

Report

	SAMPLE2_PE.consensus	SAMPLE1_PE.consensus	SAMPLE3_SE.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)	29903	29903	29903
Total length (>= 1000 bp)	29903	29903	29903
Total length (>= 5000 bp)	29903	29903	29903
Total length (>= 10000 bp)	29903	29903	29903
Total length (>= 25000 bp)	29903	29903	29903
Total length (>= 50000 bp)	0	0	0
# contigs	1	1	1
Largest contig	29903	29903	29903
Total length	29903	29903	29903
Reference length	29903	29903	29903
GC (%)	38.12	37.95	37.98
Reference GC (%)	37.97	37.97	37.97
N50	29903	29903	29903
NG50	29903	29903	29903
N90	29903	29903	29903
NG90	29903	29903	29903
auN	29903.0	29903.0	29903.0
auNG	29903.0	29903.0	29903.0
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.	9	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 (%)	89.804	98.094	97.432
Duplication ratio	1.000	1.000	1.000
# N's per 100 kbp	10497.27	2193.76	3096.68
# mismatches per 100 kbp	22.34	20.45	6.86
# indels per 100 kbp	0.00	0.00	0.00
# genomic features	10 + 13 part	17 + 6 part	17 + 6 part
Largest alignment	26854	29333	29135
Total aligned length	26854	29333	29135
NA50	26854	29333	29135
NGA50	26854	29333	29135
NA90	-	29333	29135
NGA90	-	29333	29135
auNA	24115.9	28773.9	28386.7
auNGA	24115.9	28773.9	28386.7
LA50	1	1	1
LGA50	1	1	1
LA90	-	1	1
LGA90	-	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

	SAMPLE2_PE.consensus	SAMPLE1_PE.consensus	SAMPLE3_SE.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.	9	1	2
# unaligned mis. contigs	0	0	0
# mismatches	6	6	2
# indels	0	0	0
# indels (<= 5 bp)	0	0	0
# indels (> 5 bp)	0	0	0
Indels length	0	0	0

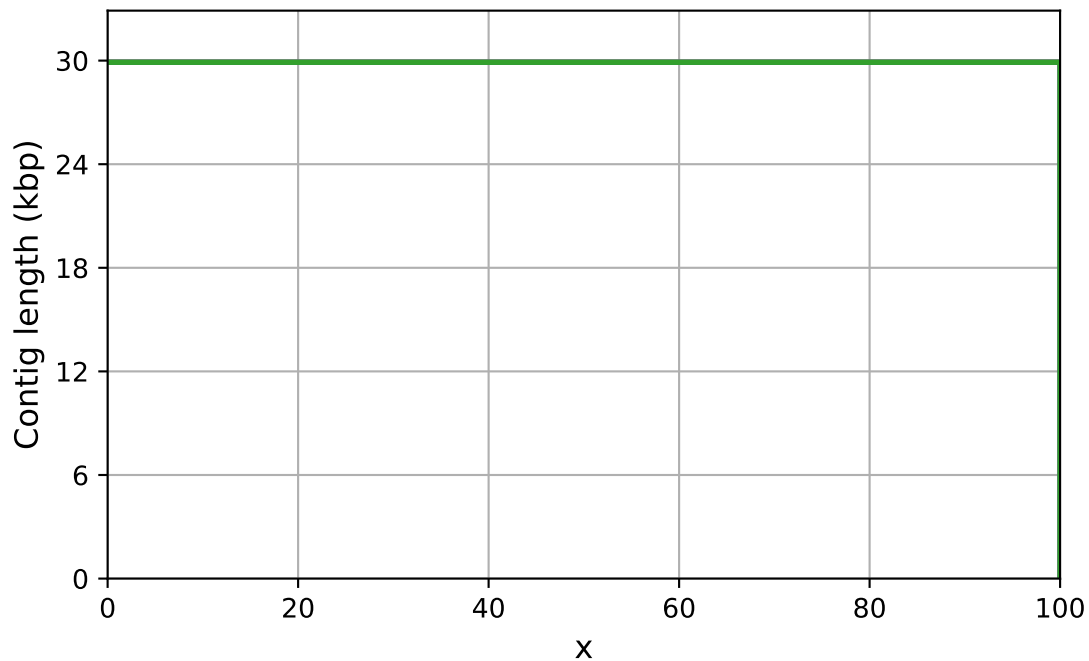
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	SAMPLE2_PE.consensus	SAMPLE1_PE.consensus	SAMPLE3_SE.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	3139	656	926

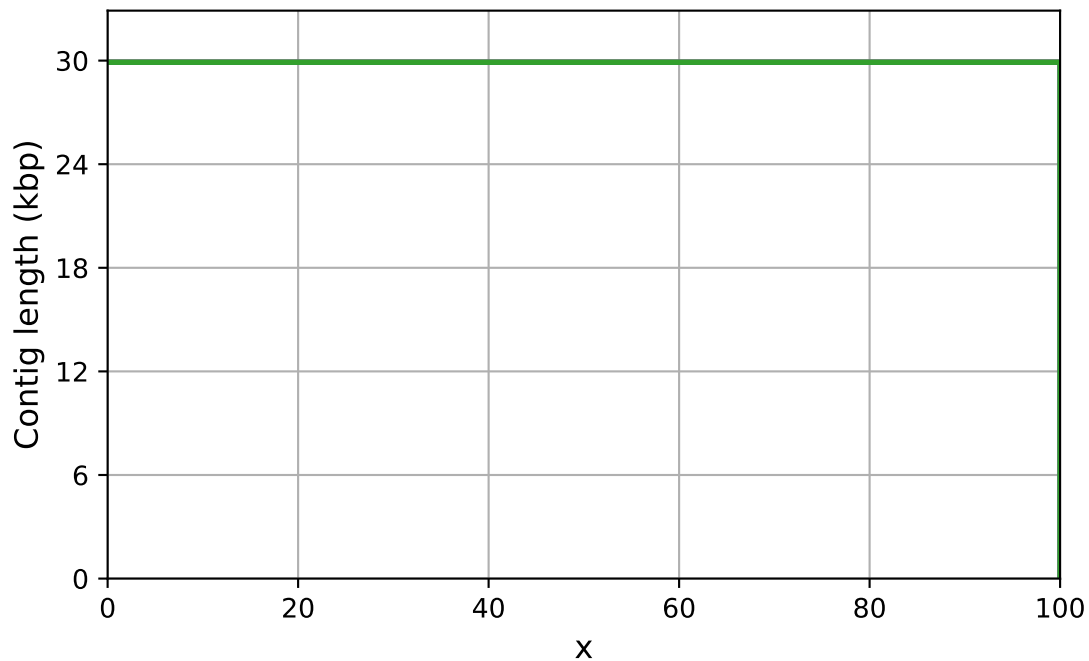
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



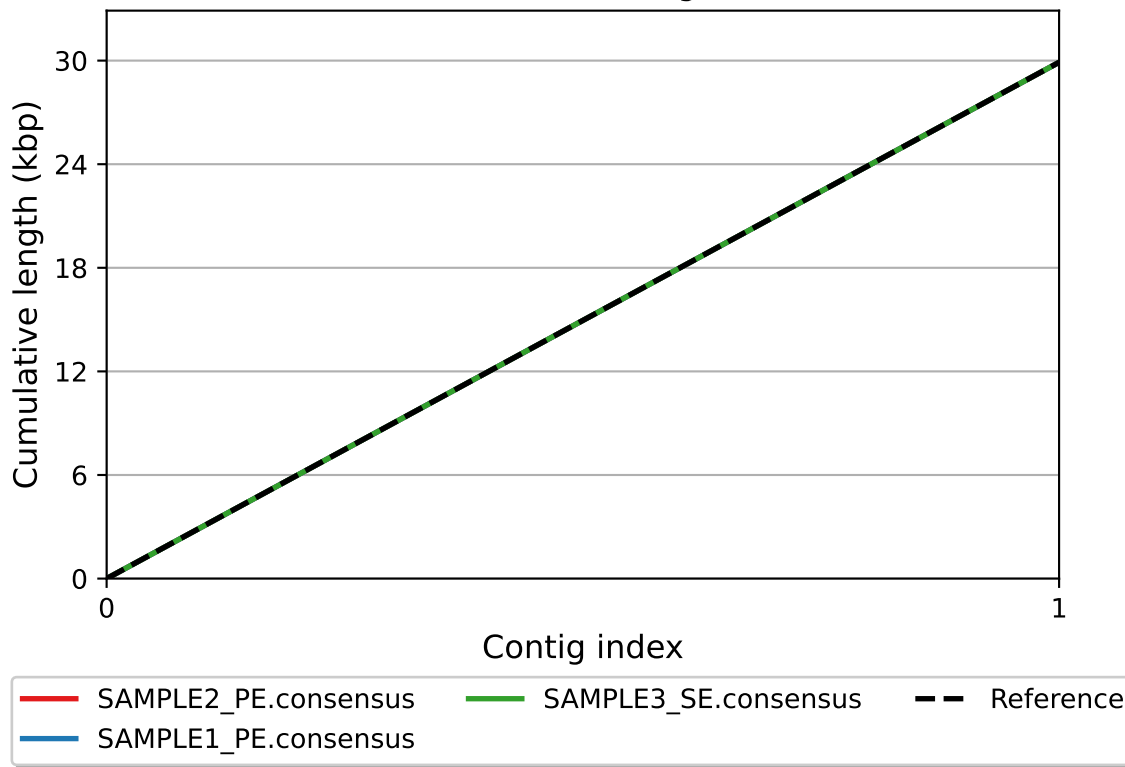
SAMPLE2_PE.consensus SAMPLE1_PE.consensus SAMPLE3_SE.consensus

NGx

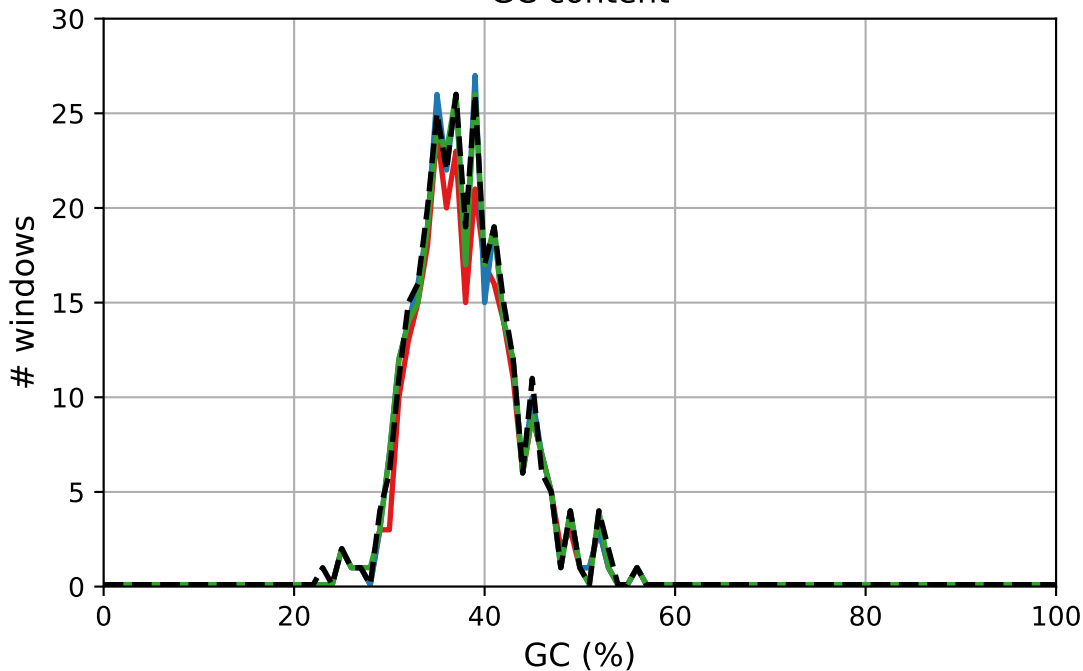


SAMPLE2_PE.consensus SAMPLE1_PE.consensus SAMPLE3_SE.consensus

Cumulative length

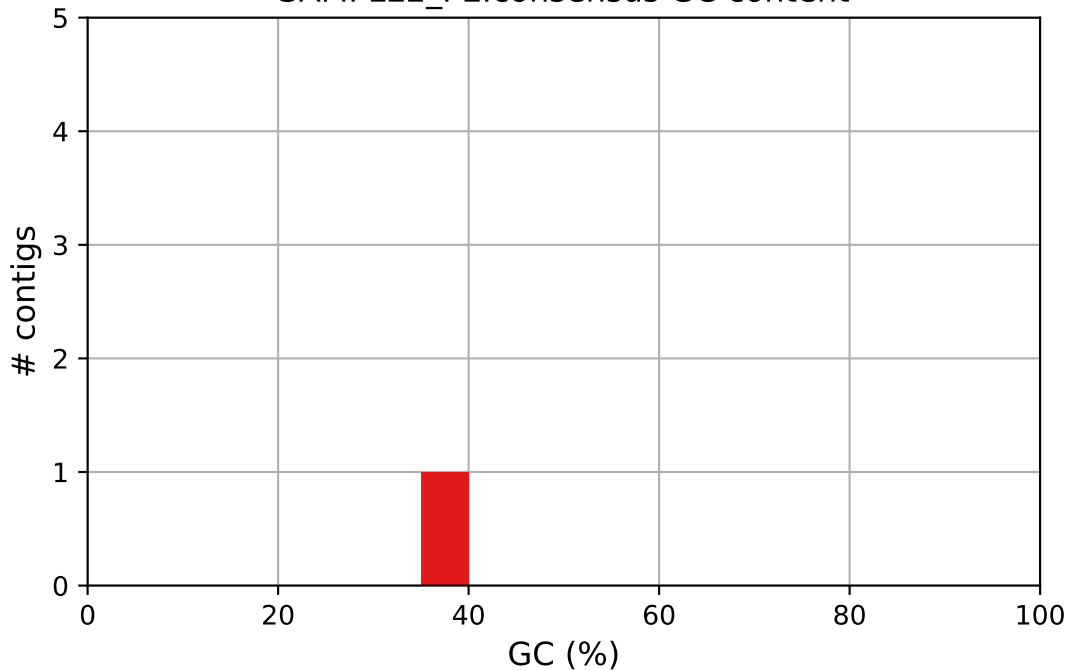


GC content



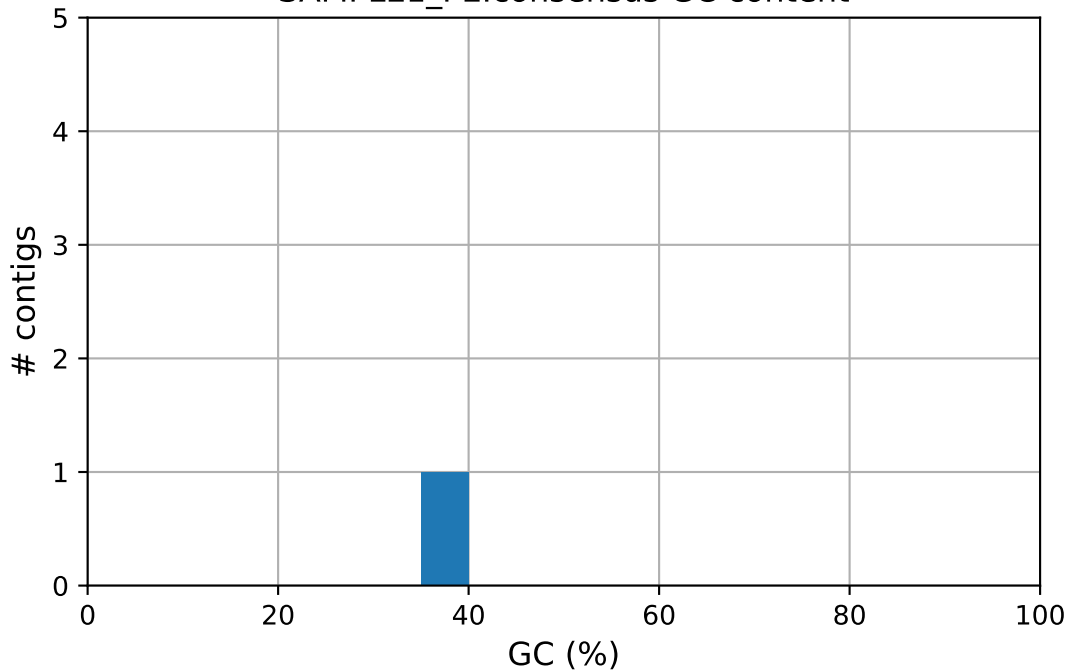
SAMPLE2_PE.consensus SAMPLE3_SE.consensus Reference
SAMPLE1_PE.consensus

SAMPLE2_PE.consensus GC content



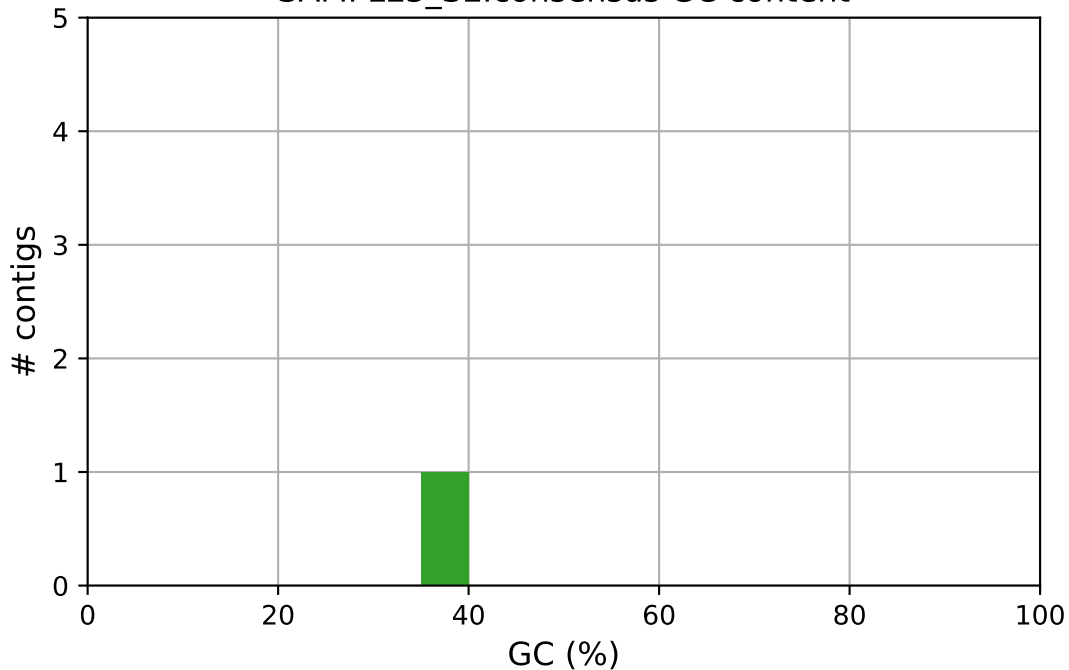
■ SAMPLE2_PE.consensus


SAMPLE1_PE.consensus GC content



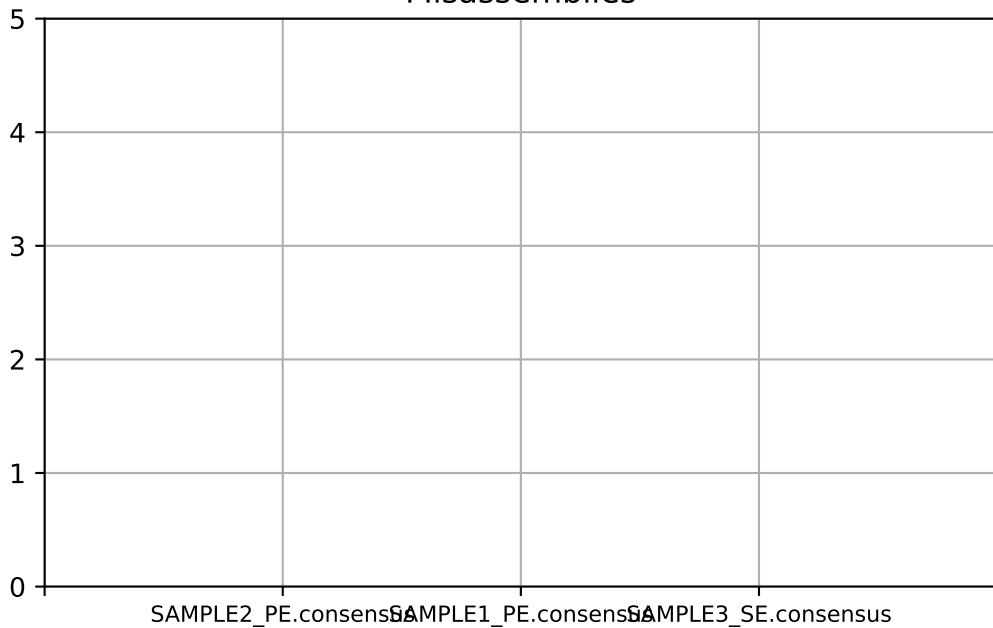
SAMPLE1_PE.consensus

SAMPLE3_SE.consensus GC content

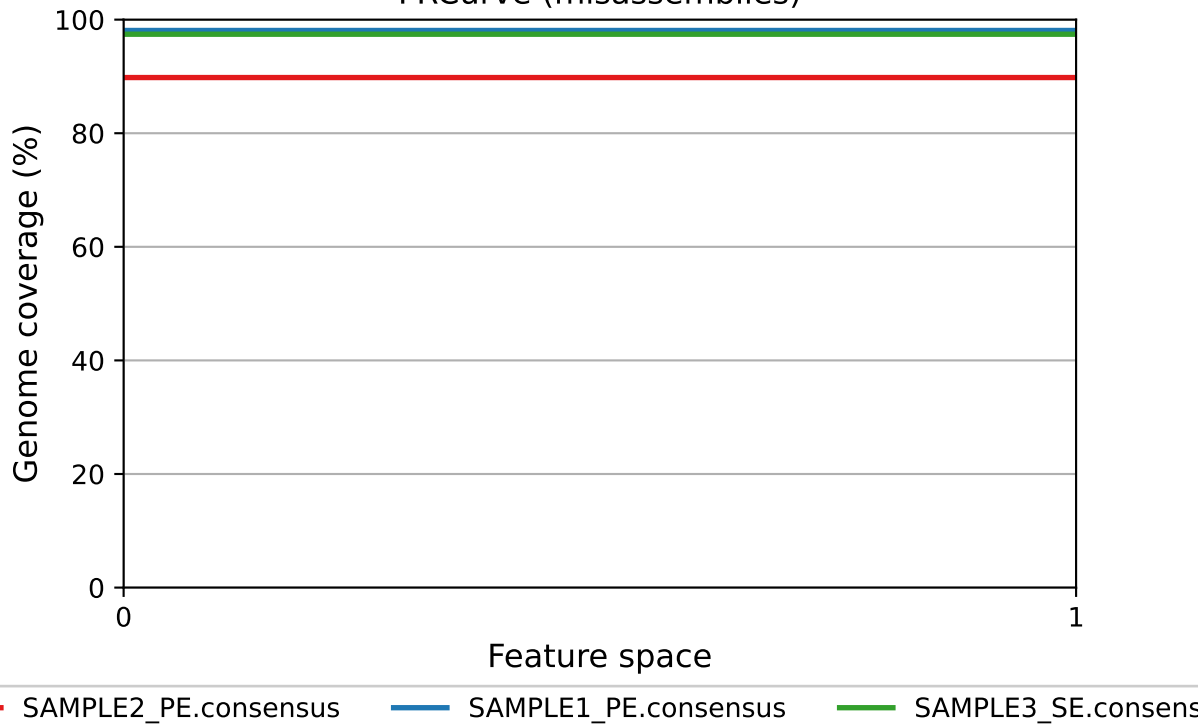


 SAMPLE3_SE.consensus

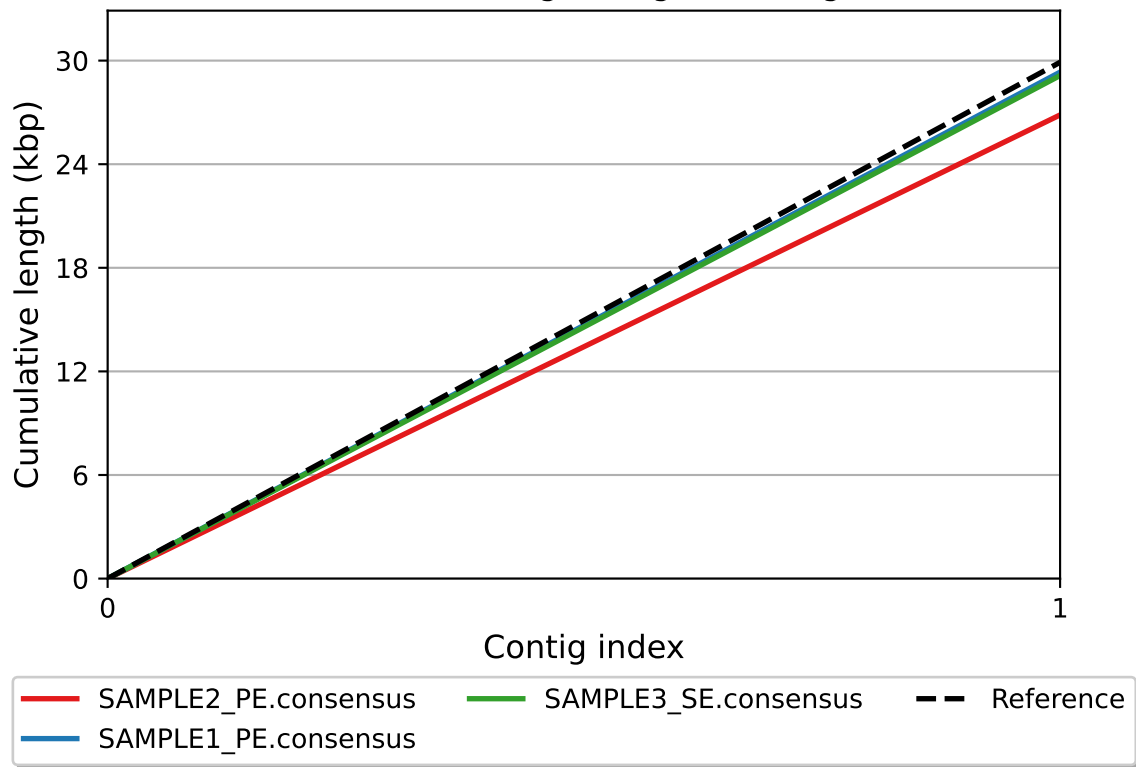
Misassemblies



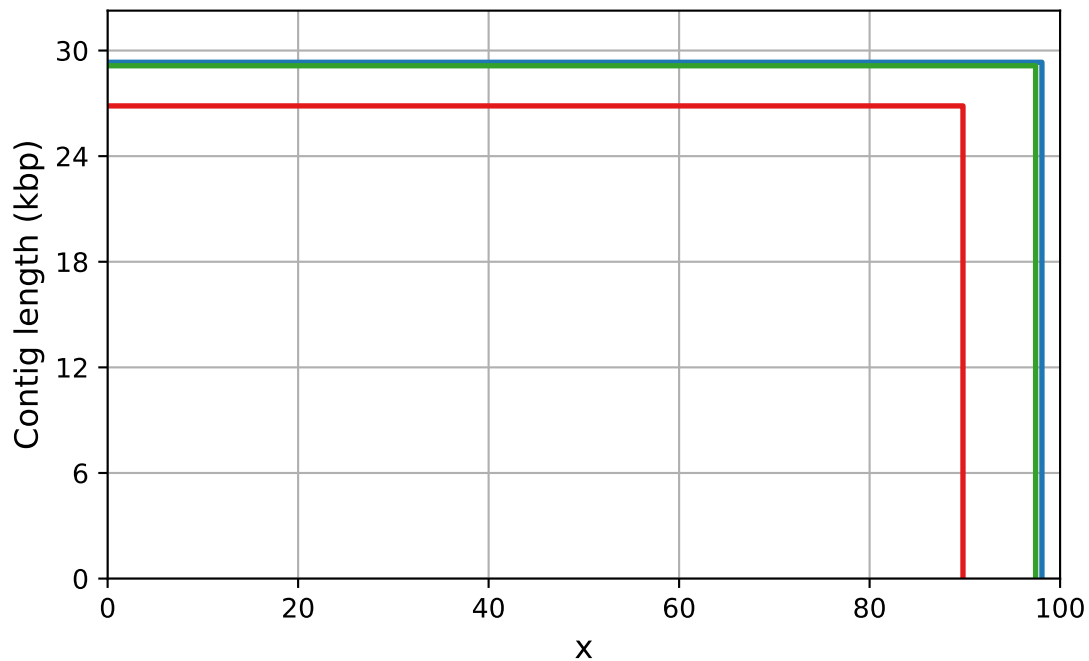
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx

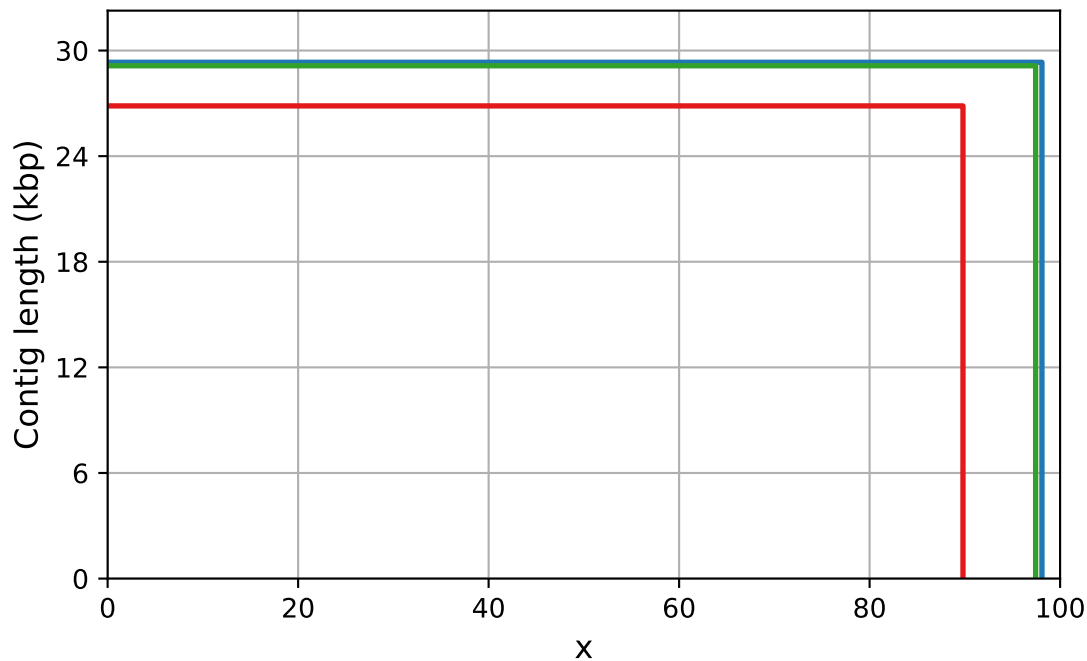


— SAMPLE2_PE.consensus

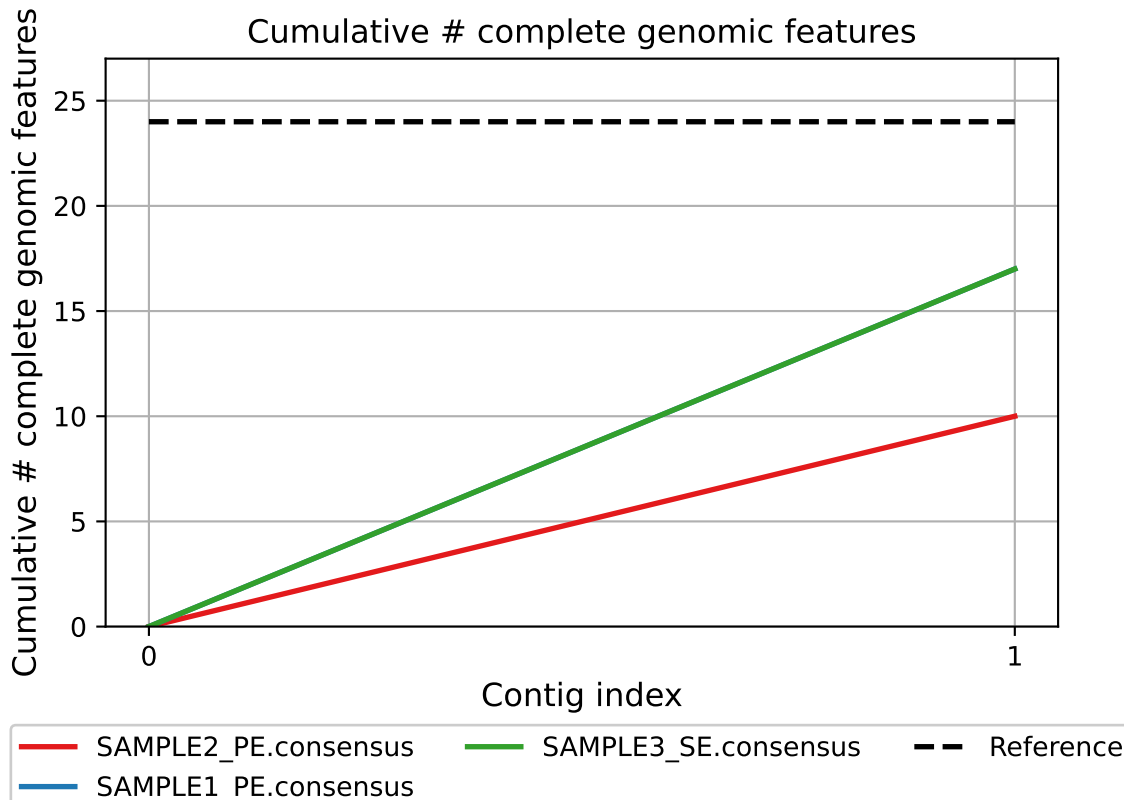
— SAMPLE1_PE.consensus

— SAMPLE3_SE.consensus

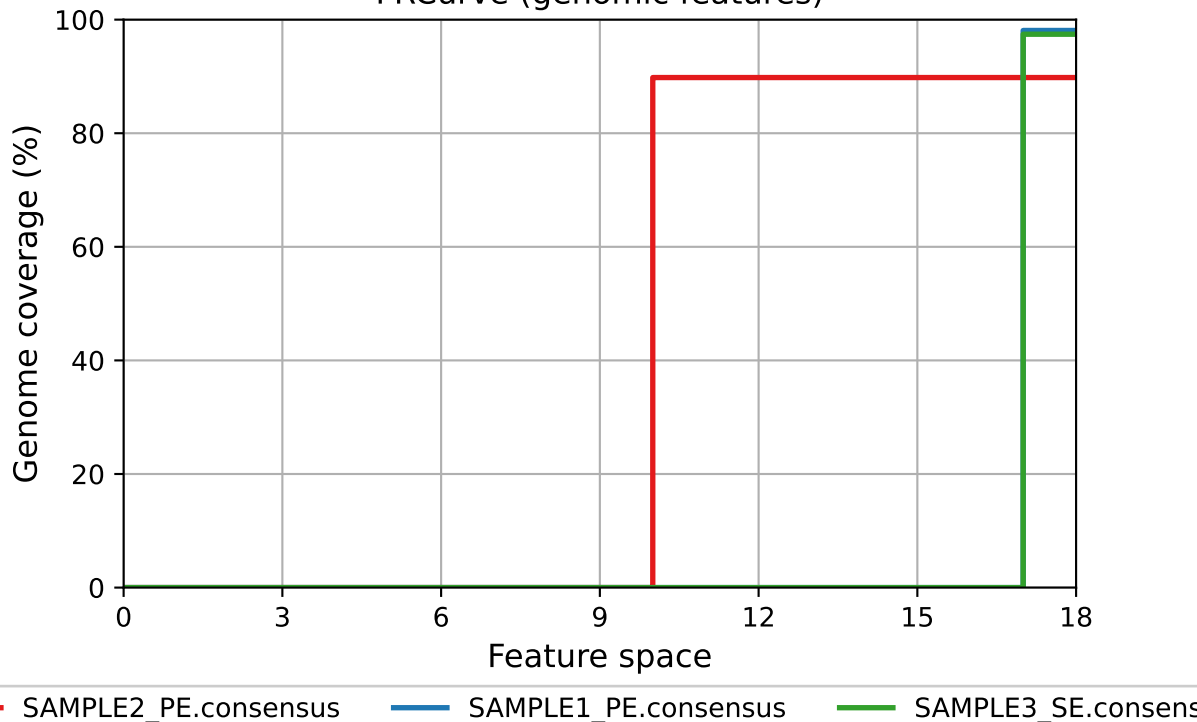
NGAx



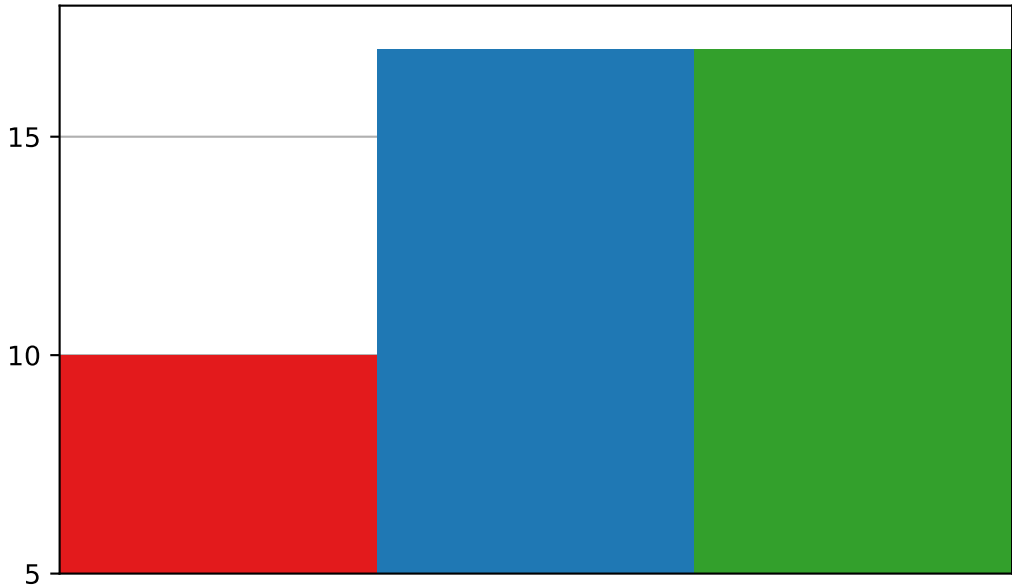
— SAMPLE2_PE.consensus — SAMPLE1_PE.consensus — SAMPLE3_SE.consensus



FRCurve (genomic features)



complete genomic features



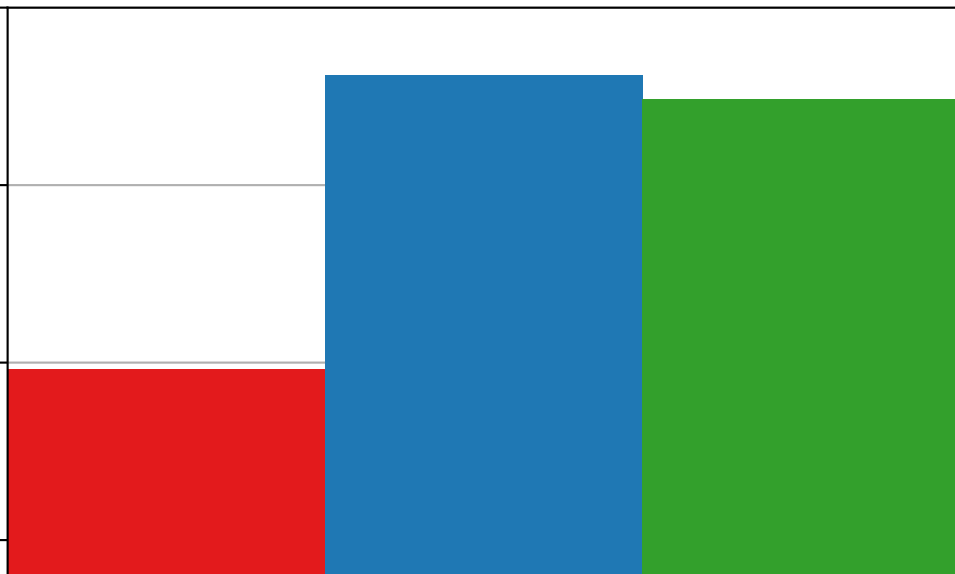
■ SAMPLE2_PE.consensus

■ SAMPLE1_PE.consensus

■ SAMPLE3_SE.consensus

Genome fraction, %

100
95
90
85



■ SAMPLE2_PE.consensus

■ SAMPLE1_PE.consensus

■ SAMPLE3_SE.consensus