

# Report

	CV115_contigs
# contigs (>= 0 bp)	28
# contigs (>= 1000 bp)	15
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	44340
Total length (>= 1000 bp)	33480
Total length (>= 5000 bp)	5225
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	28
Largest contig	5225
Total length	44340
Reference length	29903
GC (%)	43.55
Reference GC (%)	37.97
N50	2258
NG50	3060
N75	1013
NG75	2258
L50	7
LG50	4
L75	15
LG75	7
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	16 + 0 part
Unaligned length	14595
Genome fraction (%)	96.957
Duplication ratio	1.026
# N's per 100 kbp	0.00
# mismatches per 100 kbp	41.39
# indels per 100 kbp	0.00
# genomic features	38 + 21 part
Largest alignment	5152
Total aligned length	29438
NA50	2179
NGA50	3060
NGA75	2179
LA50	7
LGA50	4
LGA75	7

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

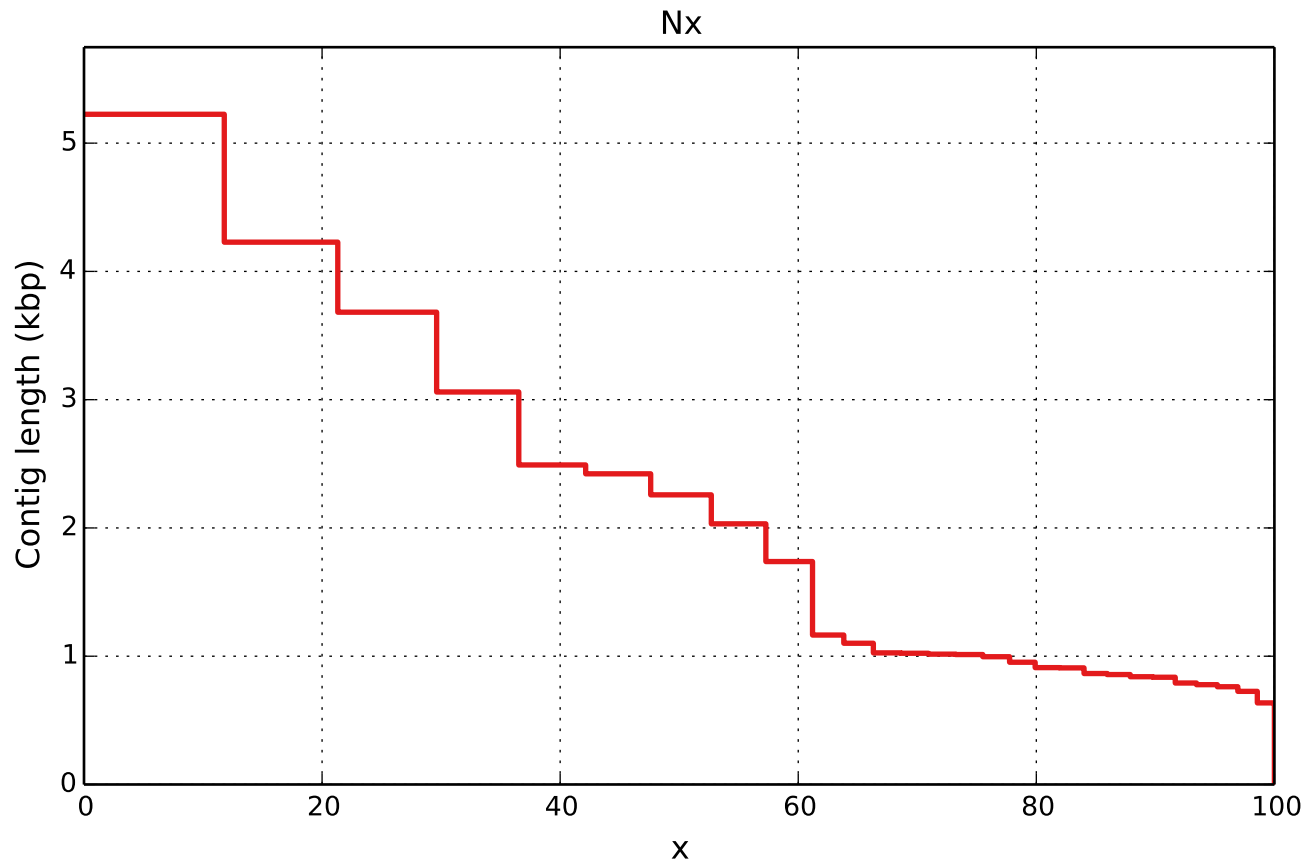
	CV115_contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	12
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	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).

## Unaligned report

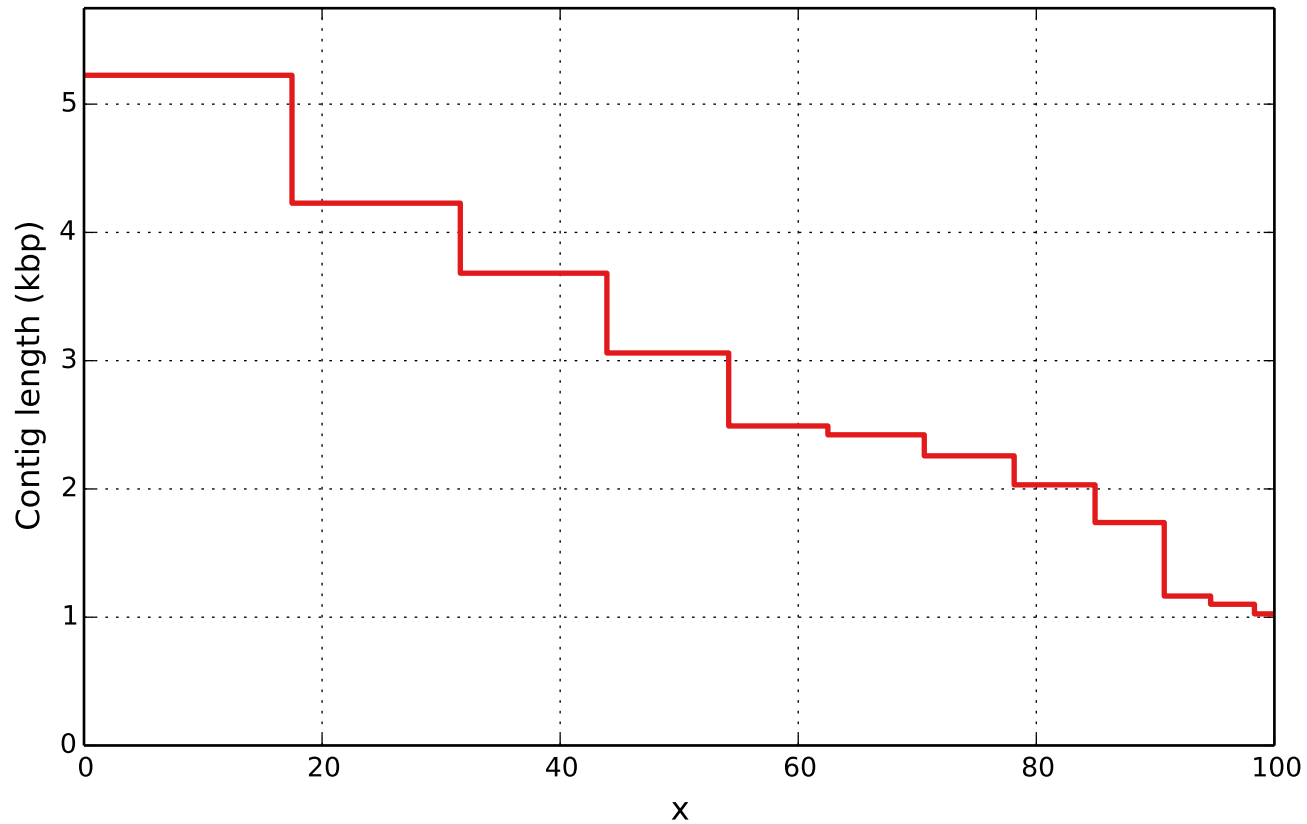
	CV115_contigs
# fully unaligned contigs	16
Fully unaligned length	14595
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).

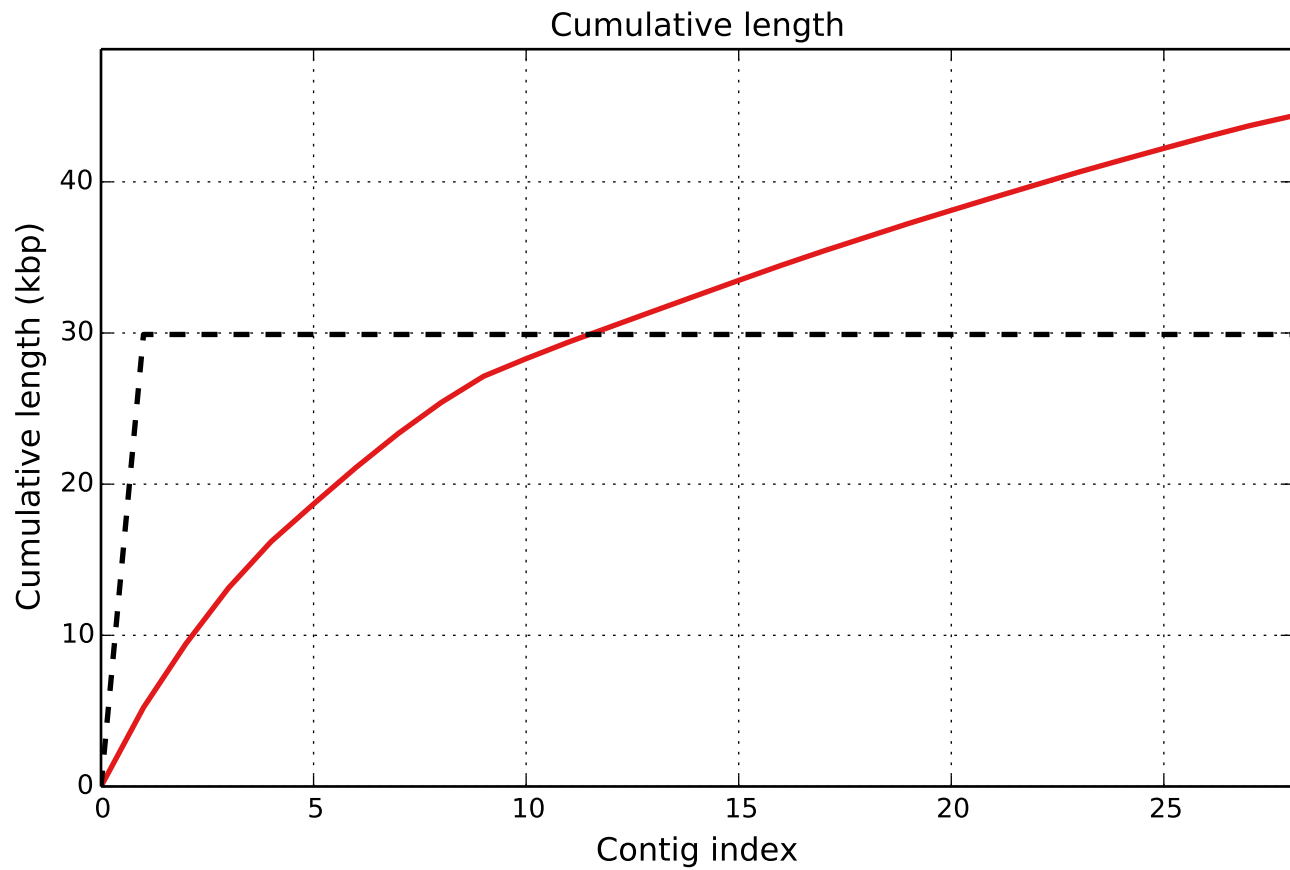


— CV115\_contigs

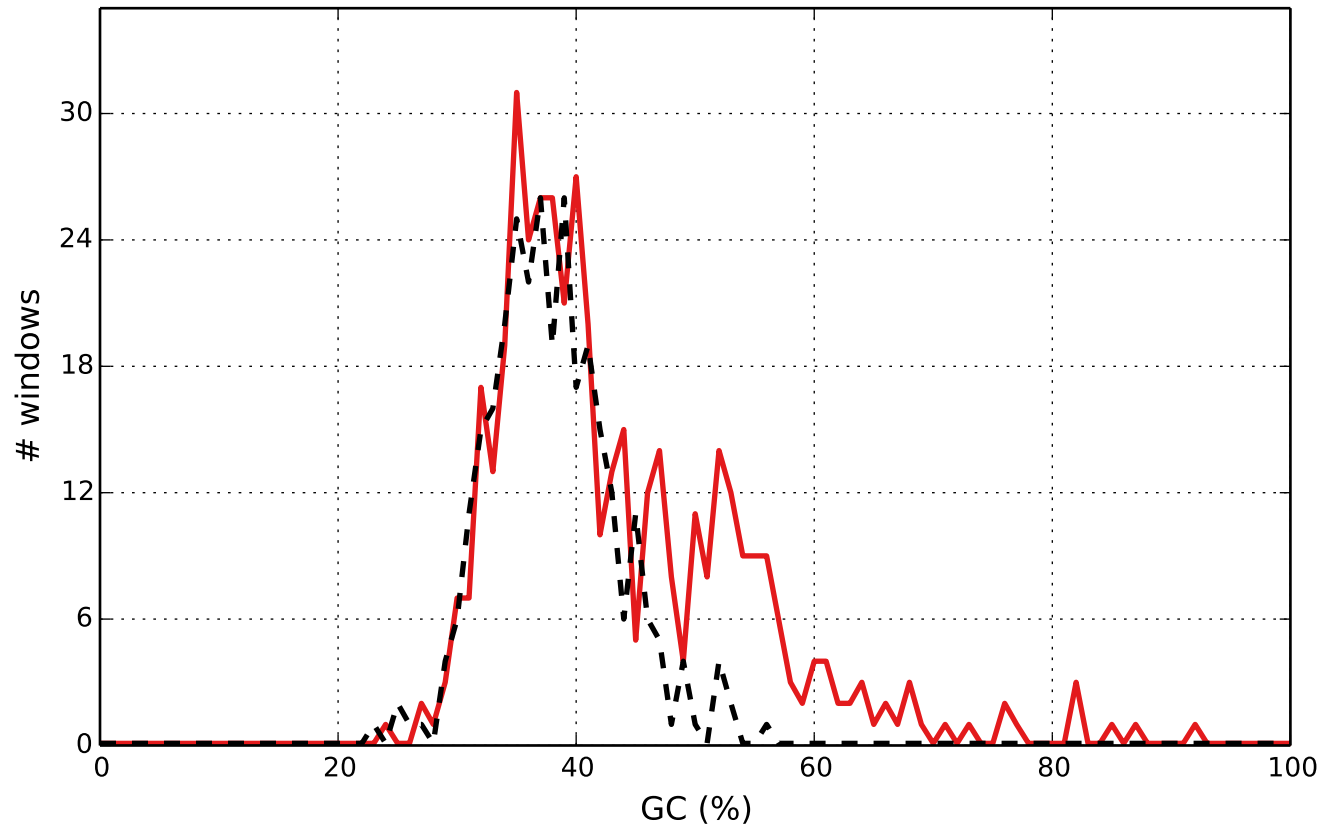
NGx



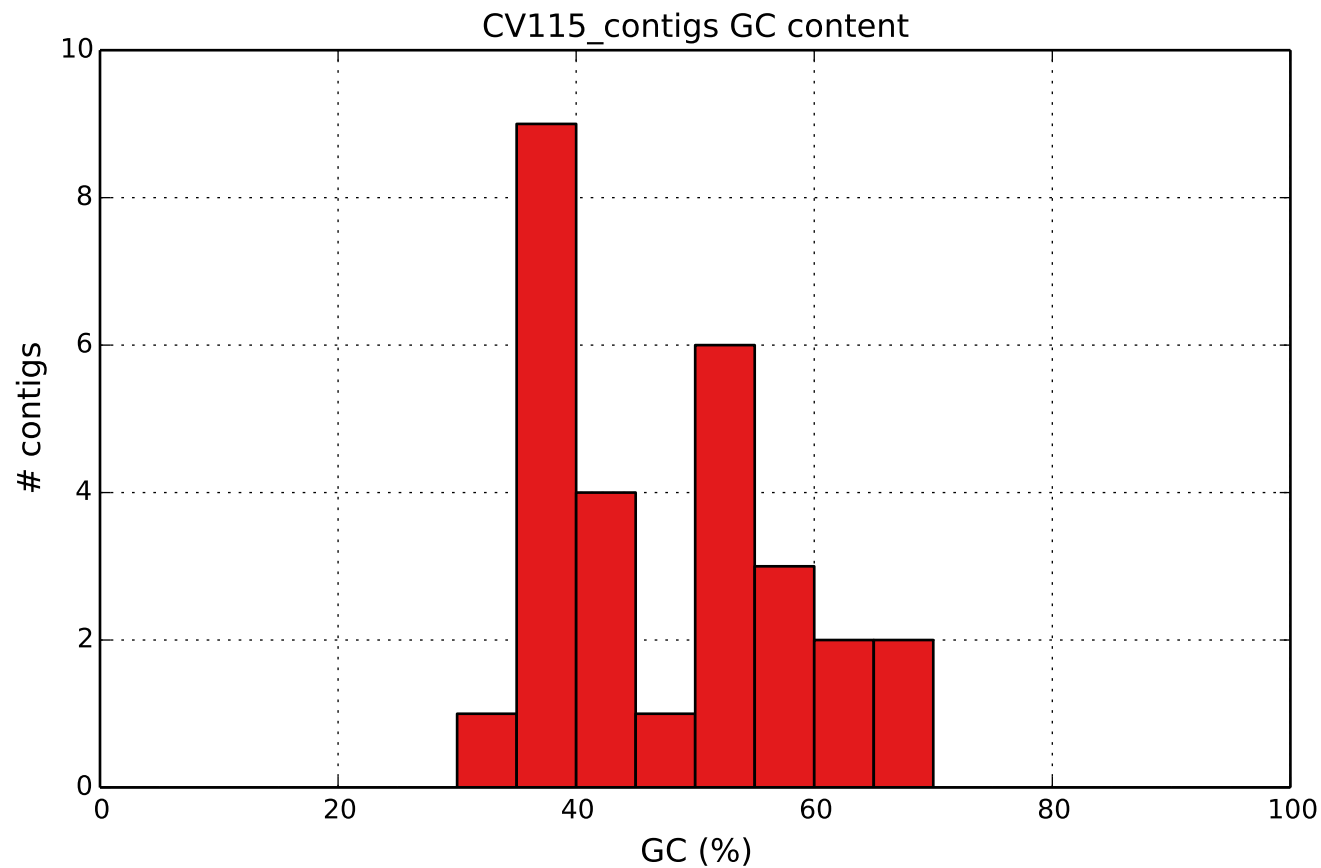
— CV115\_contigs



GC content



— CV115\_contigs    - - Reference



CV115\_contigs

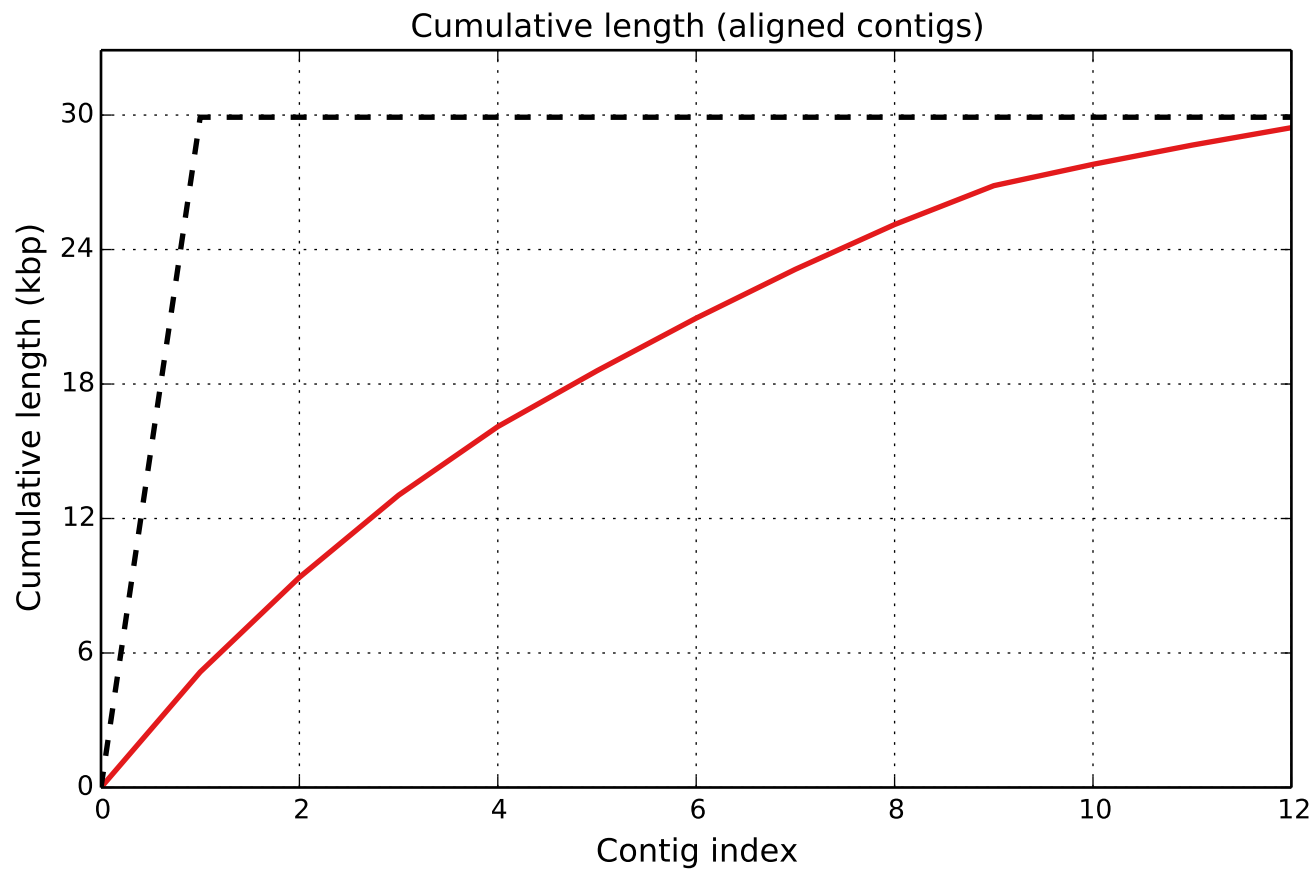




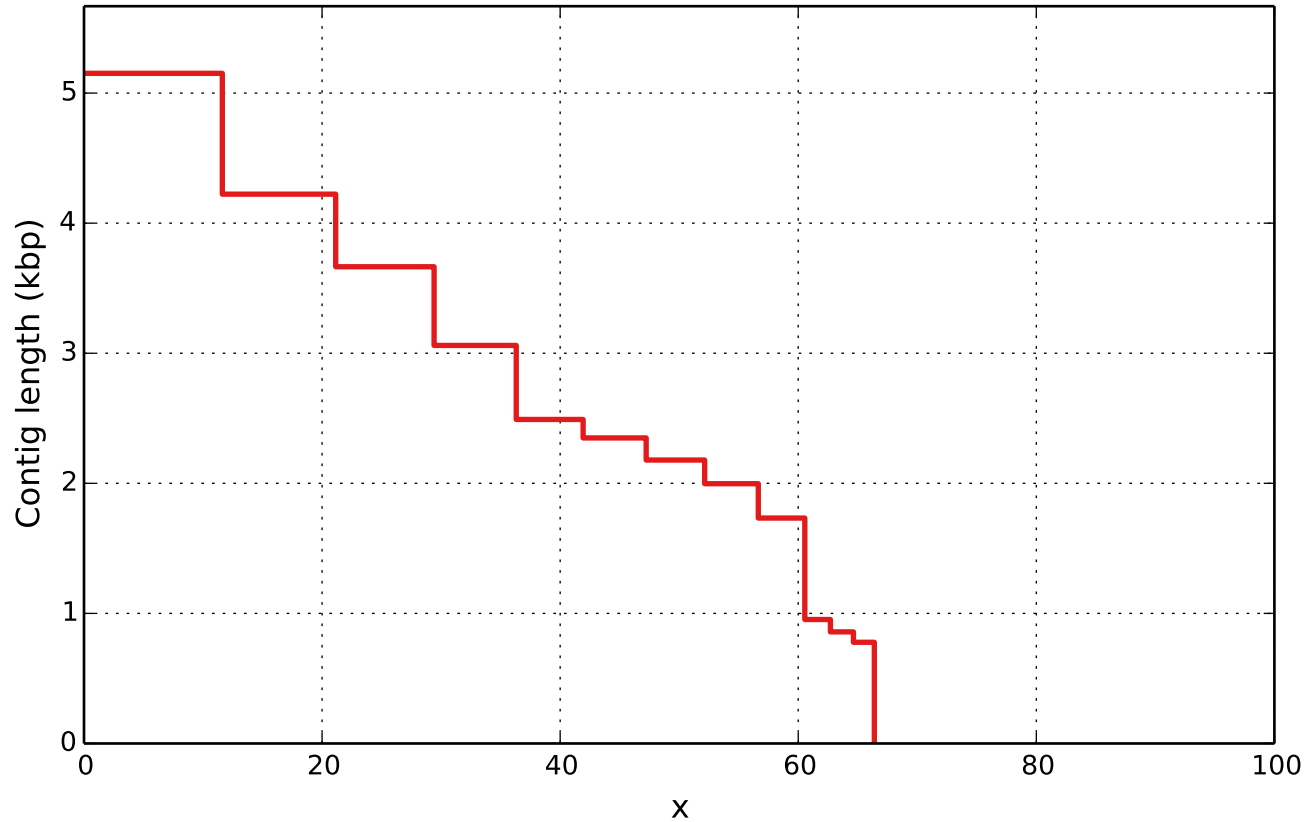
FRCurve (misassemblies)



— CV115\_contigs

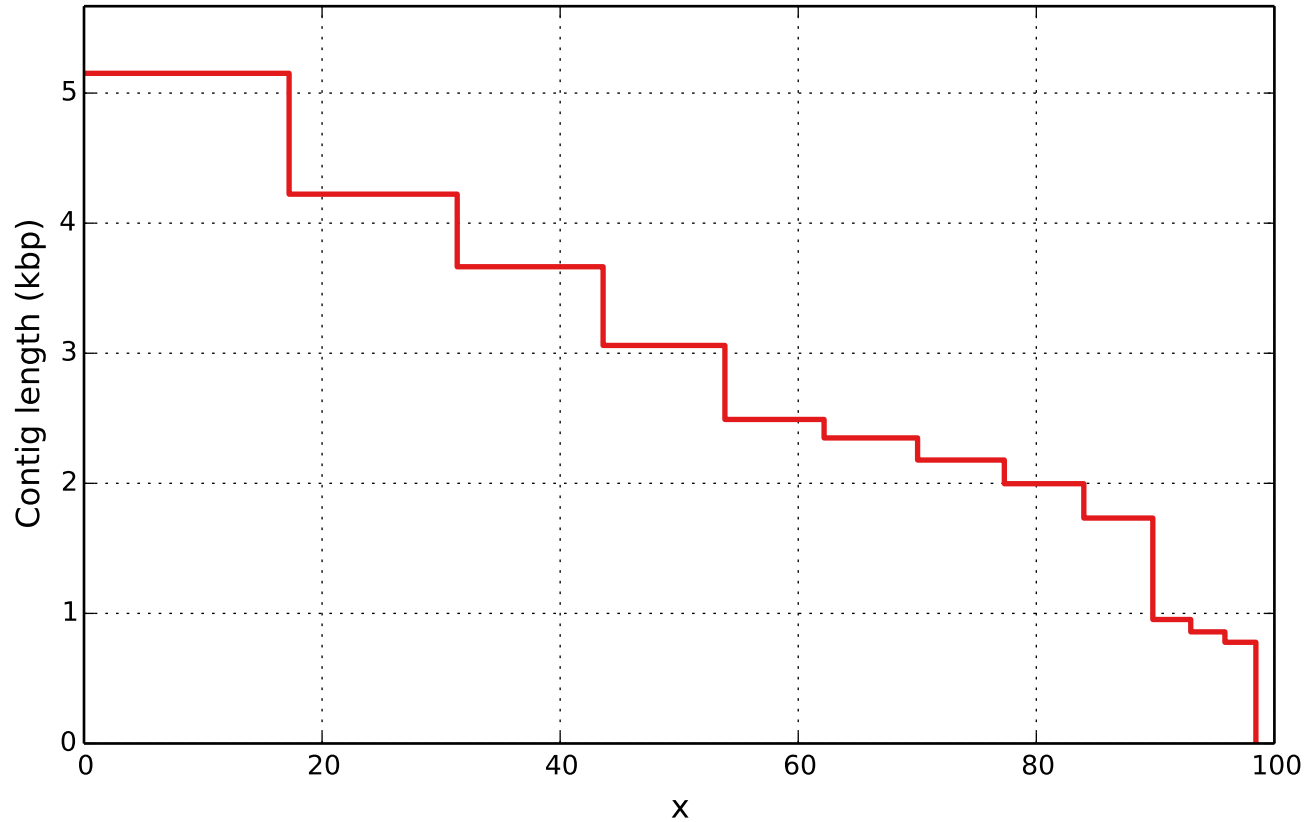


NAx



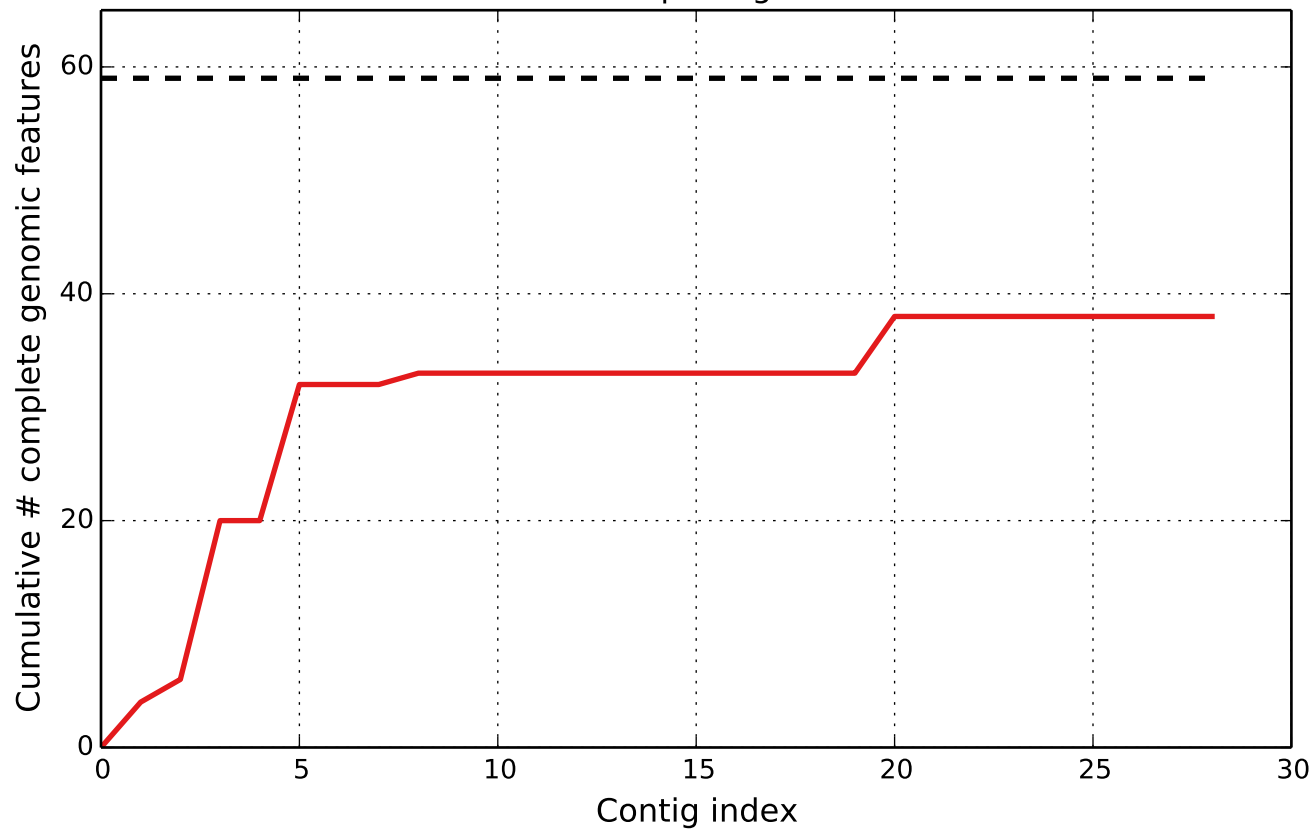
— CV115\_contigs

NGAx

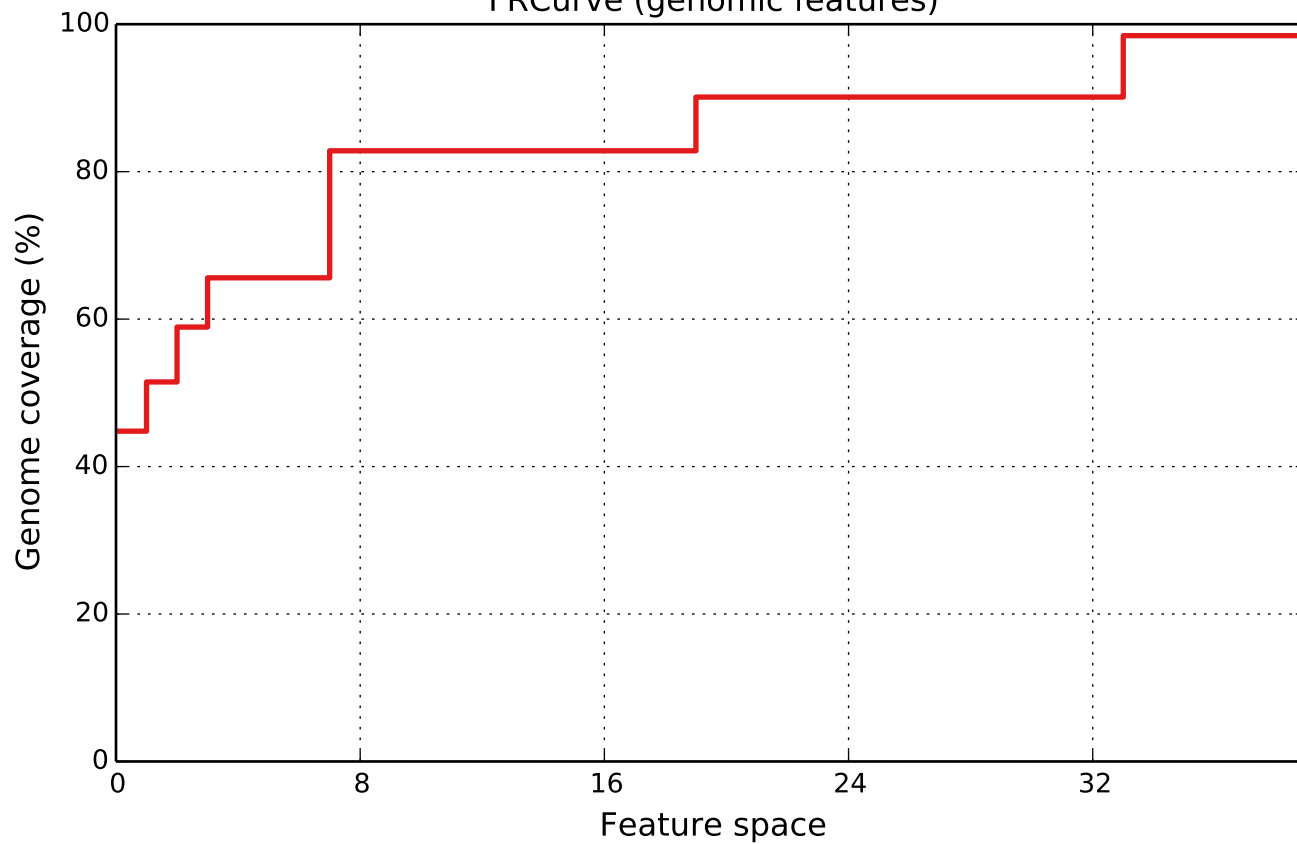


— CV115\_contigs

Cumulative # complete genomic features



FRCurve (genomic features)



— CV115\_contigs