Report

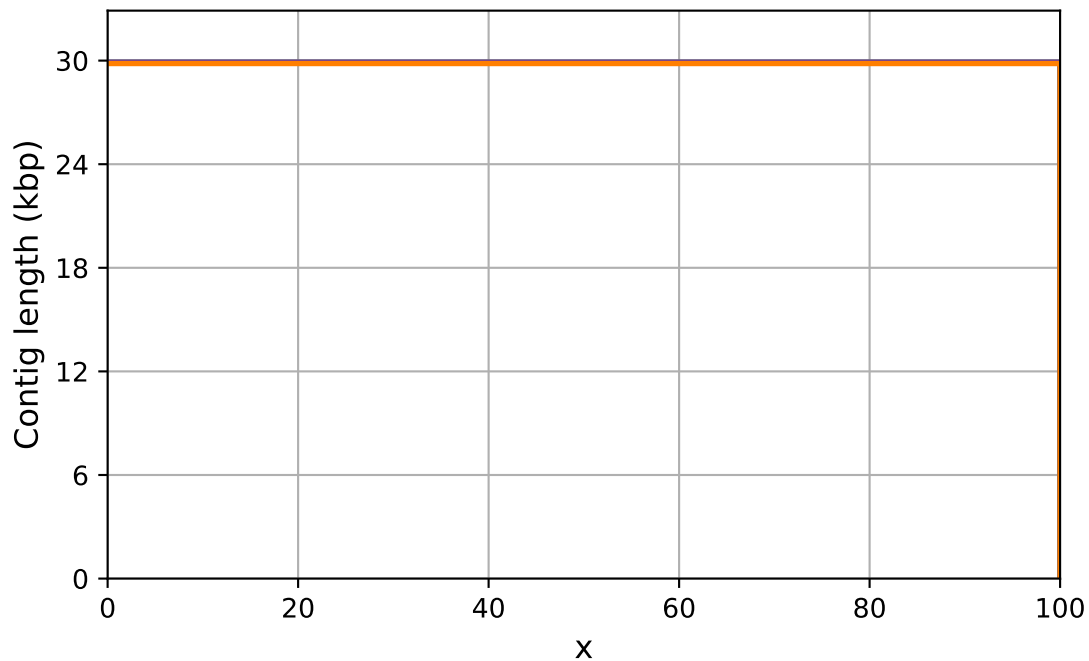|	ERR5743893.consensus	SRR13500958.consensus	ERR5405022.consensus	ERR5556343.consensus	ERR5181310.consensus
# contigs (>= 0 bp)	1	1	1	1	1
# contigs (>= 1000 bp)	1	1	1	1	1
# contigs (>= 5000 bp)	1	1	1	1	1
# contigs (>= 10000 bp)	1	1	1	1	1
# contigs (>= 25000 bp)	1	1	1	1	1
# contigs (>= 50000 bp)	0	0	0	0	0
Total length (>= 0 bp)	29902	29903	29884	29894	29830
Total length (>= 1000 bp)	29902	29903	29884	29894	29830
Total length (>= 5000 bp)	29902	29903	29884	29894	29830
Total length (>= 10000 bp)	29902	29903	29884	29894	29830
Total length (>= 25000 bp)	29902	29903	29884	29894	29830
Total length (>= 50000 bp)	0	0	0	0	0
# contigs	1	1	1	1	1
Largest contig	29902	29903	29884	29894	29830
Total length	29902	29903	29884	29894	29830
Reference length	29903	29903	29903	29903	29903
GC (%)	37.93	37.98	37.97	37.96	37.92
Reference GC (%)	37.97	37.97	37.97	37.97	37.97
N50	29902	29903	29884	29894	29830
NG50	29902	29903	29884	29894	29830
N90	29902	29903	29884	29894	29830
NG90	29902	29903	29884	29894	29830
auN	29902.0	29903.0	29884.0	29894.0	29830.0
auNG	29901.0	29903.0	29865.0	29885.0	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.	1	0	2	2	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 (%)	97.656	99.595	98.030	97.790	98.284
Duplication ratio	1.000	1.000	0.999	1.000	0.999
# N's per 100 kbp	2220.59	404.64	1977.65	2114.14	1354.34
# mismatches per 100 kbp	92.46	73.87	116.06	116.31	95.35
# indels per 100 kbp	3.42	0.00	13.65	3.42	17.03
# genomic features	19 + 4 part	21 + 3 part	17 + 7 part	17 + 7 part	19 + 4 part
Largest alignment	29201	29782	29295	29233	29366
Total aligned length	29201	29782	29295	29233	29366
NA50	29201	29782	29295	29233	29366
NGA50	29201	29782	29295	29233	29366
NA90	29201	29782	29295	29233	29366
NGA90	29201	29782	29295	29233	29366
auNA	28516.4	29661.5	28717.6	28586.6	28909.2
auNGA	28515.5	29661.5	28699.4	28578.0	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
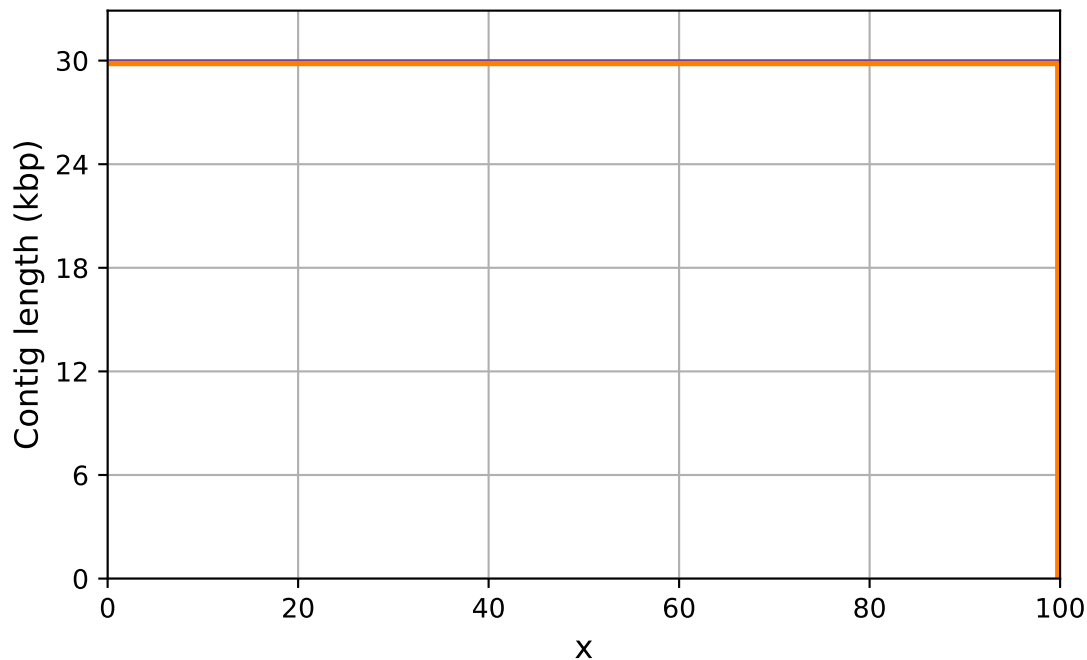
	ERR5743893.consensus	SRR13500958.consensus	ERR5405022.consensus	ERR5556343.consensus	ERR5181310.consensus
# misassemblies	0	0	0	0	0
# contig misassemblies	0	0	0	0	0
# c. relocations	0	0	0	0	0
# c. translocations	0	0	0	0	0
# c. inversions	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0
# s. relocations	0	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.	1	0	2	2	1
# unaligned mis. contigs	0	0	0	0	0
# mismatches	27	22	34	34	28
# indels	1	0	4	1	5
# indels (<= 5 bp)	1	0	2	0	3
# indels (> 5 bp)	0	0	2	1	2
Indels length	1	0	19	9	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

	ERR5743893.consensus	SRR13500958.consensus	ERR5405022.consensus	ERR5556343.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	664	121	591	632	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

Cumulative length

Contig index

Cumulative length (kbp)
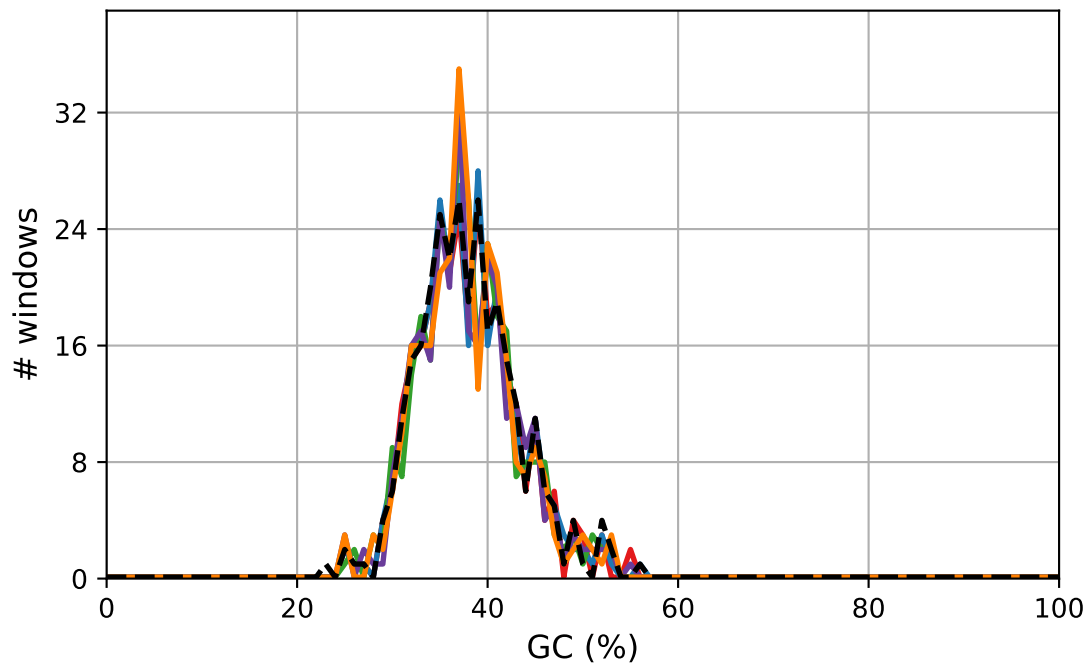
ERR5743893.consensus	ERR5405022.consensus	ERR5181310.consen
SRR13500958.consensus	ERR5556343.consensus	Reference

GC content

ERR5743893.consensus	ERR5405022.consensus
SRR13500958.consensus	ERR5556343.consensus
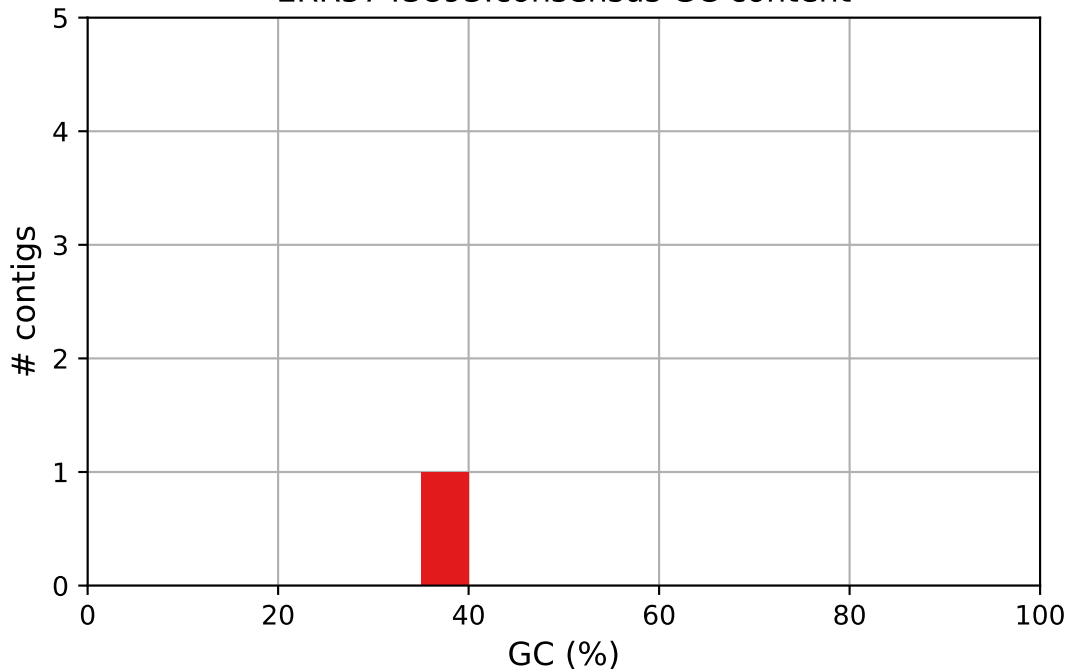
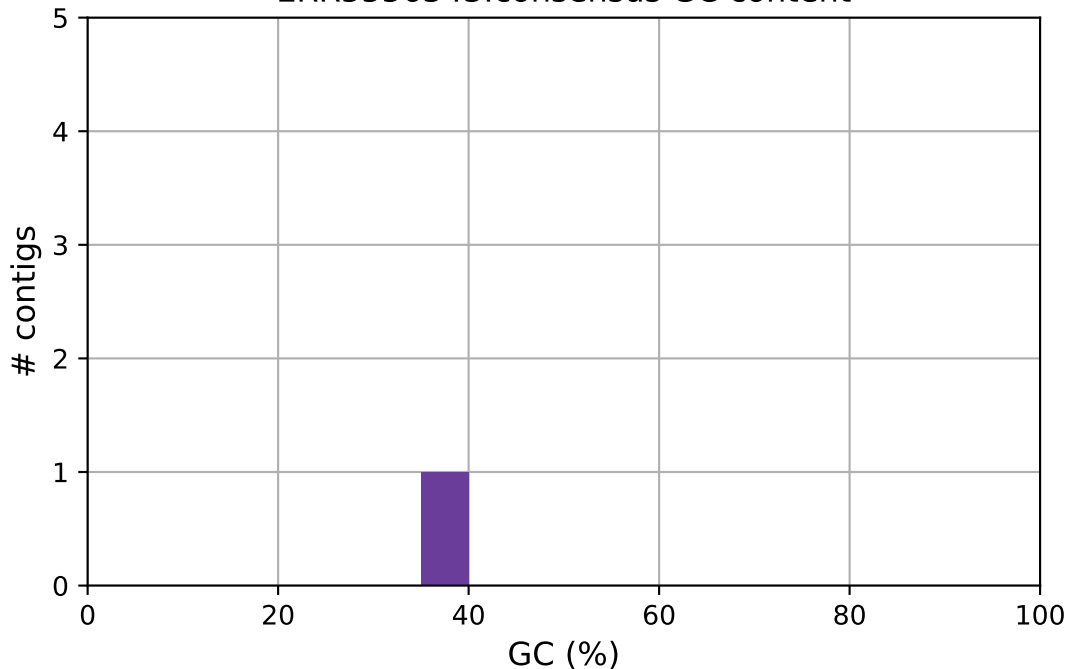ERR5743893.consensus GC content

SRR13500958.consensus GC content
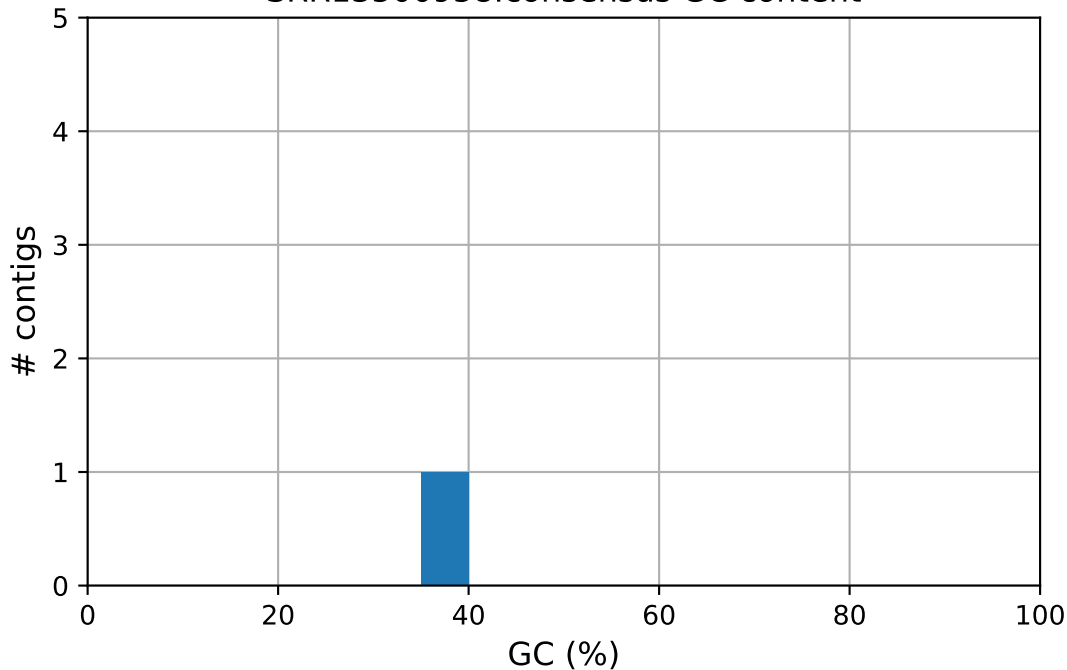
ERR5405022.consensus GC content
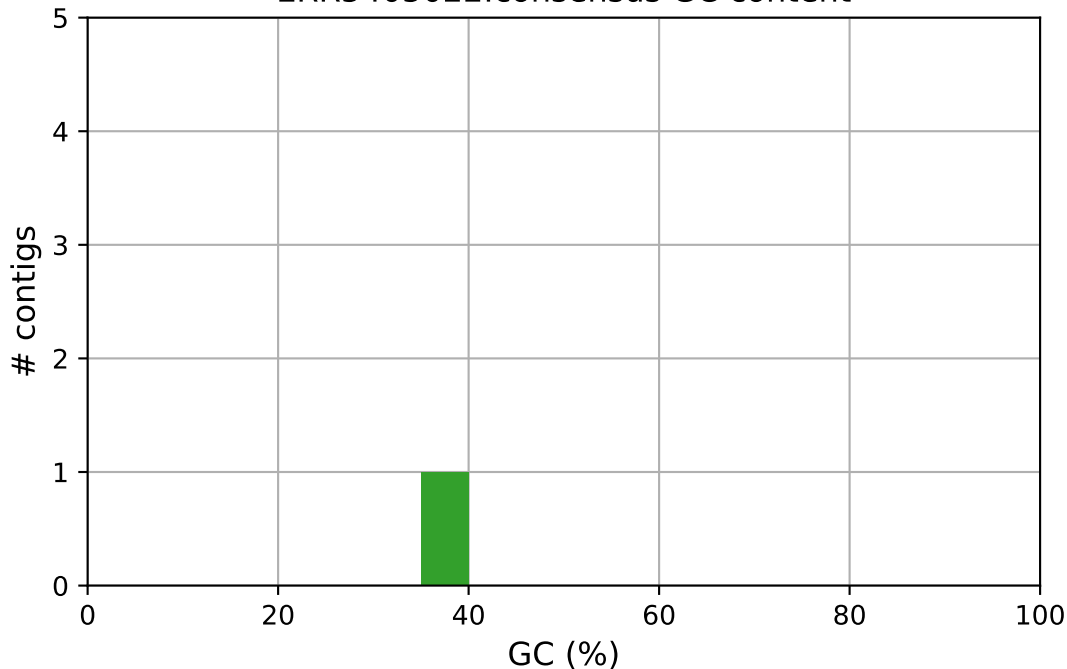
ERR5556343.consensus GC content

ERR5181310.consensus GC content
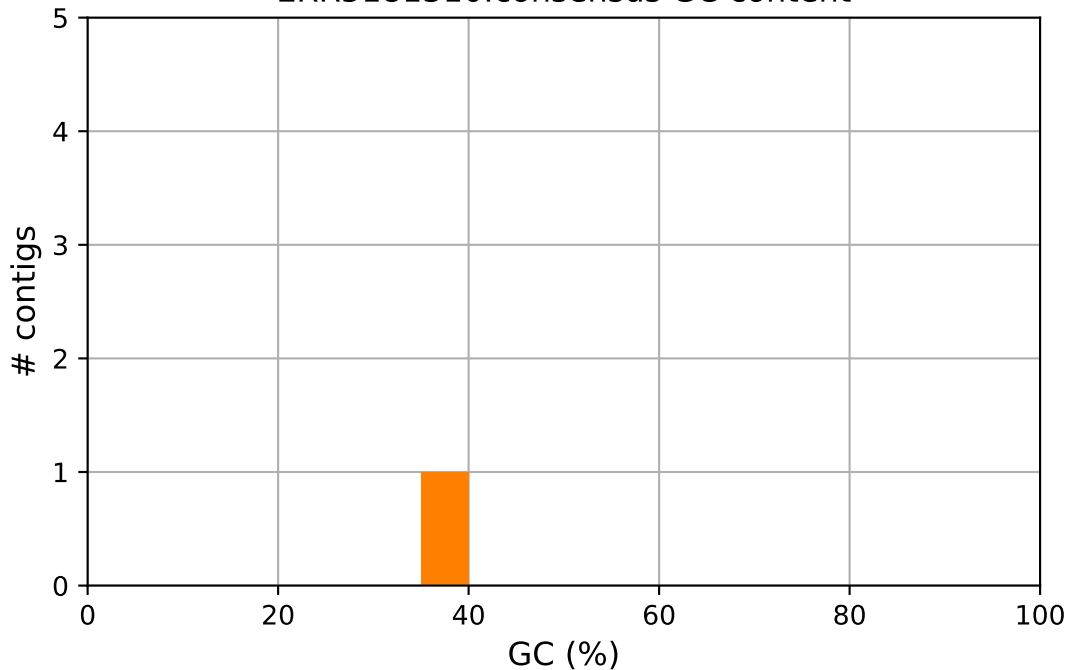
Misassemblies
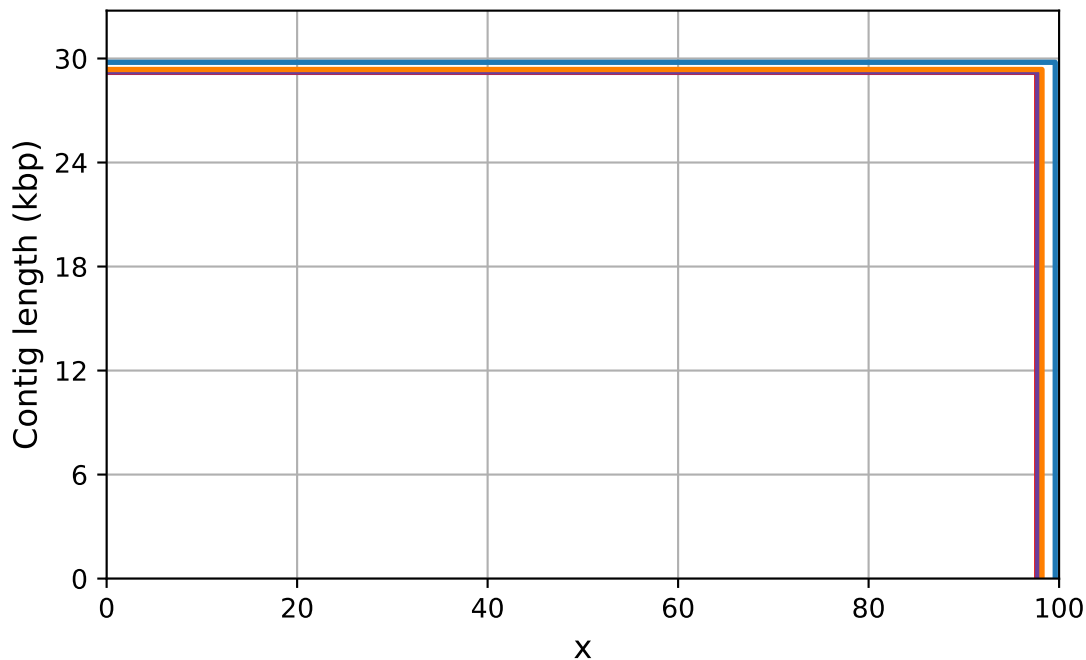
FRCurve (misassemblies)

Genome coverage (%)

Feature space

ERR5743893.consensus — ERR5405022.consensus — ERR5181310.consen
SRR13500958.consensus — ERR5556343.consensus
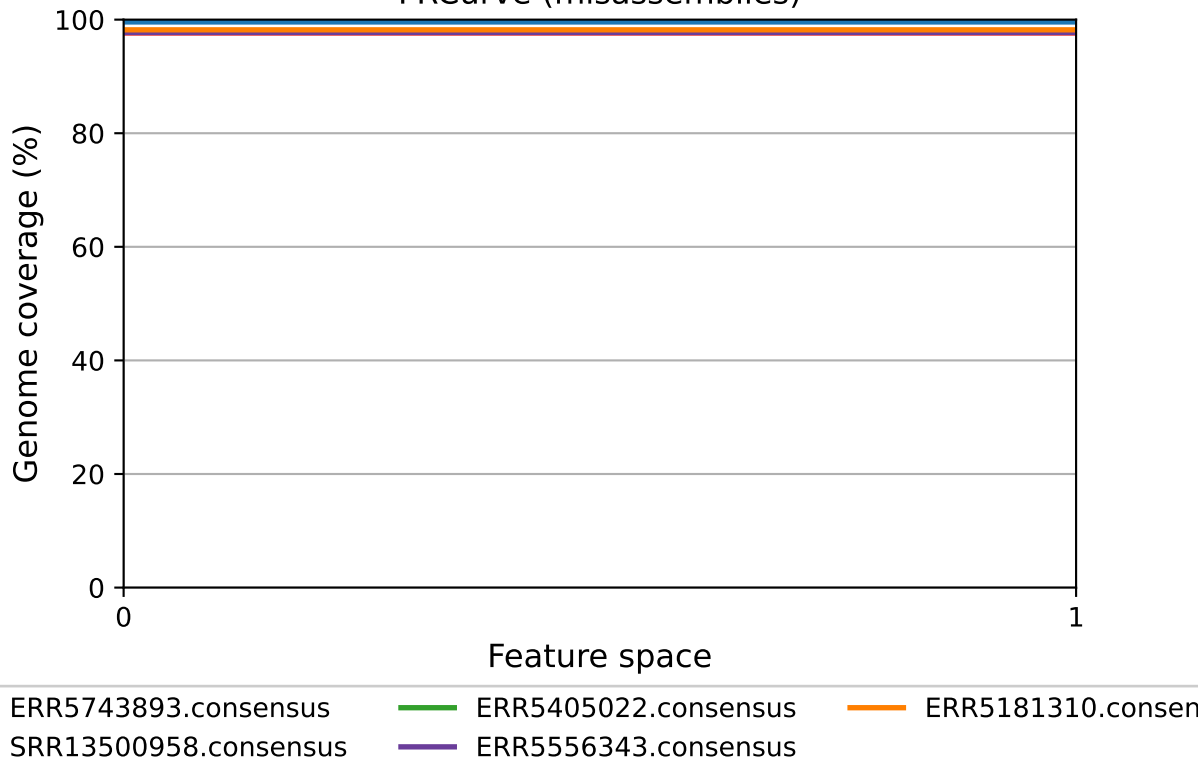
Cumulative length (aligned contigs)
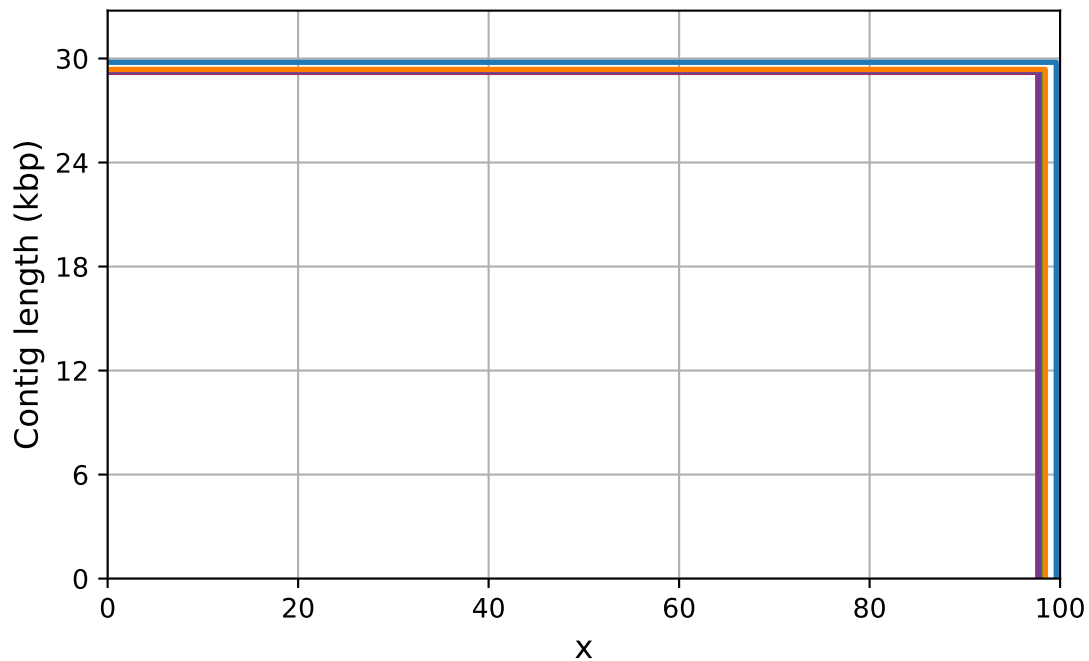
ERR5743893.consensus
SRR13500958.consensus
ERR5405022.consensus
ERR5556343.consensus
ERR5181310.consen
Reference

NAx

NGAx

Contig length (kbp)

x

ERR5743893.consensus
ERR5405022.consensus
ERR5181310.consen
SRR13500958.consensus
ERR5556343.consensus

Cumulative # complete genomic features

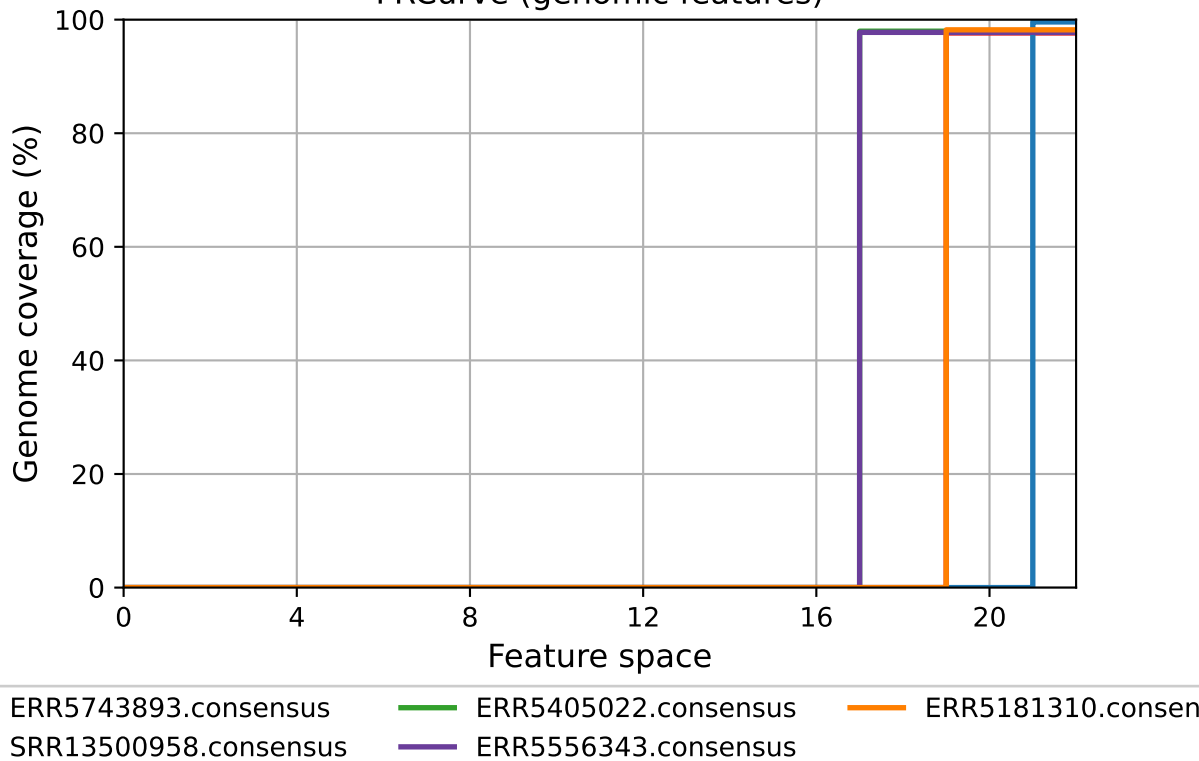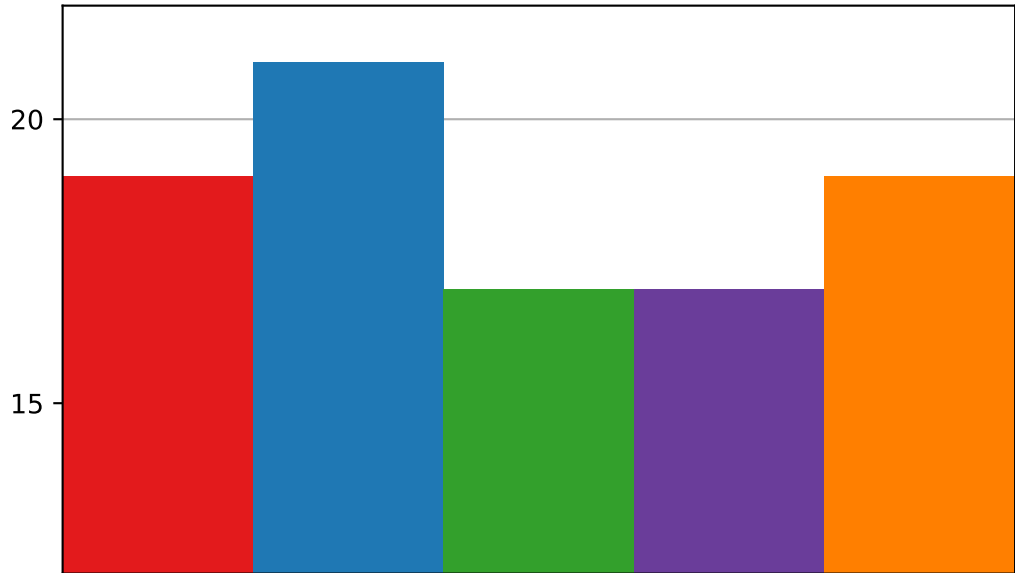|	
ERR5743893.consensus	ERR5405022.consensus
SRR13500958.consensus	ERR5556343.consensus
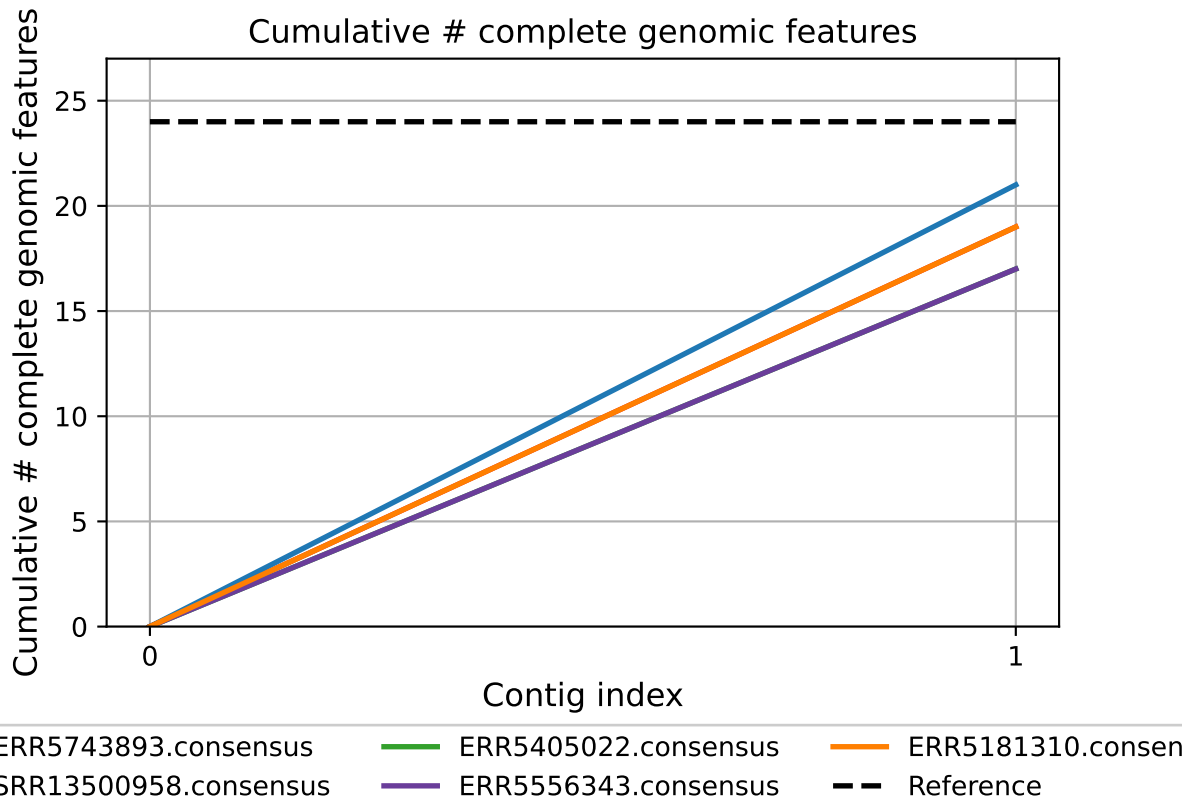
FRCurve (genomic features)

Feature space

Genome coverage (%)

ERR5743893.consensus ERR5405022.consensus ERR5181310.consen

SRR13500958.consensus ERR5556343.consensus

complete genomic features

ERR5743893.consensus
SRR13500958.consensus
ERR5405022.consensus
ERR5556343.consensus
ERR5181310.consen

Genome fraction, %

ERR5743893.consensus
SRR13500958.consensus
ERR5405022.consensus
ERR5556343.consensus
ERR5181310.consen