

# Report

	SC2278.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)	29905
Total length (>= 1000 bp)	29905
Total length (>= 5000 bp)	29905
Total length (>= 10000 bp)	29905
Total length (>= 25000 bp)	29905
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	29905
Total length	29905
Reference length	29903
GC (%)	37.97
Reference GC (%)	37.97
N50	29905
NG50	29905
N75	29905
NG75	29905
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.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.803
Duplication ratio	1.002
# N's per 100 kbp	200.64
# mismatches per 100 kbp	80.42
# indels per 100 kbp	6.70
# genomic features	21 + 3 part
Largest alignment	29846
Total aligned length	29846
NA50	29846
NGA50	29846
NA75	29846
NGA75	29846
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

	SC2278.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.	0
# unaligned mis. contigs	0
# mismatches	24
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	4

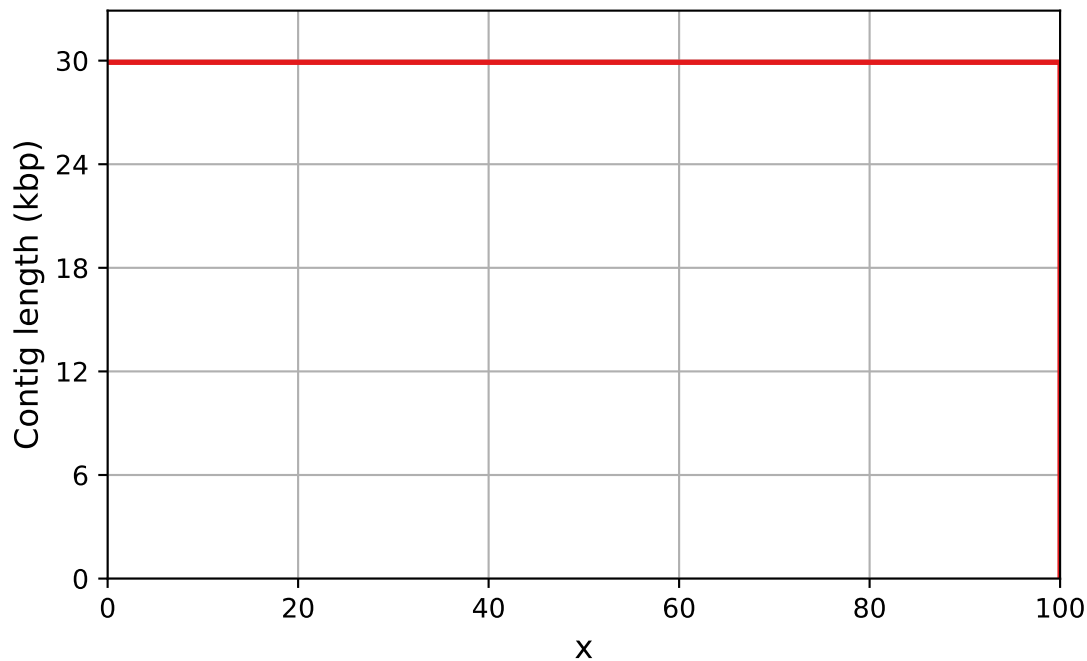
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	SC2278.consensus
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	60

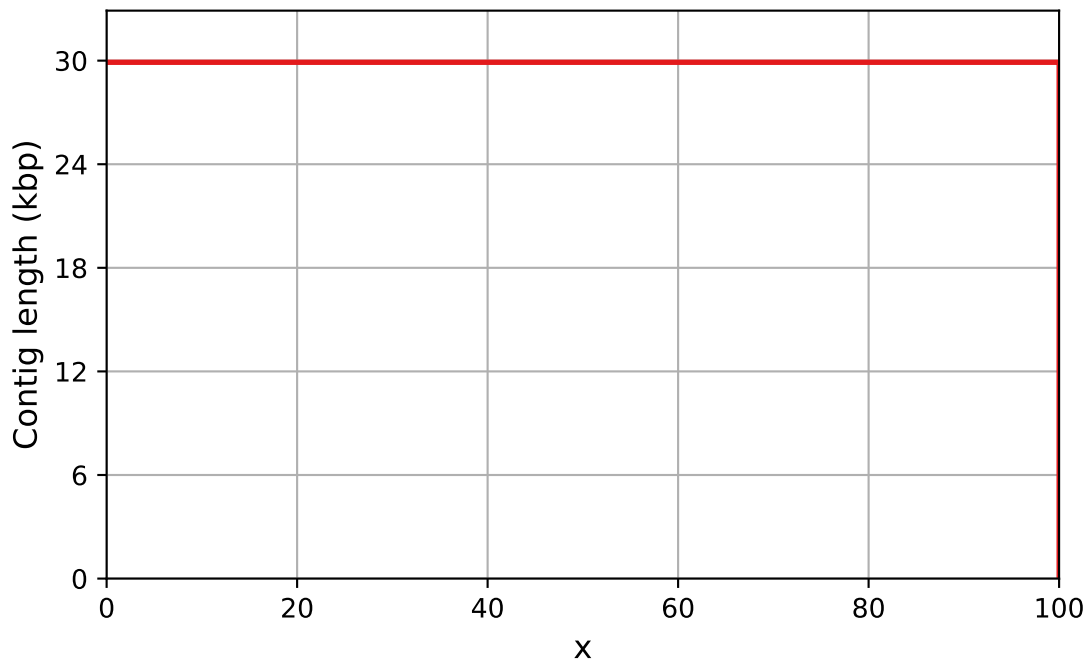
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



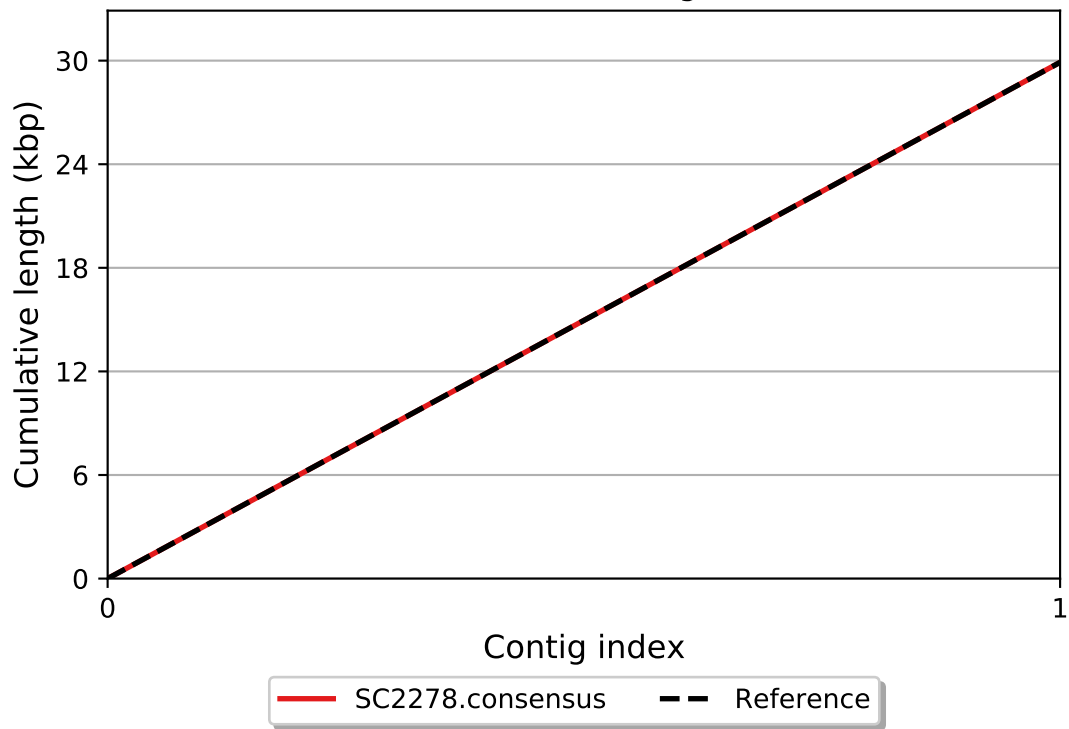
— SC2278.consensus

# NGx

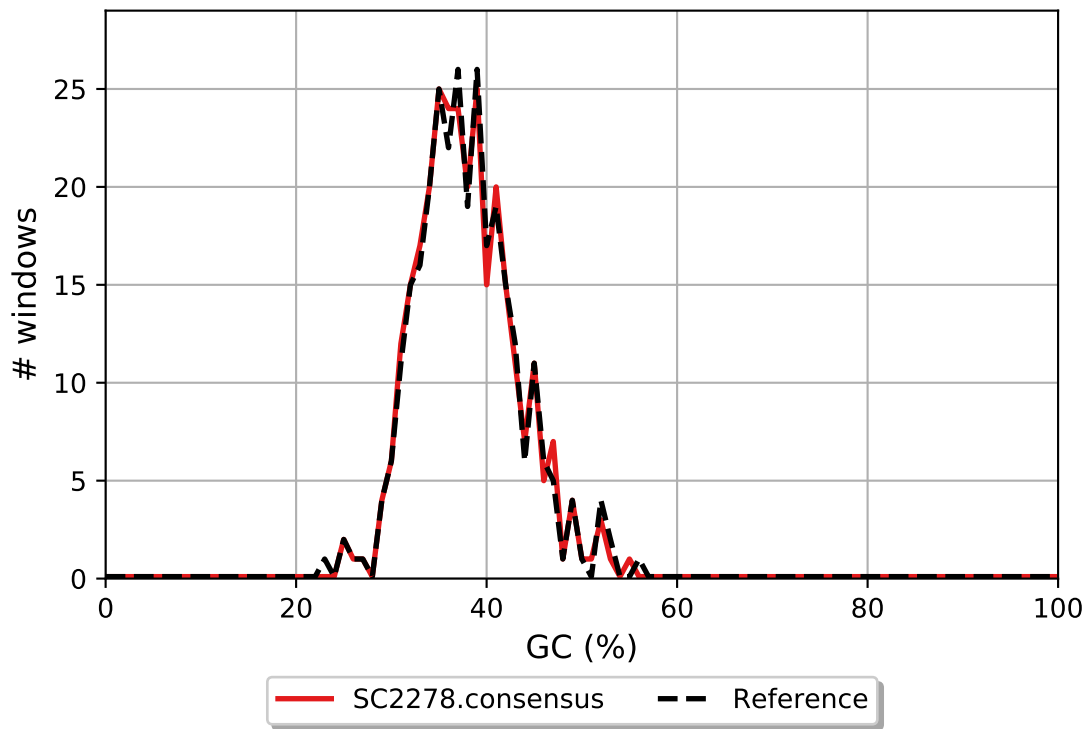


— SC2278.consensus

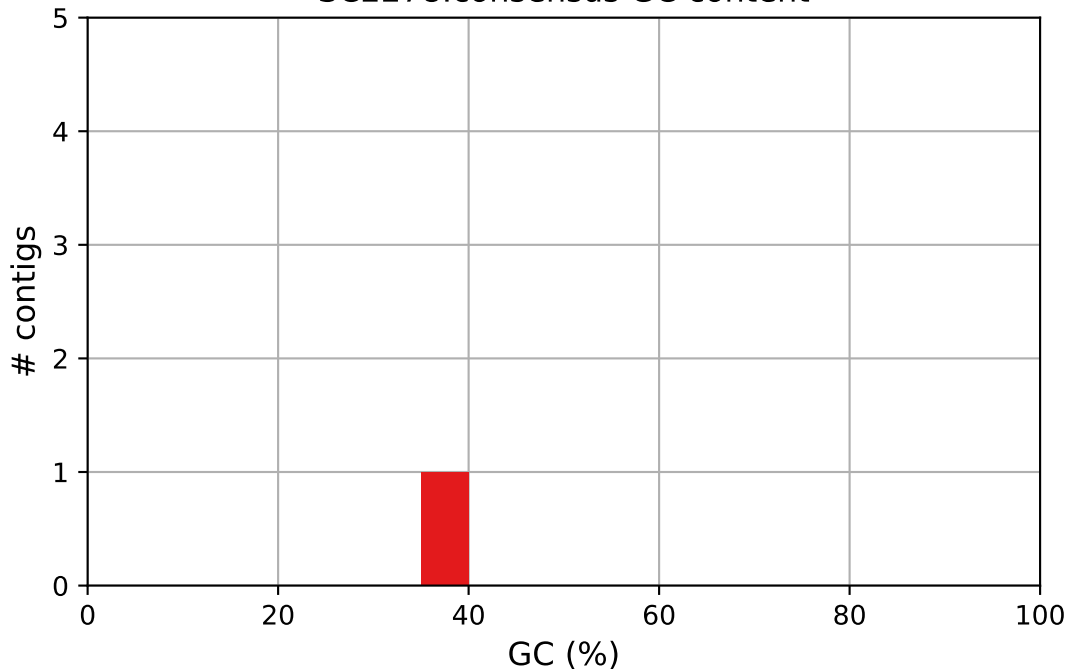
Cumulative length



## GC content



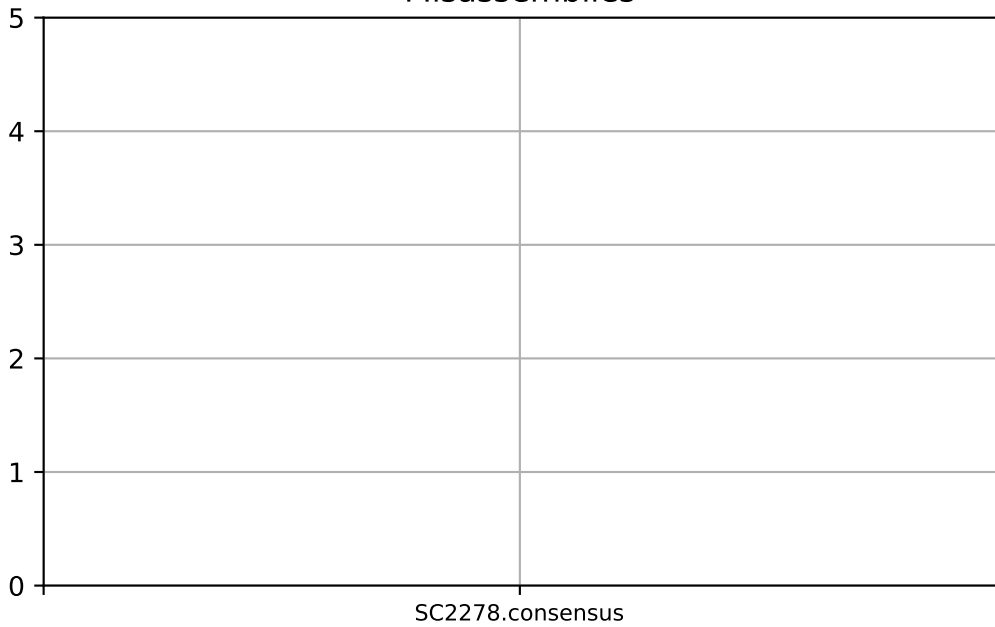
SC2278.consensus GC content



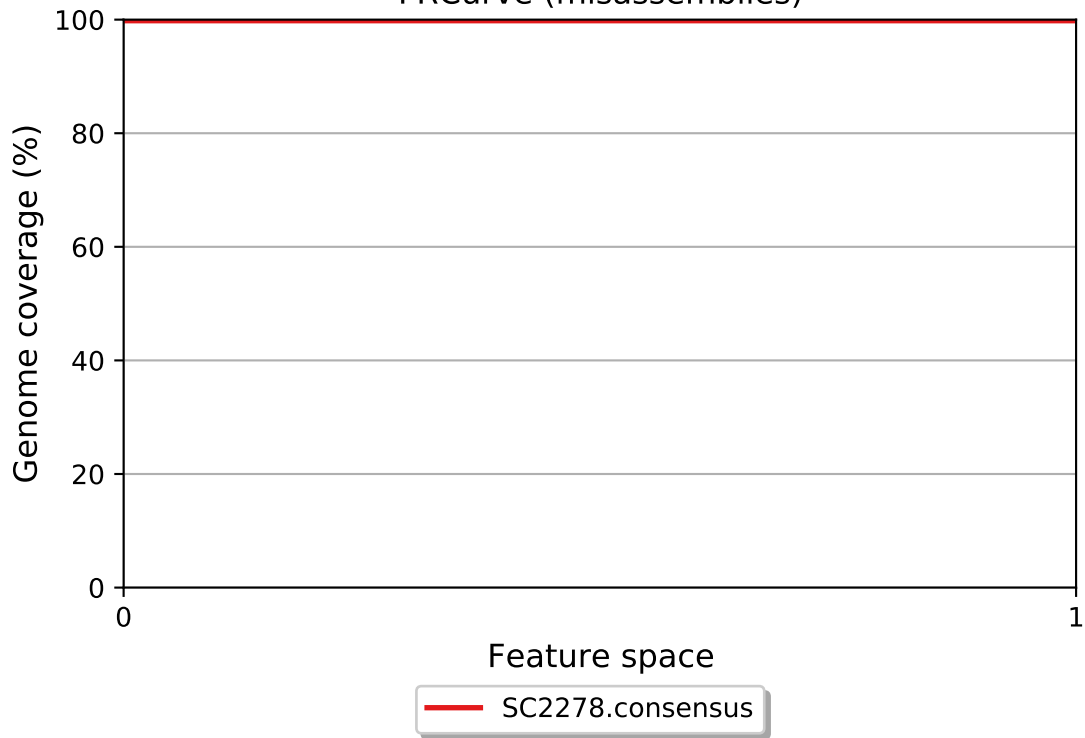
SC2278.consensus



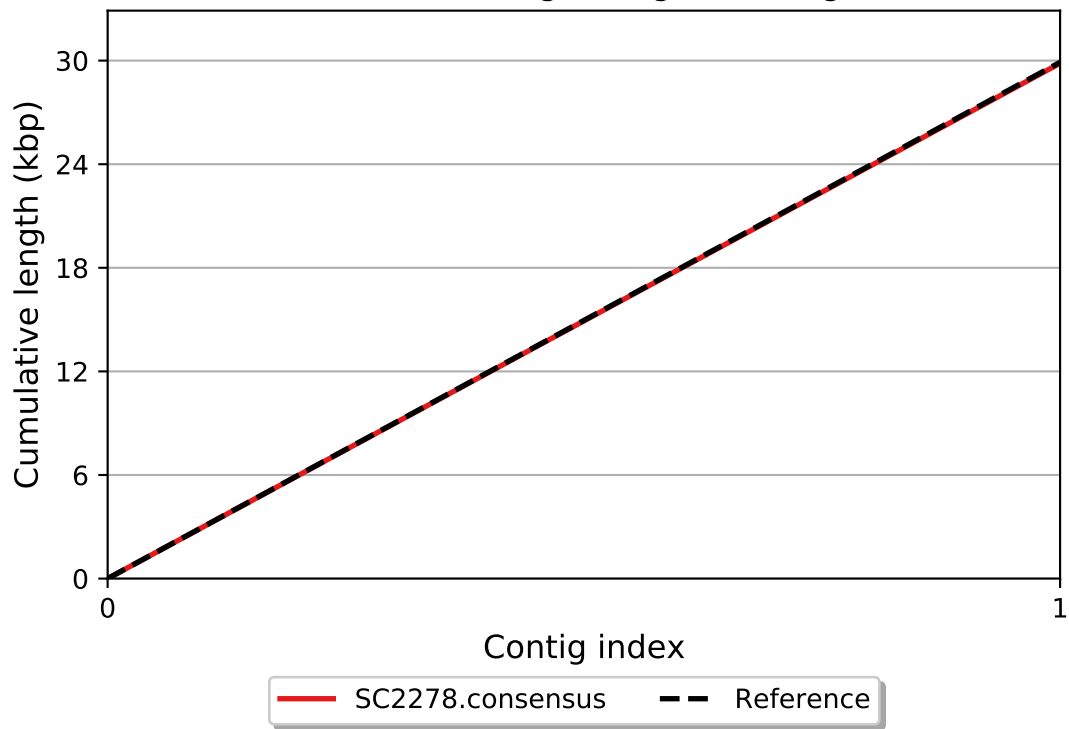
## Misassemblies



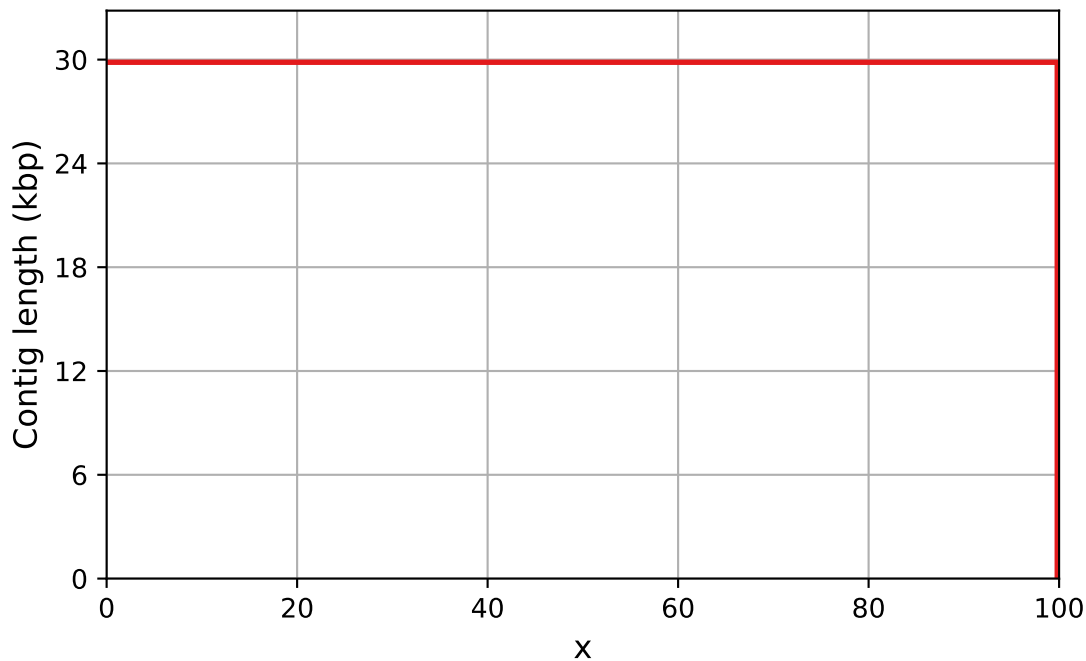
FRCurve (misassemblies)



Cumulative length (aligned contigs)

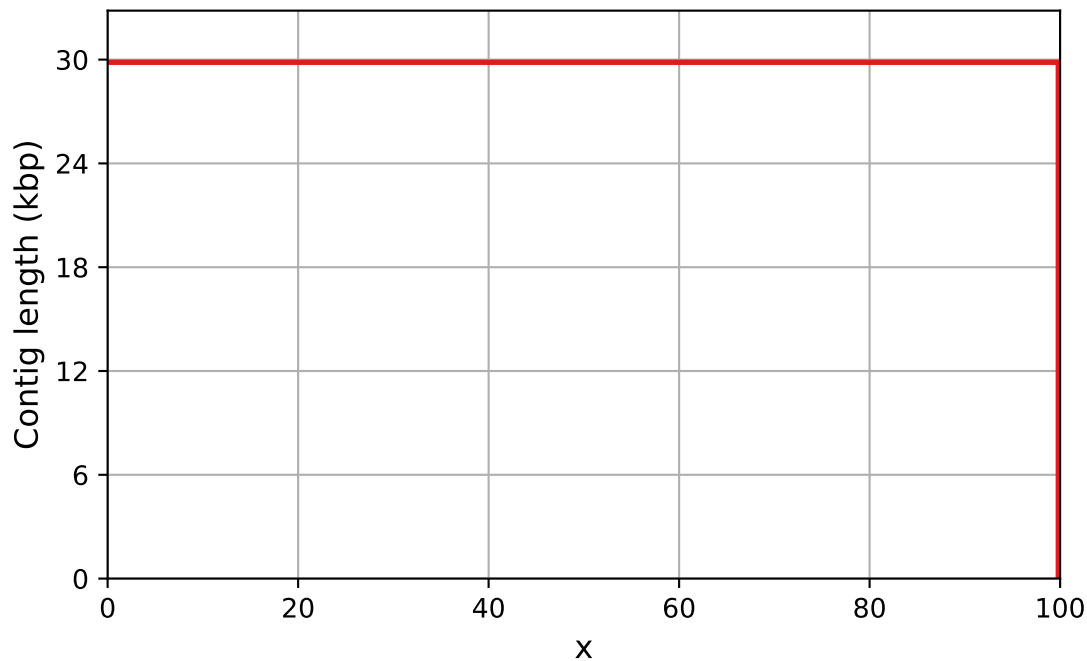


NAx

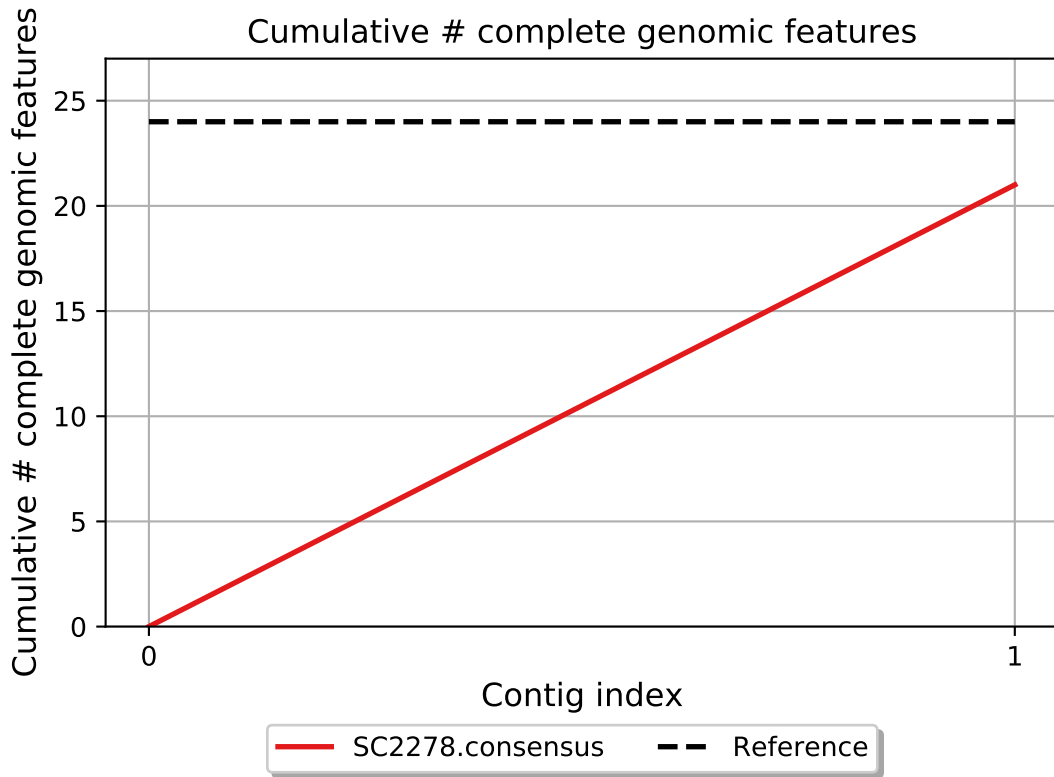


— SC2278.consensus

# NGAx



— SC2278.consensus



FRCurve (genomic features)

