

Report

	SAMPLE3_SE.scaffolds	SAMPLE1_PE.scaffolds	SAMPLE2_PE.scaffolds
# contigs (>= 0 bp)	4	4	13
# contigs (>= 1000 bp)	3	3	7
# contigs (>= 5000 bp)	2	3	2
# contigs (>= 10000 bp)	1	1	1
# contigs (>= 25000 bp)	1	0	0
# contigs (>= 50000 bp)	0	0	0
Total length (>= 0 bp)	35693	35707	36769
Total length (>= 1000 bp)	35255	35249	33578
Total length (>= 5000 bp)	31081	35249	16839
Total length (>= 10000 bp)	25568	21005	10482
Total length (>= 25000 bp)	25568	0	0
Total length (>= 50000 bp)	0	0	0
# contigs	3	3	9
Largest contig	25568	21005	10482
Total length	35255	35249	34940
Reference length	29903	29903	29903
GC (%)	39.06	39.05	39.14
Reference GC (%)	37.97	37.97	37.97
N50	25568	21005	4107
NG50	25568	21005	6357
N75	5513	8770	3823
NG75	25568	8770	4070
L50	1	1	3
LG50	1	1	2
L75	2	2	5
LG75	1	2	4
# misassemblies	0	0	0
# misassembled contigs	0	0	0
Misassembled contigs length	0	0	0
# local misassemblies	1	0	0
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	0	0	0
# unaligned contigs	1 + 0 part	1 + 0 part	3 + 0 part
Unaligned length	5513	5474	5432
Genome fraction (%)	98.950	98.983	98.064
Duplication ratio	1.005	1.006	1.006
# N's per 100 kbp	0.00	0.00	0.00
# mismatches per 100 kbp	13.52	20.27	34.10
# indels per 100 kbp	0.00	0.00	3.41
# genomic features	26 + 6 part	26 + 6 part	20 + 10 part
Largest alignment	25542	20949	10414
Total aligned length	29716	29599	29323
NA50	25542	20949	3990
NGA50	25542	20949	6357
NA75	4174	8650	3177
NGA75	25542	8650	3823
LA50	1	1	3
LGA50	1	1	2
LA75	2	2	5
LGA75	1	2	4

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.scaffolds	SAMPLE1_PE.scaffolds	SAMPLE2_PE.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	1	0	0
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	0	0	0
# mismatches	4	6	10
# indels	0	0	1
# indels (<= 5 bp)	0	0	1
# indels (> 5 bp)	0	0	0
Indels length	0	0	1

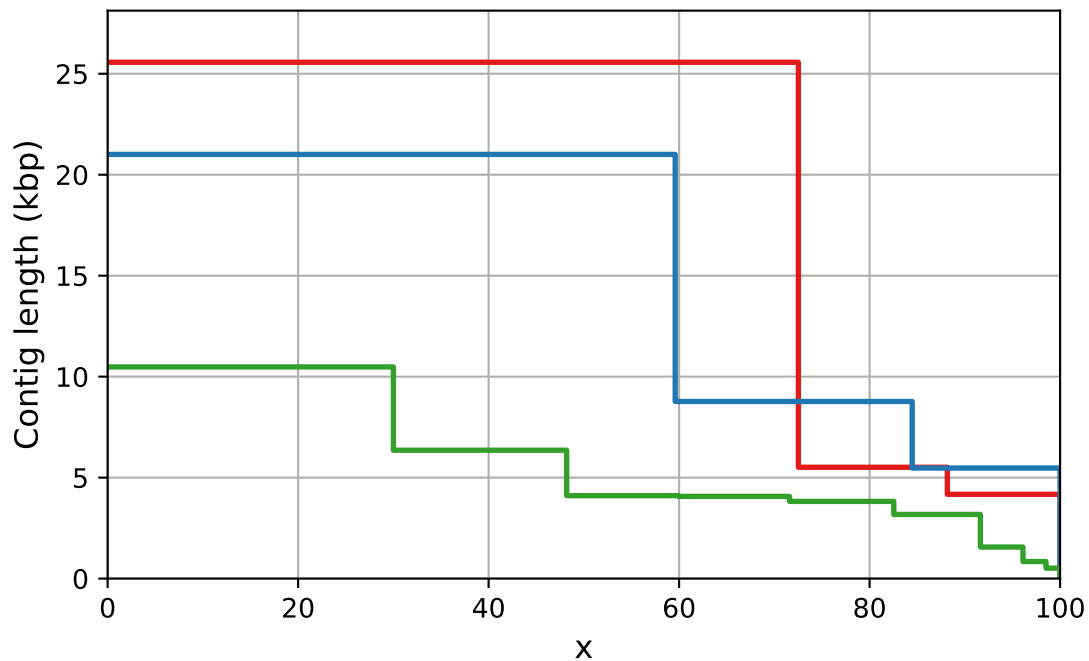
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	SAMPLE3_SE.scaffolds	SAMPLE1_PE.scaffolds	SAMPLE2_PE.scaffolds
# fully unaligned contigs	1	1	3
Fully unaligned length	5513	5474	5432
# partially unaligned contigs	0	0	0
Partially unaligned length	0	0	0
# N's	0	0	0

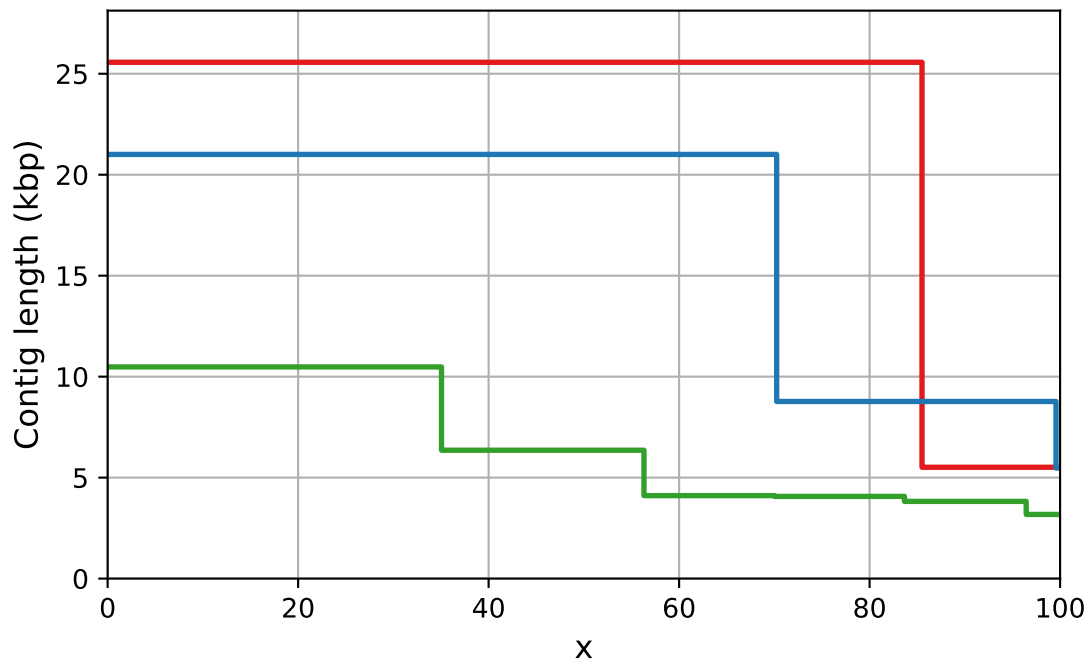
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



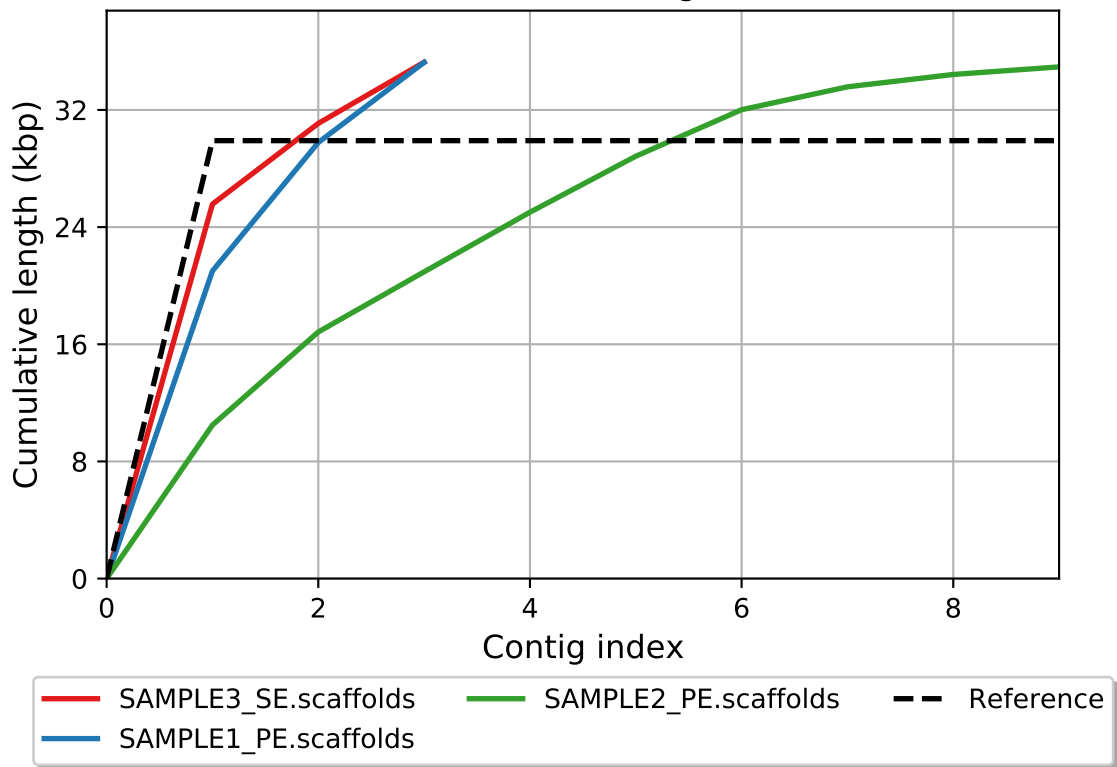
— SAMPLE3_SE.scaffolds — SAMPLE1_PE.scaffolds — SAMPLE2_PE.scaffolds

NGx

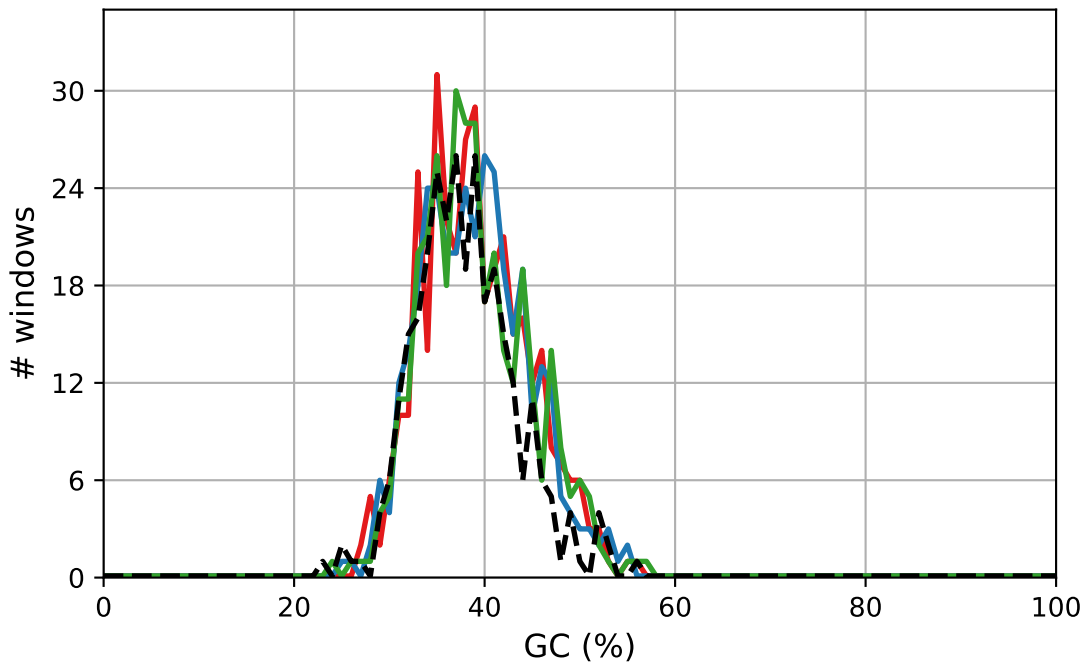


— SAMPLE3_SE.scaffolds — SAMPLE1_PE.scaffolds — SAMPLE2_PE.scaffolds

Cumulative length

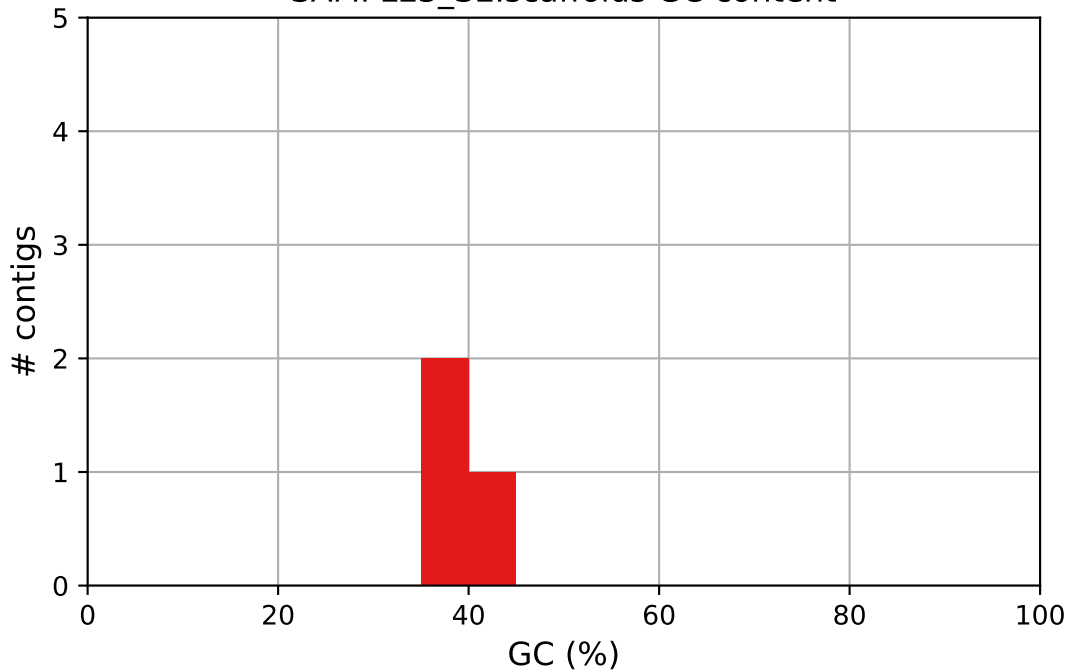


GC content



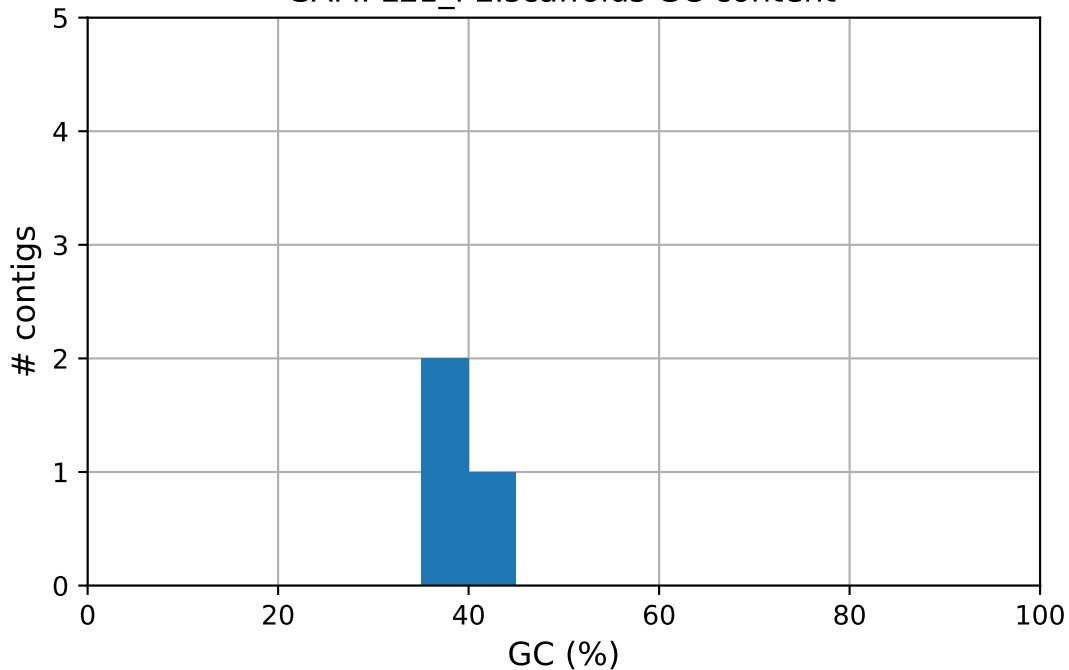
SAMPLE3_SE.scaffolds SAMPLE2_PE.scaffolds Reference
SAMPLE1_PE.scaffolds

SAMPLE3_SE.scaffolds GC content



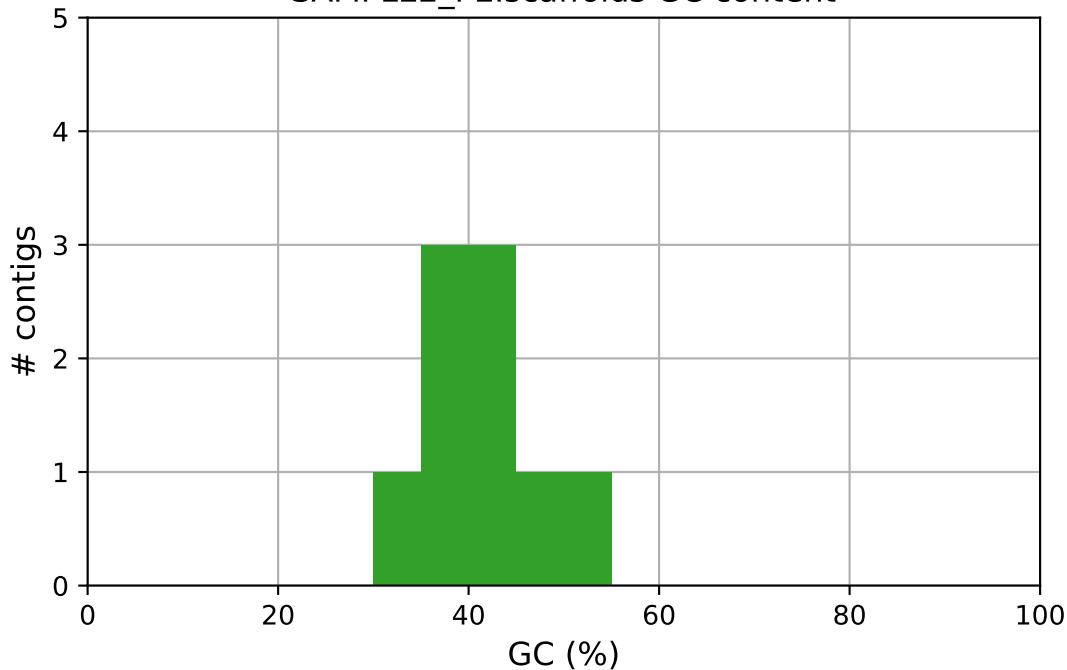
■ SAMPLE3_SE.scaffolds

SAMPLE1_PE.scaffolds GC content



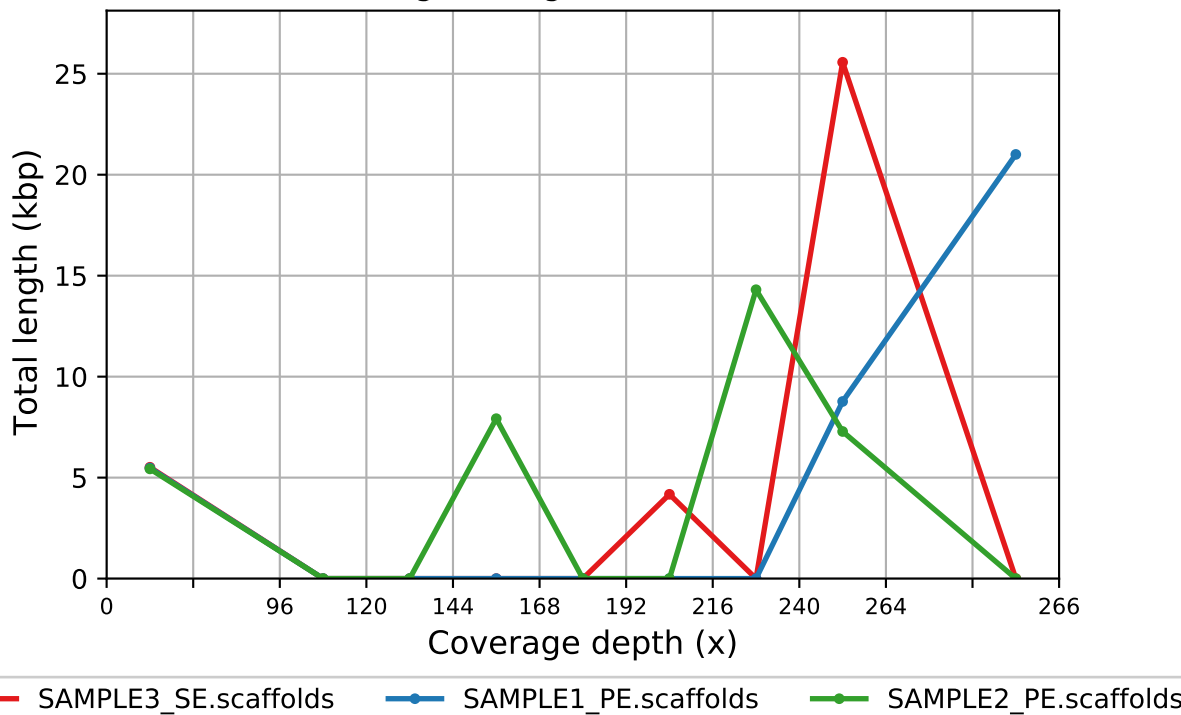
SAMPLE1_PE.scaffolds

SAMPLE2_PE.scaffolds GC content

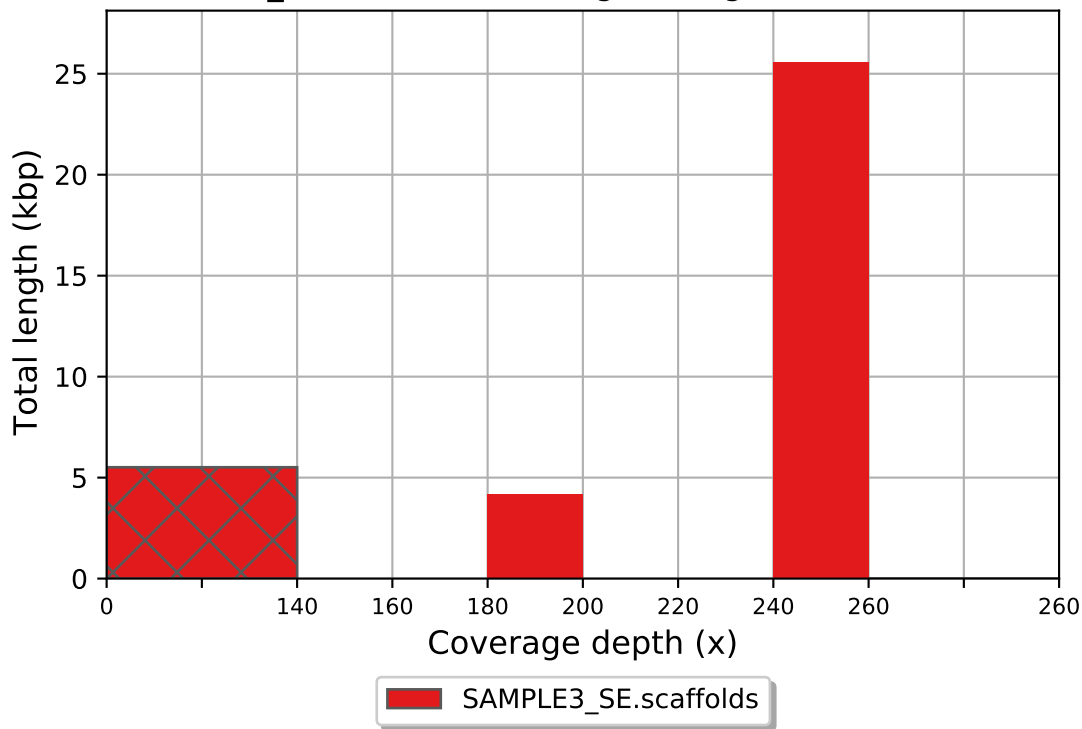


SAMPLE2_PE.scaffolds

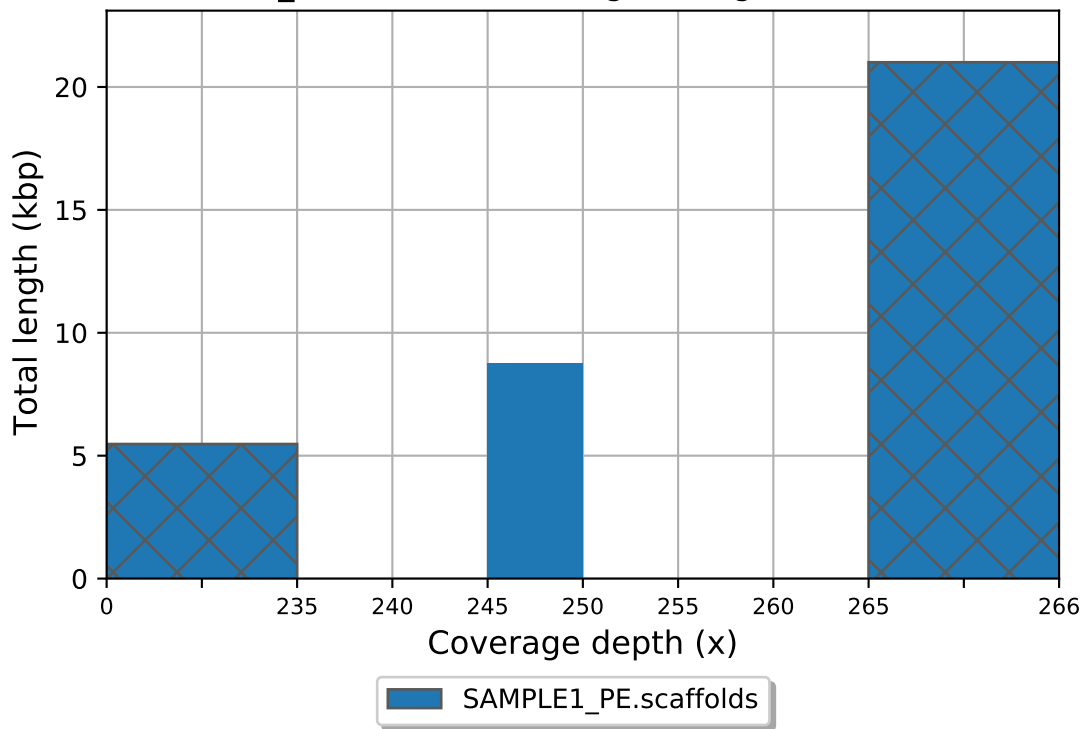
Coverage histogram (bin size: 24x)



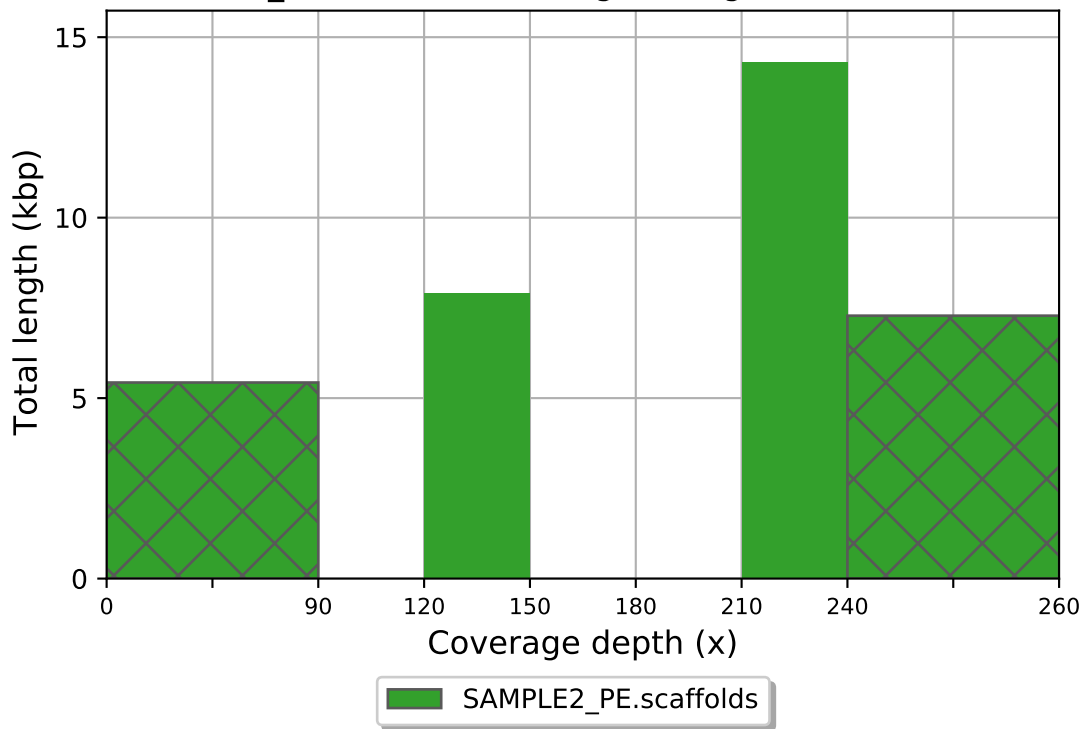
SAMPLE3_SE.scaffolds coverage histogram (bin size: 20x)



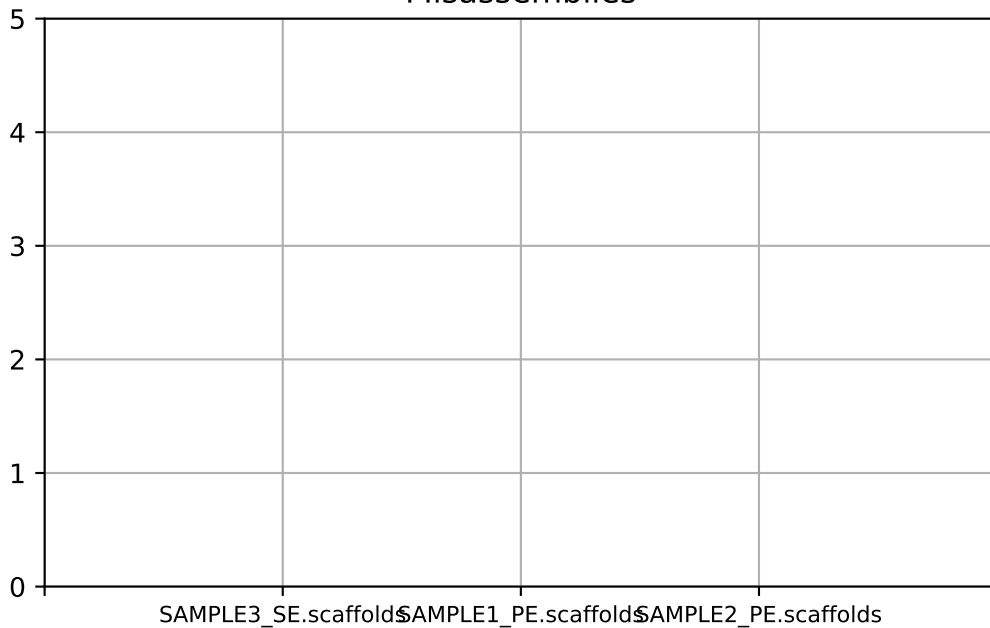
SAMPLE1_PE.scaffolds coverage histogram (bin size: 5x)



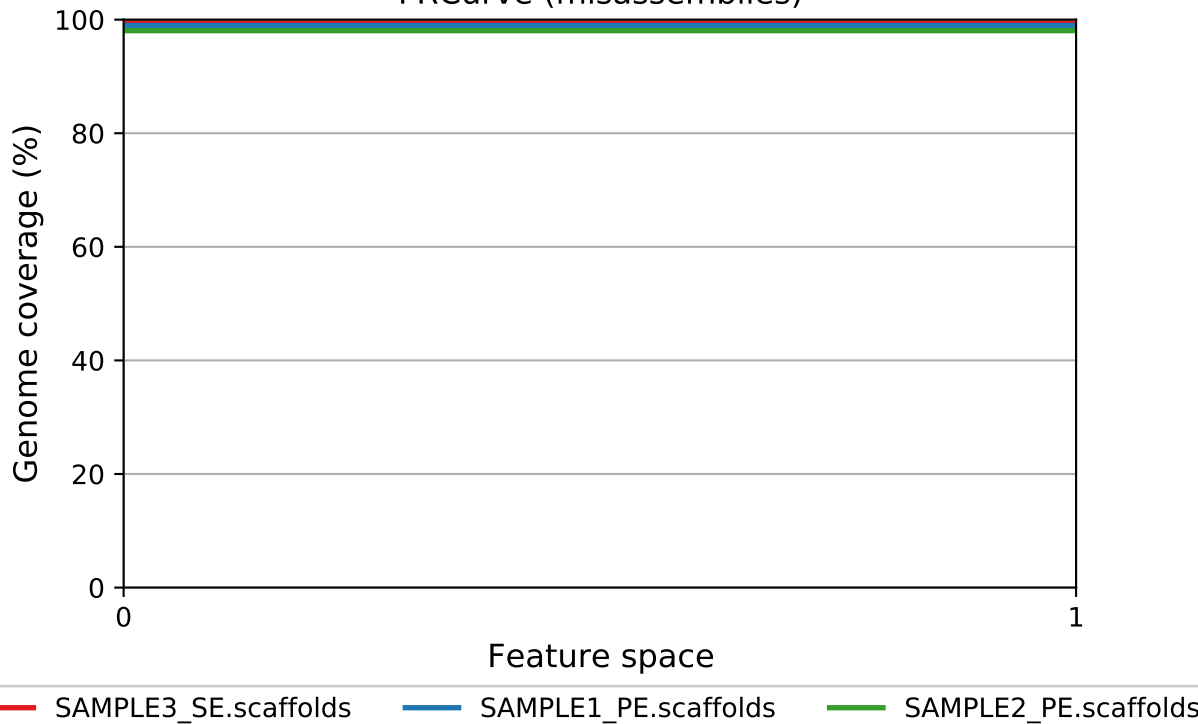
SAMPLE2_PE.scaffolds coverage histogram (bin size: 30x)



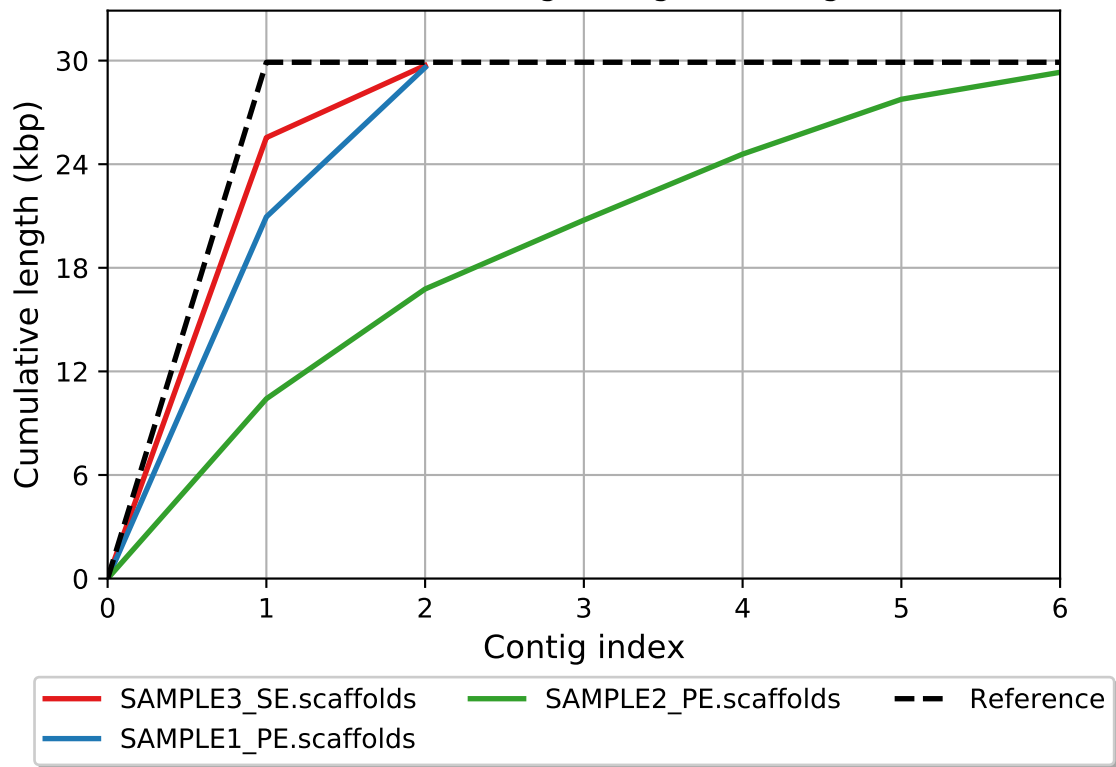
Misassemblies



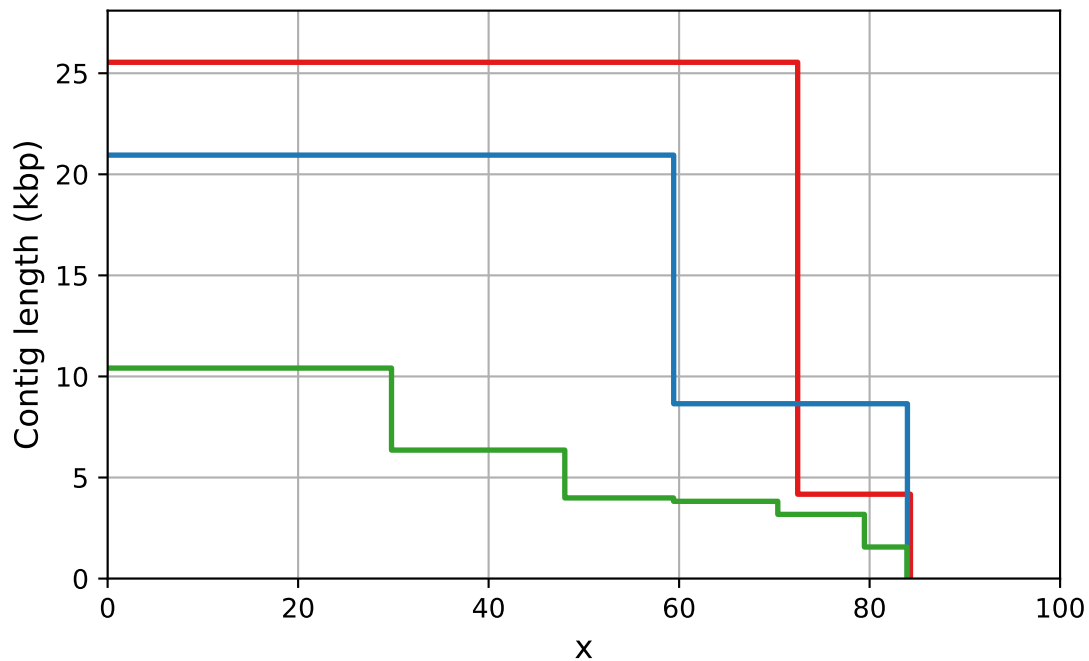
FRCurve (misassemblies)



Cumulative length (aligned contigs)

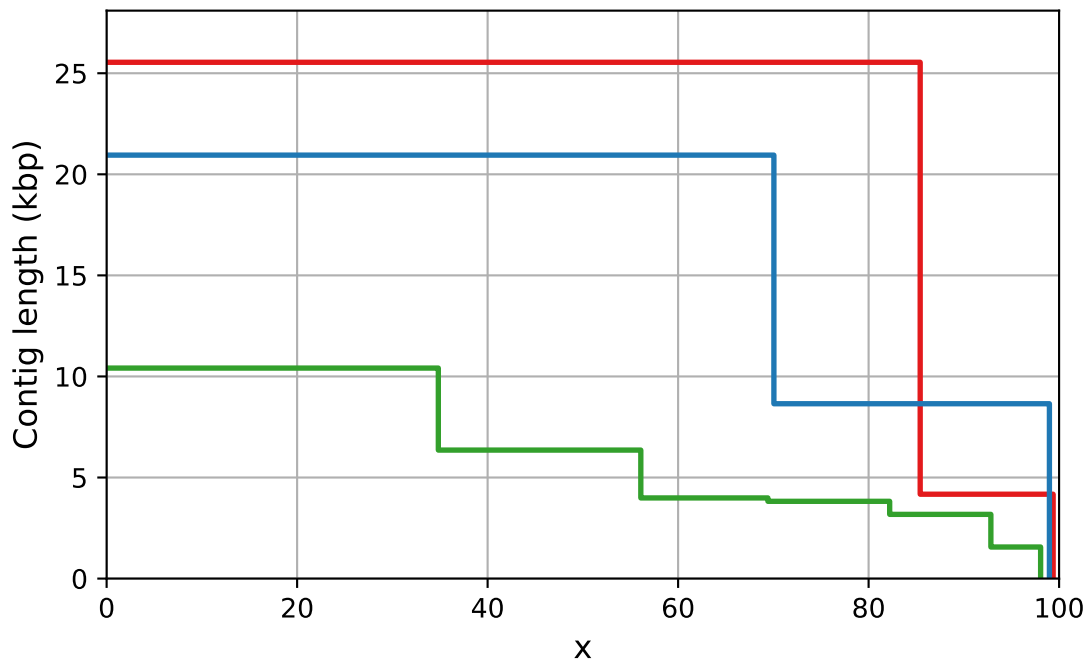


NAx

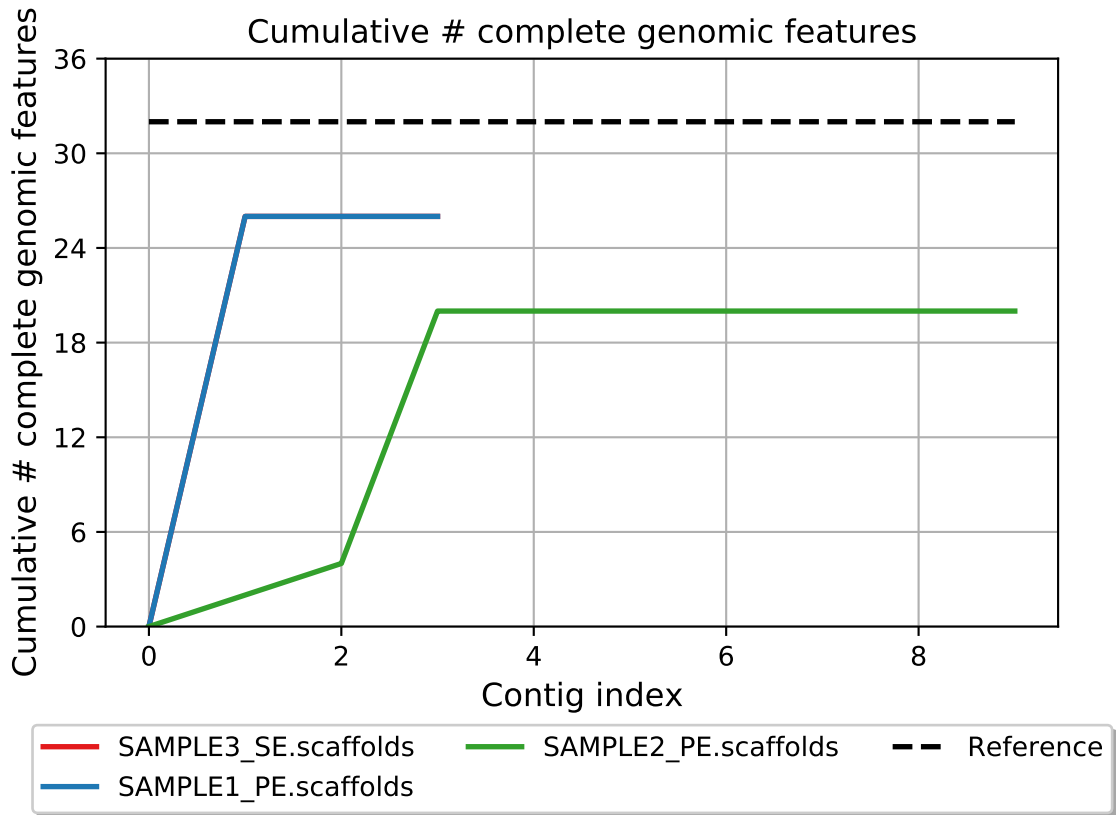


— SAMPLE3_SE.scaffolds — SAMPLE1_PE.scaffolds — SAMPLE2_PE.scaffolds

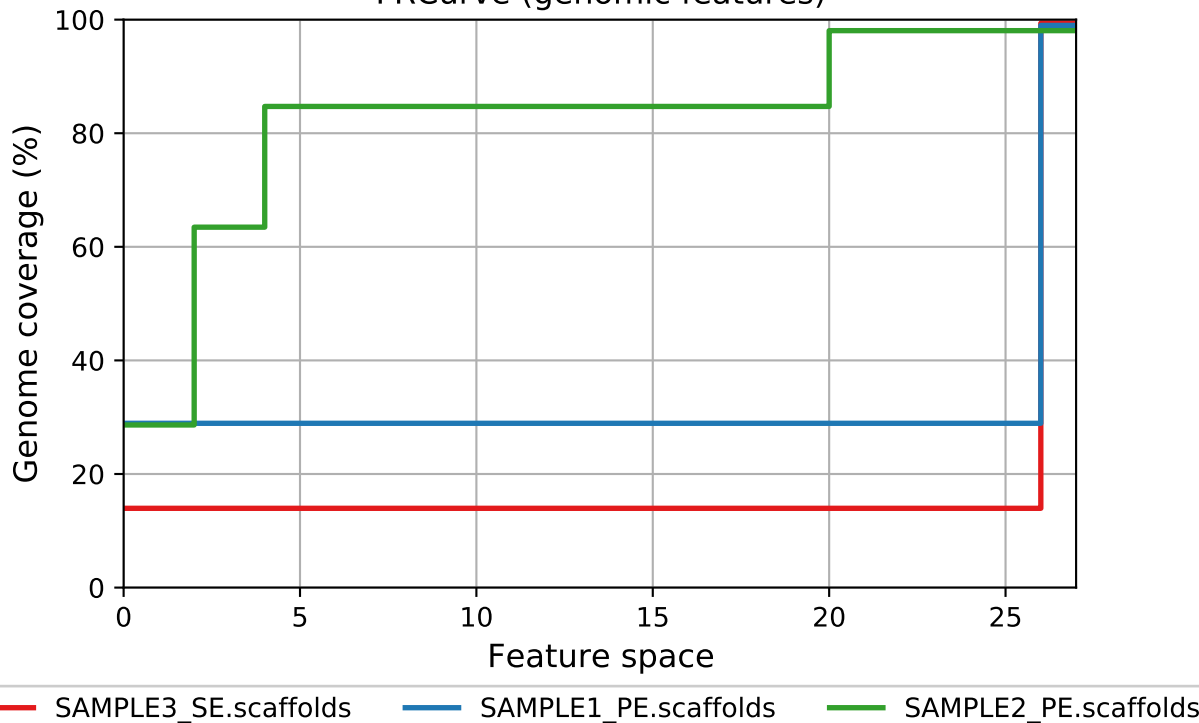
NGAx



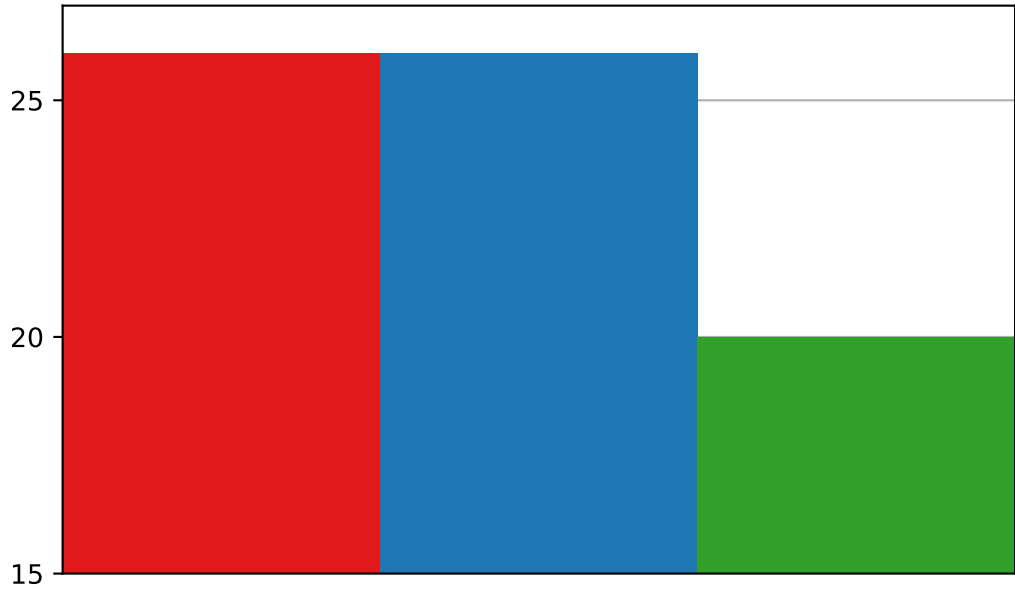
— SAMPLE3_SE.scaffolds — SAMPLE1_PE.scaffolds — SAMPLE2_PE.scaffolds



FRCurve (genomic features)



complete genomic features






■ SAMPLE3_SE.scaffolds ■ SAMPLE1_PE.scaffolds ■ SAMPLE2_PE.scaffolds

Genome fraction, %

100

99

98

 SAMPLE3_SE.scaffolds  SAMPLE1_PE.scaffolds  SAMPLE2_PE.scaffolds

