

# Report

	SC2254.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)	29900
Total length (>= 1000 bp)	29900
Total length (>= 5000 bp)	29900
Total length (>= 10000 bp)	29900
Total length (>= 25000 bp)	29900
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	29900
Total length	29900
Reference length	29903
GC (%)	38.15
Reference GC (%)	37.97
N50	29900
NG50	29900
N75	29900
NG75	29900
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.	19
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	68.057
Duplication ratio	1.469
# N's per 100 kbp	31478.26
# mismatches per 100 kbp	49.14
# indels per 100 kbp	24.57
# genomic features	12 + 8 part
Largest alignment	20349
Total aligned length	20349
NA50	20349
NGA50	20349
LA50	1
LGA50	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

	SC2254.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.	19
# unaligned mis. contigs	0
# mismatches	10
# indels	5
# indels (<= 5 bp)	5
# indels (> 5 bp)	0
Indels length	6

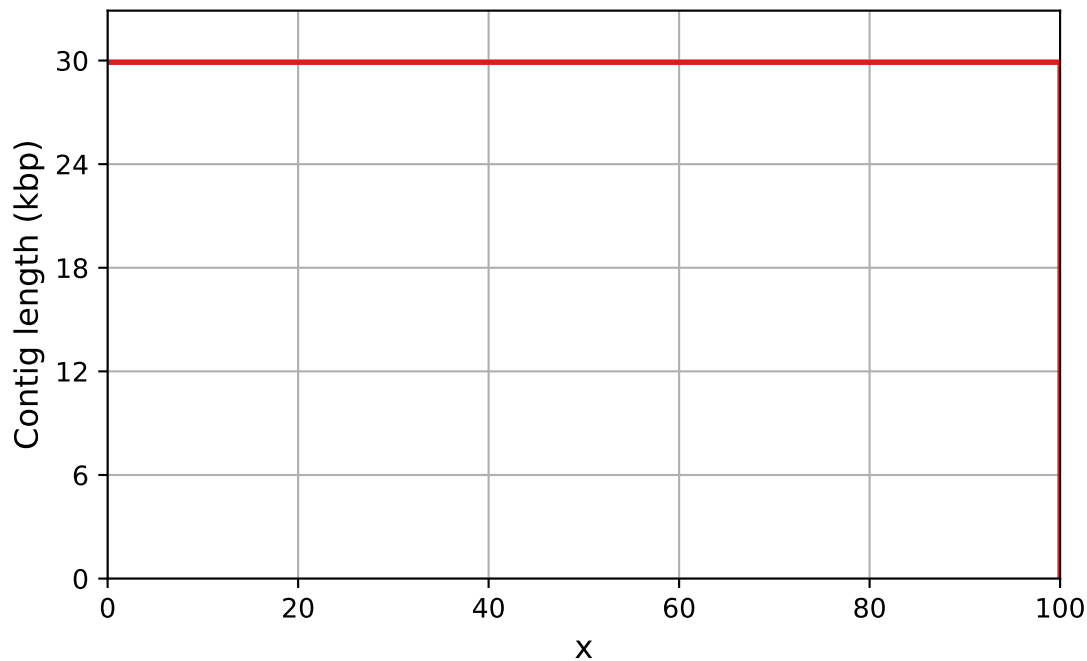
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	SC2254.consensus
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	9412

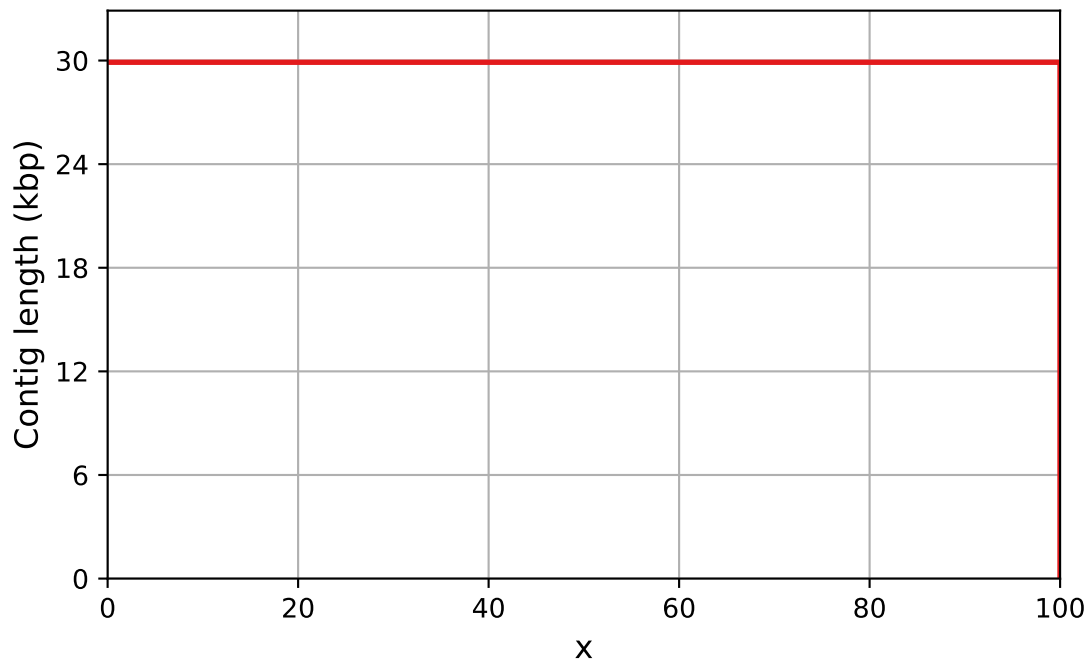
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



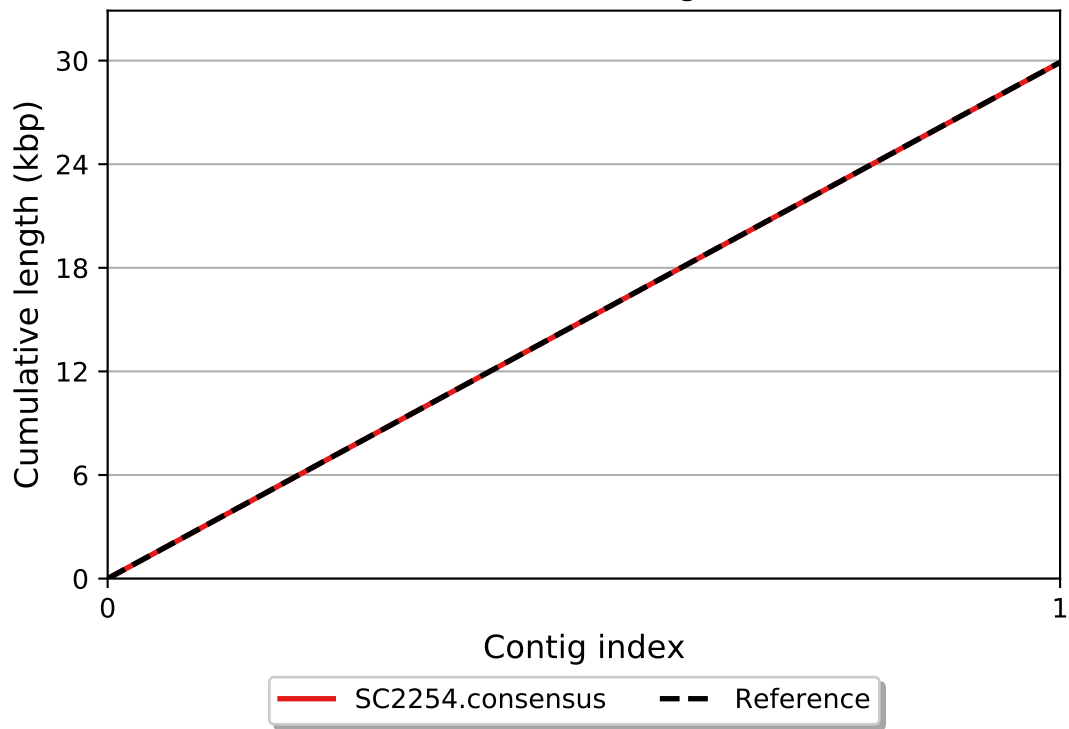
— SC2254.consensus

# NGx

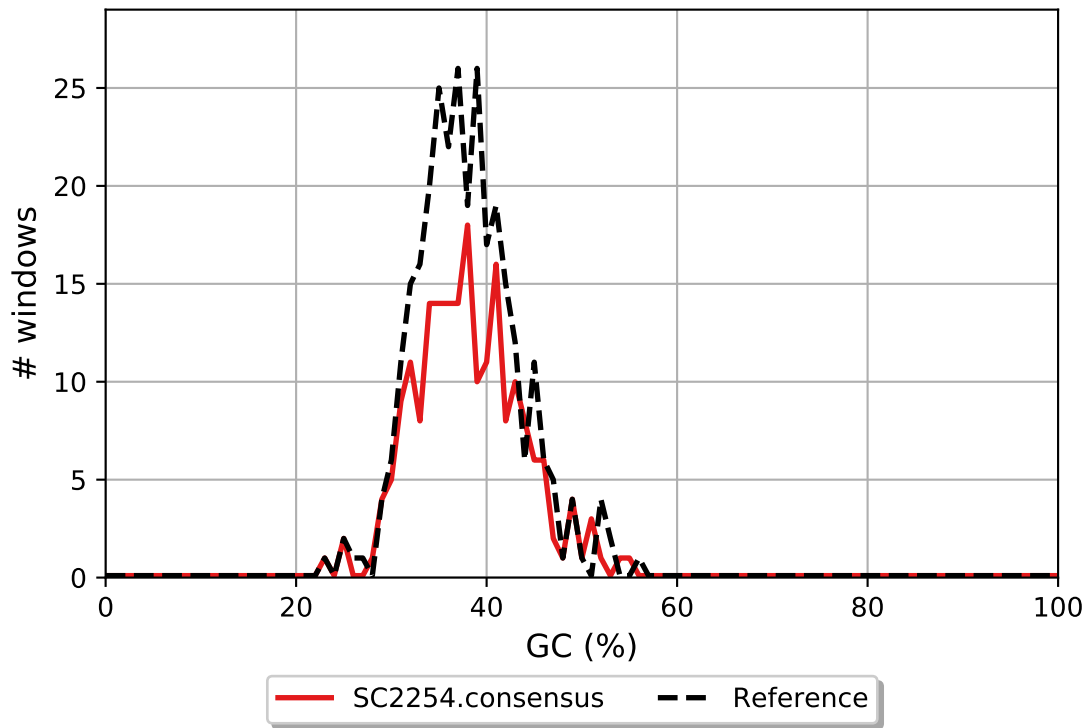


— SC2254.consensus

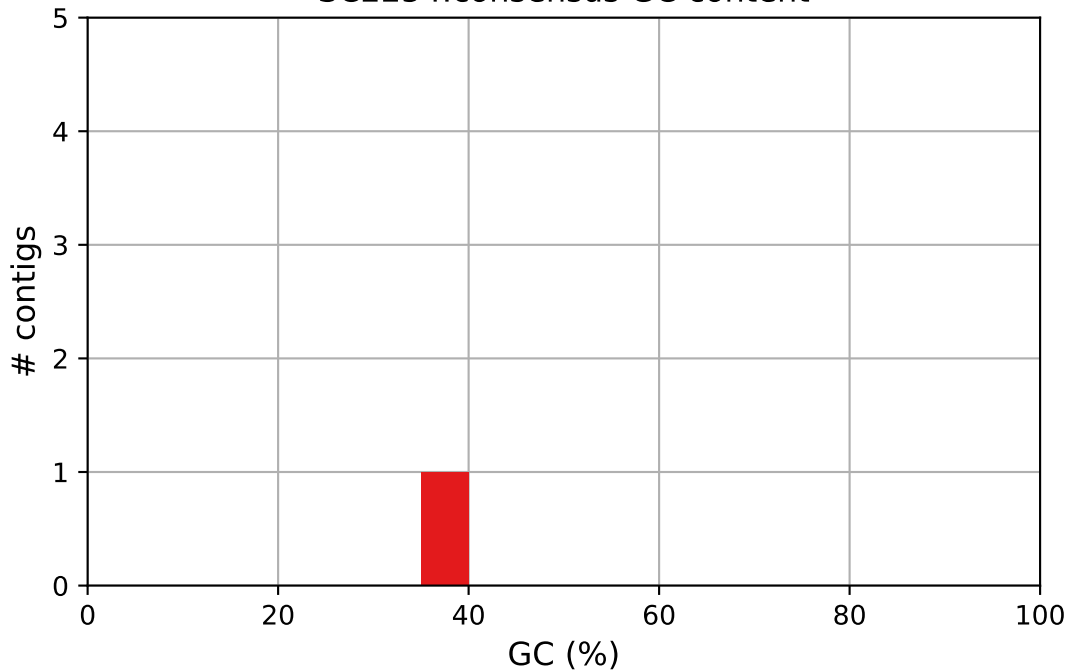
Cumulative length



## GC content



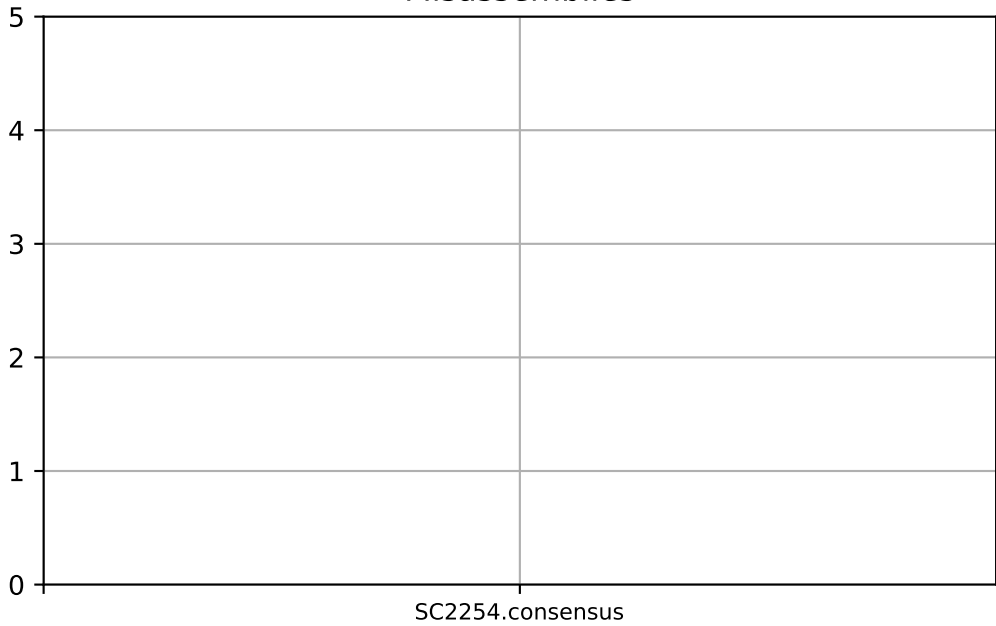
SC2254.consensus GC content



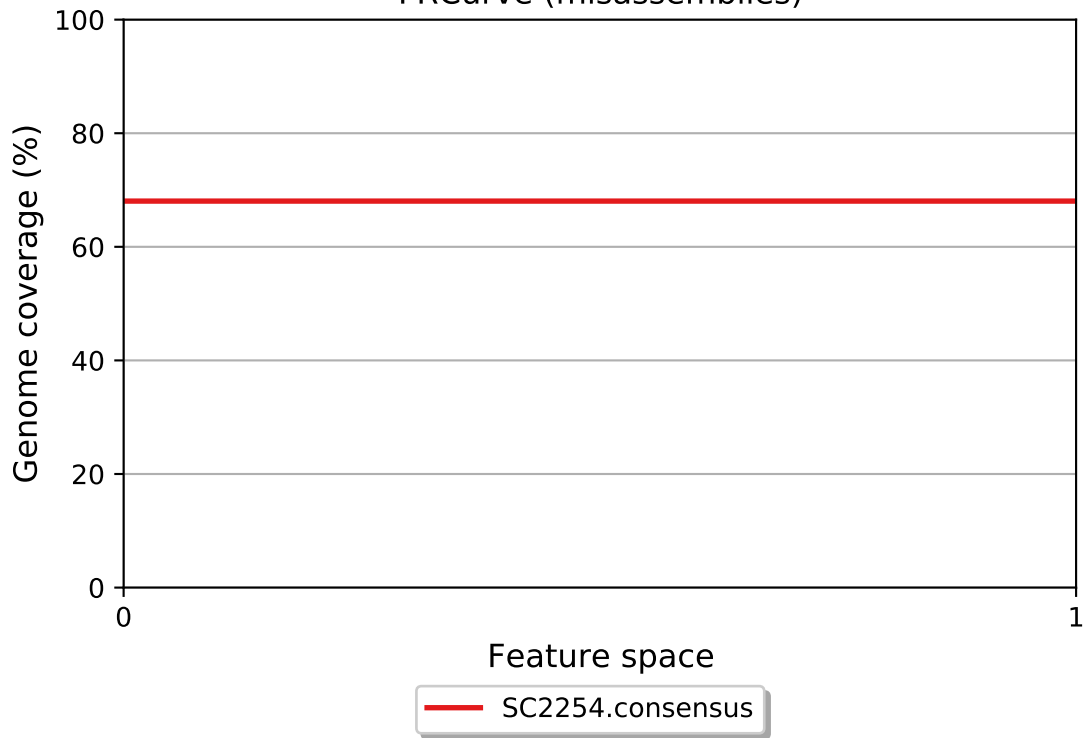
SC2254.consensus



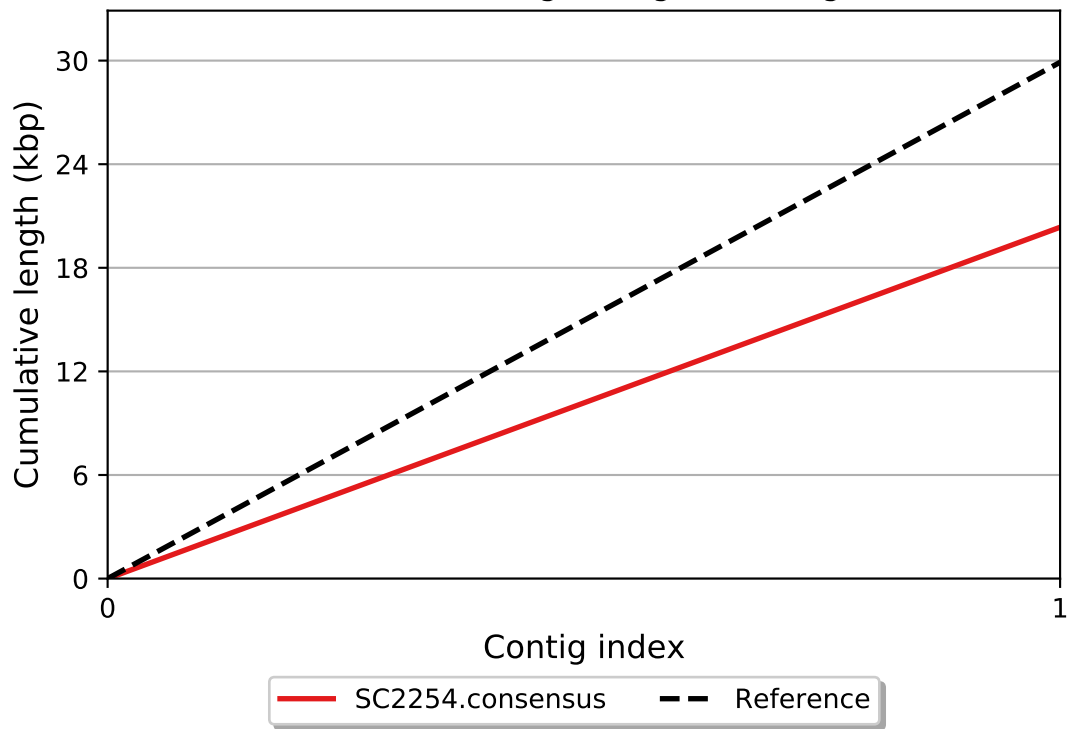
## Misassemblies



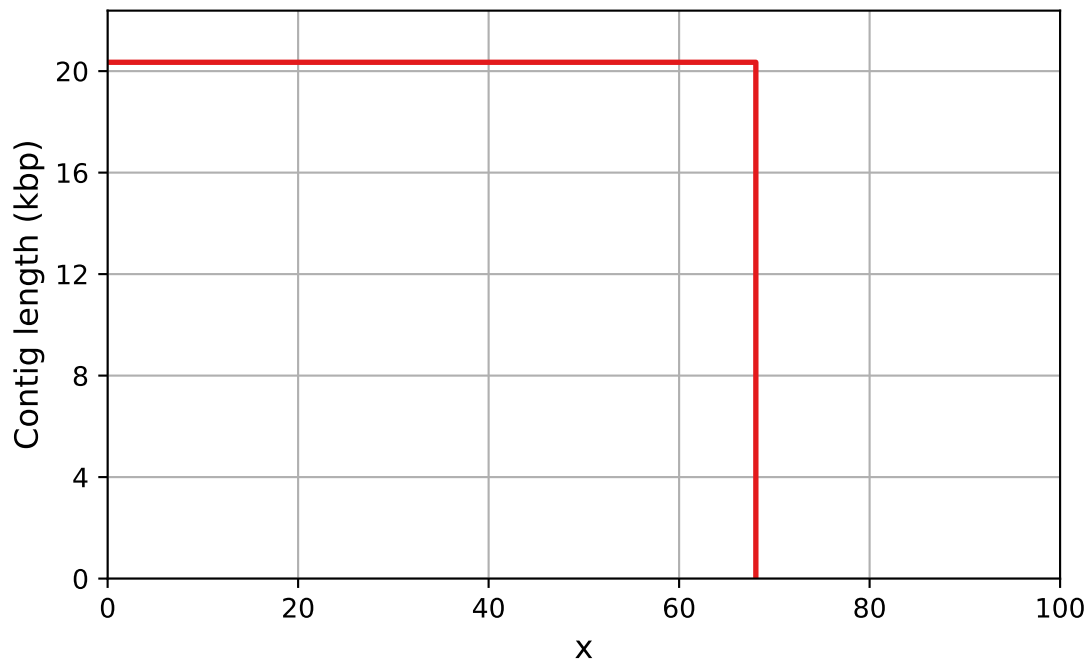
FRCurve (misassemblies)



Cumulative length (aligned contigs)

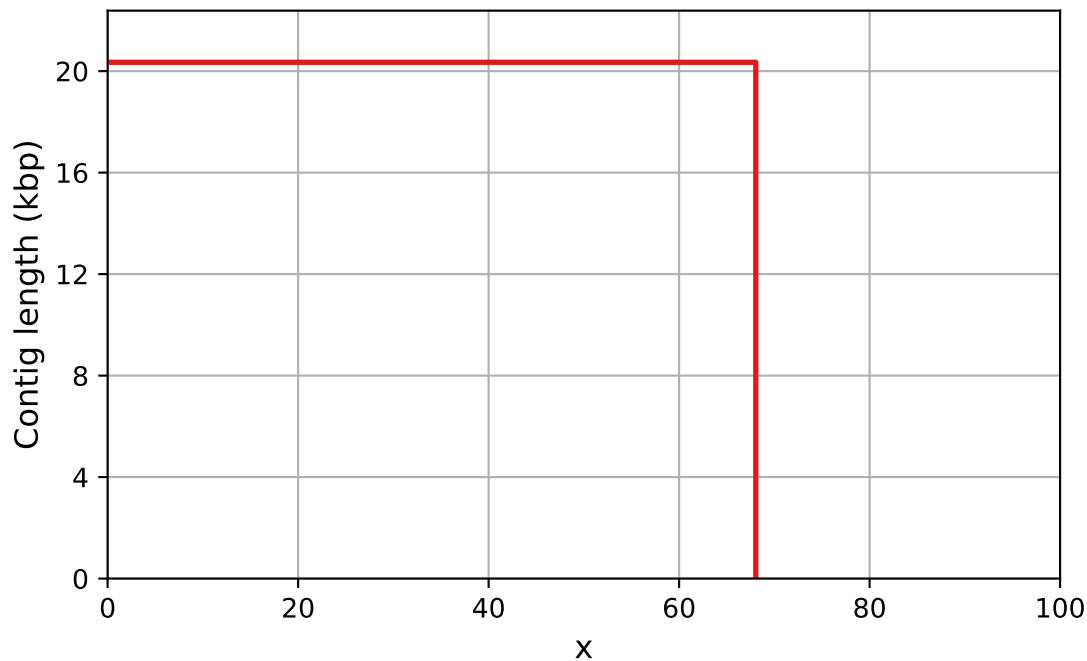


NAx

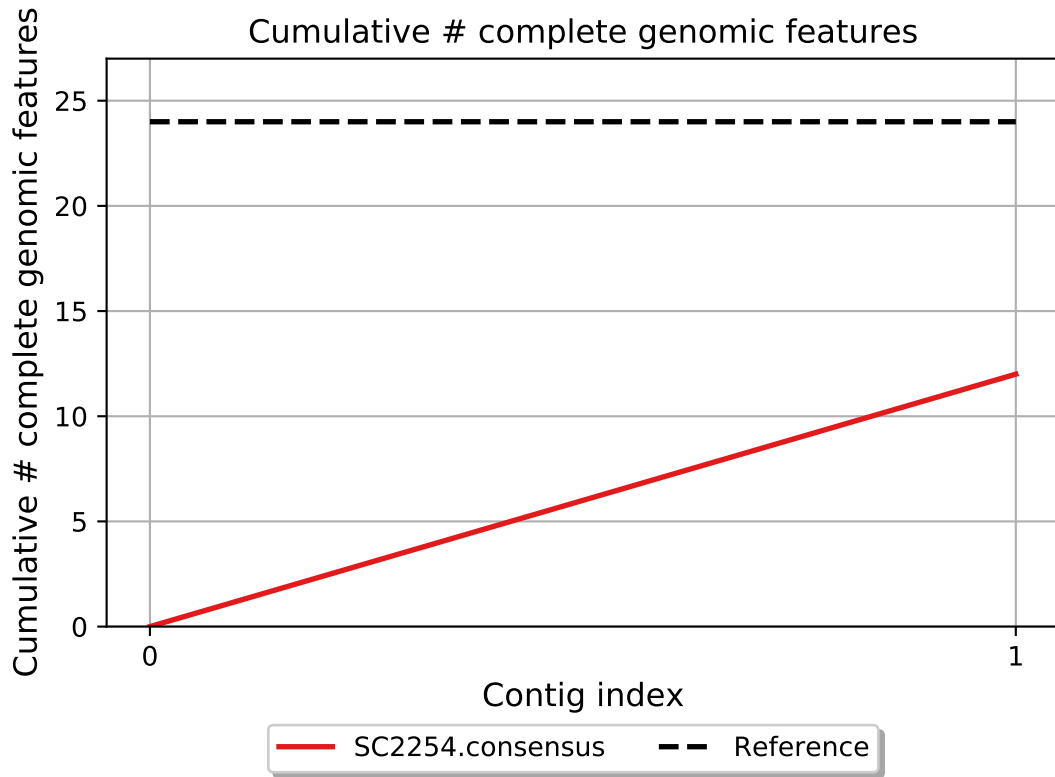


— SC2254.consensus

# NGAx



— SC2254.consensus



FRCurve (genomic features)

