Report

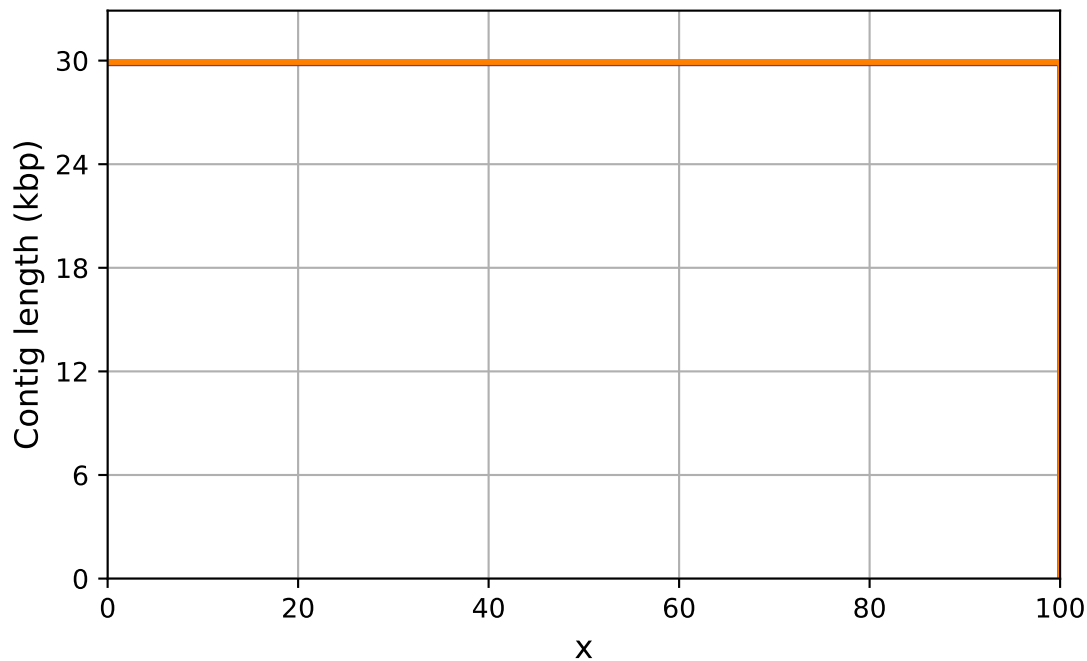|	ERR5405022.consensus	ERR5556343.consensus	ERR5743893.consensus	ERR5181310.consensus	SRR13500958.consensus
# contigs (>= 0 bp)	1	1	1	1	1
# contigs (>= 1000 bp)	1	1	1	1	1
# contigs (>= 5000 bp)	1	1	1	1	1
# contigs (>= 10000 bp)	1	1	1	1	1
# contigs (>= 25000 bp)	1	1	1	1	1
# contigs (>= 50000 bp)	0	0	0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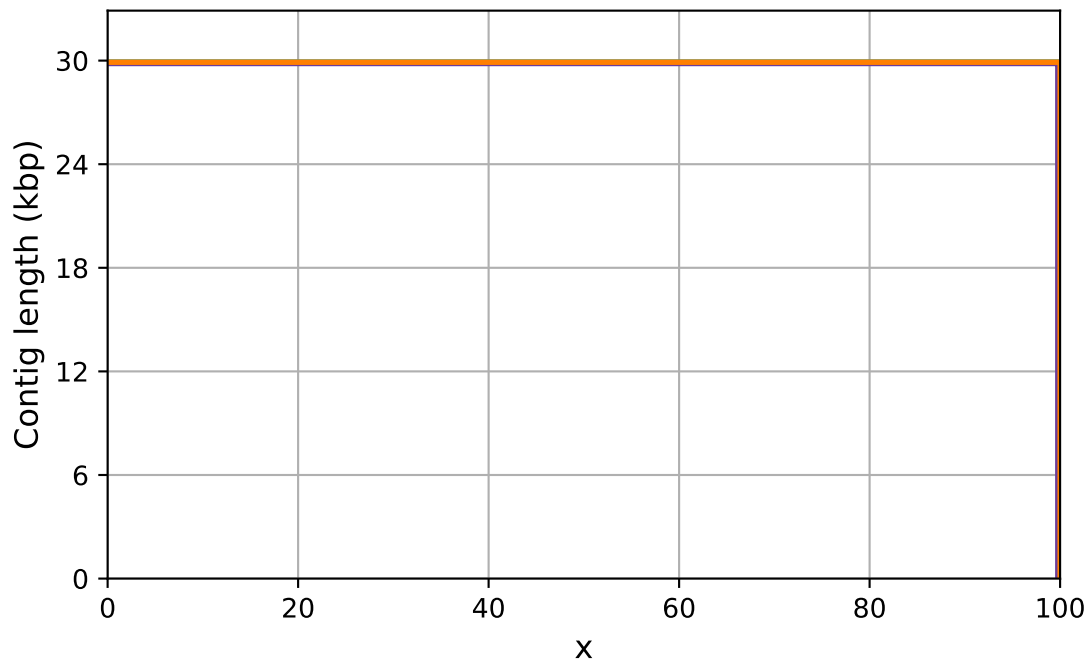
	ERR5405022.consensus	ERR5556343.consensus	ERR5743893.consensus	ERR5181310.consensus	SRR13500958.consensus
# misassemblies	0	0	0	0	0
# contig misassemblies	0	0	0	0	0
# c. relocations	0	0	0	0	0
# c. translocations	0	0	0	0	0
# c. inversions	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0
# s. relocations	0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

	ERR5405022.consensus	ERR5556343.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	591	632	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

Contig length (kbp)

x

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

NGx

Contig length (kbp)

x

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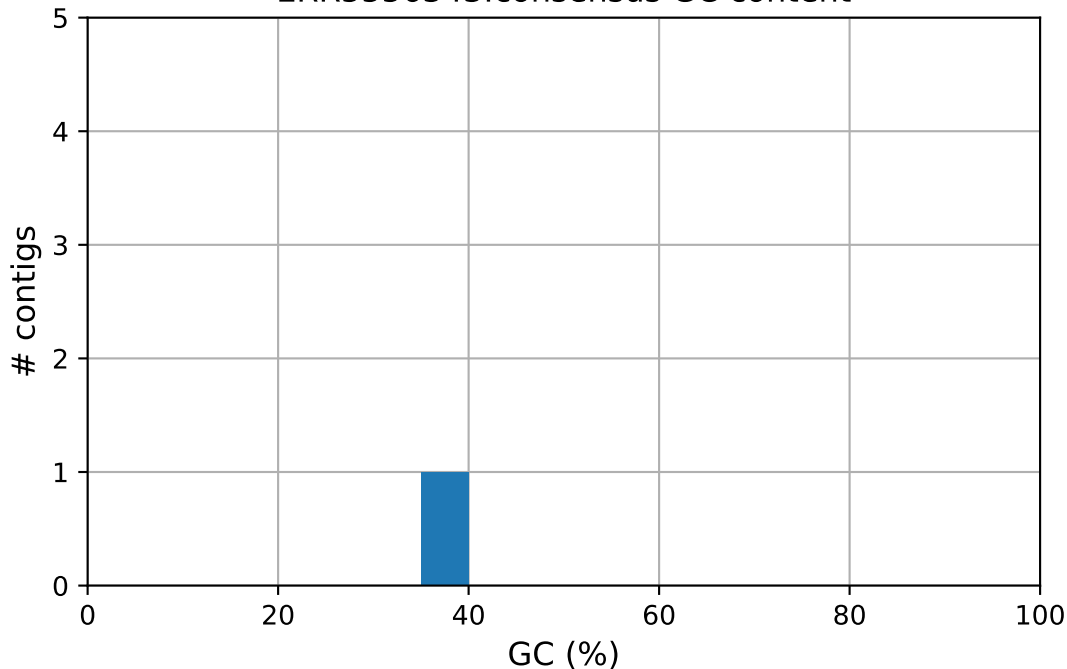ERR5181310.consensus
SRR13500958.consen

Cumulative length

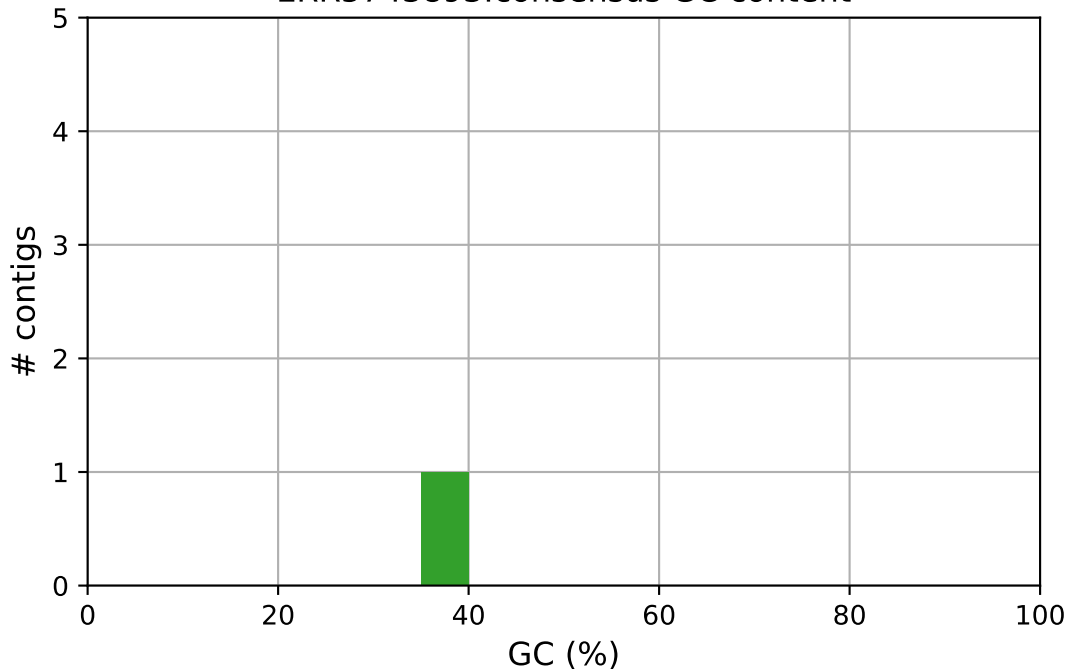| ERR5405022.consensus | ERR5743893.consensus | SRR13500958.consen |
| ERR5556343.consensus | ERR5181310.consensus | Reference |

GC content
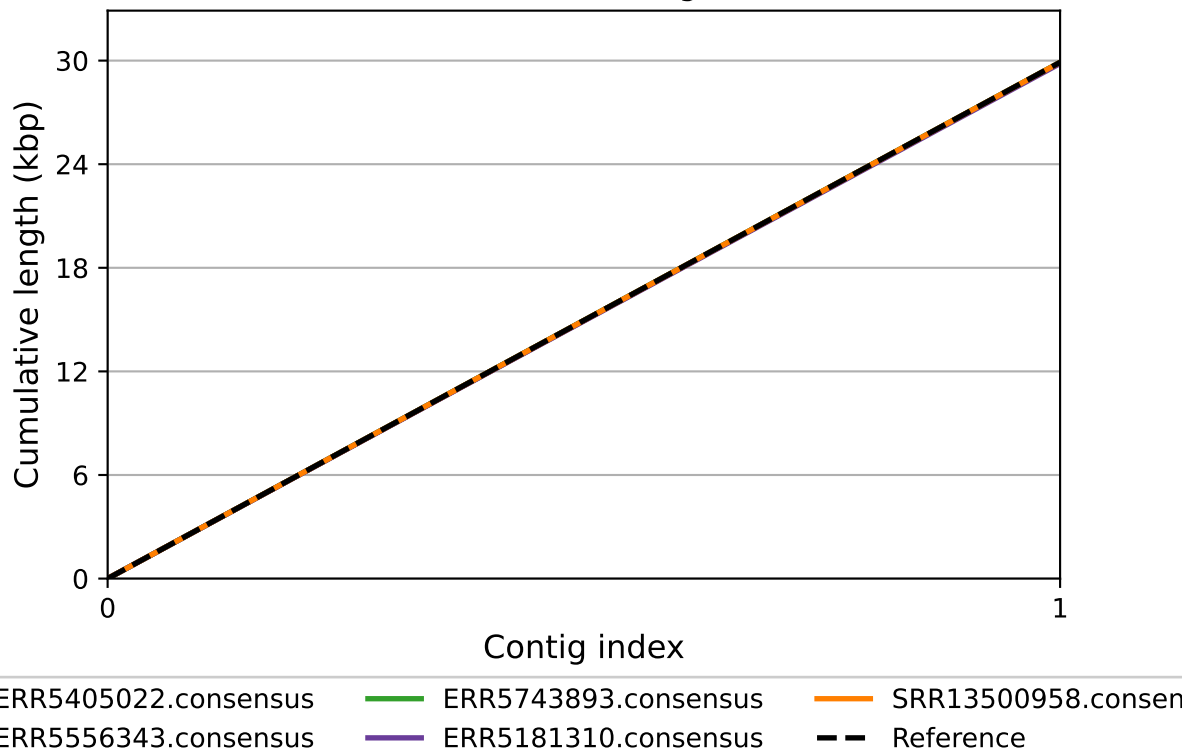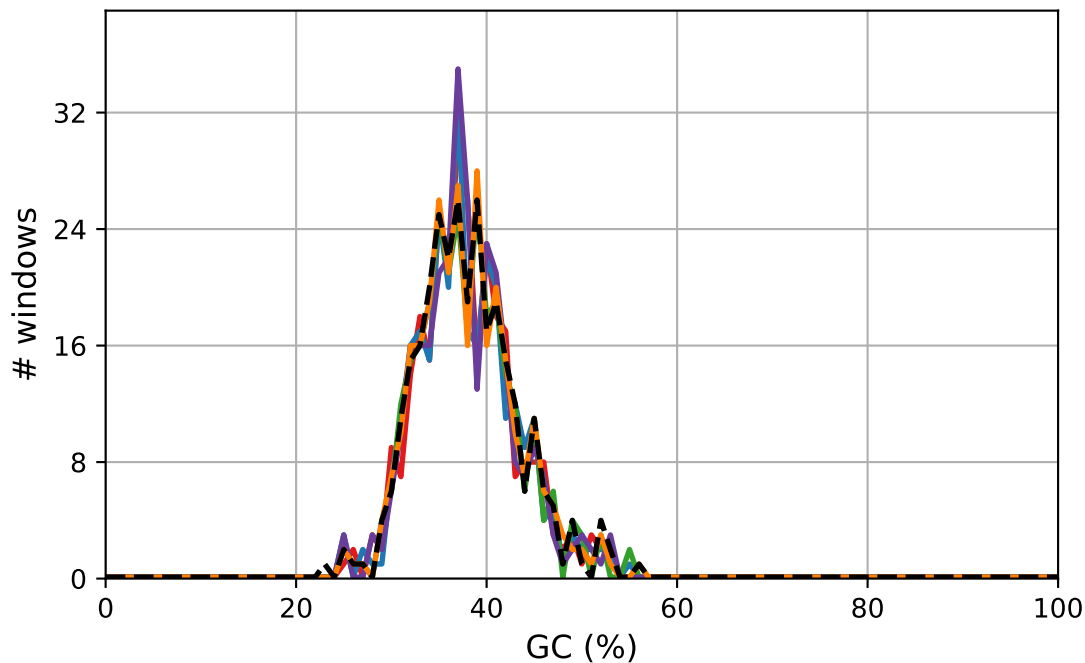
![GC content plot showing # windows versus GC (%), with legend: ERR5405022.consensus, ERR5556343.consensus, ERR5743893.consensus, ERR5181310.consensus, SRR13500958.consensus, Reference]

ERR5405022.consensus GC content
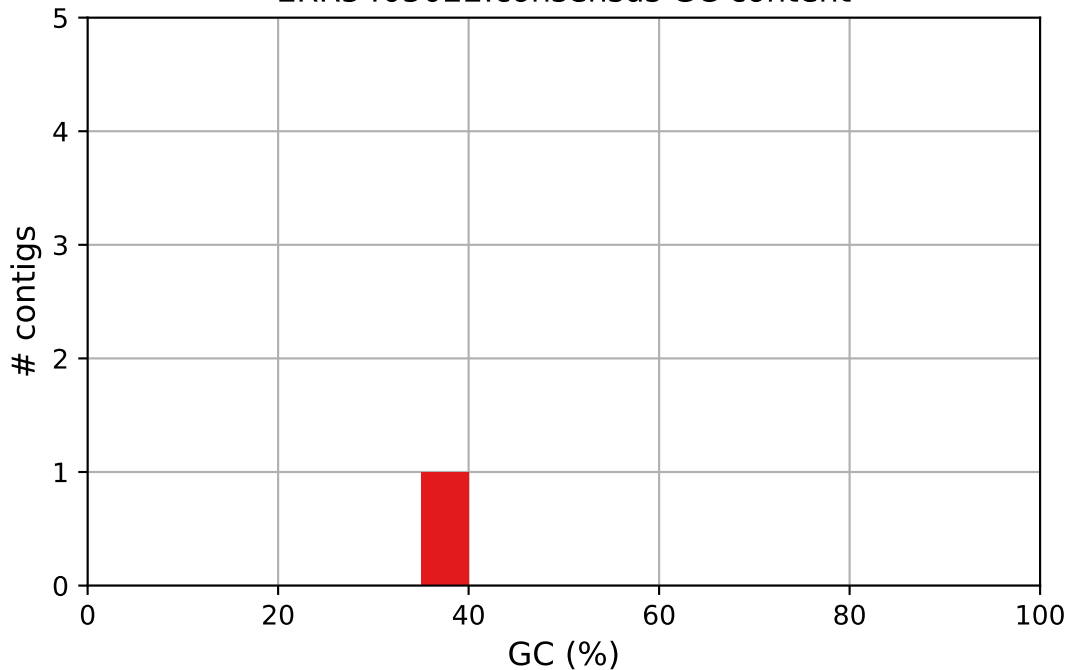
ERR5556343.consensus GC content

ERR5743893.consensus GC content

ERR5181310.consensus GC content
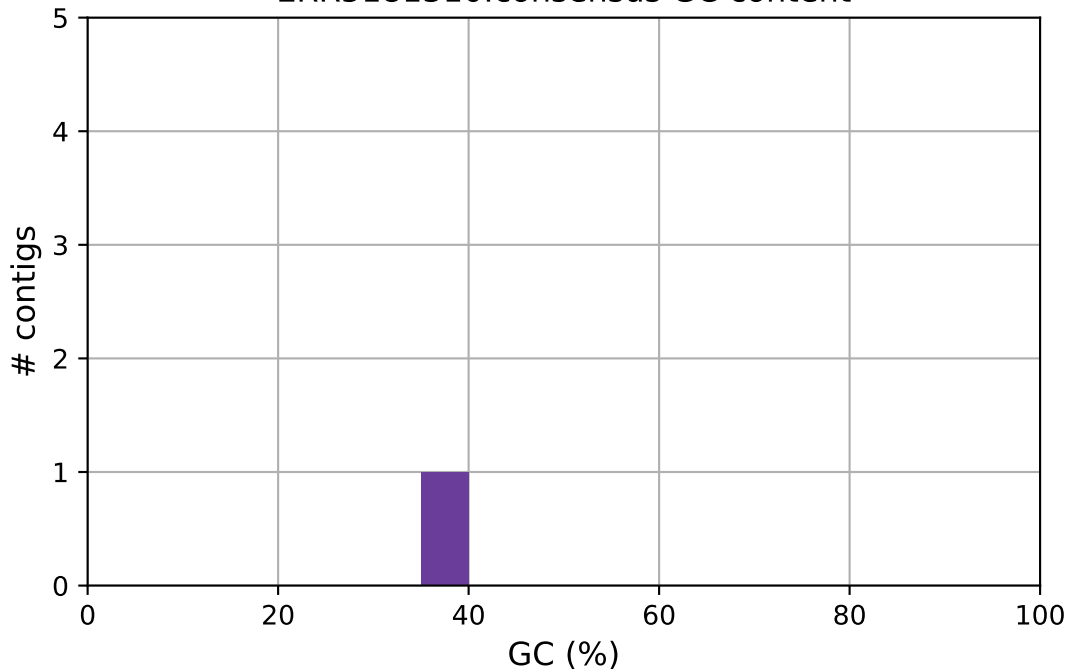
Misassemblies
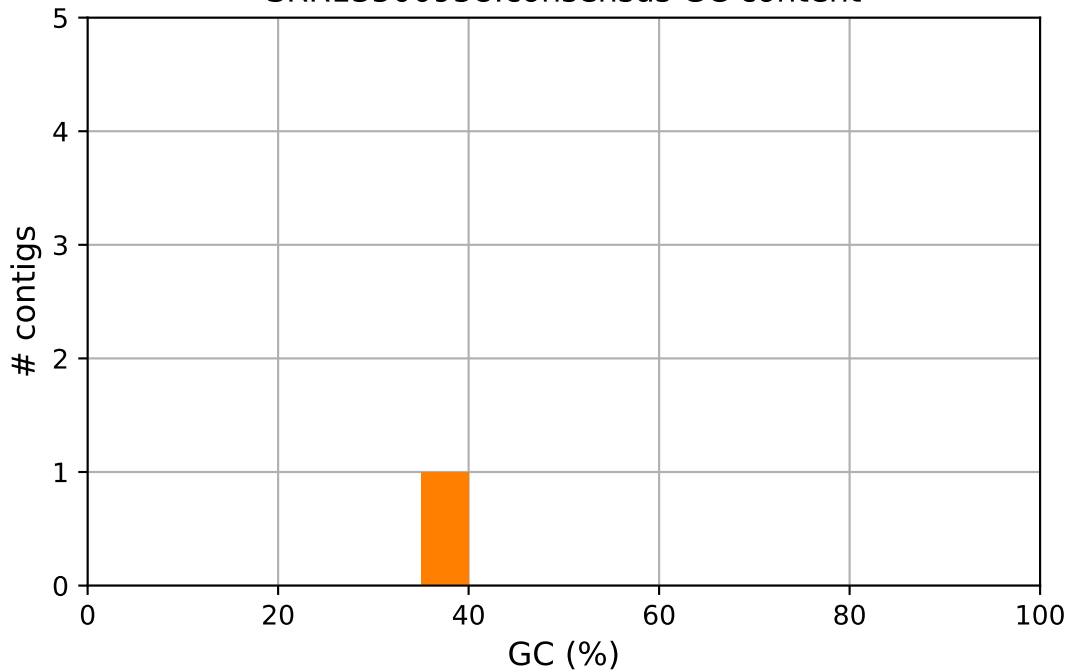
ERR5405022.consensus ERR5556343.consensus ERR5743893.consensus ERR5181310.consensus ERR5356958.consensus

FRCurve (misassemblies)

Legend:
- ERR5405022.consensus
- ERR5556343.consensus
- ERR5743893.consensus
- ERR5181310.consensus
- SRR13500958.consen
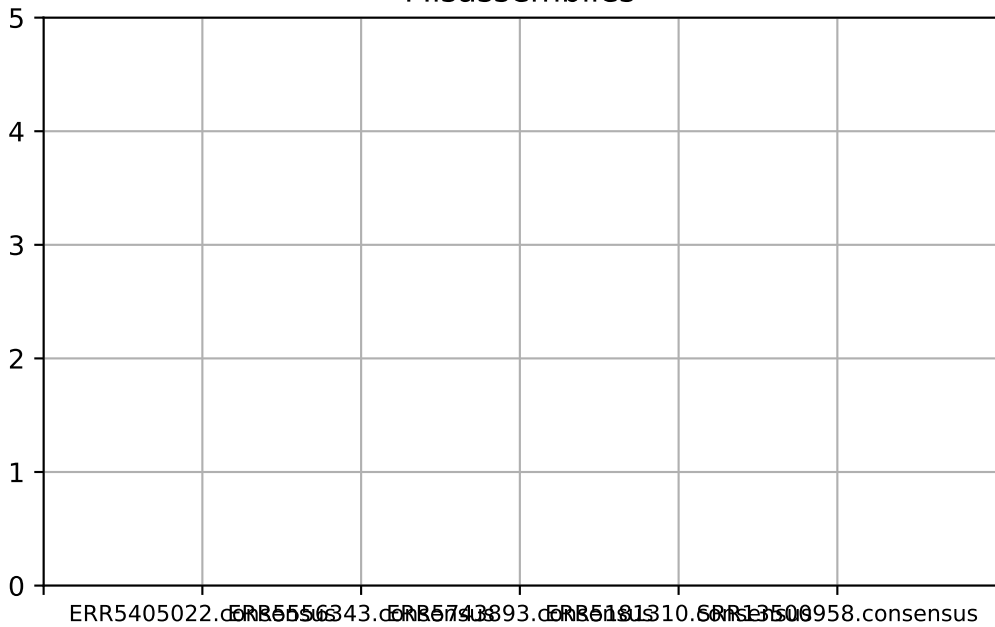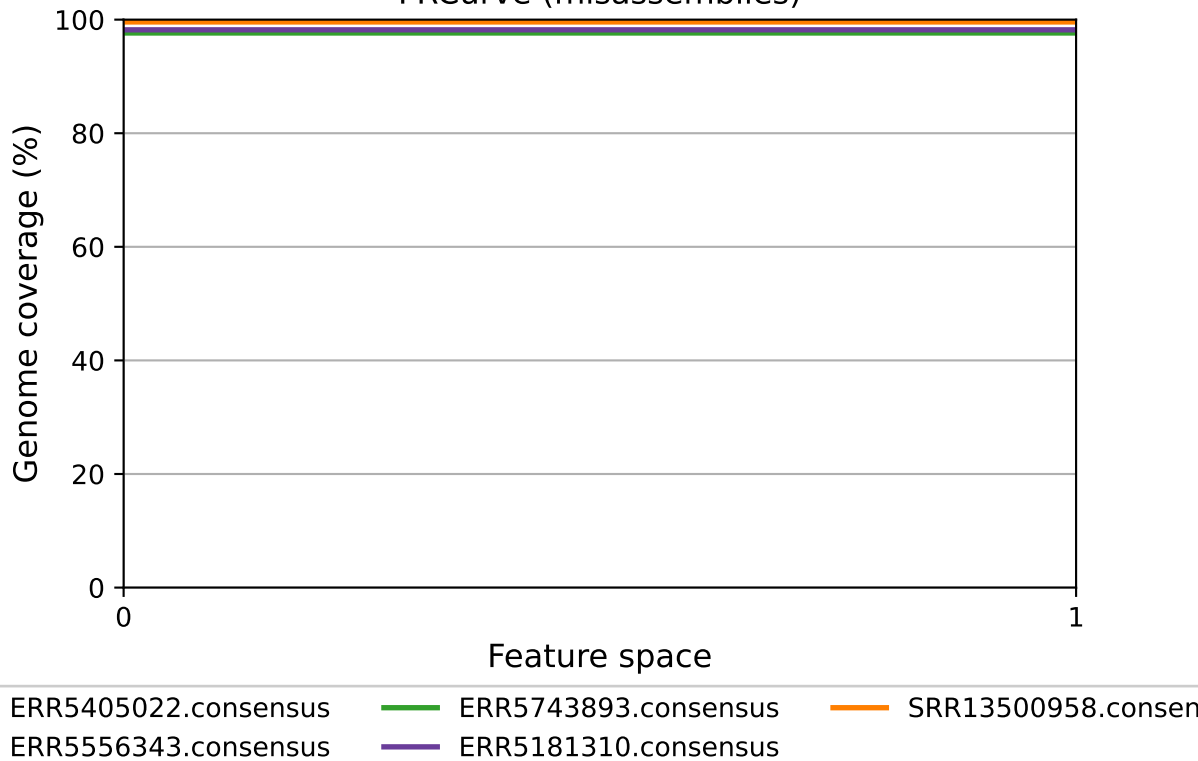
Cumulative length (aligned contigs)
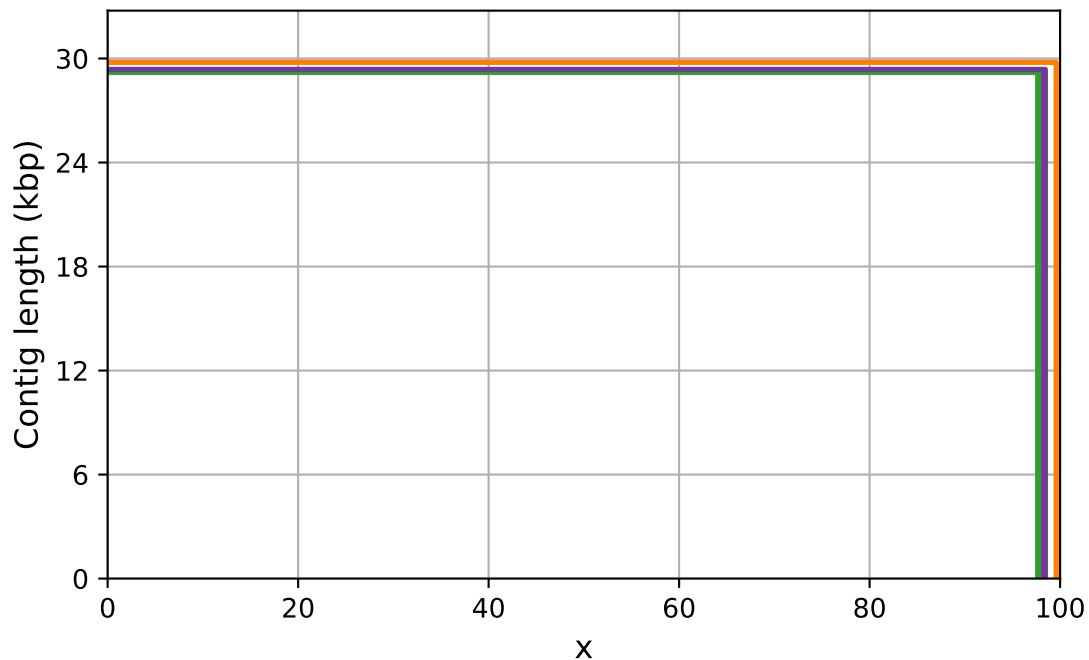
Legend	
ERR5405022.consensus	ERR5743893.consensus	SRR13500958.consen
ERR5556343.consensus	ERR5181310.consensus	Reference

NAx

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

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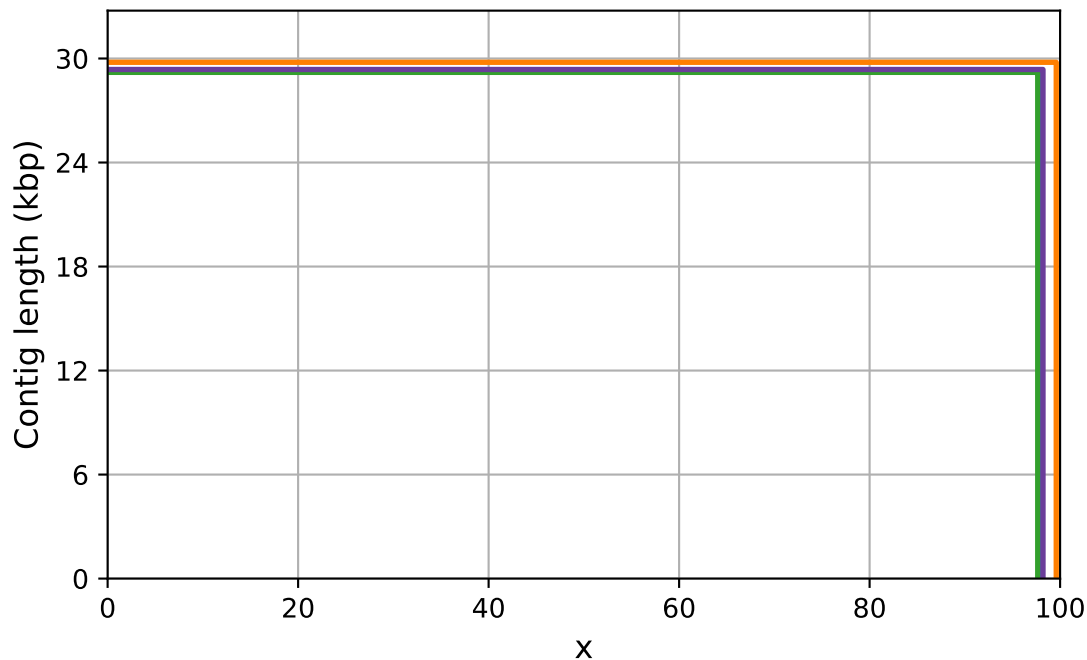
| ERR5405022.consensus | ERR5743893.consensus | SRR13500958.consen |
| ERR5556343.consensus | ERR5181310.consensus | |

Genome fraction, %

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