Report

	SC2250.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)	29895
Total length (>= 1000 bp)	29895
Total length (>= 5000 bp)	29895
Total length (>= 10000 bp)	29895
Total length (>= 25000 bp)	29895
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	29895
Total length	29895
Reference length	29903
GC (%)	38.03
Reference GC (%)	37.97
N50	29895
NG50	29895
N75	29895
NG75	29895
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.	10
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	89.590
Duplication ratio	1.116
# N's per 100 kbp	12303.06
# mismatches per 100 kbp	85.85
# indels per 100 kbp	3.73
# genomic features	14 + 8 part
Largest alignment	26782
Total aligned length	26782
NA50	26782
NGA50	26782
NA75	26782
NGA75	26782
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

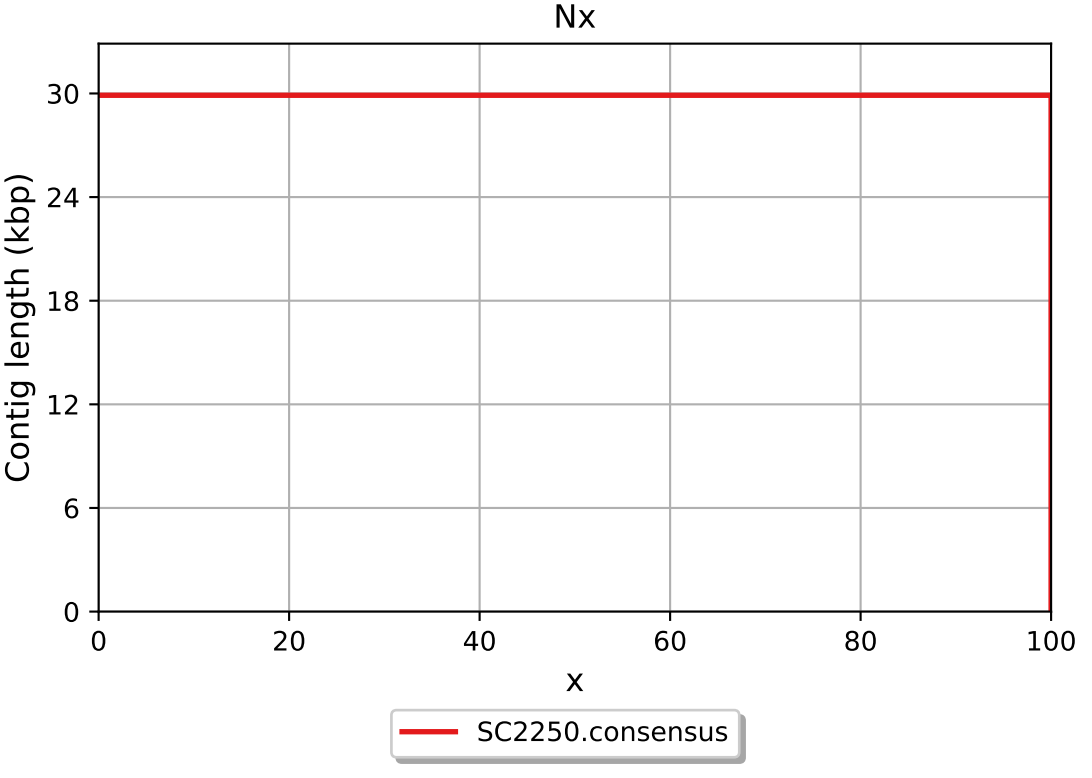
	SC2250.consensus
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	10
# unaligned mis. contigs	0
# mismatches	23
# indels	1
# indels (<= 5 bp)	0
# indels (> 5 bp)	1
Indels length	8

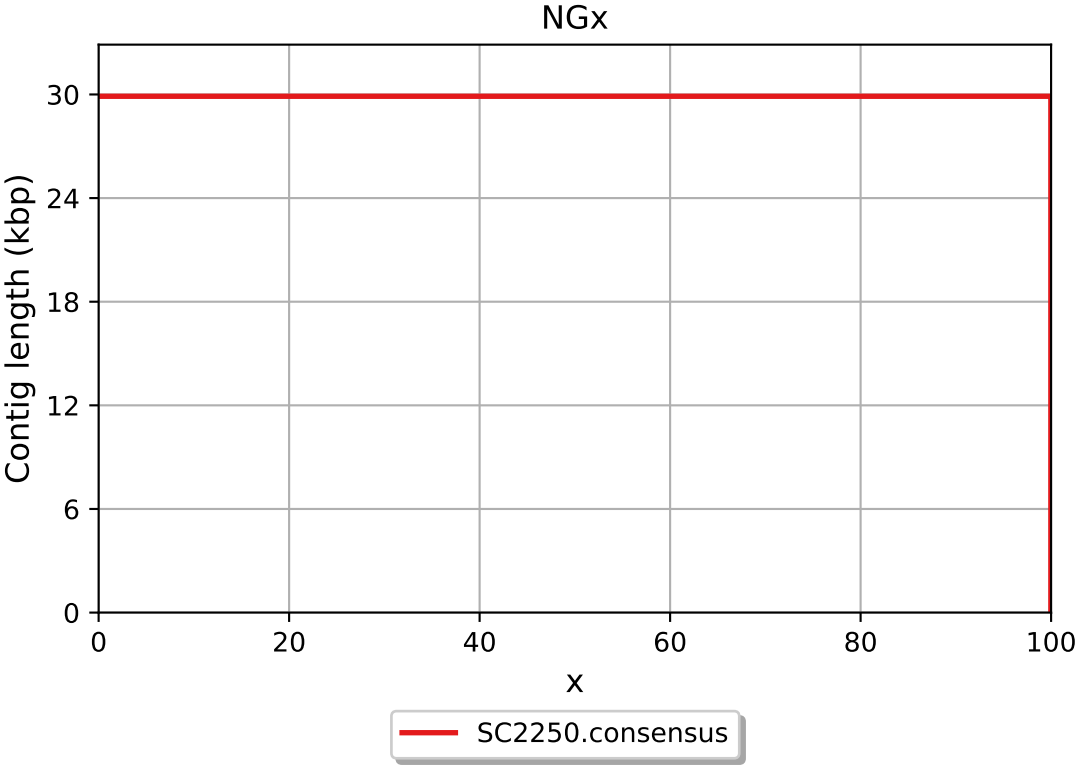
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

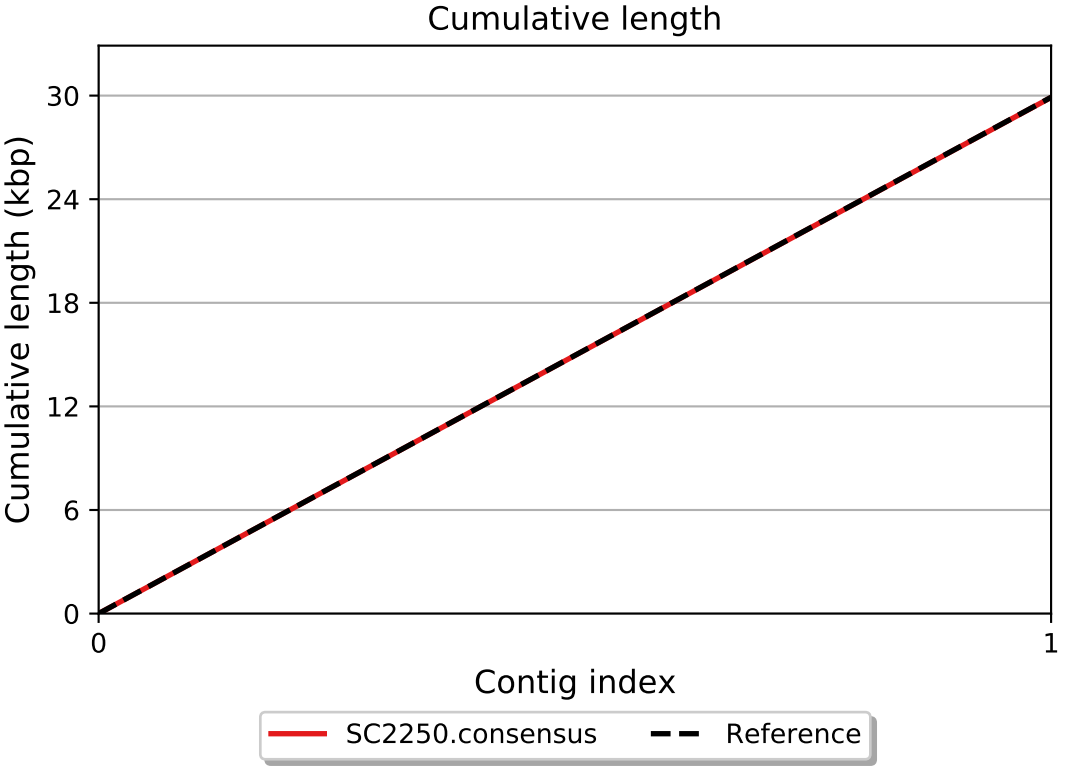
Unaligned report

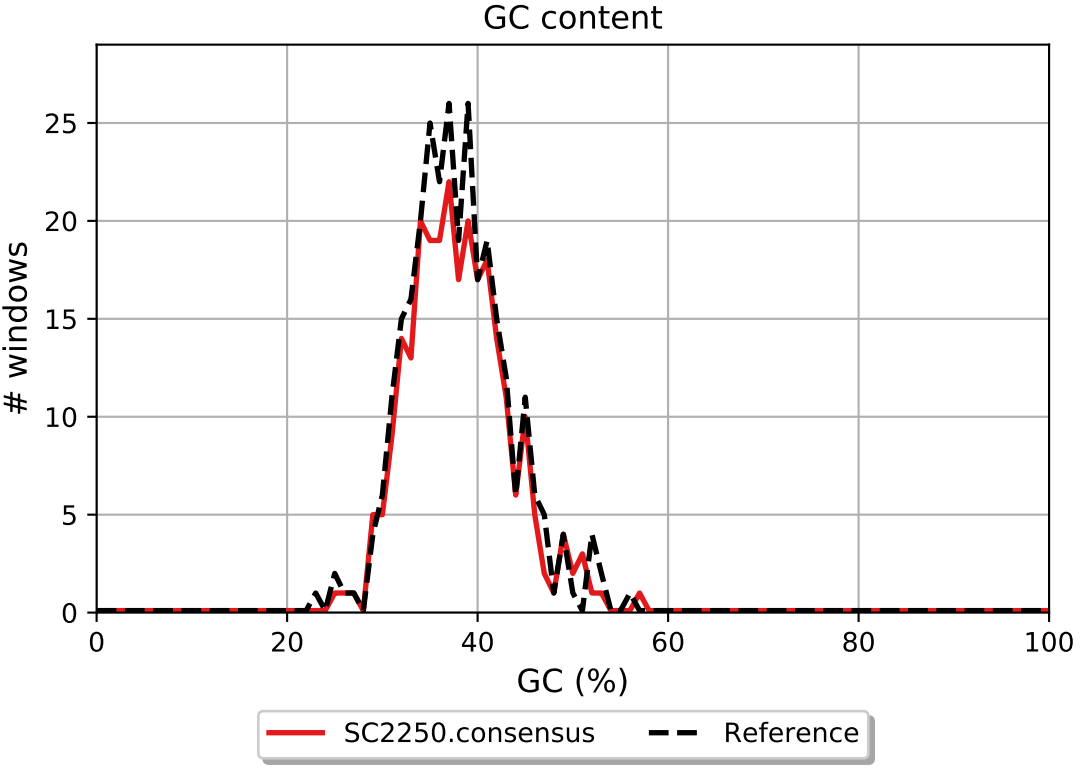
	SC2250.consensus
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	3678

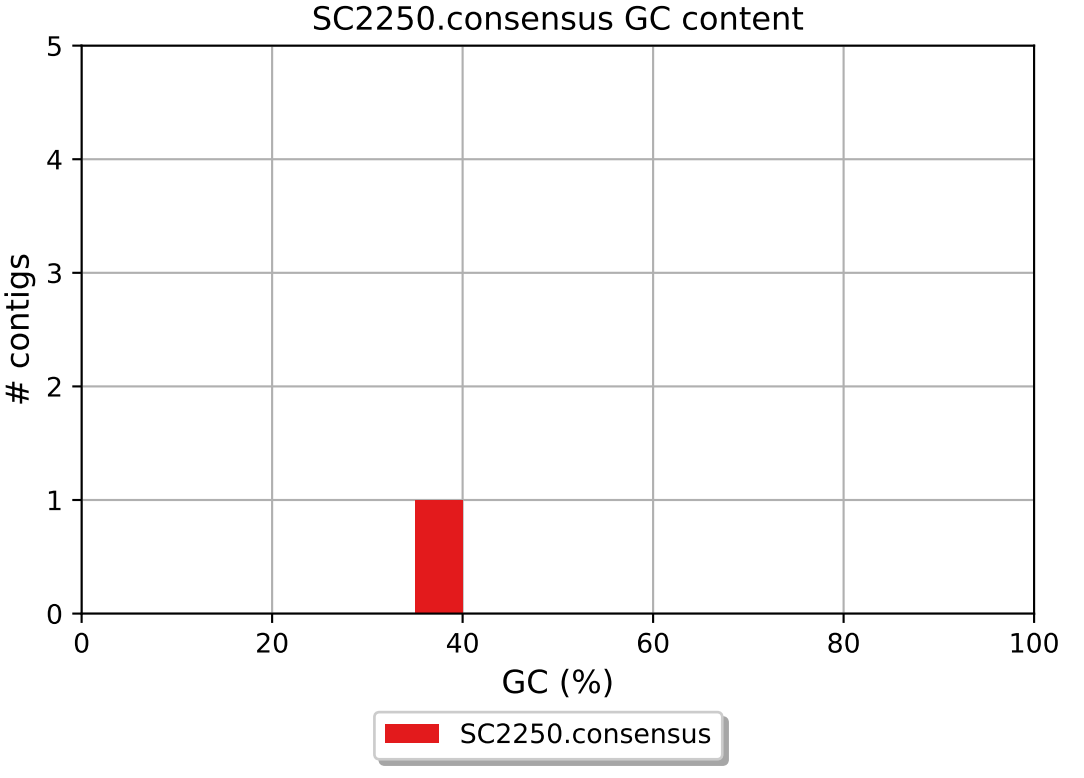
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
SC2250.consensus

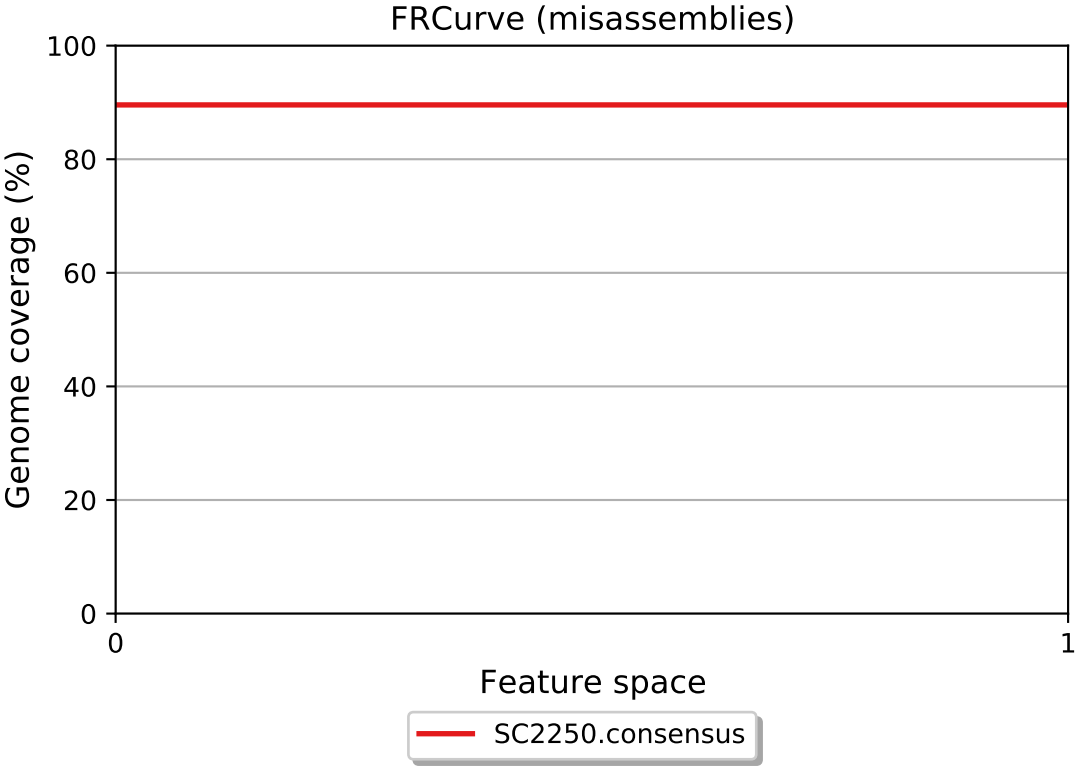

NGx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
SC2250.consensus

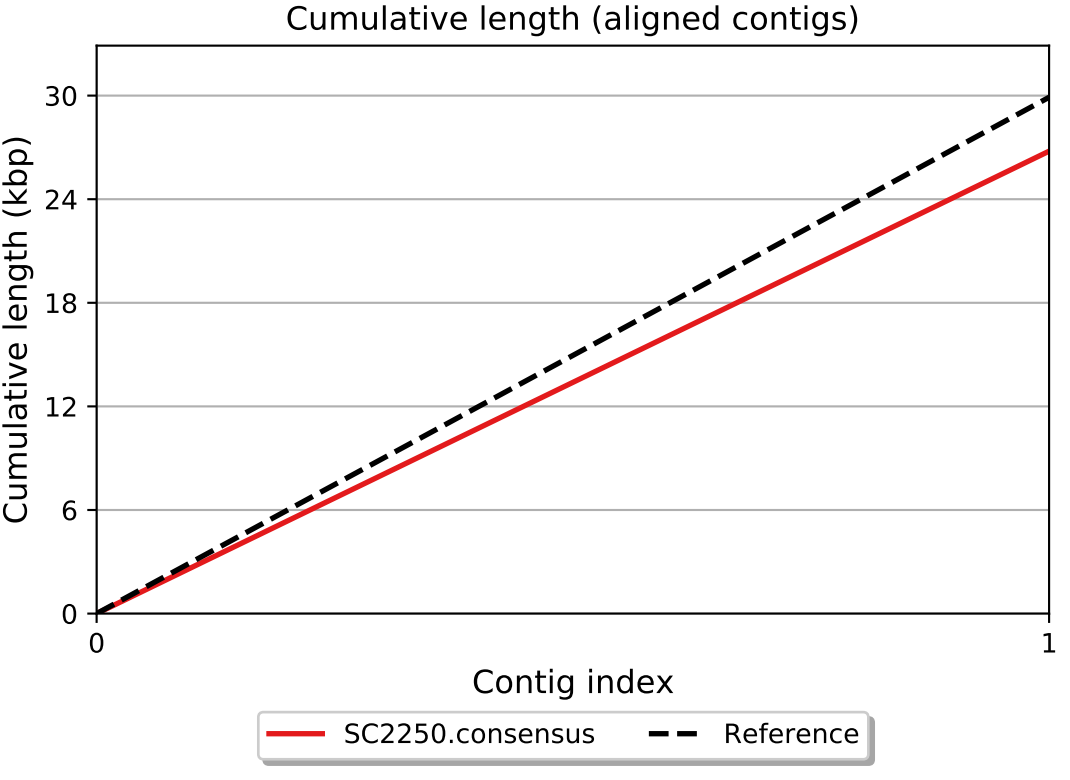

Cumulative length
Cumulative length (kbp)
30
24
18
12
6
0
0
1
Contig index
SC2250.consensus
Reference

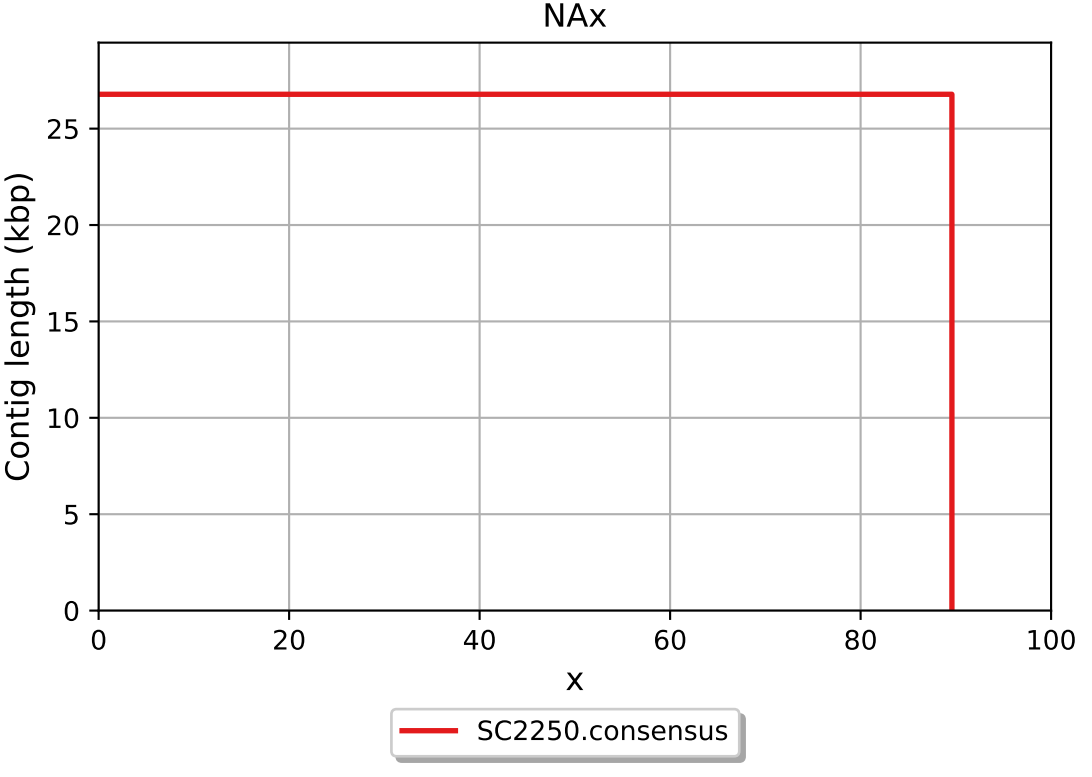

GC content
windows
GC (%)
0
5
10
15
20
25
0
20
40
60
80
100
SC2250.consensus
Reference

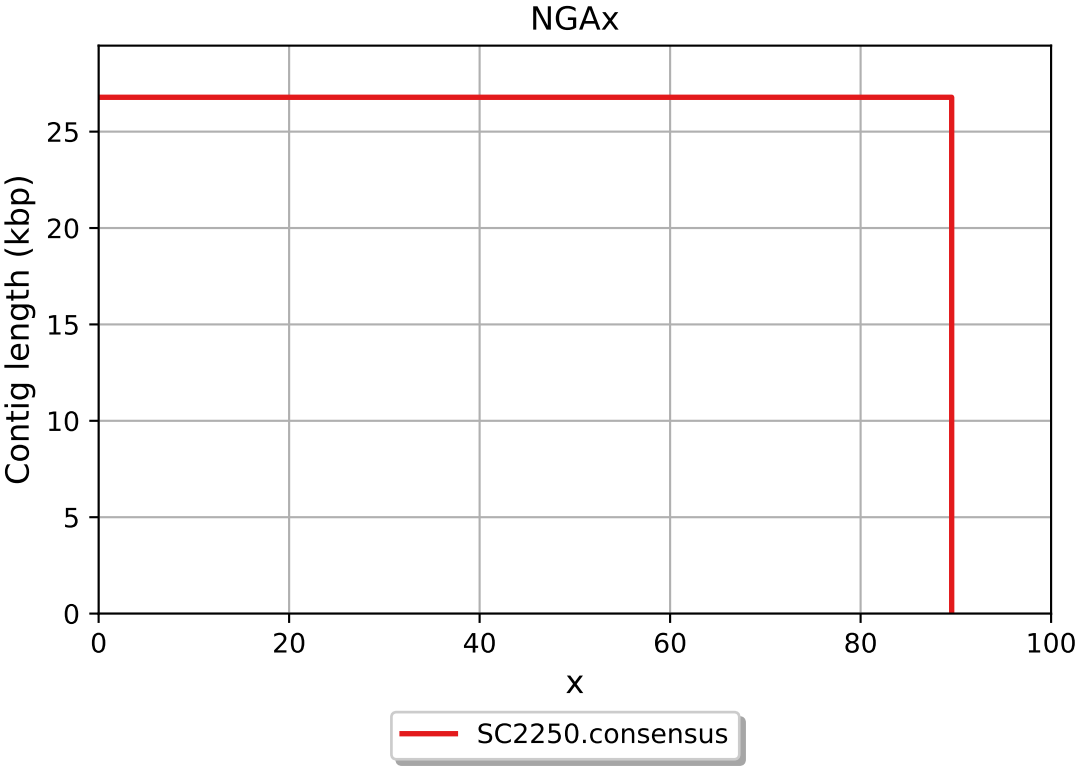

SC2250.consensus GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
SC2250.consensus

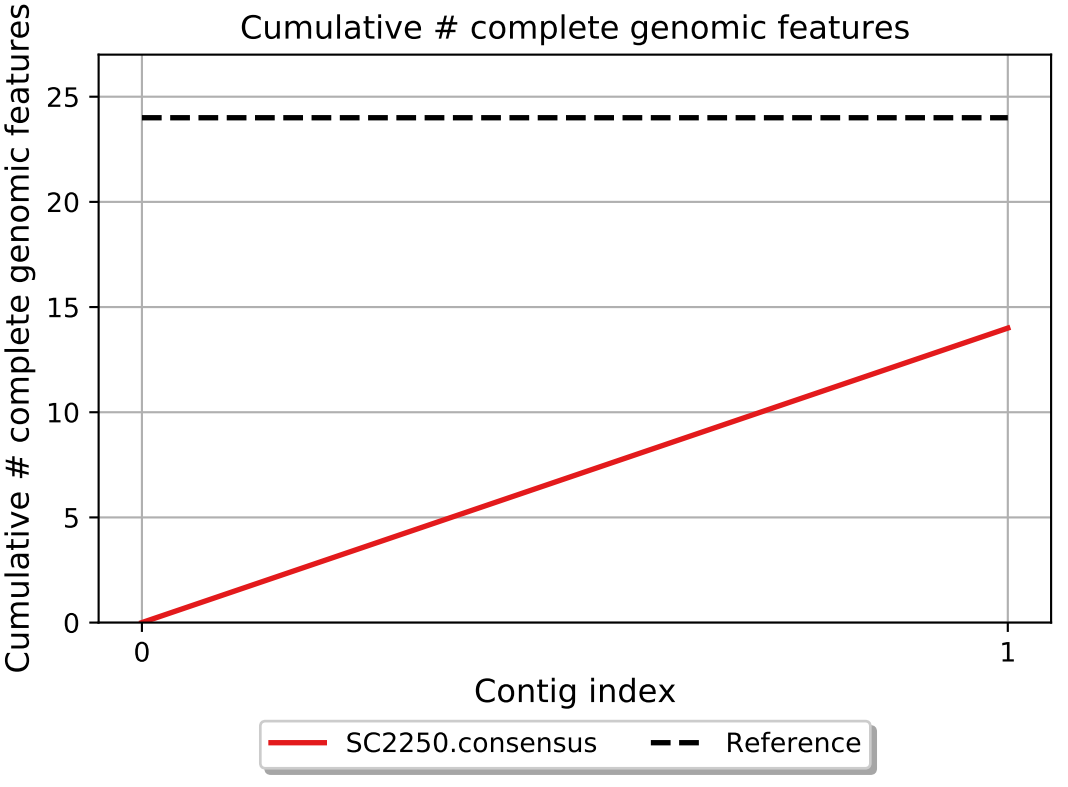
Misassemblies
5
4
3
2
1
0
SC2250.consensus

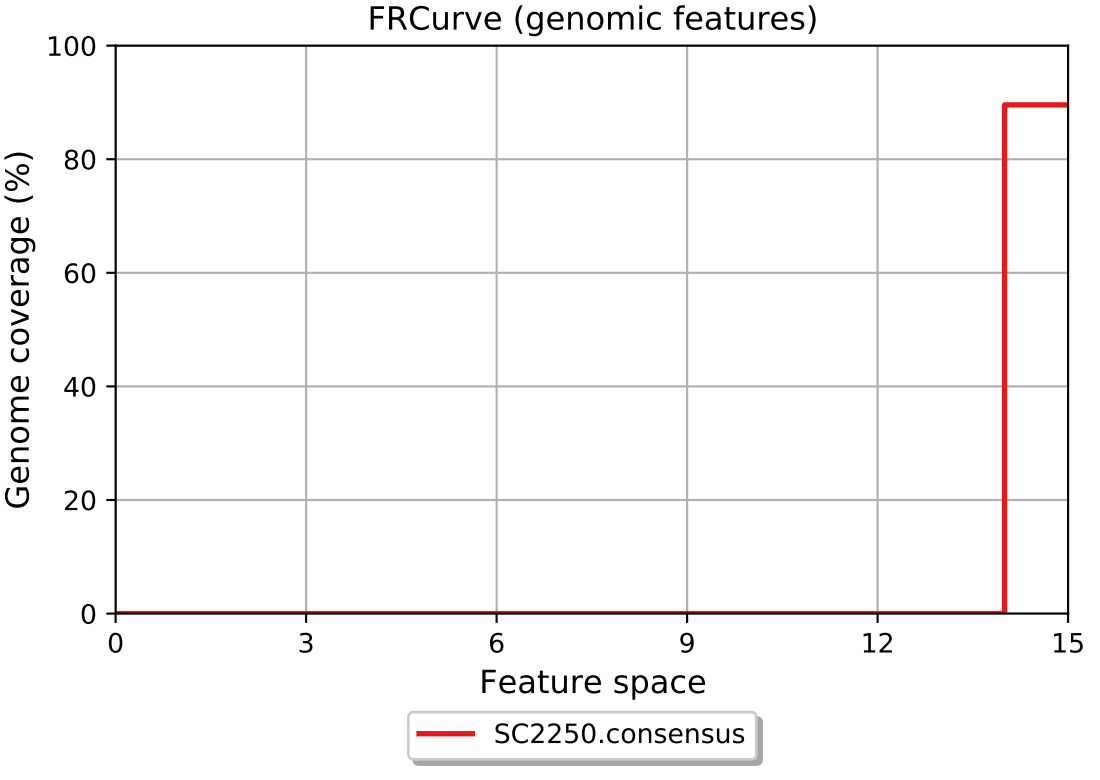

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
SC2250.consensus


Cumulative length (aligned contigs)
Cumulative length (kbp)
30
24
18
12
6
0
0
1
Contig index
SC2250.consensus
Reference


NAx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
SC2250.consensus


NGAx
Contig length (kbp)
0
5
10
15
20
25
0
20
40
60
80
100
x
SC2250.consensus


Cumulative # complete genomic features
Cumulative # complete genomic features
25
20
15
10
5
0
0
1
Contig index
SC2250.consensus
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
3
6
9
12
15
Feature space
SC2250.consensus