigs of size  $\geq 400$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## 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

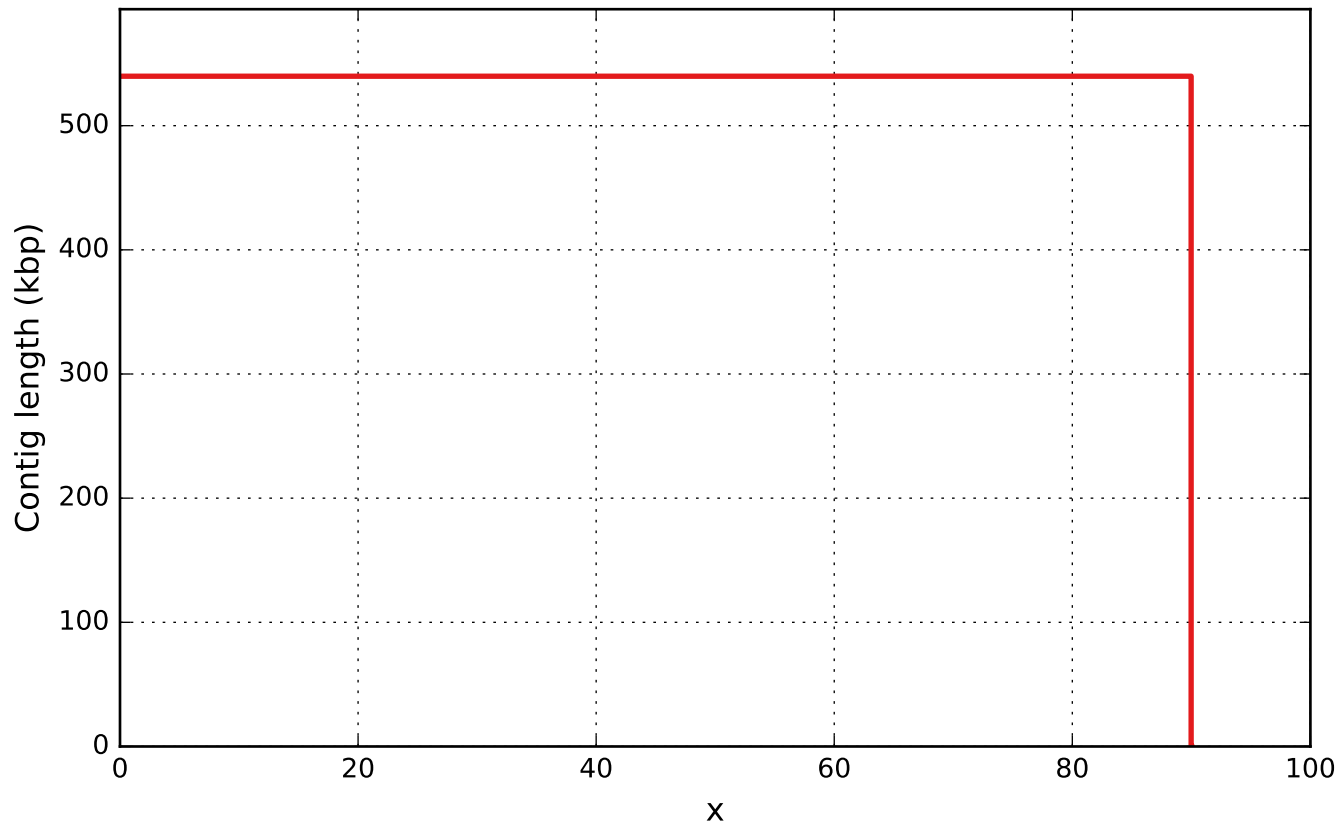
All statistics are based on contigs of size  $\geq 400$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



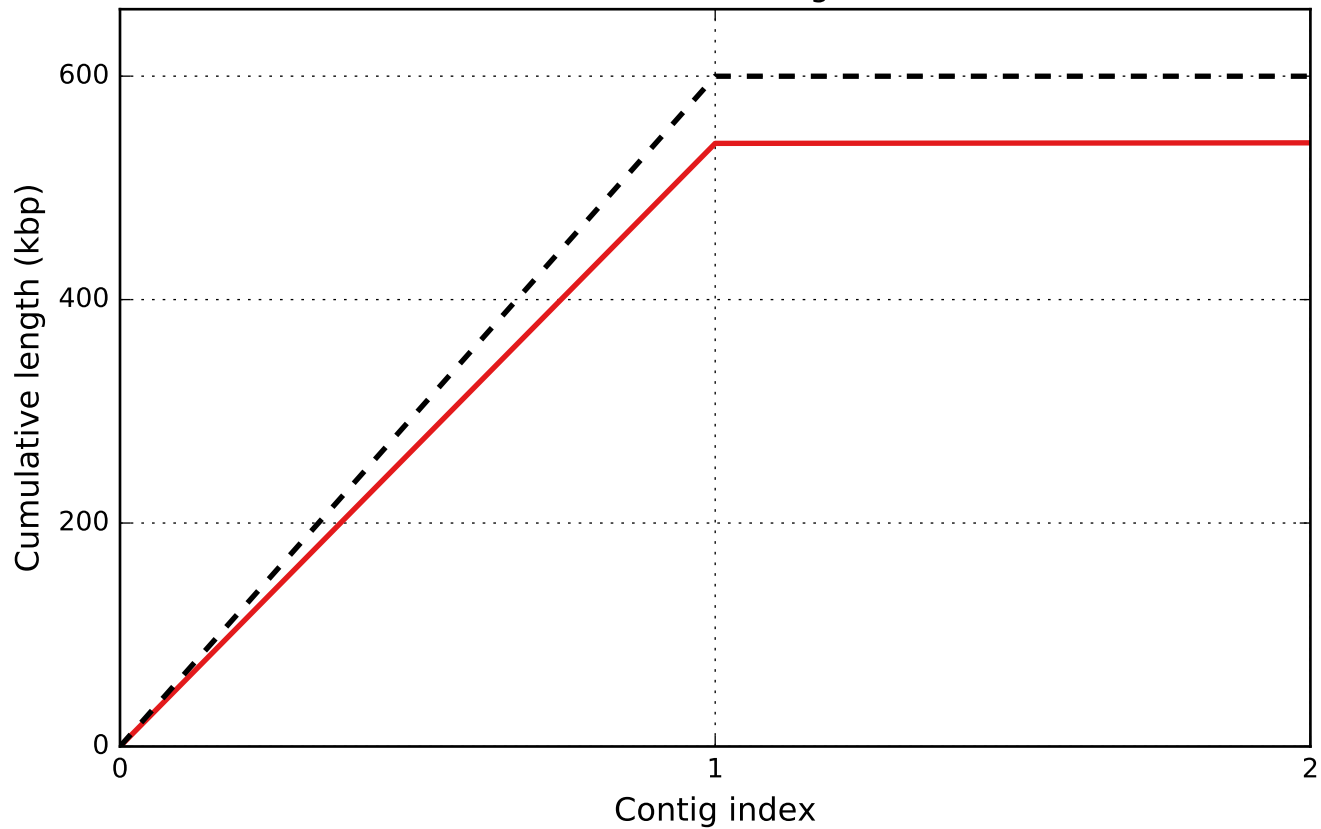
— uniq-contigs-contigs-contigs-contigs-contigs

NGx

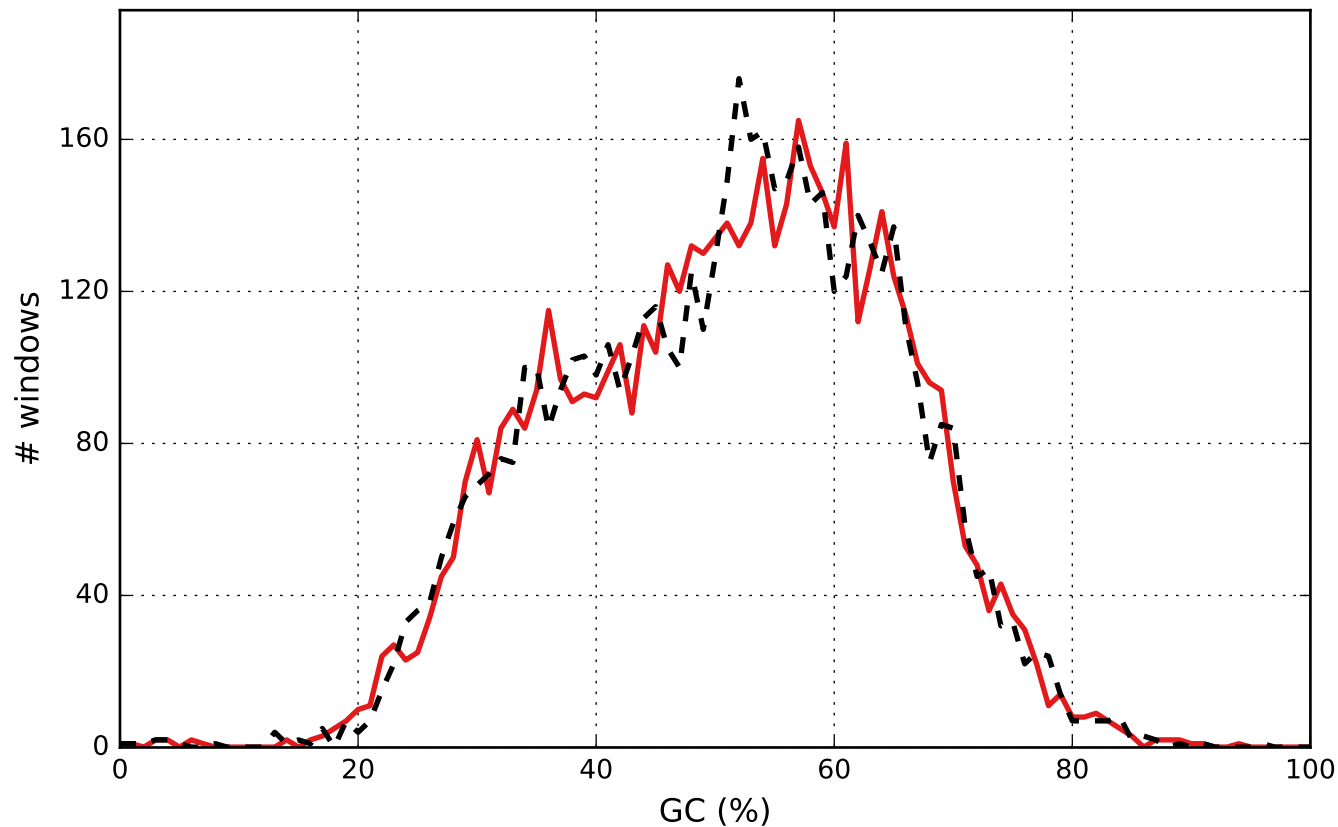


— uniq-contigs-contigs-contigs-contigs-contigs

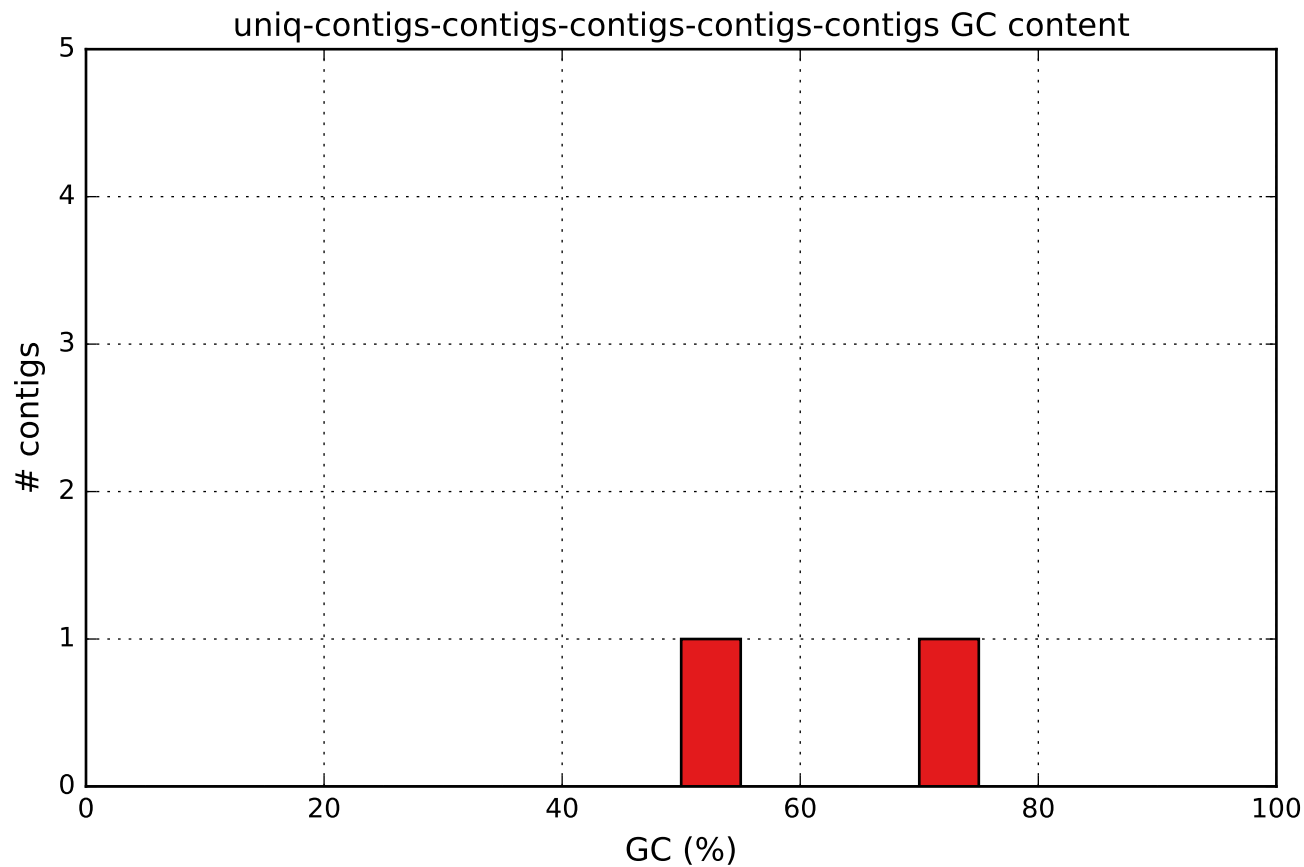
Cumulative length



GC content

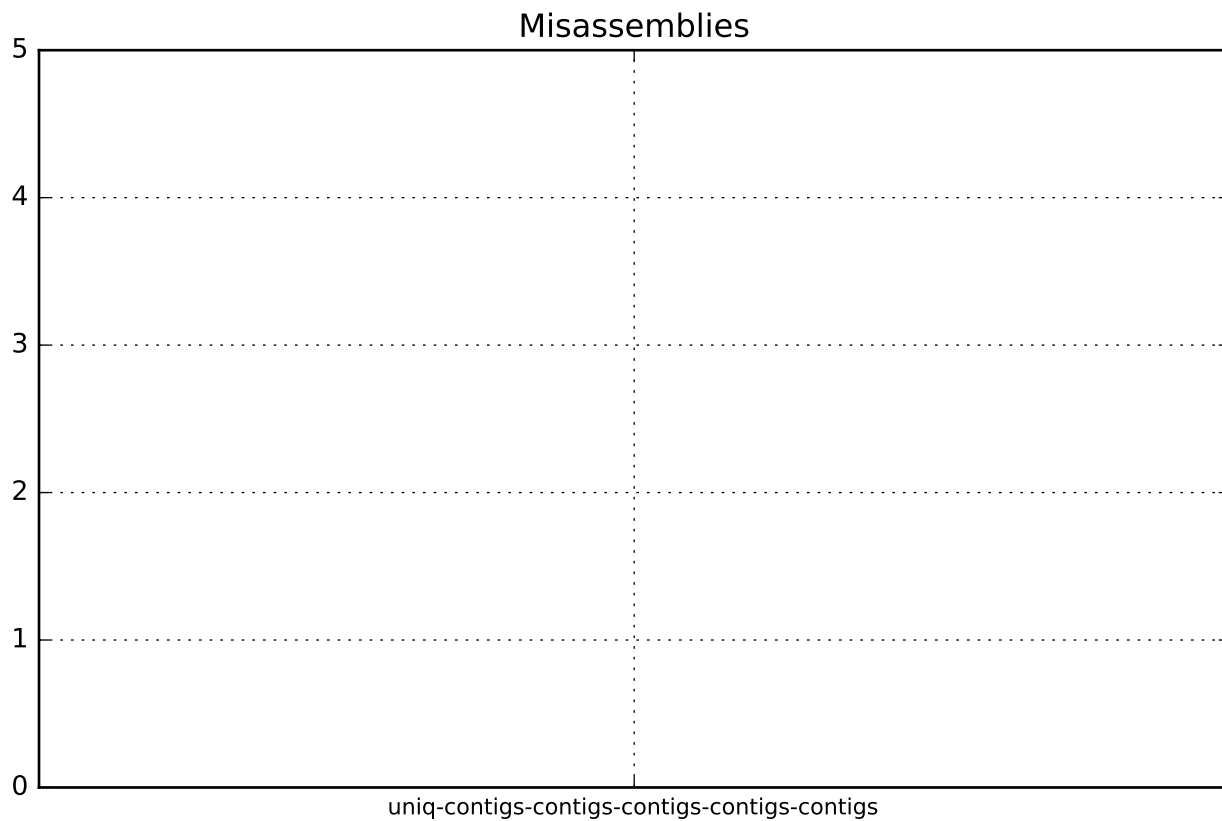


— uniq-contigs-contigs-contigs-contigs-contigs    - - Reference

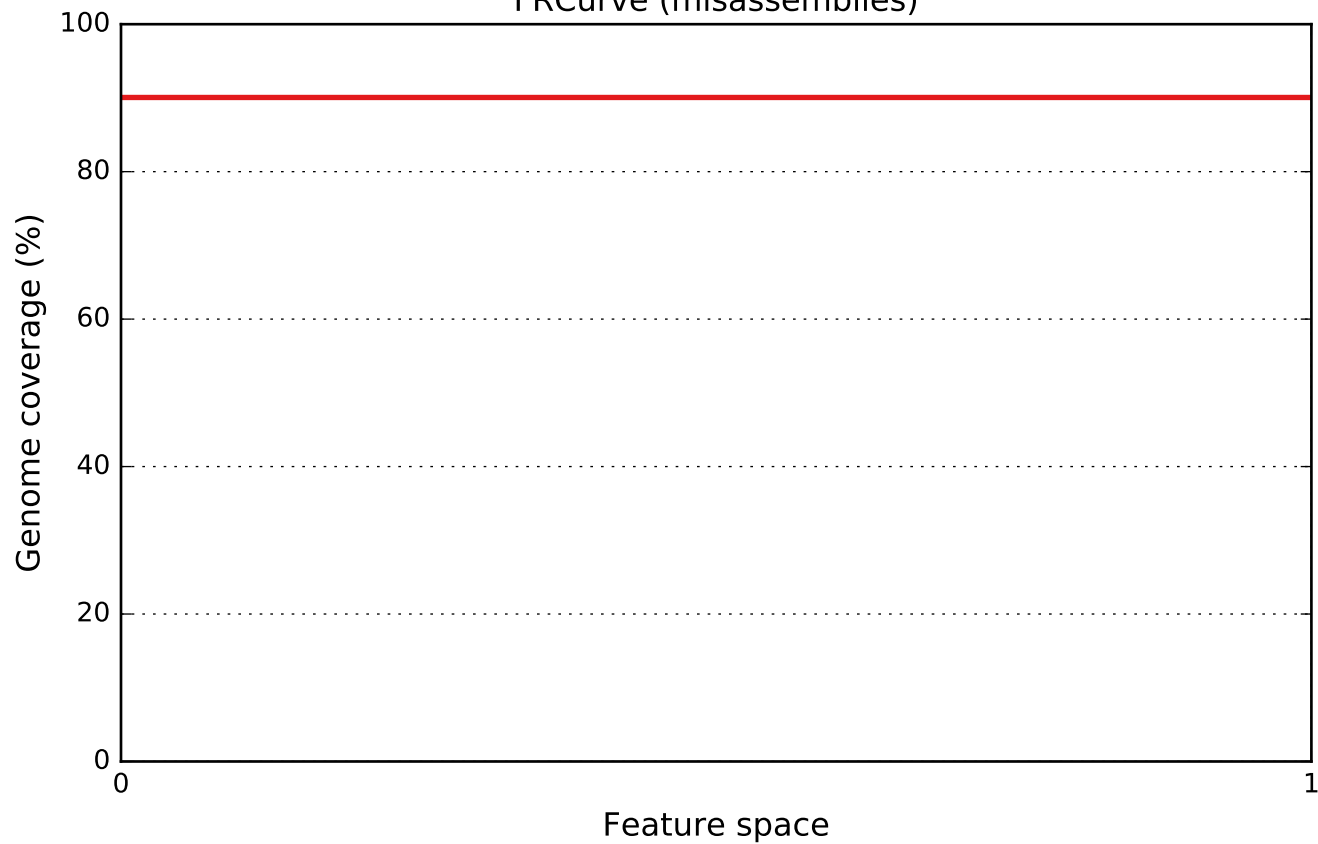


uniq-contigs-contigs-contigs-contigs-contigs

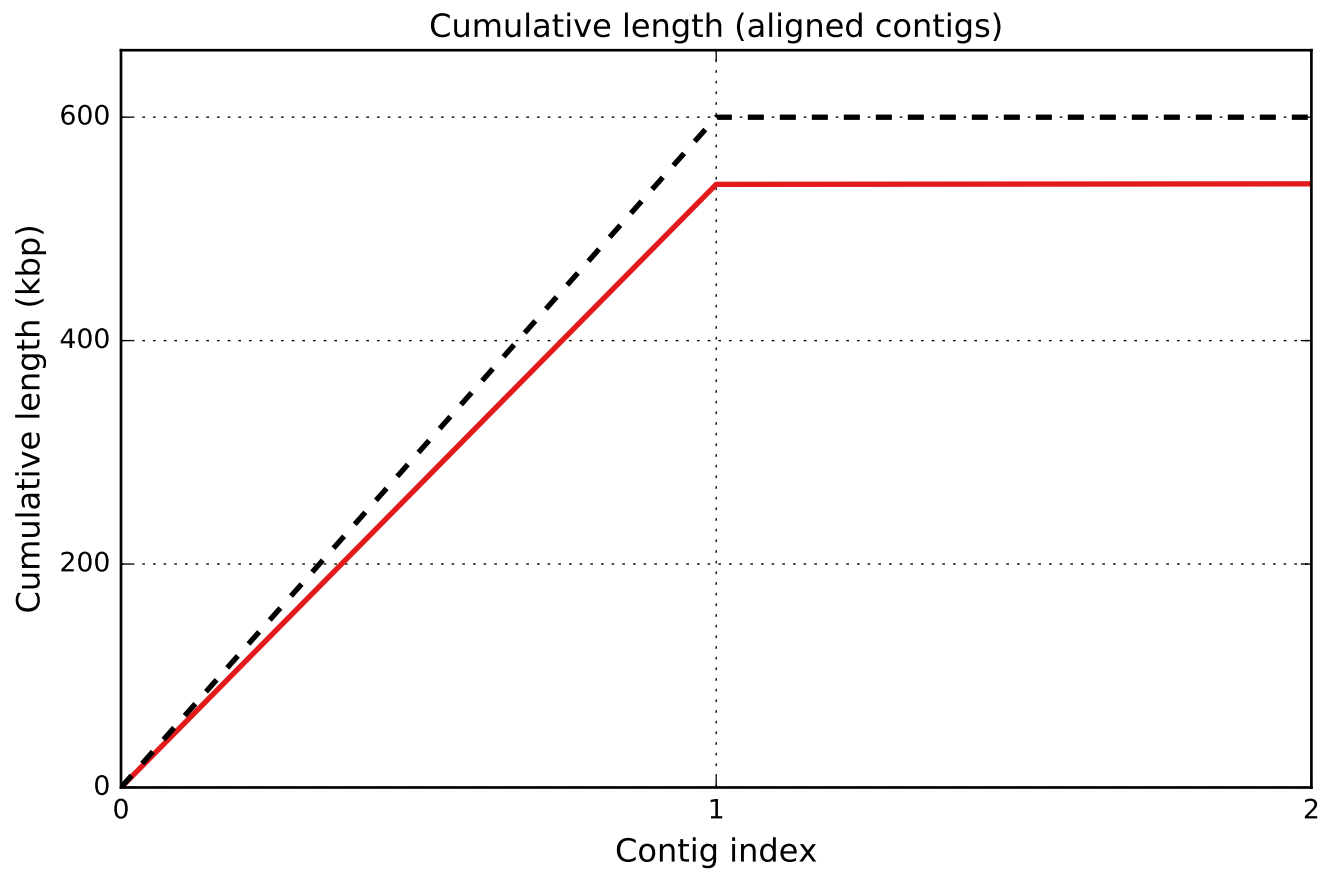




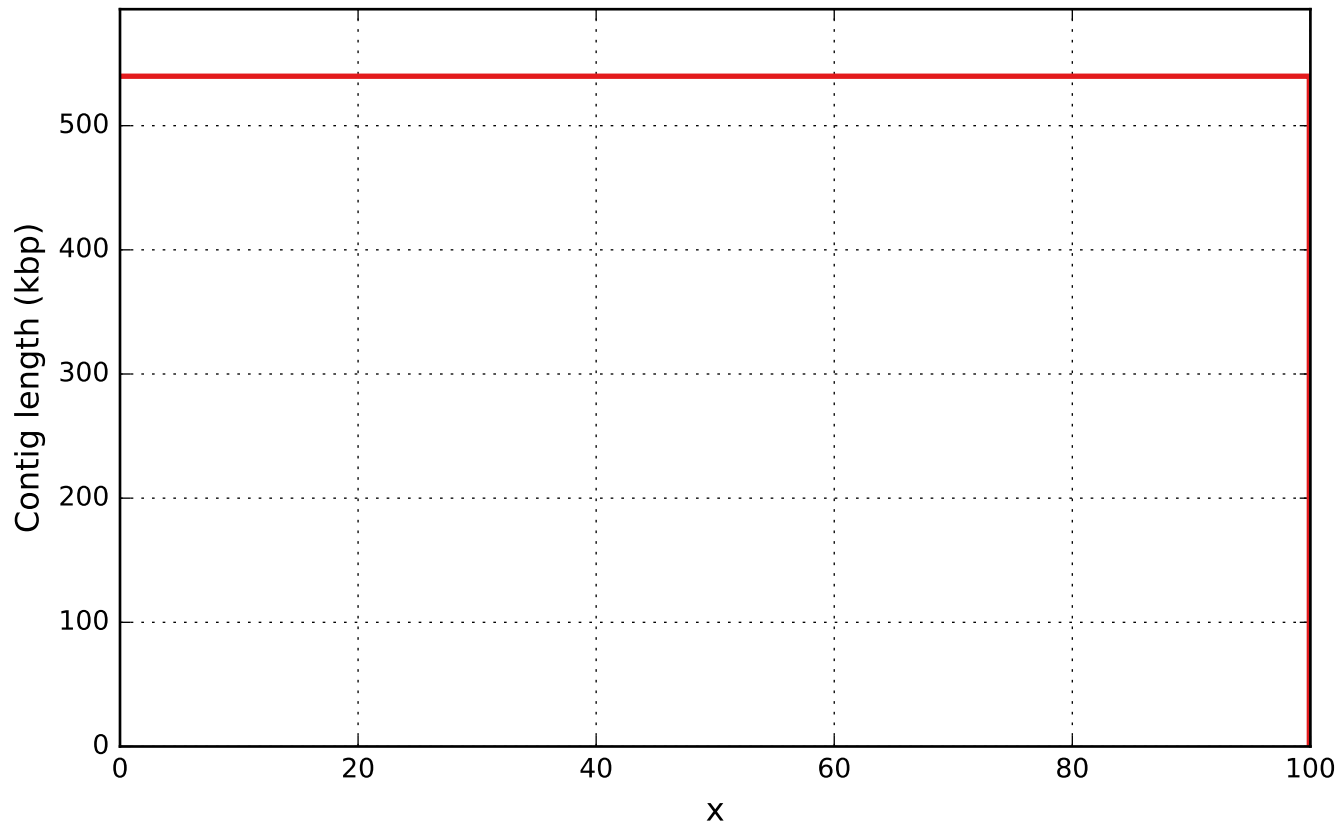
FRCurve (misassemblies)



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

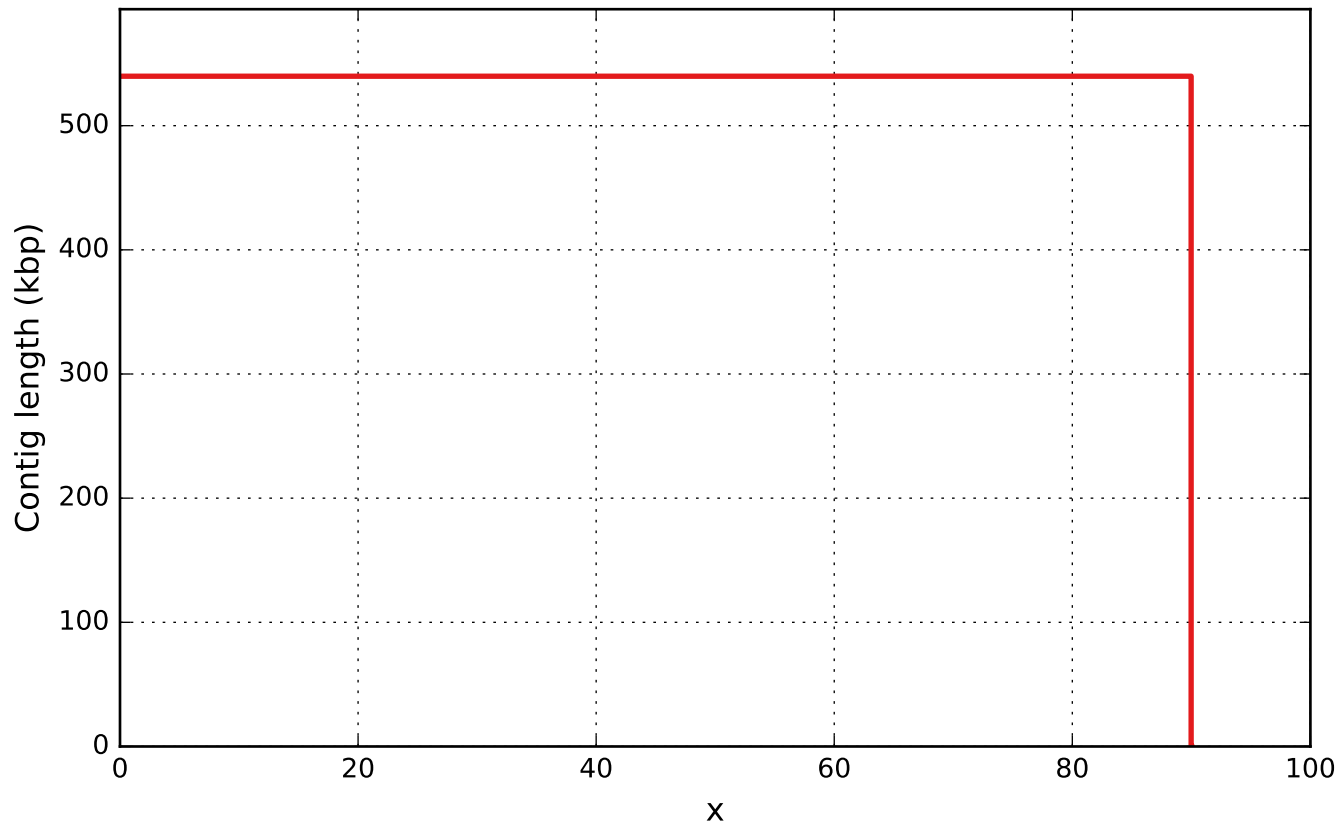


NAx



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

NGAx



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