

# Report

	SC2244.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)	29891
Total length (>= 1000 bp)	29891
Total length (>= 5000 bp)	29891
Total length (>= 10000 bp)	29891
Total length (>= 25000 bp)	29891
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	29891
Total length	29891
Reference length	29903
GC (%)	37.90
Reference GC (%)	37.97
N50	29891
NG50	29891
N75	29891
NG75	29891
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.	22
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	62.907
Duplication ratio	1.589
# N's per 100 kbp	37292.16
# mismatches per 100 kbp	116.95
# indels per 100 kbp	21.26
# genomic features	10 + 10 part
Largest alignment	18799
Total aligned length	18799
NA50	18799
NGA50	18799
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

	SC2244.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.	22
# unaligned mis. contigs	0
# mismatches	22
# indels	4
# indels (<= 5 bp)	3
# indels (> 5 bp)	1
Indels length	12

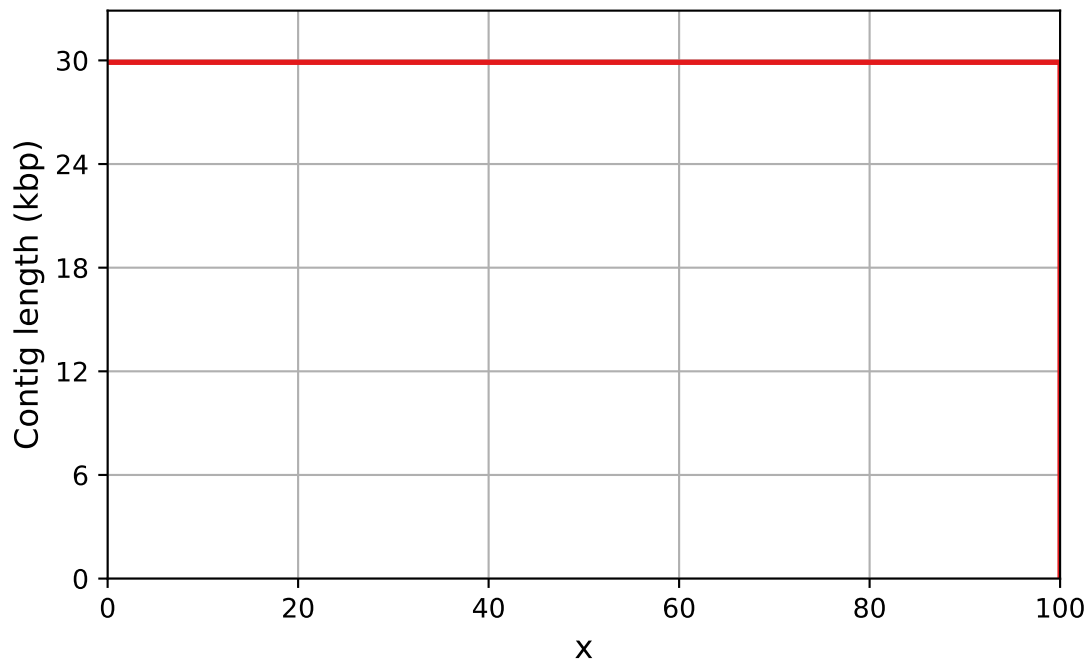
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	SC2244.consensus
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	11147

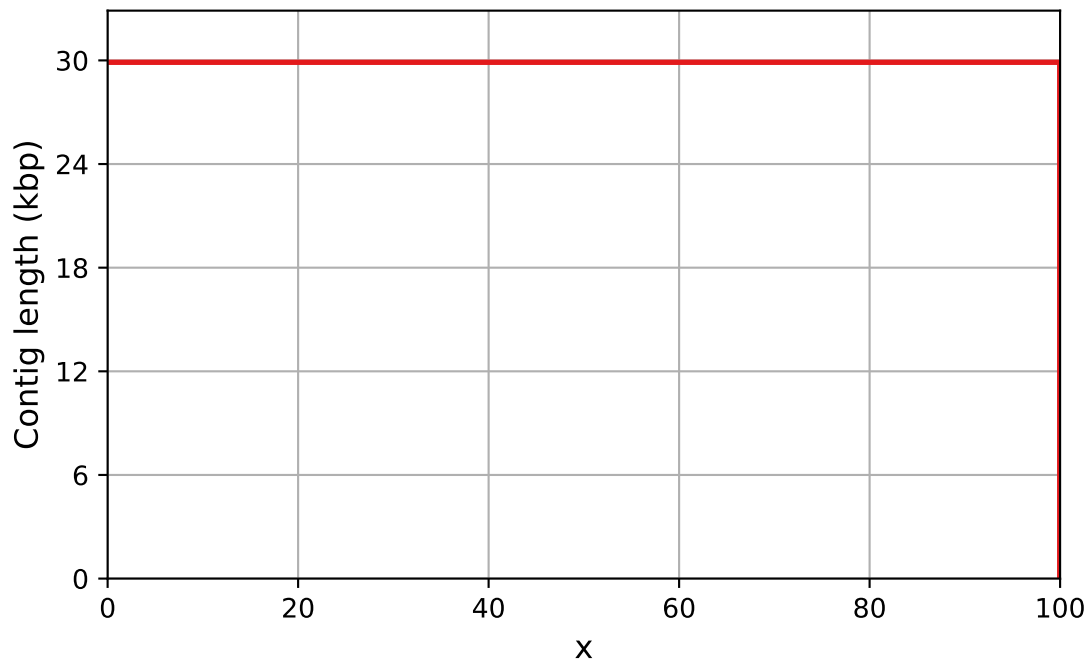
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



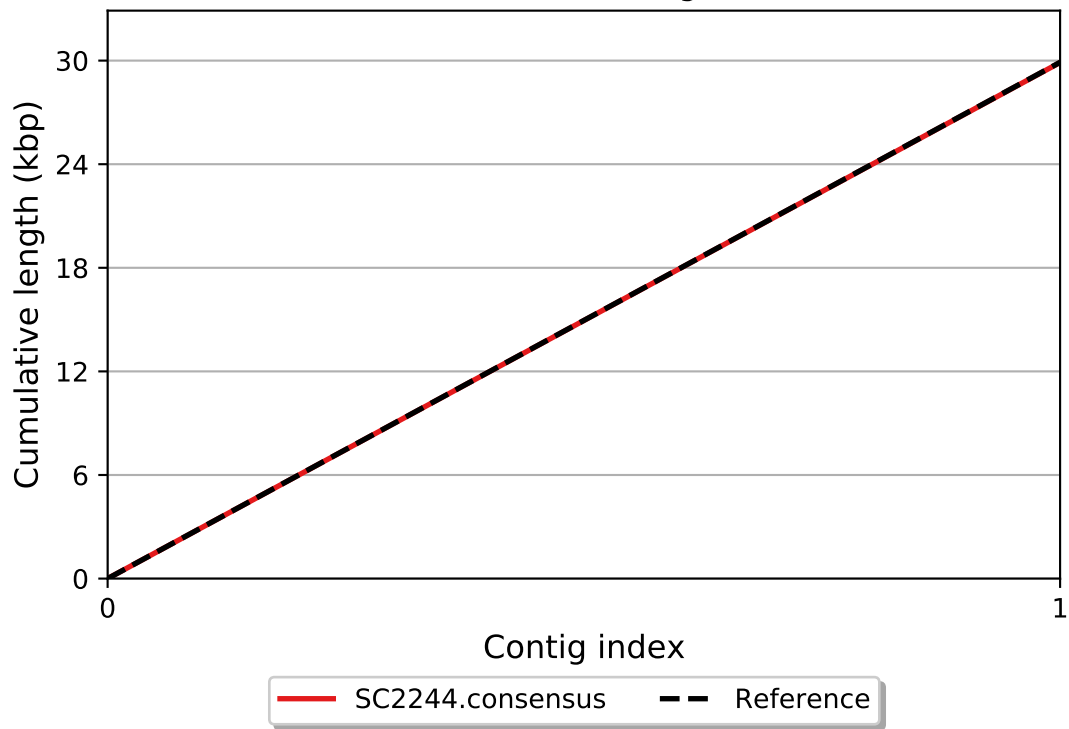
— SC2244.consensus

# NGx

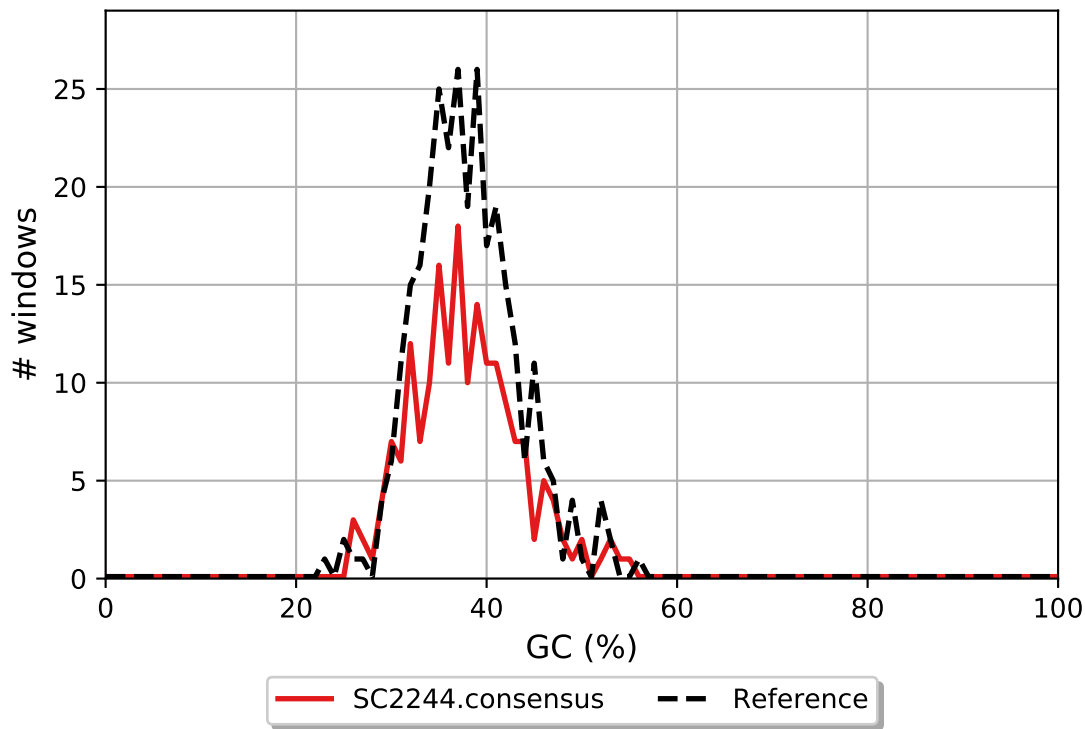


— SC2244.consensus

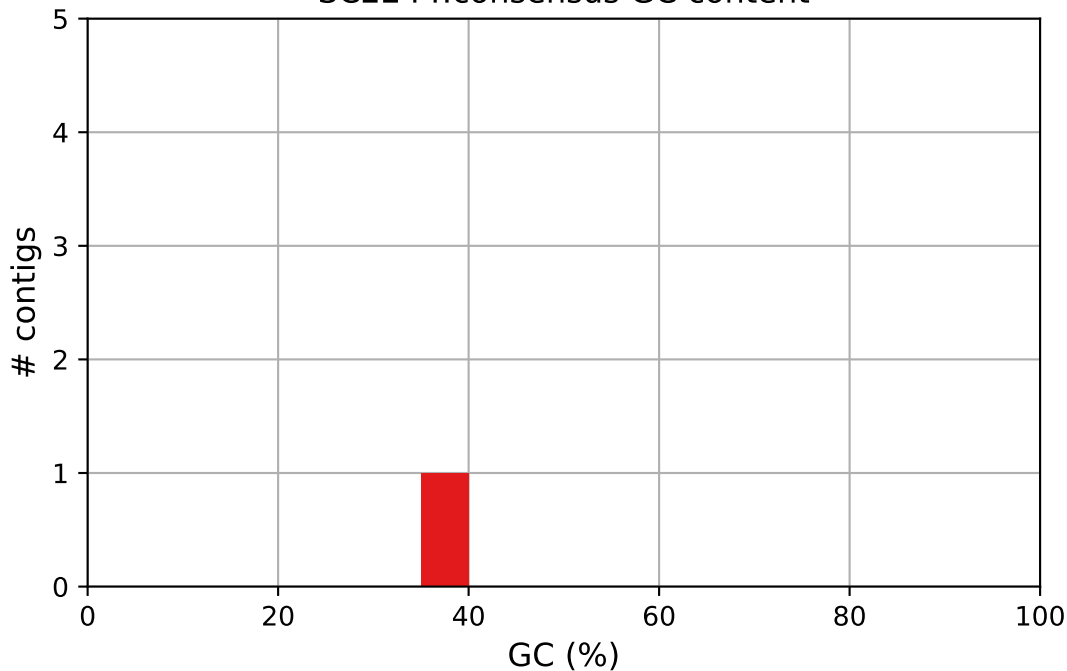
Cumulative length



GC content



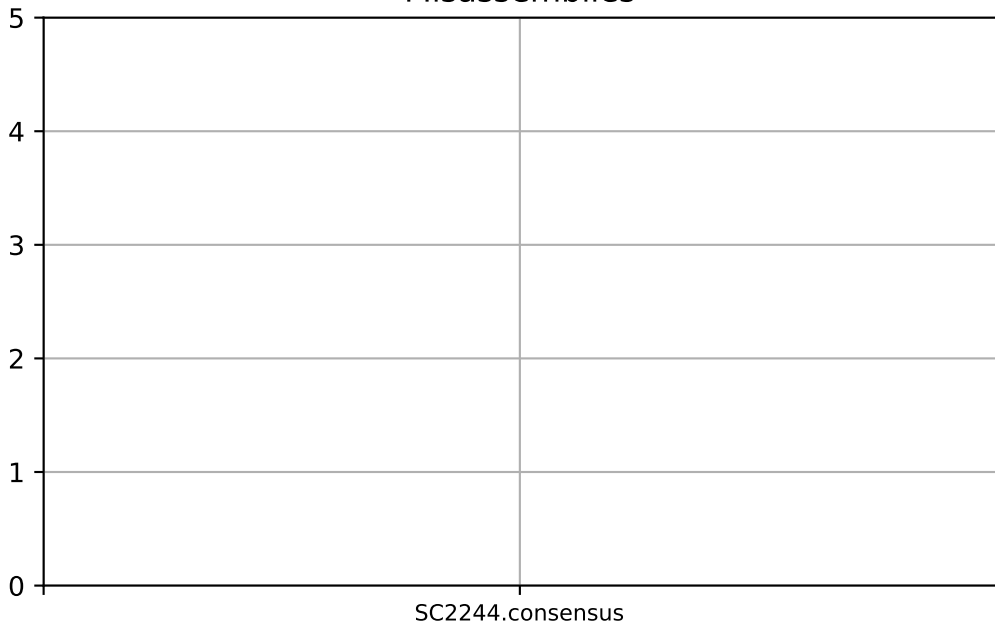
SC2244.consensus GC content



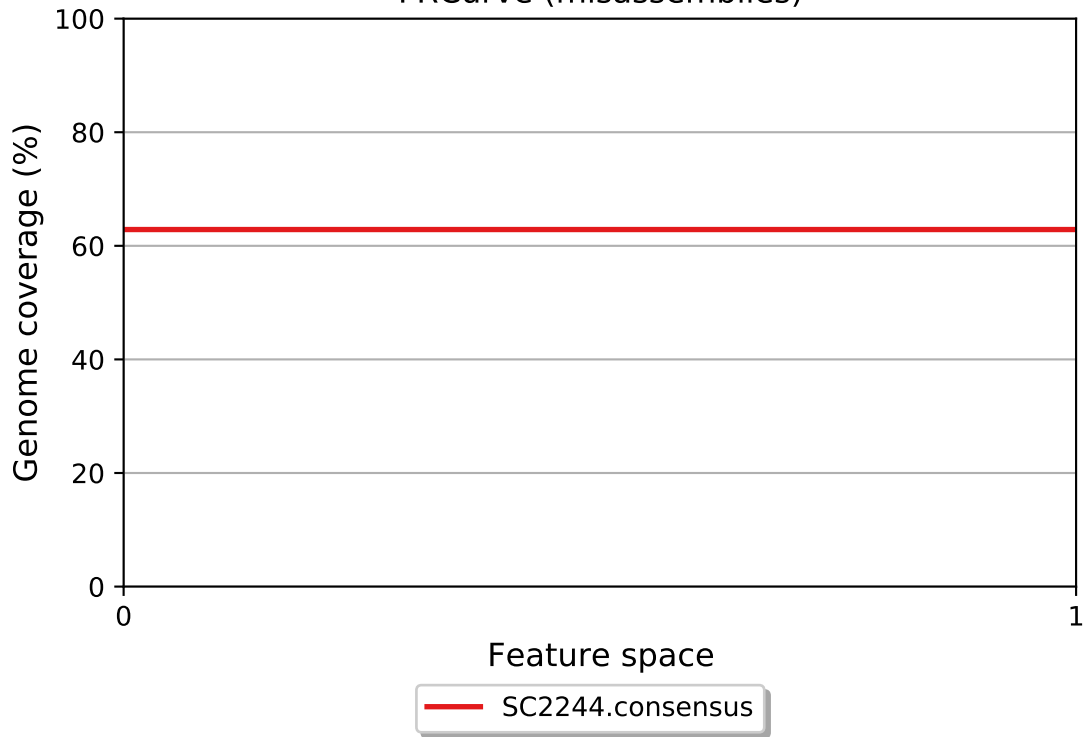
SC2244.consensus



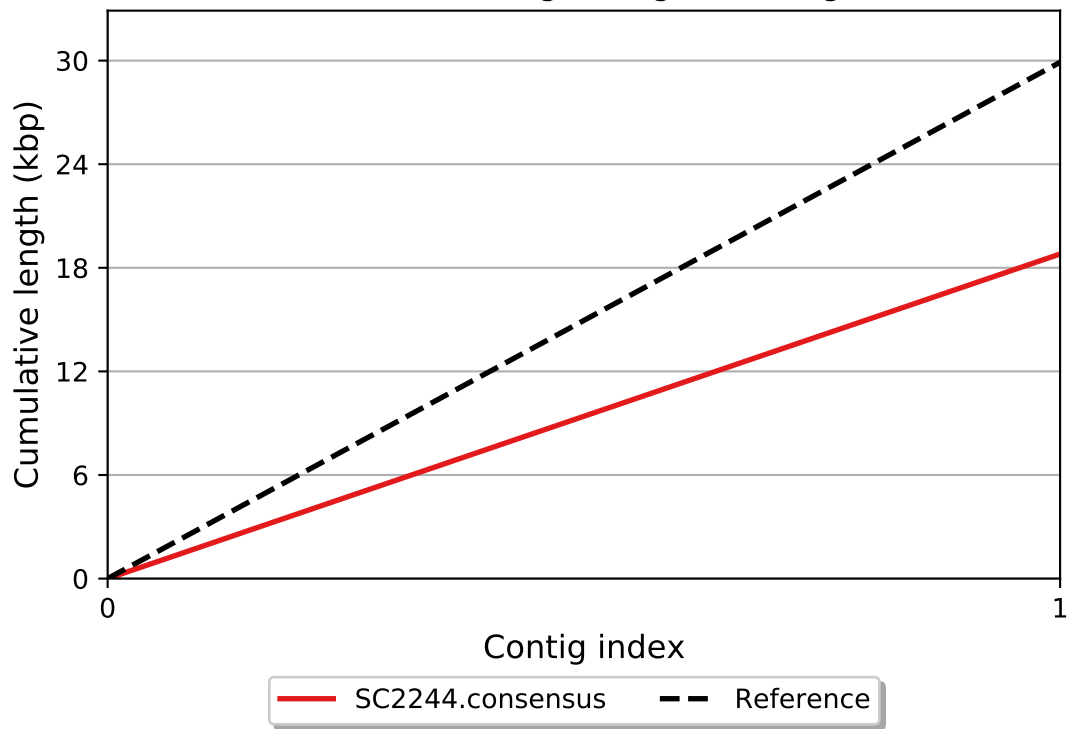
## Misassemblies



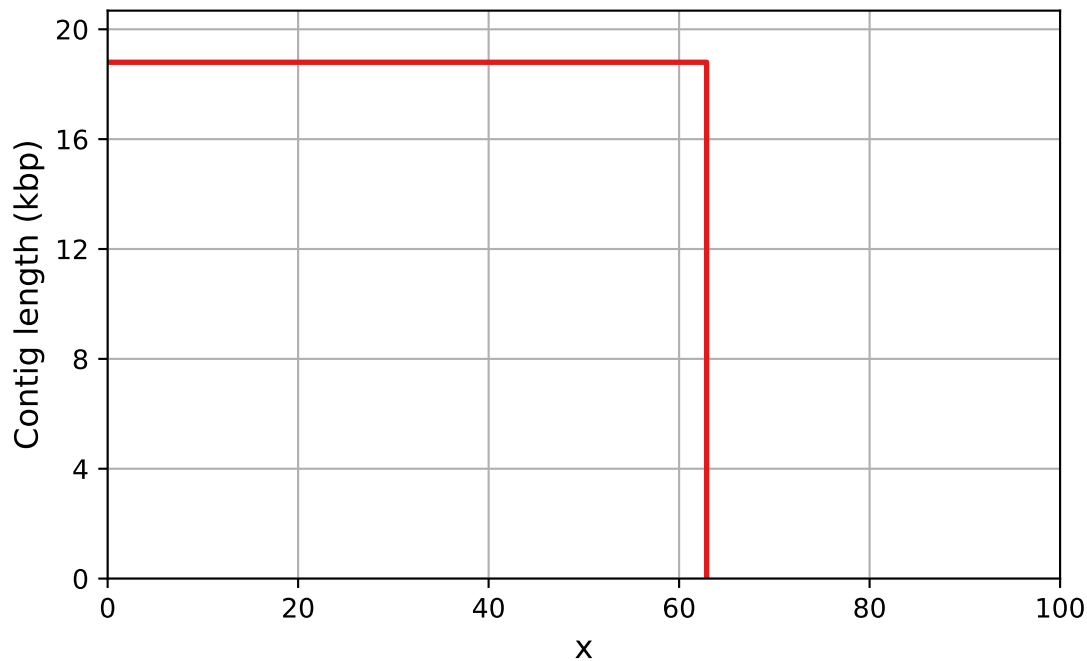
FRCurve (misassemblies)



Cumulative length (aligned contigs)

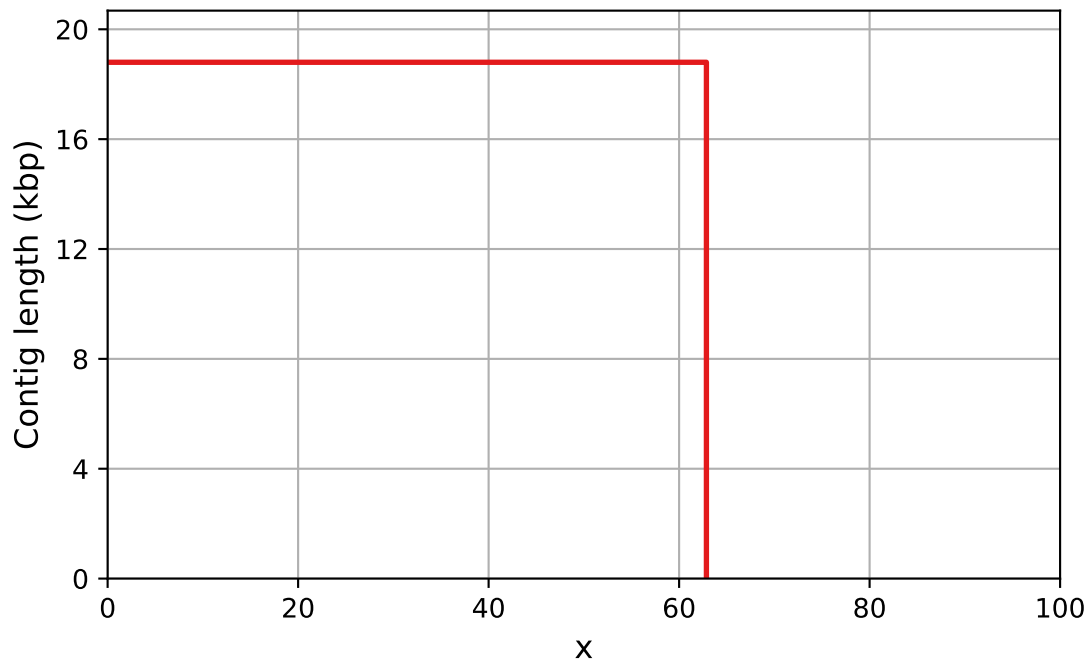


NAx

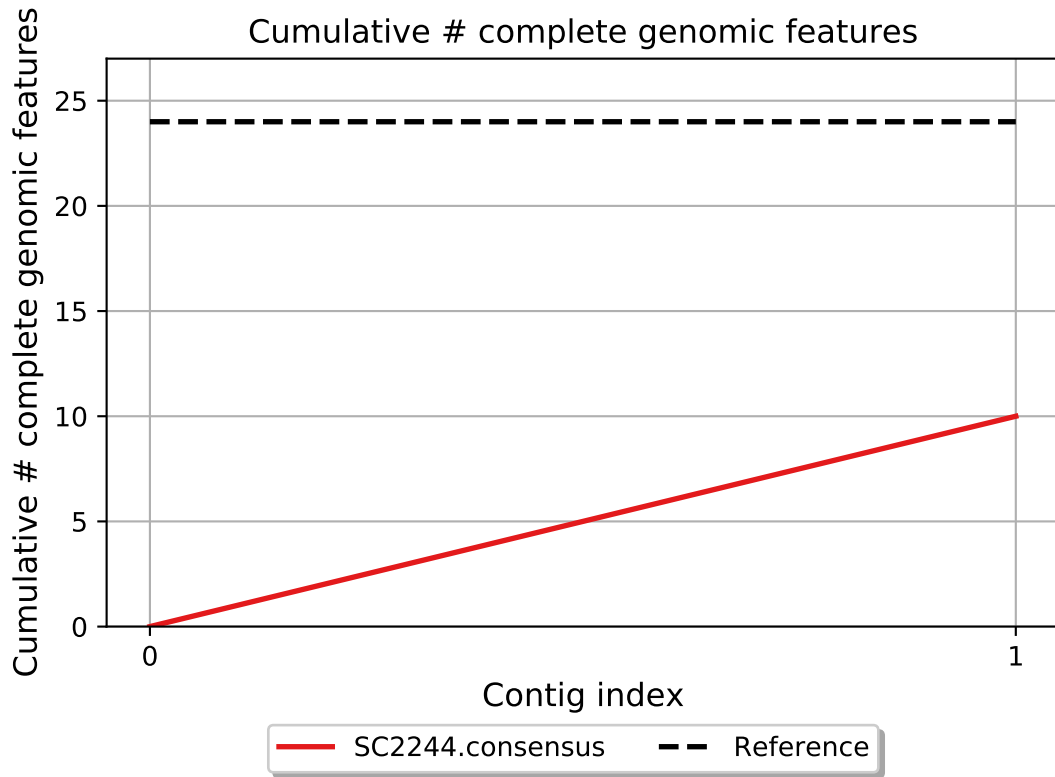


— SC2244.consensus

# NGAx



— SC2244.consensus



FRCurve (genomic features)

