

Report

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

	SRR13500958.consensus	ERR5556343.consensus	ERR5405022.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.	0	2	2	1	1
# unaligned mis. contigs	0	0	0	0	0
# mismatches	22	34	34	27	28
# indels	0	1	4	1	5
# indels (<= 5 bp)	0	0	2	1	3
# indels (> 5 bp)	0	1	2	0	2
Indels length	0	9	19	1	24

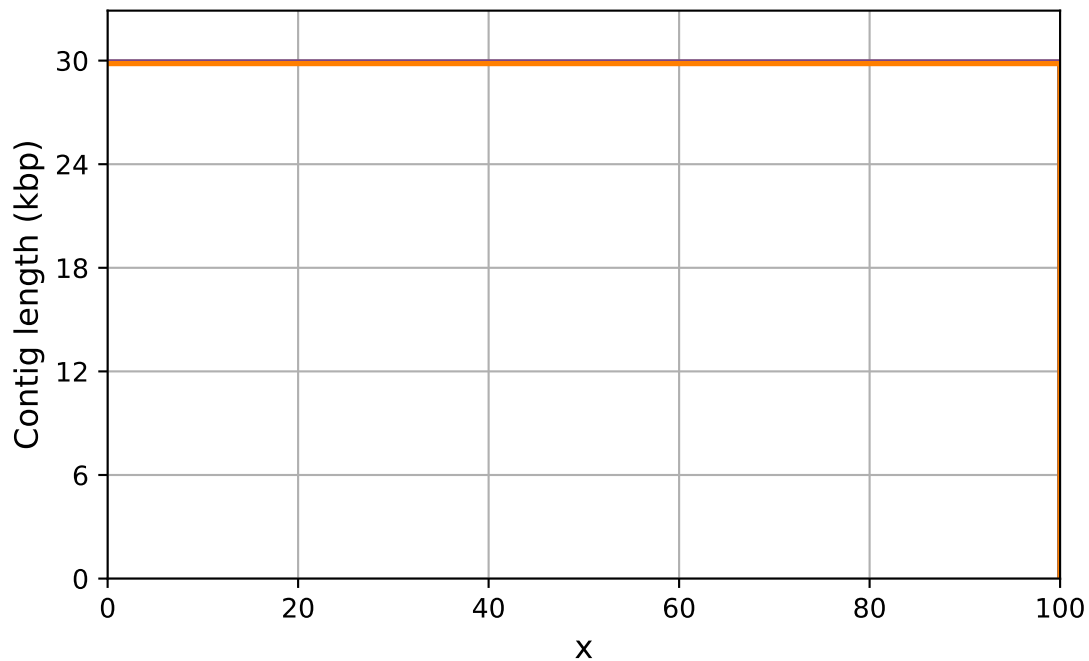
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	SRR13500958.consensus	ERR5556343.consensus	ERR5405022.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	121	632	591	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



SRR13500958.consensus

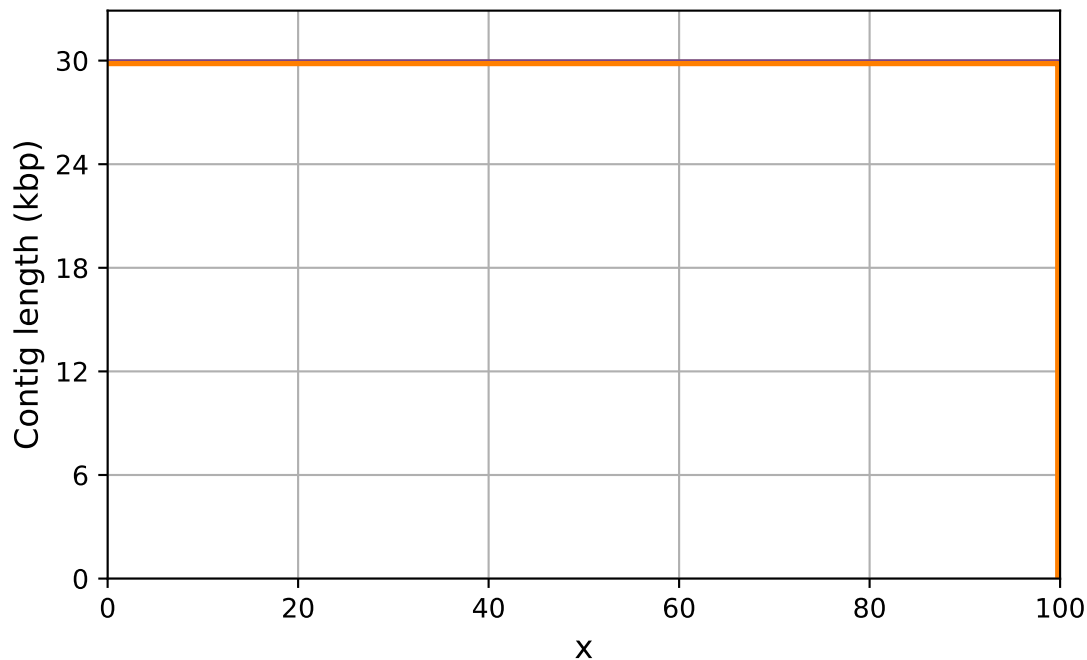
ERR5405022.consensus

ERR5181310.consensus

ERR5556343.consensus

ERR5743893.consensus

NGx



SRR13500958.consensus

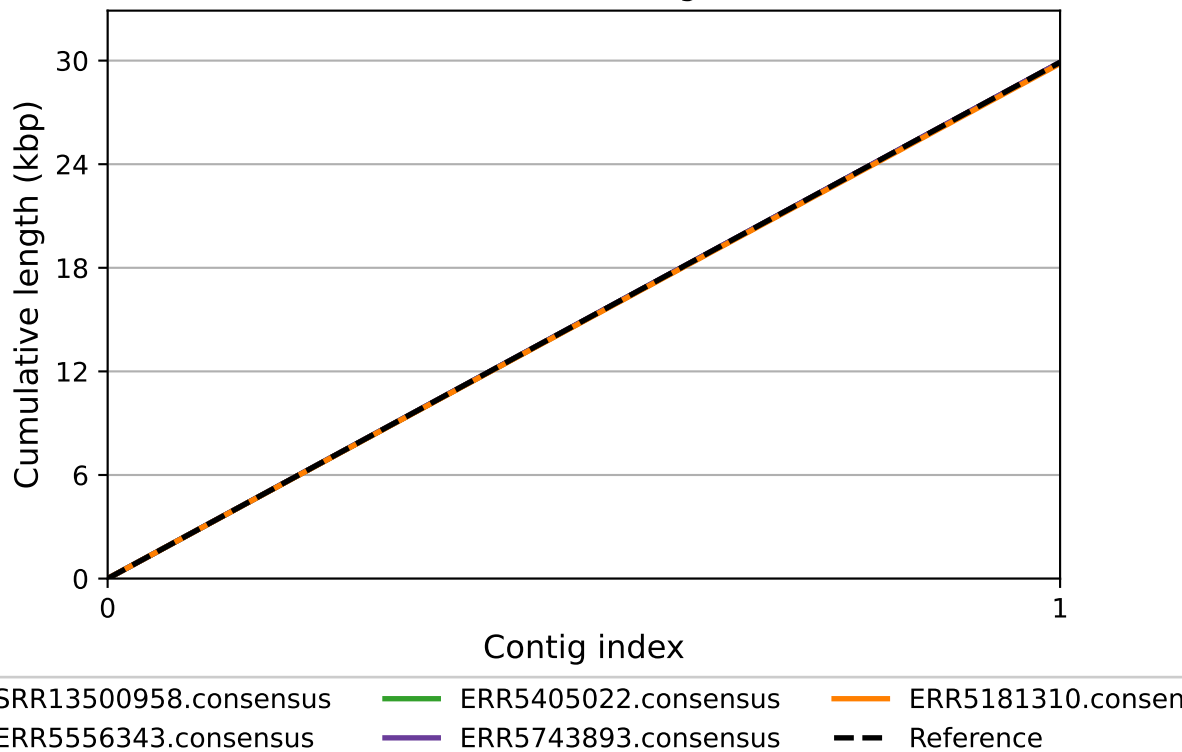
ERR5405022.consensus

ERR5181310.consensus

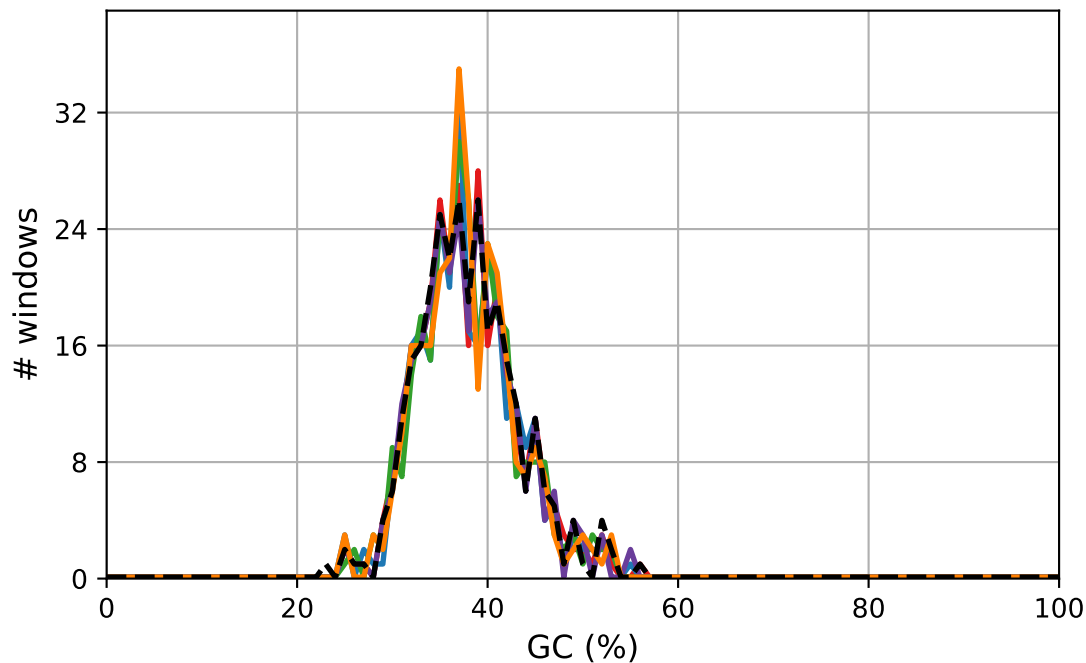
ERR5556343.consensus

ERR5743893.consensus

Cumulative length

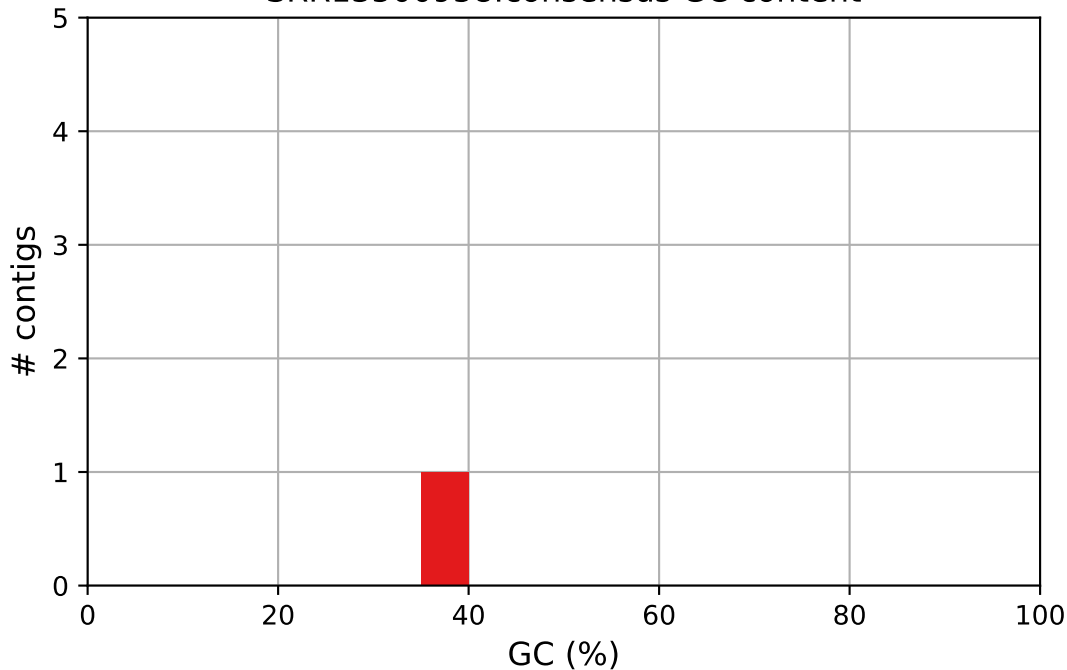


GC content



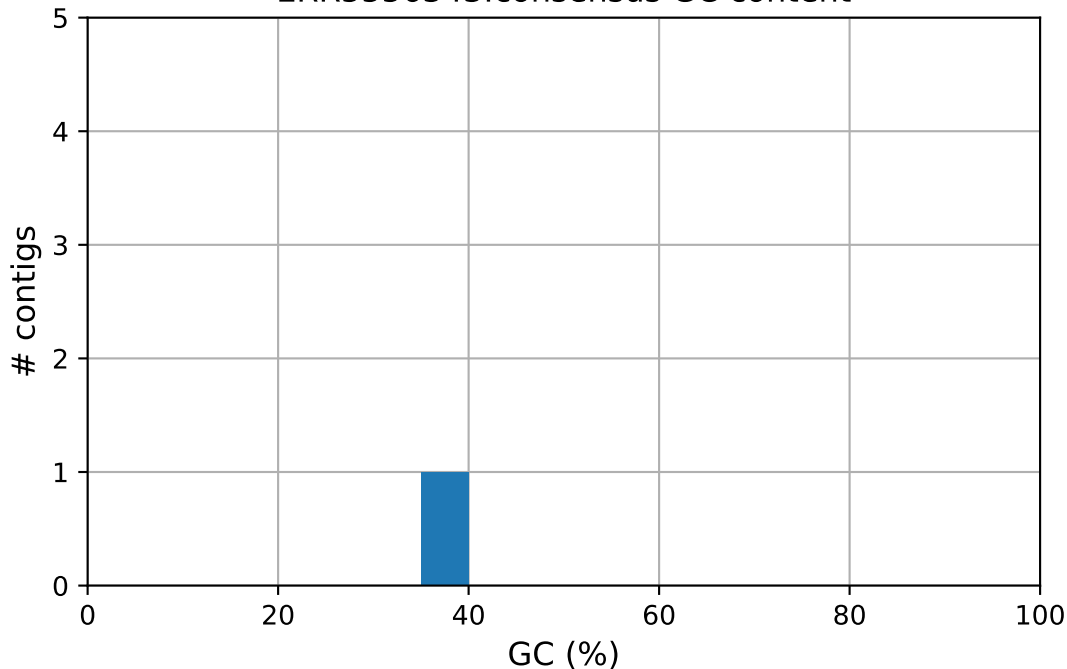
SRR13500958.consensus ERR5405022.consensus ERR5181310.consensus
ERR5556343.consensus ERR5743893.consensus Reference

SRR13500958.consensus GC content



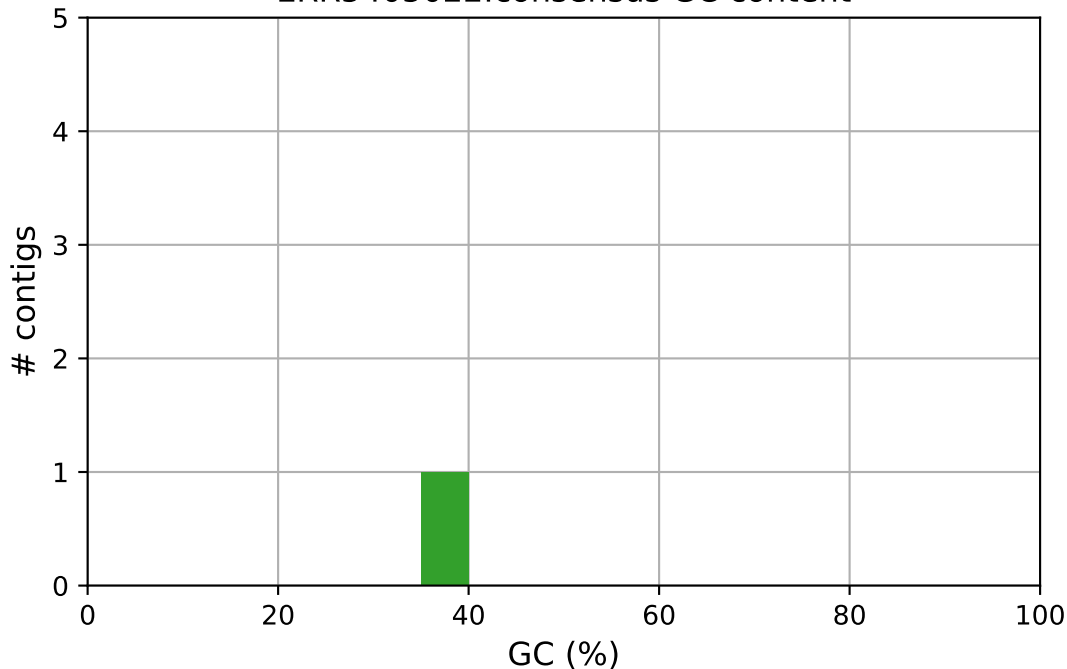
 SRR13500958.consensus

ERR5556343.consensus GC content



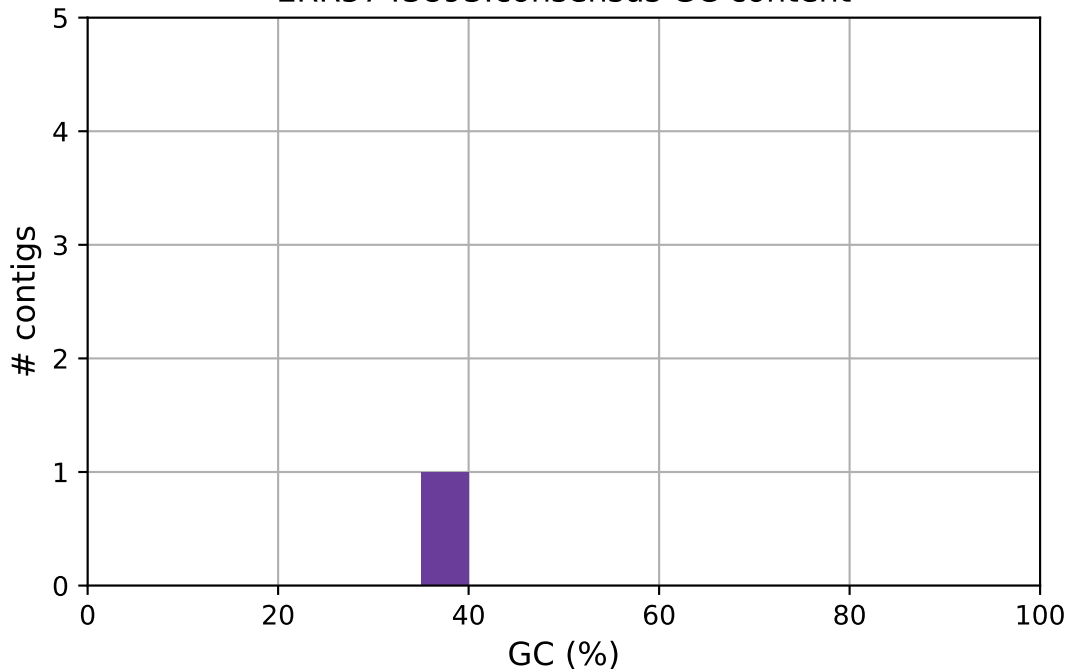
ERR5556343.consensus

ERR5405022.consensus GC content



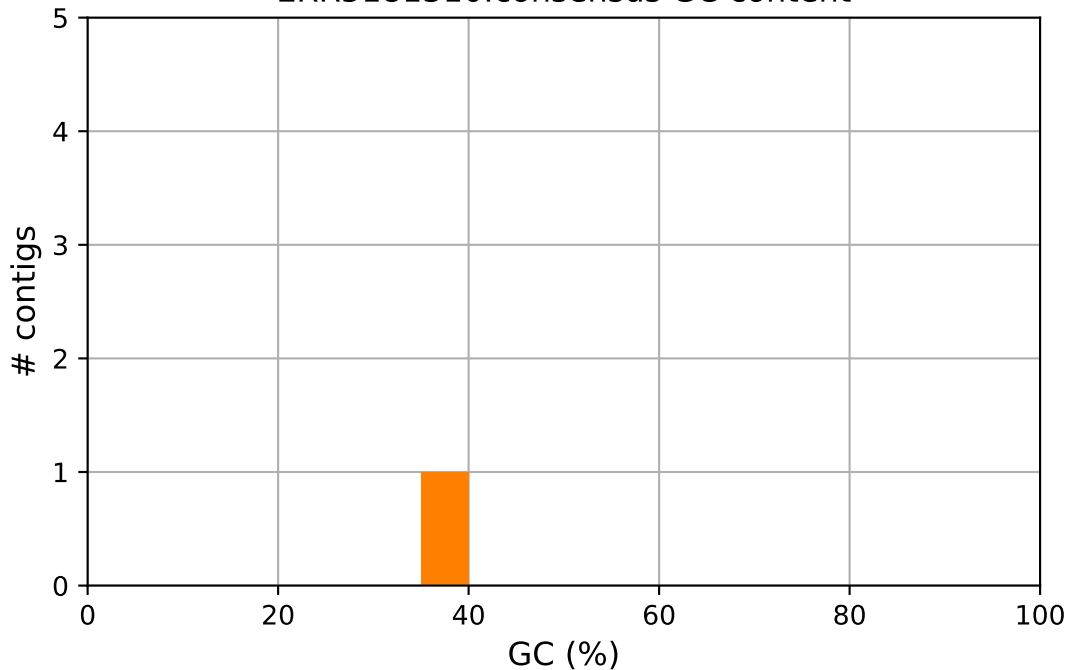
ERR5405022.consensus

ERR5743893.consensus GC content



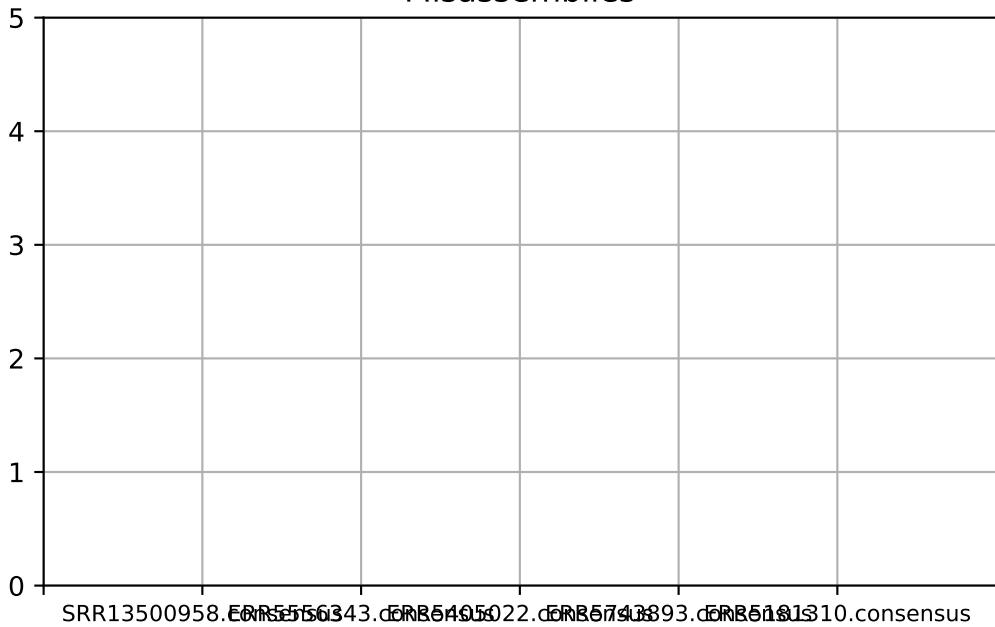
ERR5743893.consensus

ERR5181310.consensus GC content

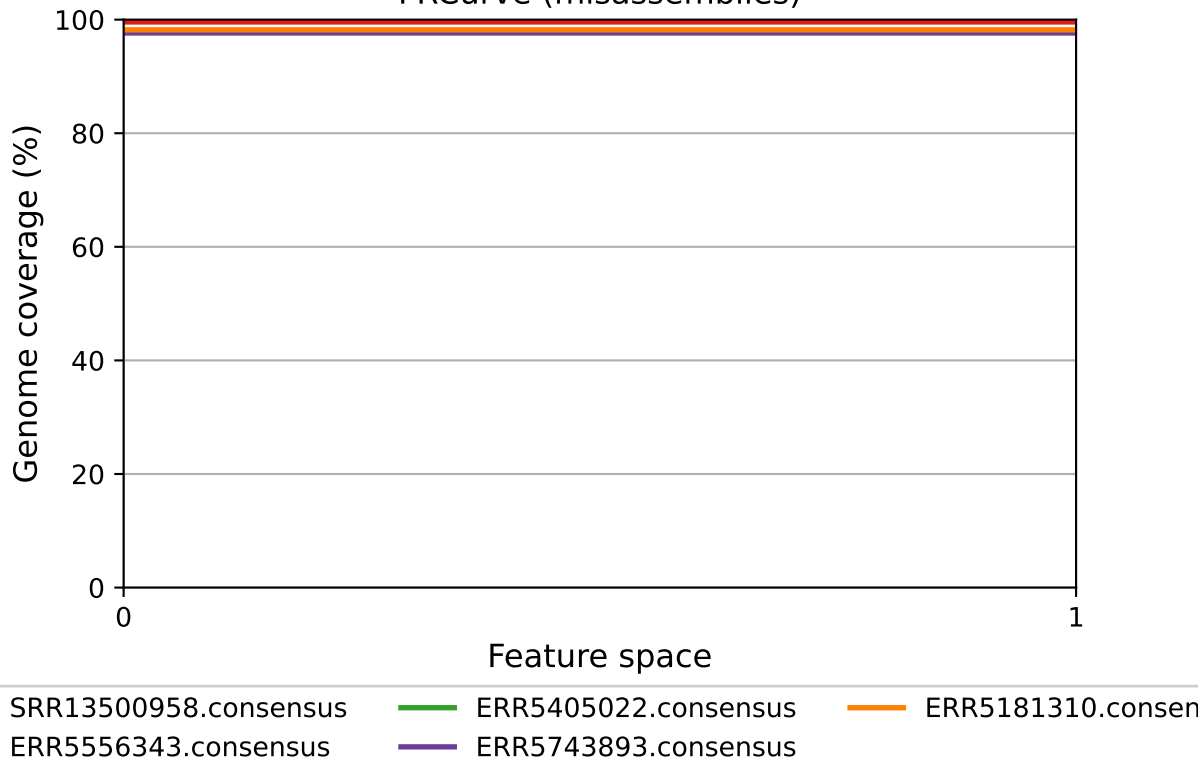


ERR5181310.consensus

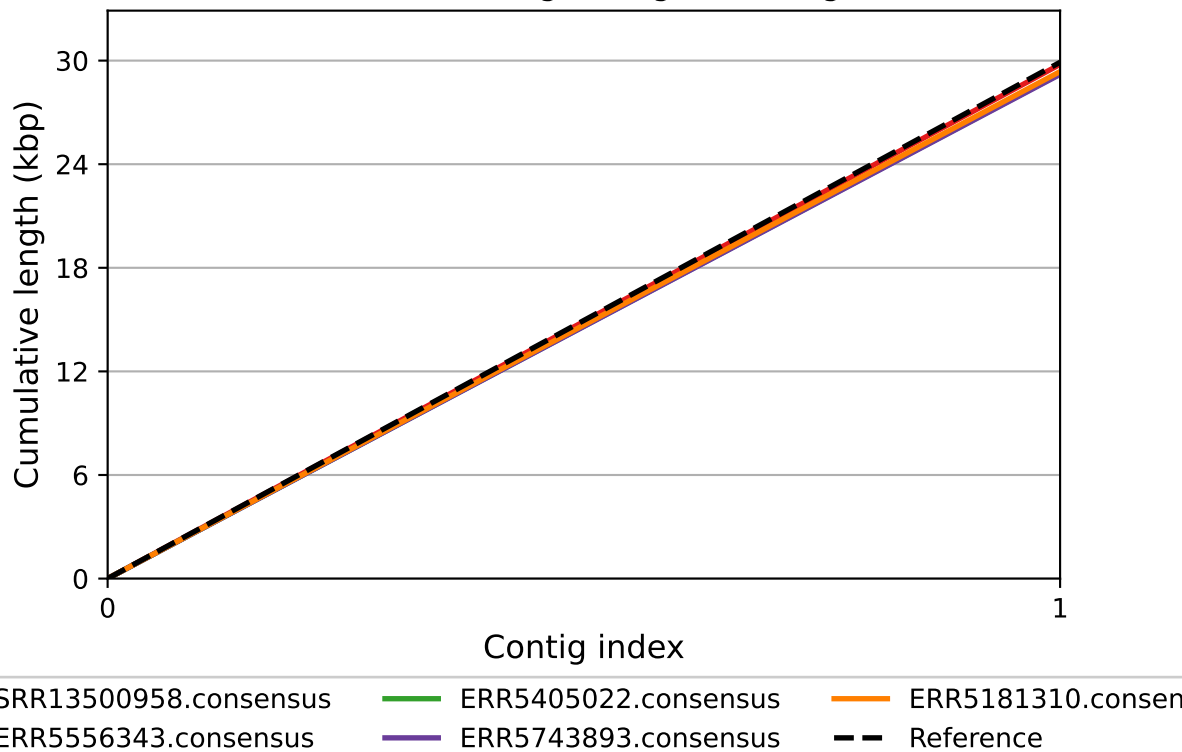
Misassemblies



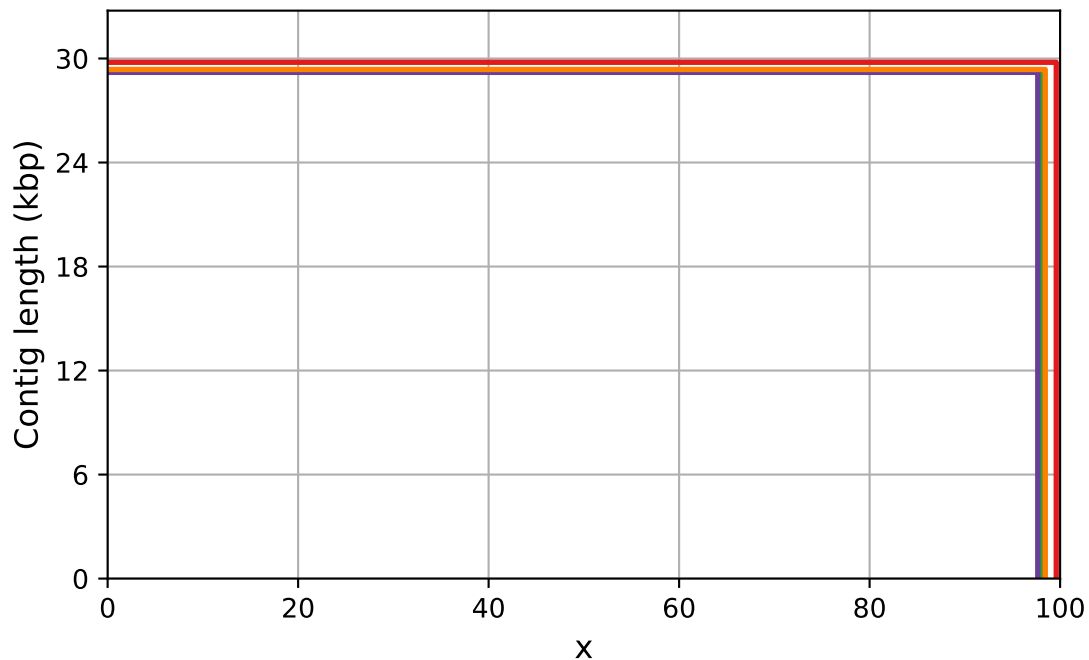
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



SRR13500958.consensus

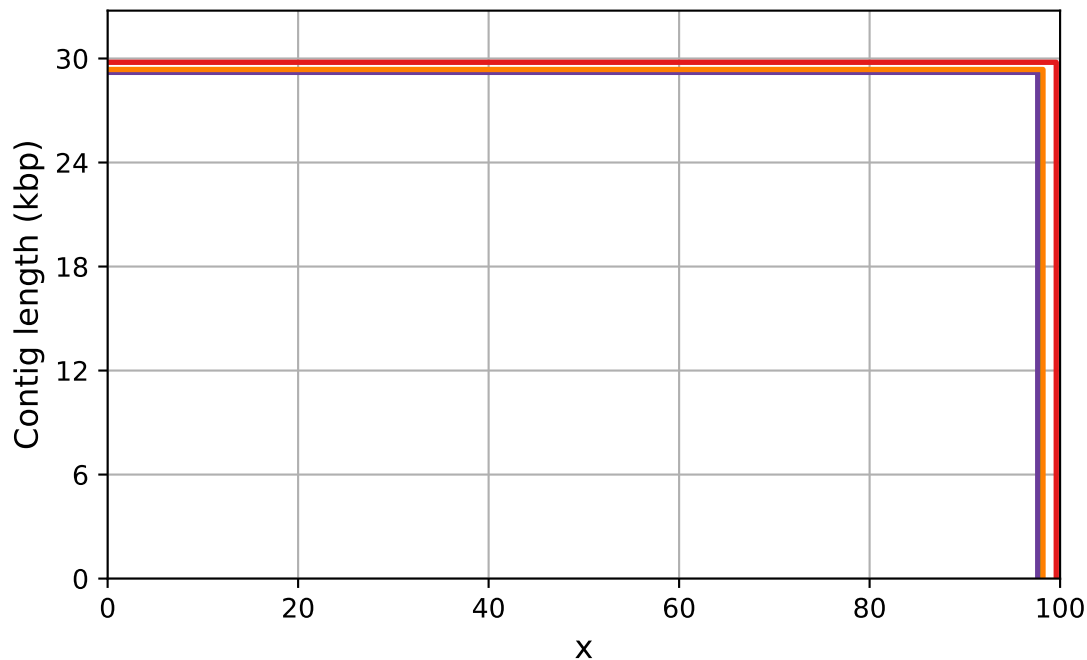
ERR5405022.consensus

ERR5181310.consensus

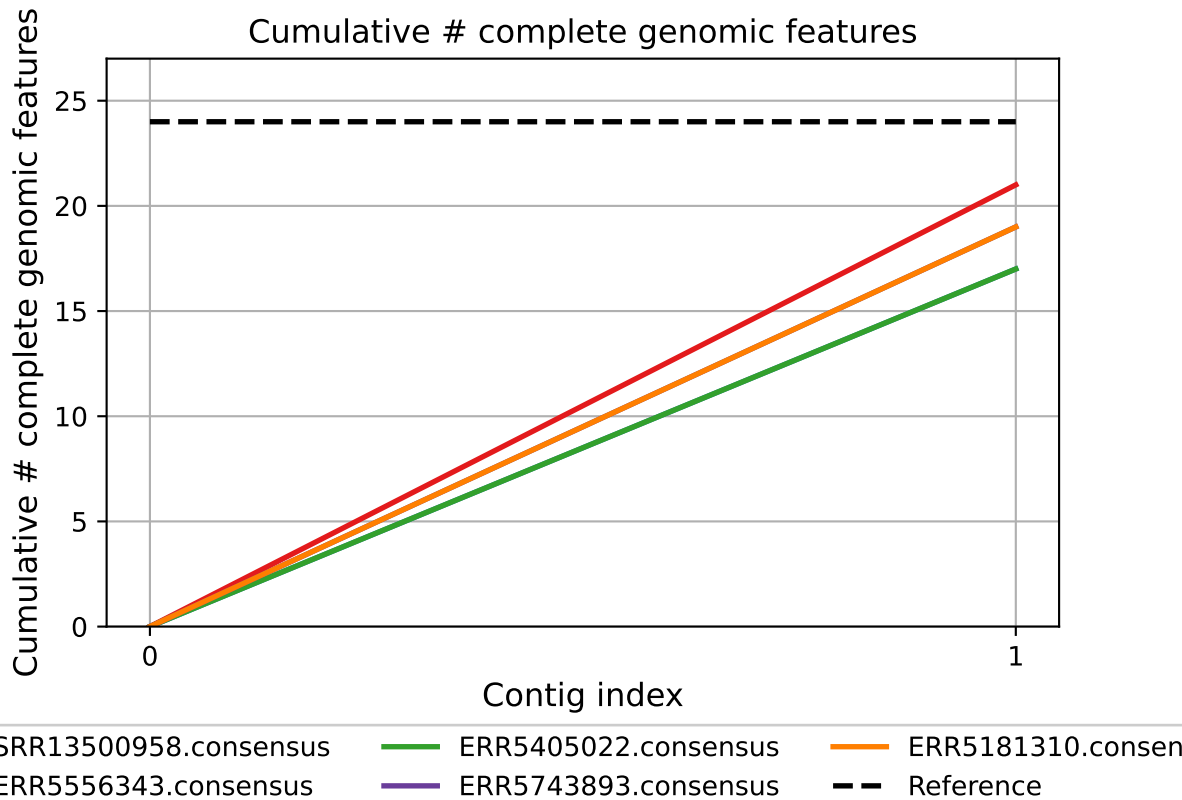
ERR5556343.consensus

ERR5743893.consensus

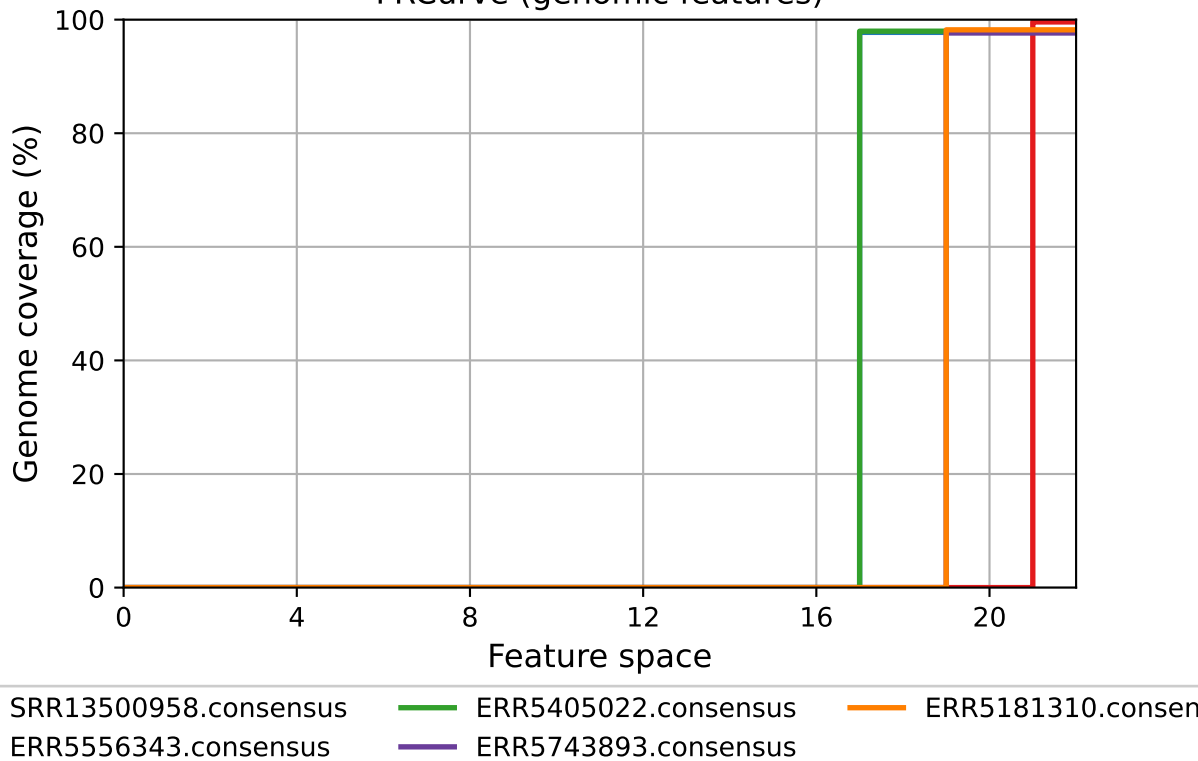
NGAx



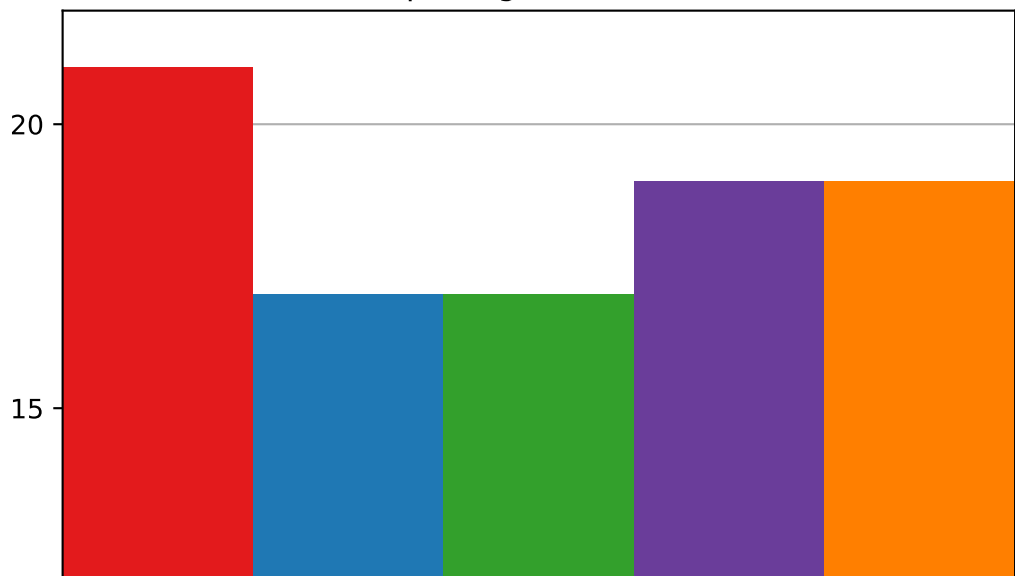
— SRR13500958.consensus — ERR5405022.consensus — ERR5181310.consensus
— ERR5556343.consensus — ERR5743893.consensus



FRCurve (genomic features)



complete genomic features



SRR13500958.consensus

ERR5405022.consensus

ERR5181310.consensus

ERR5556343.consensus

ERR5743893.consensus

Genome fraction, %

100

95

