Report

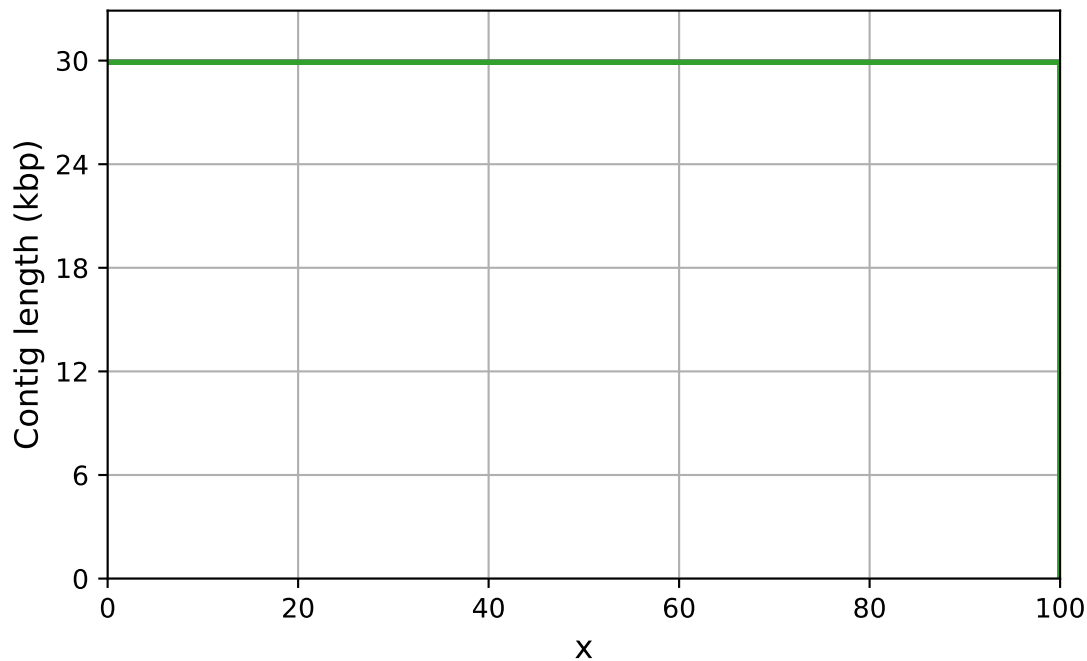|	SAMPLE3_SE.consensus.masked	SAMPLE1_PE.consensus.masked	SAMPLE2_PE.consensus.masked
# contigs (>= 0 bp)	1	1	1
# contigs (>= 1000 bp)	1	1	1
# contigs (>= 5000 bp)	1	1	1
# contigs (>= 10000 bp)	1	1	1
# contigs (>= 25000 bp)	1	1	1
# contigs (>= 50000 bp)	0	0	0
Total length (>= 0 bp)	29903	29903	29903
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 (%)	37.98	37.95	38.13
Reference GC (%)	37.97	37.97	37.97
N50	29903	29903	29903
NG50	29903	29903	29903
N75	29903	29903	29903
NG75	29903	29903	29903
L50	1	1	1
LG50	1	1	1
L75	1	1	1
LG75	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.	2	1	9
# unaligned mis. contigs	0	0	0
# unaligned contigs	0 + 0 part	0 + 0 part	0 + 0 part
Unaligned length	0	0	0
Genome fraction (%)	97.432	98.094	89.804
Duplication ratio	1.026	1.019	1.114
# N's per 100 kbp	3100.02	2193.76	10497.27
# mismatches per 100 kbp	17.16	20.45	18.62
# indels per 100 kbp	0.00	0.00	0.00
# genomic features	23 + 7 part	23 + 7 part	14 + 14 part
Largest alignment	29135	29333	26854
Total aligned length	29135	29333	26854
NA50	29135	29333	26854
NGA50	29135	29333	26854
NA75	29135	29333	26854
NGA75	29135	29333	26854
LA50	1	1	1
LGA50	1	1	1
LA75	1	1	1
LGA75	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).
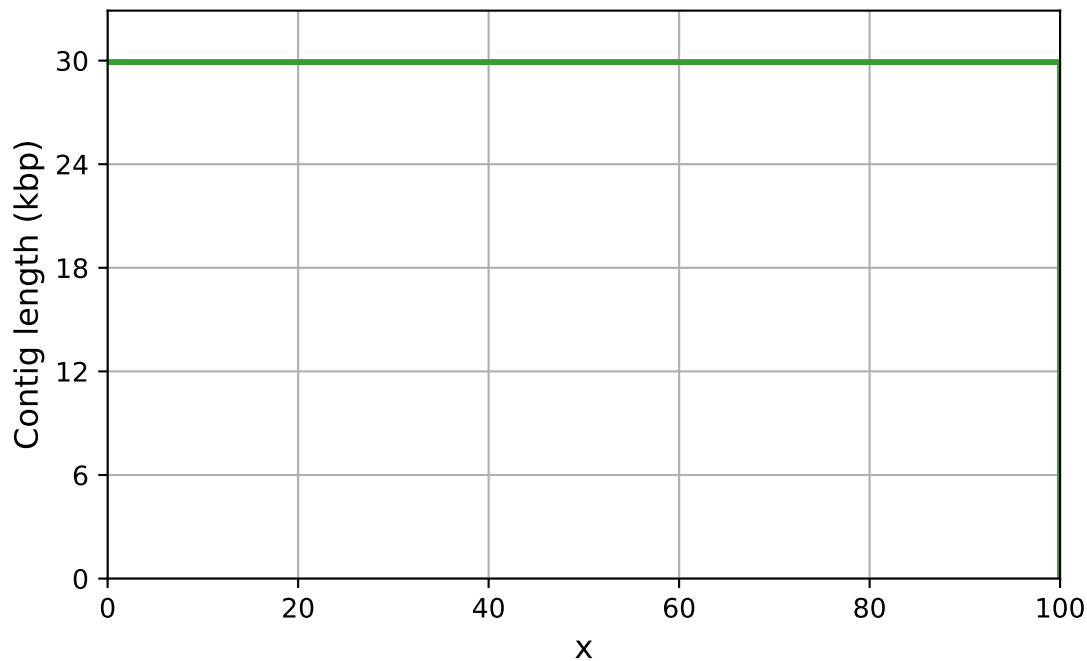
Misassemblies report

	SAMPLE3_SE.consensus.masked	SAMPLE1_PE.consensus.masked	SAMPLE2_PE.consensus.masked
# 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.	2	1	9
# unaligned mis. contigs	0	0	0
# mismatches	5	6	5
# 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

	SAMPLE3_SE.consensus.masked	SAMPLE1_PE.consensus.masked	SAMPLE2_PE.consensus.masked
# 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	927	656	3139

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

3_SE.consensus.masked ——— SAMPLE1_PE.consensus.masked ——— SAMPLE2_PE.con

NGx

Cumulative length

SAMPLE3_SE.consensus.masked   SAMPLE2_PE.consensus.masked   Refere

SAMPLE1_PE.consensus.masked
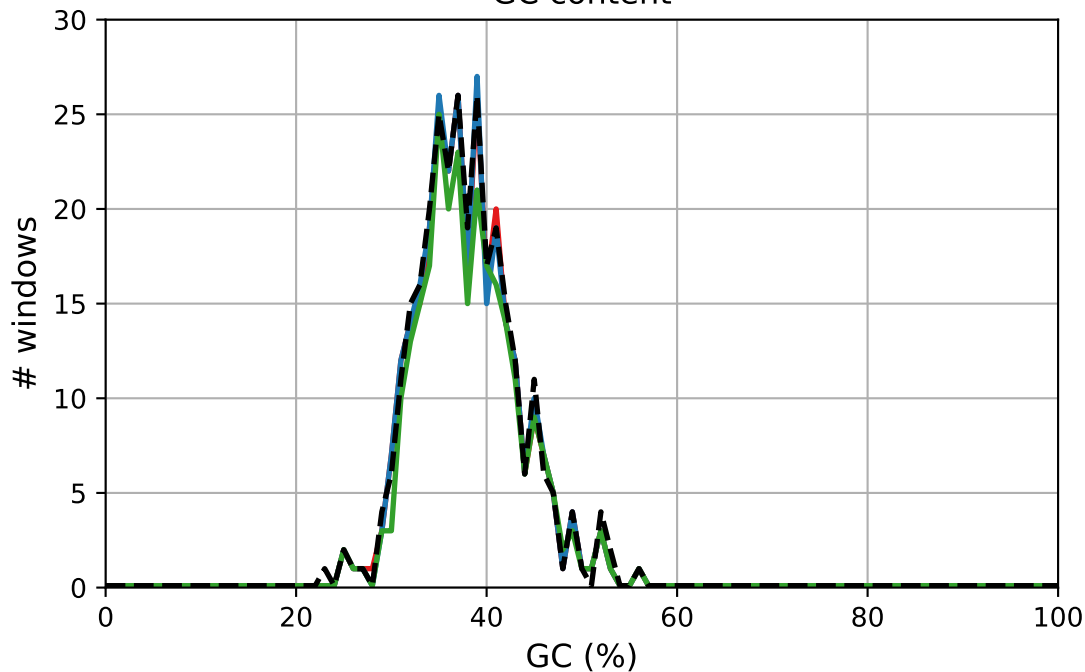
GC content

SAMPLE3_SE.consensus.masked   SAMPLE2_PE.consensus.masked   Refere

SAMPLE1_PE.consensus.masked
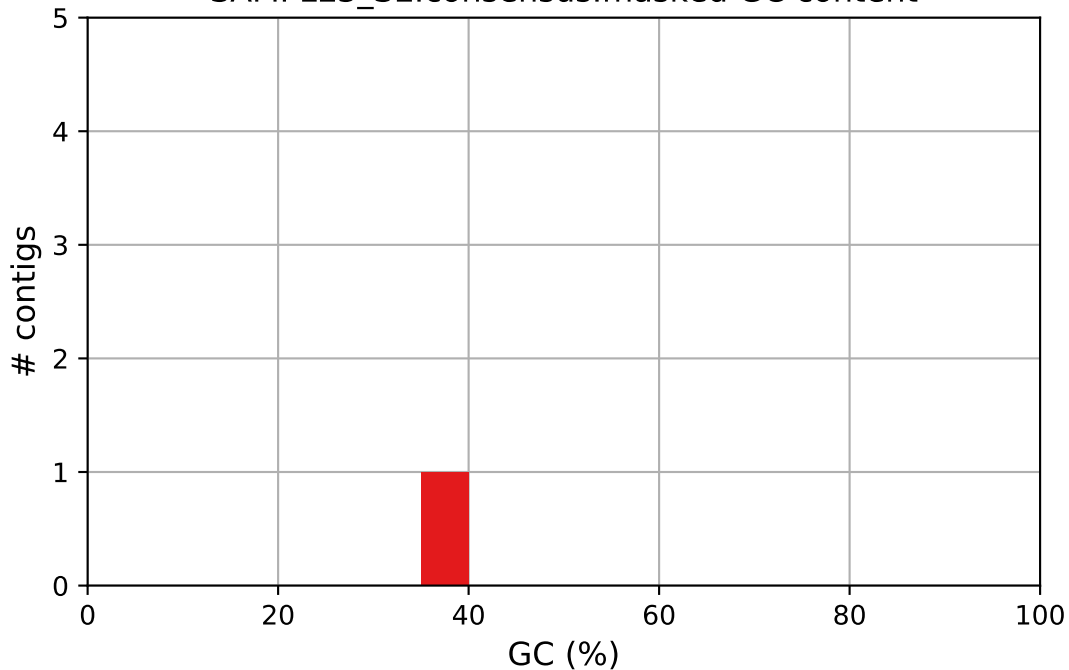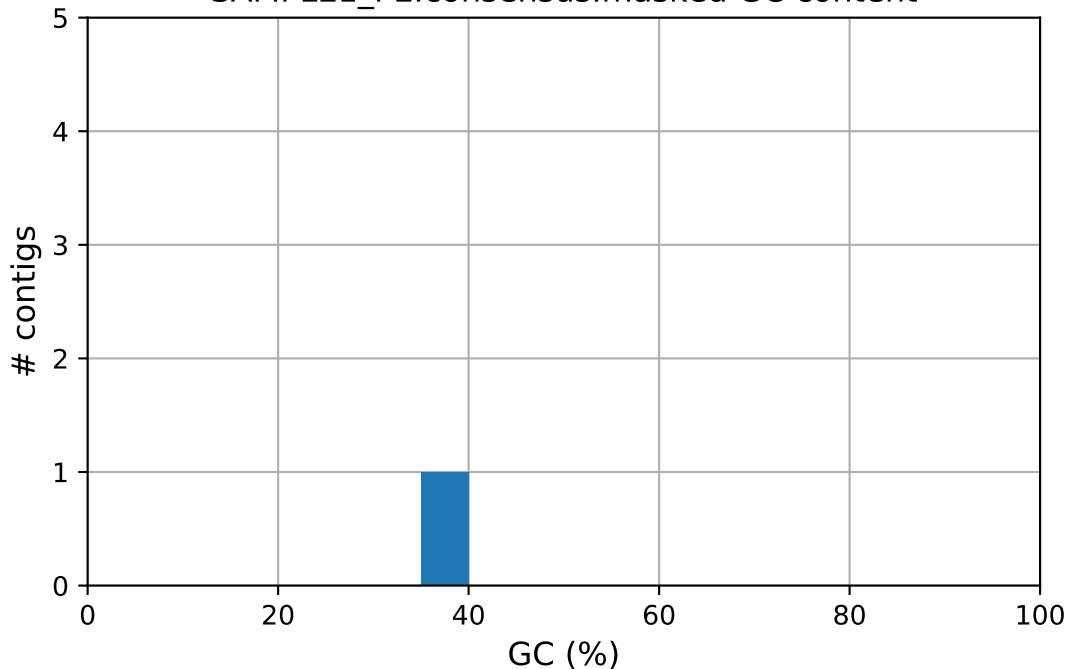
SAMPLE3_SE.consensus.masked GC content

SAMPLE1_PE.consensus.masked GC content
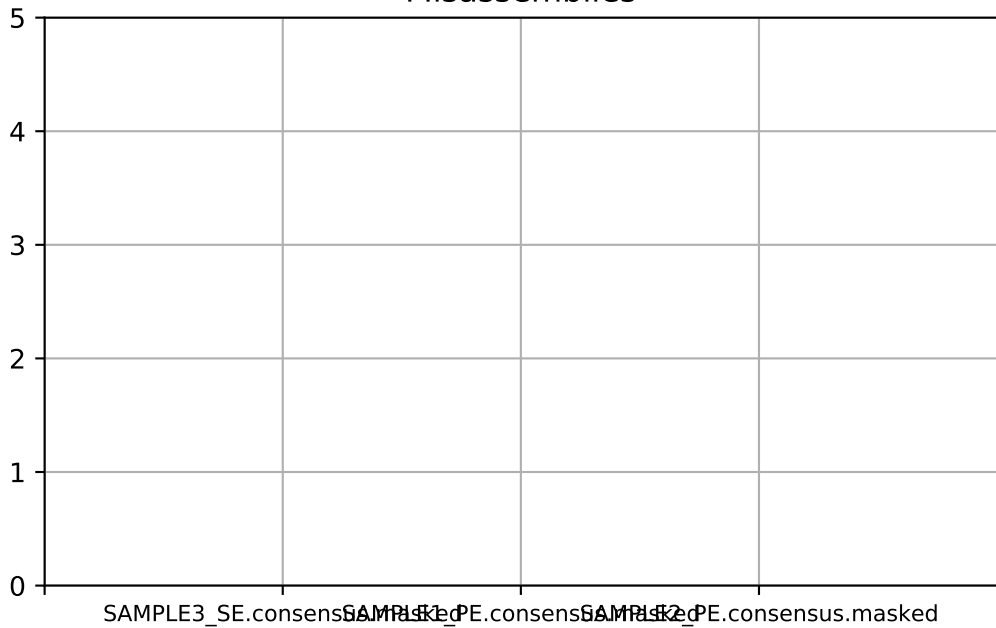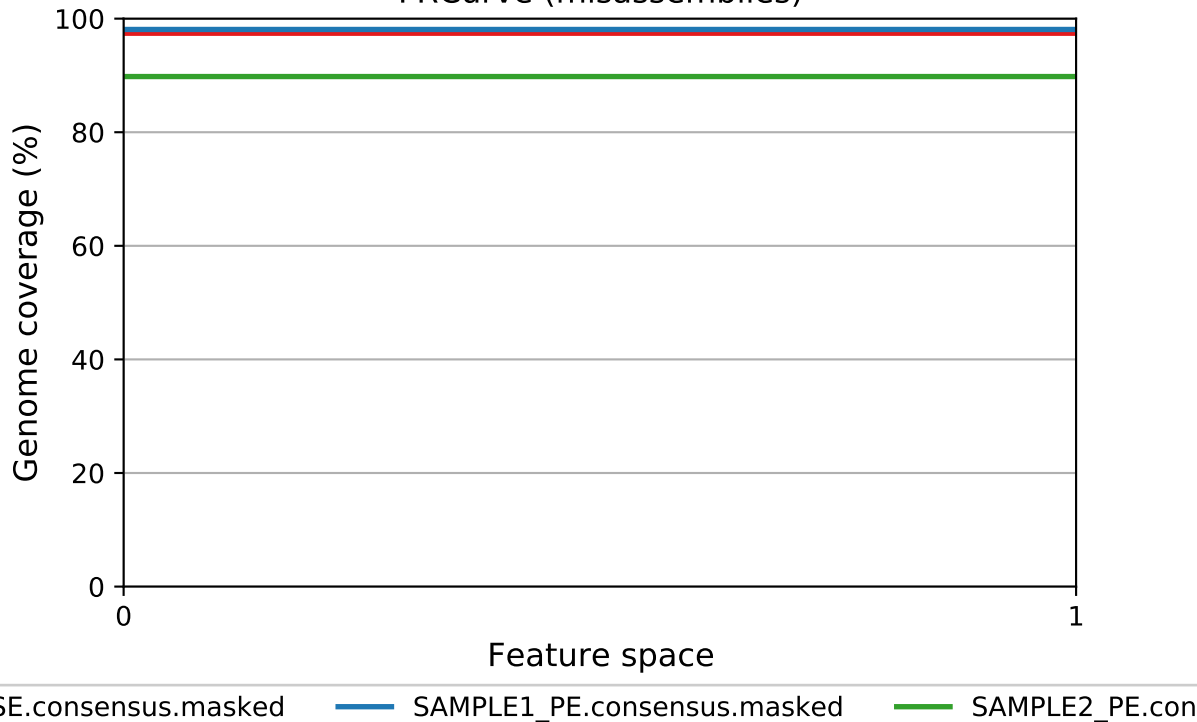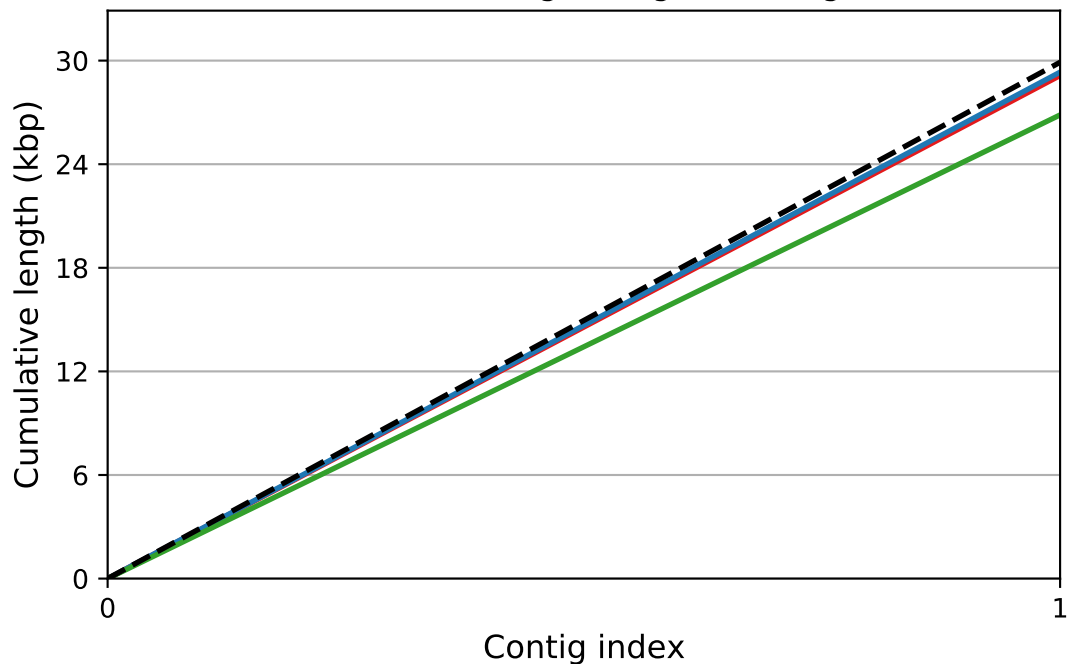
SAMPLE2_PE.consensus.masked GC content

contigs

GC (%)

SAMPLE2_PE.consensus.masked

Misassemblies

SAMPLE3_SE.consensus.masked SAMPLE1_PE.consensus.masked SAMPLE2_PE.consensus.masked
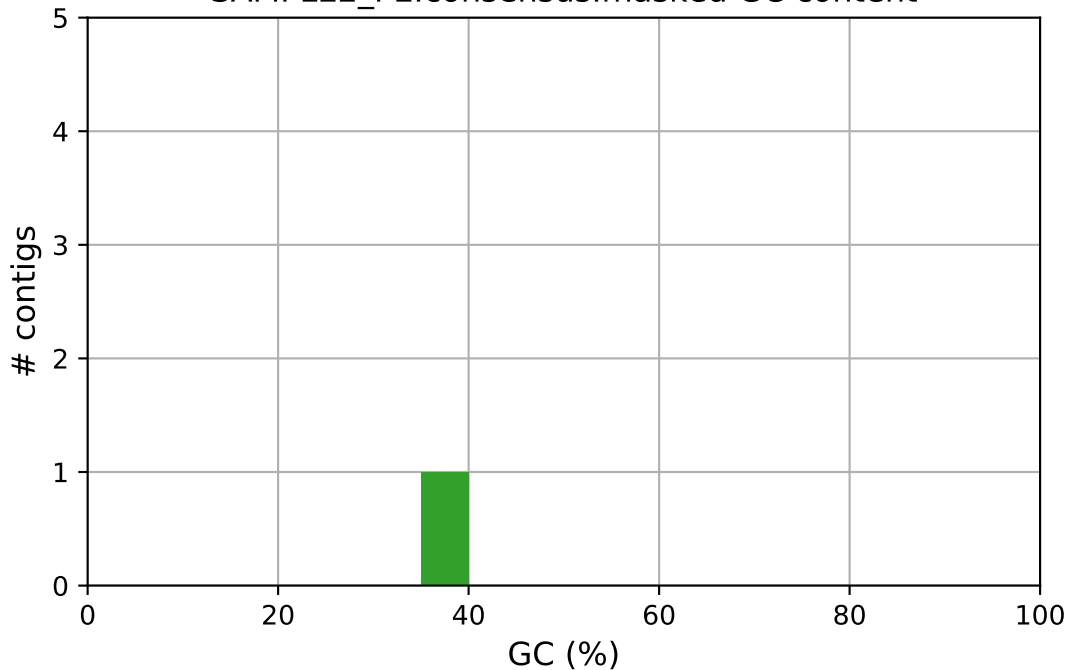
FRCurve (misassemblies)

Cumulative length (aligned contigs)

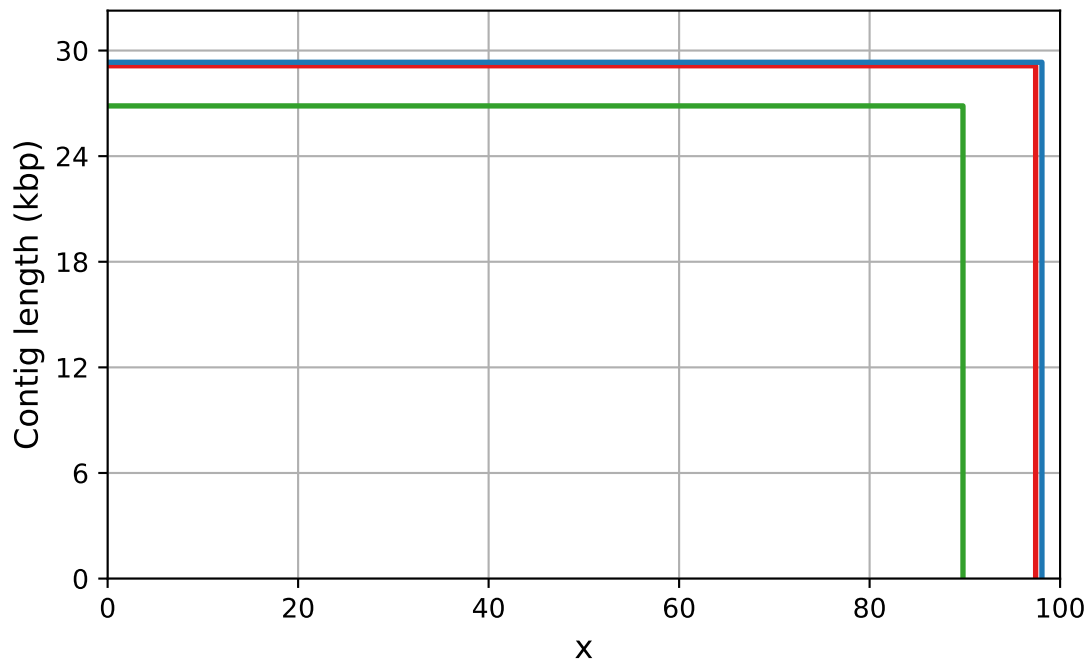— SAMPLE3_SE.consensus.masked   — SAMPLE2_PE.consensus.masked   -- Refere
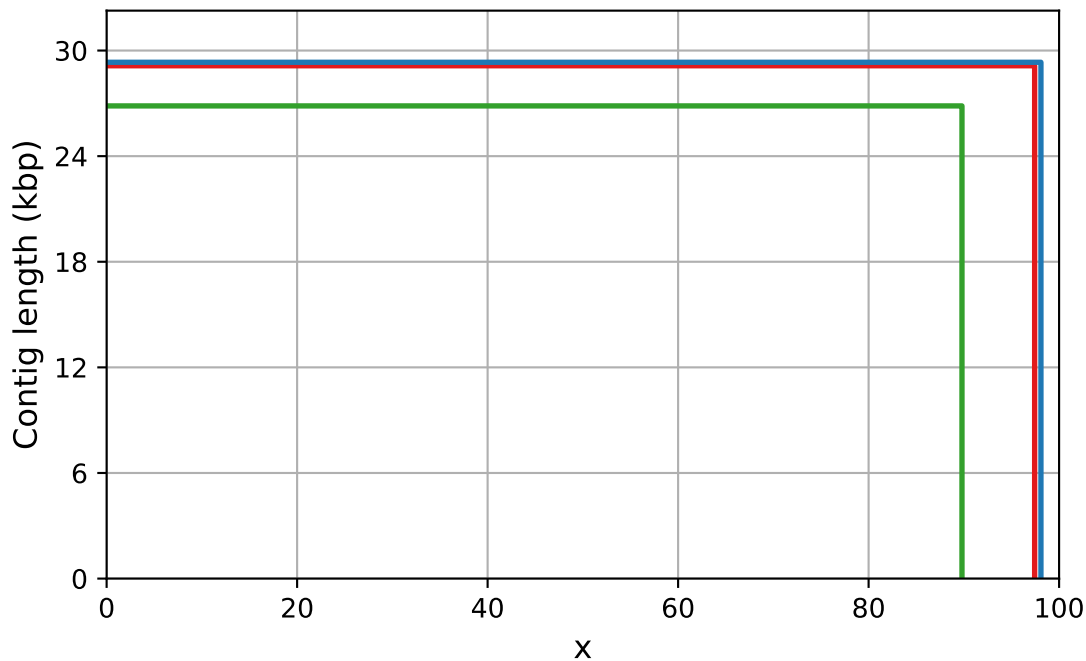
— SAMPLE1_PE.consensus.masked

NAx

Contig length (kbp) vs x

3_SE.consensus.masked   SAMPLE1_PE.consensus.masked   SAMPLE2_PE.con

NGAx

Cumulative # complete genomic features

— SAMPLE3_SE.consensus.masked	— SAMPLE2_PE.consensus.masked
— SAMPLE1_PE.consensus.masked	- - Refere
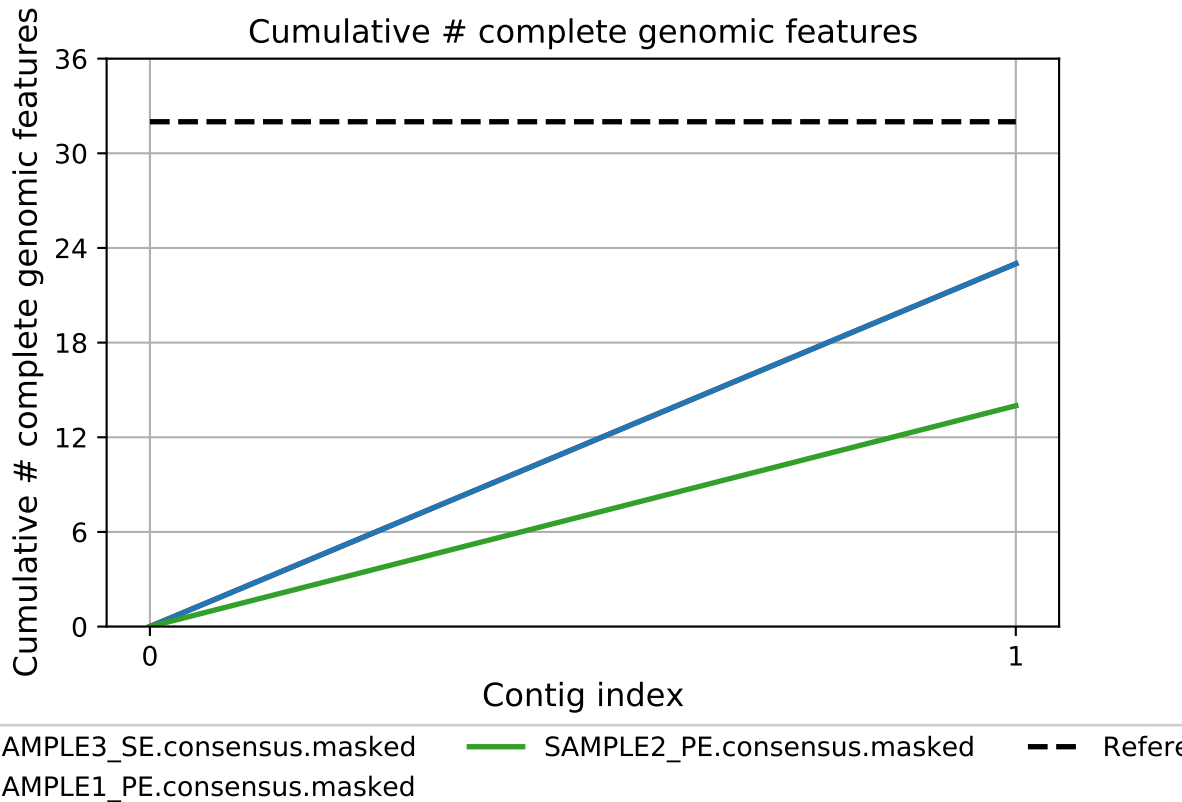
FRCurve (genomic features)

SAMPLE3_SE.consensus.masked SAMPLE1_PE.consensus.masked SAMPLE2_PE.con

complete genomic features

Genome fraction, %

Legend:
- 3_SE.consensus.masked
- SAMPLE1_PE.consensus.masked
- SAMPLE2_PE.con...