

Report

	SAMPLE2_PE.scaffolds	SAMPLE1_PE.scaffolds	SAMPLE3_SE.scaffolds
# contigs (>= 0 bp)	13	5	5
# contigs (>= 1000 bp)	7	3	4
# contigs (>= 5000 bp)	1	3	3
# contigs (>= 10000 bp)	1	1	1
# contigs (>= 25000 bp)	0	0	0
# contigs (>= 50000 bp)	0	0	0
Total length (>= 0 bp)	36064	36164	35820
Total length (>= 1000 bp)	32873	35260	35382
Total length (>= 5000 bp)	10409	35260	31208
Total length (>= 10000 bp)	10409	20973	16925
Total length (>= 25000 bp)	0	0	0
Total length (>= 50000 bp)	0	0	0
# contigs	9	3	4
Largest contig	10409	20973	16925
Total length	34235	35260	35382
Reference length	29903	29903	29903
GC (%)	39.18	39.05	39.06
Reference GC (%)	37.97	37.97	37.97
N50	4093	20973	8770
NG50	4093	20973	16925
N90	3823	5513	4174
NG90	4051	8774	5513
auN	5775.0	15520.2	11621.3
auNG	6611.6	18300.6	13750.6
L50	3	1	2
LG50	3	1	1
L90	6	3	4
LG90	5	2	3
# 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.	0	0	0
# unaligned mis. contigs	0	0	0
# unaligned contigs	3 + 0 part	1 + 0 part	1 + 0 part
Unaligned length	5432	5513	5513
Genome fraction (%)	96.010	98.987	98.973
Duplication ratio	1.002	1.000	1.004
# N's per 100 kbp	0.00	0.00	0.00
# mismatches per 100 kbp	38.24	20.27	10.09
# indels per 100 kbp	3.48	0.00	0.00
# genomic features	14 + 9 part	19 + 5 part	19 + 5 part
Largest alignment	10408	20951	16899
Total aligned length	28764	29600	29723
NA50	4093	20951	8650
NGA50	4093	20951	16899
NA90	-	-	-
NGA90	1913	8649	4174
auNA	5252.5	14570.3	10678.3
auNGA	6013.4	17180.5	12634.9
LA50	3	1	2
LGA50	3	1	1
LA90	-	-	-
LGA90	6	2	3

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.scaffolds	SAMPLE1_PE.scaffolds	SAMPLE3_SE.scaffolds
# 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.	0	0	0
# unaligned mis. contigs	0	0	0
# mismatches	11	6	3
# indels	1	0	0
# indels (<= 5 bp)	1	0	0
# indels (> 5 bp)	0	0	0
Indels length	1	0	0

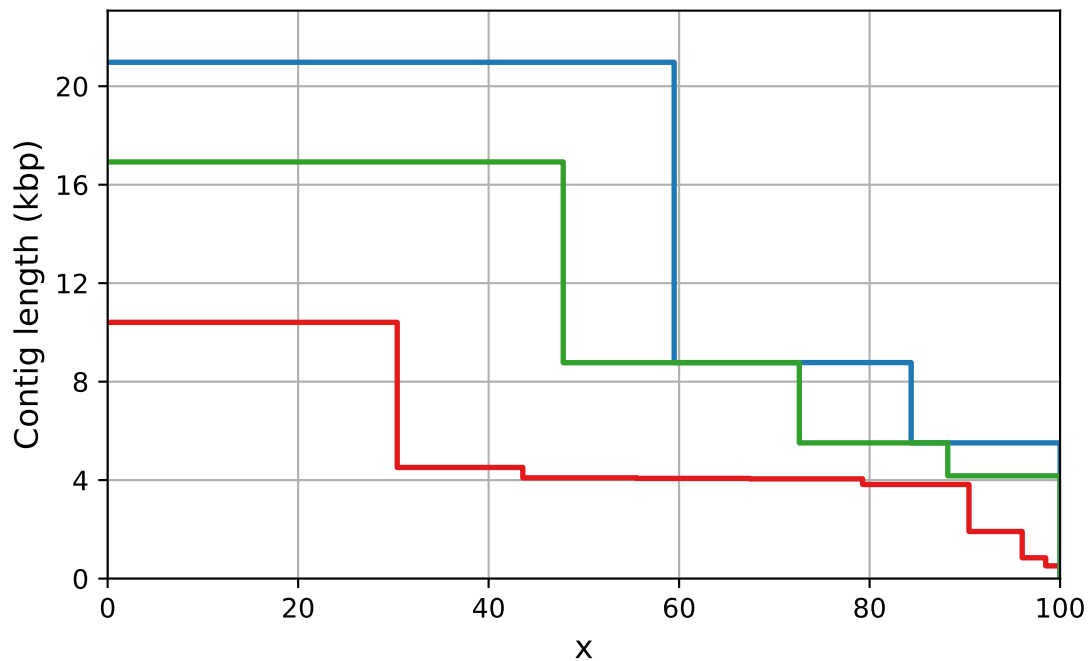
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	SAMPLE2_PE.scaffolds	SAMPLE1_PE.scaffolds	SAMPLE3_SE.scaffolds
# fully unaligned contigs	3	1	1
Fully unaligned length	5432	5513	5513
# partially unaligned contigs	0	0	0
Partially unaligned length	0	0	0
# N's	0	0	0

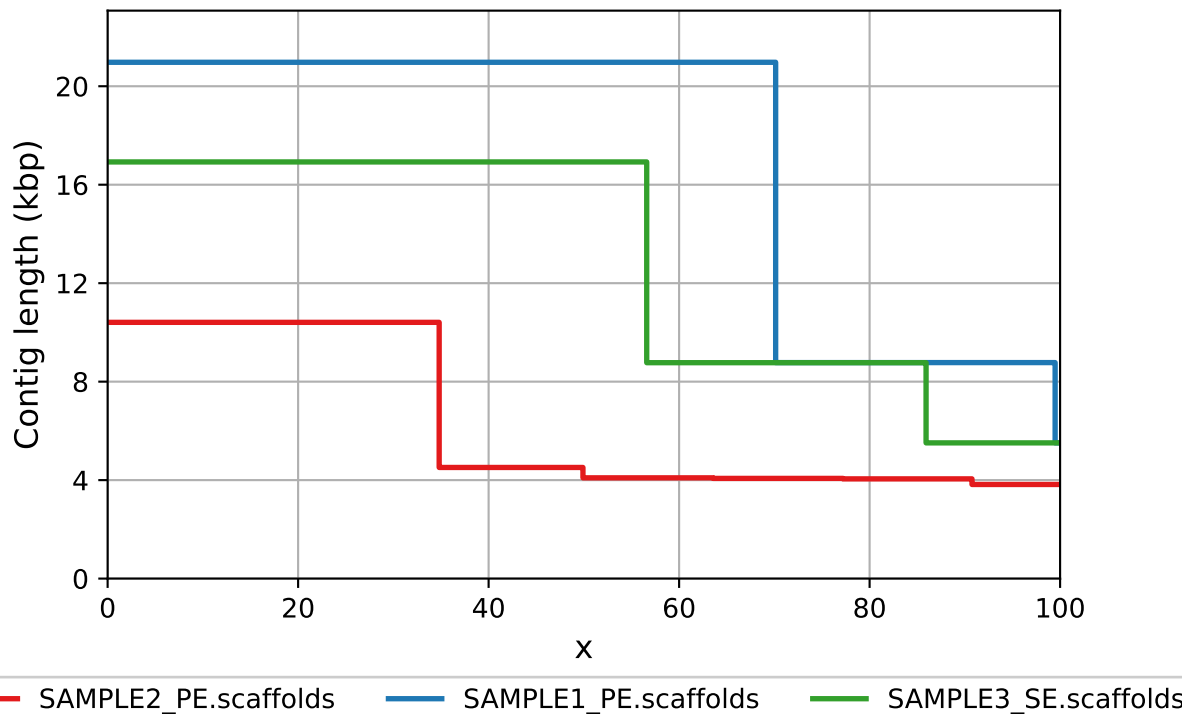
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

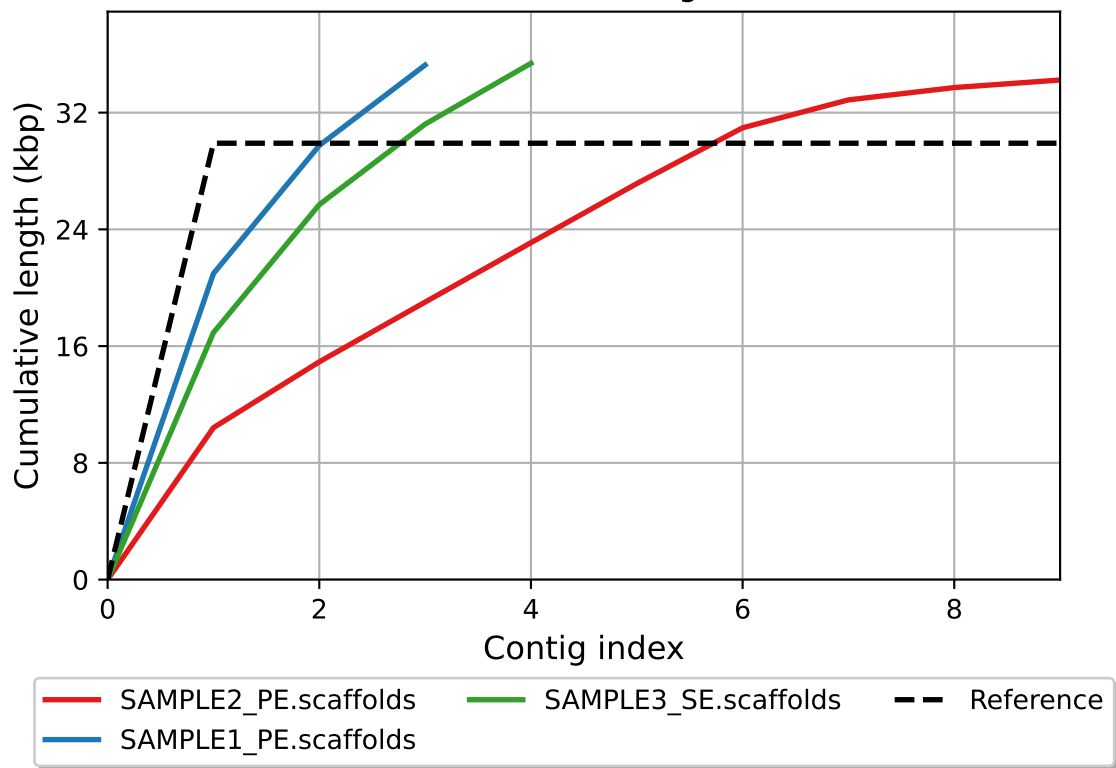


SAMPLE2_PE.scaffolds SAMPLE1_PE.scaffolds SAMPLE3_SE.scaffolds

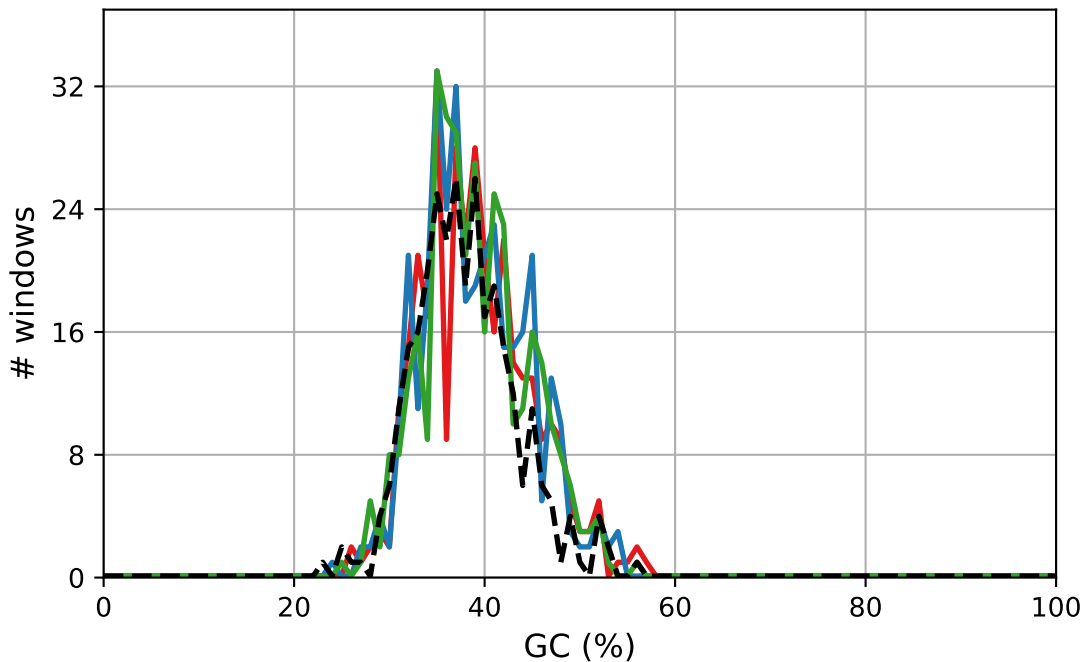
NGx



Cumulative length

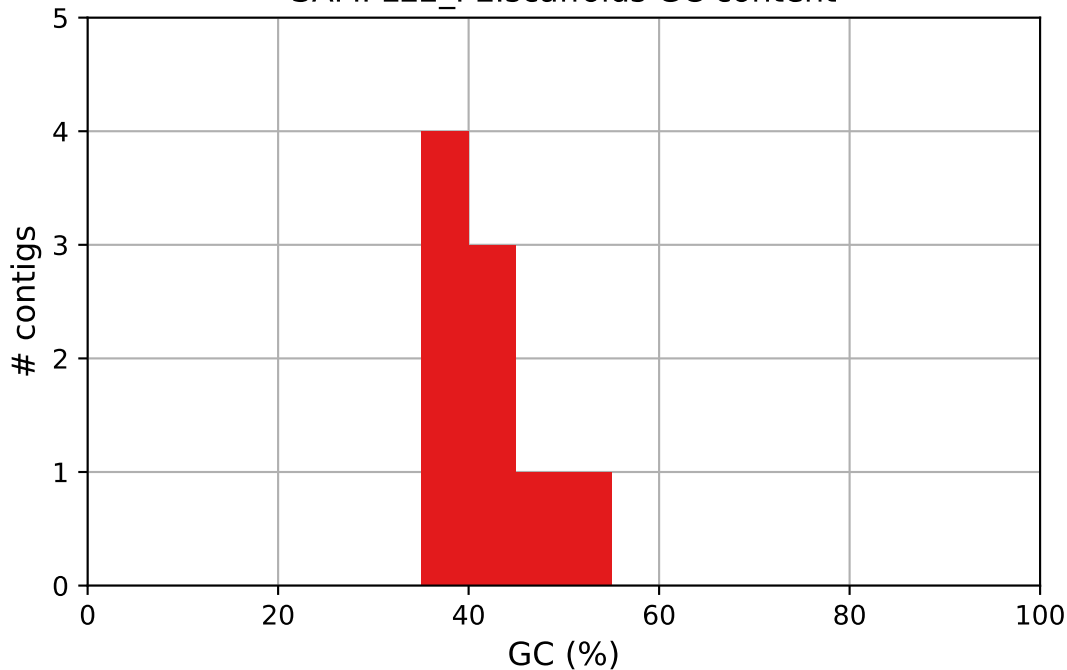


GC content



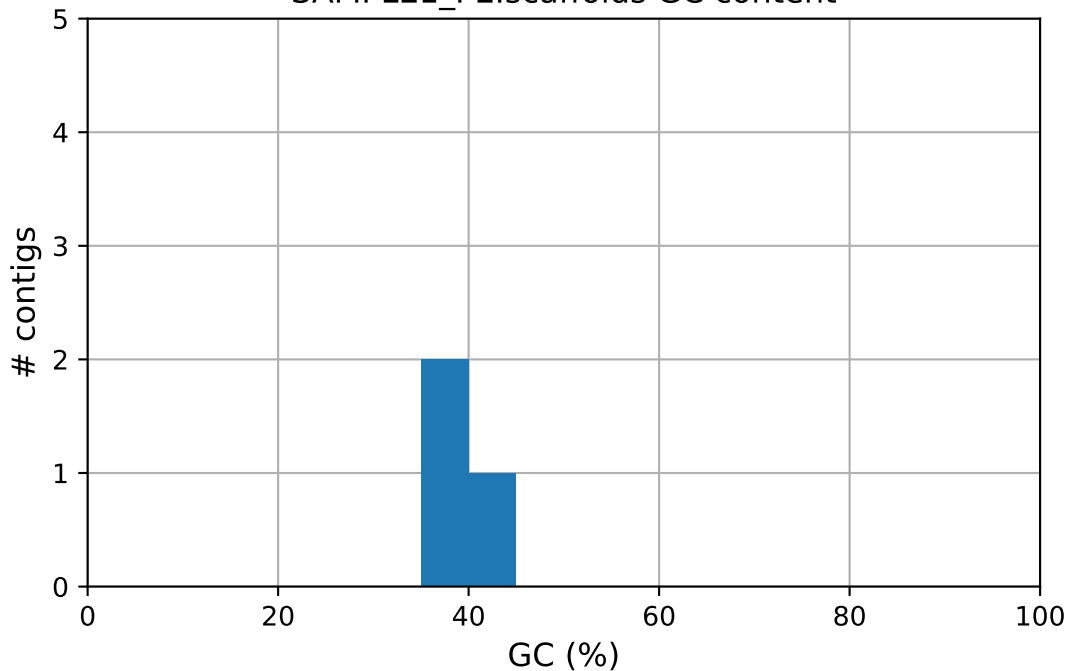
SAMPLE2_PE.scaffolds SAMPLE3_SE.scaffolds Reference
SAMPLE1_PE.scaffolds

SAMPLE2_PE.scaffolds GC content



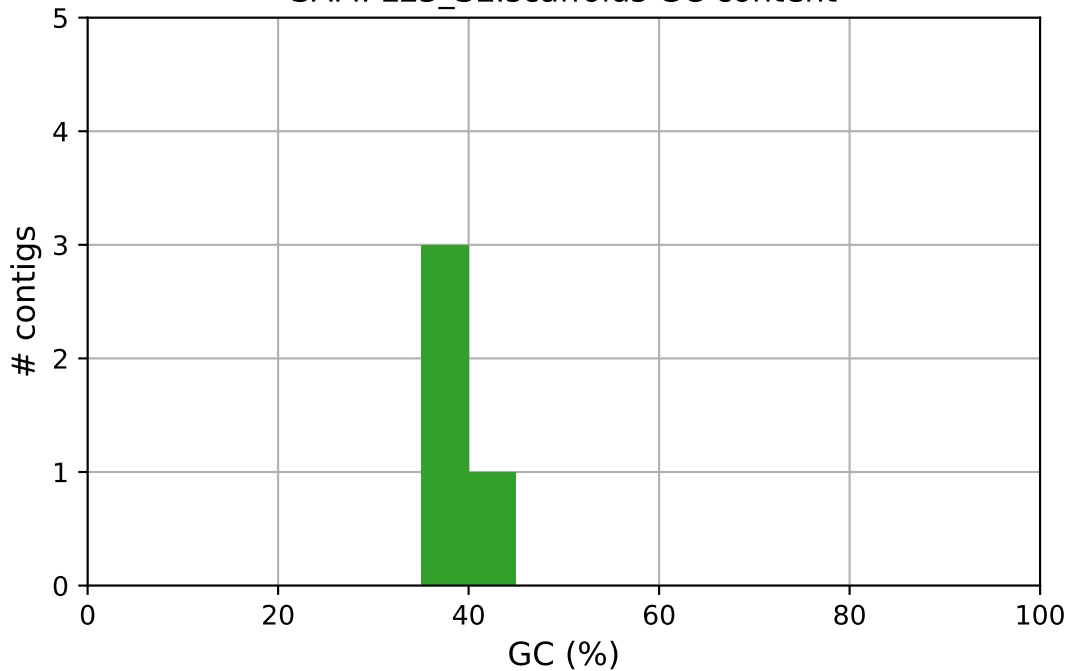
■ SAMPLE2_PE.scaffolds


SAMPLE1_PE.scaffolds GC content



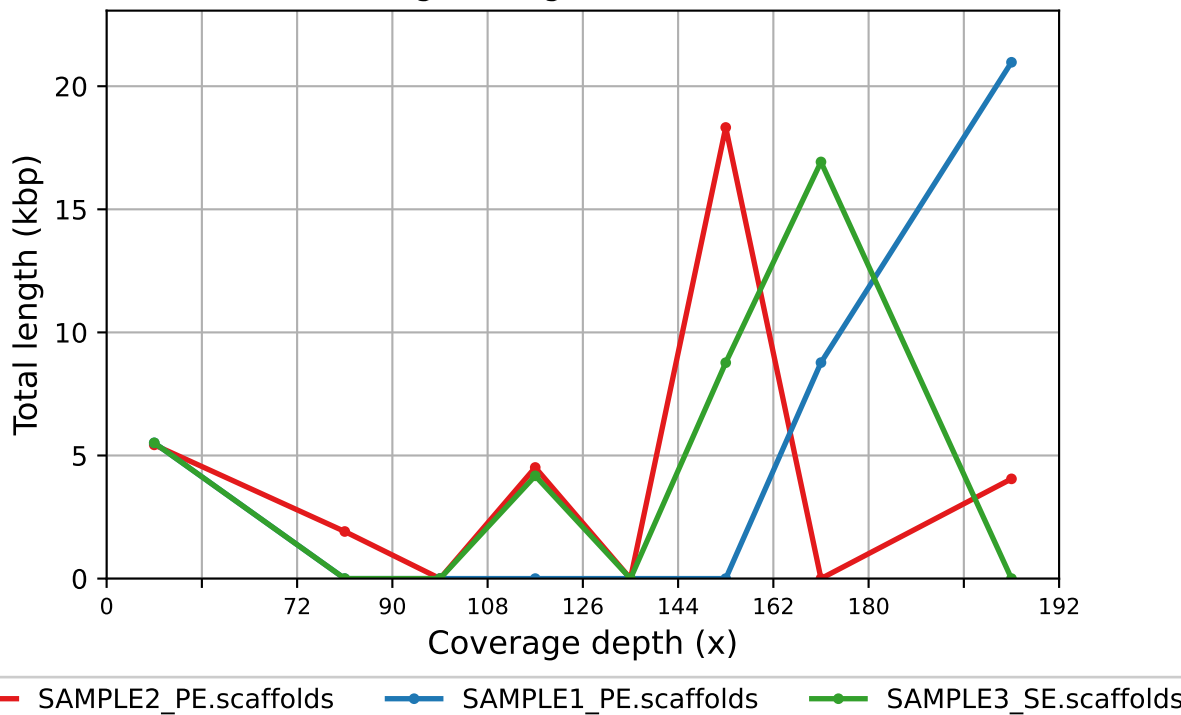
SAMPLE1_PE.scaffolds

SAMPLE3_SE.scaffolds GC content

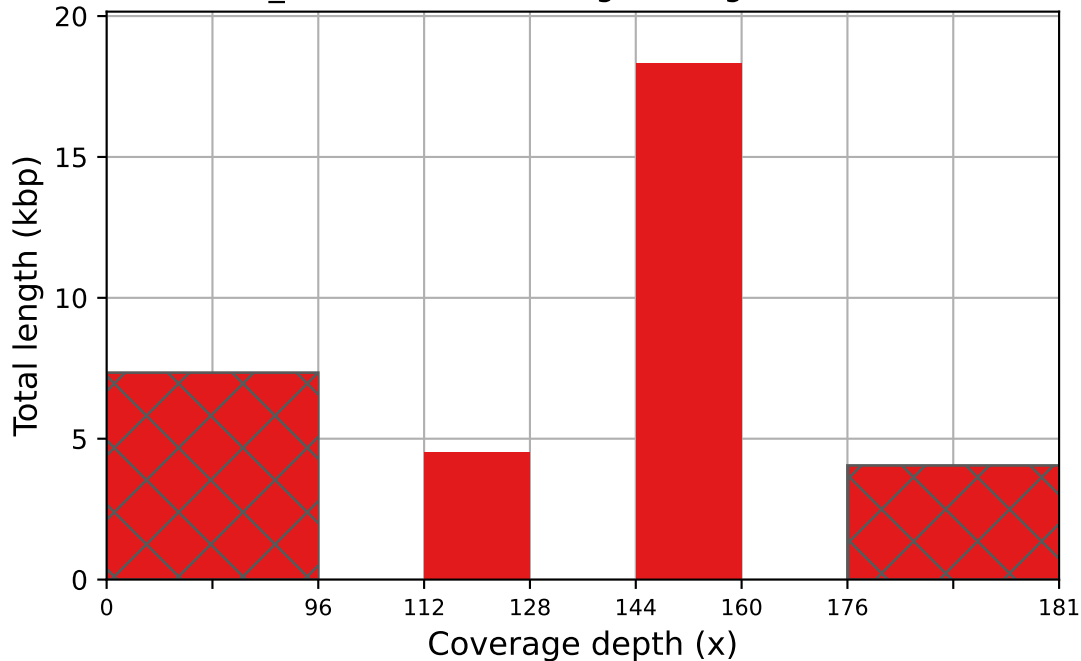


 SAMPLE3_SE.scaffolds

Coverage histogram (bin size: 18x)

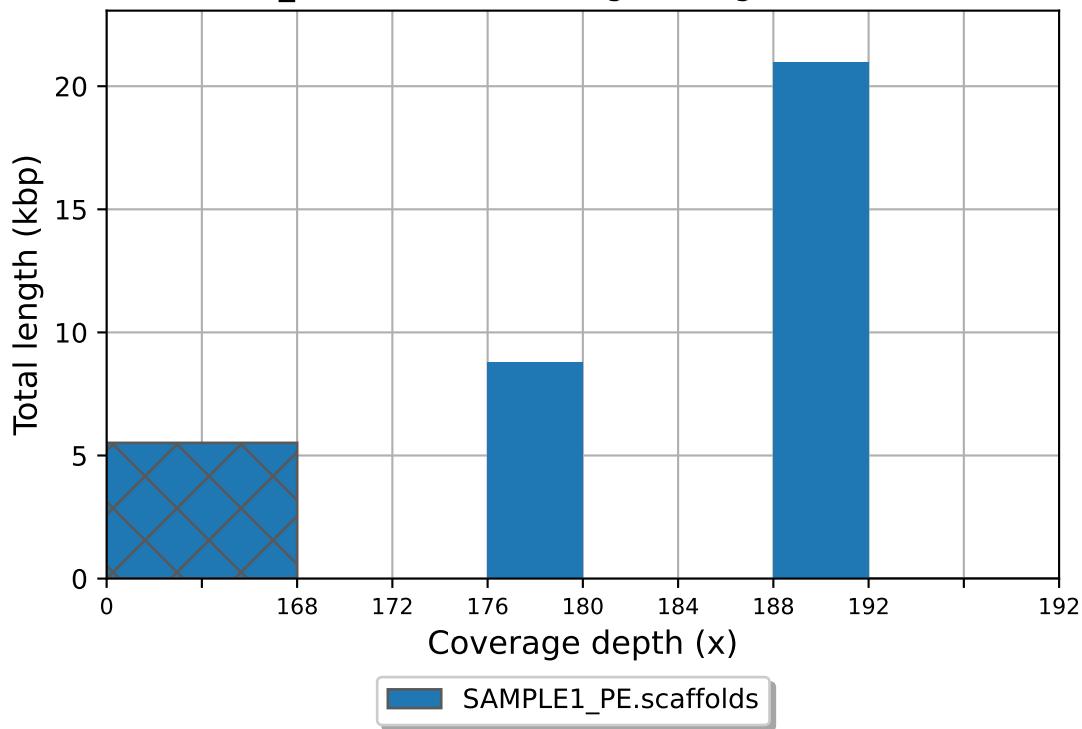


SAMPLE2_PE.scaffolds coverage histogram (bin size: 16x)

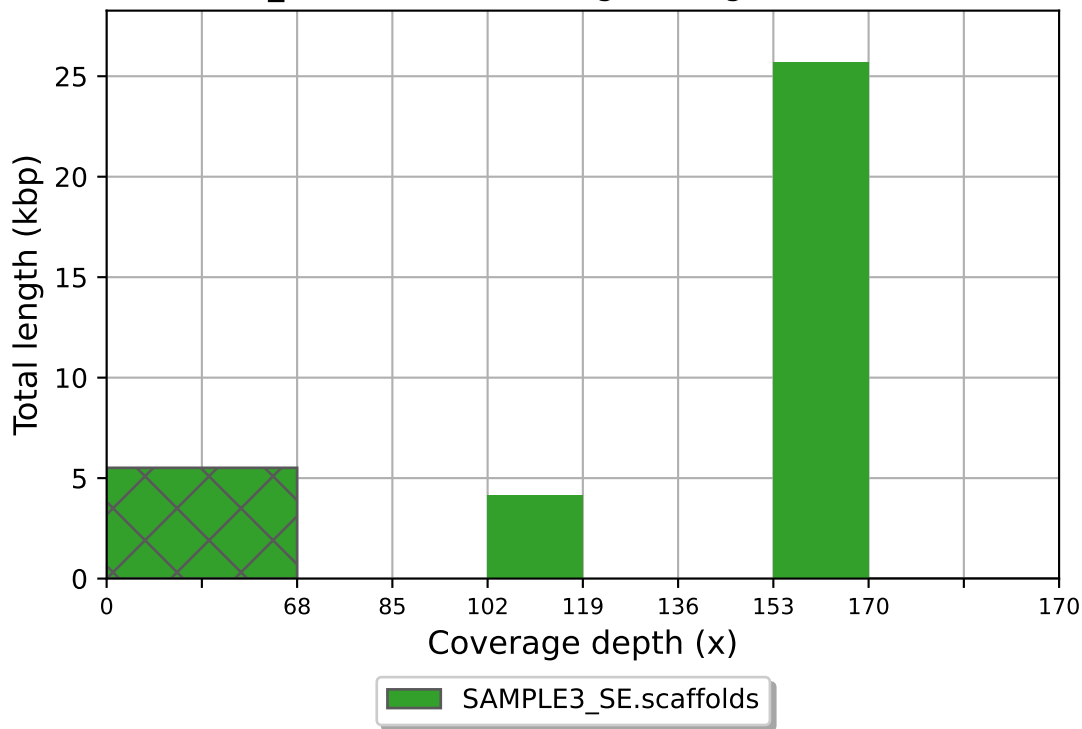


SAMPLE2_PE.scaffolds

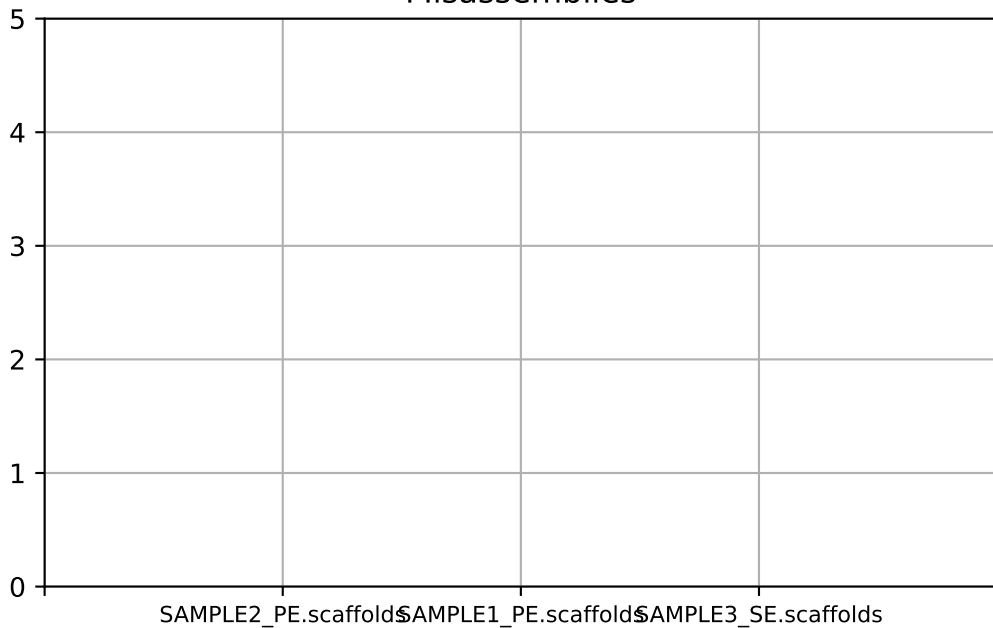
SAMPLE1_PE.scaffolds coverage histogram (bin size: 4x)



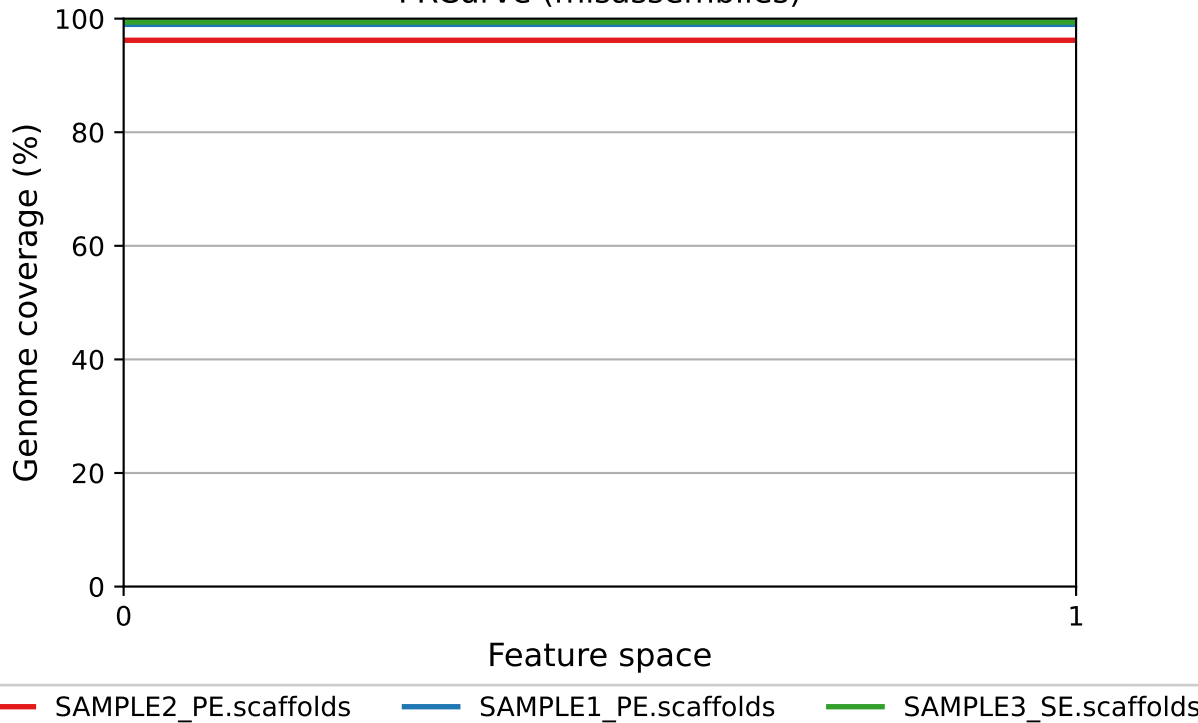
SAMPLE3_SE.scaffolds coverage histogram (bin size: 17x)



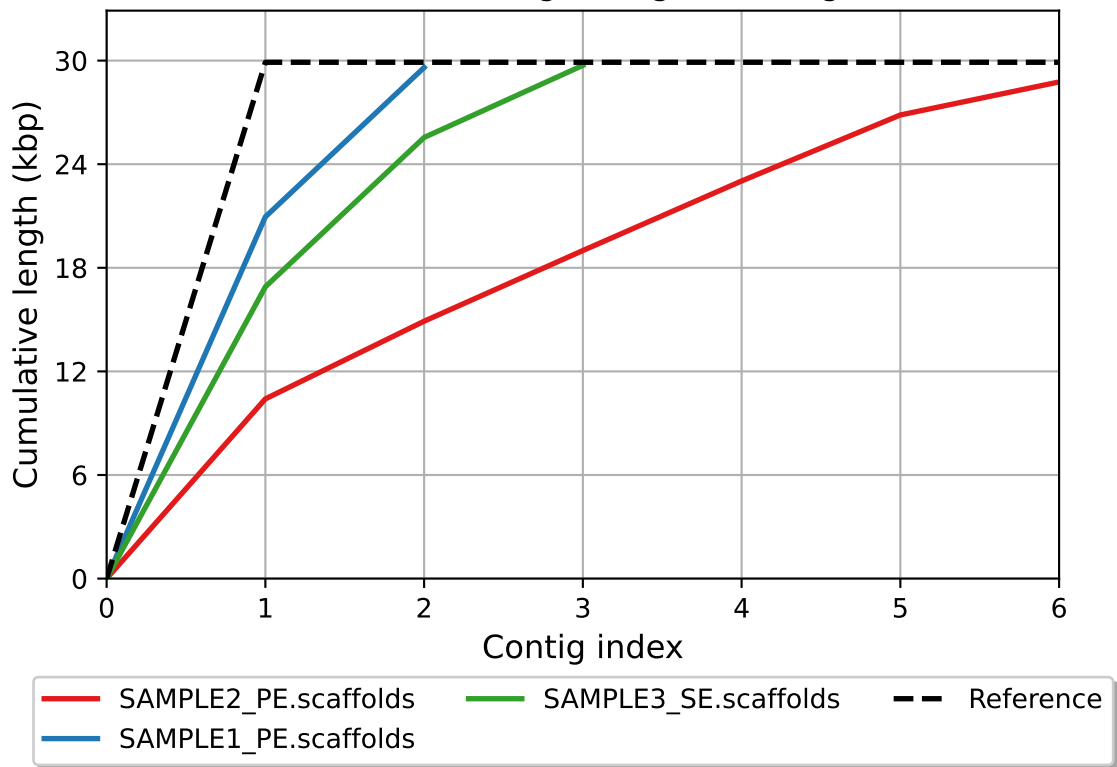
Misassemblies



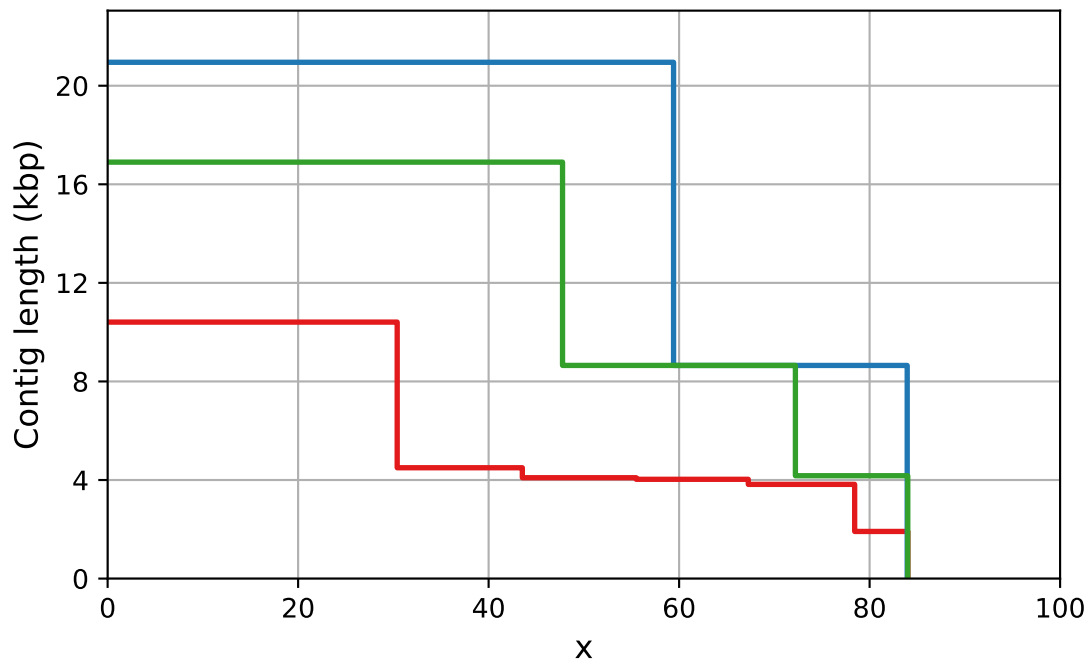
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx

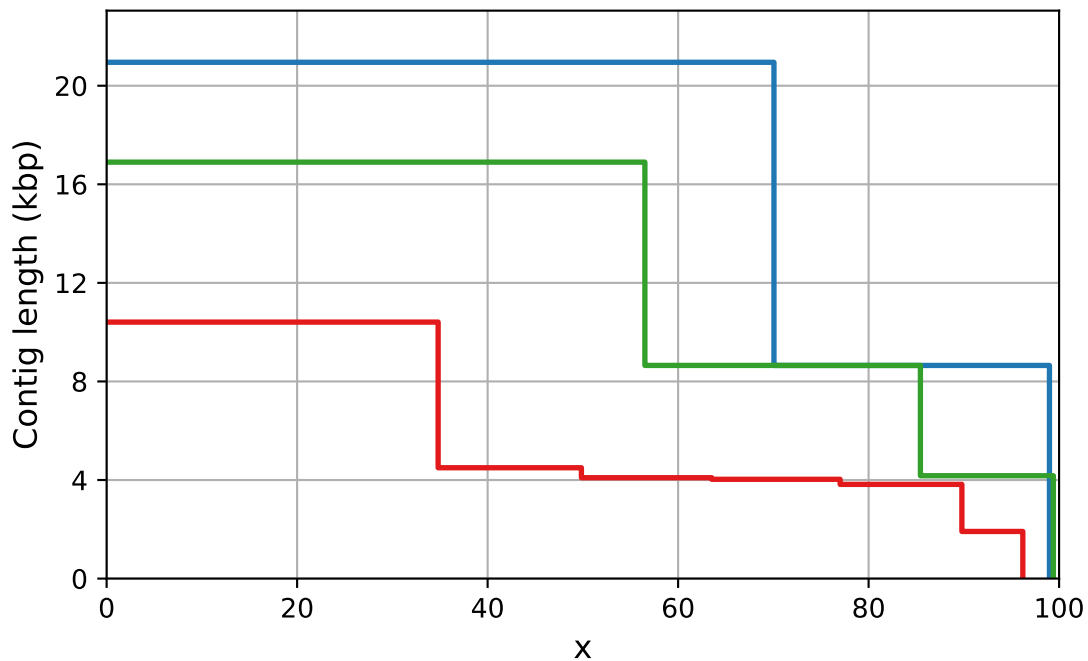


— SAMPLE2_PE.scaffolds

— SAMPLE1_PE.scaffolds

— SAMPLE3_SE.scaffolds

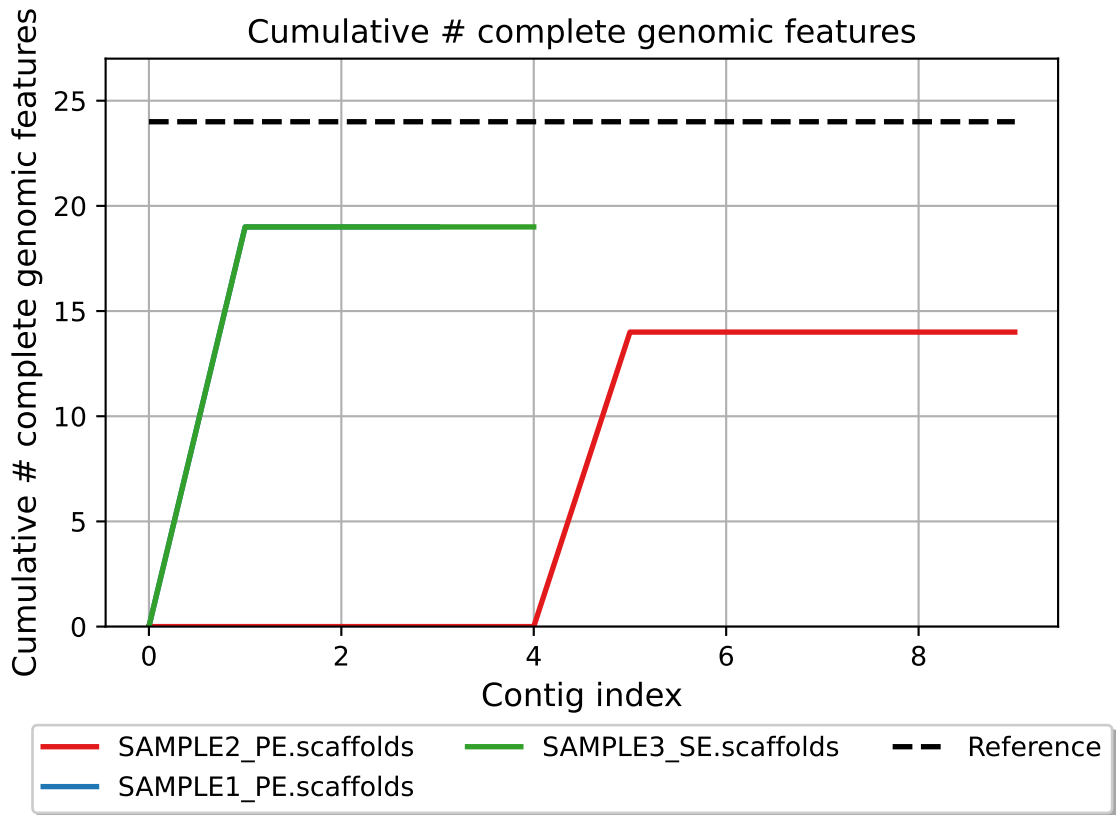
NGAx



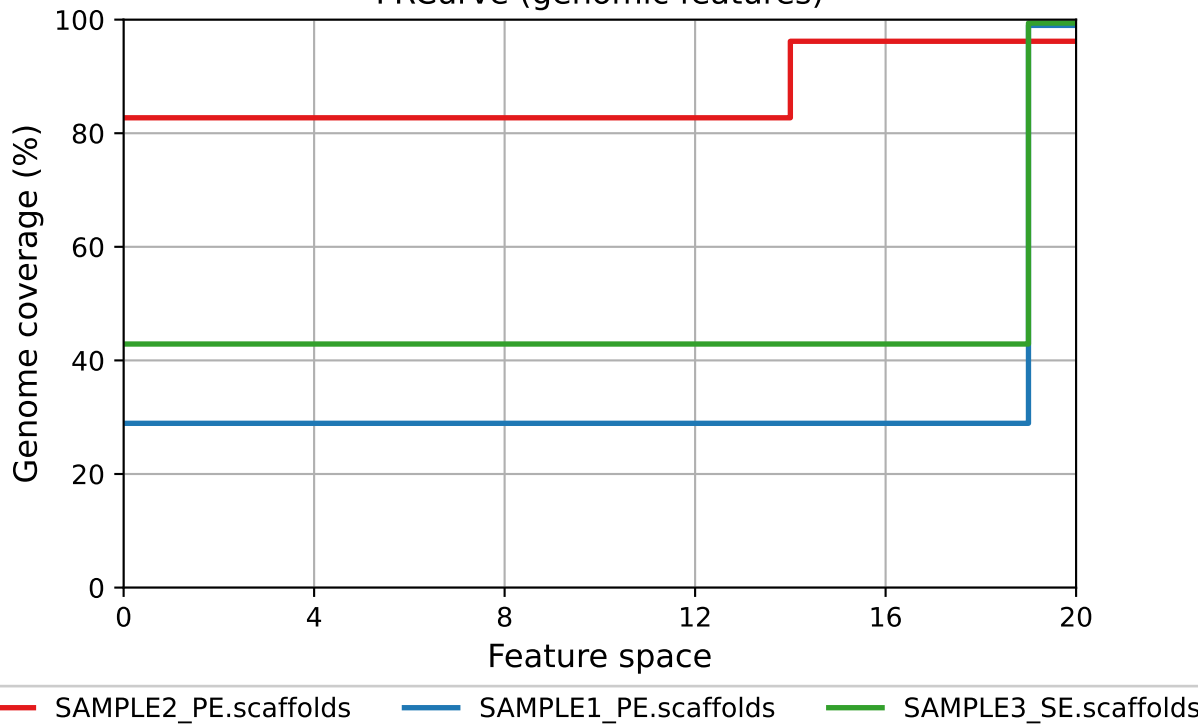
— SAMPLE2_PE.scaffolds

— SAMPLE1_PE.scaffolds

— SAMPLE3_SE.scaffolds



FRCurve (genomic features)






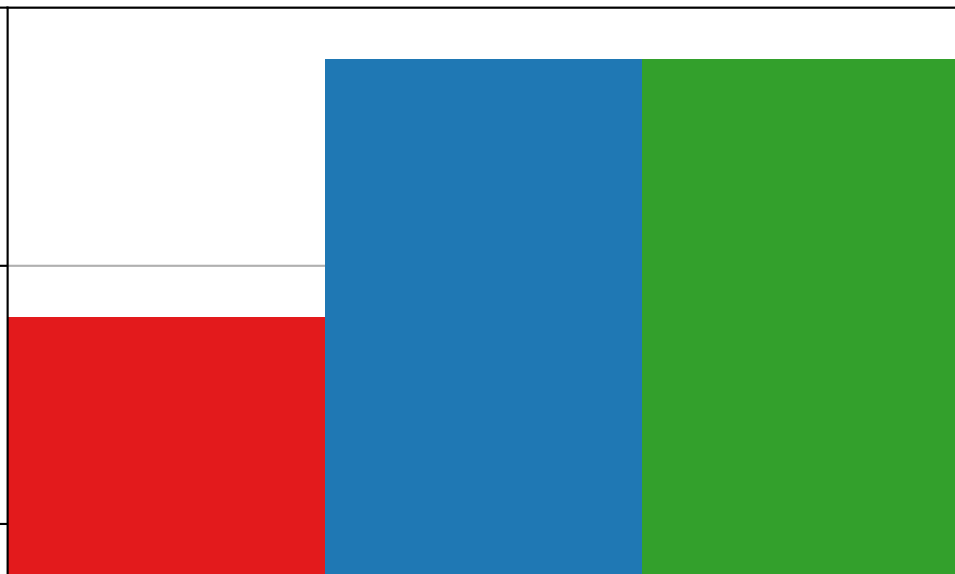
complete genomic features

20

15

10




 SAMPLE2_PE.scaffolds  SAMPLE1_PE.scaffolds  SAMPLE3_SE.scaffolds



Genome fraction, %

100

95

 SAMPLE2_PE.scaffolds  SAMPLE1_PE.scaffolds  SAMPLE3_SE.scaffolds

