

## Report

	SAMPLE1_PE.scaffolds	SAMPLE2_PE.scaffolds
# contigs (>= 0 bp)	7	27
# contigs (>= 1000 bp)	3	6
# contigs (>= 5000 bp)	3	2
# contigs (>= 10000 bp)	1	1
# contigs (>= 25000 bp)	0	0
# contigs (>= 50000 bp)	0	0
Total length (>= 0 bp)	36445	41598
Total length (>= 1000 bp)	35151	32606
Total length (>= 5000 bp)	35151	16798
Total length (>= 10000 bp)	20973	10441
Total length (>= 25000 bp)	0	0
Total length (>= 50000 bp)	0	0
# contigs	3	9
Largest contig	20973	10441
Total length	35151	34939
Reference length	29903	29903
GC (%)	39.03	39.13
Reference GC (%)	37.97	37.97
N50	20973	4738
NG50	20973	6357
N75	8704	4051
NG75	8704	4070
L50	1	3
LG50	1	2
L75	2	5
LG75	2	4
# misassemblies	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# unaligned contigs	1 + 0 part	3 + 0 part
Unaligned length	5474	5432
Genome fraction (%)	98.870	98.151
Duplication ratio	1.004	1.005
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	23.68	34.07
# indels per 100 kbp	0.00	3.41
# genomic features	26 + 6 part	22 + 8 part
Largest alignment	20951	10414
Total aligned length	29565	29404
NA50	20951	4738
NGA50	20951	6357
NA75	8614	2895
NGA75	8614	4029
LA50	1	3
LGA50	1	2
LA75	2	5
LGA75	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

	SAMPLE1_PE.scaffolds	SAMPLE2_PE.scaffolds
# misassemblies	0	0
# contig misassemblies	0	0
# c. relocations	0	0
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# mismatches	7	10
# indels	0	1
# indels (<= 5 bp)	0	1
# indels (> 5 bp)	0	0
Indels length	0	1

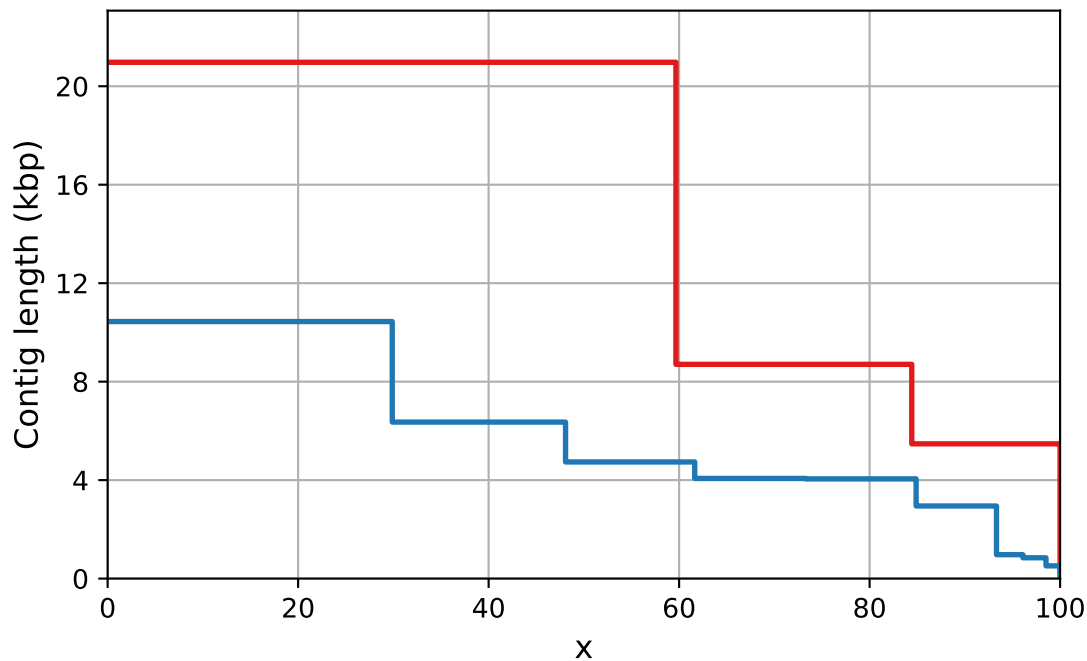
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

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

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

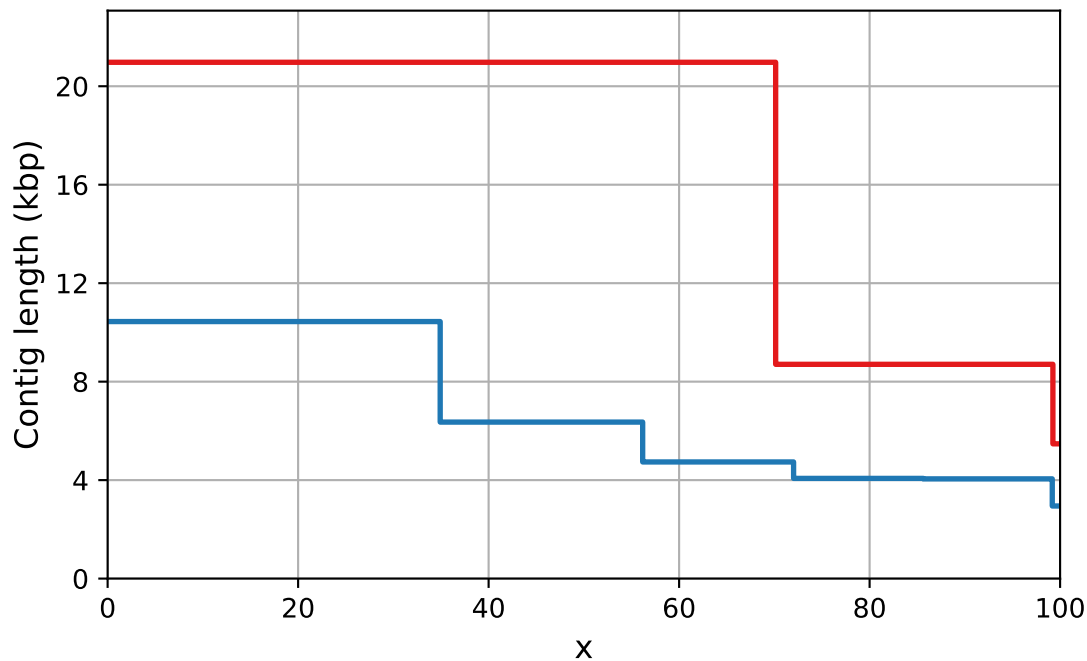
Nx



SAMPLE1\_PE.scaffolds

SAMPLE2\_PE.scaffolds

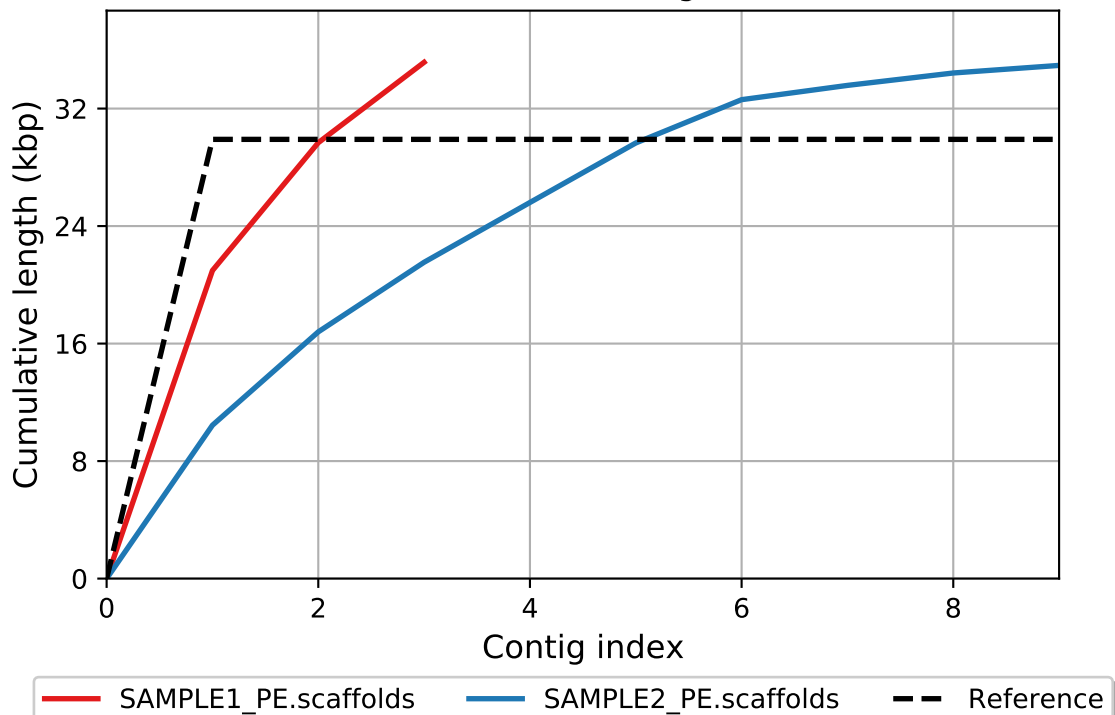
# NGx



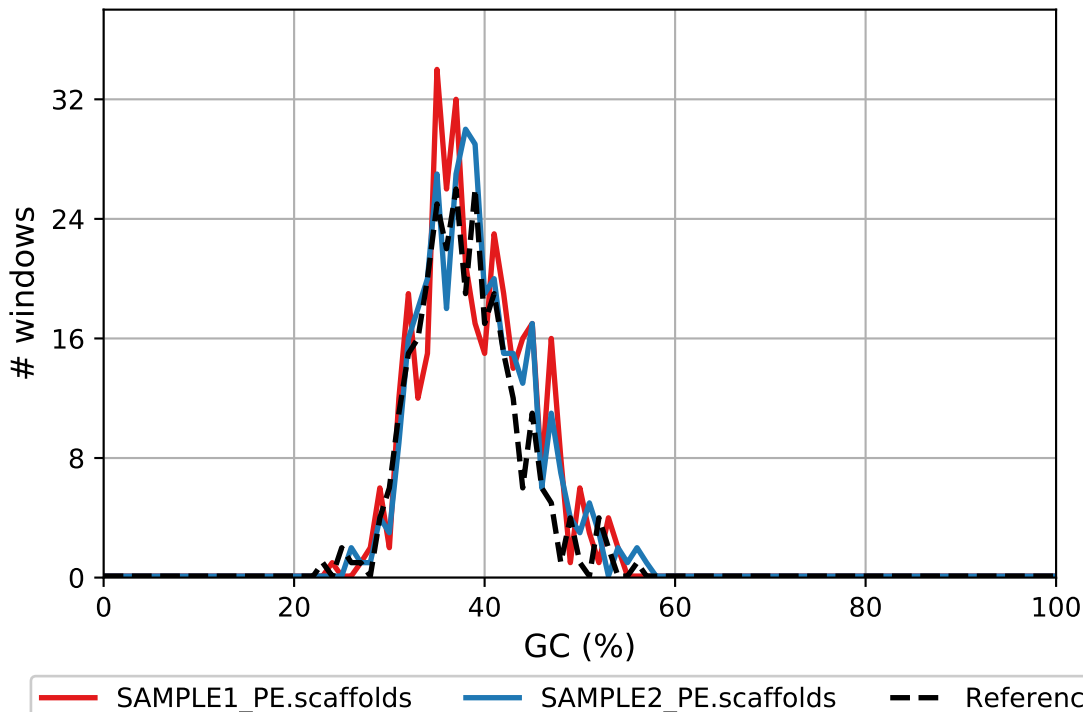
— SAMPLE1\_PE.scaffolds

— SAMPLE2\_PE.scaffolds

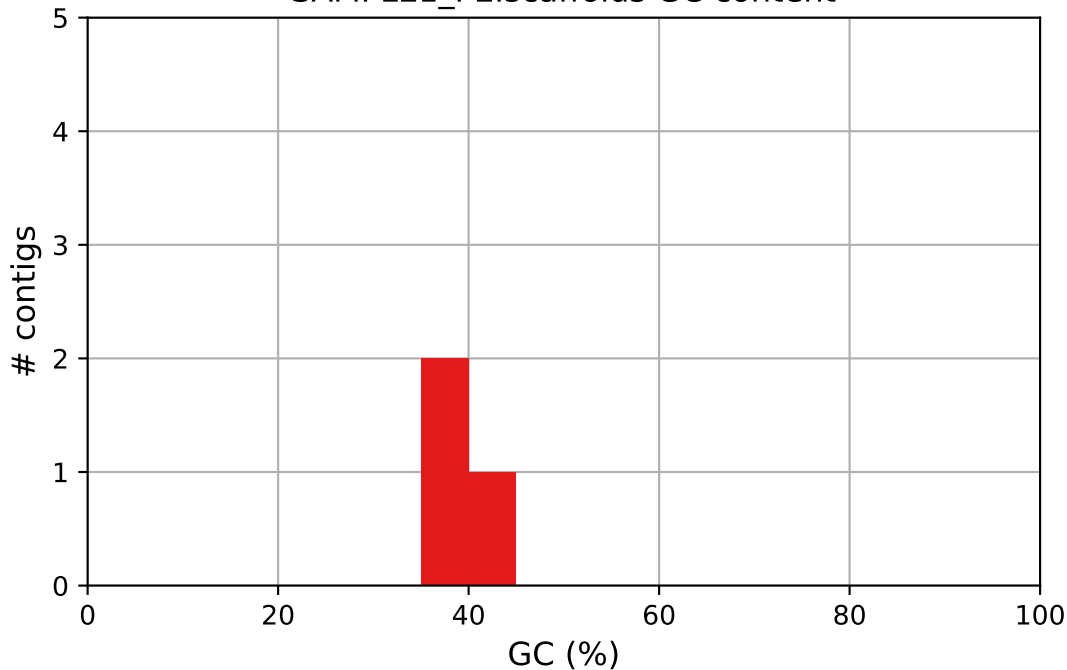
Cumulative length



GC content



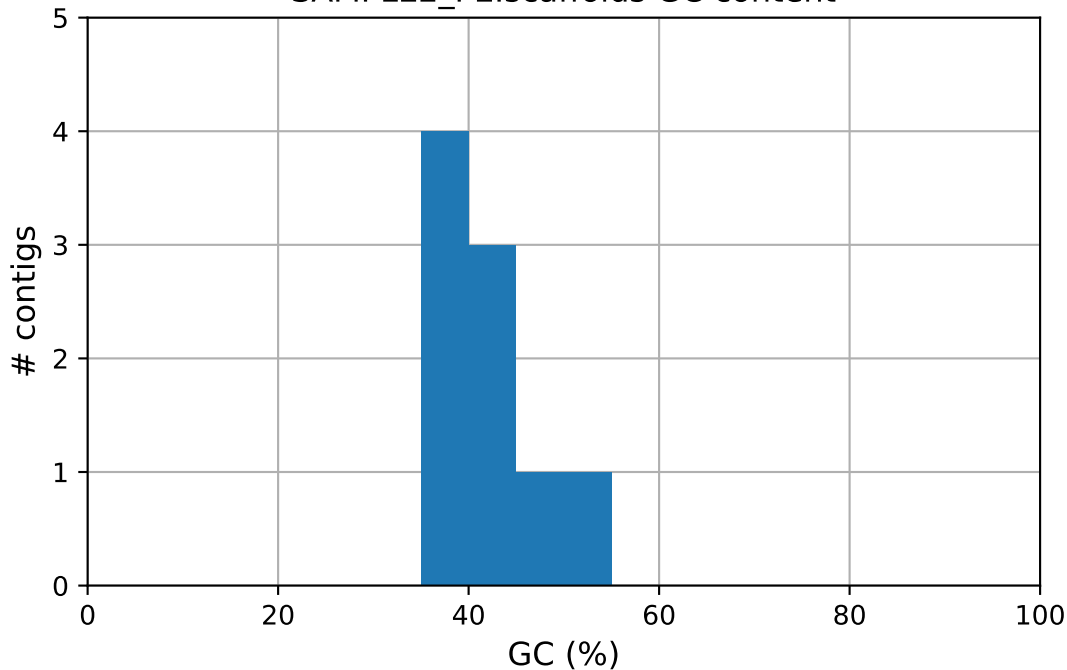
SAMPLE1\_PE.scaffolds GC content



■ SAMPLE1\_PE.scaffolds

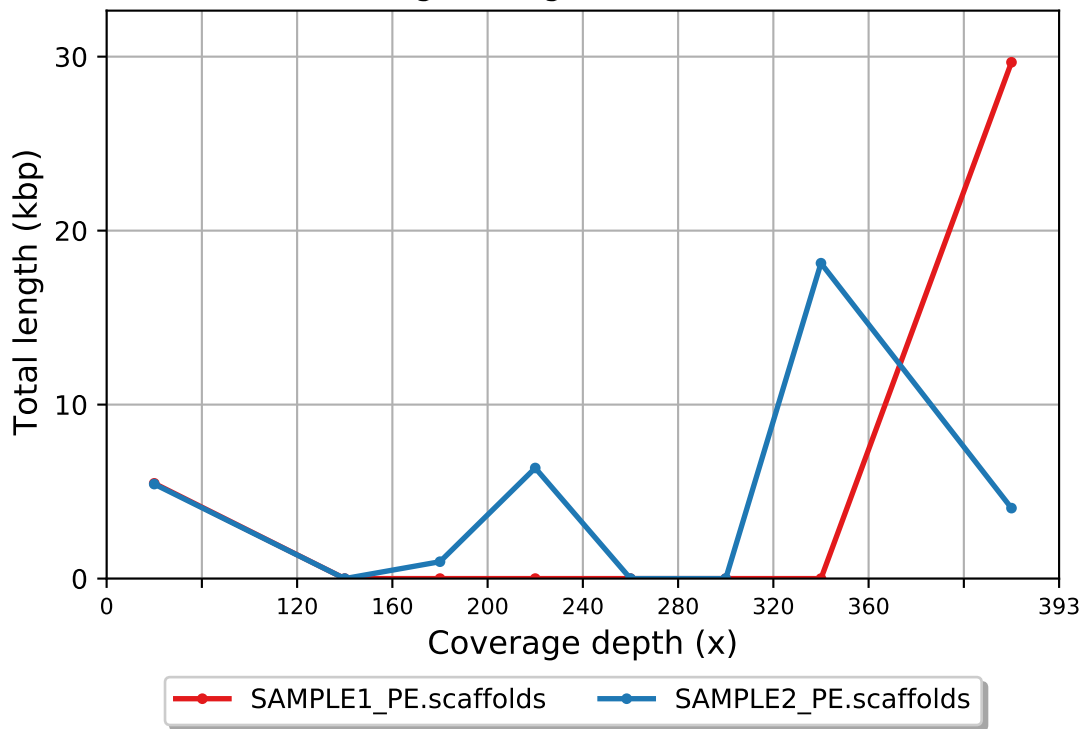


SAMPLE2\_PE.scaffolds GC content

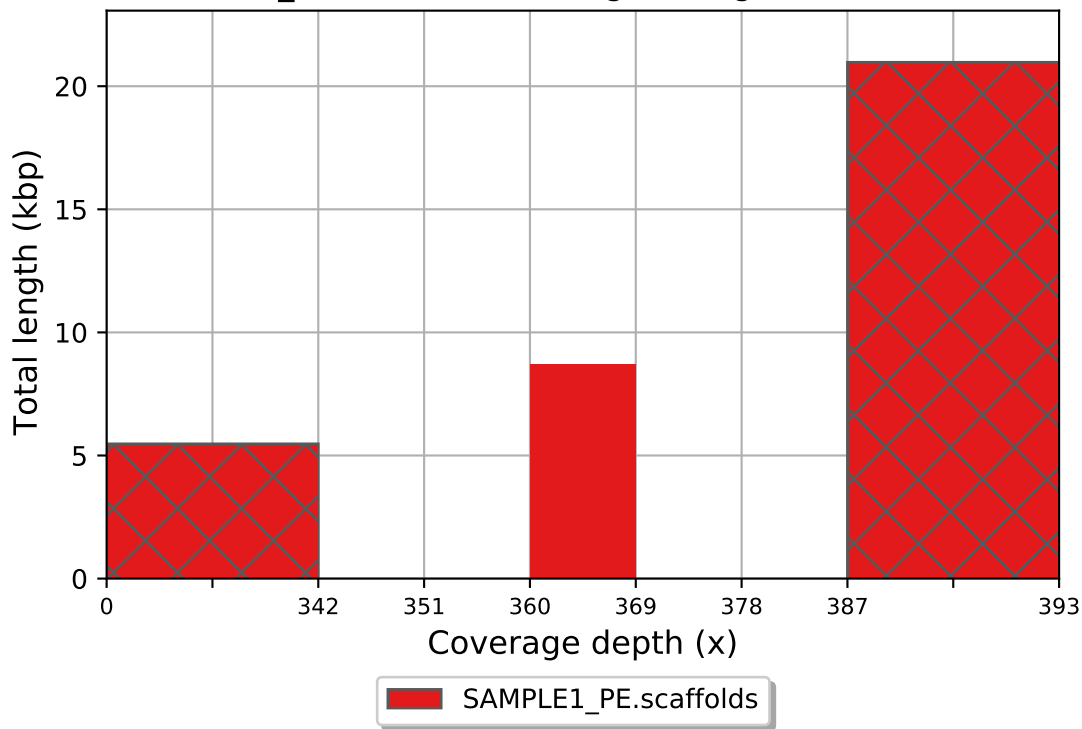


SAMPLE2\_PE.scaffolds

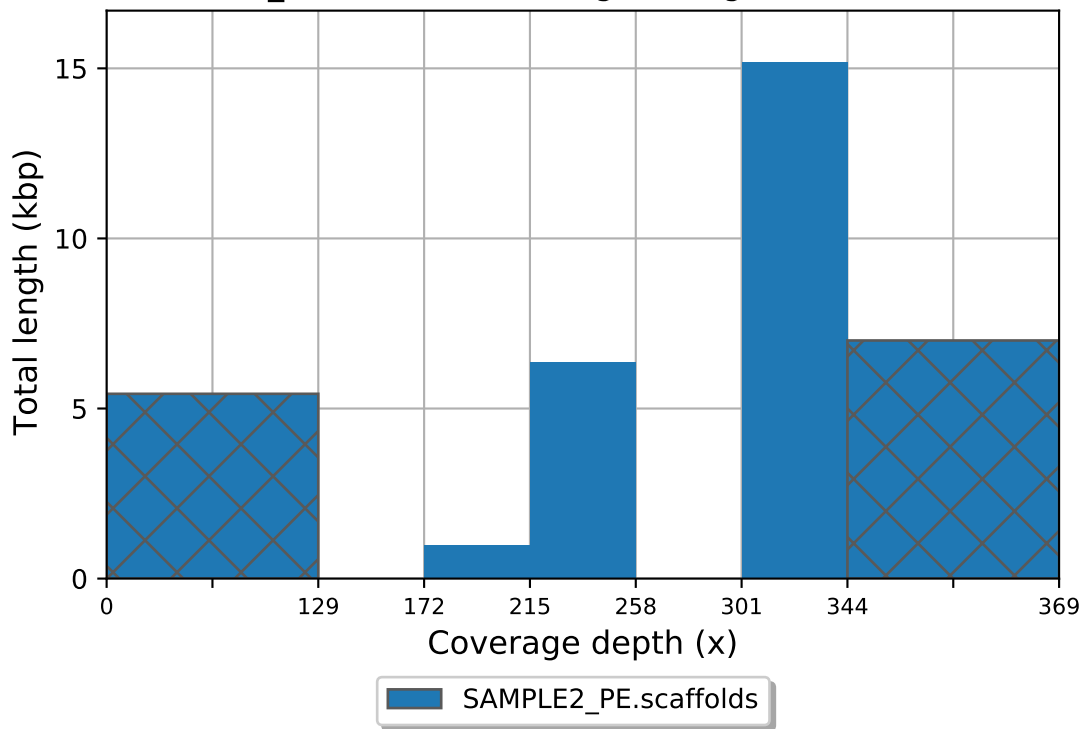
Coverage histogram (bin size: 40x)



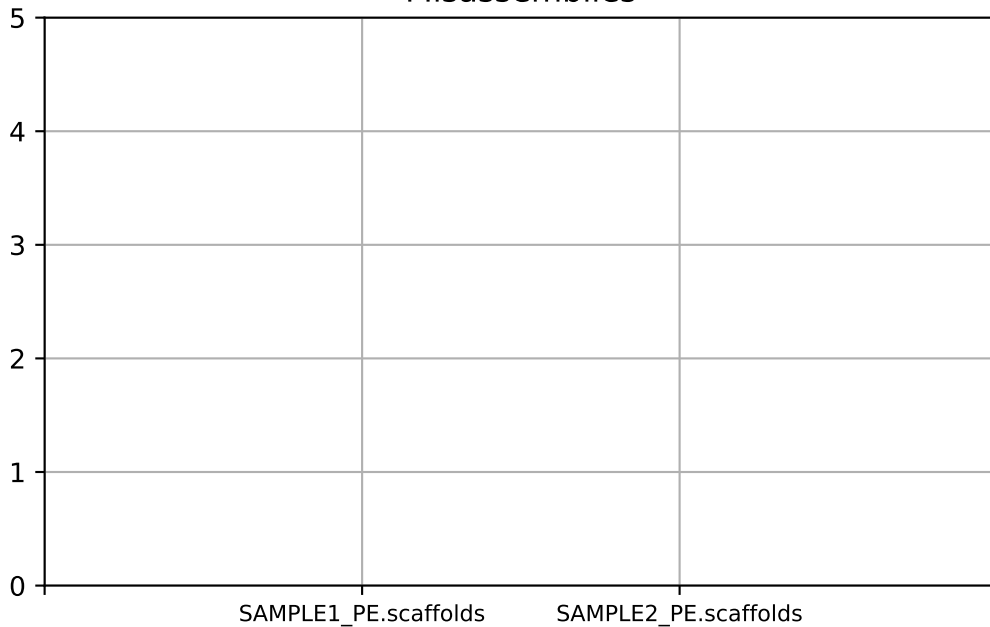
SAMPLE1\_PE.scaffolds coverage histogram (bin size: 9x)



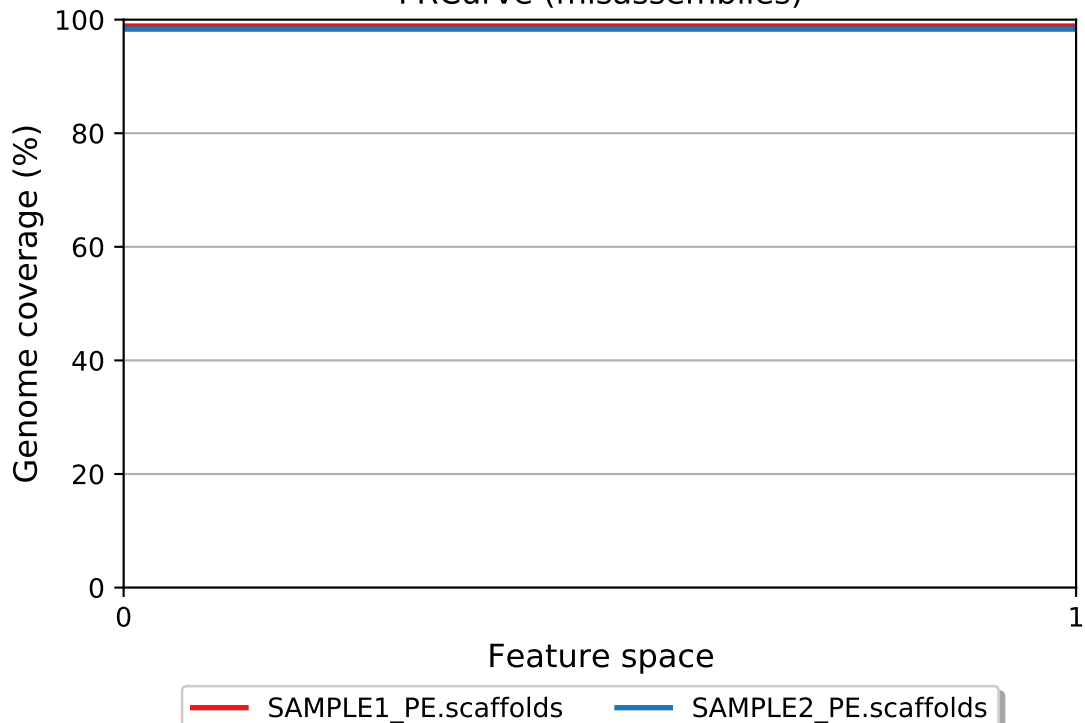
SAMPLE2\_PE.scaffolds coverage histogram (bin size: 43x)



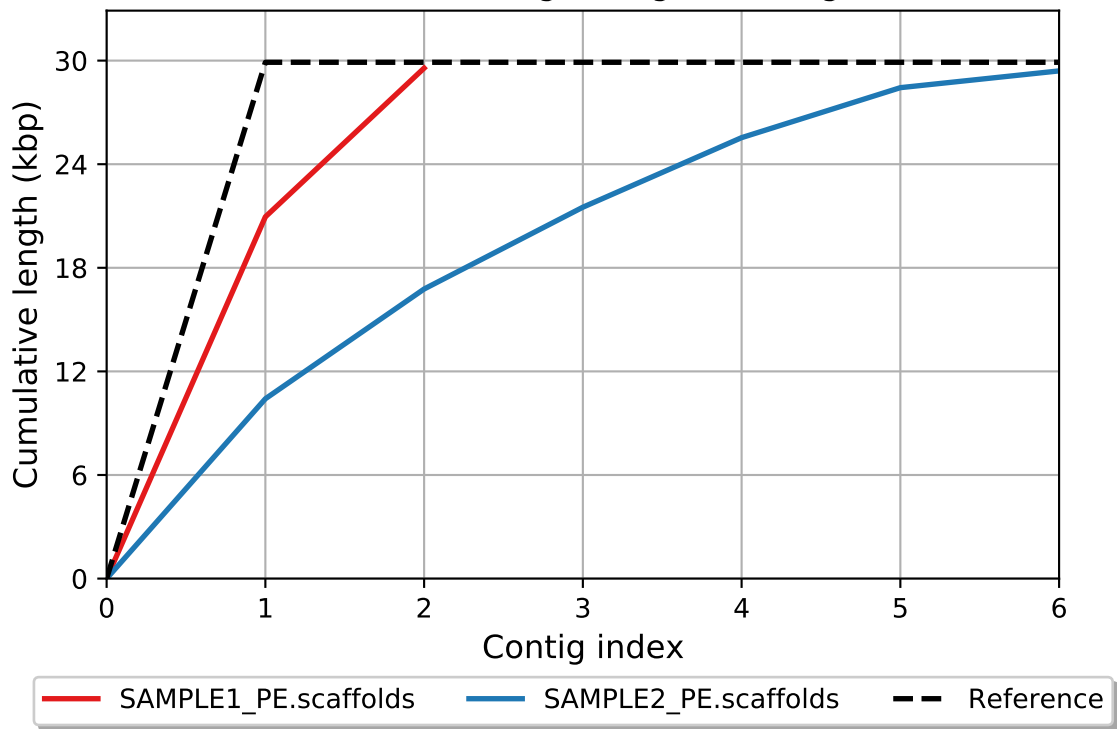
## Misassemblies



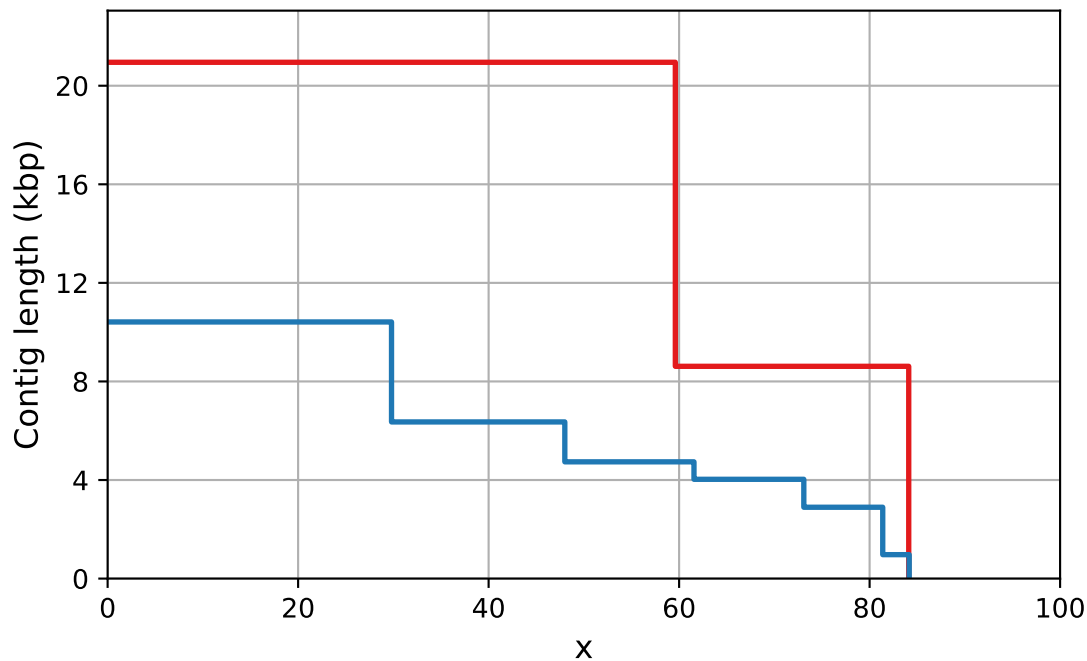
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx

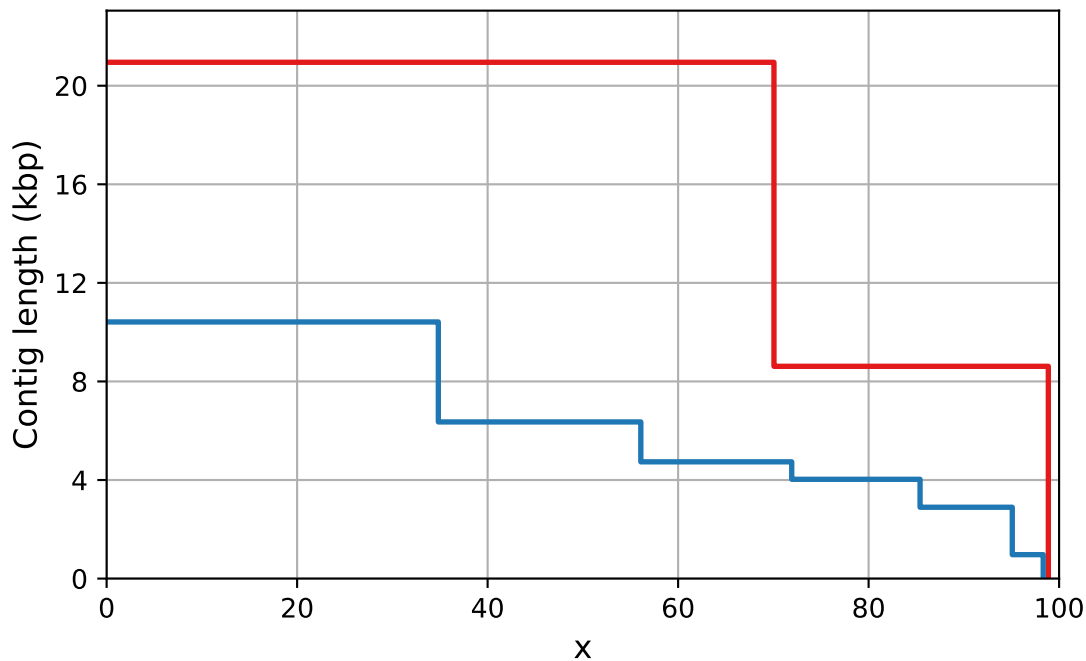


SAMPLE1\_PE.scaffolds

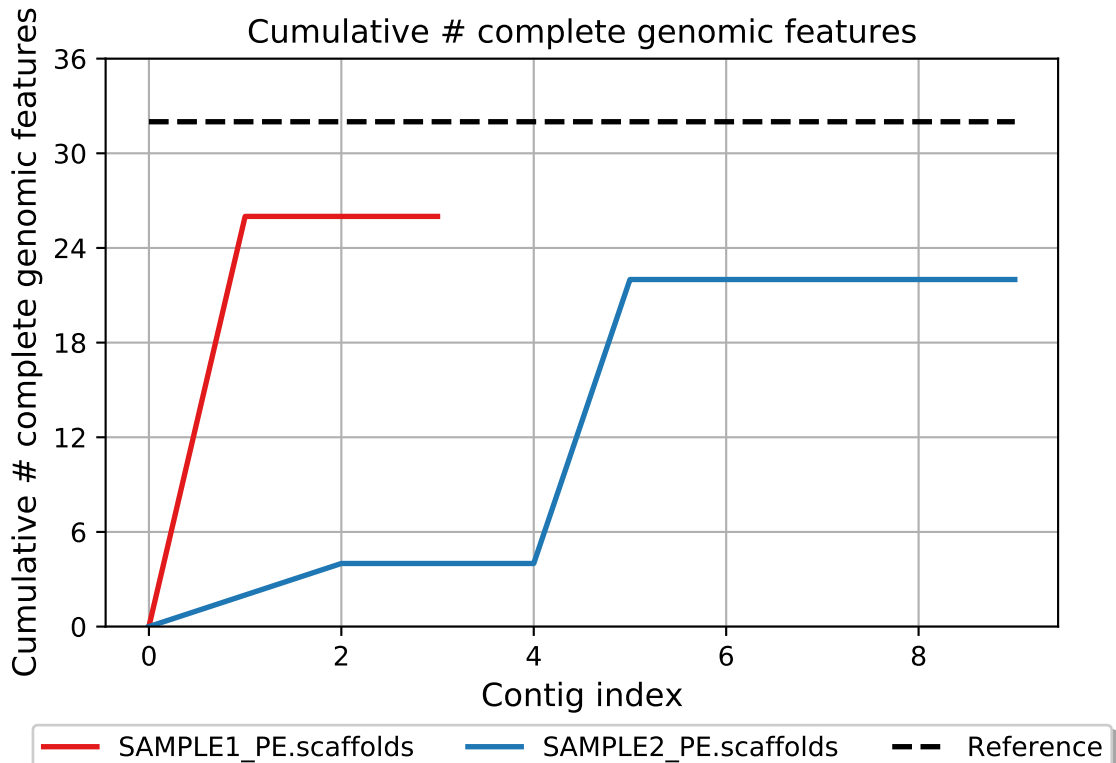
SAMPLE2\_PE.scaffolds



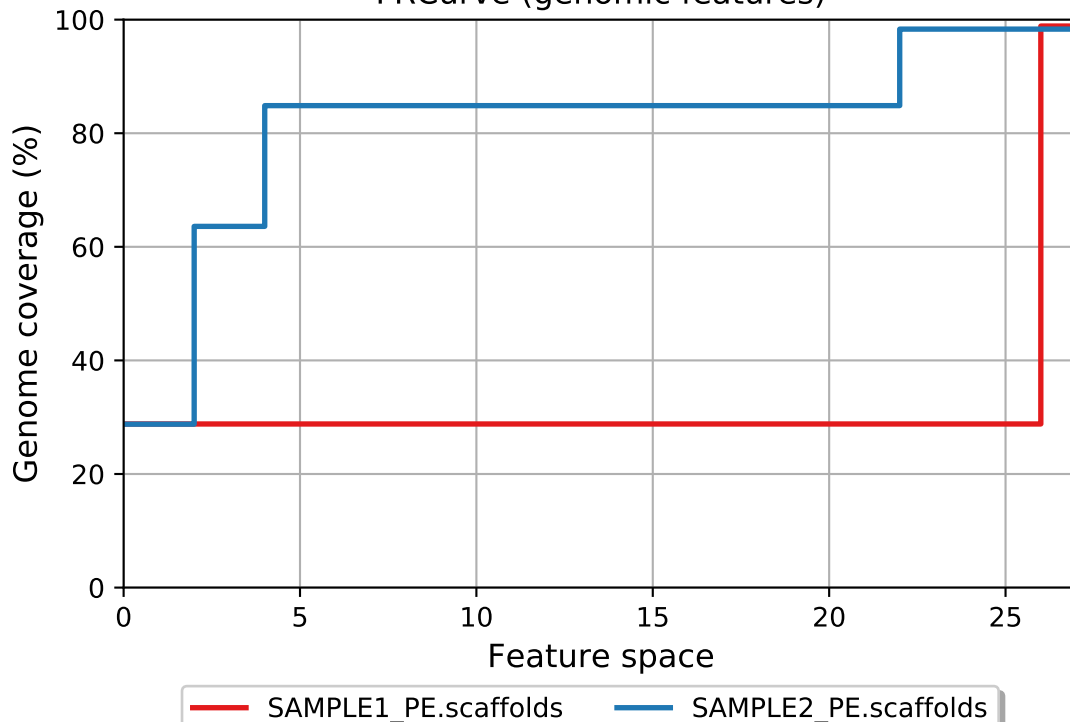
# NGAx



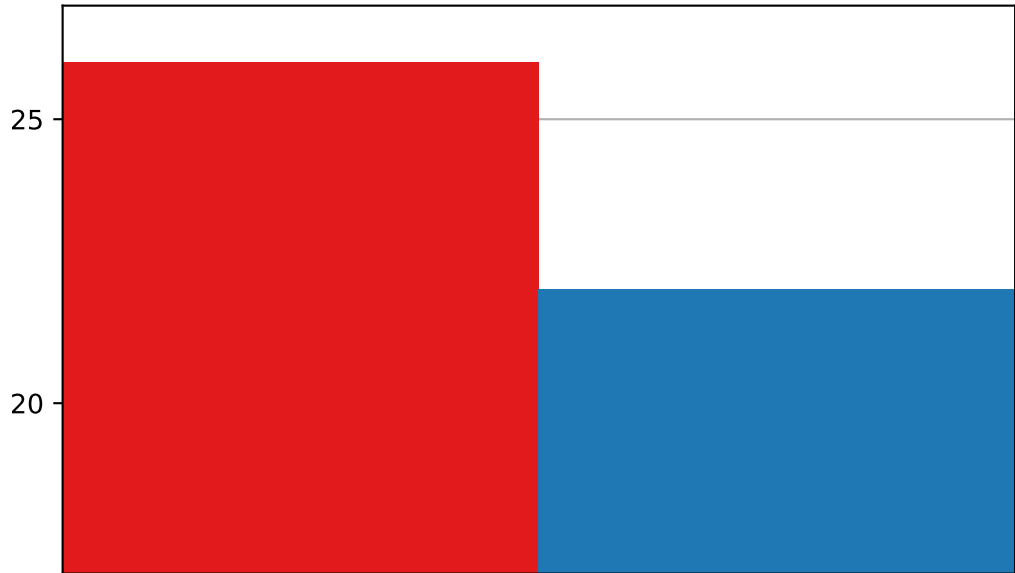
— SAMPLE1\_PE.scaffolds — SAMPLE2\_PE.scaffolds



FRCurve (genomic features)



# complete genomic features

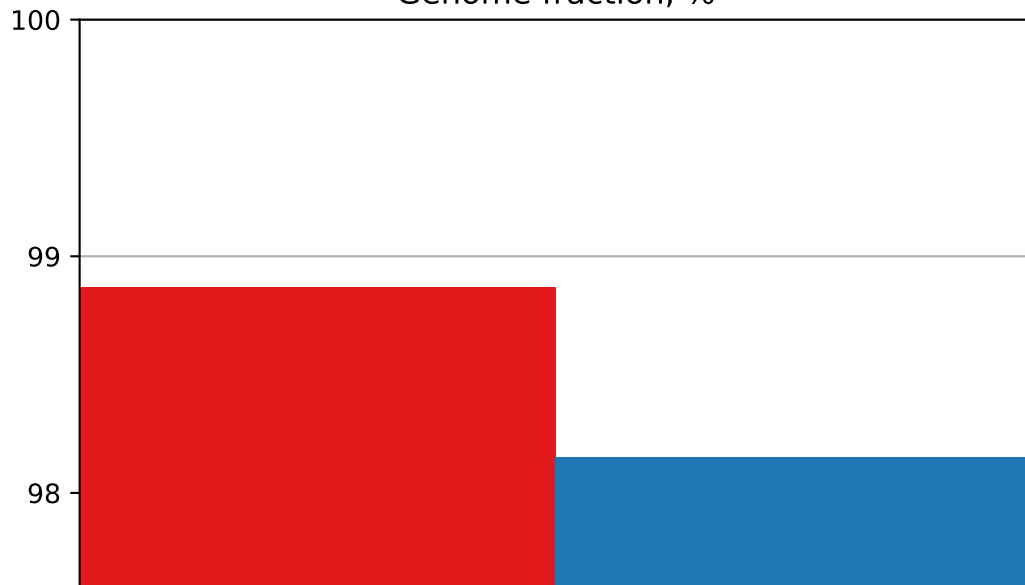


SAMPLE1\_PE.scaffolds



SAMPLE2\_PE.scaffolds

Genome fraction, %



SAMPLE1\_PE.scaffolds



SAMPLE2\_PE.scaffolds