Report

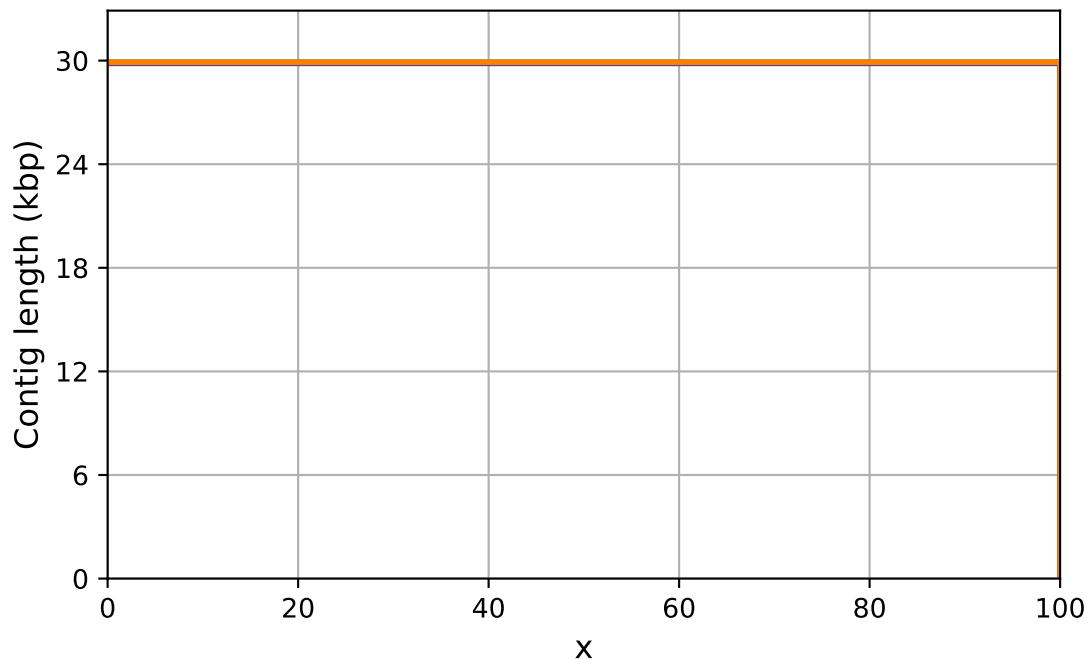|	ERR5556343.consensus	ERR5405022.consensus	ERR5743893.consensus	ERR5181310.consensus	SRR13500958.consensus
# contigs (>= 0 bp)	1	1	1	1	1
# contigs (>= 1000 bp)	1	1	1	1	1
# contigs (>= 5000 bp)	1	1	1	1	1
# contigs (>= 10000 bp)	1	1	1	1	1
# contigs (>= 25000 bp)	1	1	1	1	1
# contigs (>= 50000 bp)	0	0	0	0	0
Total length (>= 0 bp)	29894	29884	29902	29830	29903
Total length (>= 1000 bp)	29894	29884	29902	29830	29903
Total length (>= 5000 bp)	29894	29884	29902	29830	29903
Total length (>= 10000 bp)	29894	29884	29902	29830	29903
Total length (>= 25000 bp)	29894	29884	29902	29830	29903
Total length (>= 50000 bp)	0	0	0	0	0
# contigs	1	1	1	1	1
Largest contig	29894	29884	29902	29830	29903
Total length	29894	29884	29902	29830	29903
Reference length	29903	29903	29903	29903	29903
GC (%)	37.96	37.97	37.93	37.92	37.98
Reference GC (%)	37.97	37.97	37.97	37.97	37.97
N50	29894	29884	29902	29830	29903
NG50	29894	29884	29902	29830	29903
N90	29894	29884	29902	29830	29903
NG90	29894	29884	29902	29830	29903
auN	29894.0	29884.0	29902.0	29830.0	29903.0
auNG	29885.0	29865.0	29901.0	29757.2	29903.0
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.	2	2	1	1	0
# 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 (%)	97.790	98.030	97.656	98.284	99.595
Duplication ratio	1.000	0.999	1.000	0.999	1.000
# N's per 100 kbp	2114.14	1977.65	2220.59	1354.34	404.64
# mismatches per 100 kbp	116.31	116.06	92.46	95.35	73.87
# indels per 100 kbp	3.42	13.65	3.42	17.03	0.00
# genomic features	17 + 7 part	17 + 7 part	19 + 4 part	19 + 4 part	21 + 3 part
Largest alignment	29233	29295	29201	29366	29782
Total aligned length	29233	29295	29201	29366	29782
NA50	29233	29295	29201	29366	29782
NGA50	29233	29295	29201	29366	29782
NA90	29233	29295	29201	29366	29782
NGA90	29233	29295	29201	29366	29782
auNA	28586.6	28717.6	28516.4	28909.2	29661.5
auNGA	28578.0	28699.4	28515.5	28838.6	29661.5
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
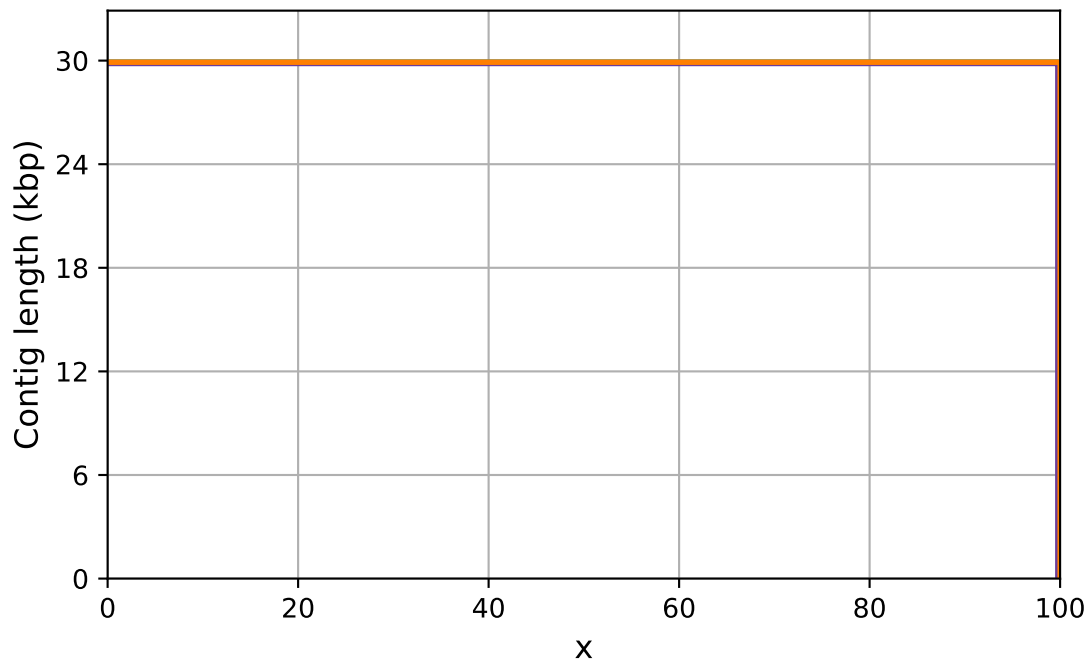
	ERR5556343.consensus	ERR5405022.consensus	ERR5743893.consensus	ERR5181310.consensus	SRR13500958.consensus
# misassemblies	0	0	0	0	0
# contig misassemblies	0	0	0	0	0
# c. relocations	0	0	0	0	0
# c. translocations	0	0	0	0	0
# c. inversions	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0
# s. relocations	0	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	1	1	0
# unaligned mis. contigs	0	0	0	0	0
# mismatches	34	34	27	28	22
# indels	1	4	1	5	0
# indels (<= 5 bp)	0	2	1	3	0
# indels (> 5 bp)	1	2	0	2	0
Indels length	9	19	1	24	0

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

	ERR5556343.consensus	ERR5405022.consensus	ERR5743893.consensus	ERR5181310.consensus	SRR13500958.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	632	591	664	404	121

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

NGx

Contig length (kbp)

x

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

Cumulative length
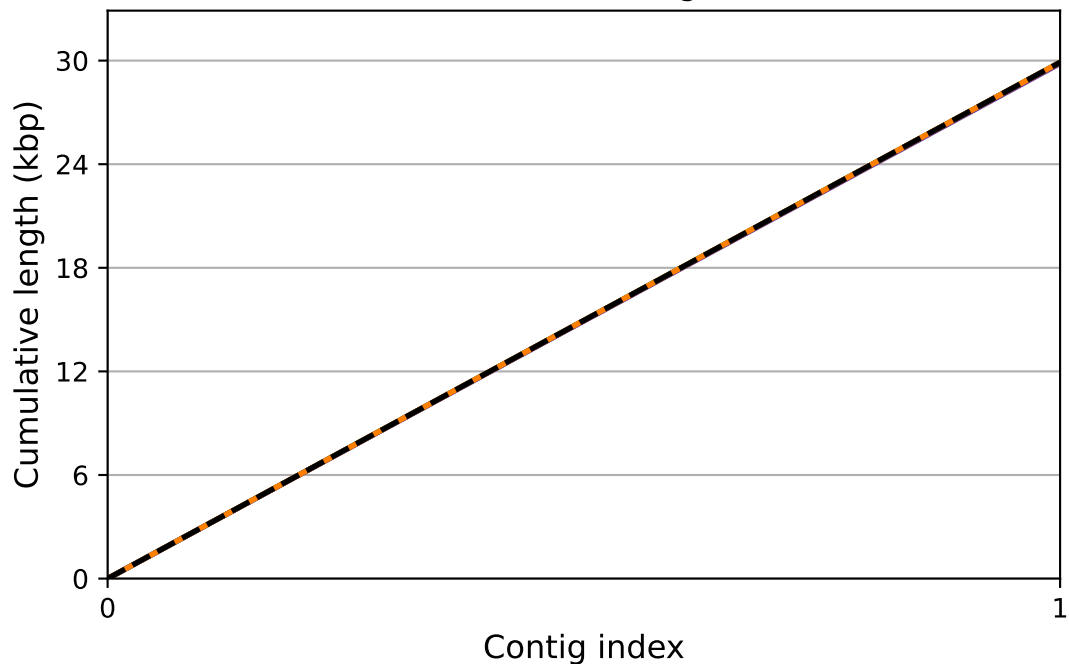
ERR5556343.consensus

ERR5405022.consensus

ERR5743893.consensus

ERR5181310.consensus

SRR13500958.consen

Reference

GC content
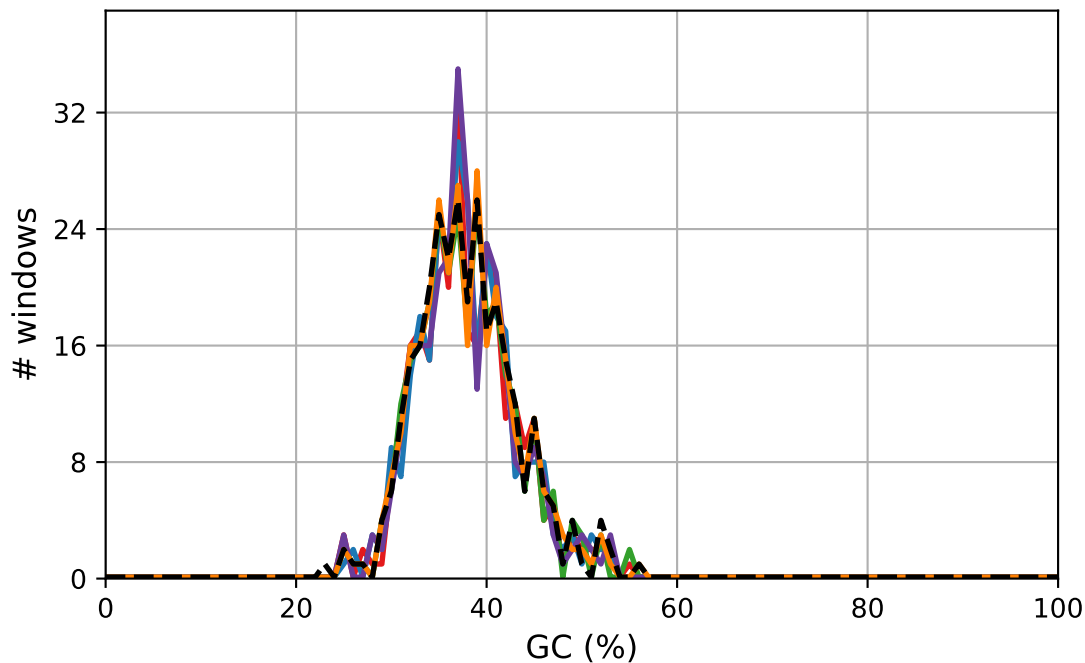
ERR5556343.consensus   ERR5743893.consensus   SRR13500958.consen
ERR5405022.consensus   ERR5181310.consensus   Reference
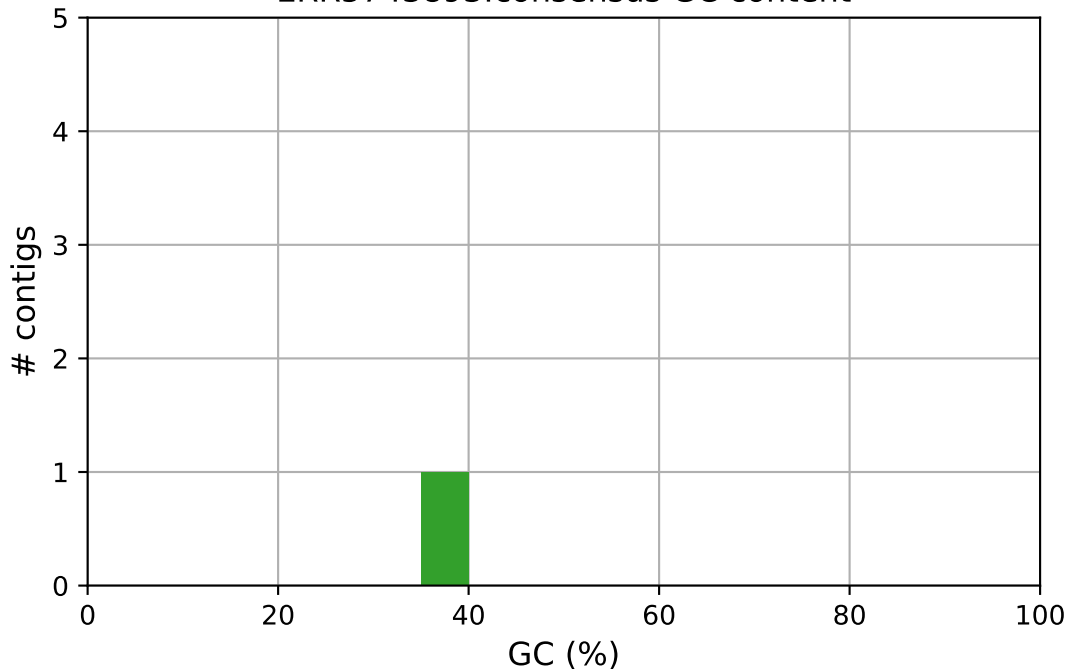
ERR5556343.consensus GC content
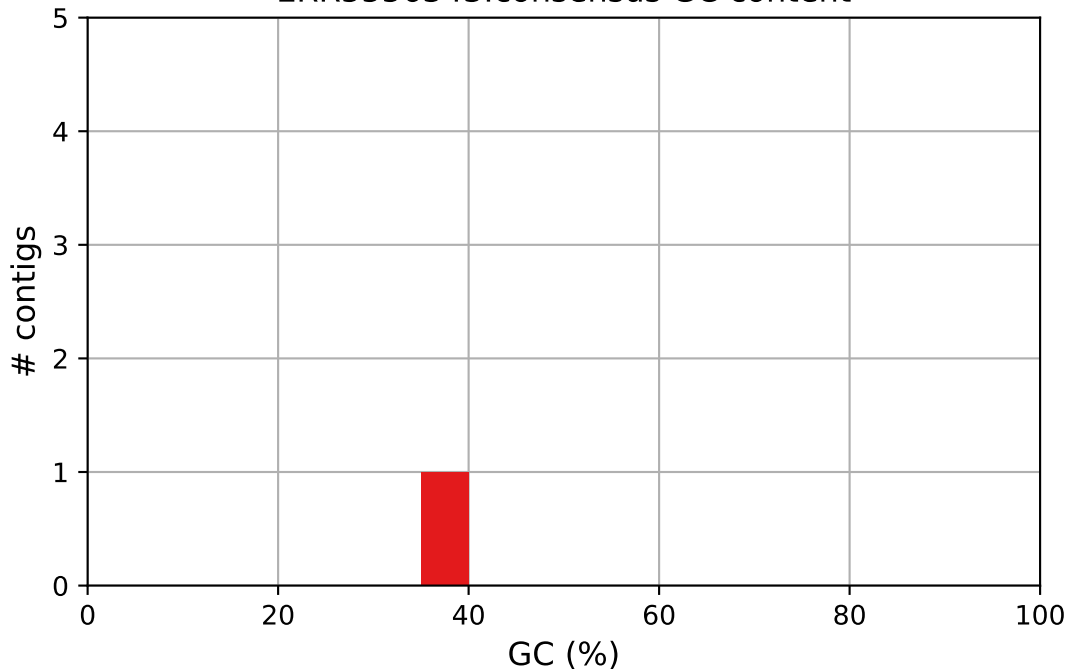
ERR5405022.consensus GC content
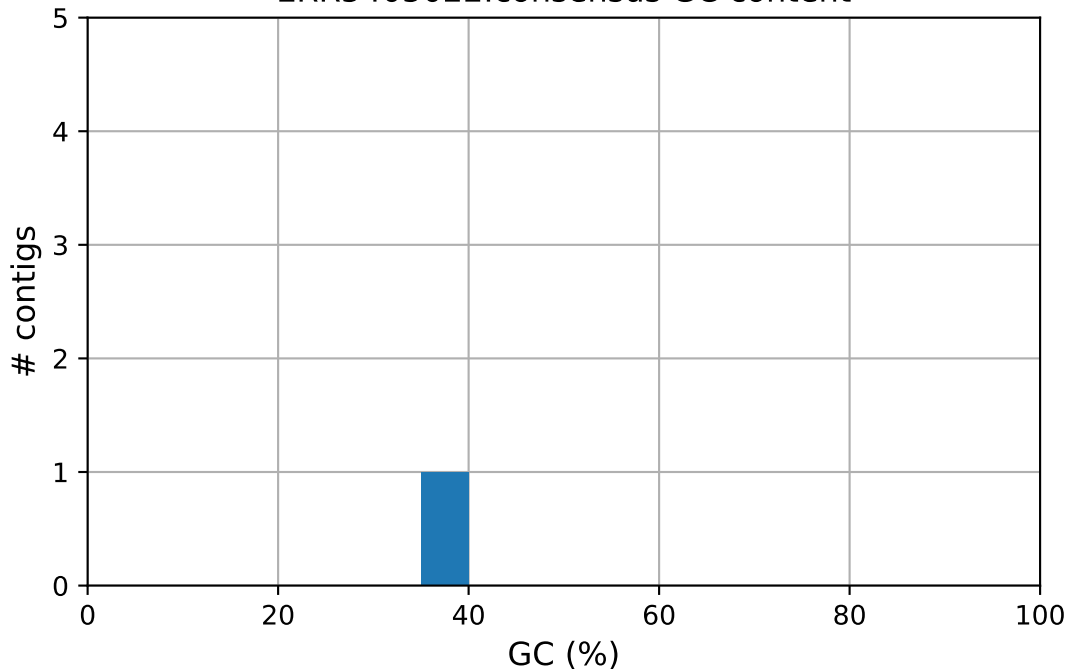
ERR5743893.consensus GC content

ERR5181310.consensus GC content
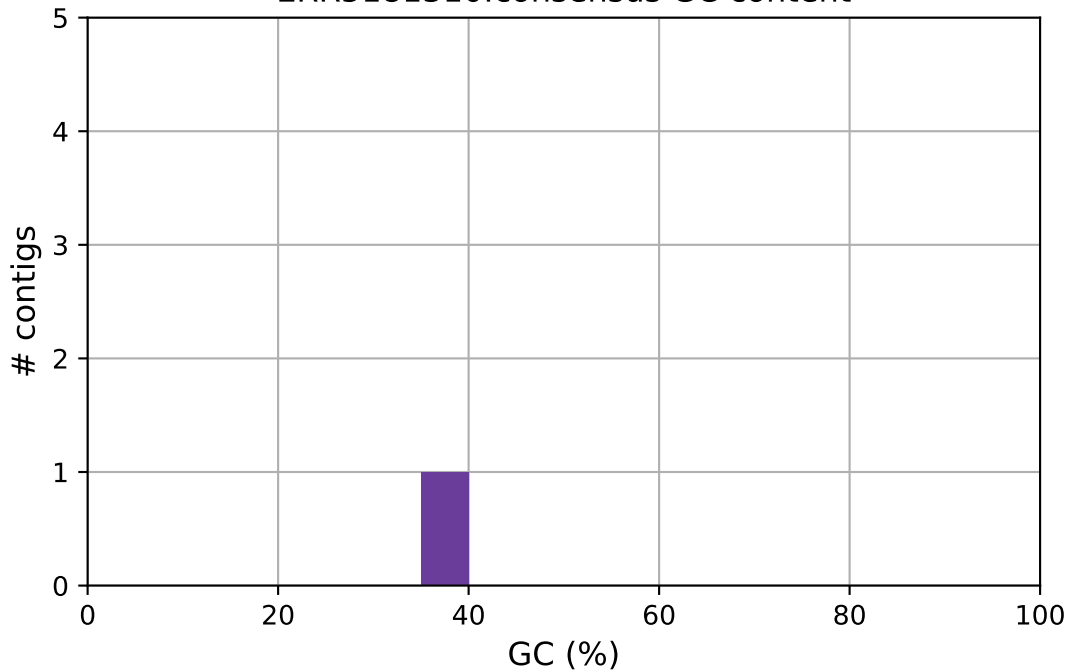
SRR13500958.consensus GC content

Misassemblies
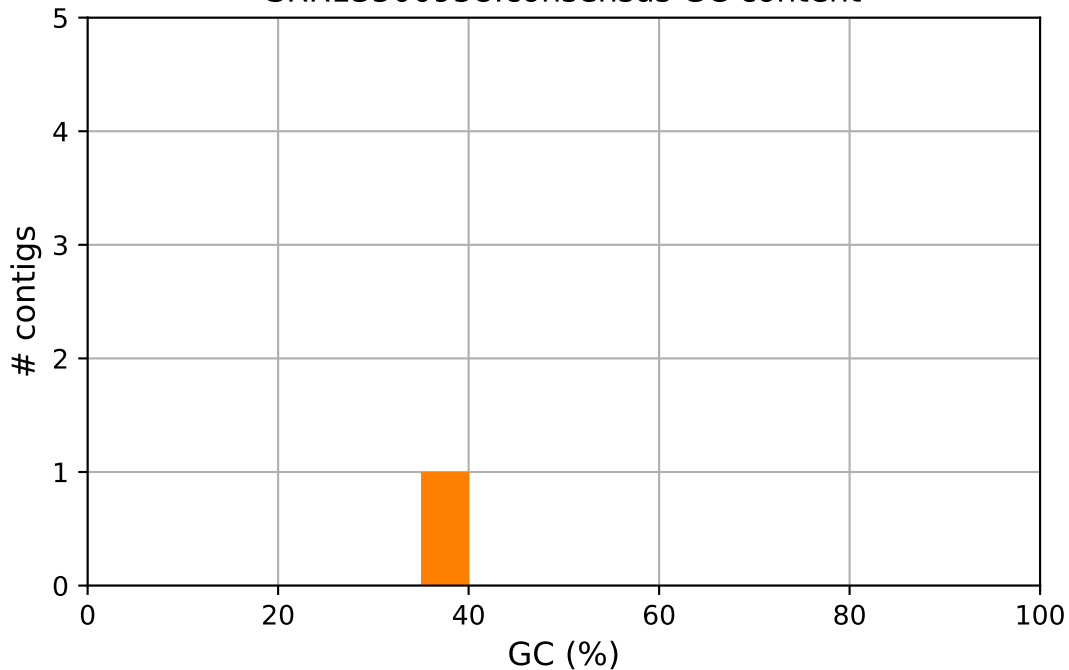
ERR5556343.consensus ERR5495022.consensus ERR5743893.consensus ERR5181310.consensus ERR5506958.consensus

FRCurve (misassemblies)

Genome coverage (%)

Feature space

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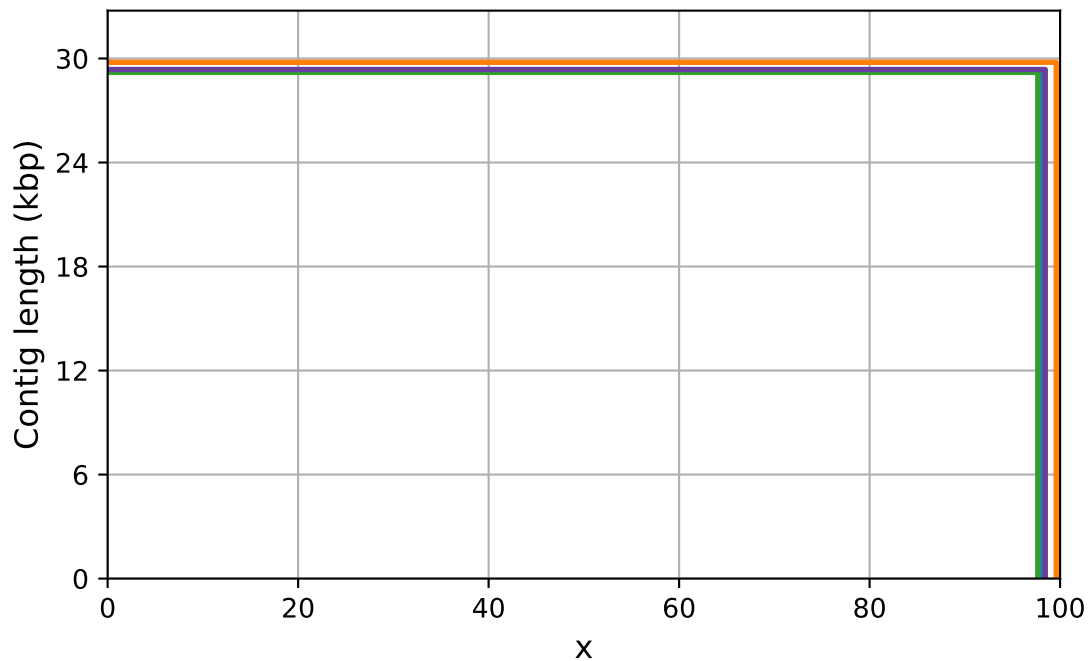ERR5405022.consensus
ERR5743893.consensus
ERR5181310.consensus
SRR13500958.consen
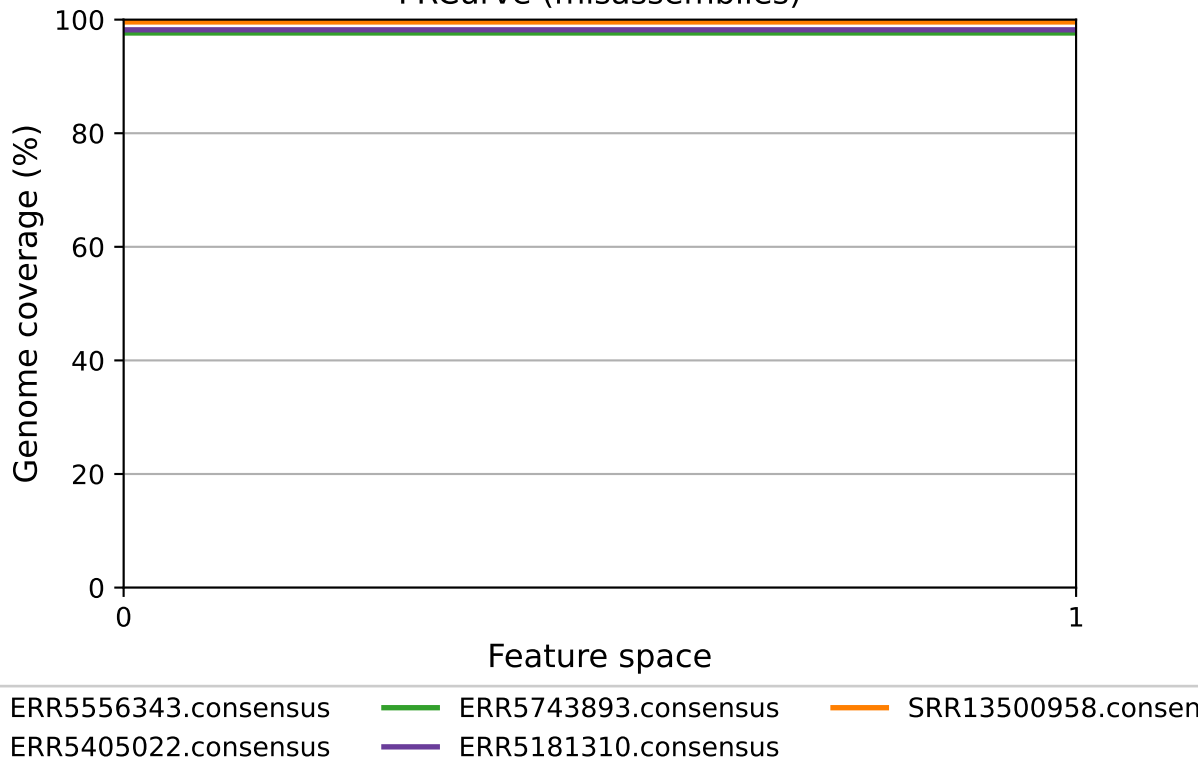
Cumulative length (aligned contigs)

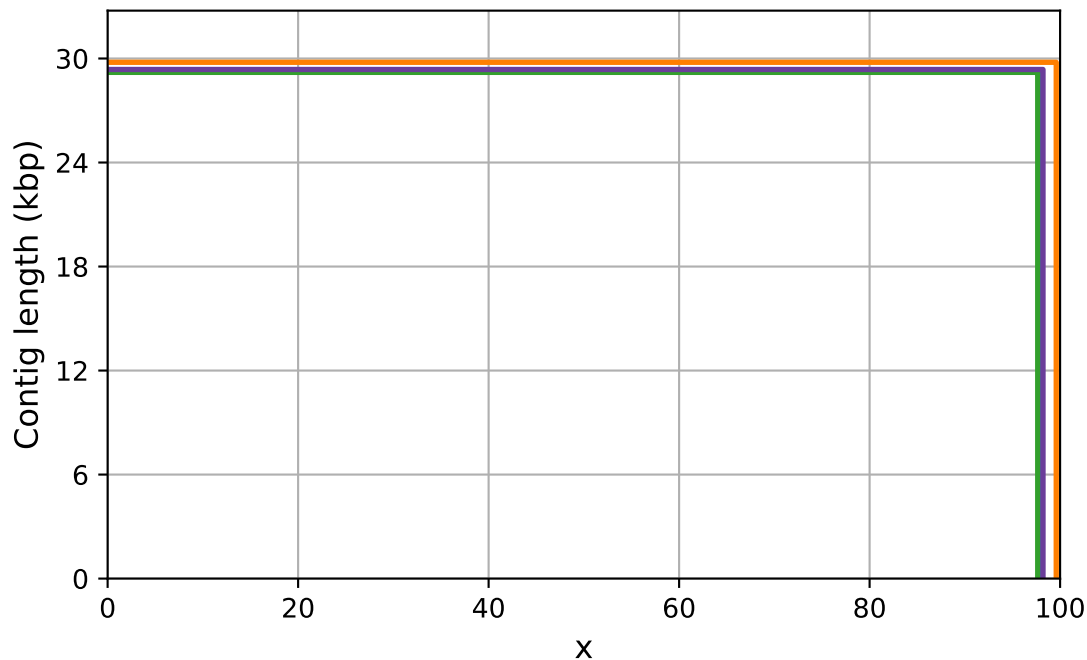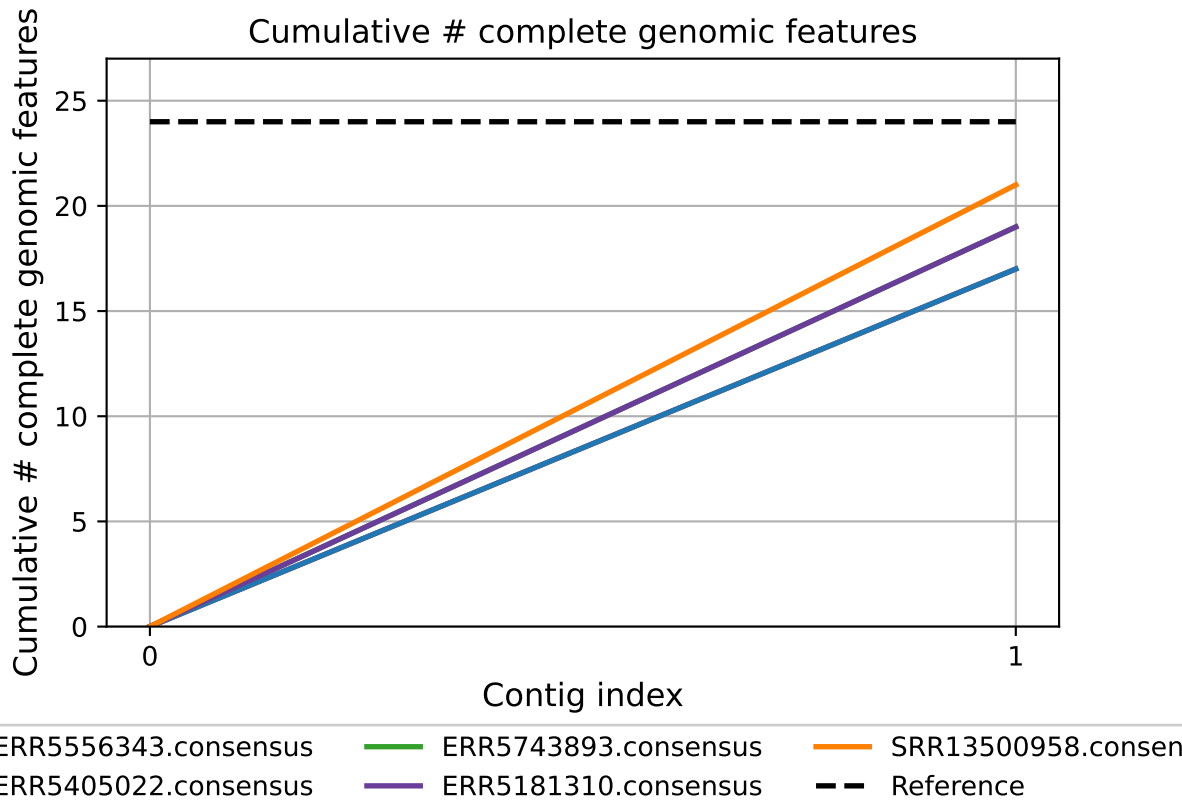| ERR5556343.consensus | ERR5743893.consensus | SRR13500958.consen |
| ERR5405022.consensus | ERR5181310.consensus | Reference |

NAx

ERR5556343.consensus ERR5743893.consensus SRR13500958.consen

ERR5405022.consensus ERR5181310.consensus

NGAx

Contig length (kbp) vs x

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

Cumulative # complete genomic features

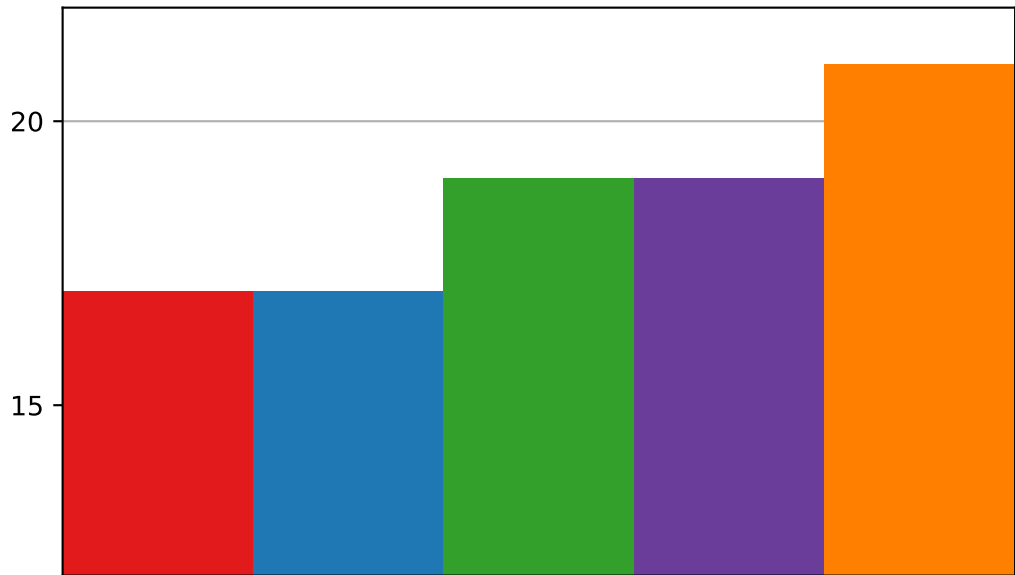|	
ERR5556343.consensus	ERR5743893.consensus	SRR13500958.consen
ERR5405022.consensus	ERR5181310.consensus	Reference

FRCurve (genomic features)

Legend:
- ERR5556343.consensus
- ERR5405022.consensus
- ERR5743893.consensus
- ERR5181310.consensus
- SRR13500958.consen

complete genomic features

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

Genome fraction, %

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