

# Report

	uniq-contigs-contigs-contigs-contigs
# contigs (>= 0 bp)	7
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	3
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	543654
Total length (>= 1000 bp)	540436
Total length (>= 5000 bp)	540436
Total length (>= 10000 bp)	540436
Total length (>= 25000 bp)	540436
Total length (>= 50000 bp)	540436
# contigs	7
Largest contig	257853
Total length	543654
Reference length	599940
GC (%)	51.06
Reference GC (%)	51.01
N50	207406
NG50	207406
N75	207406
NG75	207406
L50	2
LG50	2
L75	2
LG75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	89.950
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5.37
# indels per 100 kbp	1.85
Largest alignment	257853
Total aligned length	543654
NA50	207406
NGA50	207406
NA75	207406
NGA75	207406
LA50	2
LGA50	2
LA75	2
LGA75	2

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
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned mis. contigs	0
# mismatches	29
# indels	10
# indels ( $\leq 5$ bp)	5
# indels ( $> 5$ bp)	5
Indels length	178

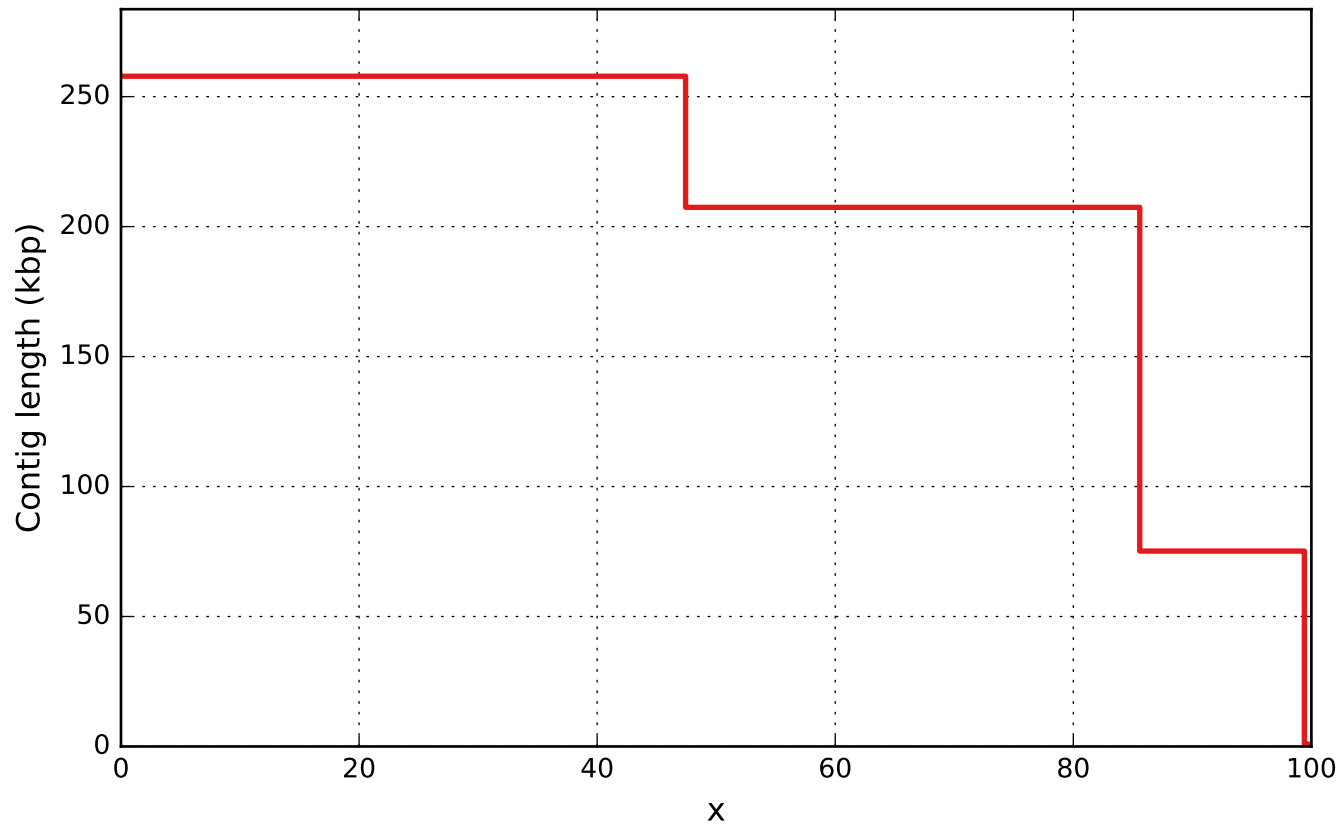
All statistics are based on contigs of size  $\geq 400$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

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

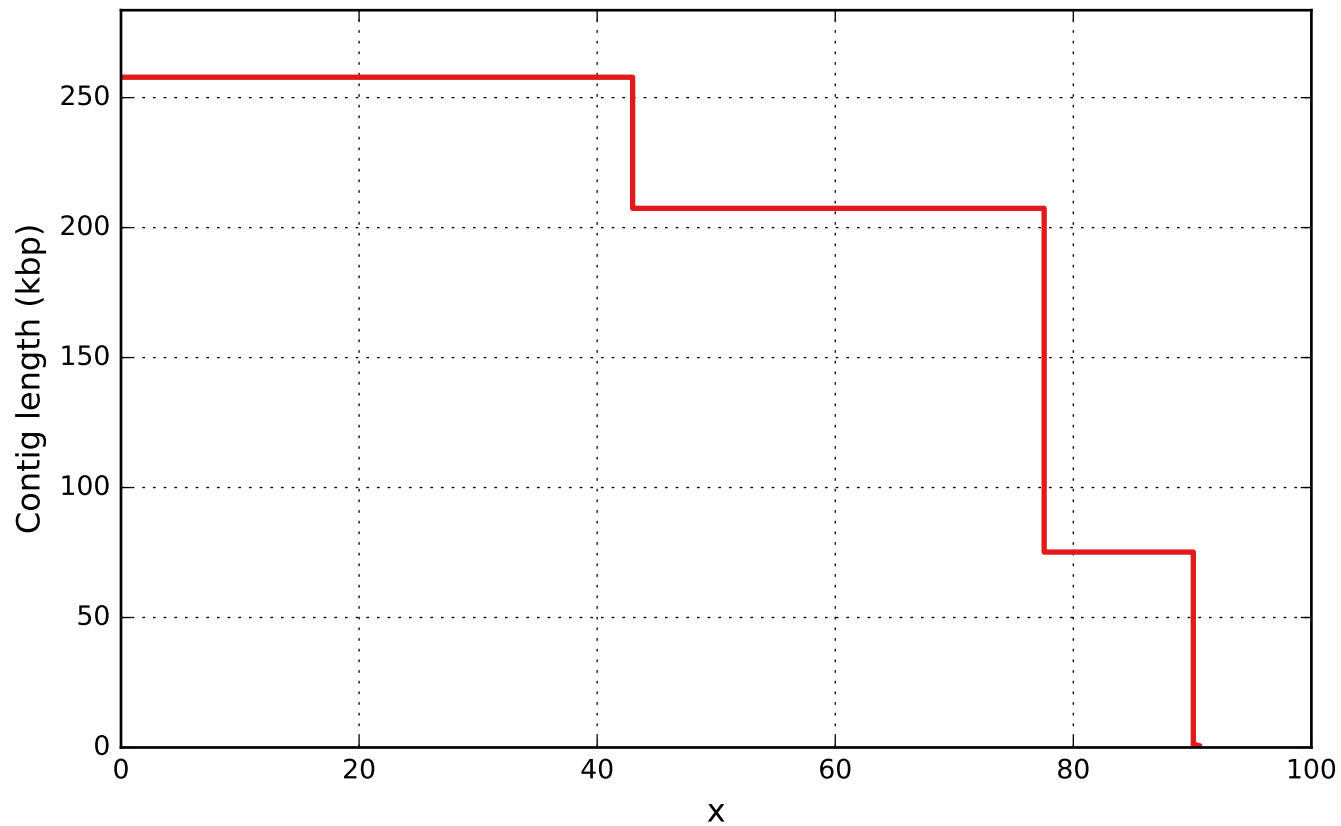
All statistics are based on contigs of size  $\geq 400$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



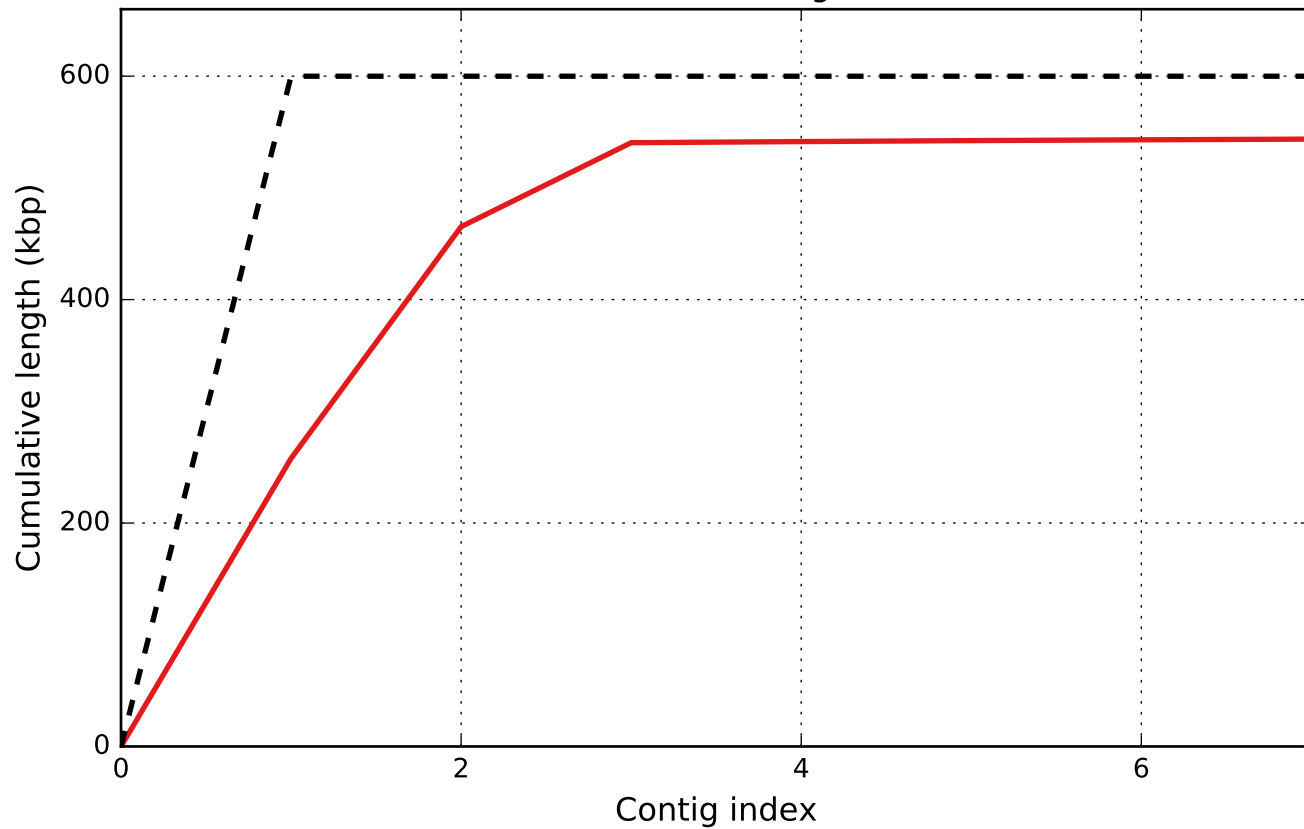
— uniq-contigs-contigs-contigs-contigs

NGx

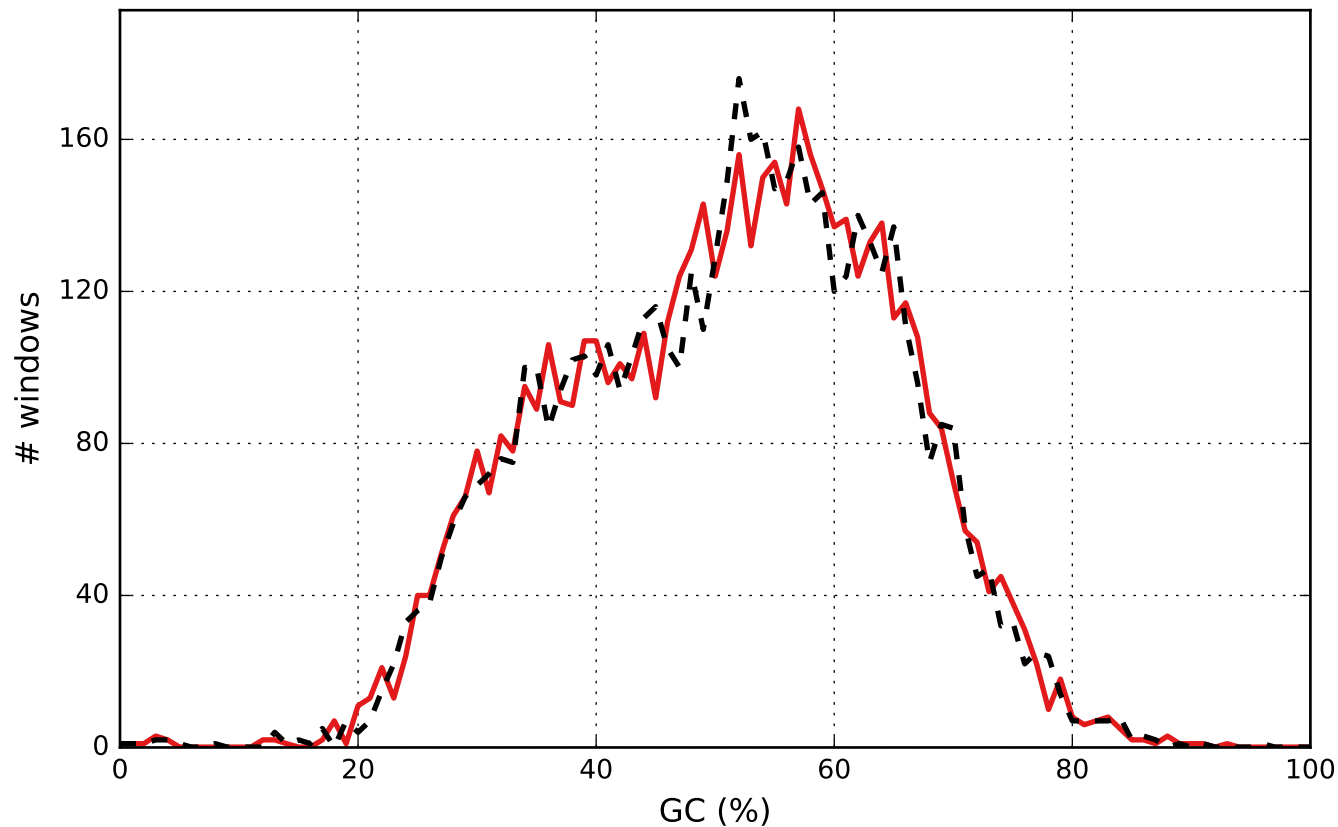


— uniq-contigs-contigs-contigs-contigs

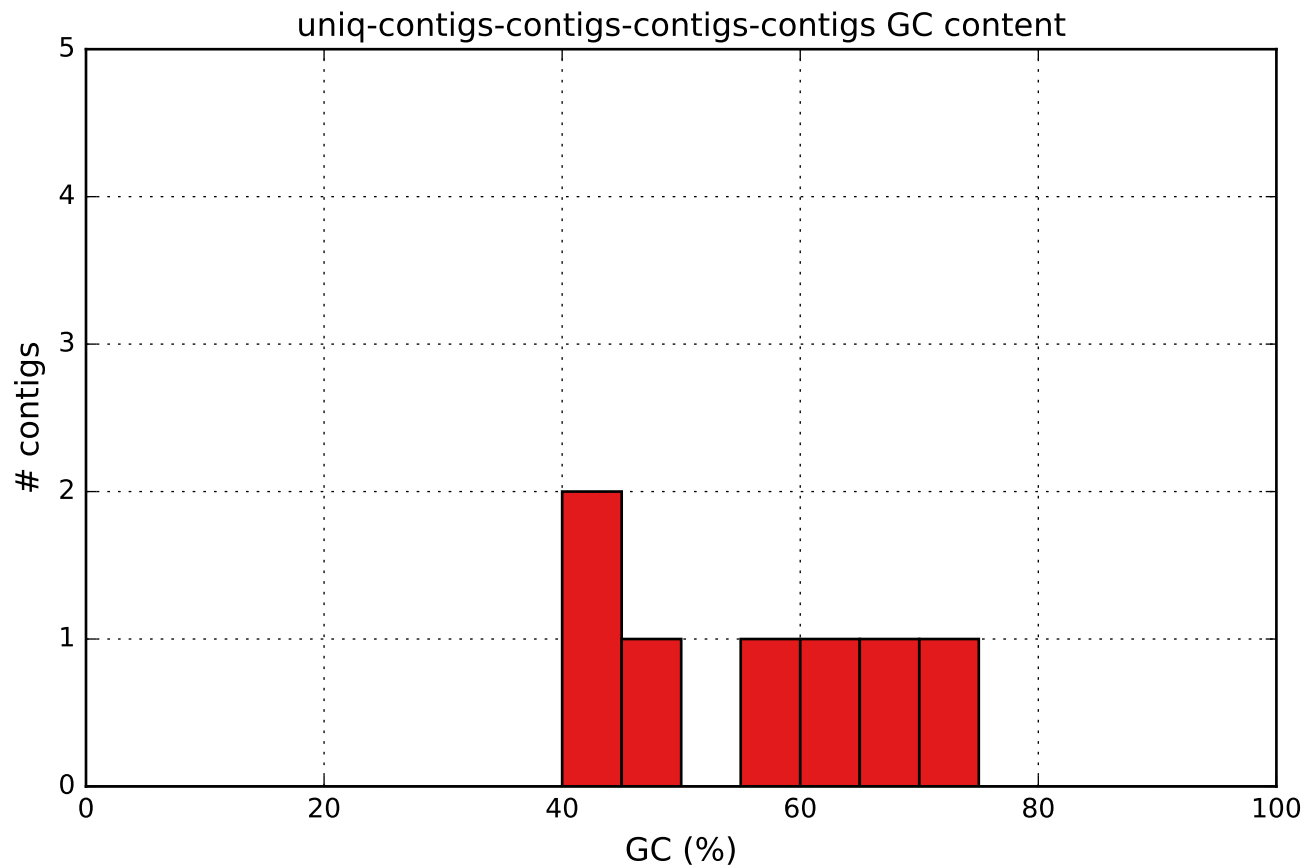
Cumulative length



GC content

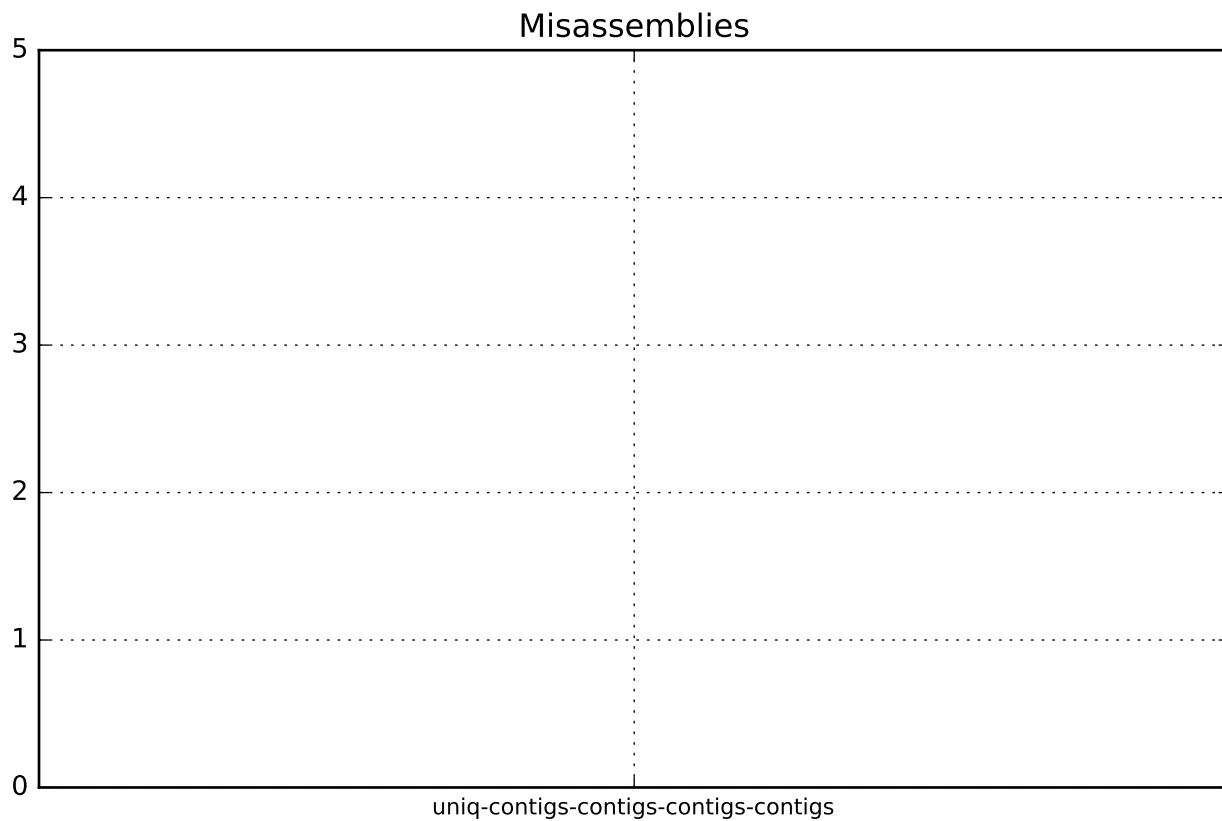


— uniq-contigs-contigs-contigs-contigs    - - Reference



uniq-contigs-contigs-contigs-contigs

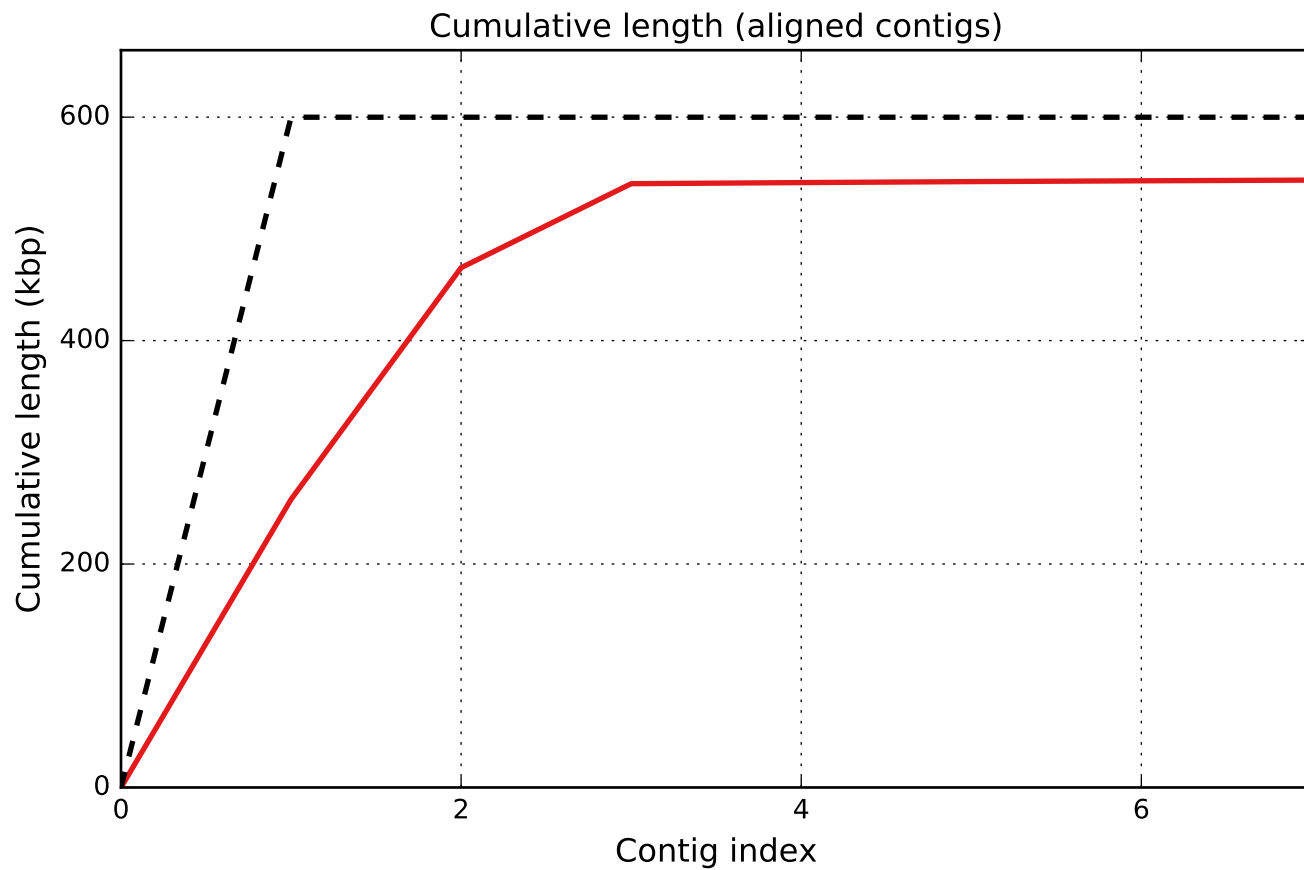




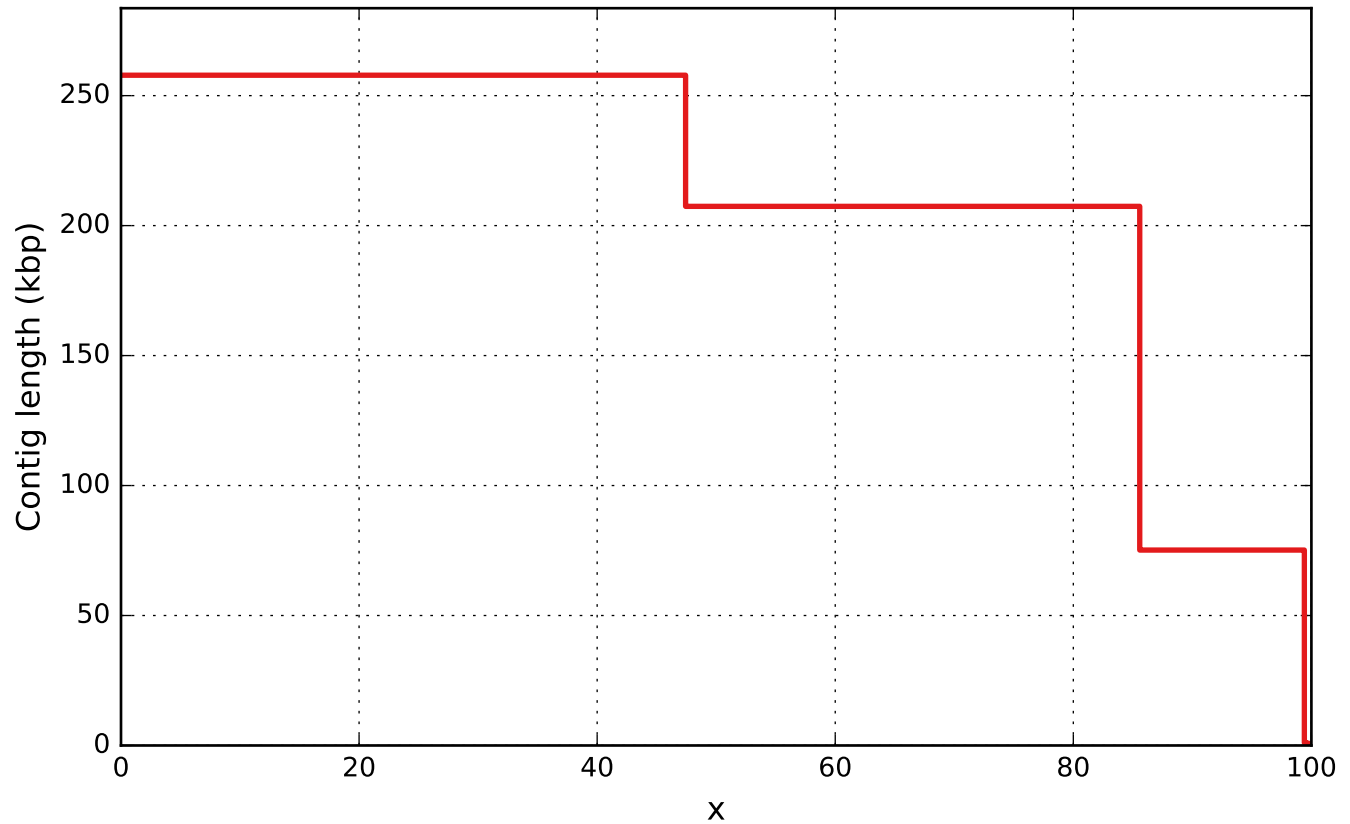
FRCurve (misassemblies)



— uniq-contigs-contigs-contigs-contigs

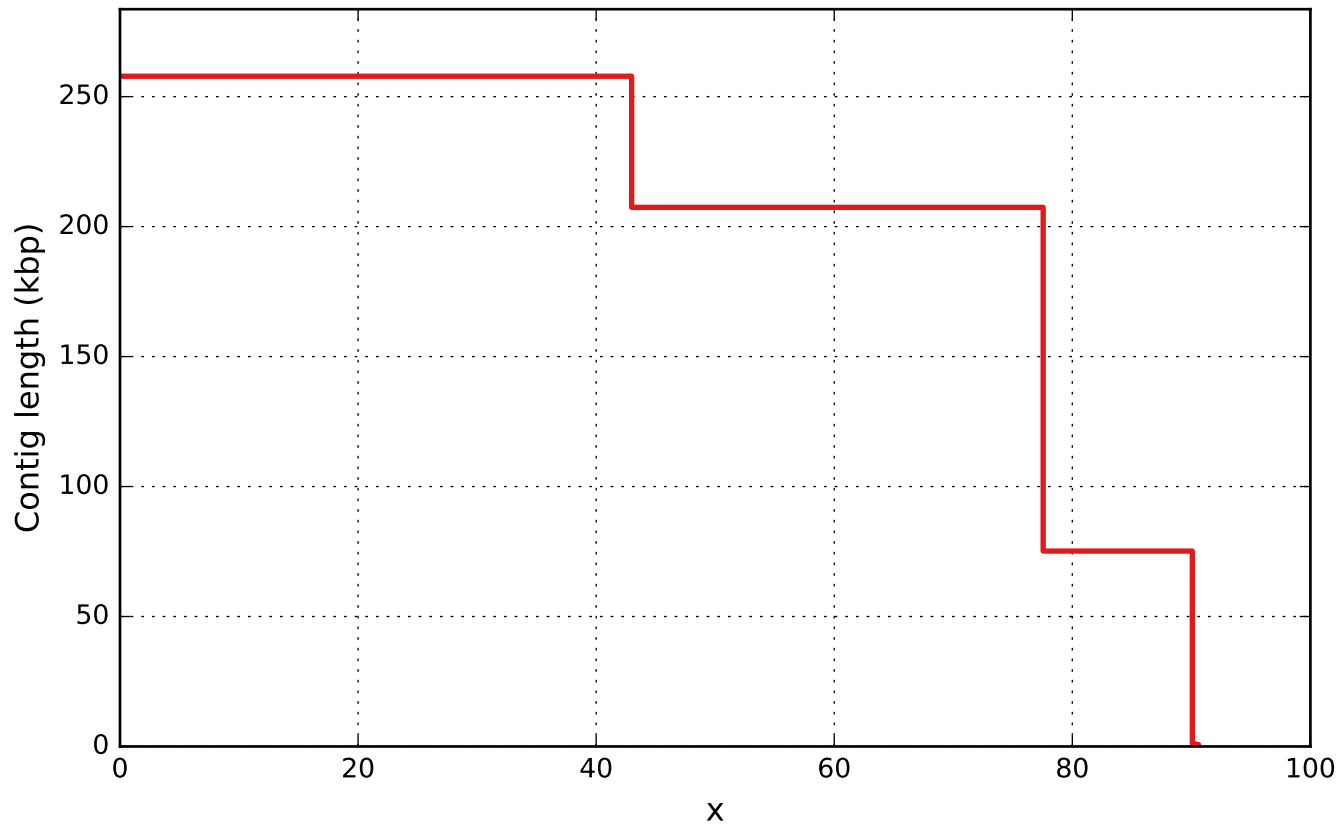


NAx



— uniq-contigs-contigs-contigs-contigs

NGAx



— uniq-contigs-contigs-contigs-contigs