Report

	SC2285.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)	29904
Total length (>= 1000 bp)	29904
Total length (>= 5000 bp)	29904
Total length (>= 10000 bp)	29904
Total length (>= 25000 bp)	29904
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	29904
Total length	29904
Reference length	29903
GC (%)	38.01
Reference GC (%)	37.97
N50	29904
NG50	29904
N75	29904
NG75	29904
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.	9
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	88.045
Duplication ratio	1.136
# N's per 100 kbp	12225.79
# mismatches per 100 kbp	98.75
# indels per 100 kbp	11.39
# genomic features	14 + 8 part
Largest alignment	26329
Total aligned length	26329
NA50	26329
NGA50	26329
NA75	26329
NGA75	26329
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

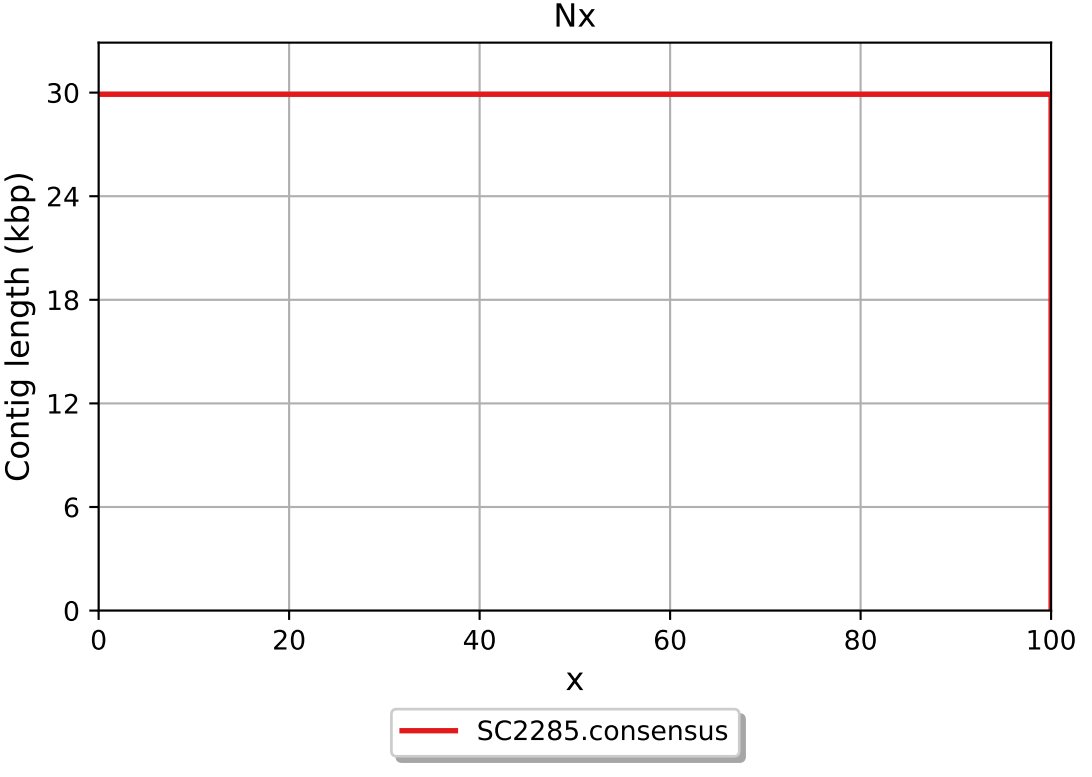
	SC2285.consensus
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	9
# unaligned mis. contigs	0
# mismatches	26
# indels	3
# indels (<= 5 bp)	3
# indels (> 5 bp)	0
Indels length	3

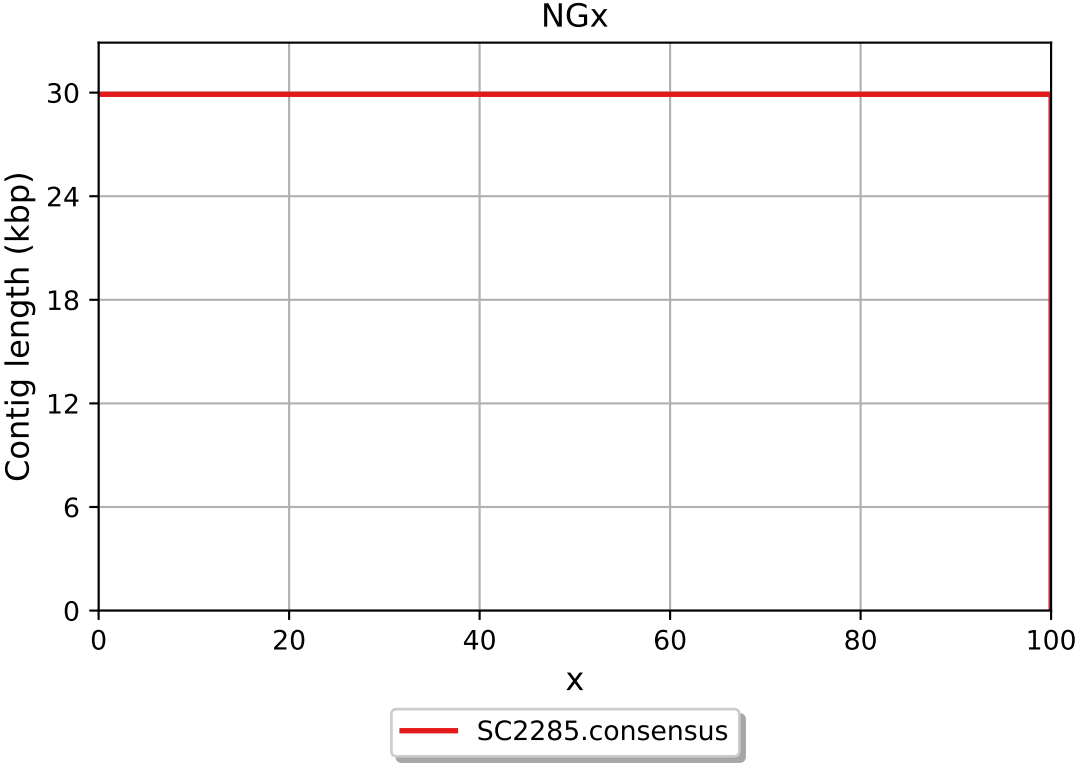
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

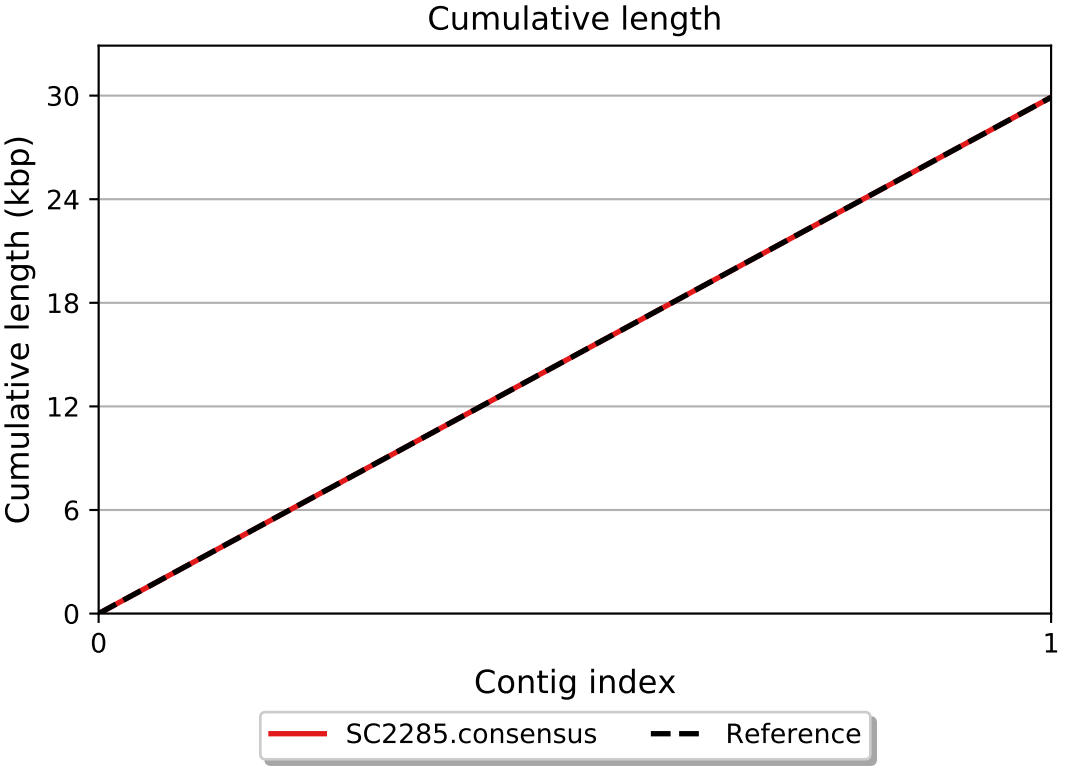
Unaligned report

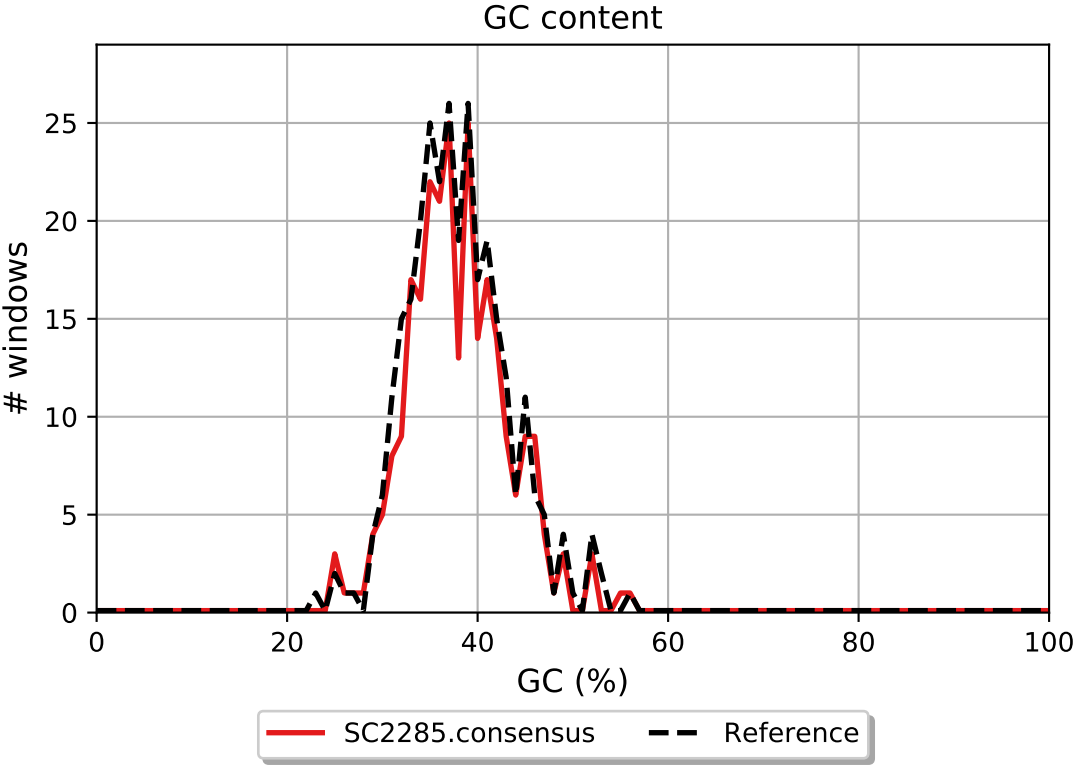
	SC2285.consensus
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	3656

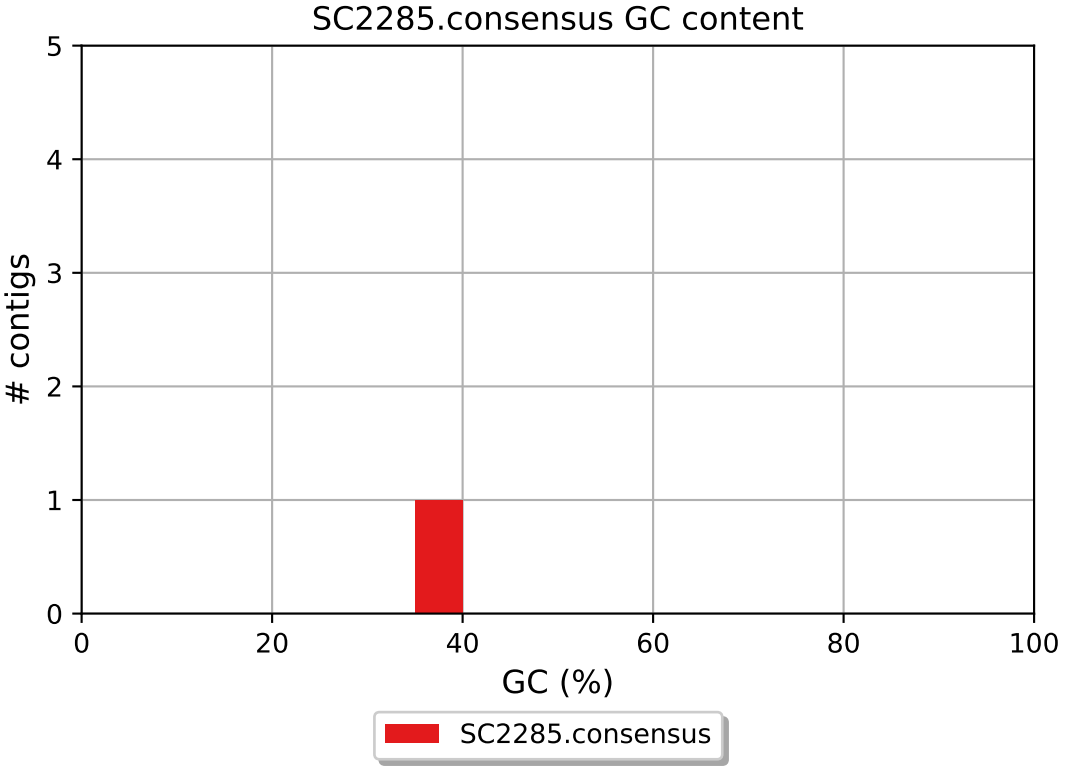
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
SC2285.consensus

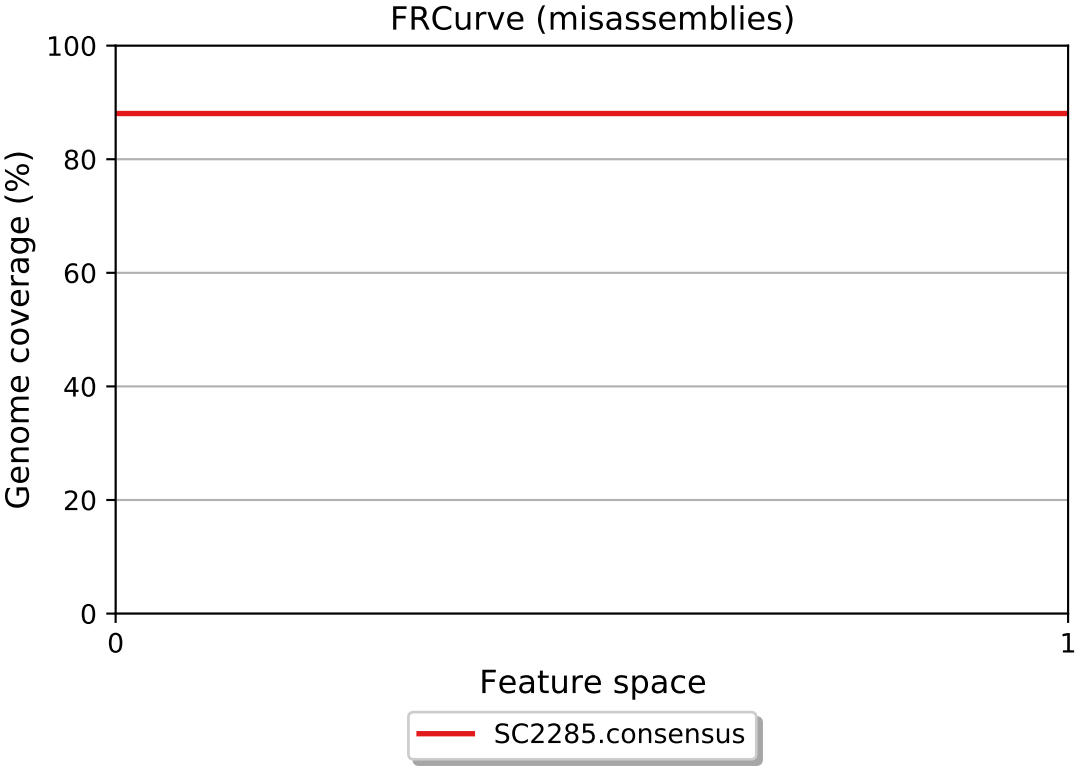

NGx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
SC2285.consensus

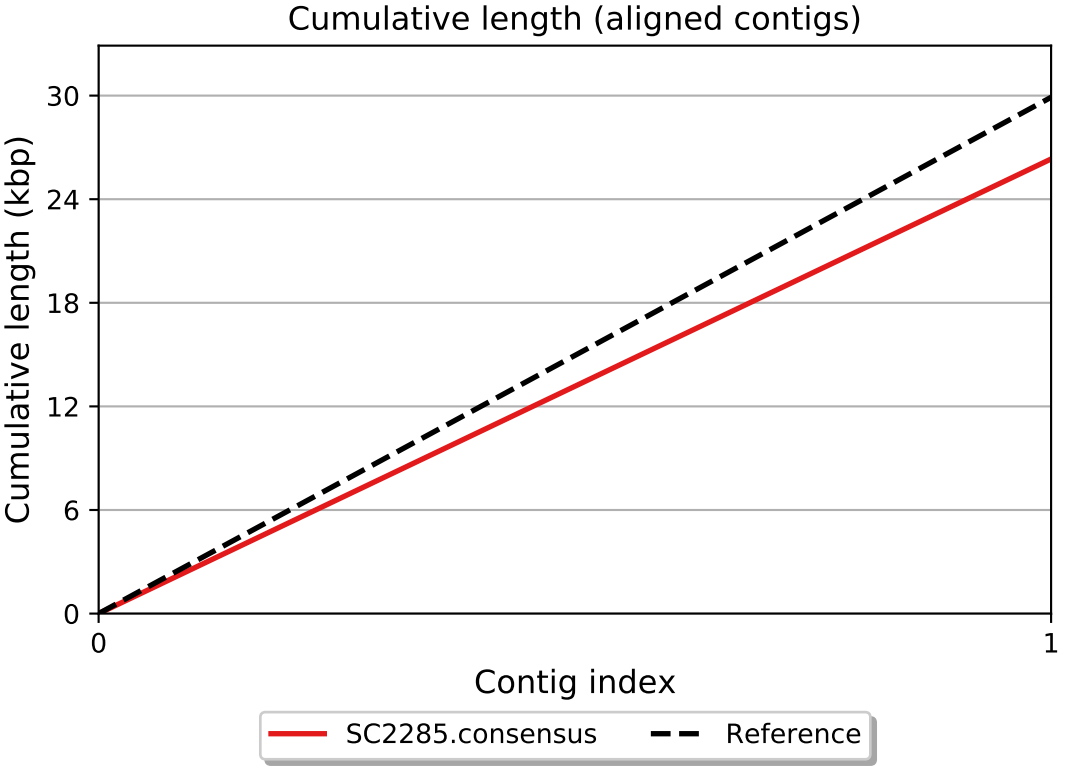

Cumulative length
Cumulative length (kbp)
30
24
18
12
6
0
0
1
Contig index
SC2285.consensus
Reference

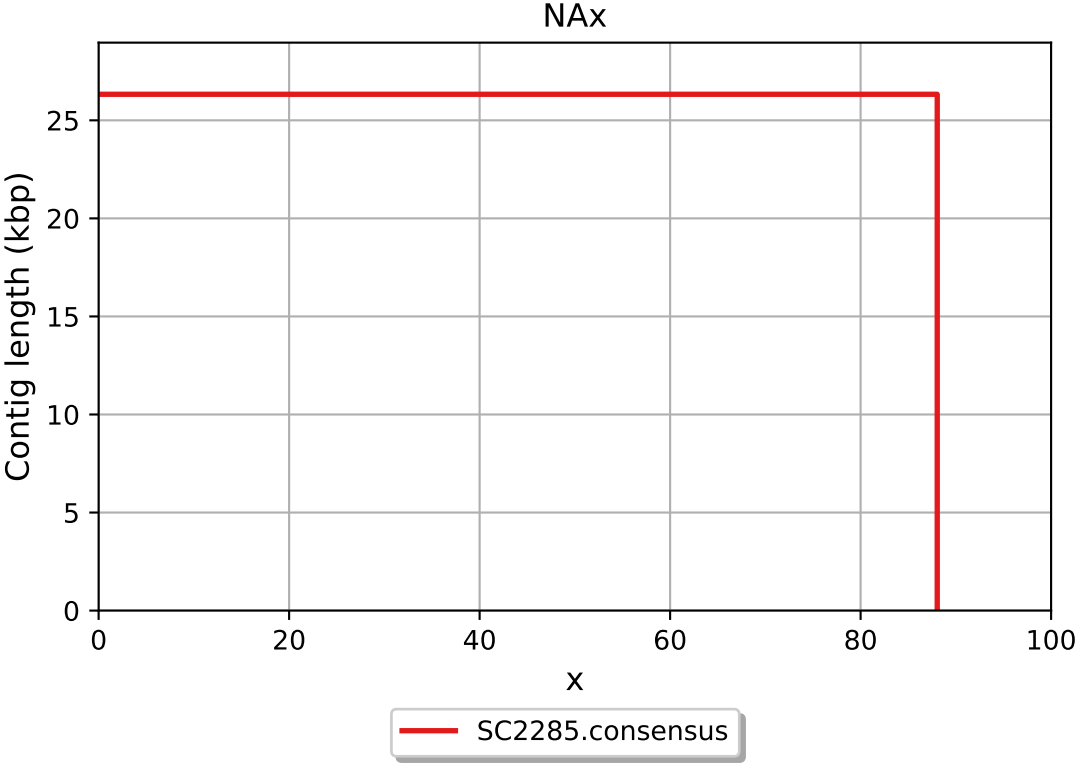

GC content
windows
GC (%)
0
5
10
15
20
25
0
20
40
60
80
100
SC2285.consensus
Reference

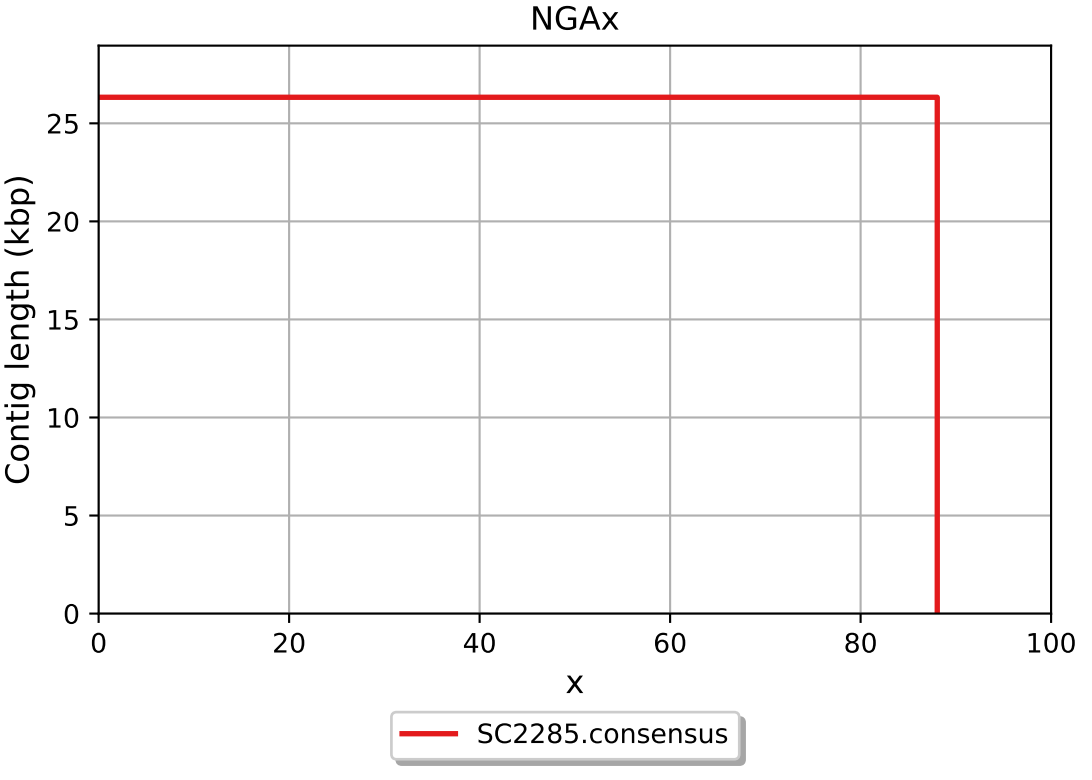

SC2285.consensus GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
SC2285.consensus

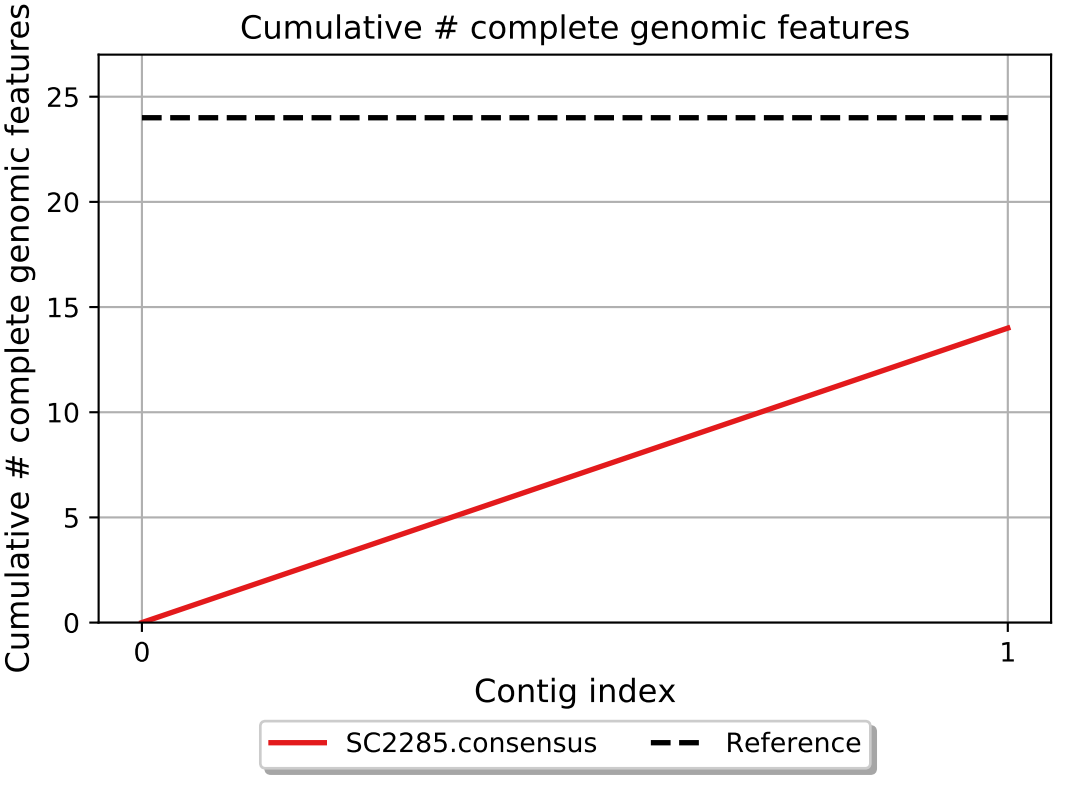
Misassemblies
5
4
3
2
1
0
SC2285.consensus

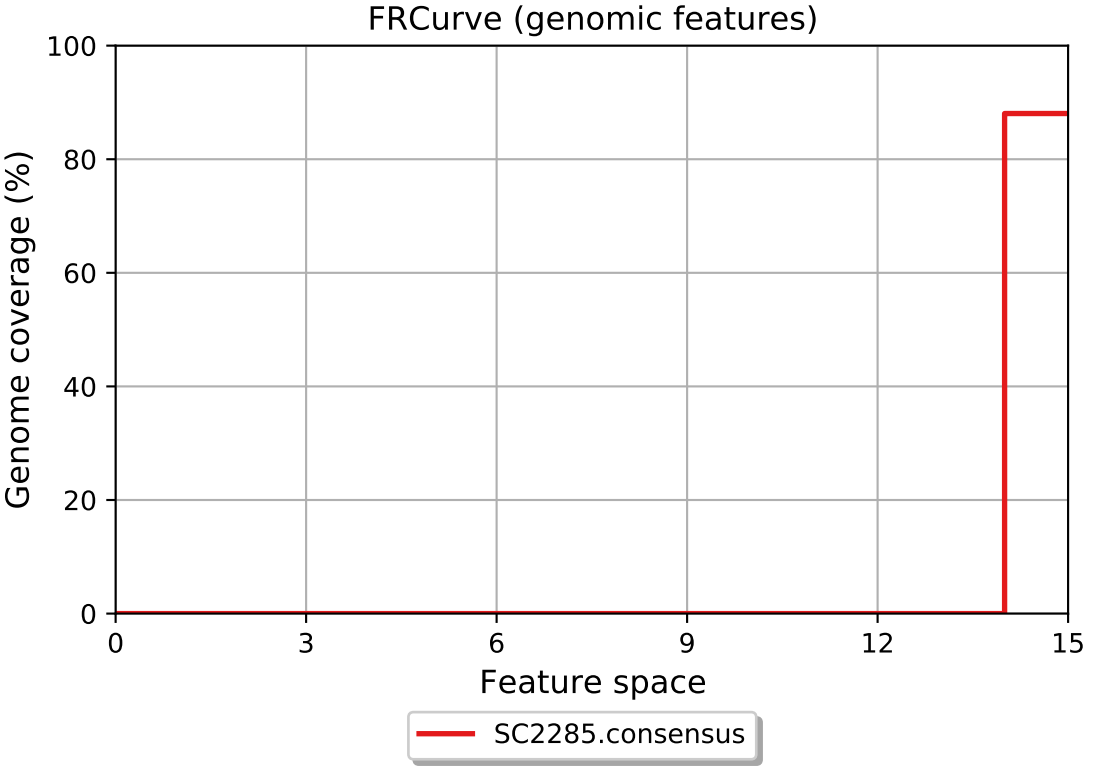

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
SC2285.consensus


Cumulative length (aligned contigs)
Cumulative length (kbp)
30
24
18
12
6
0
0
1
Contig index
SC2285.consensus
Reference


NAx
Contig length (kbp)
0
5
10
15
20
25
0
20
40
60
80
100
x
SC2285.consensus


NGAx
Contig length (kbp)
0
5
10
15
20
25
0
20
40
60
80
100
x
SC2285.consensus


Cumulative # complete genomic features
Cumulative # complete genomic features
25
20
15
10
5
0
0
1
Contig index
SC2285.consensus
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
3
6
9
12
15
Feature space
SC2285.consensus