

Report

	SRR33436961_pipecov_consensus	ref_majority	SRR33436961_viralrecon_consensus
# contigs (>= 0 bp)	1	1	1
# contigs (>= 1000 bp)	1	1	1
# contigs (>= 5000 bp)	1	1	1
# contigs (>= 10000 bp)	1	1	1
# contigs (>= 25000 bp)	1	1	1
# contigs (>= 50000 bp)	0	0	0
Total length (>= 0 bp)	29735	29903	29867
Total length (>= 1000 bp)	29735	29903	29867
Total length (>= 5000 bp)	29735	29903	29867
Total length (>= 10000 bp)	29735	29903	29867
Total length (>= 25000 bp)	29735	29903	29867
Total length (>= 50000 bp)	0	0	0
# contigs	1	1	1
Largest contig	29735	29903	29867
Total length	29735	29903	29867
Reference length	29903	29903	29903
GC (%)	37.81	37.80	37.83
Reference GC (%)	37.97	37.97	37.97
N50	29735	29903	29867
NG50	29735	29903	29867
N90	29735	29903	29867
NG90	29735	29903	29867
auN	29735.0	29903.0	29867.0
auNG	29567.9	29903.0	29831.0
L50	1	1	1
LG50	1	1	1
L90	1	1	1
LG90	1	1	1
# misassemblies	0	0	0
# misassembled contigs	0	0	0
Misassembled contigs length	0	0	0
# local misassemblies	0	0	0
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	1	1	2
# unaligned mis. contigs	0	0	0
# unaligned contigs	0 + 0 part	0 + 0 part	0 + 0 part
Unaligned length	0	0	0
Genome fraction (%)	99.034	99.084	98.301
Duplication ratio	0.998	1.000	0.999
# N's per 100 kbp	605.35	1140.35	1640.61
# mismatches per 100 kbp	443.24	459.01	405.29
# indels per 100 kbp	40.60	6.75	27.25
Largest alignment	29555	29629	29362
Total aligned length	29555	29629	29362
NA50	29555	29629	29362
NGA50	29555	29629	29362
NA90	29555	29629	29362
NGA90	29555	29629	29362
auNA	29376.1	29357.5	28865.5
auNGA	29211.0	29357.5	28830.8
LA50	1	1	1
LGA50	1	1	1
LA90	1	1	1
LGA90	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

	SRR33436961_pipecov_consensus	ref_majority	SRR33436961_viralrecon_consensus
# misassemblies	0	0	0
# contig misassemblies	0	0	0
# c. relocations	0	0	0
# c. translocations	0	0	0
# c. inversions	0	0	0
# scaffold misassemblies	0	0	0
# s. relocations	0	0	0
# s. translocations	0	0	0
# s. inversions	0	0	0
# misassembled contigs	0	0	0
Misassembled contigs length	0	0	0
# local misassemblies	0	0	0
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	1	1	2
# unaligned mis. contigs	0	0	0
# mismatches	131	136	119
# indels	12	2	8
# indels (<= 5 bp)	6	2	5
# indels (> 5 bp)	6	0	3
Indels length	85	2	35

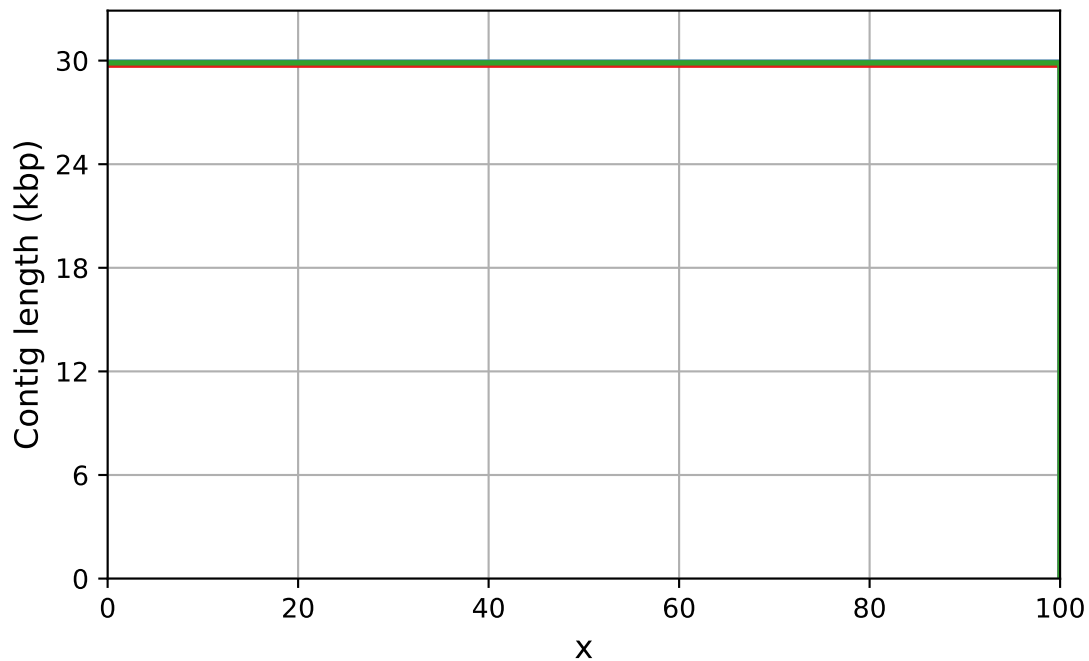
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	SRR33436961_pipecov_consensus	ref_majority	SRR33436961_viralrecon_consensus
# fully unaligned contigs	0	0	0
Fully unaligned length	0	0	0
# partially unaligned contigs	0	0	0
Partially unaligned length	0	0	0
# N's	180	341	490

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

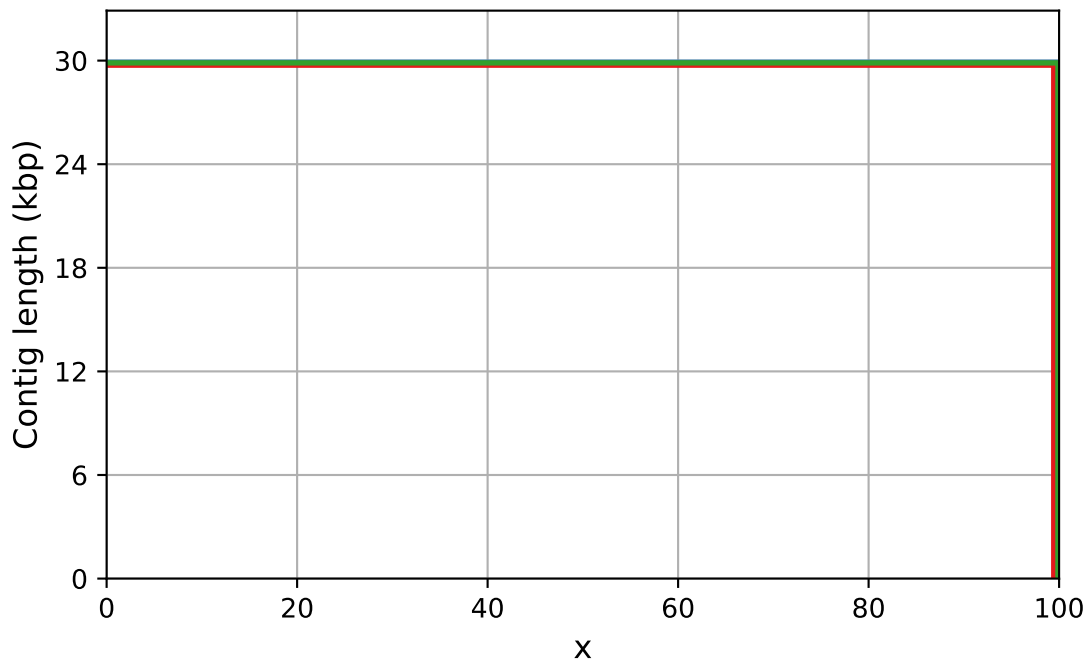


RR33436961_pipecov_consensus

ref_majority

SRR33436961_viralrecon_co

NGx

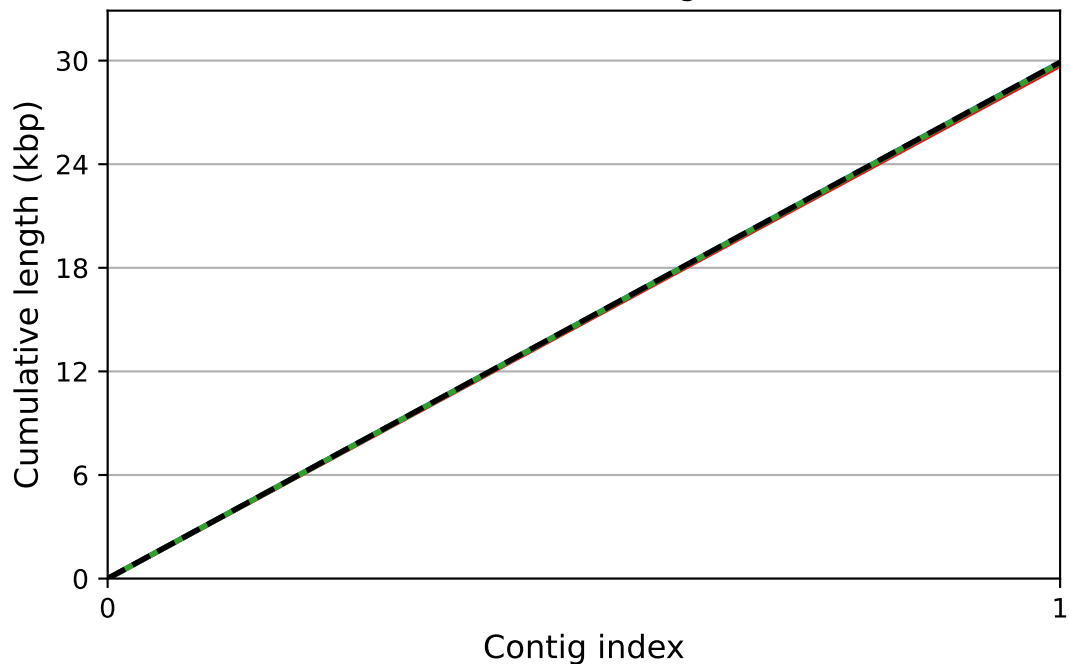


RR33436961_pipecov_consensus

ref_majority

SRR33436961_viralrecon_co

Cumulative length

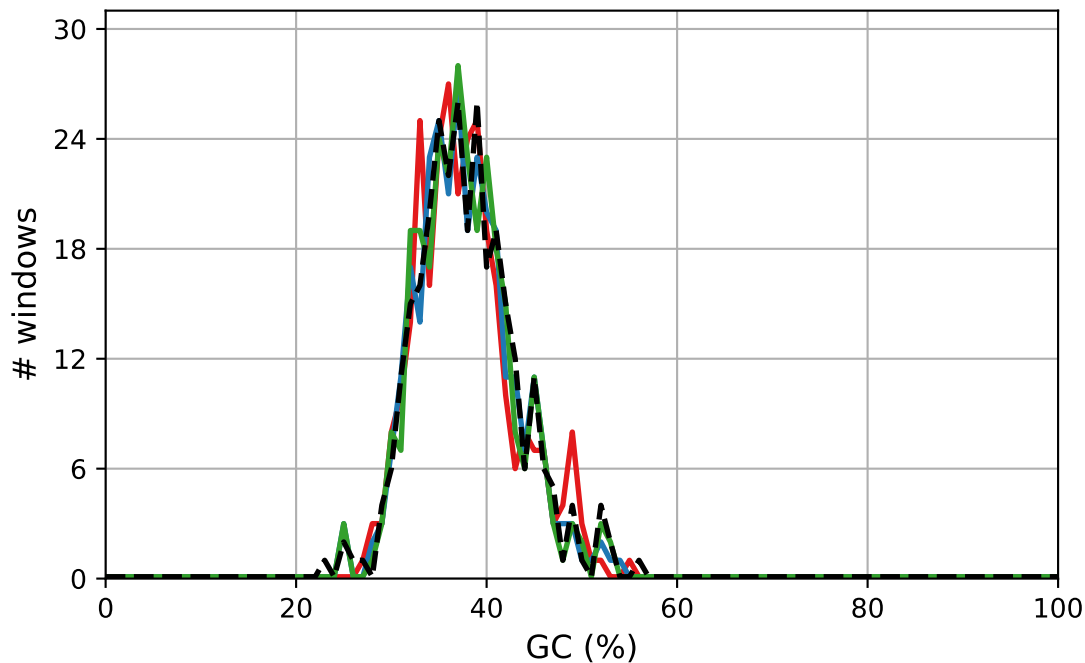


SRR33436961_pipecov_consensus
Refef_majority

SRR33436961_viralrecon_consensus

Refef_majority

GC content



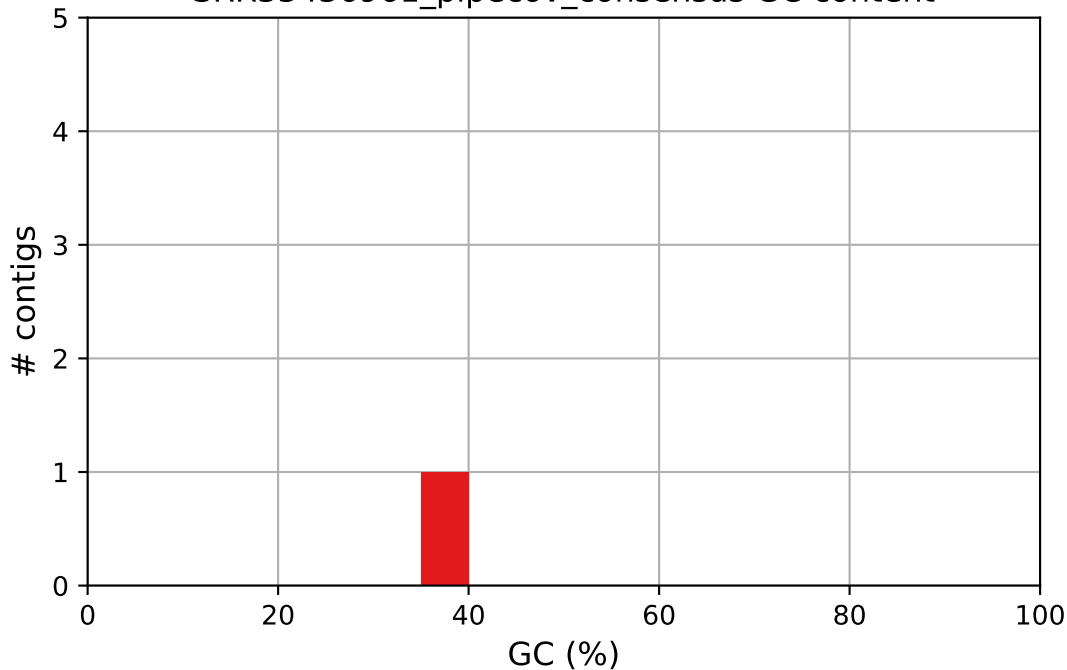
SRR33436961_pipecov_consensus

SRR33436961_viralrecon_consensus

Ref_majority

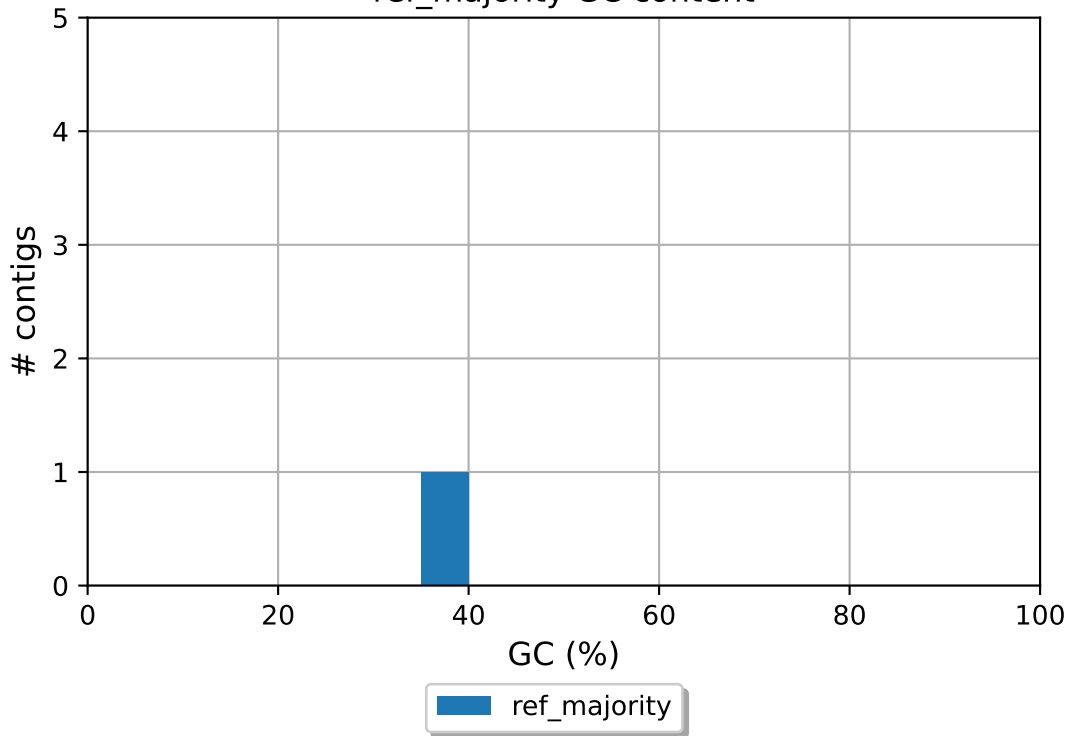
ef_majority

SRR33436961_pipecov_consensus GC content

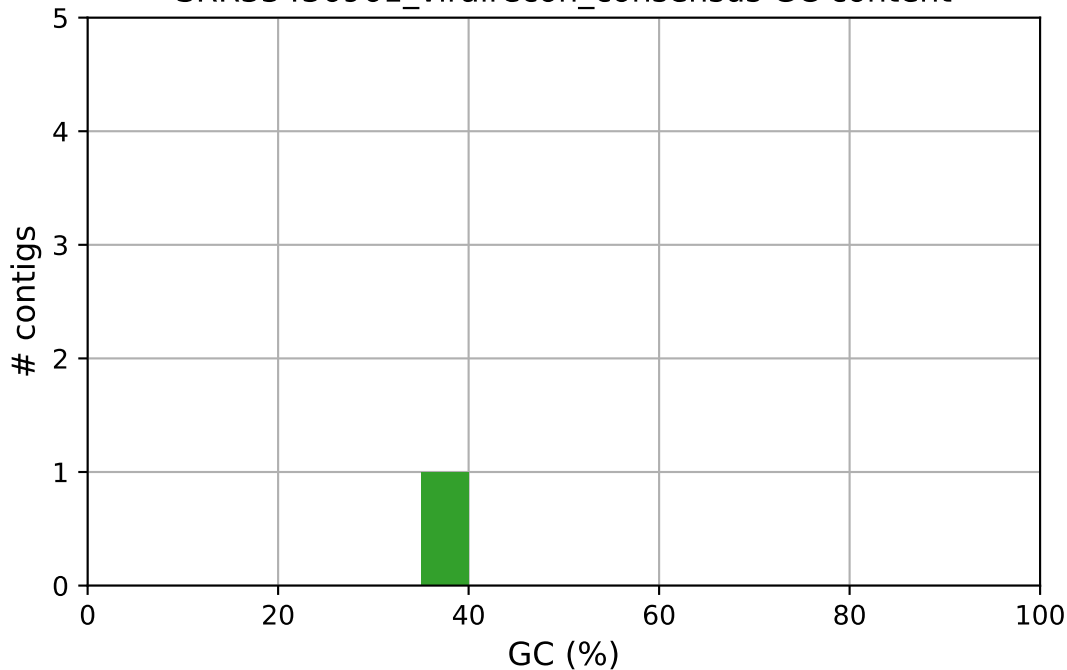


■ SRR33436961_pipecov_consensus

ref_majority GC content

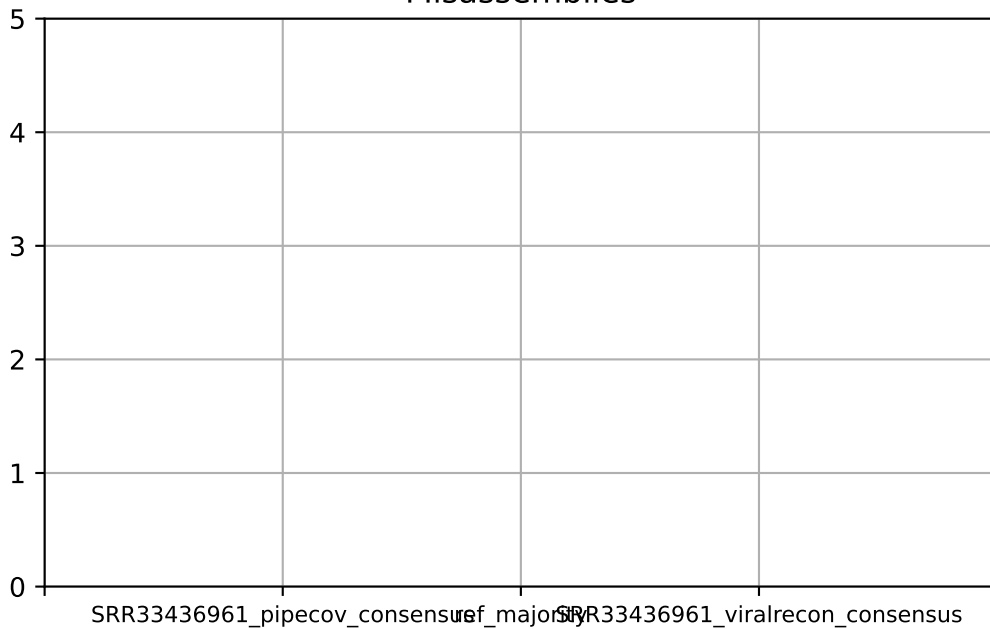


SRR33436961_viralrecon_consensus GC content

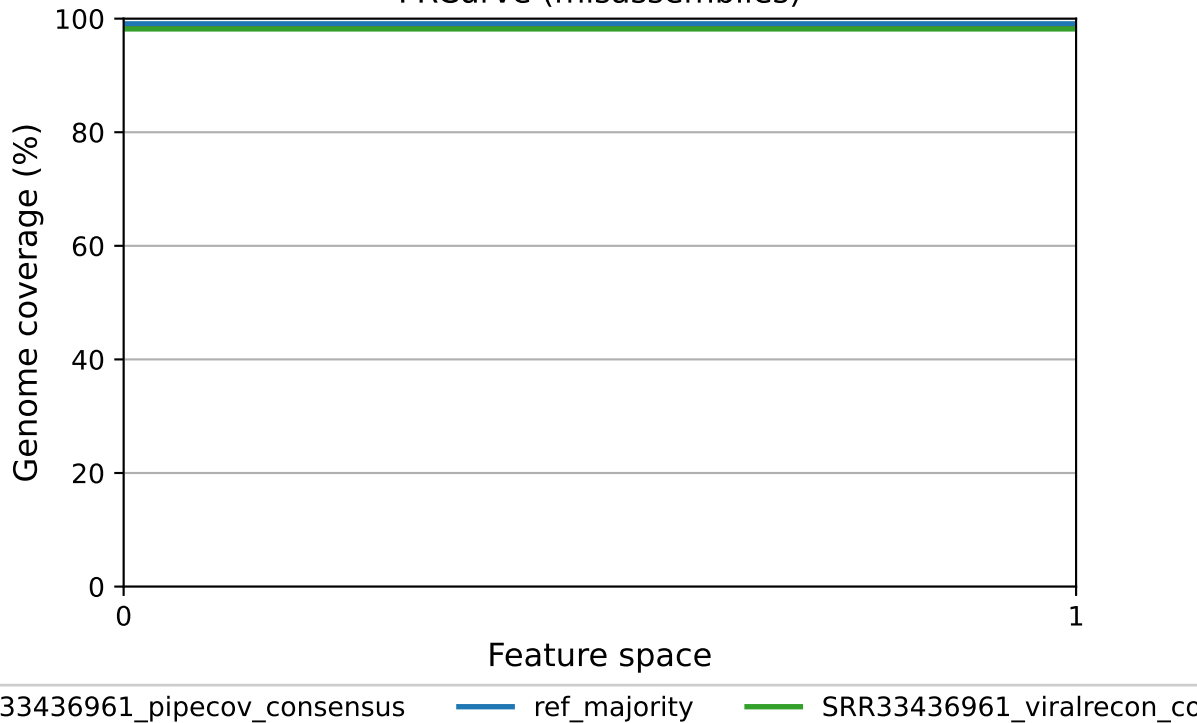


SRR33436961_viralrecon_consensus

Misassemblies



FRCurve (misassemblies)



Cumulative length (aligned contigs)

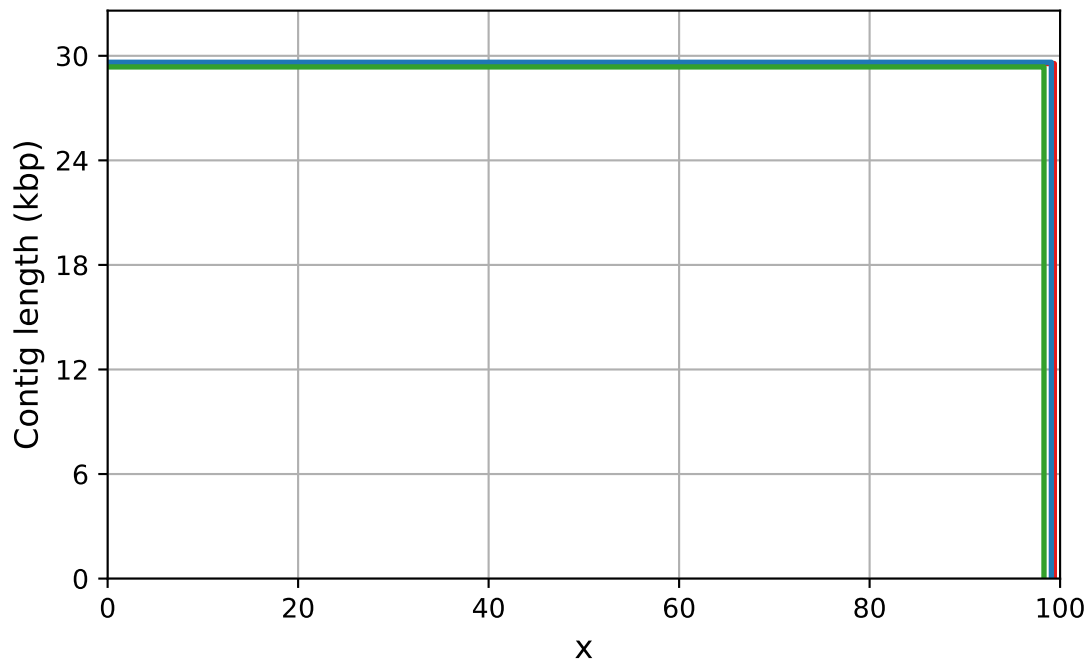


SRR33436961_pipecov_consensus
ref_majority

SRR33436961_viralrecon_consensus

Re

NAx

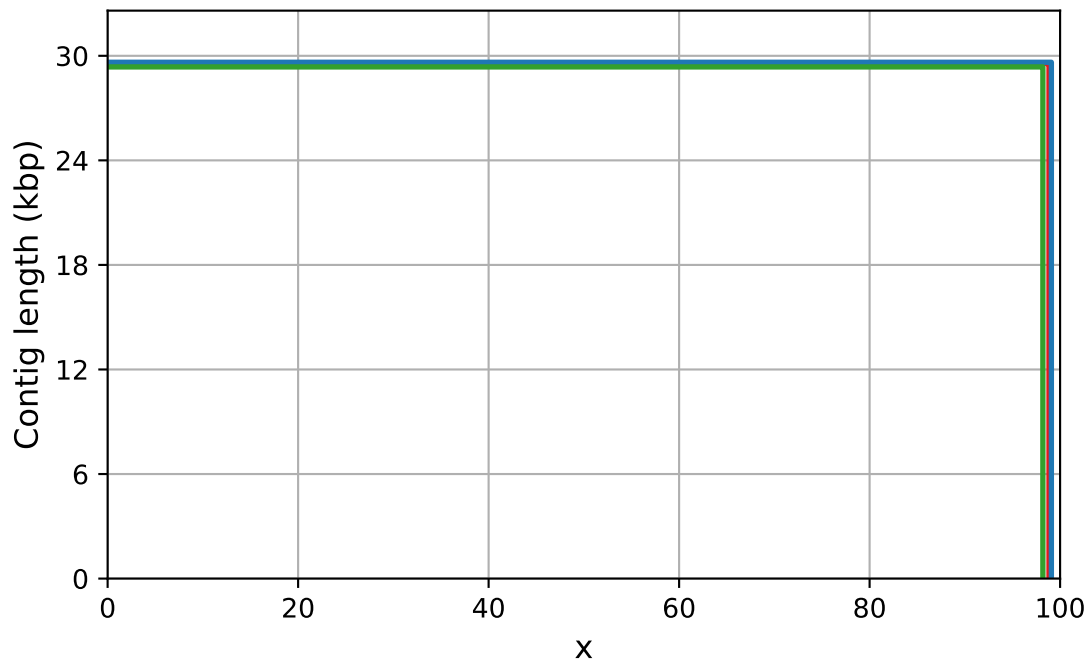


RR33436961_pipcov_consensus

ref_majority

SRR33436961_viralrecon_co

NGAx



RR33436961_pipecov_consensus

ref_majority

SRR33436961_viralrecon_co

Genome fraction, %

100

99

98

RR33436961_pipecov_consensus

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SRR33436961_viralrecon_co

