

Report

	ERR5743893.consensus	ERR5556343.consensus	SRR13500958.consensus	ERR5181310.consensus	ERR5405022.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	29894	29903	29830	29884
Total length (>= 1000 bp)	29902	29894	29903	29830	29884
Total length (>= 5000 bp)	29902	29894	29903	29830	29884
Total length (>= 10000 bp)	29902	29894	29903	29830	29884
Total length (>= 25000 bp)	29902	29894	29903	29830	29884
Total length (>= 50000 bp)	0	0	0	0	0
# contigs	1	1	1	1	1
Largest contig	29902	29894	29903	29830	29884
Total length	29902	29894	29903	29830	29884
Reference length	29903	29903	29903	29903	29903
GC (%)	37.93	37.96	37.98	37.92	37.97
Reference GC (%)	37.97	37.97	37.97	37.97	37.97
N50	29902	29894	29903	29830	29884
NG50	29902	29894	29903	29830	29884
N90	29902	29894	29903	29830	29884
NG90	29902	29894	29903	29830	29884
auN	29902.0	29894.0	29903.0	29830.0	29884.0
auNG	29901.0	29885.0	29903.0	29757.2	29865.0
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	2	0	1	2
# 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	97.790	99.595	98.284	98.030
Duplication ratio	1.000	1.000	1.000	0.999	0.999
# N's per 100 kbp	2220.59	2114.14	404.64	1354.34	1977.65
# mismatches per 100 kbp	92.46	116.31	73.87	95.35	116.06
# indels per 100 kbp	3.42	3.42	0.00	17.03	13.65
# genomic features	19 + 4 part	17 + 7 part	21 + 3 part	19 + 4 part	17 + 7 part
Largest alignment	29201	29233	29782	29366	29295
Total aligned length	29201	29233	29782	29366	29295
NA50	29201	29233	29782	29366	29295
NGA50	29201	29233	29782	29366	29295
NA90	29201	29233	29782	29366	29295
NGA90	29201	29233	29782	29366	29295
auNA	28516.4	28586.6	29661.5	28909.2	28717.6
auNGA	28515.5	28578.0	29661.5	28838.6	28699.4
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	ERR5556343.consensus	SRR13500958.consensus	ERR5181310.consensus	ERR5405022.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	2	0	1	2
# unaligned mis. contigs	0	0	0	0	0
# mismatches	27	34	22	28	34
# indels	1	1	0	5	4
# indels (<= 5 bp)	1	0	0	3	2
# indels (> 5 bp)	0	1	0	2	2
Indels length	1	9	0	24	19

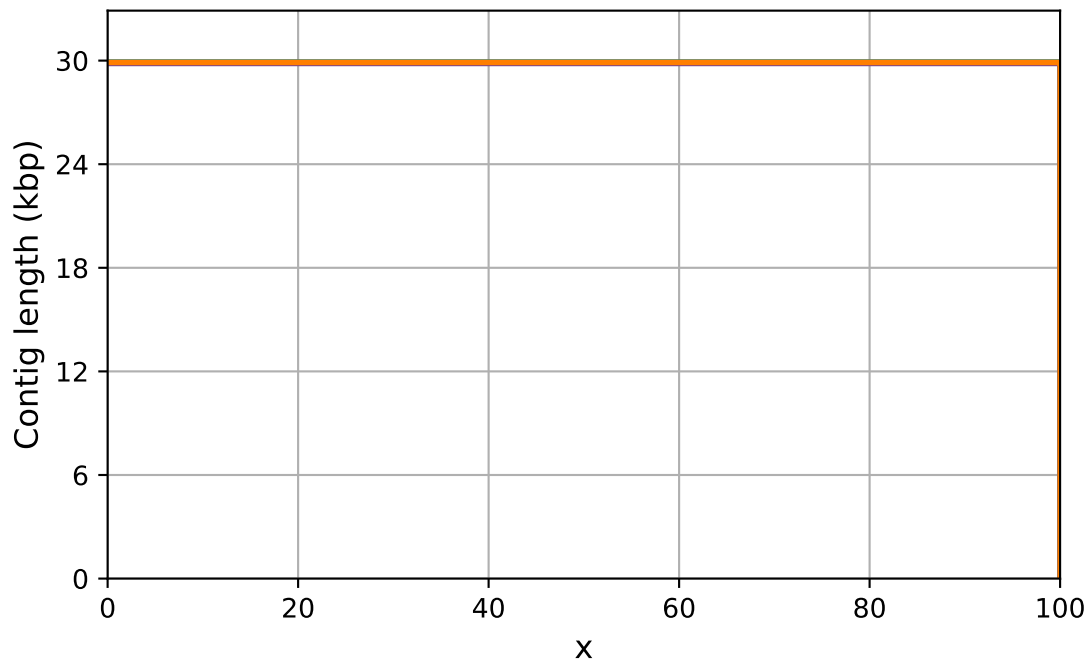
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	ERR5743893.consensus	ERR5556343.consensus	SRR13500958.consensus	ERR5181310.consensus	ERR5405022.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	632	121	404	591

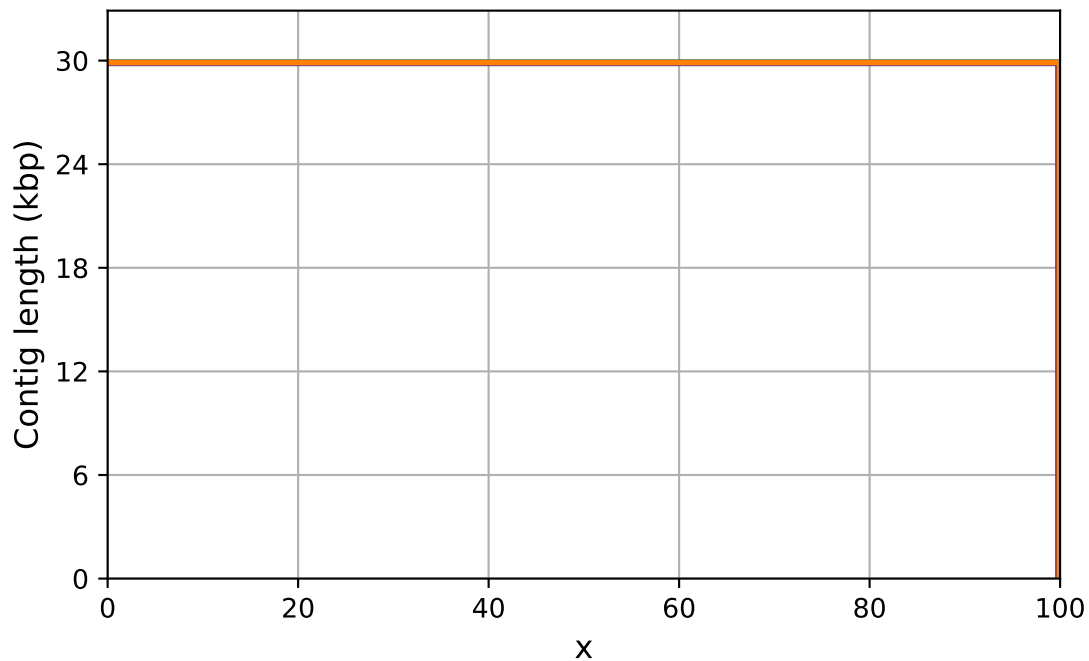
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



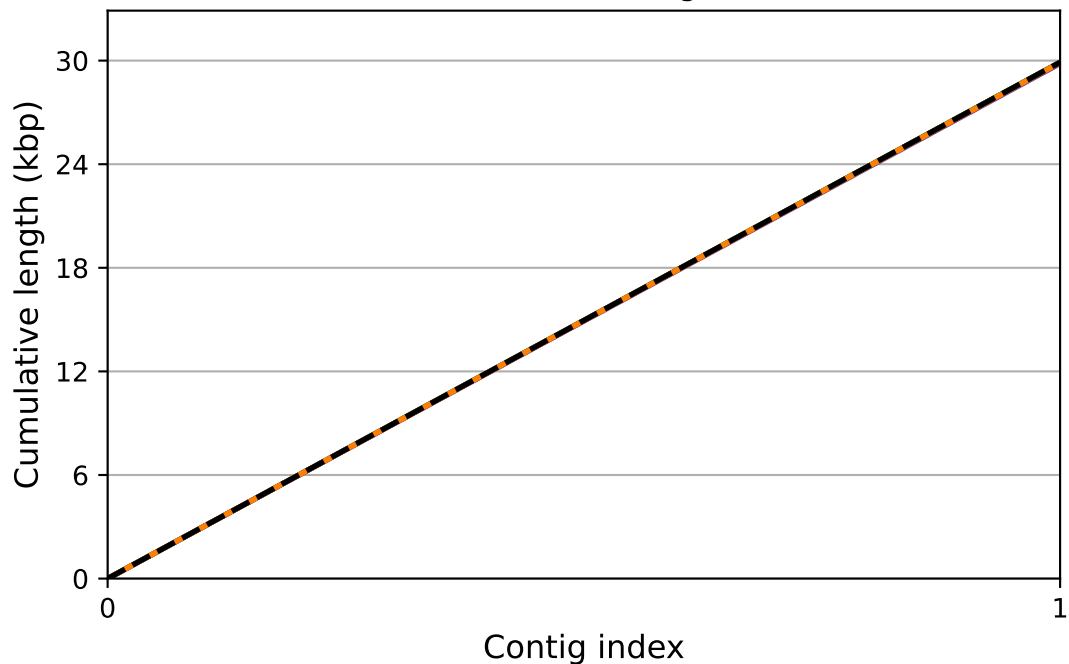
ERR5743893.consensus SRR13500958.consensus ERR5405022.consensus
ERR5556343.consensus ERR5181310.consensus

NGx



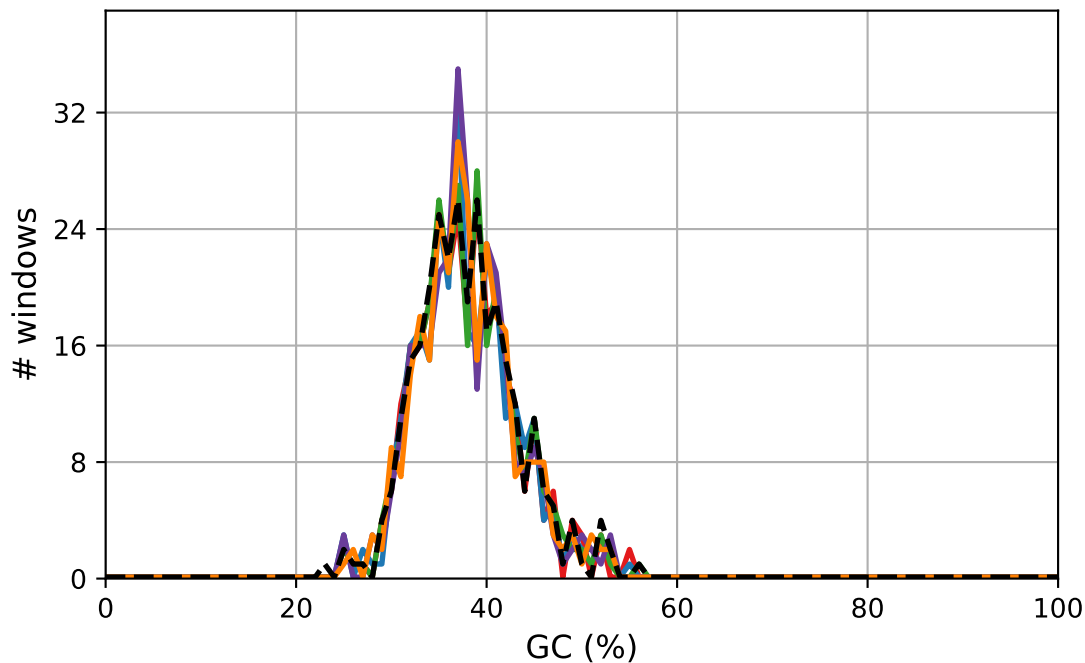
ERR5743893.consensus SRR13500958.consensus ERR5405022.consensus
ERR5556343.consensus ERR5181310.consensus

Cumulative length



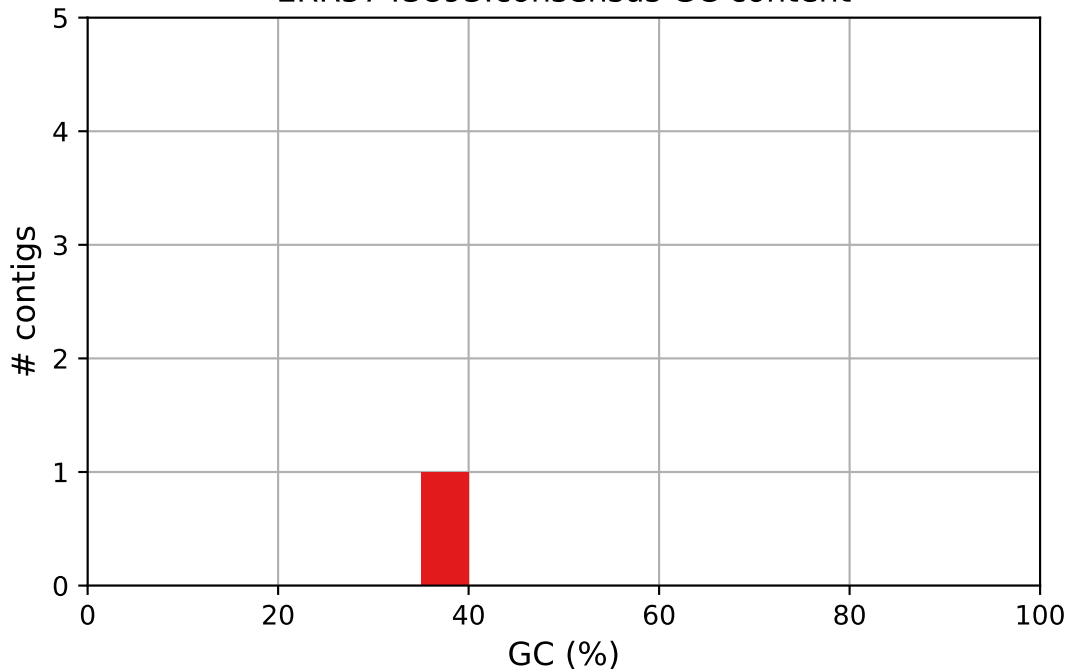
ERR5743893.consensus SRR13500958.consensus ERR5405022.consensus
ERR5556343.consensus ERR5181310.consensus Reference

GC content



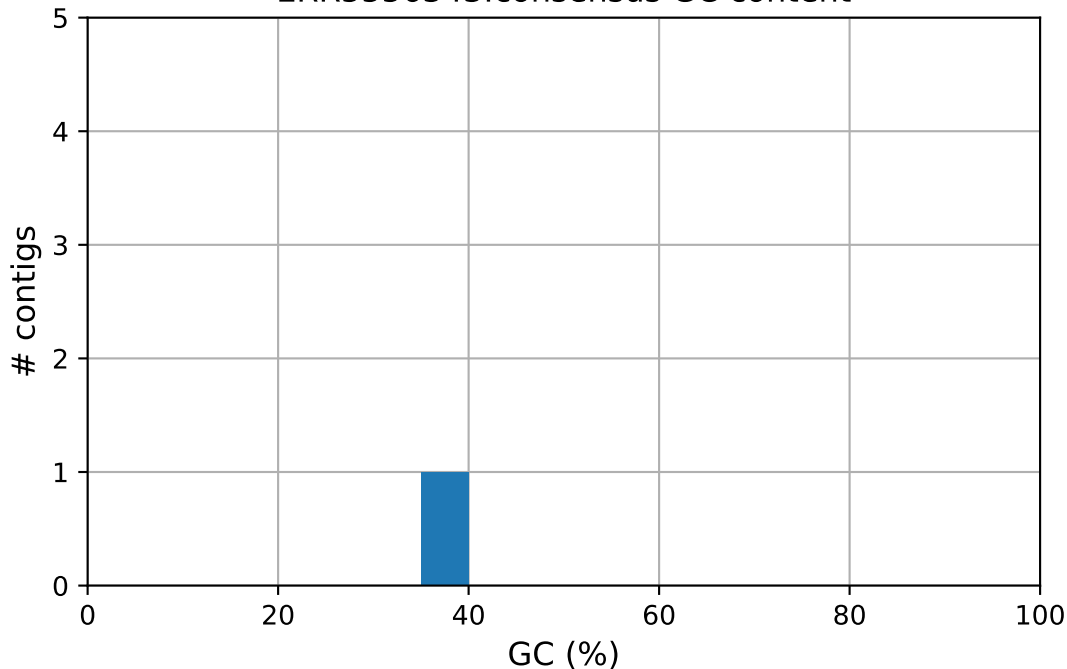
ERR5743893.consensus SRR13500958.consensus ERR5405022.consensus
ERR5556343.consensus ERR5181310.consensus Reference

ERR5743893.consensus GC content



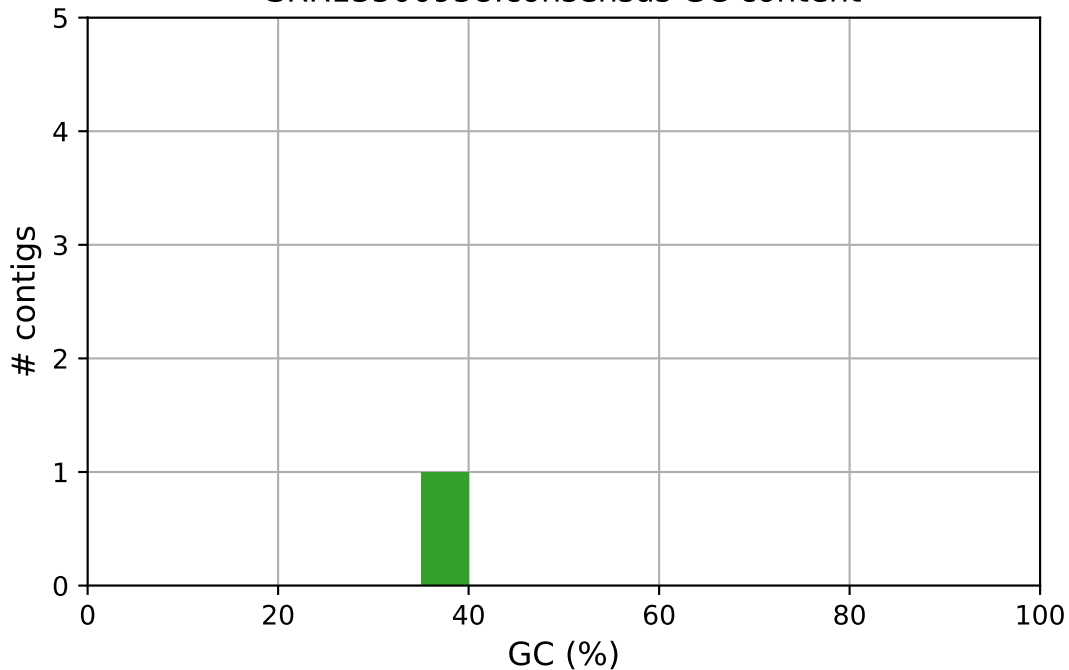
ERR5743893.consensus

ERR5556343.consensus GC content



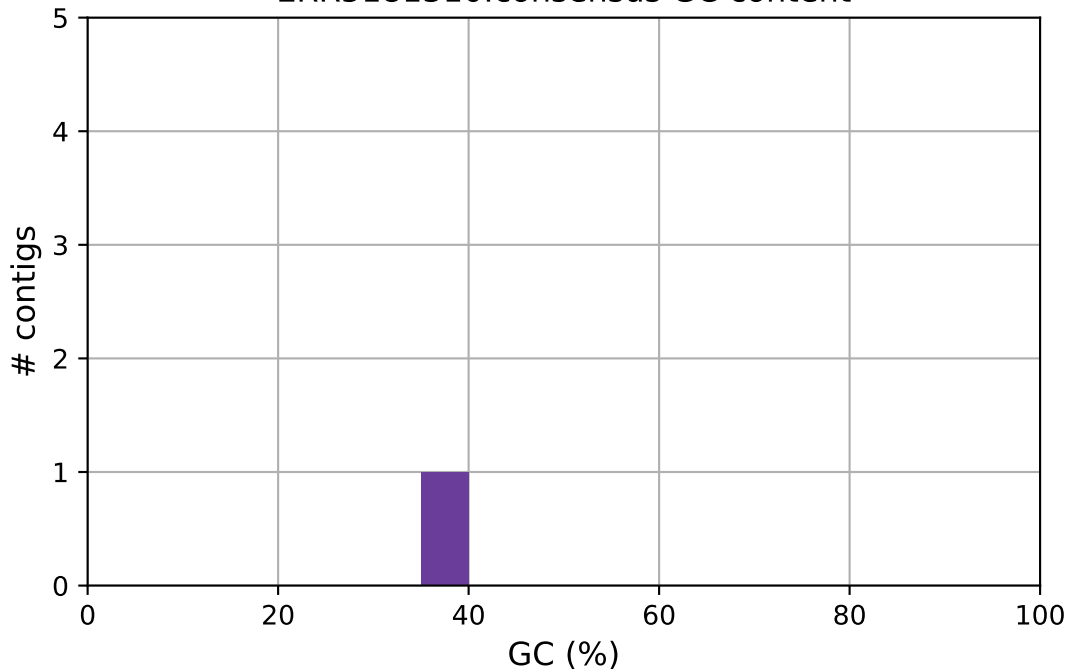
ERR5556343.consensus

SRR13500958.consensus GC content



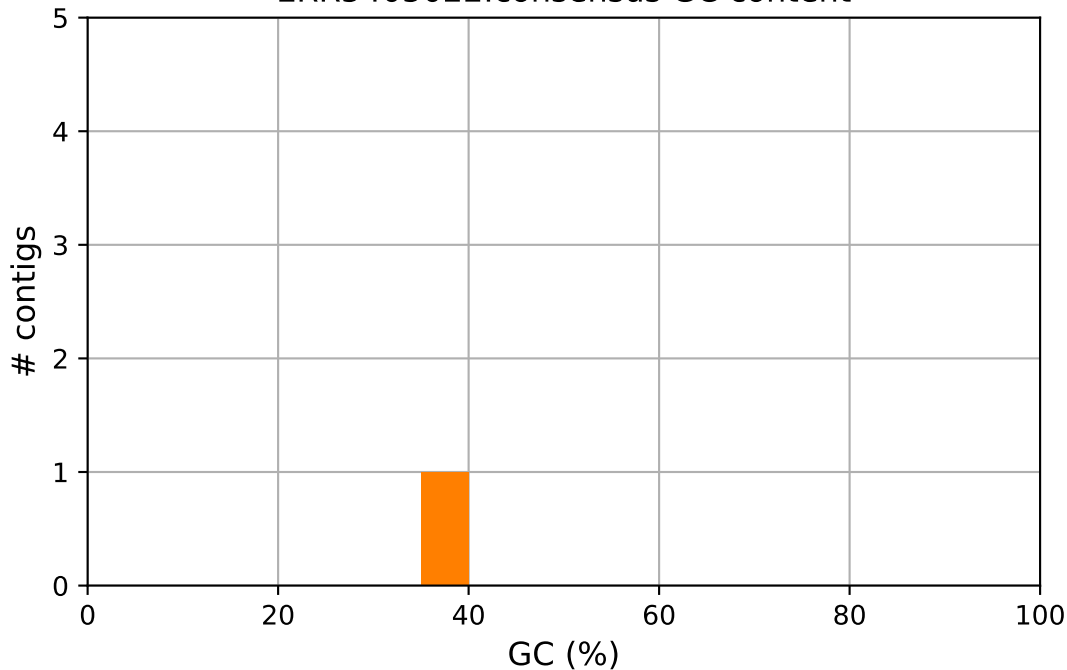
 SRR13500958.consensus

ERR5181310.consensus GC content



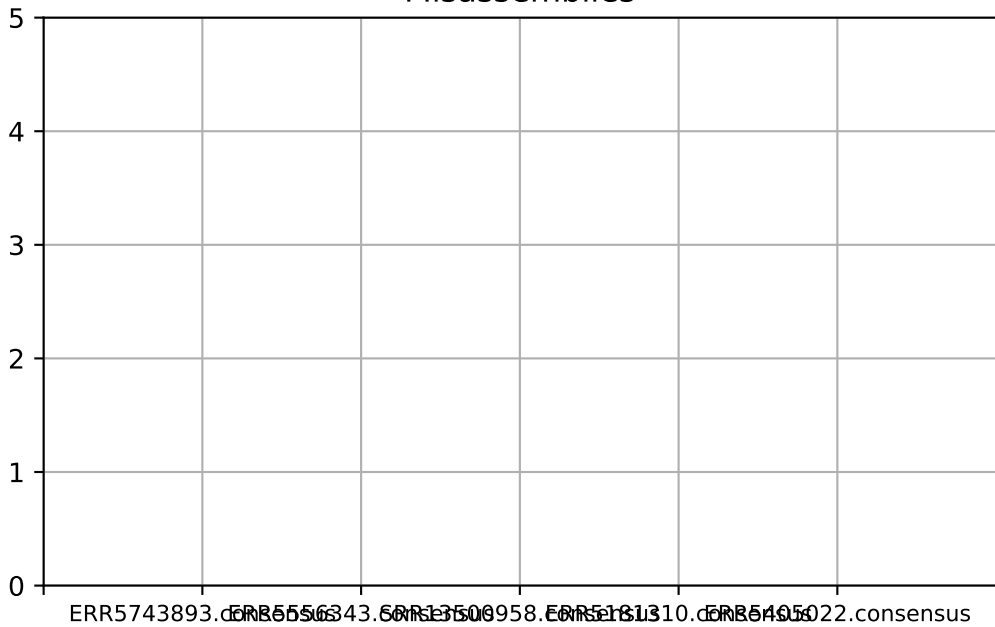
ERR5181310.consensus

ERR5405022.consensus GC content

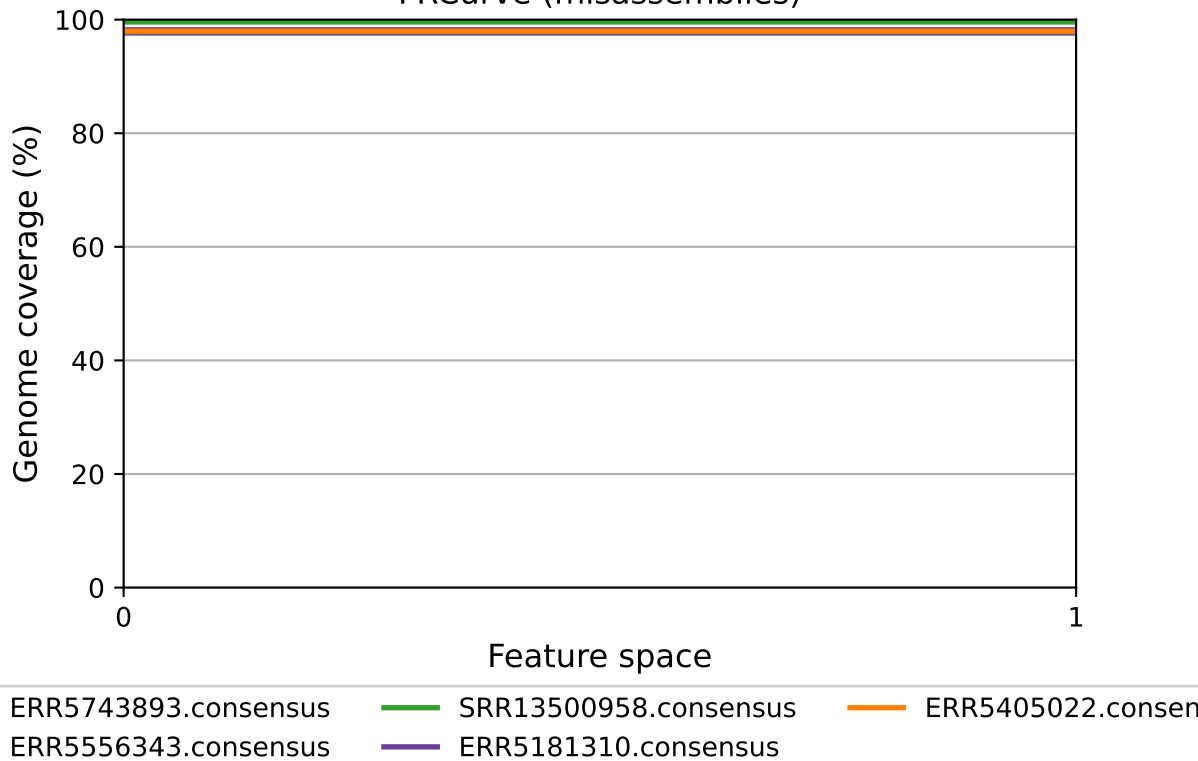


ERR5405022.consensus

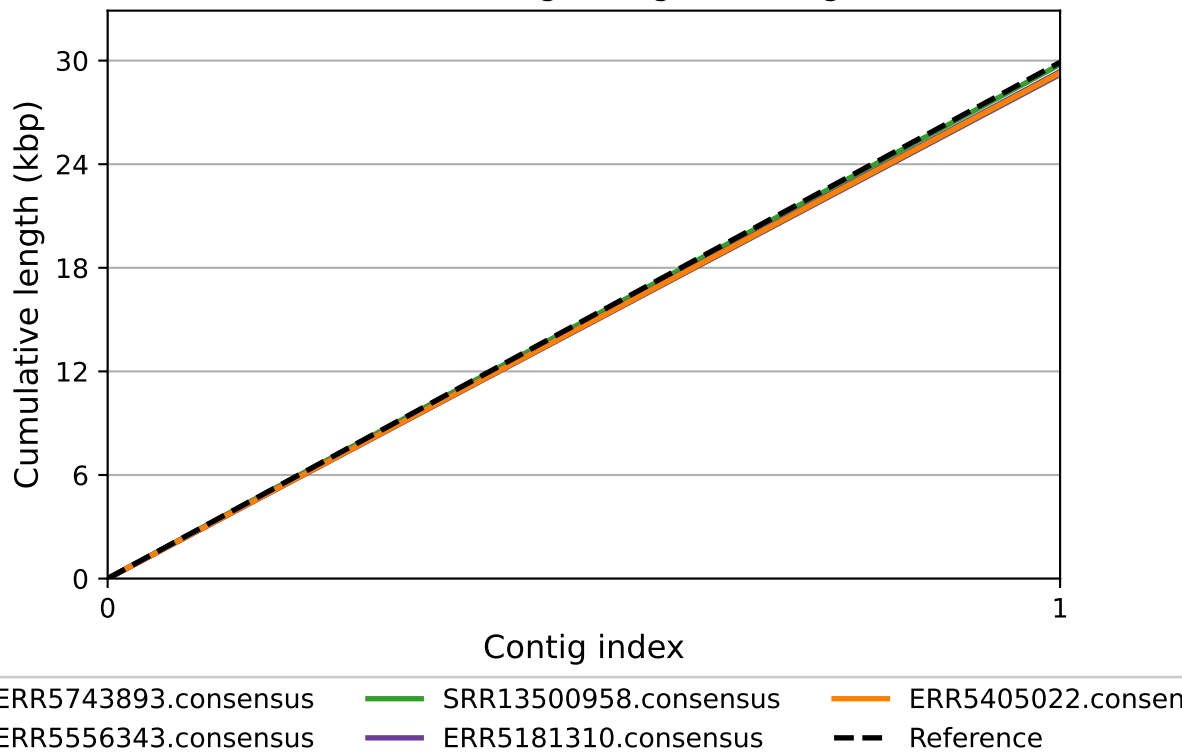
Misassemblies



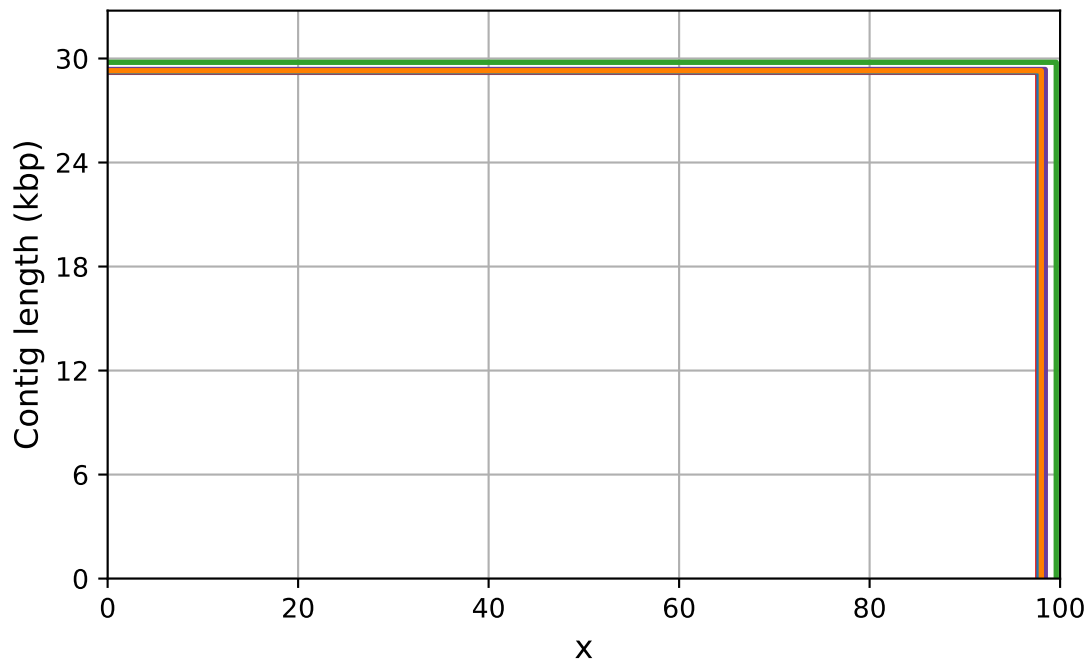
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



ERR5743893.consensus

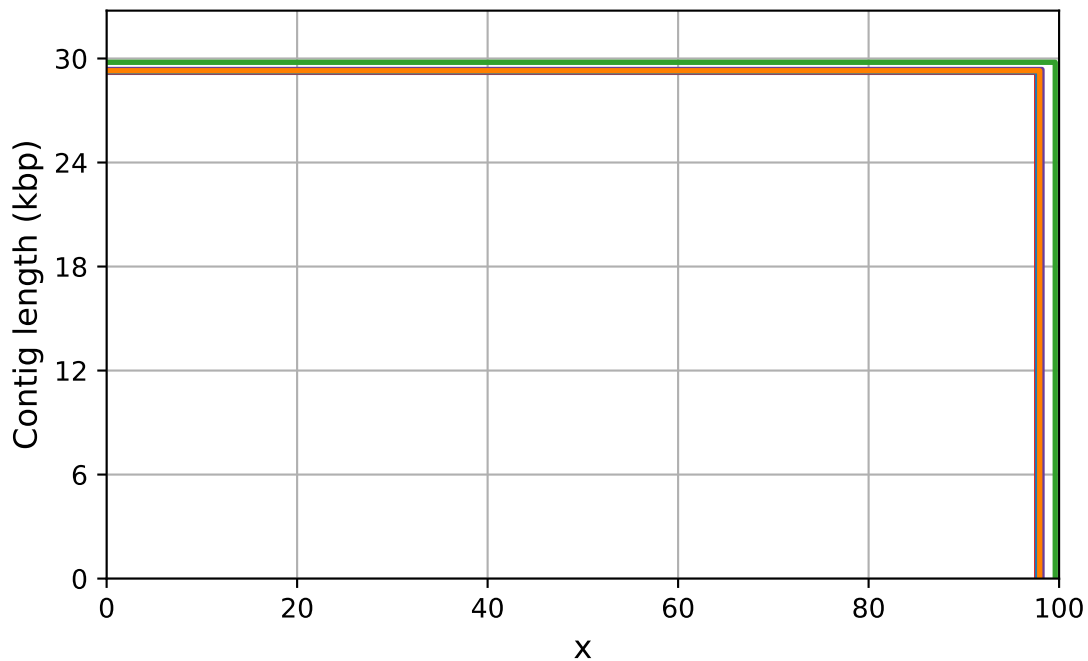
SRR13500958.consensus

ERR5405022.consensus

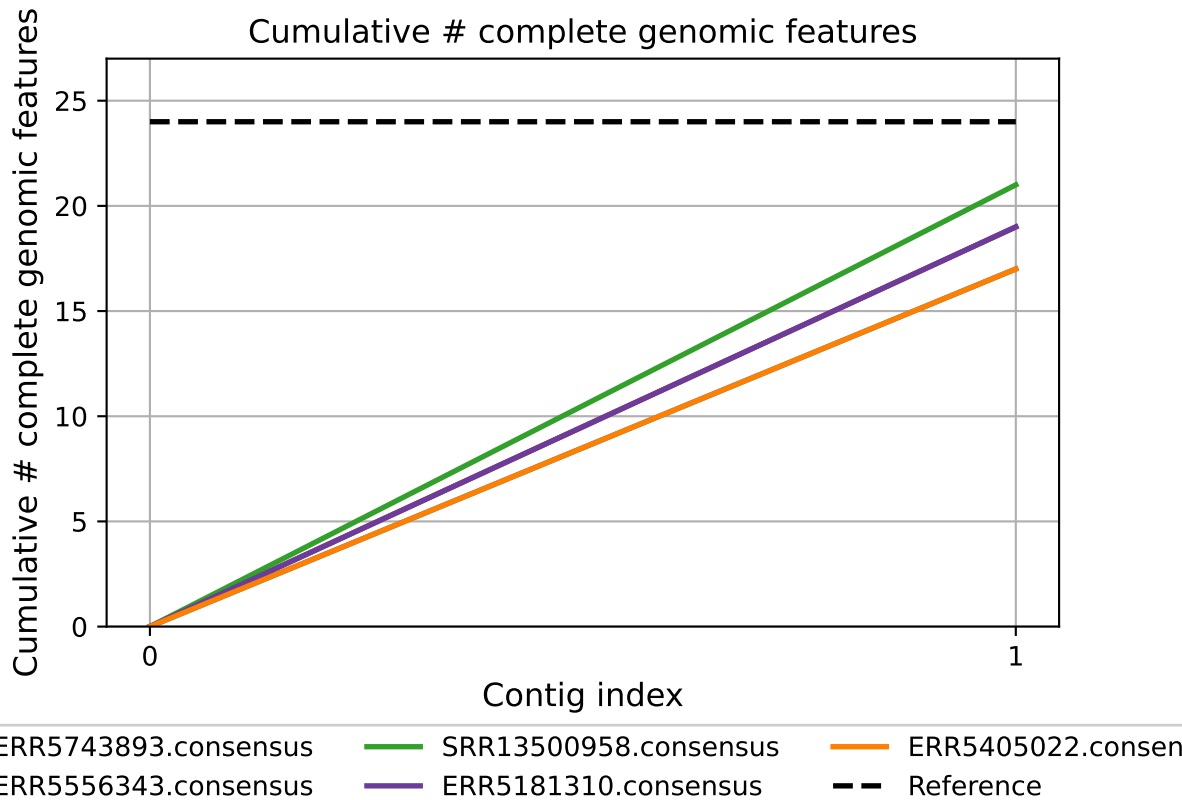
ERR5556343.consensus

ERR5181310.consensus

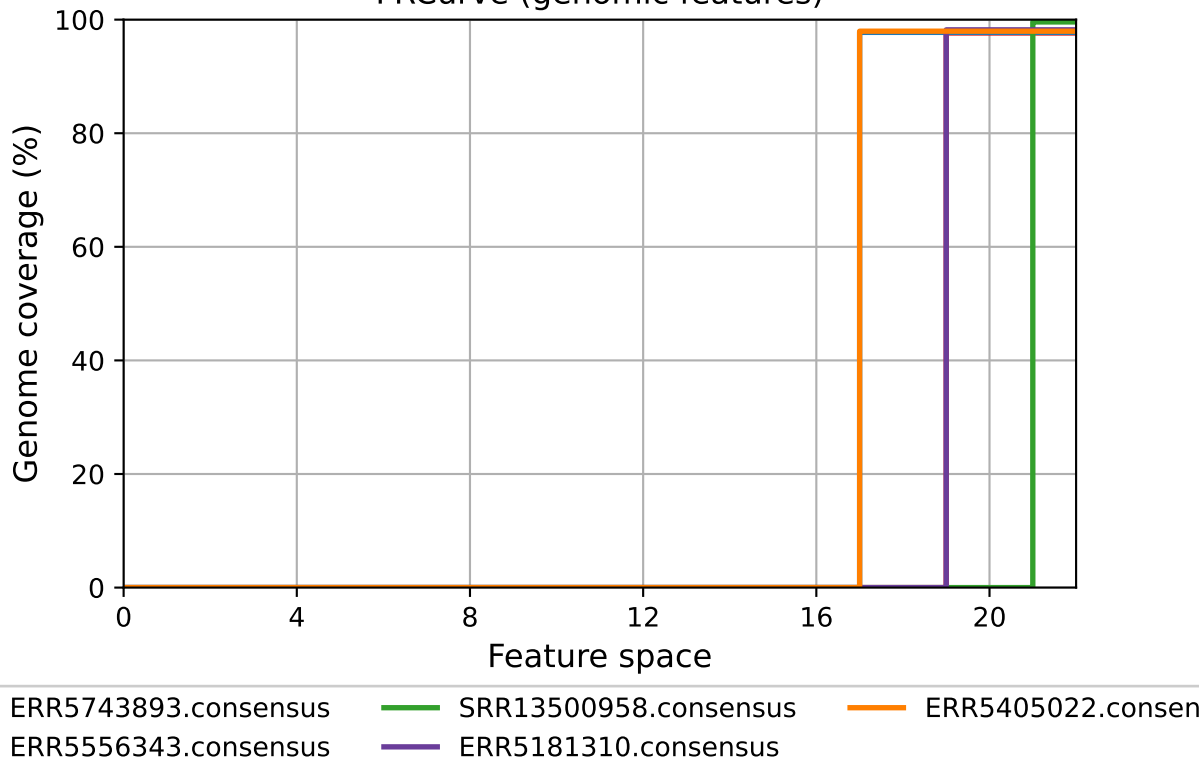
NGAx



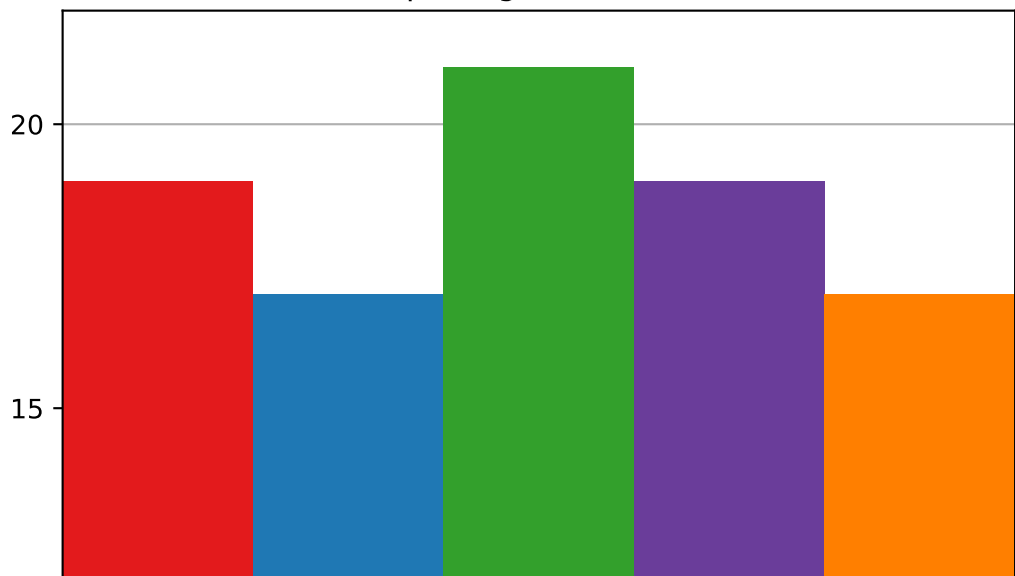
ERR5743893.consensus SRR13500958.consensus ERR5405022.consensus
ERR5556343.consensus ERR5181310.consensus



FRCurve (genomic features)



complete genomic features



ERR5743893.consensus

SRR13500958.consensus

ERR5405022.consensus

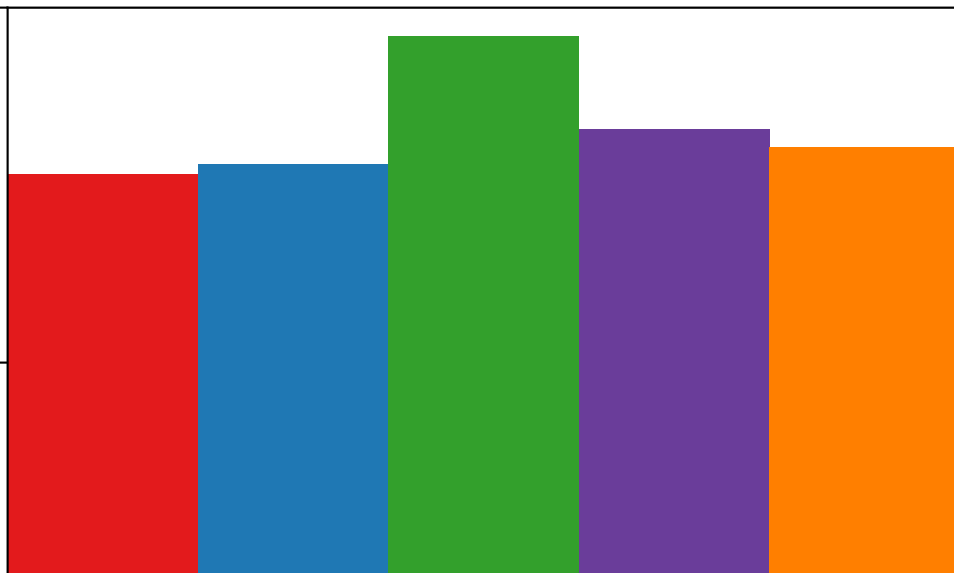
ERR5556343.consensus

ERR5181310.consensus

Genome fraction, %

100

95



ERR5743893.consensus

SRR13500958.consensus

ERR5405022.consensus

ERR5556343.consensus

ERR5181310.consensus