Report

	ERR5405022.consensus	ERR5556343.consensus	SRR13500958.consensus	ERR5743893.consensus	ERR5181310.consensus
# contigs (>= 0 bp)	1	1	1	1	1
# contigs (>= 1000 bp)	1	1	1	1	1
# contigs (>= 5000 bp)	1	1	1	1	1
# contigs (>= 10000 bp)	1	1	1	1	1
# contigs (>= 25000 bp)	1	1	1	1	1
# contigs (>= 50000 bp)	0	0	0	0	0
Total length (>= 0 bp)	29884	29894	29903	29902	29830
Total length (>= 1000 bp)	29884	29894	29903	29902	29830
Total length (>= 5000 bp)	29884	29894	29903	29902	29830
Total length (>= 10000 bp)	29884	29894	29903	29902	29830
Total length (>= 25000 bp)	29884	29894	29903	29902	29830
Total length (>= 50000 bp)	0	0	0	0	0
# contigs	1	1	1	1	1
Largest contig	29884	29894	29903	29902	29830
Total length	29884	29894	29903	29902	29830
Reference length	29903	29903	29903	29903	29903
GC (%)	37.97	37.96	37.98	37.93	37.92
Reference GC (%)	37.97	37.97	37.97	37.97	37.97
N50	29884	29894	29903	29902	29830
NG50	29884	29894	29903	29902	29830
N90	29884	29894	29903	29902	29830
NG90	29884	29894	29903	29902	29830
auN	29884.0	29894.0	29903.0	29902.0	29830.0
auNG	29865.0	29885.0	29903.0	29901.0	29757.2
L50	1	1	1	1	1
LG50	1	1	1	1	1
L90	1	1	1	1	1
LG90	1	1	1	1	1
# misassemblies	0	0	0	0	0
# misassembled contigs	0	0	0	0	0
Misassembled contigs length	0	0	0	0	0
# local misassemblies	0	0	0	0	0
# scaffold gap ext. mis.	0	0	0	0	0
# scaffold gap loc. mis.	2	2	0	1	1
# unaligned mis. contigs	0	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part
Unaligned length	0	0	0	0	0
Genome fraction (%)	98.030	97.790	99.595	97.656	98.284
Duplication ratio	0.999	1.000	1.000	1.000	0.999
# N's per 100 kbp	1977.65	2114.14	404.64	2220.59	1354.34
# mismatches per 100 kbp	116.06	116.31	73.87	92.46	95.35
# indels per 100 kbp	13.65	3.42	0.00	3.42	17.03
# genomic features	17 + 7 part	17 + 7 part	21 + 3 part	19 + 4 part	19 + 4 part
Largest alignment	29295	29233	29782	29201	29366
Total aligned length	29295	29233	29782	29201	29366
NA50	29295	29233	29782	29201	29366
NGA50	29295	29233	29782	29201	29366
NA90	29295	29233	29782	29201	29366
NGA90	29295	29233	29782	29201	29366
auNA	28717.6	28586.6	29661.5	28516.4	28909.2
auNGA	28699.4	28578.0	29661.5	28515.5	28838.6
LA50	1	1	1	1	1
LGA50	1	1	1	1	1
LA90	1	1	1	1	1
LGA90	1	1	1	1	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

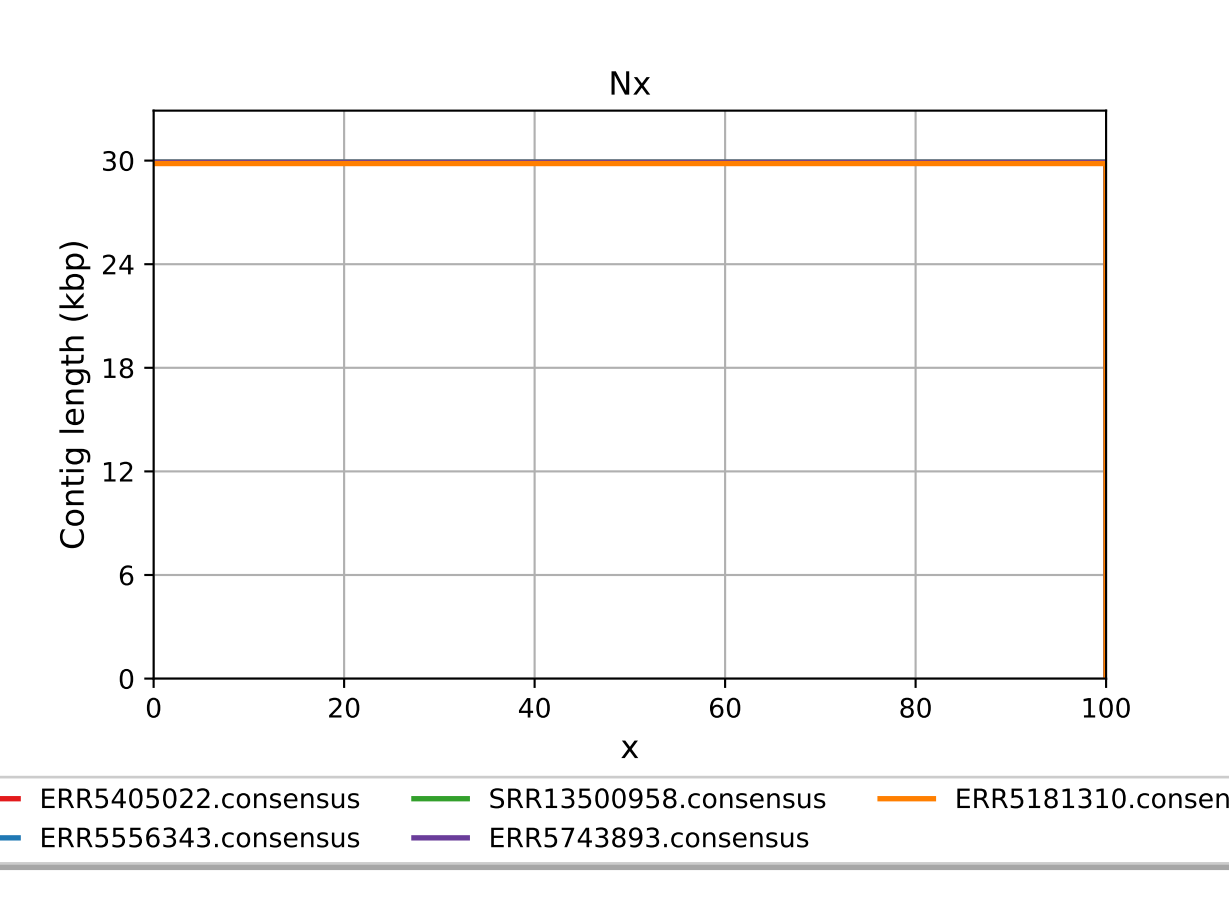
	ERR5405022.consensus	ERR5556343.consensus	SRR13500958.consensus	ERR5743893.consensus	ERR5181310.consensus
# misassemblies	0	0	0	0	0
# contig misassemblies	0	0	0	0	0
# c. relocations	0	0	0	0	0
# c. translocations	0	0	0	0	0
# c. inversions	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0
# s. relocations	0	0	0	0	0
# s. translocations	0	0	0	0	0
# s. inversions	0	0	0	0	0
# misassembled contigs	0	0	0	0	0
Misassembled contigs length	0	0	0	0	0
# local misassemblies	0	0	0	0	0
# scaffold gap ext. mis.	0	0	0	0	0
# scaffold gap loc. mis.	2	2	0	1	1
# unaligned mis. contigs	0	0	0	0	0
# mismatches	34	34	22	27	28
# indels	4	1	0	1	5
# indels (<= 5 bp)	2	0	0	1	3
# indels (> 5 bp)	2	1	0	0	2
Indels length	19	9	0	1	24

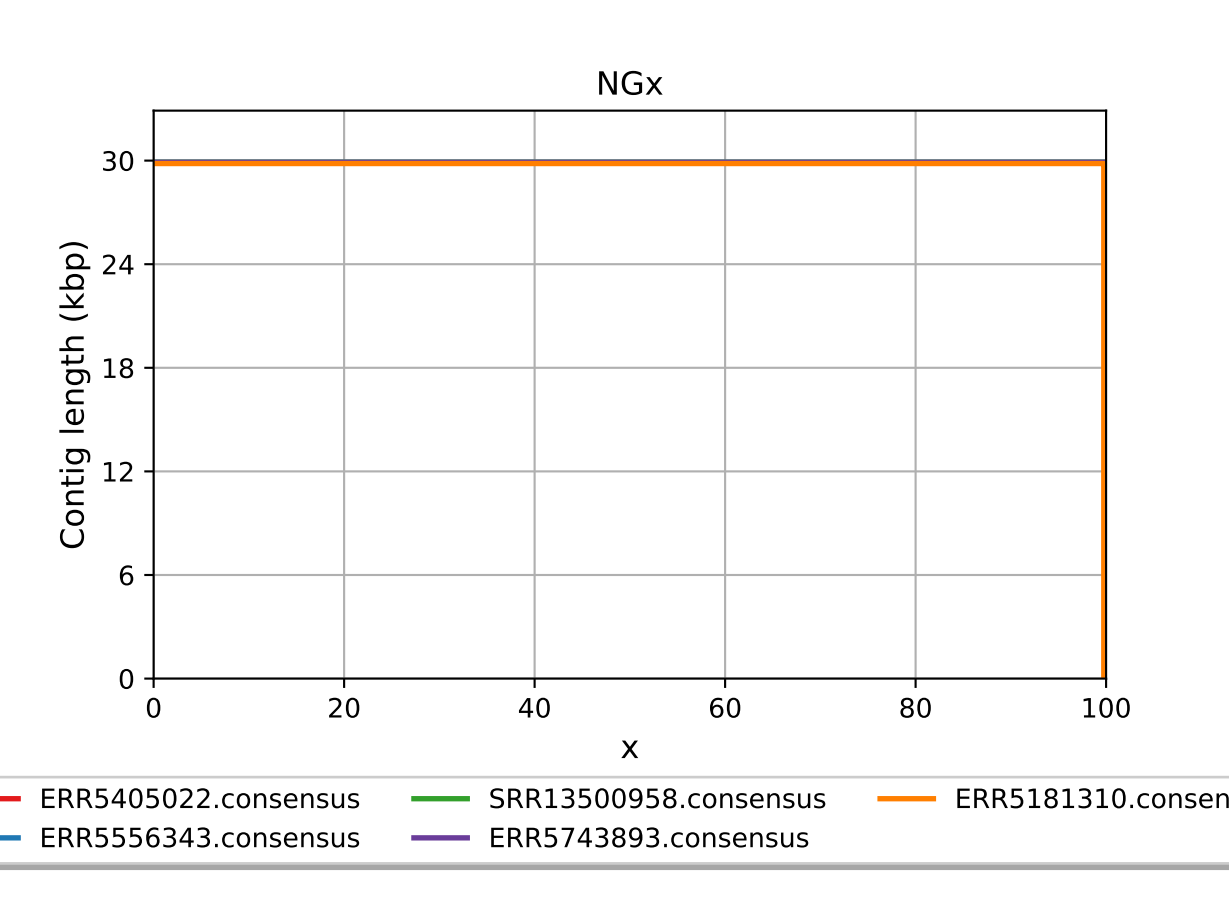
All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

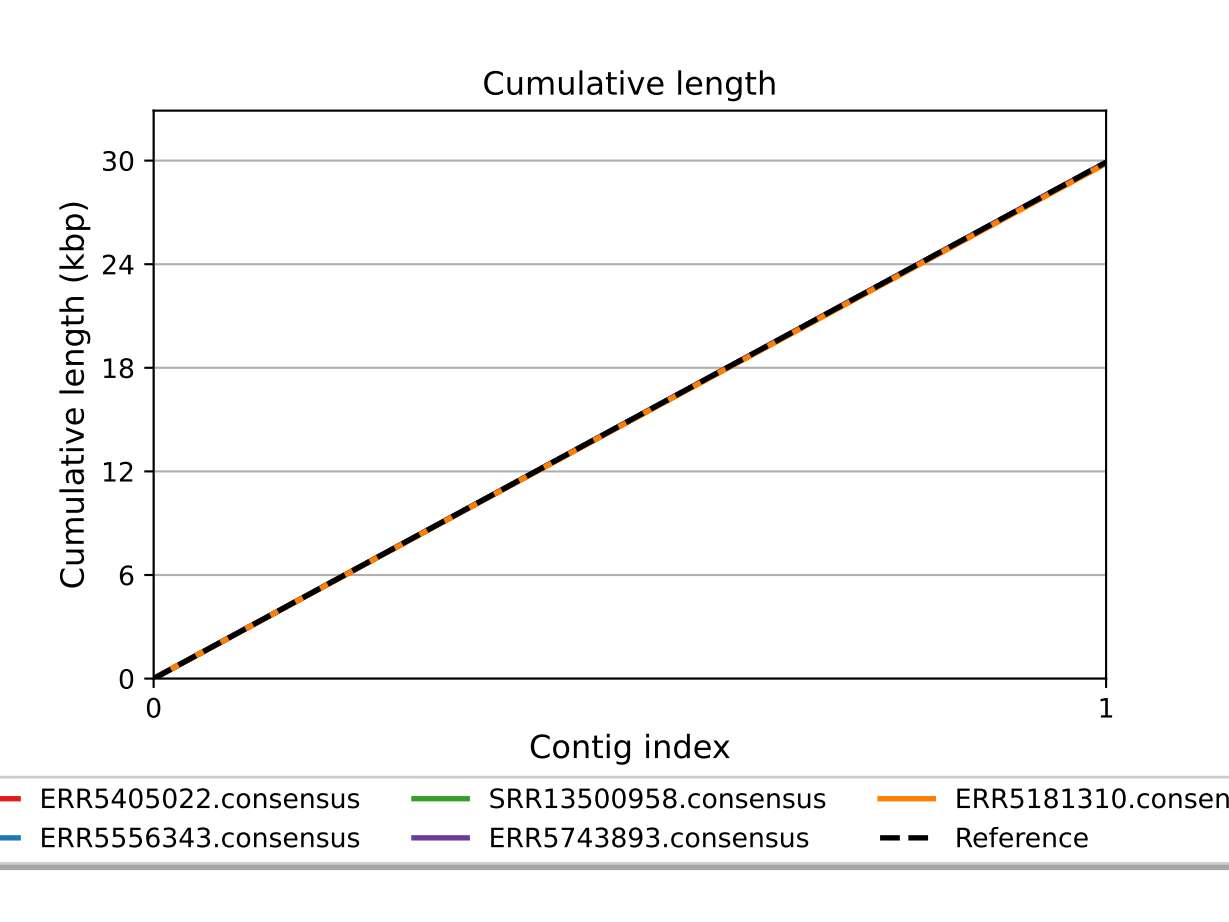
Unaligned report

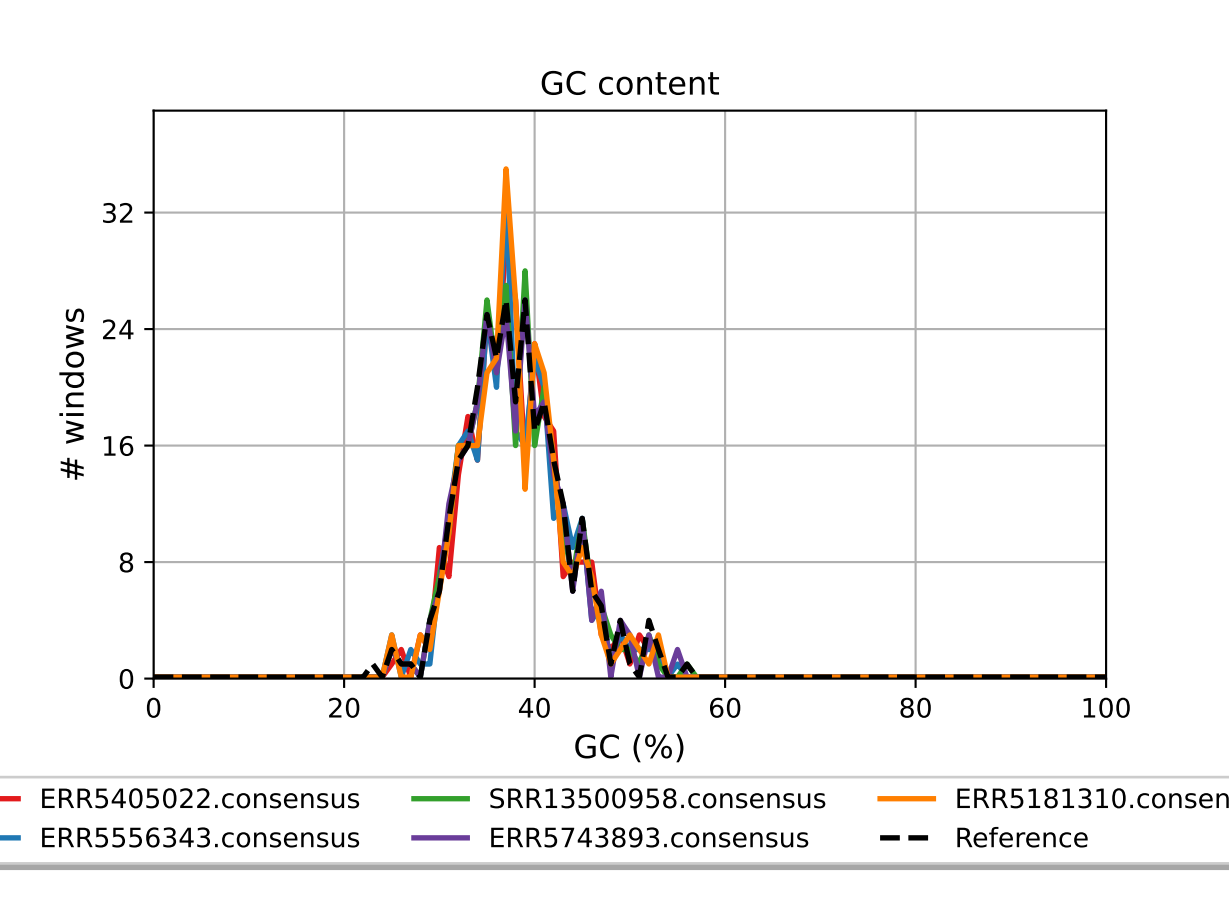
	ERR5405022.consensus	ERR5556343.consensus	SRR13500958.consensus	ERR5743893.consensus	ERR5181310.consensus
# fully unaligned contigs	0	0	0	0	0
Fully unaligned length	0	0	0	0	0
# partially unaligned contigs	0	0	0	0	0
Partially unaligned length	0	0	0	0	0
# N's	591	632	121	664	404

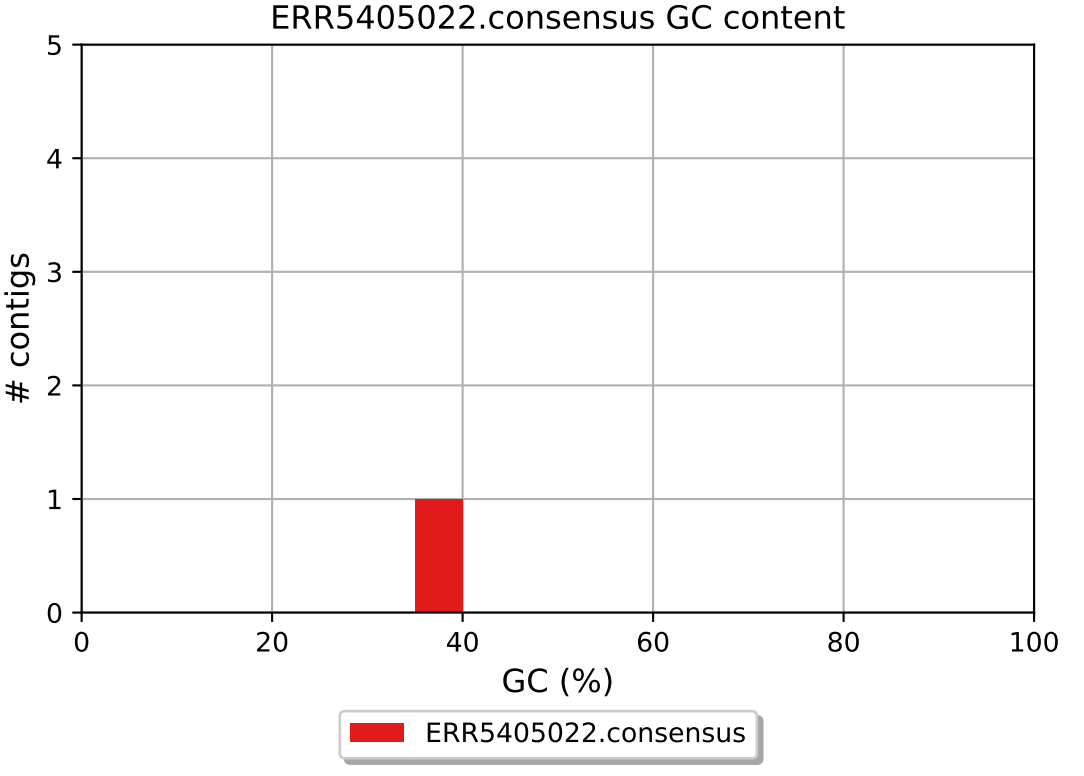
All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

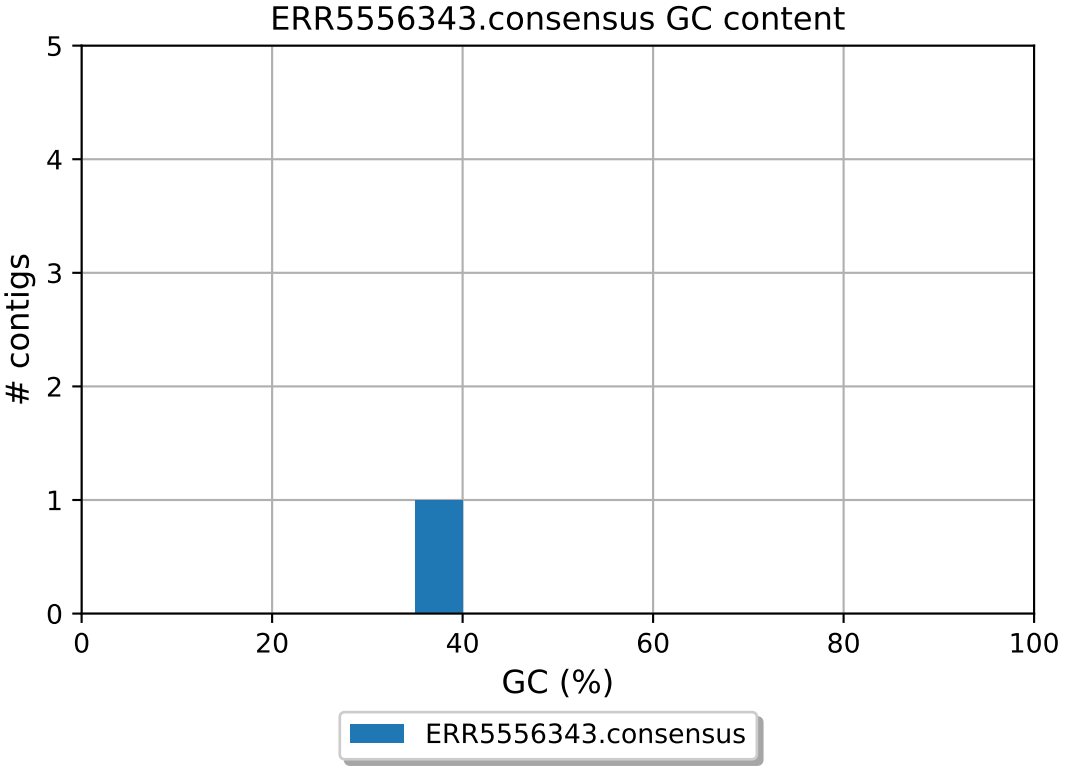

Nx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
ERR5405022.consensus
ERR5556343.consensus
SRR13500958.consensus
ERR5743893.consensus
ERR5181310.consen

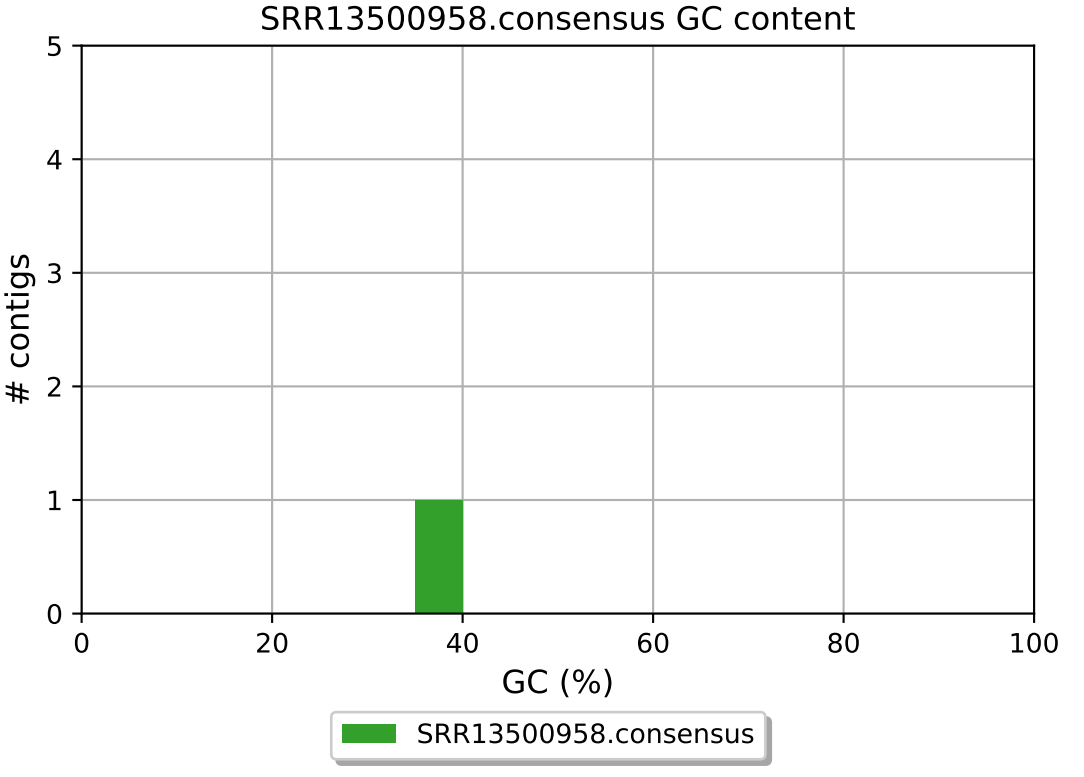

NGx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
ERR5405022.consensus
ERR5556343.consensus
SRR13500958.consensus
ERR5743893.consensus
ERR5181310.consen

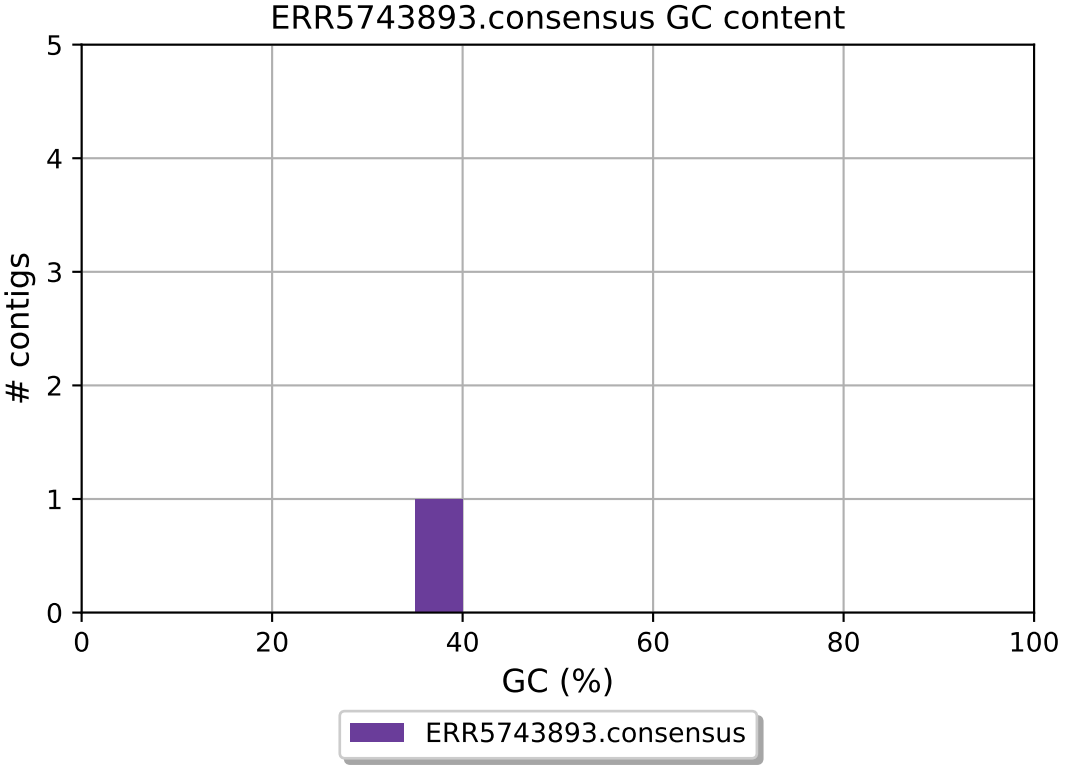

Cumulative length
Cumulative length (kbp)
30
24
18
12
6
0
0
1
Contig index
ERR5405022.consensus
ERR5556343.consensus
SRR13500958.consensus
ERR5743893.consensus
ERR5181310.consen
Reference

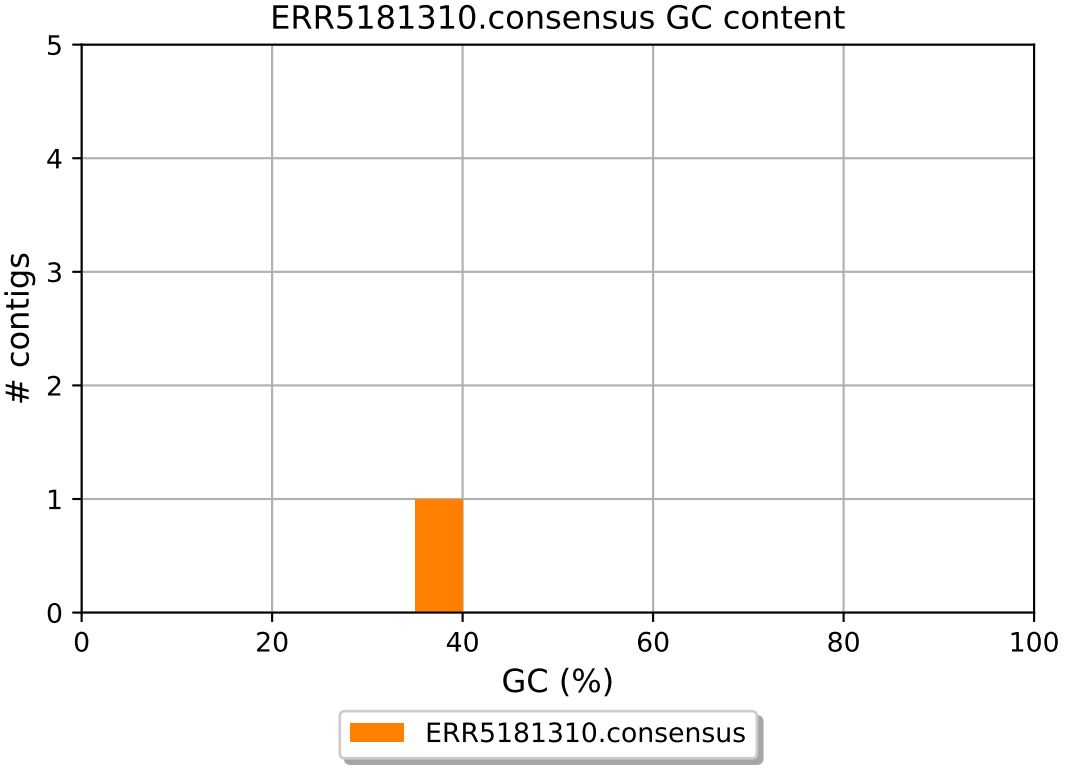

GC content
windows
GC (%)
0
8
16
24
32
0
20
40
60
80
100
ERR5405022.consensus
ERR5556343.consensus
SRR13500958.consensus
ERR5743893.consensus
ERR5181310.consen
Reference

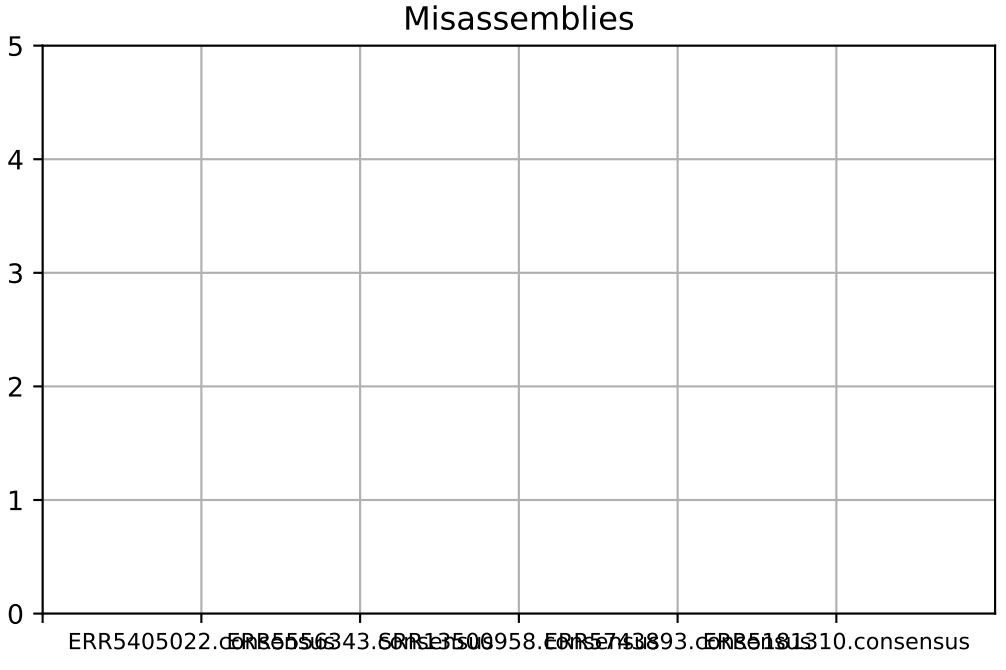

ERR5405022.consensus GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
ERR5405022.consensus

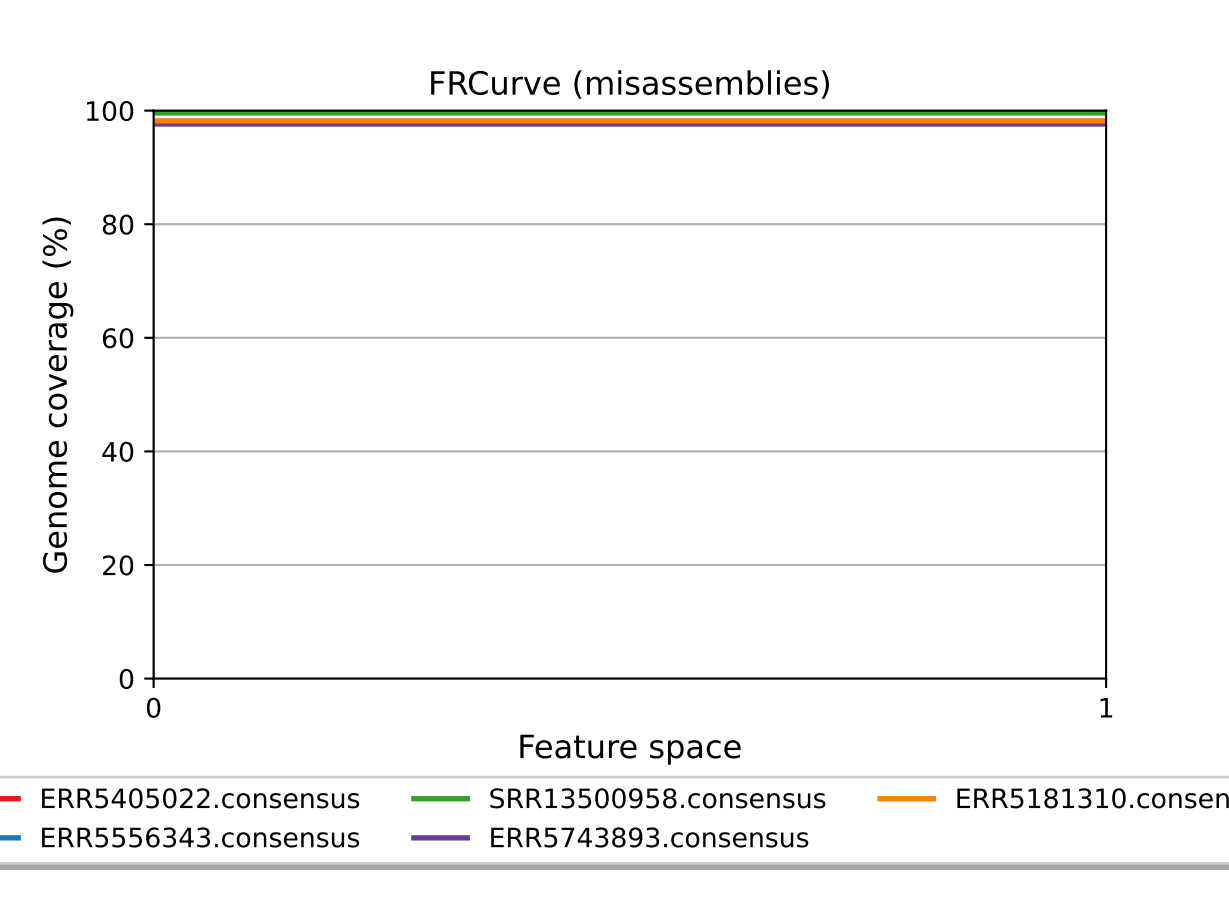

ERR5556343.consensus GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
ERR5556343.consensus

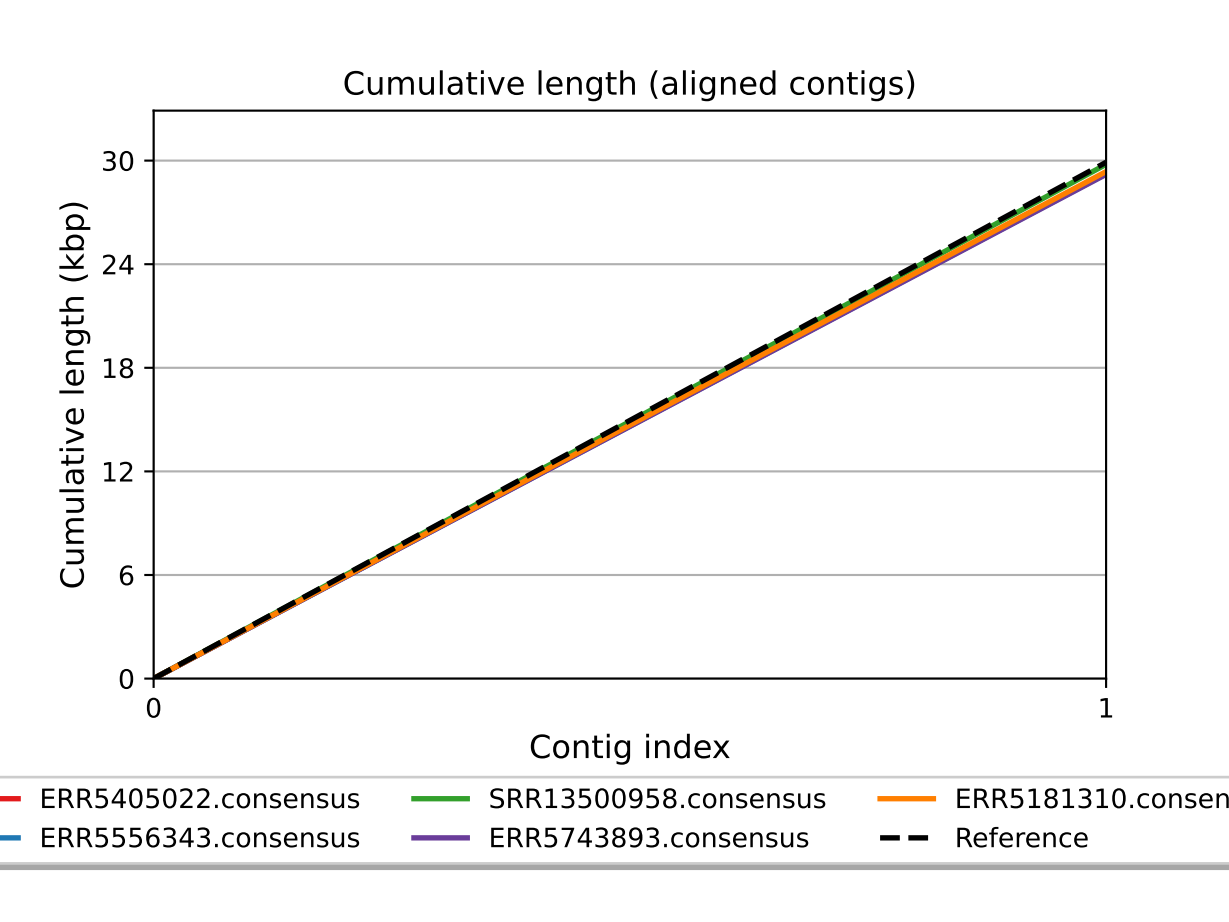

SRR13500958.consensus GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
SRR13500958.consensus

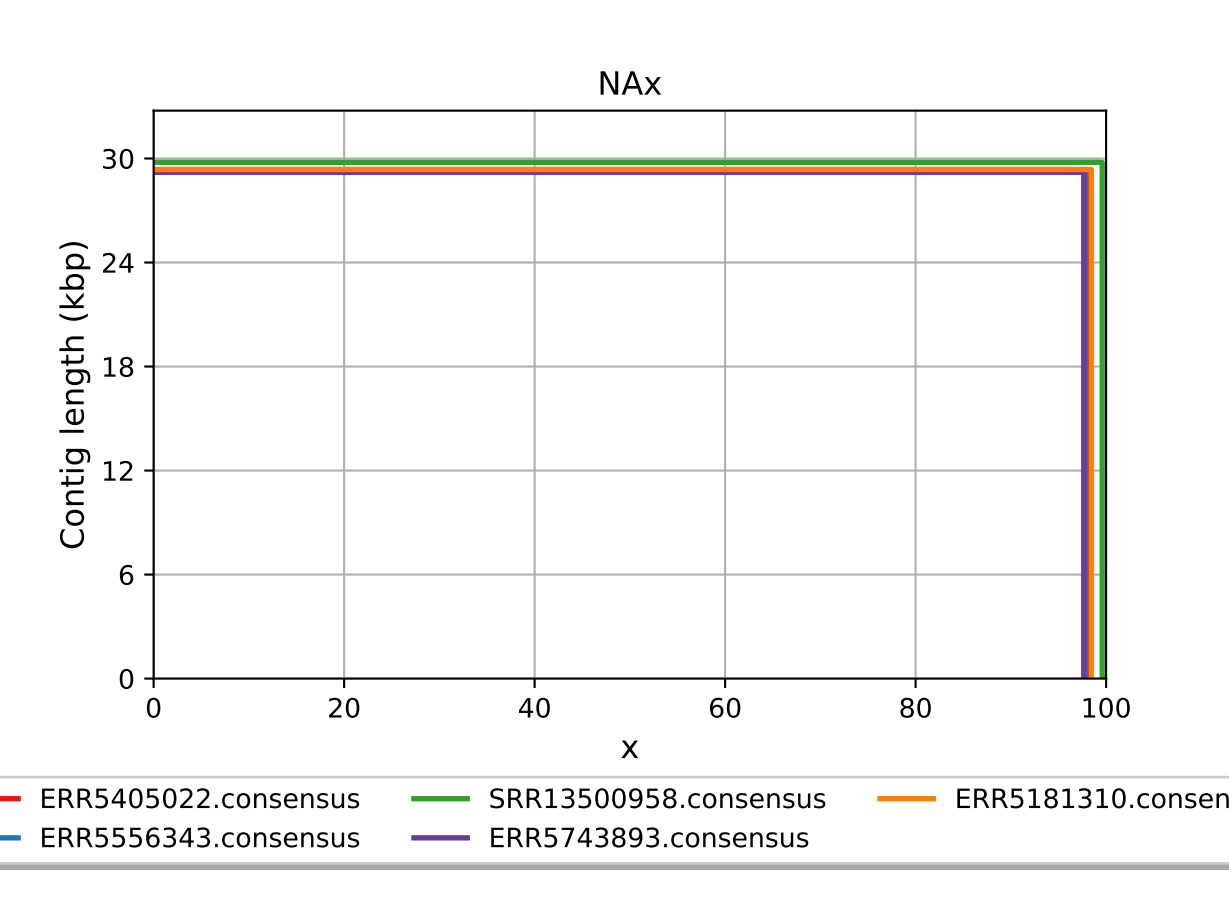

ERR5743893.consensus GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
ERR5743893.consensus

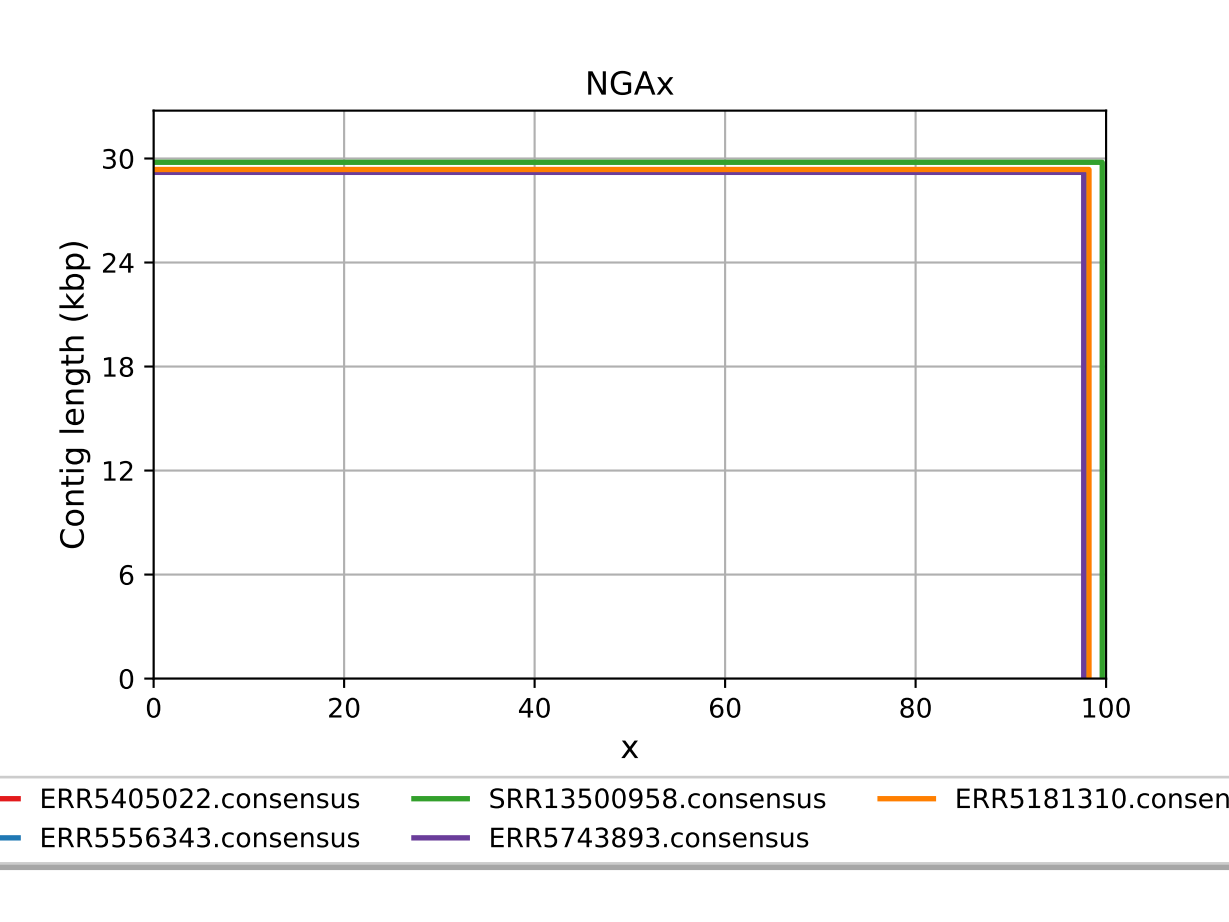

ERR5181310.consensus GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
ERR5181310.consensus

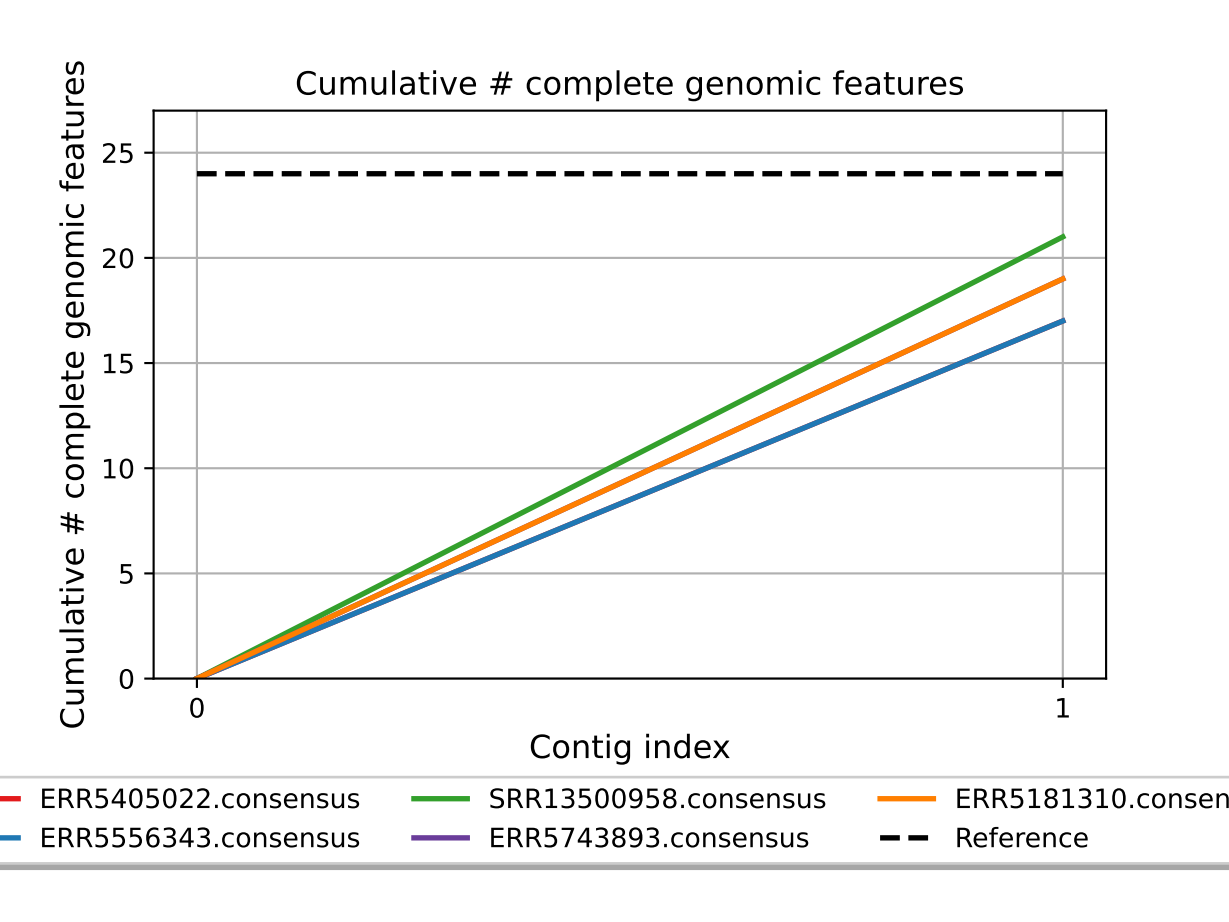

Misassemblies
5
4
3
2
1
0
ERR5405022.consensus
ERR5556343.consensus
ERR13500958.consensus
ERR5743893.consensus
ERR5181310.consensus

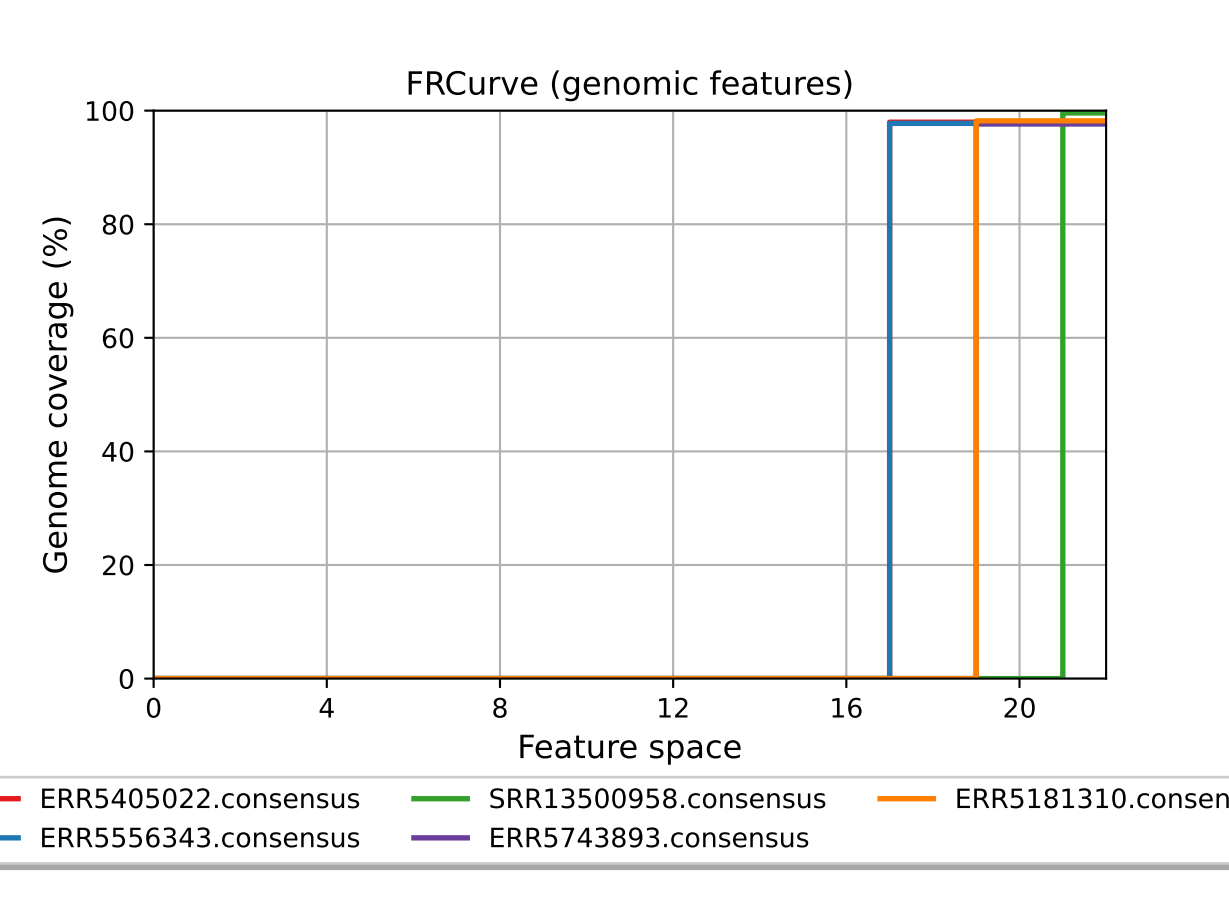

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
ERR5405022.consensus
SRR13500958.consensus
ERR5181310.consen
ERR5556343.consensus
ERR5743893.consensus

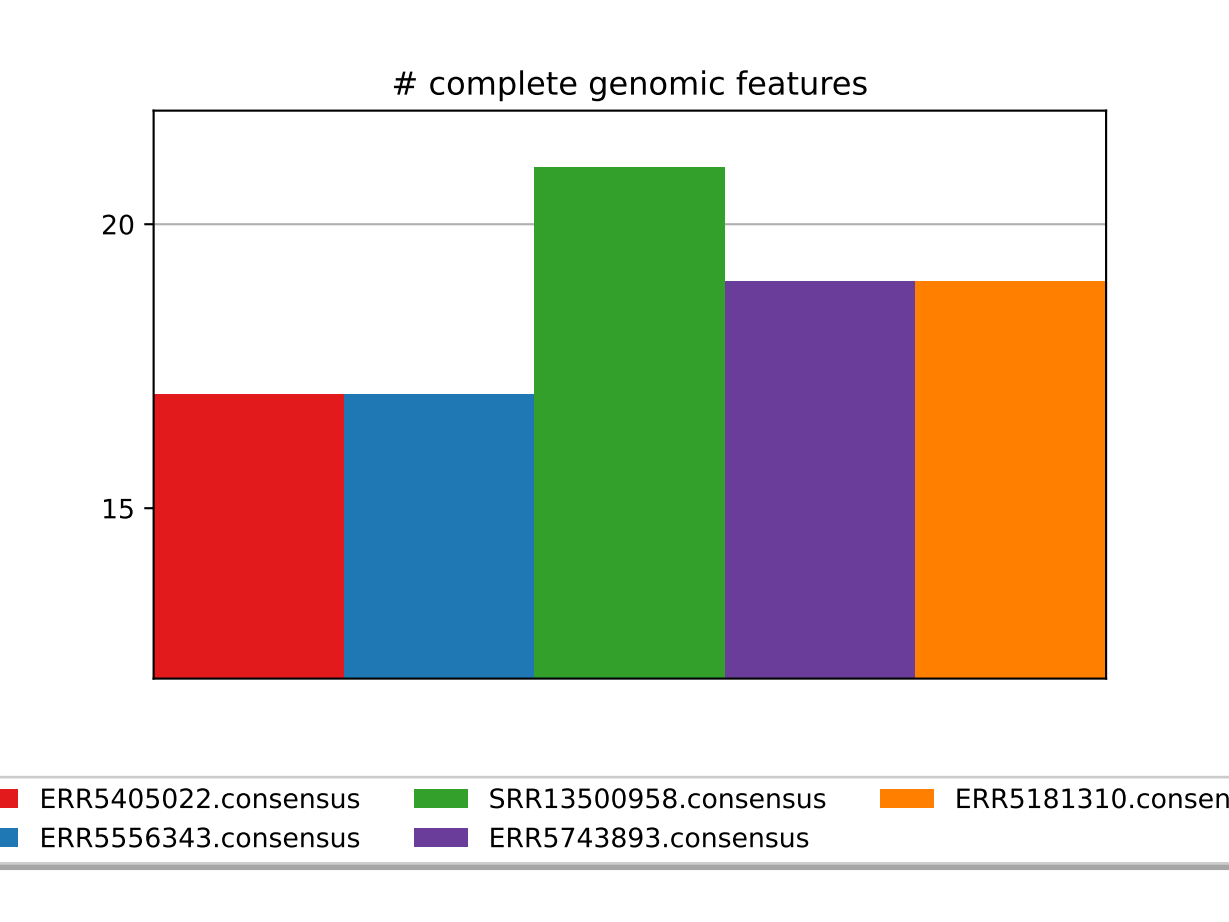

Cumulative length (aligned contigs)
Cumulative length (kbp)
30
24
18
12
6
0
0
1
Contig index
ERR5405022.consensus
ERR5556343.consensus
SRR13500958.consensus
ERR5743893.consensus
ERR5181310.consen
Reference

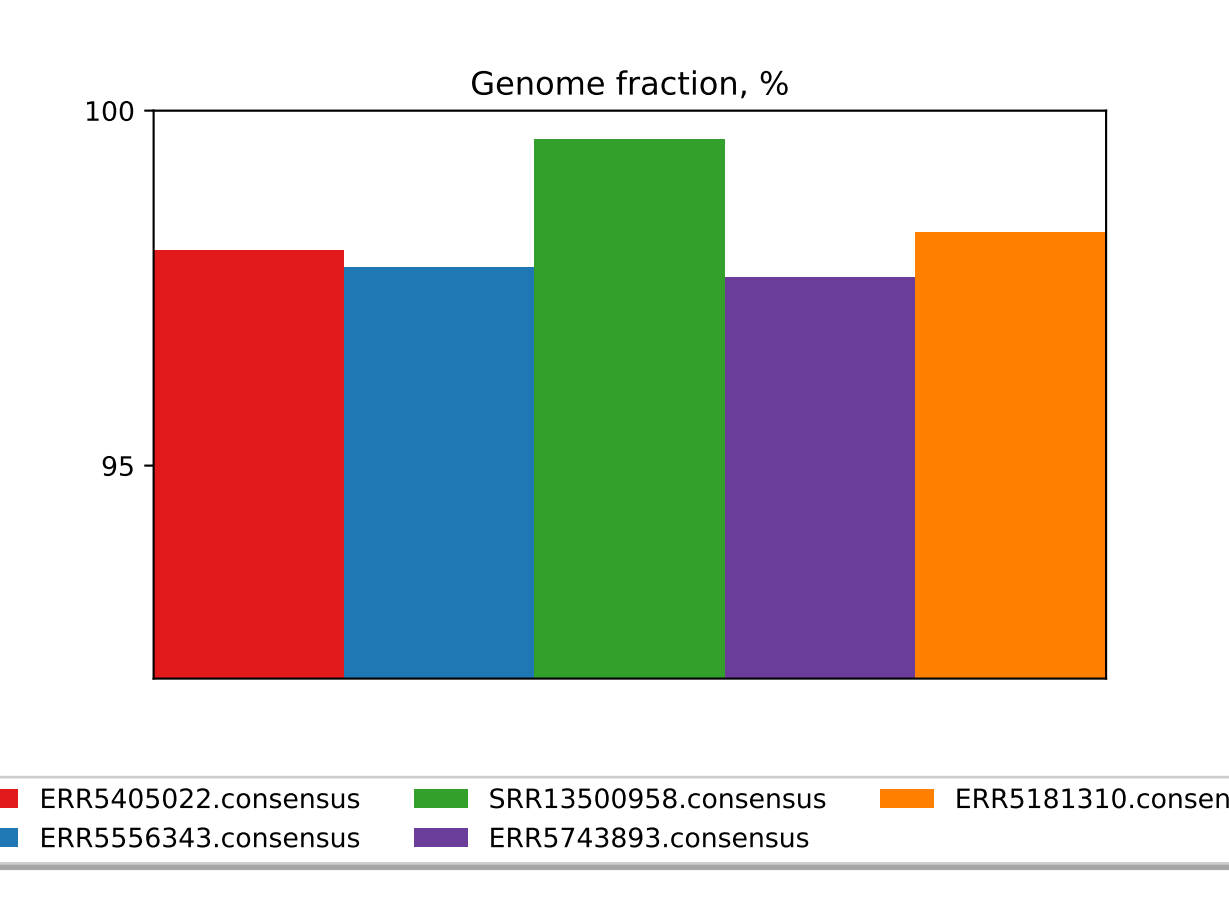

NAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
ERR5405022.consensus
SRR13500958.consensus
ERR5181310.consen
ERR5556343.consensus
ERR5743893.consensus


NGAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
ERR5405022.consensus
SRR13500958.consensus
ERR5181310.consen
ERR5556343.consensus
ERR5743893.consensus


Cumulative # complete genomic features
Cumulative # complete genomic features
25
20
15
10
5
0
0
1
Contig index
ERR5405022.consensus
SRR13500958.consensus
ERR5181310.consen
ERR5556343.consensus
ERR5743893.consensus
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
4
8
12
16
20
Feature space
ERR5405022.consensus
ERR5556343.consensus
SRR13500958.consensus
ERR5743893.consensus
ERR5181310.consen


complete genomic features
20
15
ERR5405022.consensus
ERR5556343.consensus
SRR13500958.consensus
ERR5743893.consensus
ERR5181310.consen


Genome fraction, %
100
95
ERR5405022.consensus
ERR5556343.consensus
SRR13500958.consensus
ERR5743893.consensus
ERR5181310.consen