

# Report

	SAMPLE3_SE.scaffolds	SAMPLE1_PE.scaffolds	SAMPLE2_PE.scaffolds
# contigs (>= 0 bp)	2	2	5
# contigs (>= 1000 bp)	2	2	5
# contigs (>= 5000 bp)	1	2	2
# contigs (>= 10000 bp)	1	1	1
# contigs (>= 25000 bp)	1	0	0
# contigs (>= 50000 bp)	0	0	0
Total length (>= 0 bp)	29426	29427	25591
Total length (>= 1000 bp)	29426	29427	25591
Total length (>= 5000 bp)	25442	29427	16515
Total length (>= 10000 bp)	25442	20847	10284
Total length (>= 25000 bp)	25442	0	0
Total length (>= 50000 bp)	0	0	0
# contigs	2	2	5
Largest contig	25442	20847	10284
Total length	29426	29427	25591
Reference length	29903	29903	29903
GC (%)	38.00	38.00	38.45
Reference GC (%)	37.97	37.97	37.97
N50	25442	20847	6231
NG50	25442	20847	6231
N75	25442	8580	3761
NG75	25442	8580	3753
L50	1	1	2
LG50	1	1	2
L75	1	2	3
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	0 + 0 part	0 + 0 part	0 + 0 part
Unaligned length	0	0	0
Genome fraction (%)	98.405	98.408	85.399
Duplication ratio	1.000	1.000	1.002
# N's per 100 kbp	0.00	0.00	0.00
# mismatches per 100 kbp	13.59	20.39	35.24
# indels per 100 kbp	0.00	0.00	3.92
# genomic features	26 + 6 part	26 + 6 part	20 + 10 part
Largest alignment	25442	20847	10284
Total aligned length	29426	29427	25536
NA50	25442	20847	6231
NGA50	25442	20847	6231
NA75	25442	8580	3760
NGA75	25442	8580	3699
LA50	1	1	2
LGA50	1	1	2
LA75	1	2	3
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	9
# indels	0	0	1
# indels (<= 5 bp)	0	0	1
# indels (> 5 bp)	0	0	0
Indels length	0	0	1

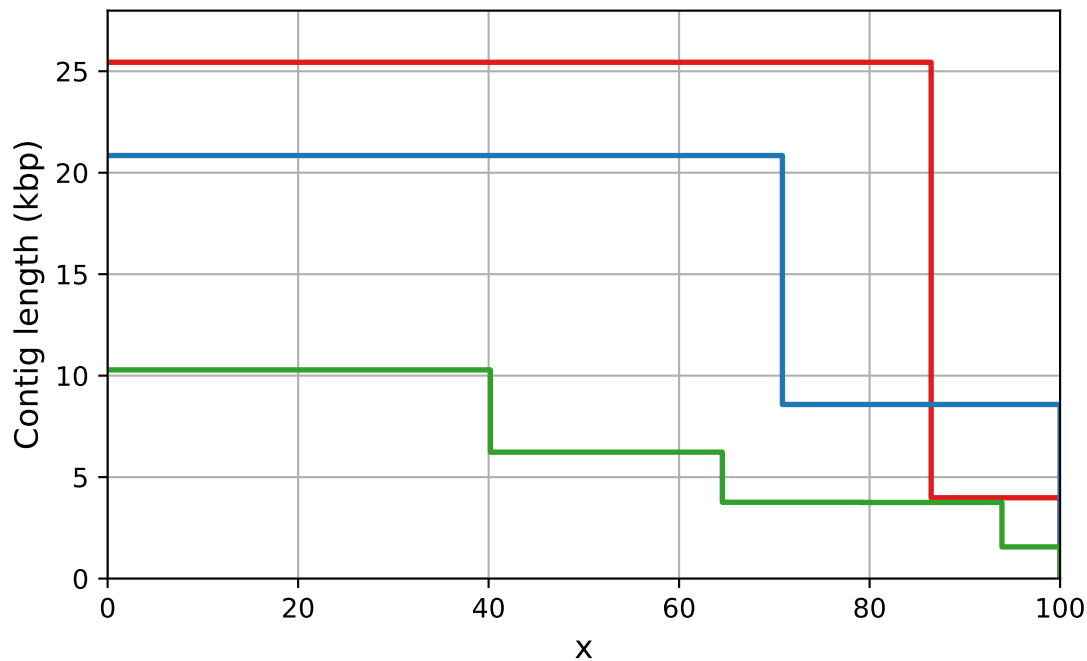
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	SAMPLE3_SE.scaffolds	SAMPLE1_PE.scaffolds	SAMPLE2_PE.scaffolds
# 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	0	0	0

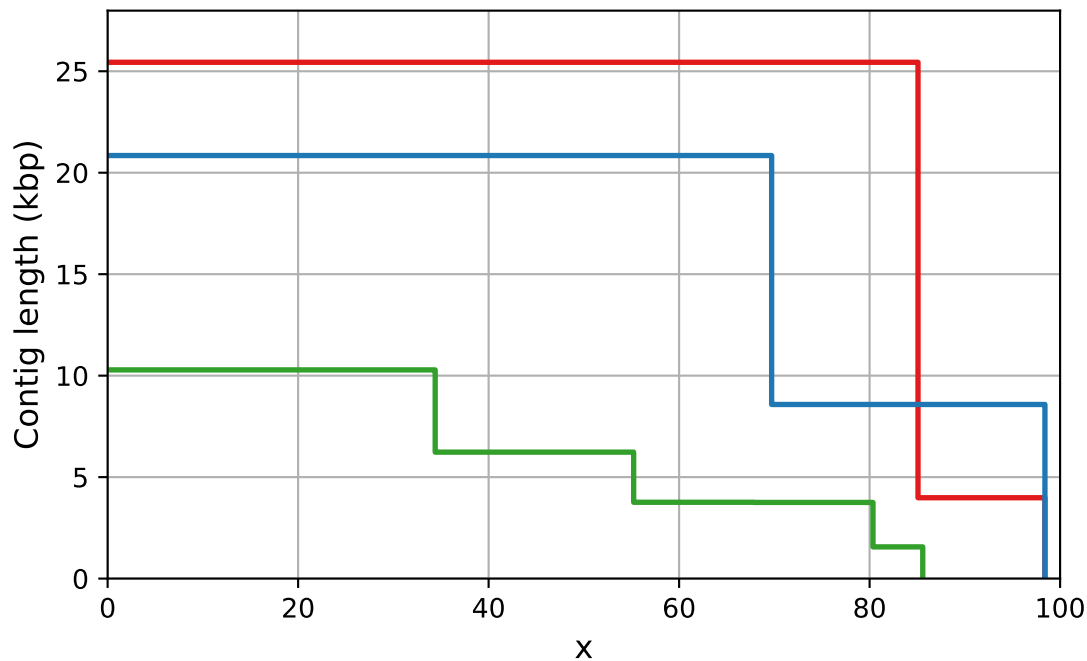
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



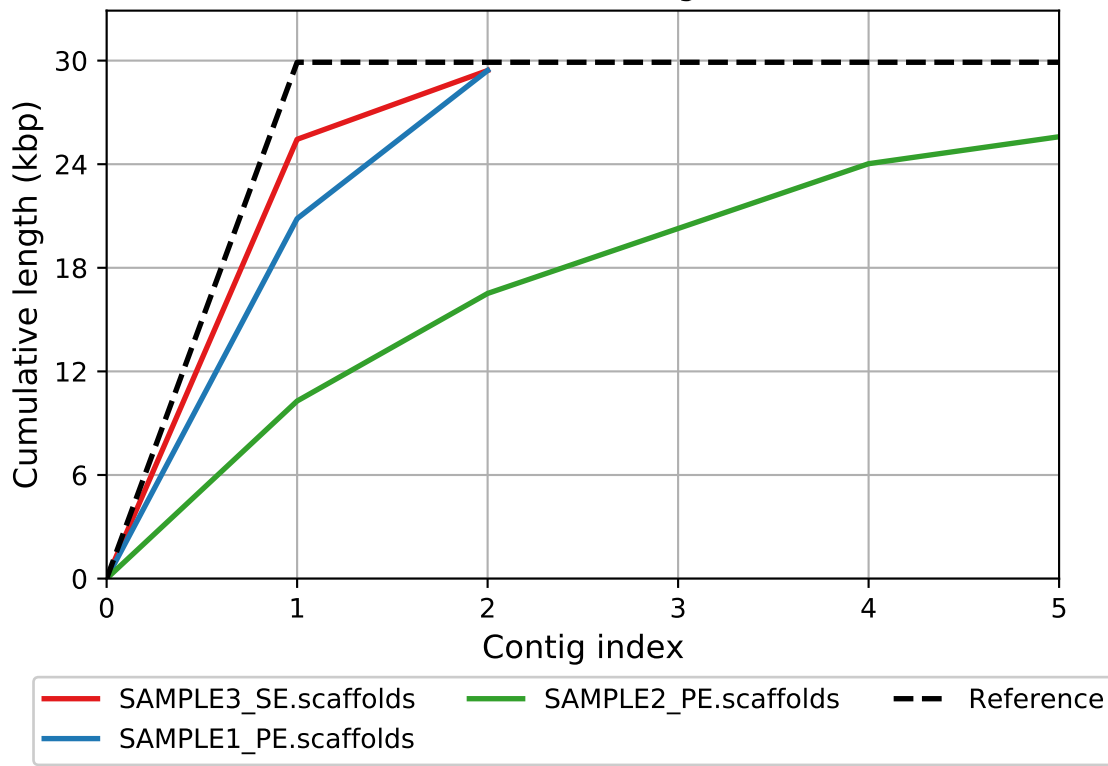
— SAMPLE3\_SE.scaffolds — SAMPLE1\_PE.scaffolds — SAMPLE2\_PE.scaffolds

# NGx

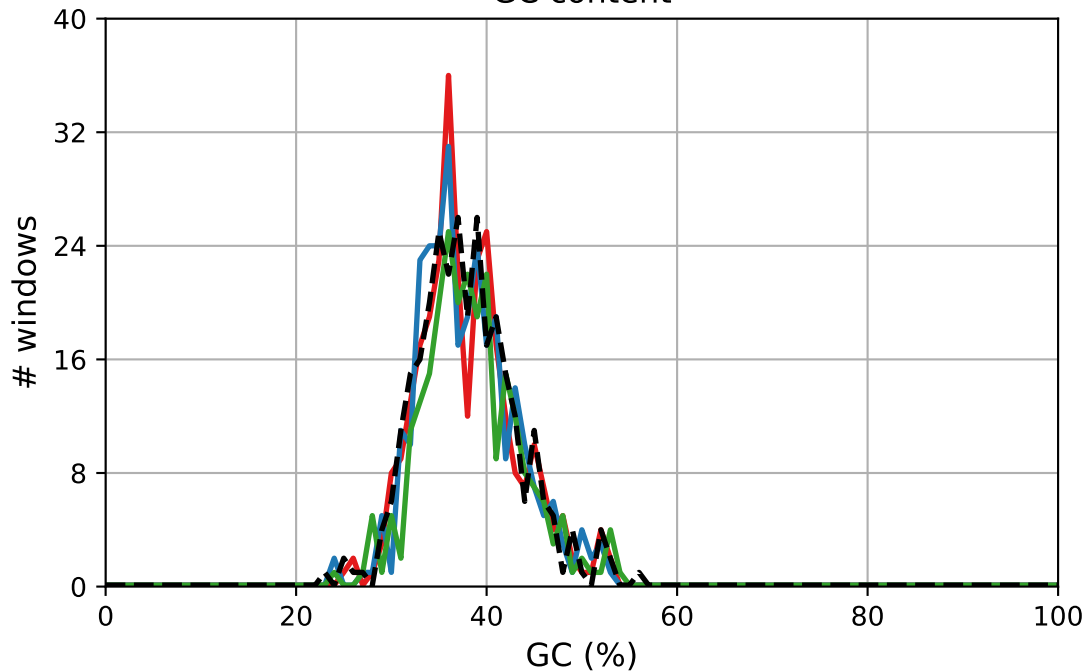


— SAMPLE3\_SE.scaffolds    — SAMPLE1\_PE.scaffolds    — SAMPLE2\_PE.scaffolds

Cumulative length

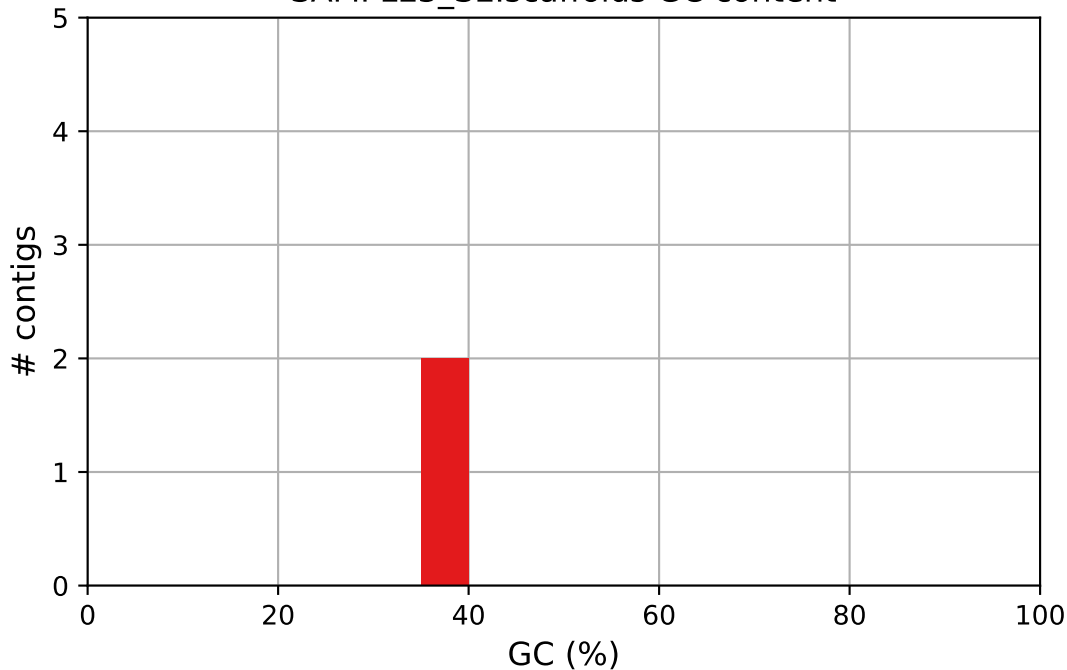


GC content



SAMPLE3\_SE.scaffolds    SAMPLE2\_PE.scaffolds    -- Reference  
SAMPLE1\_PE.scaffolds

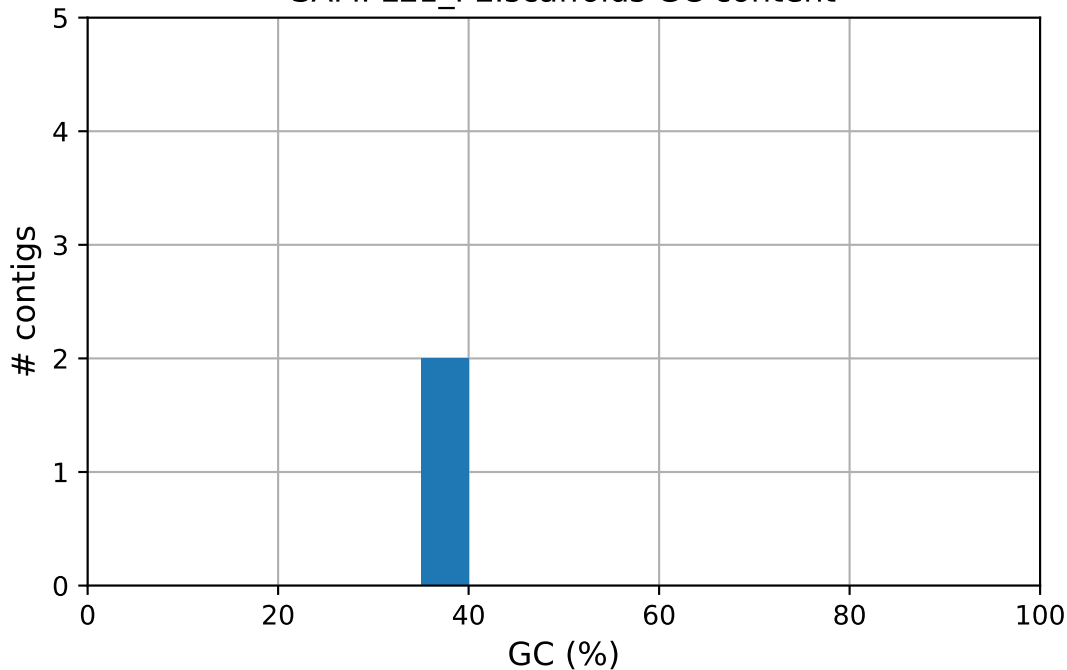
SAMPLE3\_SE.scaffolds GC content



■ SAMPLE3\_SE.scaffolds

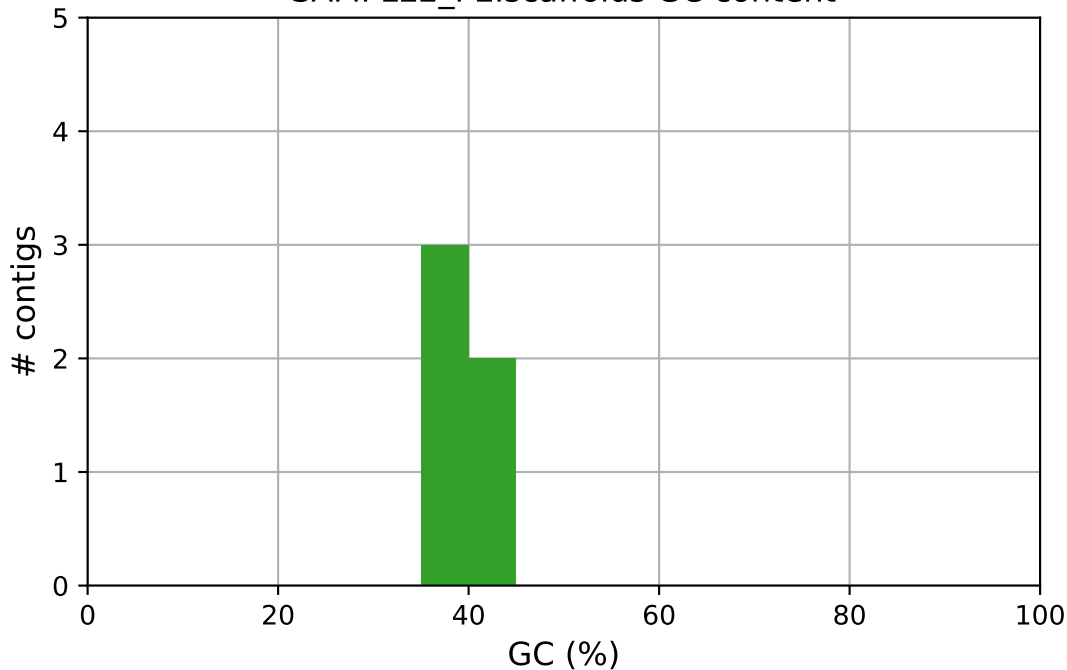


SAMPLE1\_PE.scaffolds GC content



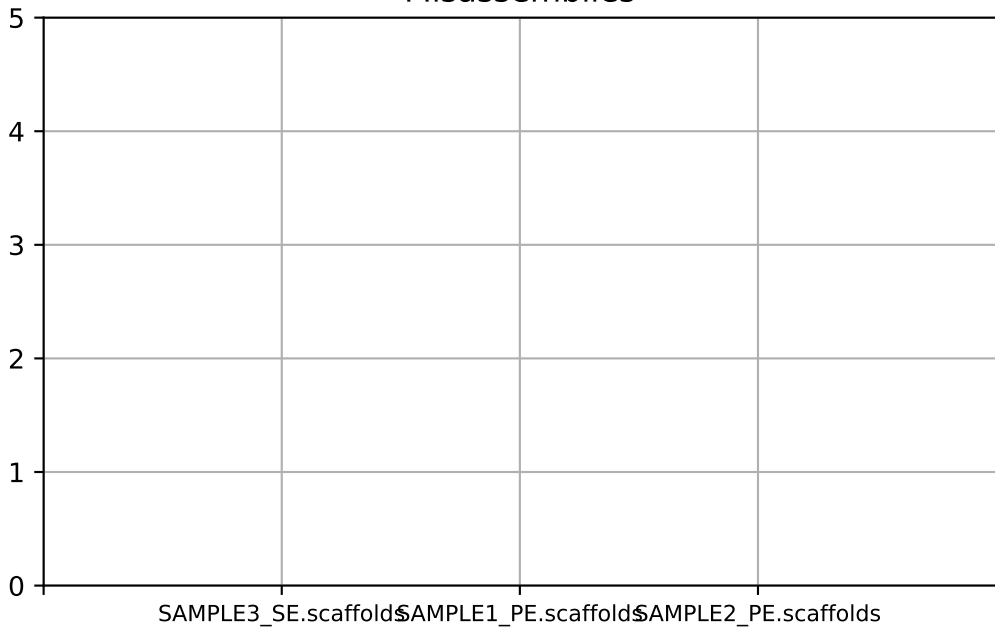
SAMPLE1\_PE.scaffolds

SAMPLE2\_PE.scaffolds GC content

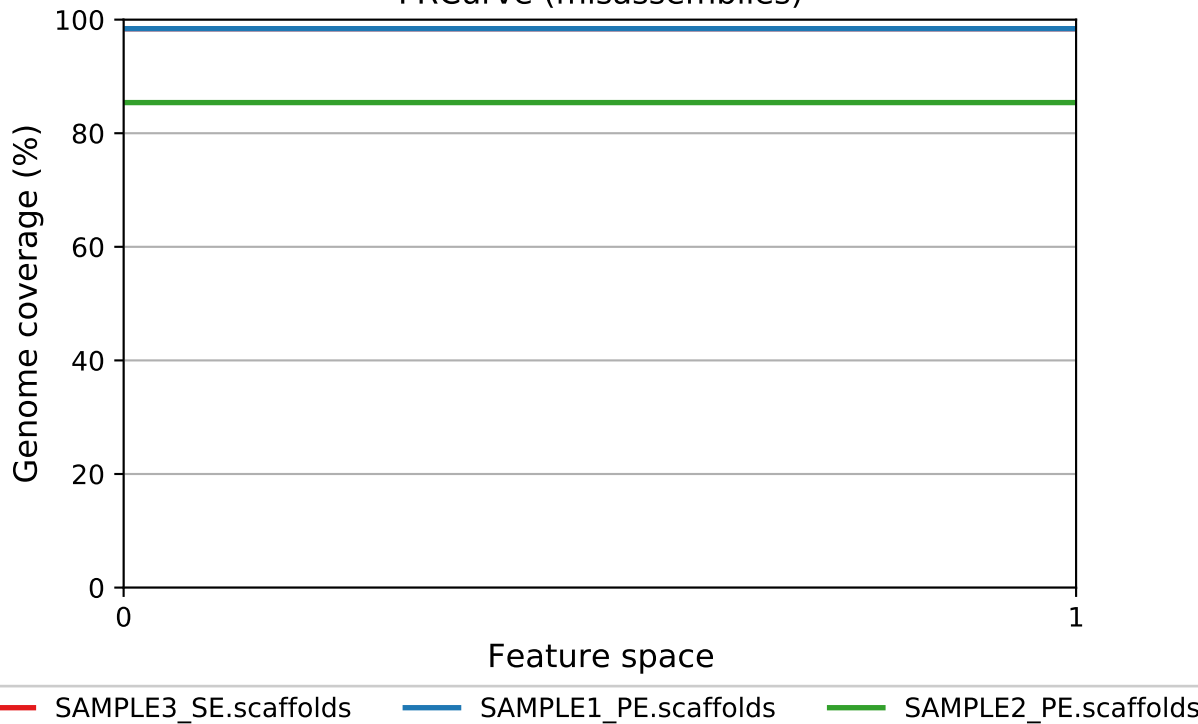


SAMPLE2\_PE.scaffolds

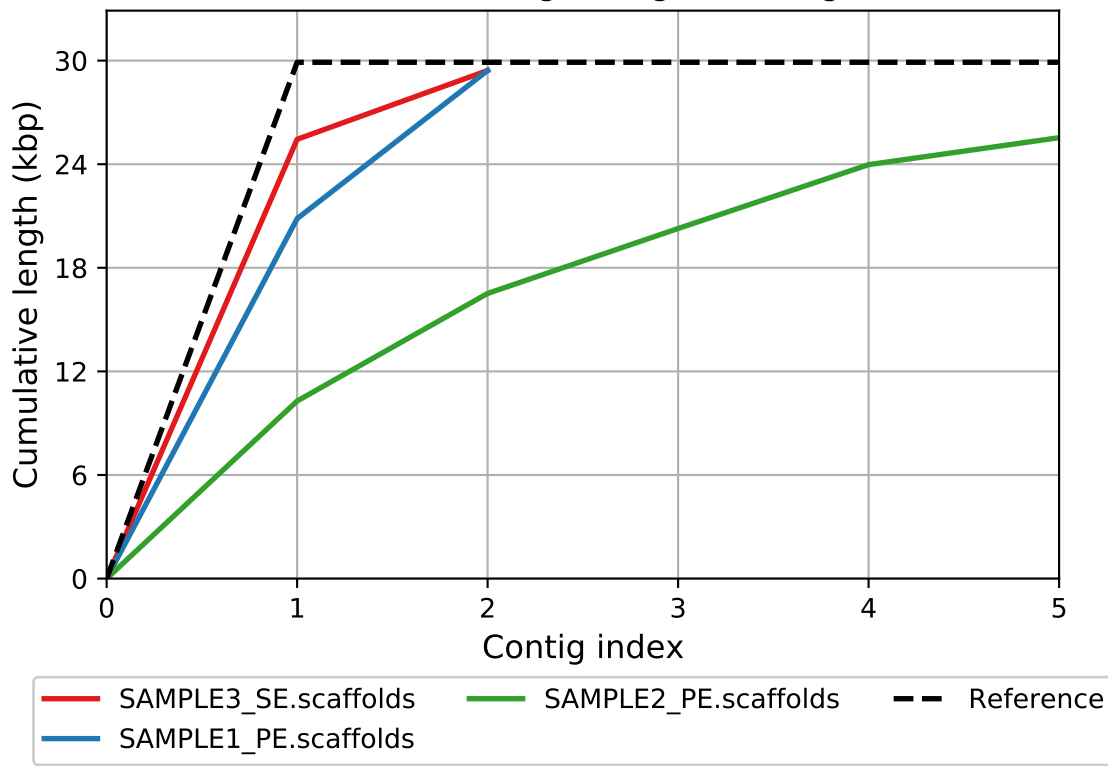
## Misassemblies



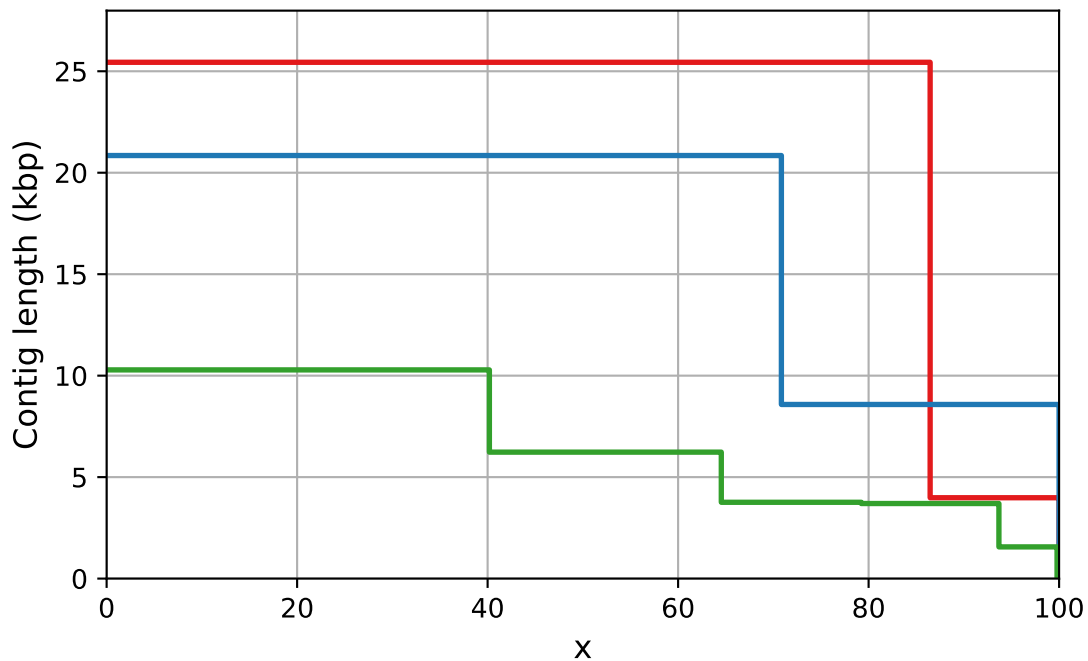
FRCurve (misassemblies)



Cumulative length (aligned contigs)

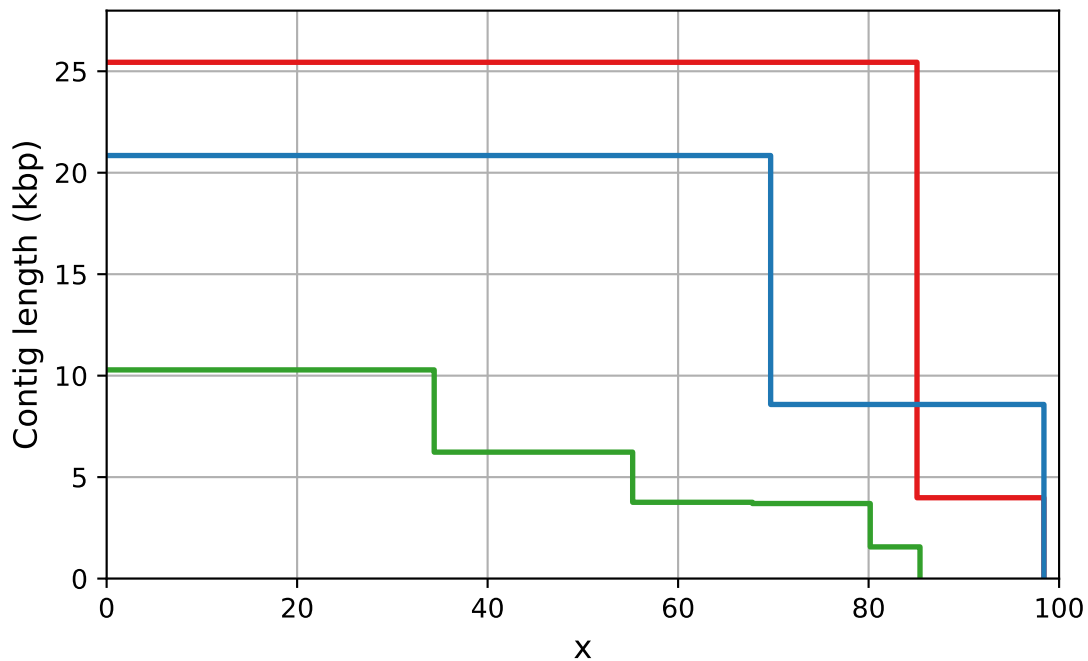


NAx

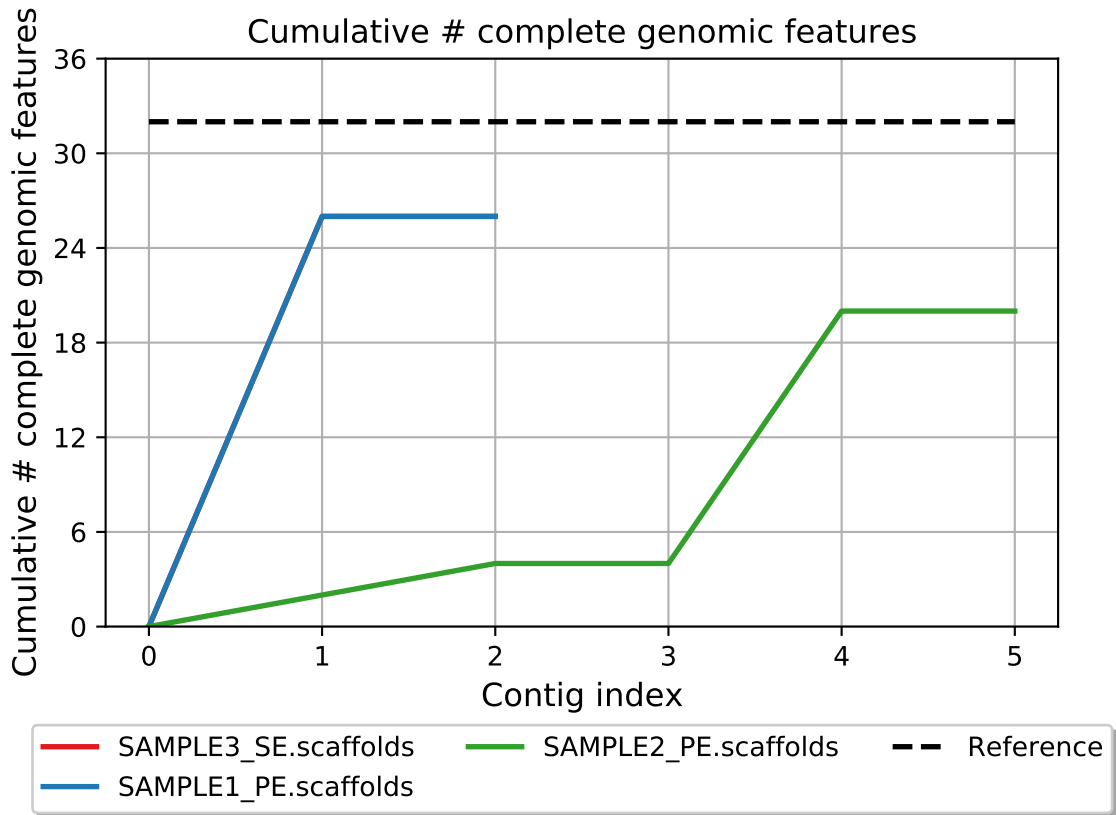


— SAMPLE3\_SE.scaffolds — SAMPLE1\_PE.scaffolds — SAMPLE2\_PE.scaffolds

# NGAx

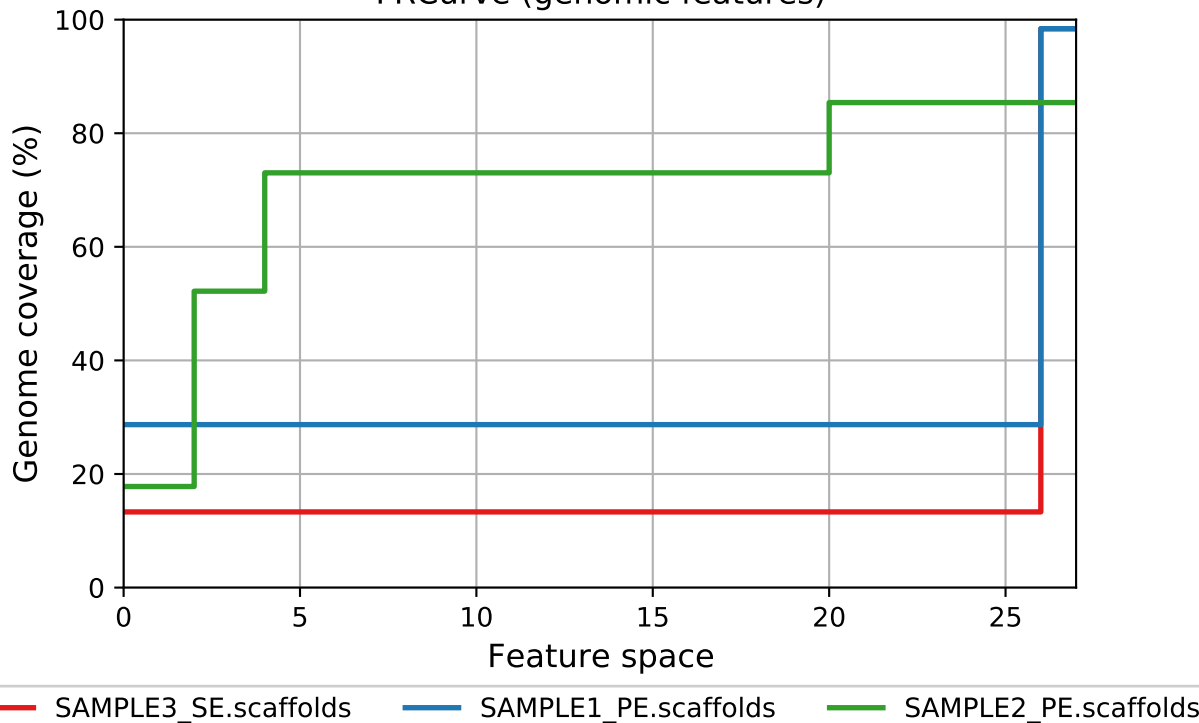


— SAMPLE3\_SE.scaffolds    — SAMPLE1\_PE.scaffolds    — SAMPLE2\_PE.scaffolds

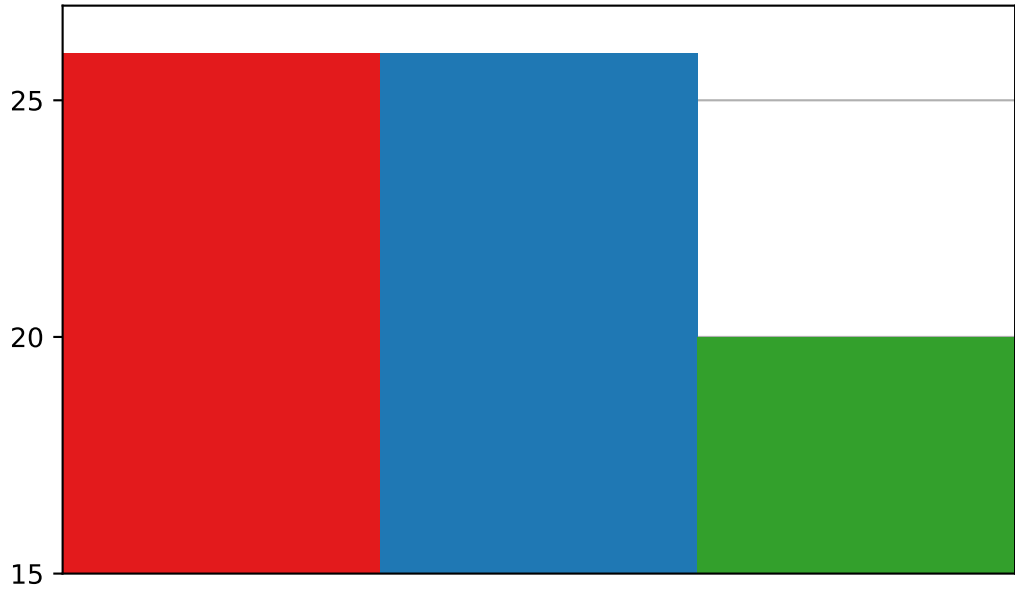




FRCurve (genomic features)



# complete genomic features






■ SAMPLE3\_SE.scaffolds    ■ SAMPLE1\_PE.scaffolds    ■ SAMPLE2\_PE.scaffolds

Genome fraction, %

100

50

 SAMPLE3\_SE.scaffolds     SAMPLE1\_PE.scaffolds     SAMPLE2\_PE.scaffolds

