

Report

	SAMPLE3_SE.AF0.8.consensus.masked	SAMPLE2_PE.AF0.8.consensus.masked	SAMPLE1_PE.AF0.8.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	38.12	37.95
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	9	1
# 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	89.804	98.094
Duplication ratio	1.026	1.114	1.019
# N's per 100 kbp	3100.02	10497.27	2193.76
# mismatches per 100 kbp	0.00	22.34	20.45
# indels per 100 kbp	0.00	0.00	0.00
# genomic features	23 + 7 part	14 + 14 part	23 + 7 part
Largest alignment	29135	26854	29333
Total aligned length	29135	26854	29333
NA50	29135	26854	29333
NGA50	29135	26854	29333
NA75	29135	26854	29333
NGA75	29135	26854	29333
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.AF0.8.consensus.masked	SAMPLE2_PE.AF0.8.consensus.masked	SAMPLE1_PE.AF0.8.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	9	1
# unaligned mis. contigs	0	0	0
# mismatches	0	6	6
# indels	0	0	0
# indels (<= 5 bp)	0	0	0
# indels (> 5 bp)	0	0	0
Indels length	0	0	0

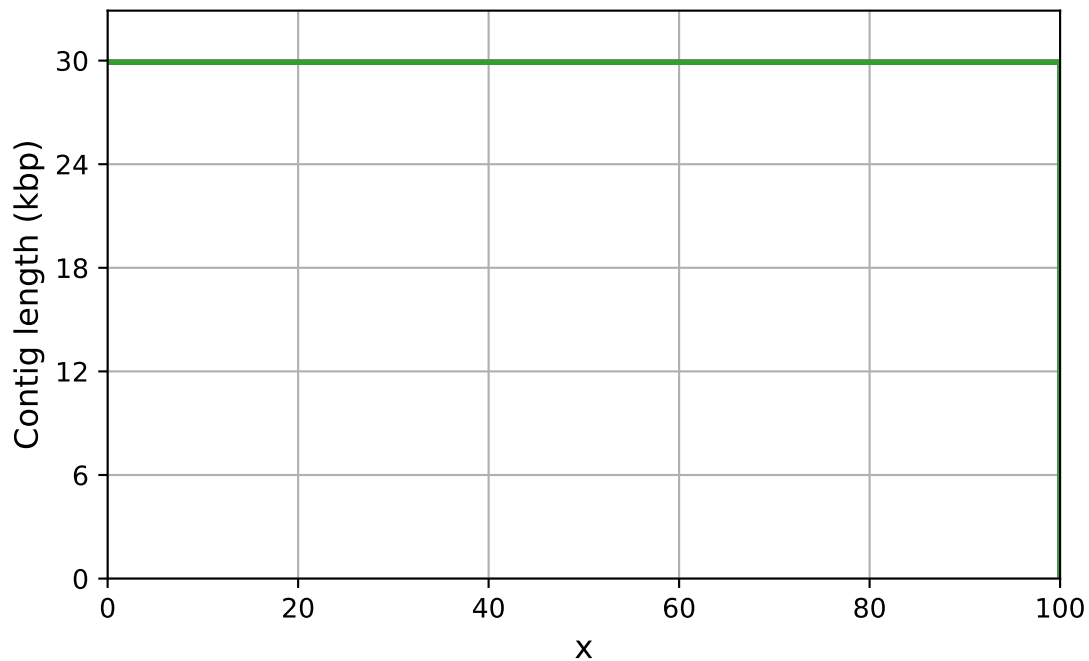
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	SAMPLE3_SE.AF0.8.consensus.masked	SAMPLE2_PE.AF0.8.consensus.masked	SAMPLE1_PE.AF0.8.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	3139	656

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

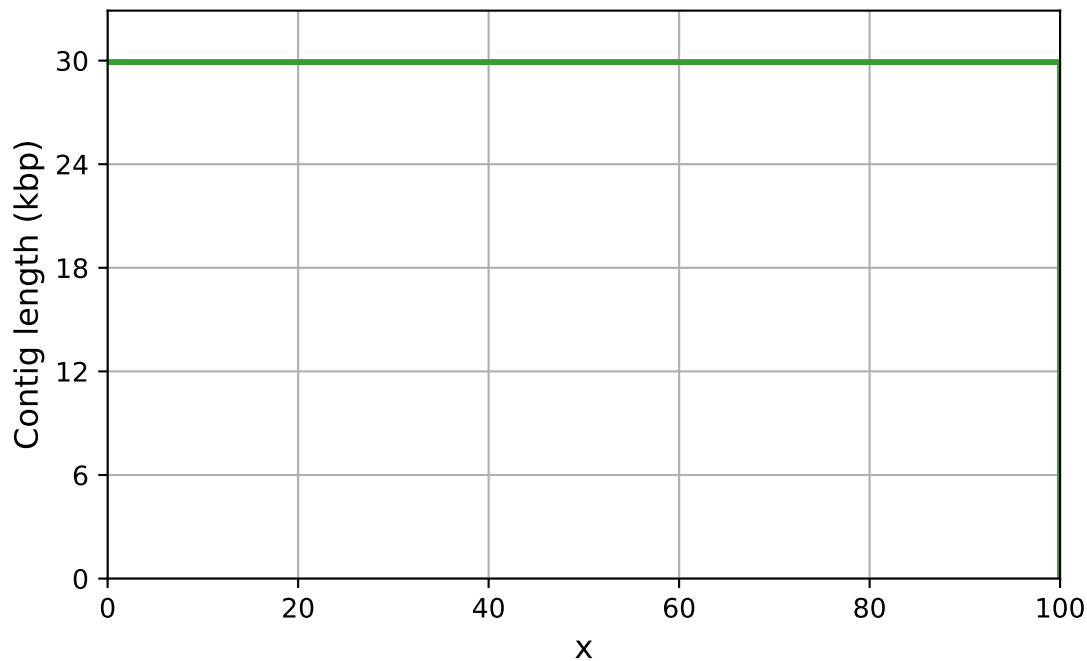


3.consensus.masked

SAMPLE2_PE.AF0.8.consensus.masked

SAMPLE1_PE.AF0.8.consensus.masked

NGx

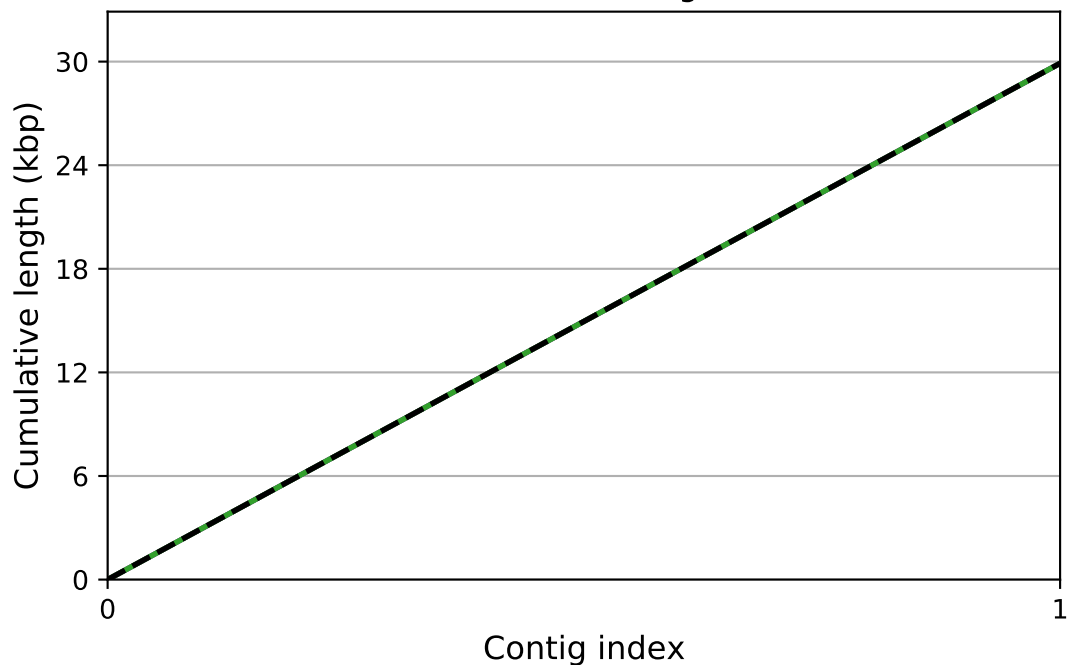


3.consensus.masked

SAMPLE2_PE.AF0.8.consensus.masked

SAMPLE1_PE.AF0.8.consensus.masked

Cumulative length

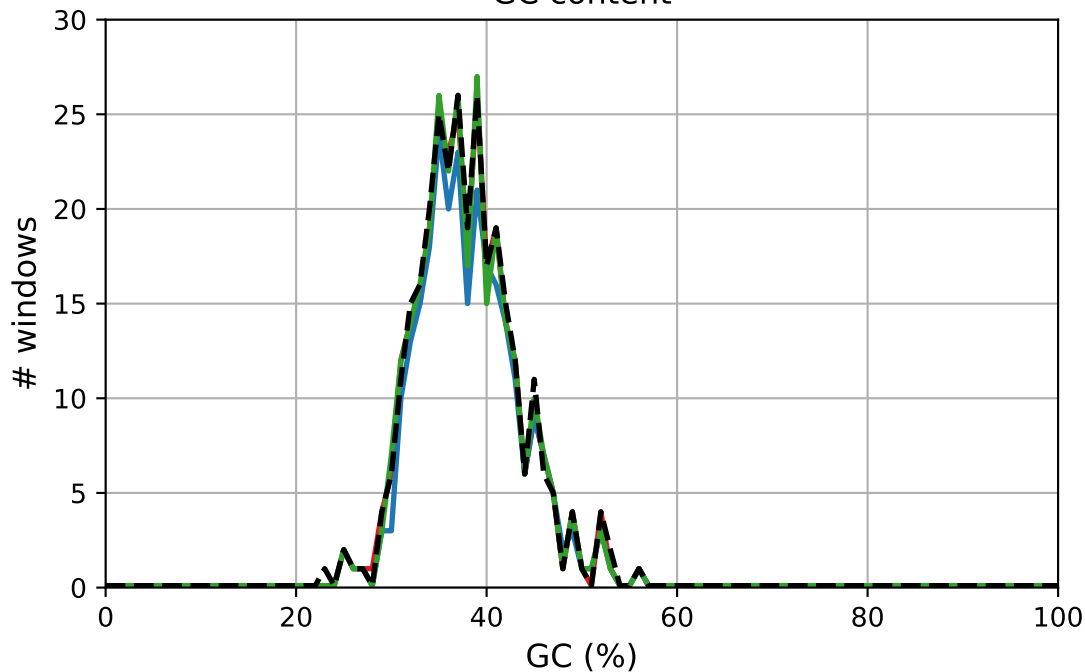


SAMPLE3_SE.AF0.8.consensus.masked
SAMPLE2_PE.AF0.8.consensus.masked

SAMPLE1_PE.AF0.8.consensus.masked

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GC content

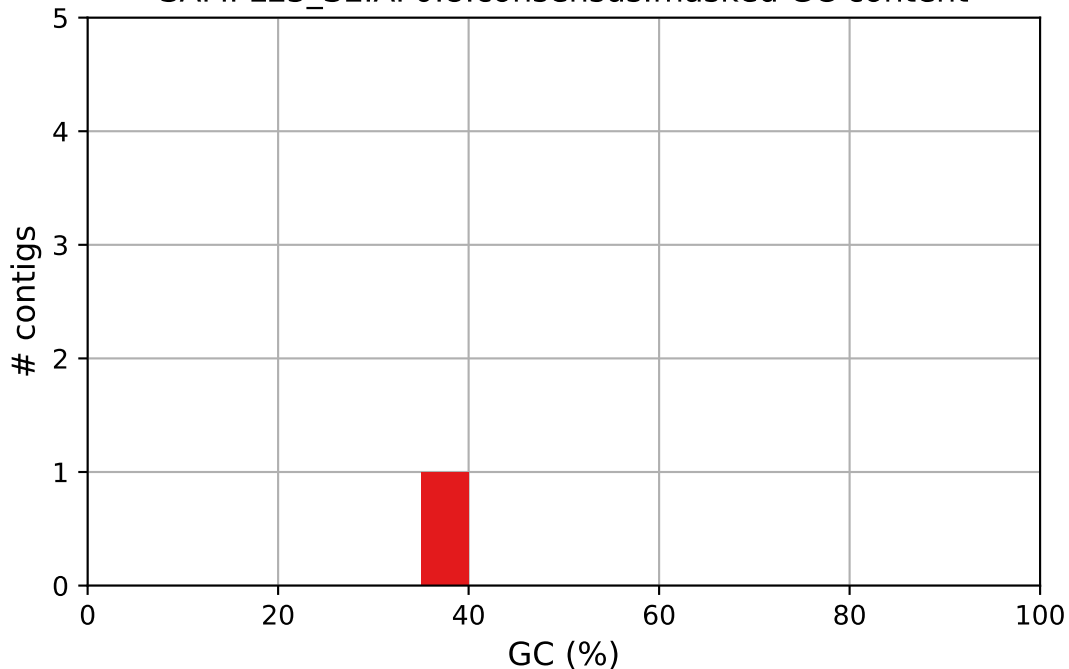


SAMPLE3_SE.AF0.8.consensus.masked
SAMPLE2_PE.AF0.8.consensus.masked

SAMPLE1_PE.AF0.8.consensus.masked

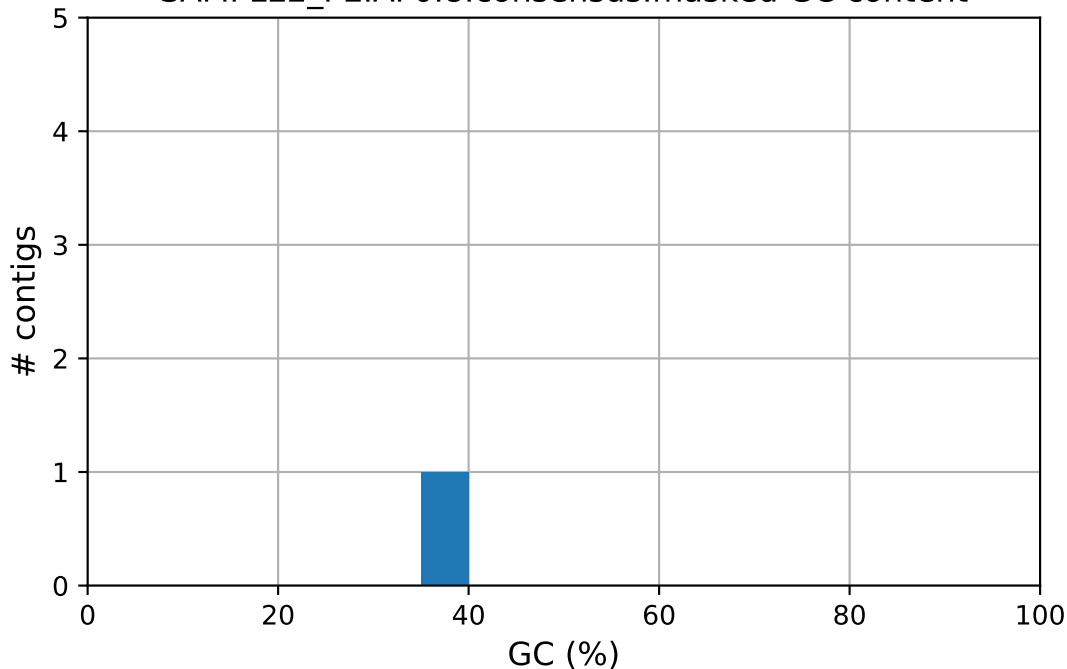
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SAMPLE3_SE.AF0.8.consensus.masked GC content



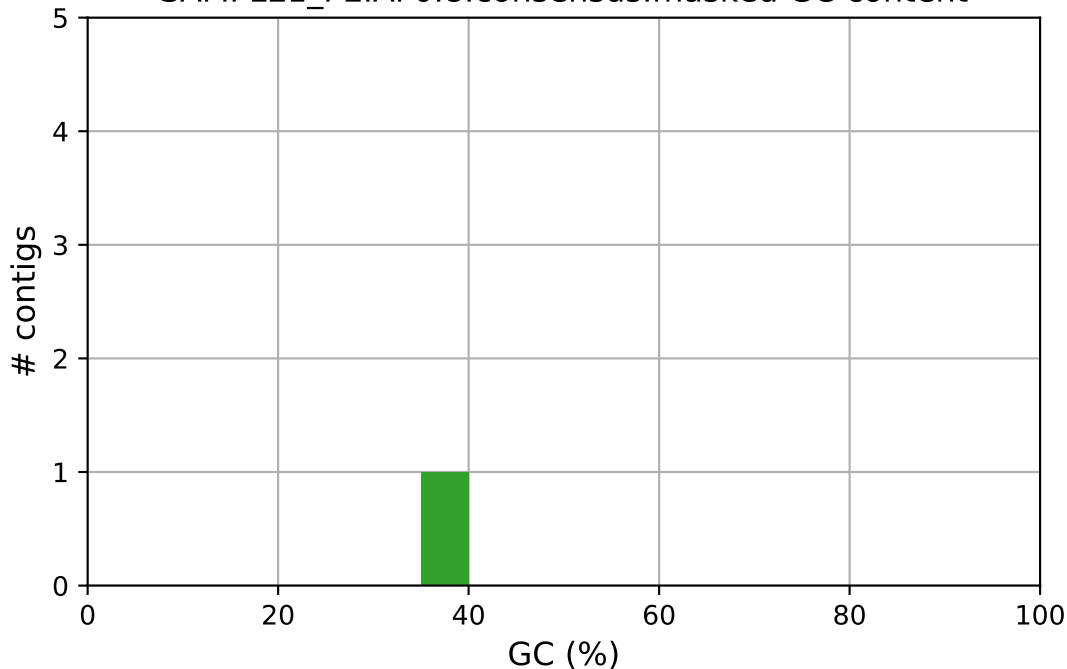
■ SAMPLE3_SE.AF0.8.consensus.masked

SAMPLE2_PE.AF0.8.consensus.masked GC content



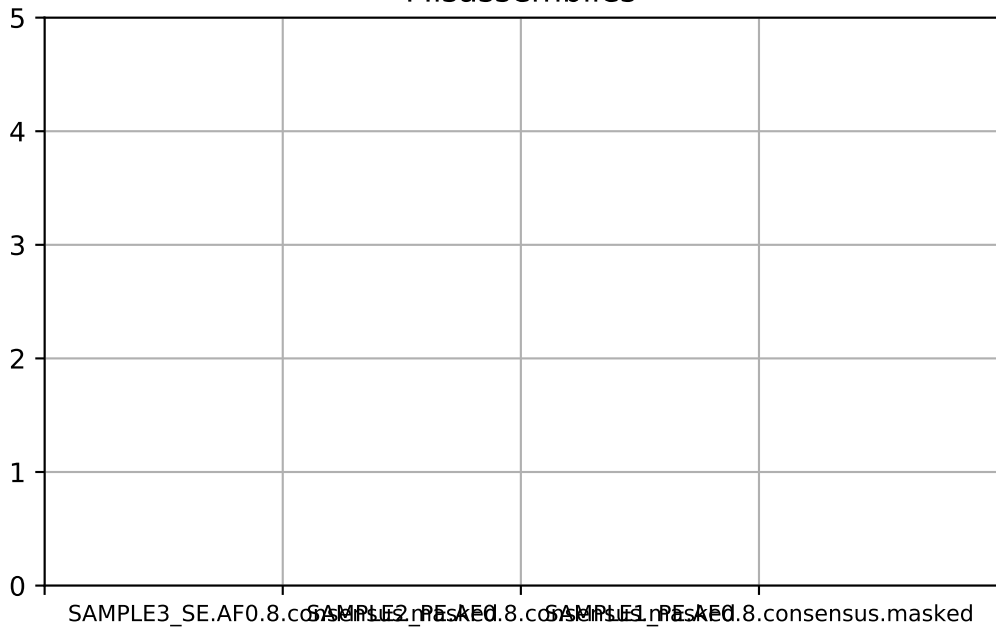
SAMPLE2_PE.AF0.8.consensus.masked

SAMPLE1_PE.AF0.8.consensus.masked GC content

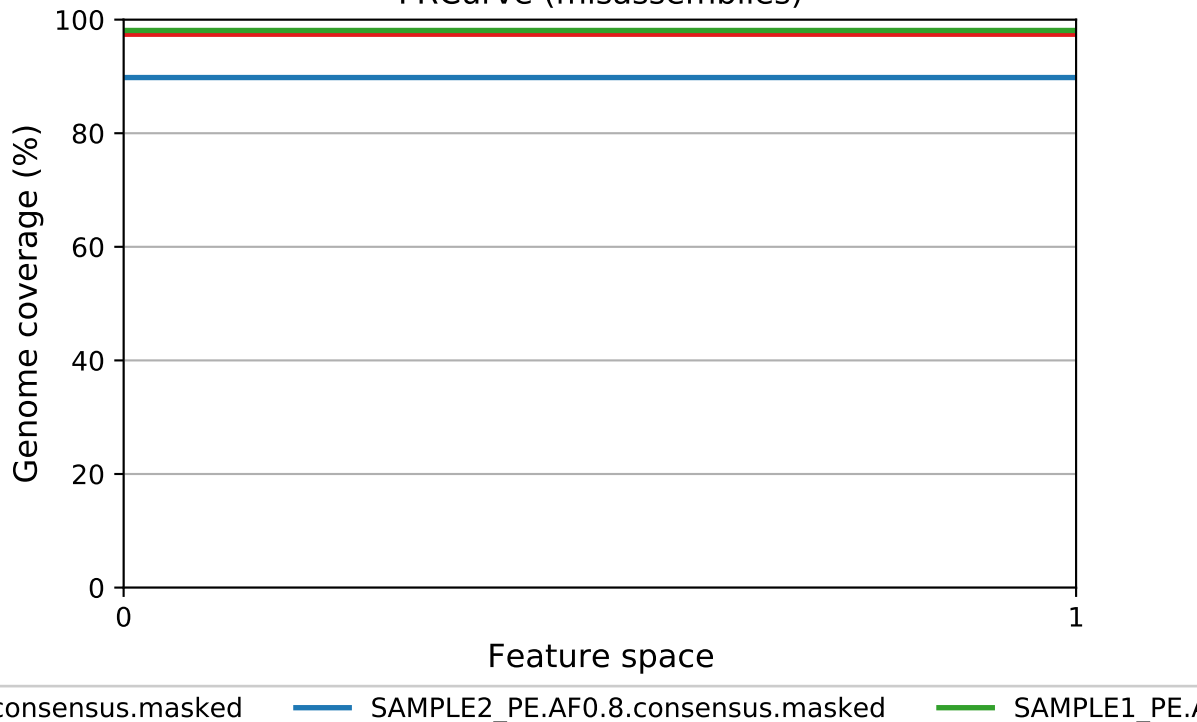


SAMPLE1_PE.AF0.8.consensus.masked

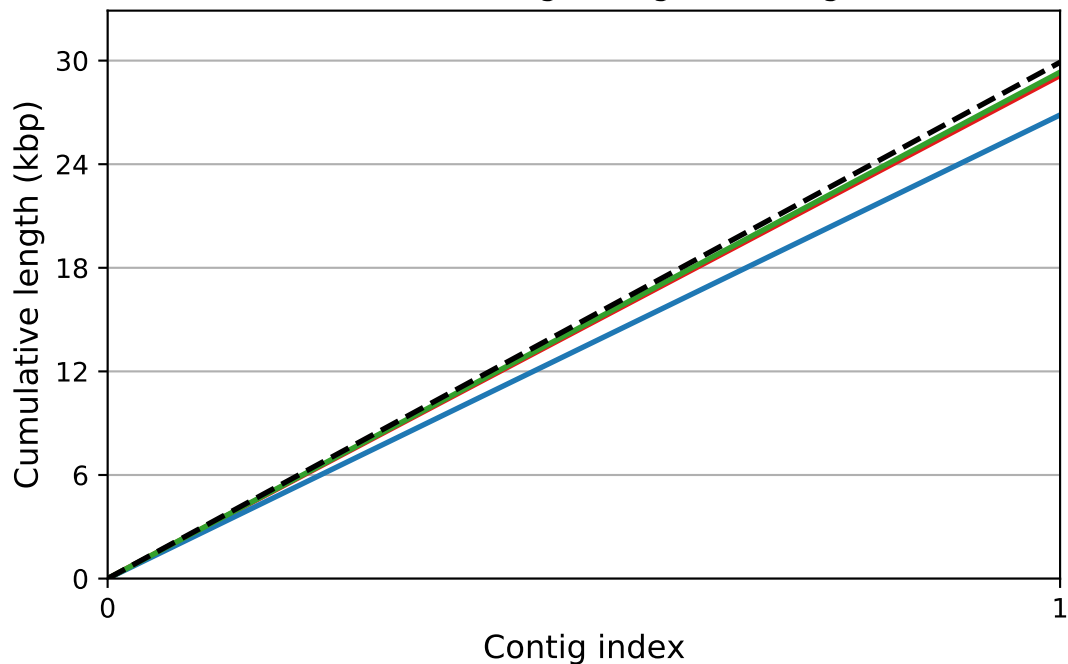
Misassemblies



FRCurve (misassemblies)



Cumulative length (aligned contigs)

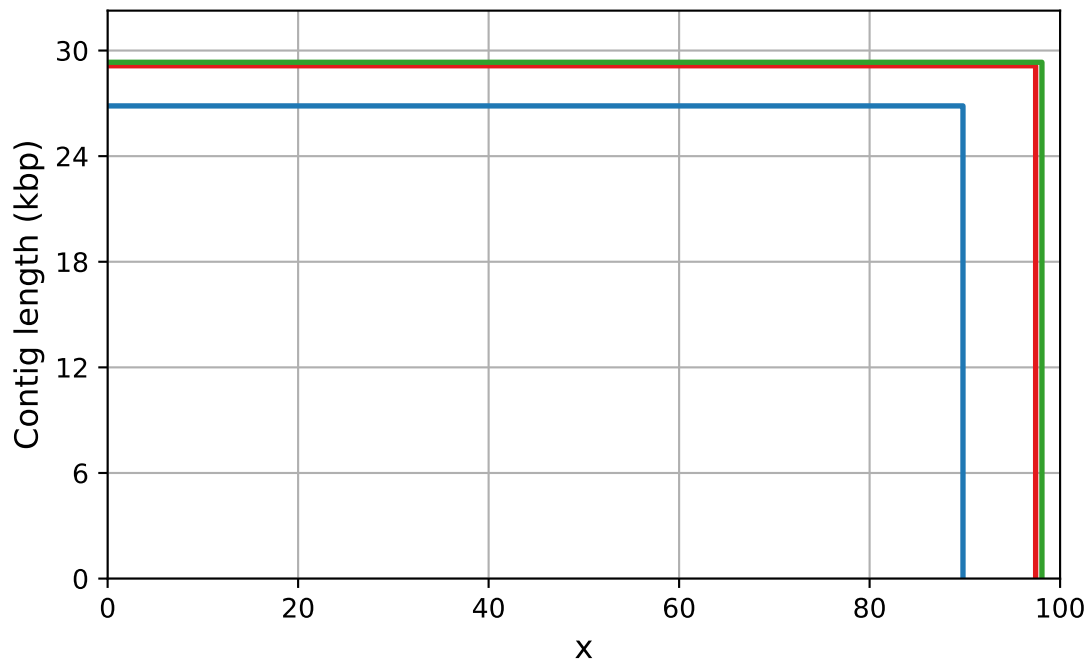


SAMPLE3_SE.AF0.8.consensus.masked
SAMPLE2_PE.AF0.8.consensus.masked

SAMPLE1_PE.AF0.8.consensus.masked

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NAx

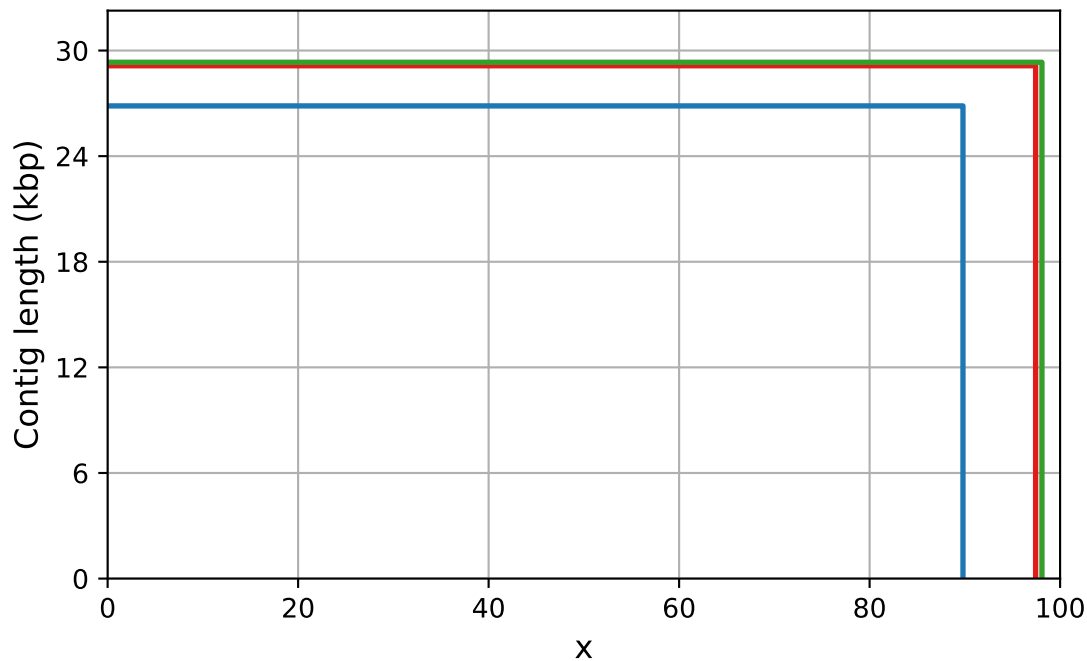


8.consensus.masked

SAMPLE2_PE.AF0.8.consensus.masked

SAMPLE1_PE.AF0.8.consensus.masked

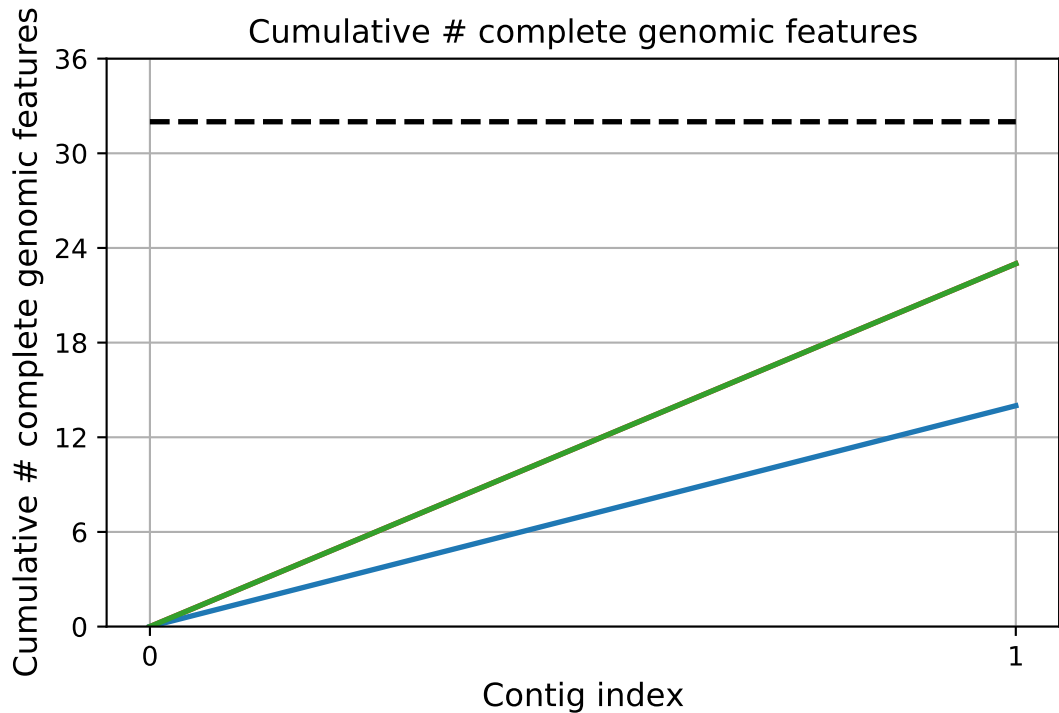
NGAx



8.consensus.masked

SAMPLE2_PE.AF0.8.consensus.masked

SAMPLE1_PE.A

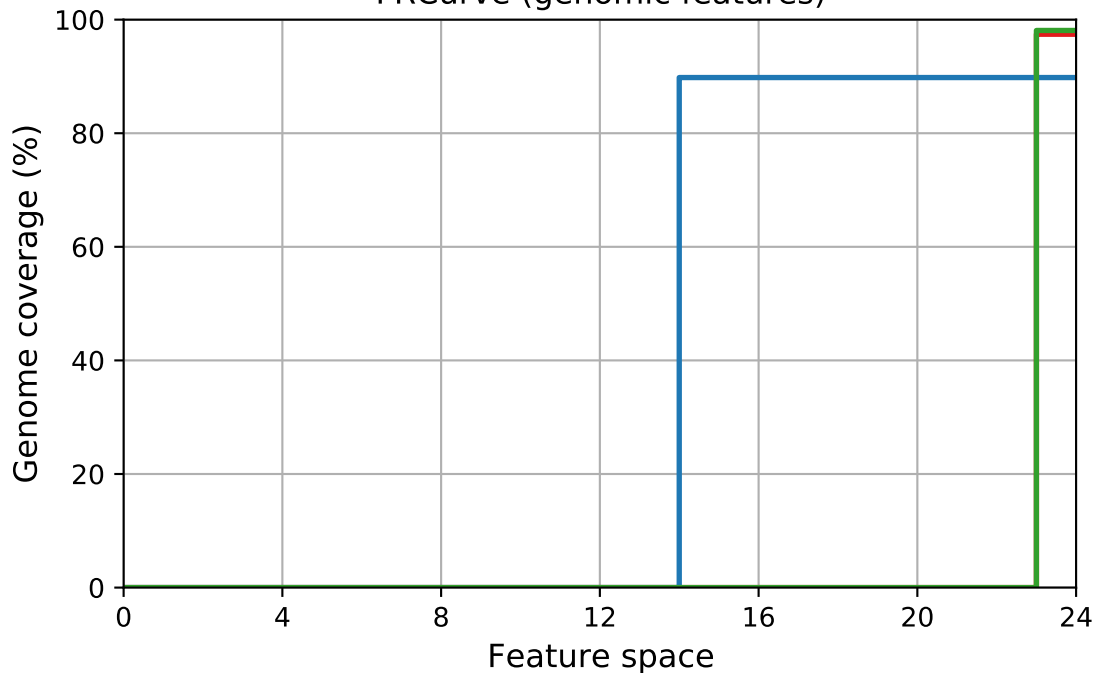


SAMPLE3_SE.AF0.8.consensus.masked
SAMPLE2_PE.AF0.8.consensus.masked

SAMPLE1_PE.AF0.8.consensus.masked

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FRCurve (genomic features)

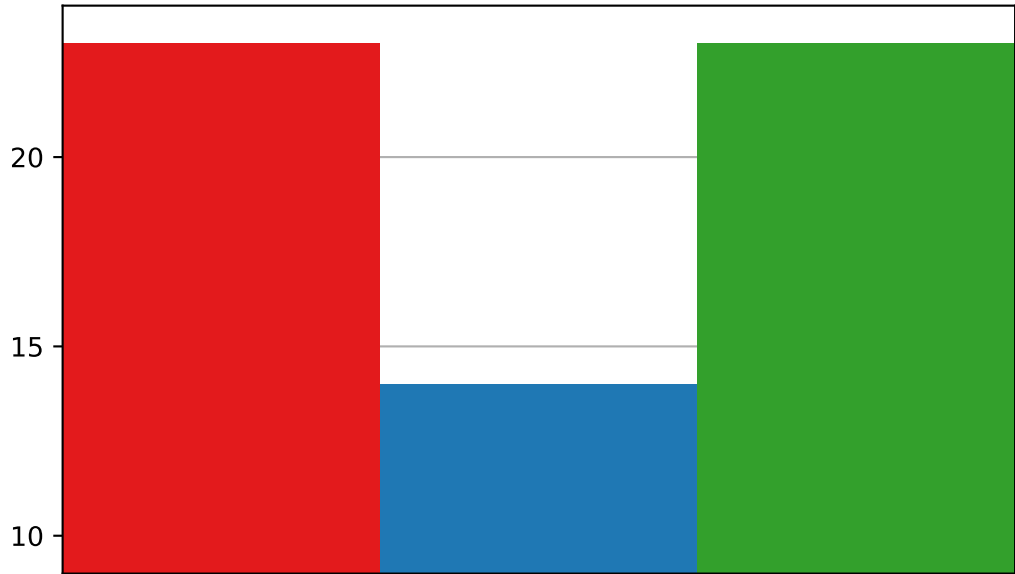


3.consensus.masked

SAMPLE2_PE.AF0.8.consensus.masked

SAMPLE1_PE.AF0.8.consensus.masked

complete genomic features

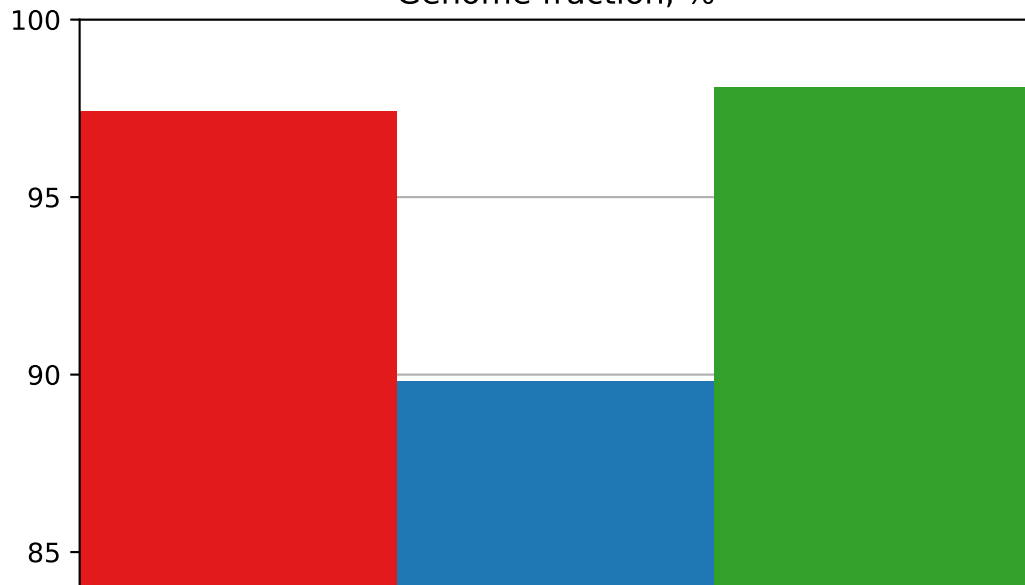


8.consensus.masked

SAMPLE2_PE.AF0.8.consensus.masked

SAMPLE1_PE.AF0.8.consensus.masked

Genome fraction, %



3.consensus.masked

SAMPLE2_PE.AF0.8.consensus.masked

SAMPLE1_PE.AF0.8.consensus.masked