

# Report

	SC2238.consensus
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	29884
Total length (>= 1000 bp)	29884
Total length (>= 5000 bp)	29884
Total length (>= 10000 bp)	29884
Total length (>= 25000 bp)	29884
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	29884
Total length	29884
Reference length	29903
GC (%)	37.91
Reference GC (%)	37.97
N50	29884
NG50	29884
N75	29884
NG75	29884
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	1
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.940
Duplication ratio	1.020
# N's per 100 kbp	1967.61
# mismatches per 100 kbp	109.26
# indels per 100 kbp	13.66
# genomic features	19 + 4 part
Largest alignment	29268
Total aligned length	29268
NA50	29268
NGA50	29268
NA75	29268
NGA75	29268
LA50	1
LGA50	1
LA75	1
LGA75	1

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

	SC2238.consensus
# 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.	1
# unaligned mis. contigs	0
# mismatches	32
# indels	4
# indels (<= 5 bp)	2
# indels (> 5 bp)	2
Indels length	19

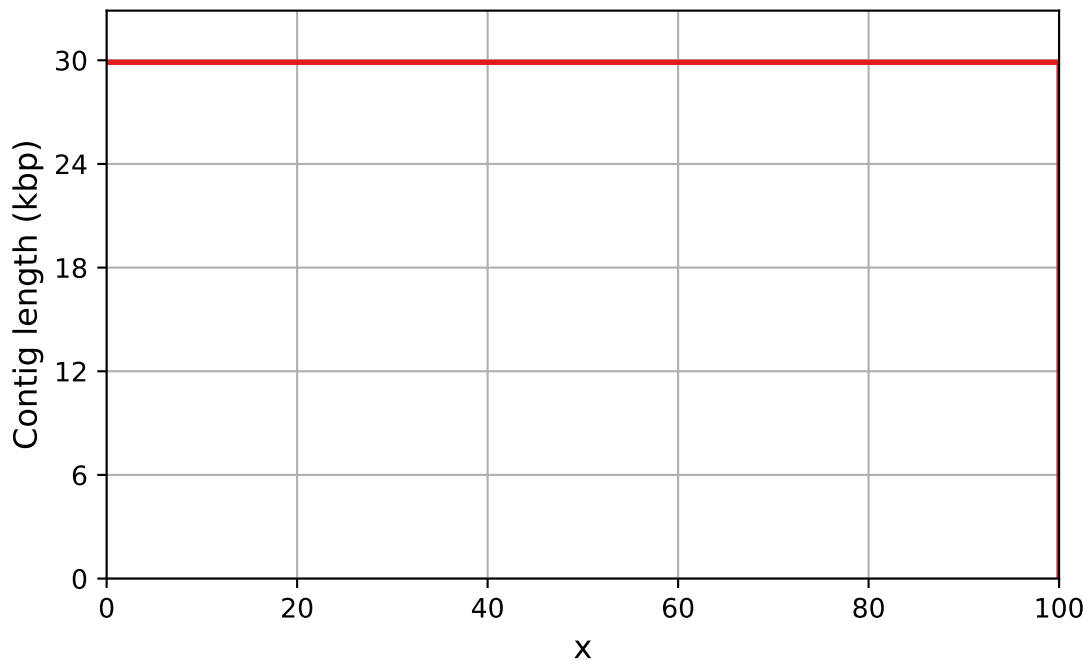
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	SC2238.consensus
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	588

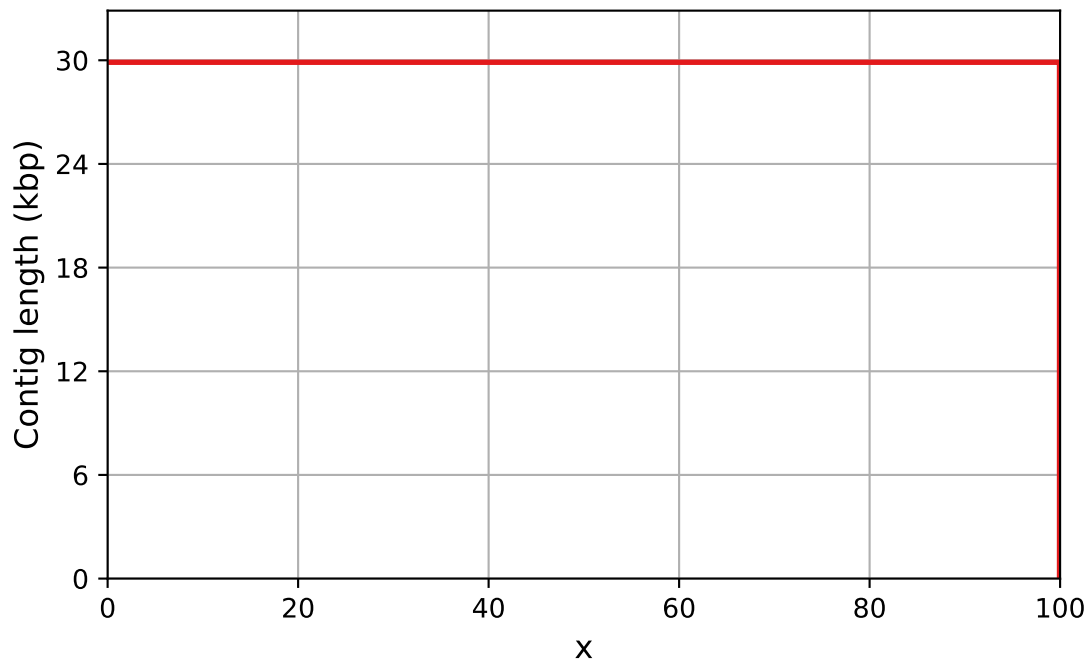
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



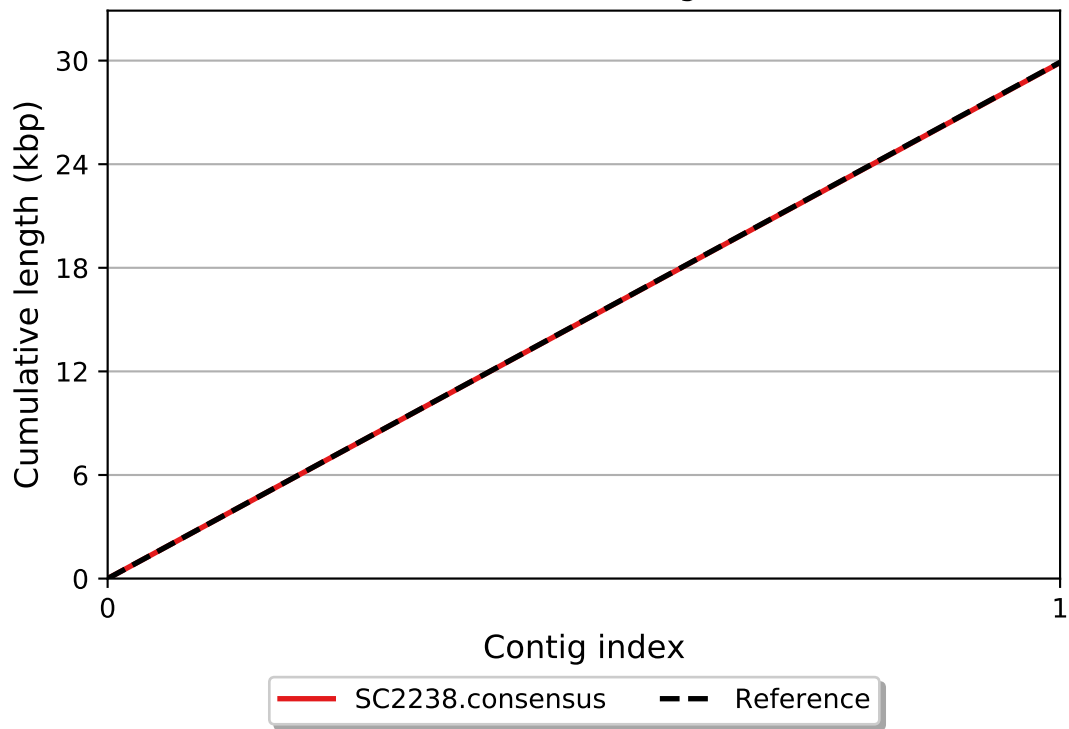
— SC2238.consensus

NGx

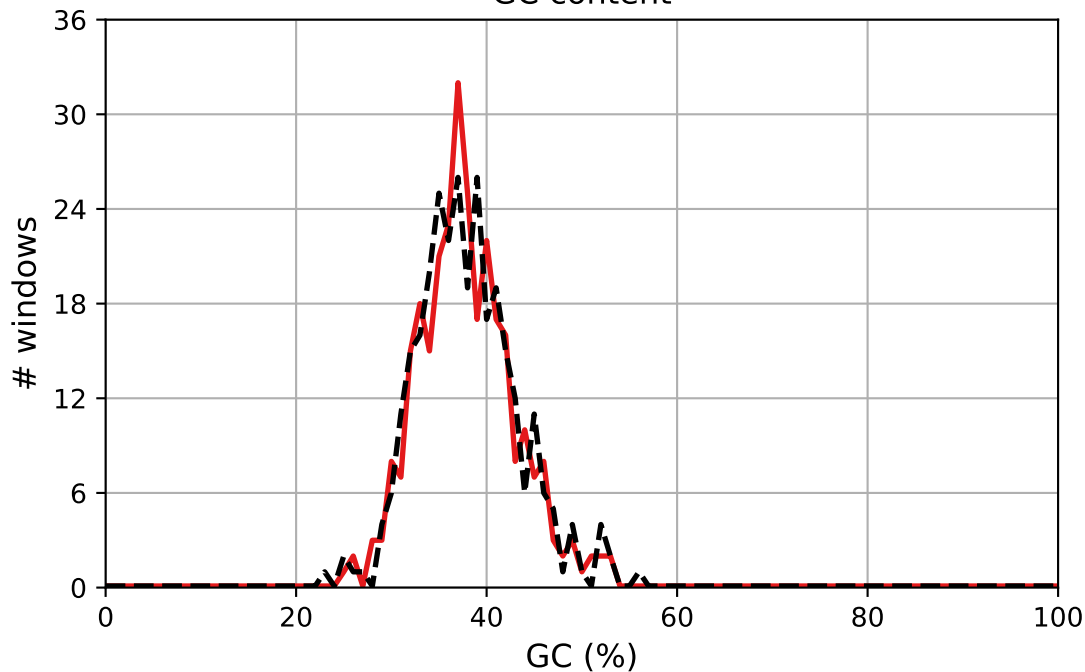


— SC2238.consensus

Cumulative length

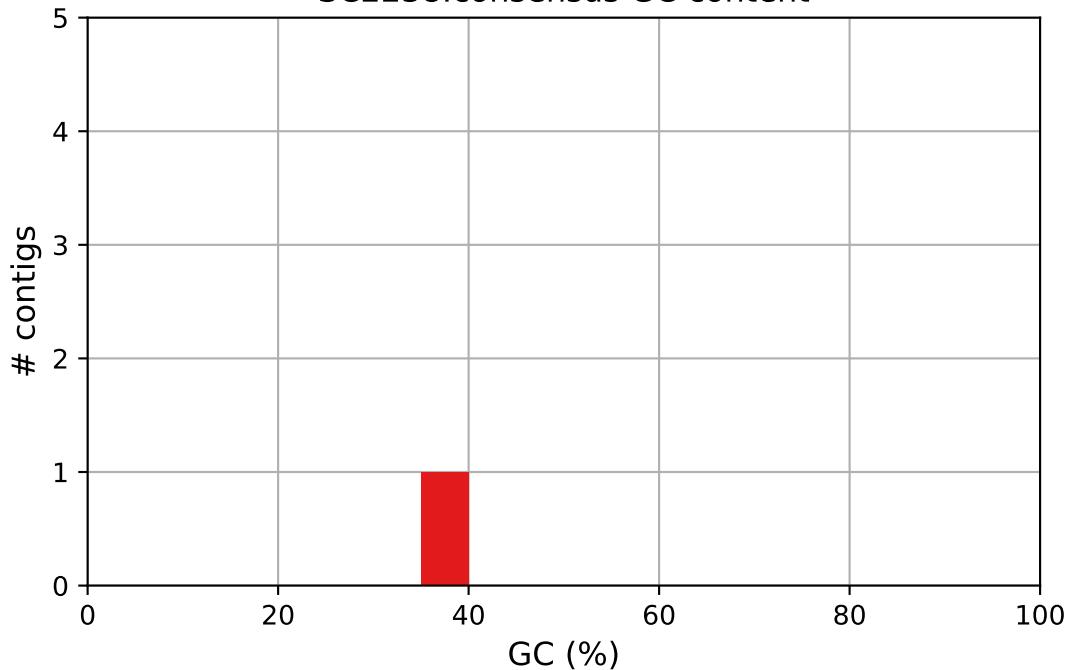


## GC content



— SC2238.consensus    - - Reference

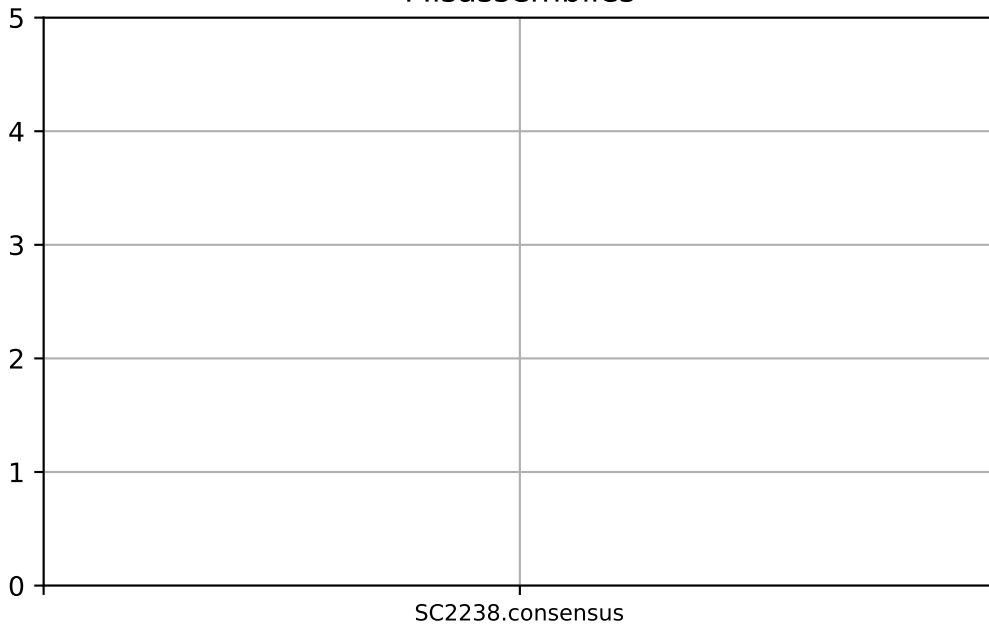
SC2238.consensus GC content



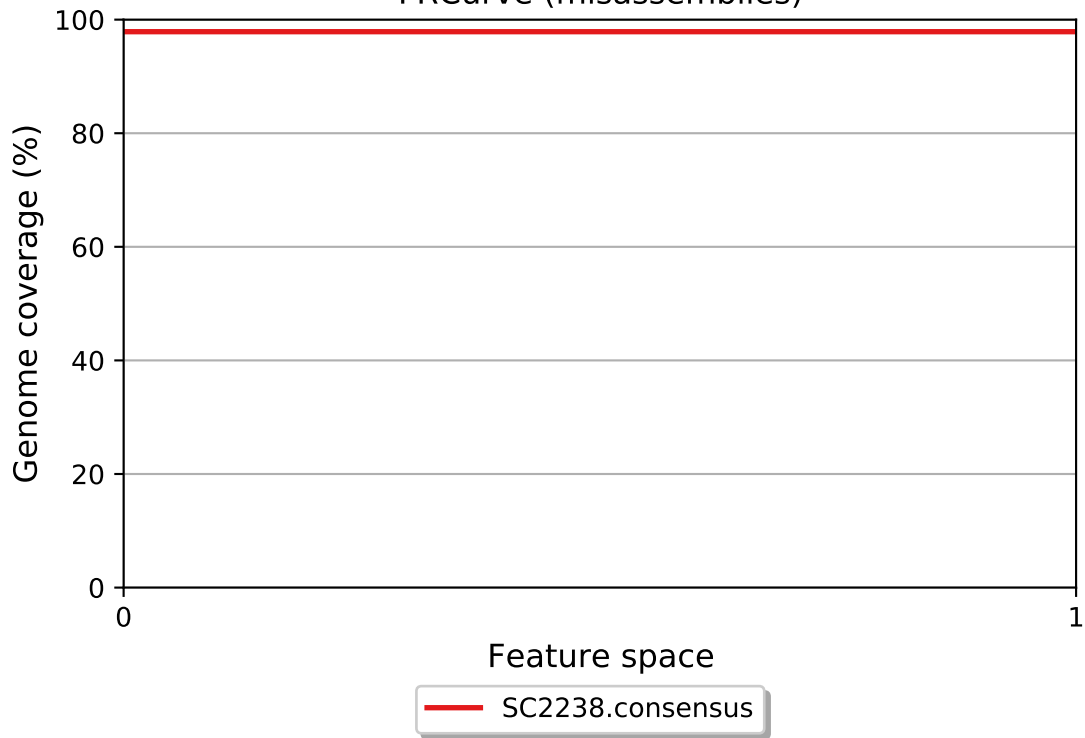
SC2238.consensus



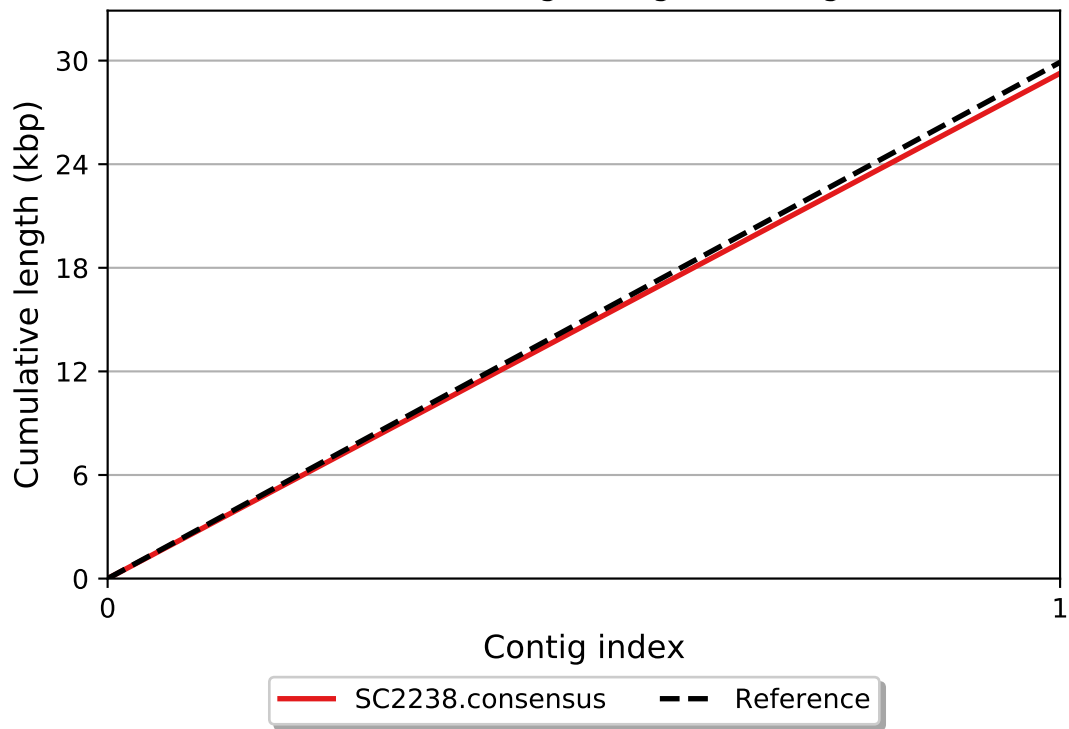
## Misassemblies



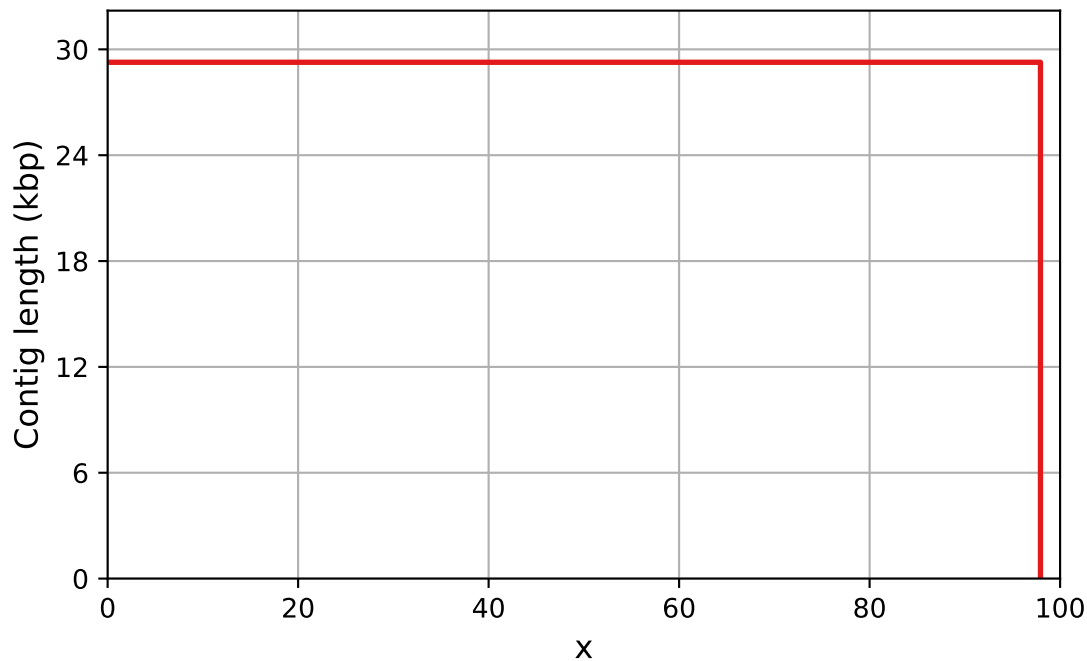
FRCurve (misassemblies)



Cumulative length (aligned contigs)

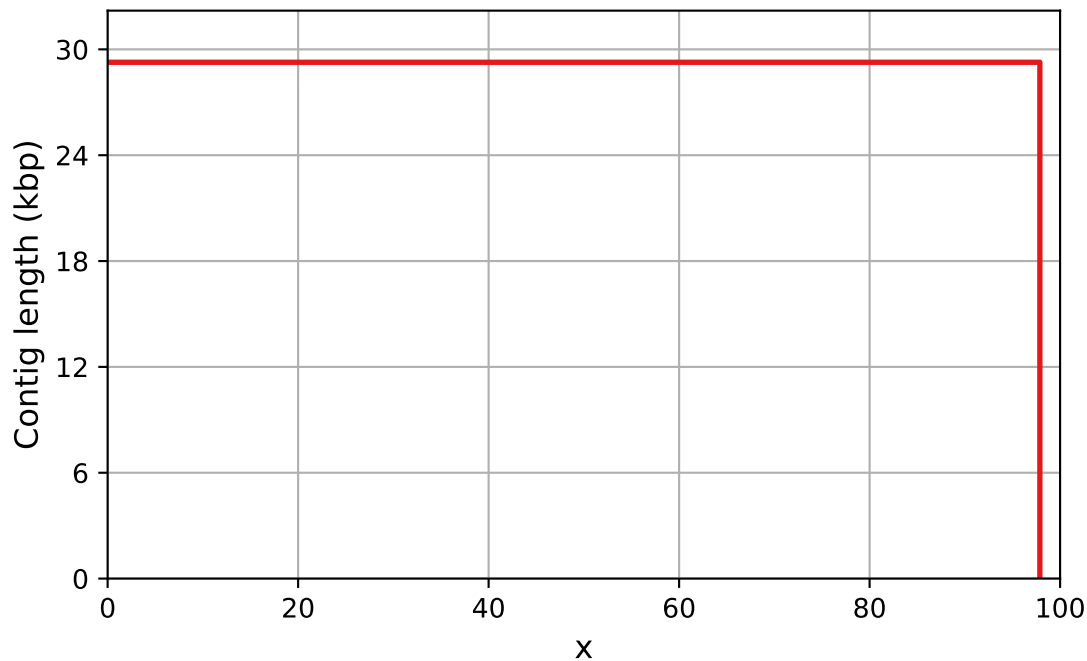


NAx

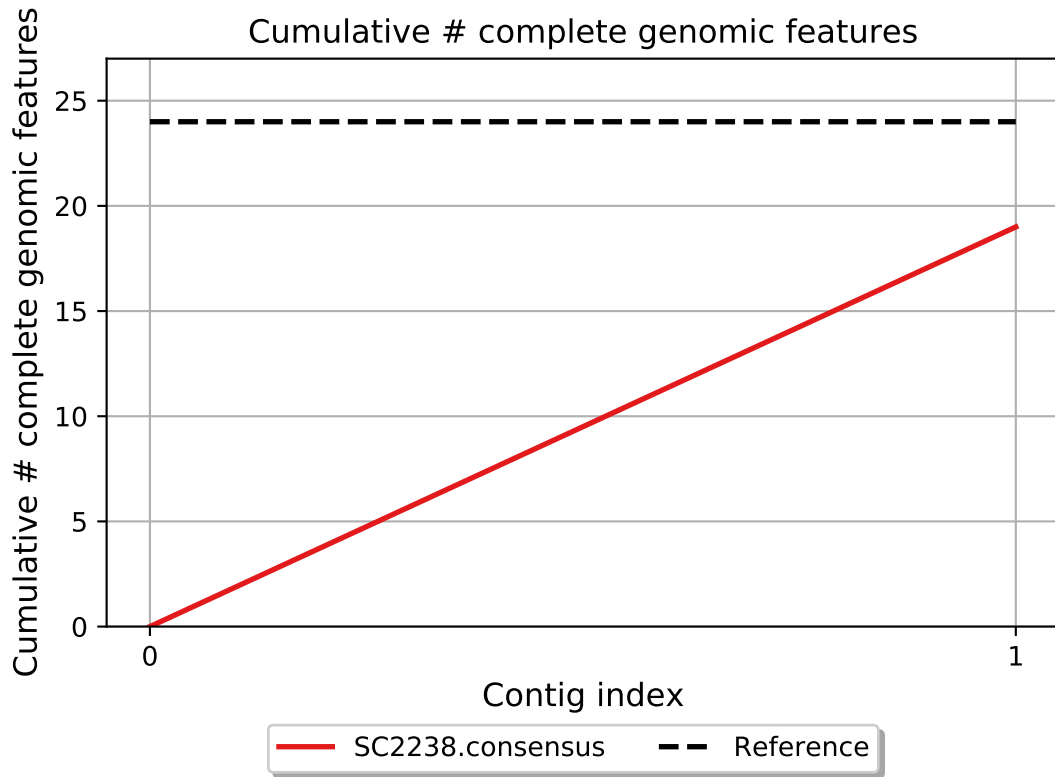


— SC2238.consensus

# NGAx



— SC2238.consensus



FRCurve (genomic features)

