Report

	SC2264.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)	29902
Total length (>= 1000 bp)	29902
Total length (>= 5000 bp)	29902
Total length (>= 10000 bp)	29902
Total length (>= 25000 bp)	29902
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	29902
Total length	29902
Reference length	29903
GC (%)	37.98
Reference GC (%)	37.97
N50	29902
NG50	29902
N75	29902
NG75	29902
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 (%)	99.699
Duplication ratio	1.003
# N's per 100 kbp	304.33
# mismatches per 100 kbp	67.08
# indels per 100 kbp	3.35
# genomic features	21 + 3 part
Largest alignment	29812
Total aligned length	29812
NA50	29812
NGA50	29812
NA75	29812
NGA75	29812
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

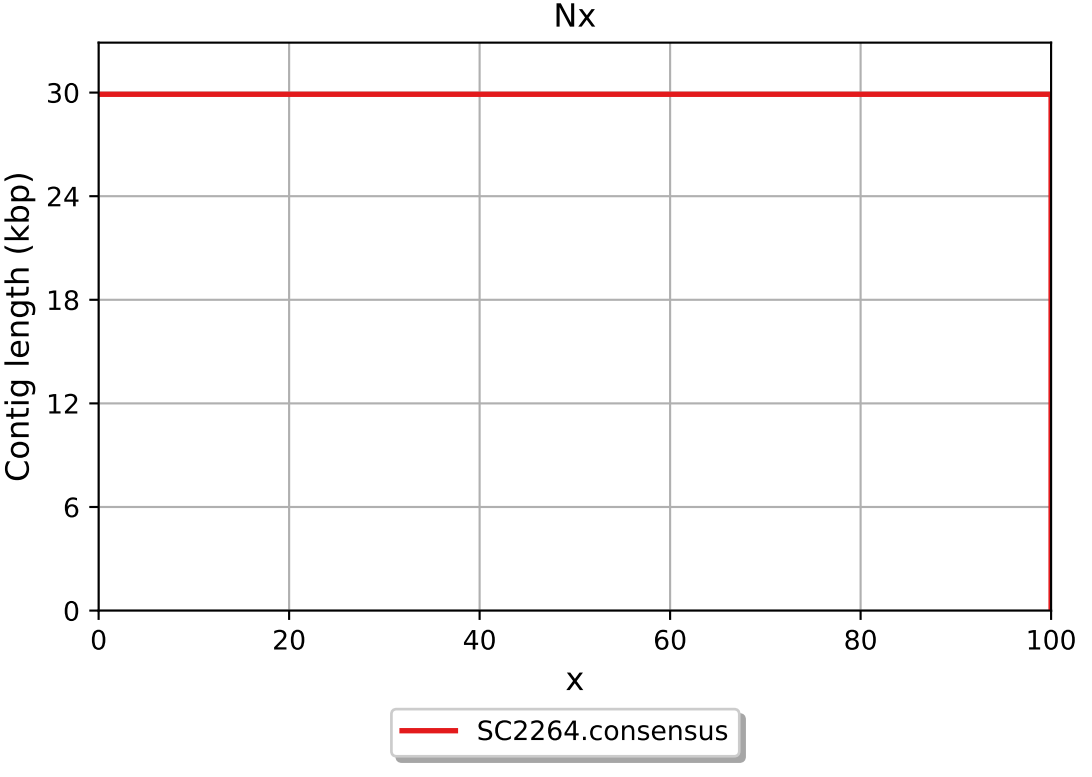
	SC2264.consensus
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	20
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	1

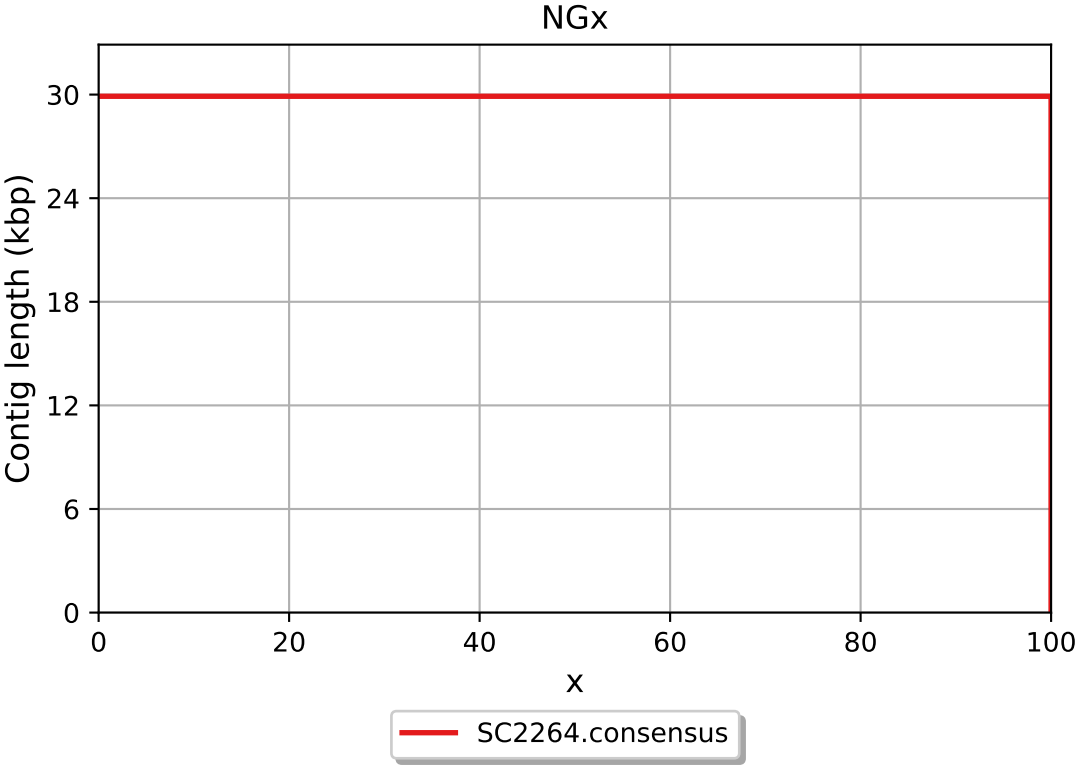
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

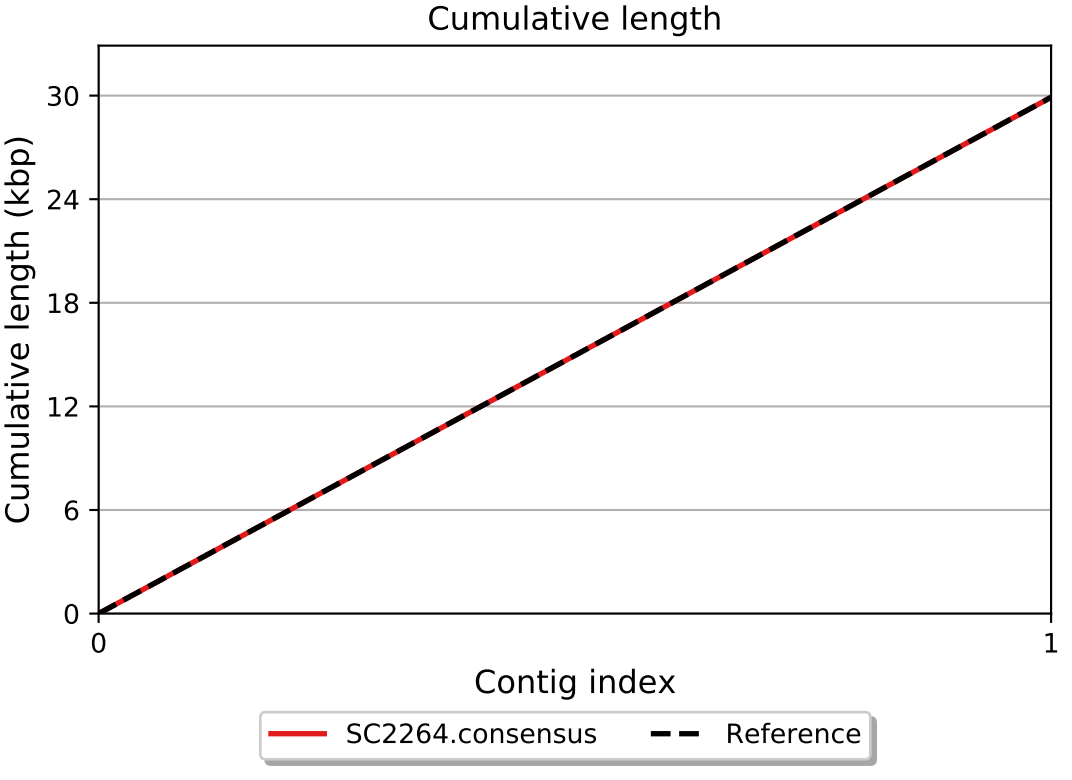
Unaligned report

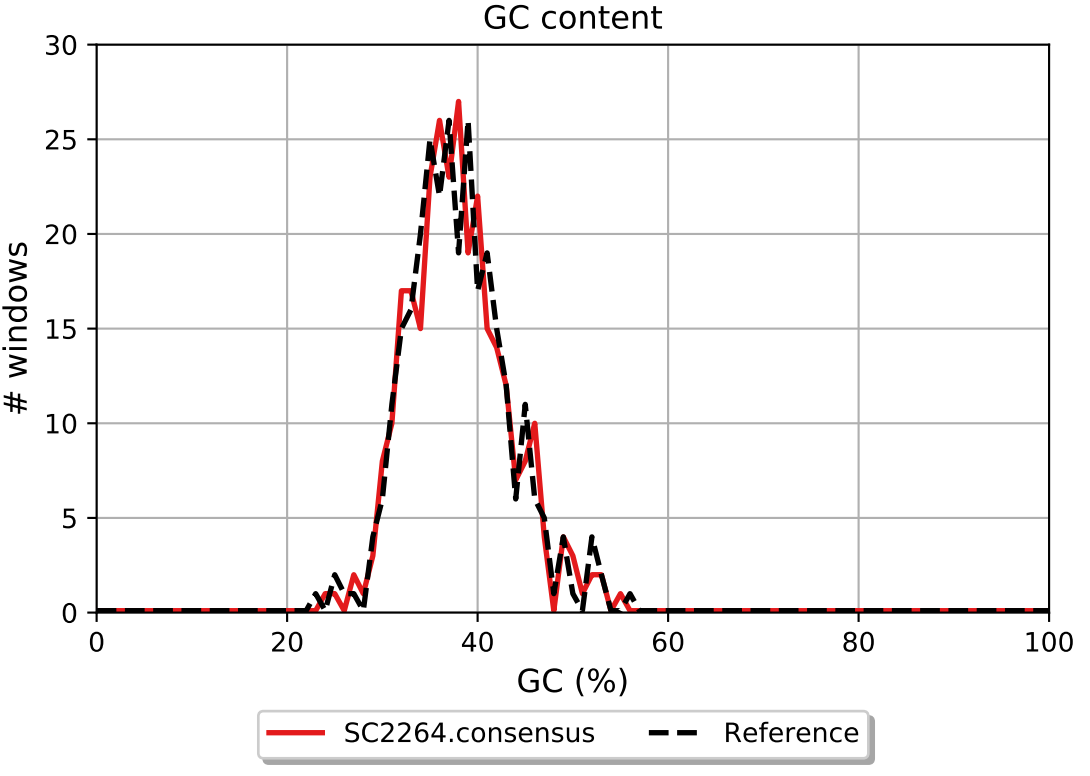
	SC2264.consensus
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	91

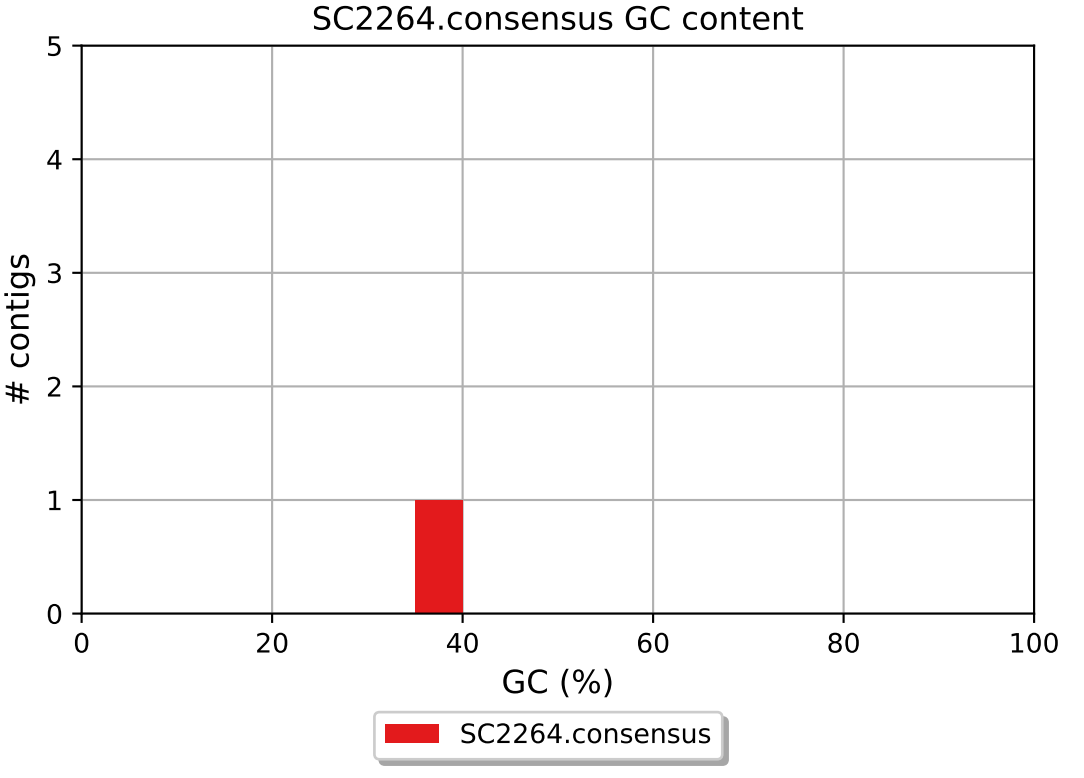
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
SC2264.consensus

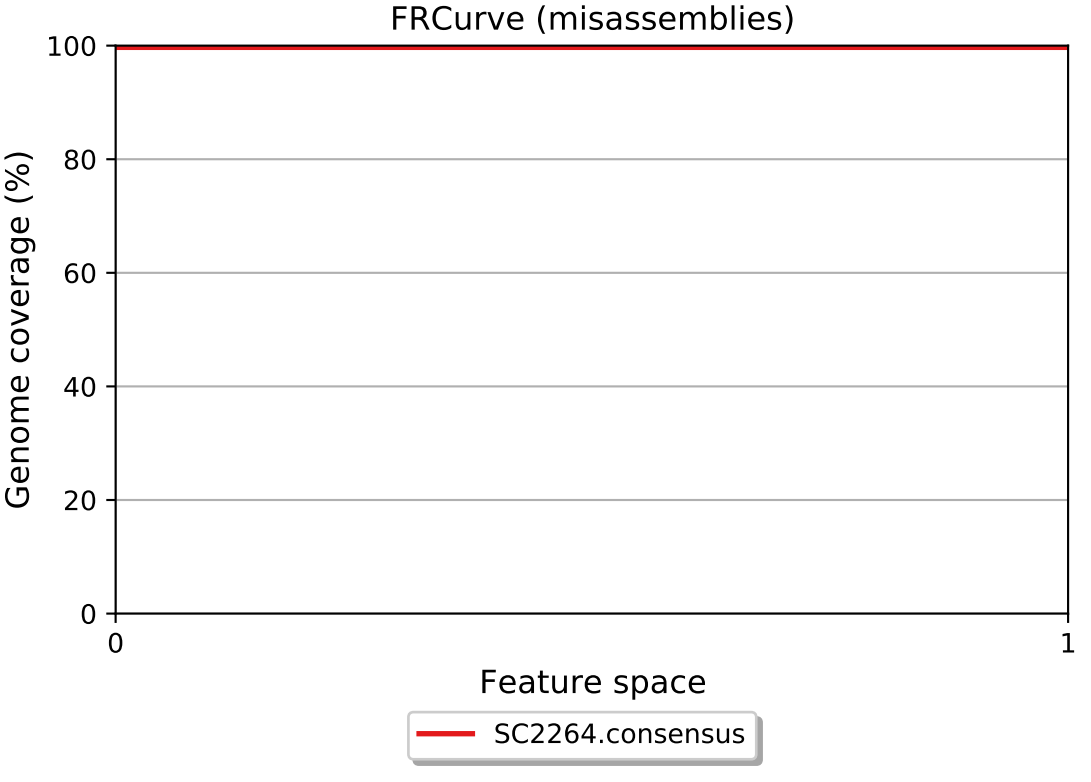

NGx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
SC2264.consensus

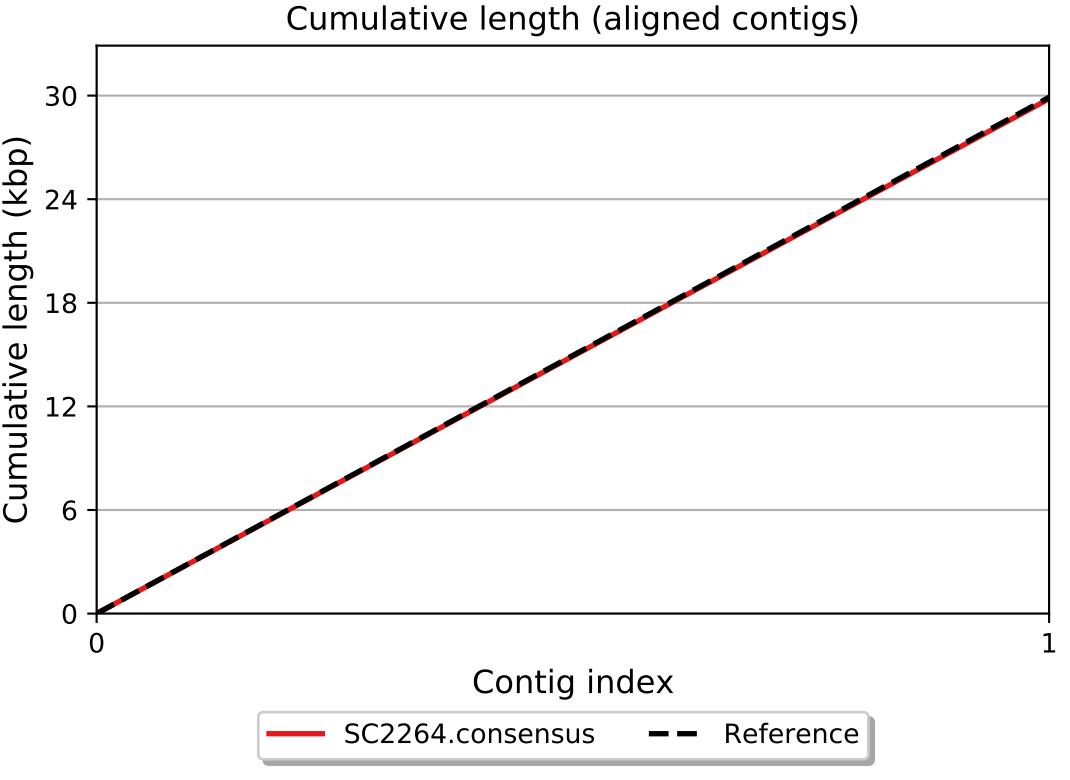

Cumulative length
Cumulative length (kbp)
30
24
18
12
6
0
0
1
Contig index
SC2264.consensus
Reference

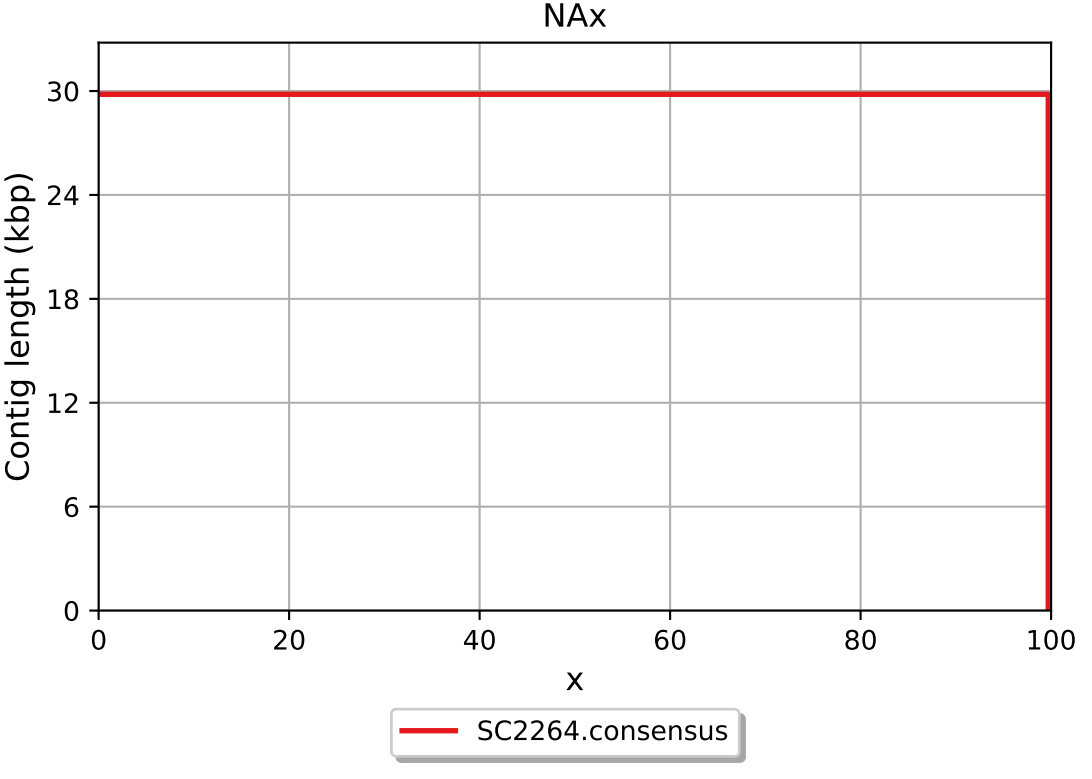

GC content
windows
GC (%)
0
5
10
15
20
25
30
0
20
40
60
80
100
SC2264.consensus
Reference

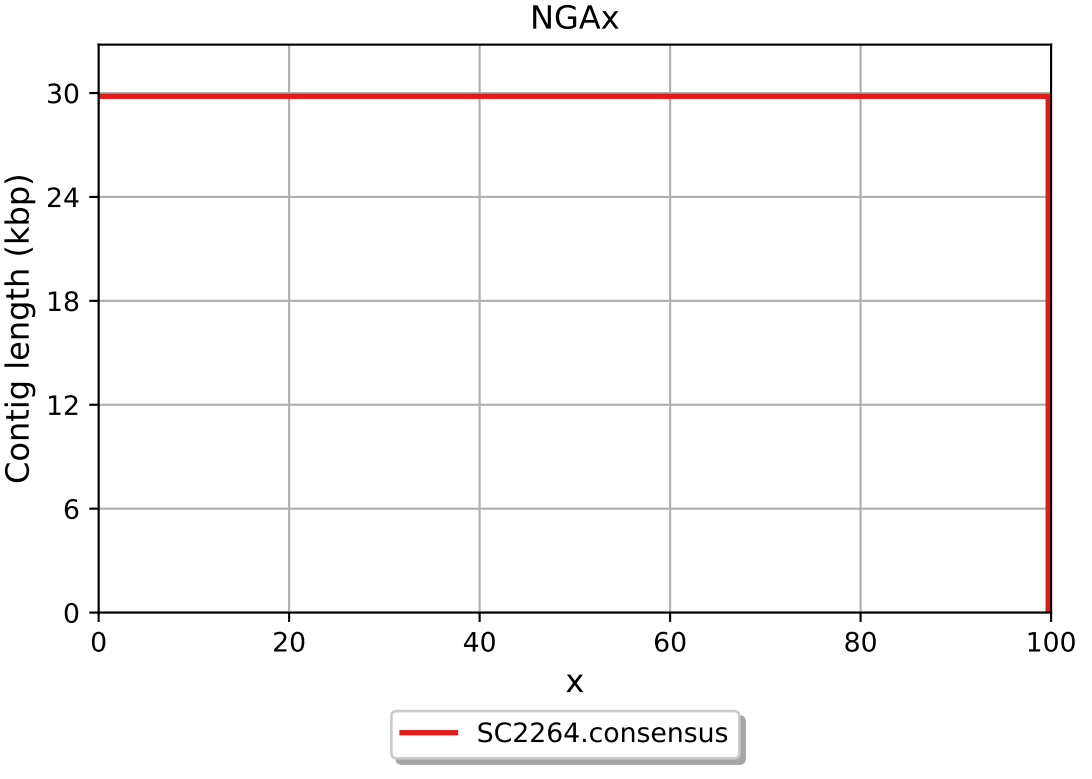

SC2264.consensus GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
SC2264.consensus

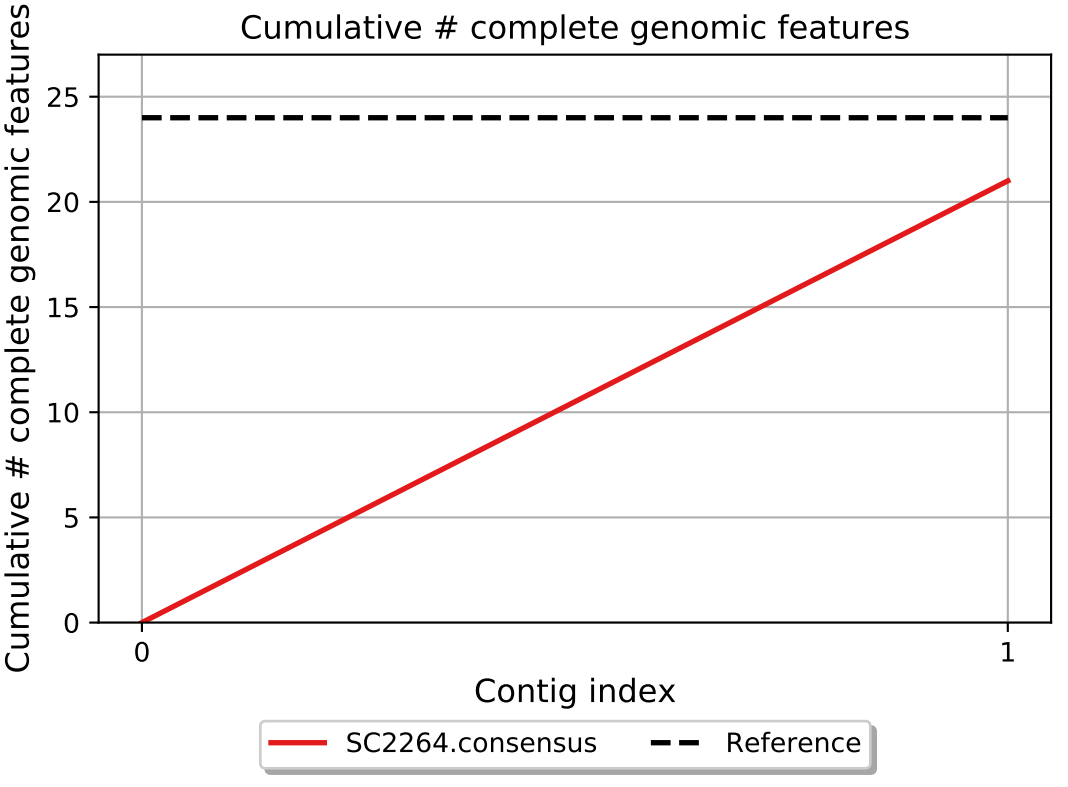
Misassemblies
5
4
3
2
1
0
SC2264.consensus

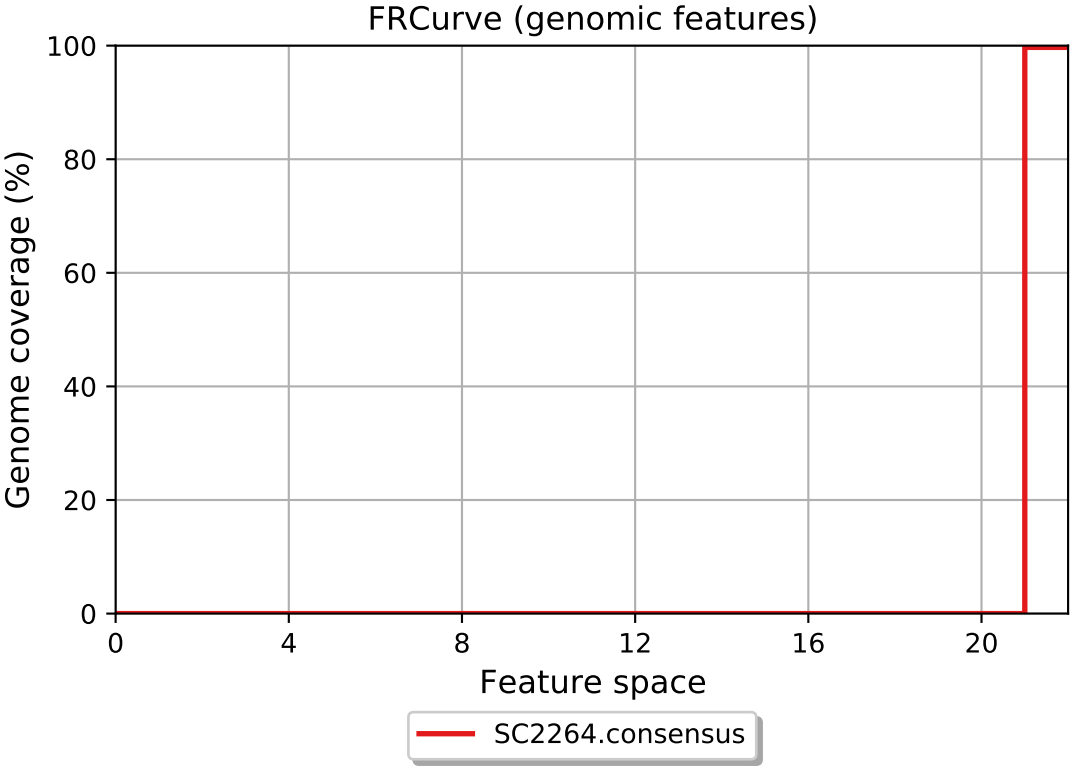

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
SC2264.consensus


Cumulative length (aligned contigs)
Cumulative length (kbp)
30
24
18
12
6
0
0
1
Contig index
SC2264.consensus
Reference


NAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
SC2264.consensus


NGAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
SC2264.consensus


Cumulative # complete genomic features
Cumulative # complete genomic features
25
20
15
10
5
0
0
1
Contig index
SC2264.consensus
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
4
8
12
16
20
Feature space
SC2264.consensus