

# Report

	SAMPLE3_SE.AF0.75.consensus	SAMPLE1_PE.AF0.75.consensus	SAMPLE2_PE.AF0.75.consensus
# 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)	29782	29782	29649
Total length (>= 1000 bp)	29782	29782	29649
Total length (>= 5000 bp)	29782	29782	29649
Total length (>= 10000 bp)	29782	29782	29649
Total length (>= 25000 bp)	29782	29782	29649
Total length (>= 50000 bp)	0	0	0
# contigs	1	1	1
Largest contig	29782	29782	29649
Total length	29782	29782	29649
Reference length	29903	29903	29903
GC (%)	37.88	37.94	38.20
Reference GC (%)	37.97	37.97	37.97
N50	29782	29782	29649
NG50	29782	29782	29649
N75	29782	29782	29649
NG75	29782	29782	29649
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.	8	2	10
# unaligned mis. contigs	0	0	0
# unaligned contigs	0 + 0 part	0 + 0 part	0 + 0 part
Unaligned length	0	0	0
Genome fraction (%)	88.891	97.606	85.700
Duplication ratio	1.120	1.020	1.157
# N's per 100 kbp	11527.10	2478.01	14364.73
# mismatches per 100 kbp	0.00	20.56	23.41
# indels per 100 kbp	0.00	0.00	0.00
# genomic features	14 + 12 part	23 + 7 part	10 + 14 part
Largest alignment	26581	29187	25627
Total aligned length	26581	29187	25627
NA50	26581	29187	25627
NGA50	26581	29187	25627
NA75	26581	29187	25627
NGA75	26581	29187	25627
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.AF0.75.consensus	SAMPLE1_PE.AF0.75.consensus	SAMPLE2_PE.AF0.75.consensus
# 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.	8	2	10
# 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

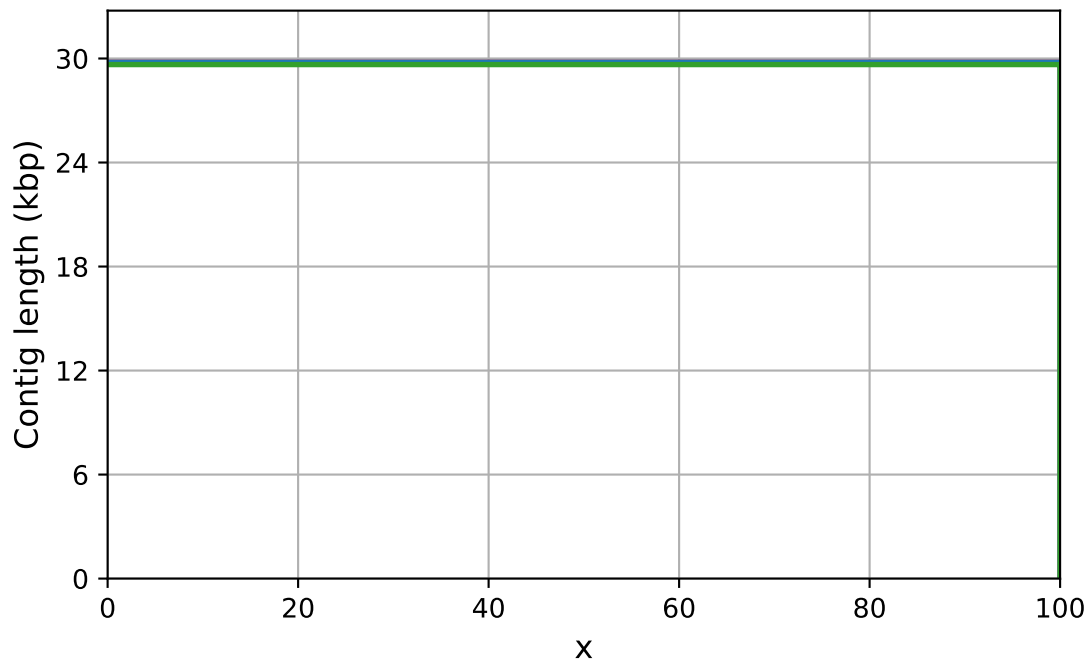
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	SAMPLE3_SE.AF0.75.consensus	SAMPLE1_PE.AF0.75.consensus	SAMPLE2_PE.AF0.75.consensus
# 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	3433	738	4259

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

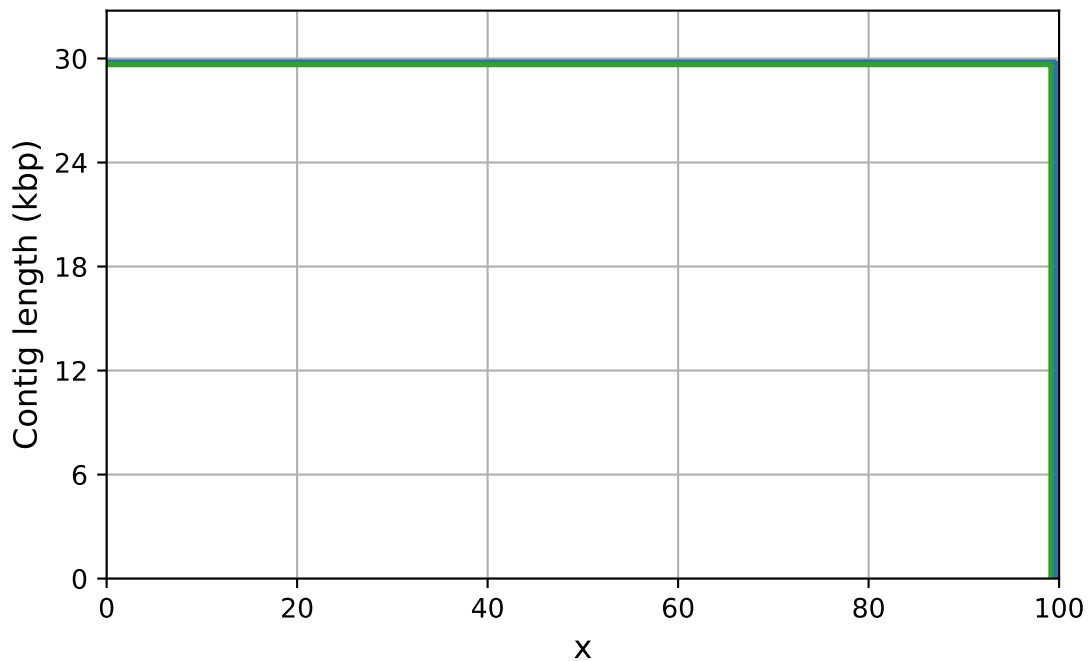


E3\_SE.AF0.75.consensus

— SAMPLE1\_PE.AF0.75.consensus

— SAMPLE2\_PE.AF0.75.consensus

# NGx

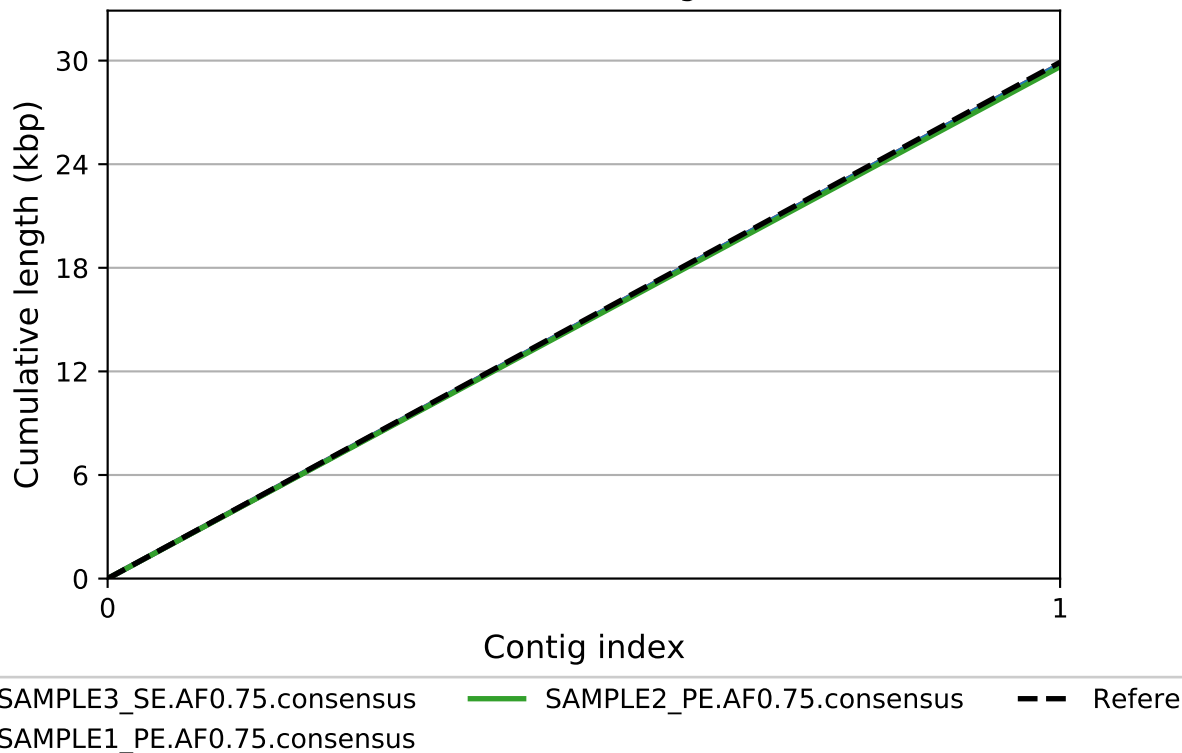


E3\_SE.AF0.75.consensus

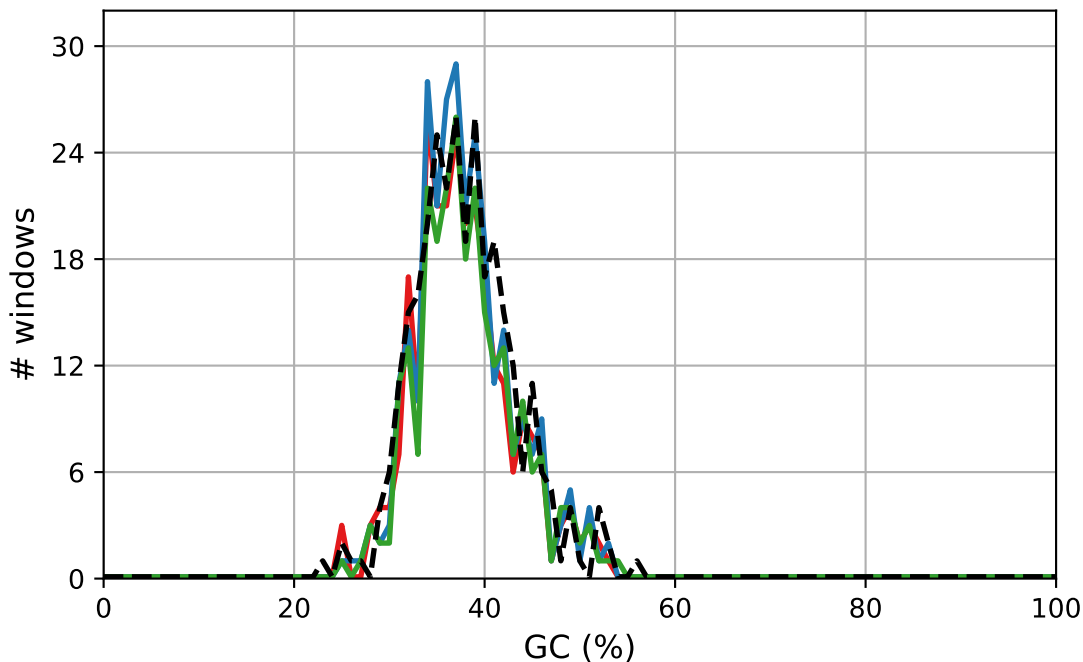
SAMPLE1\_PE.AF0.75.consensus

SAMPLE2\_PE.AF0.75.consensus

Cumulative length



GC content



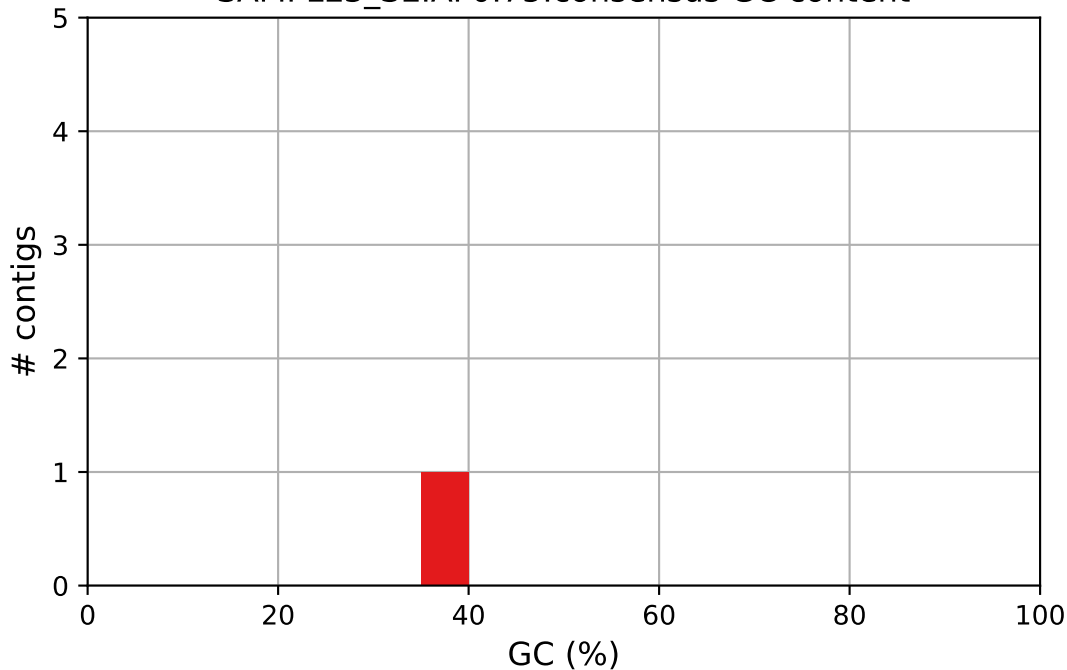
SAMPLE3\_SE.AF0.75.consensus

SAMPLE2\_PE.AF0.75.consensus

Reference

SAMPLE1\_PE.AF0.75.consensus

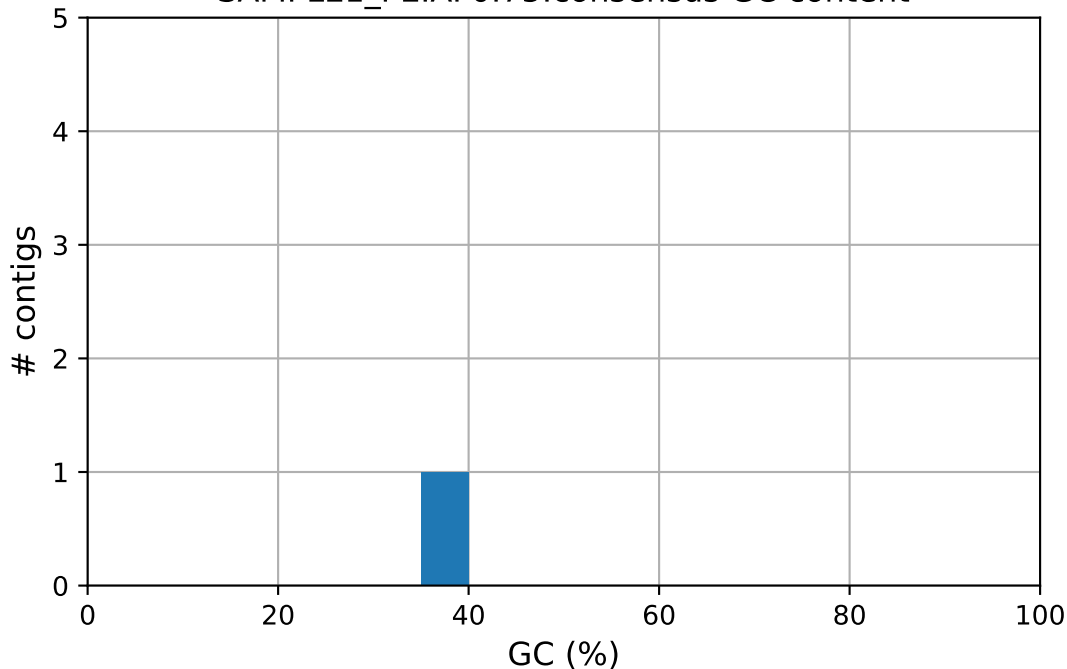
SAMPLE3\_SE.AF0.75.consensus GC content



 SAMPLE3\_SE.AF0.75.consensus

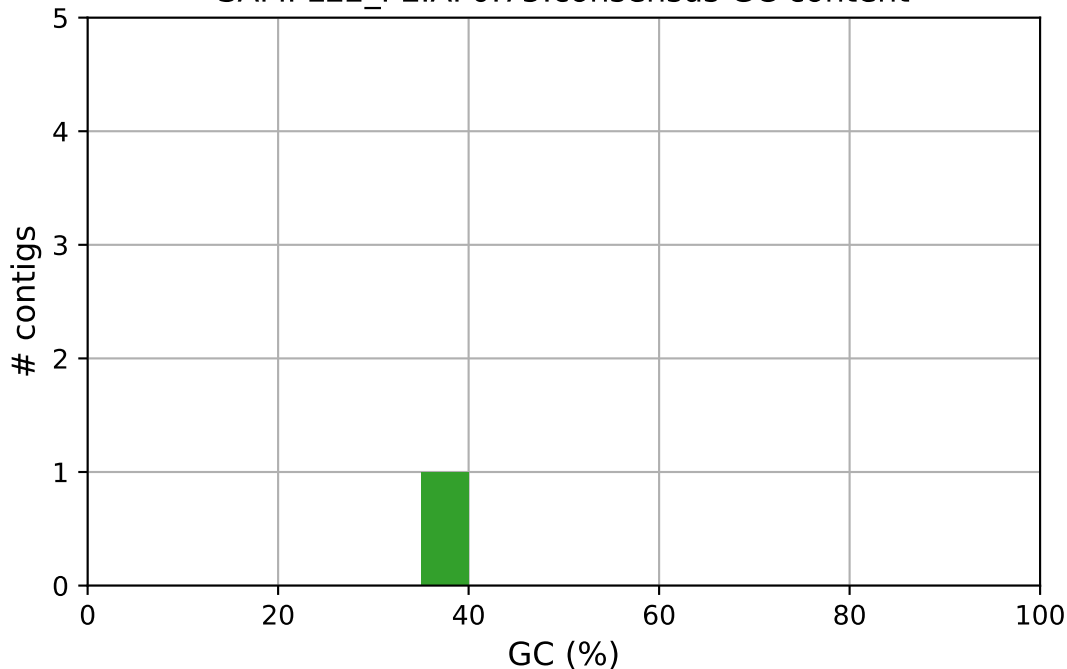


SAMPLE1\_PE.AF0.75.consensus GC content



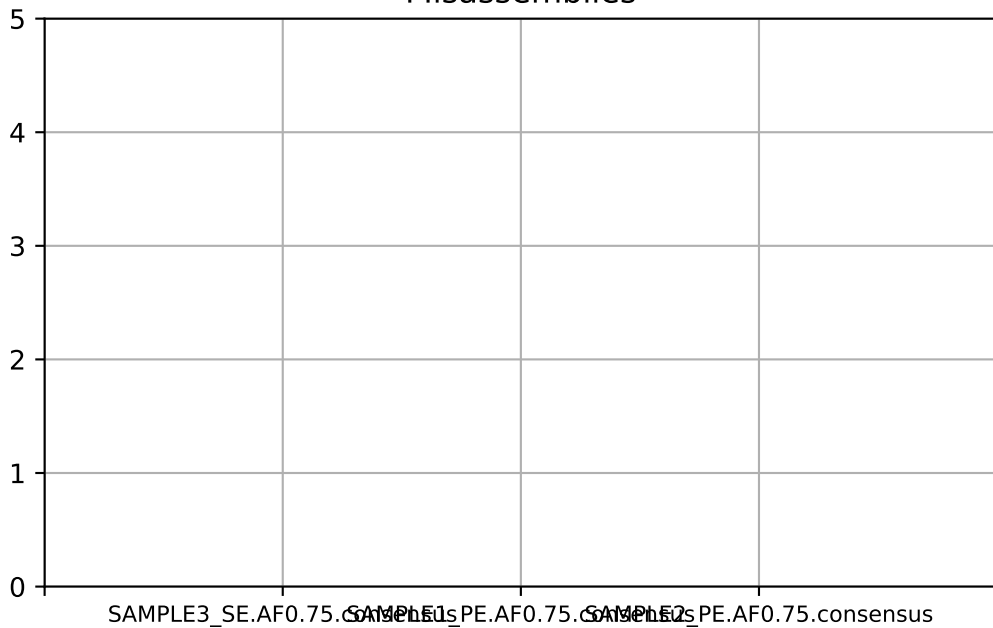
SAMPLE1\_PE.AF0.75.consensus

SAMPLE2\_PE.AF0.75.consensus GC content

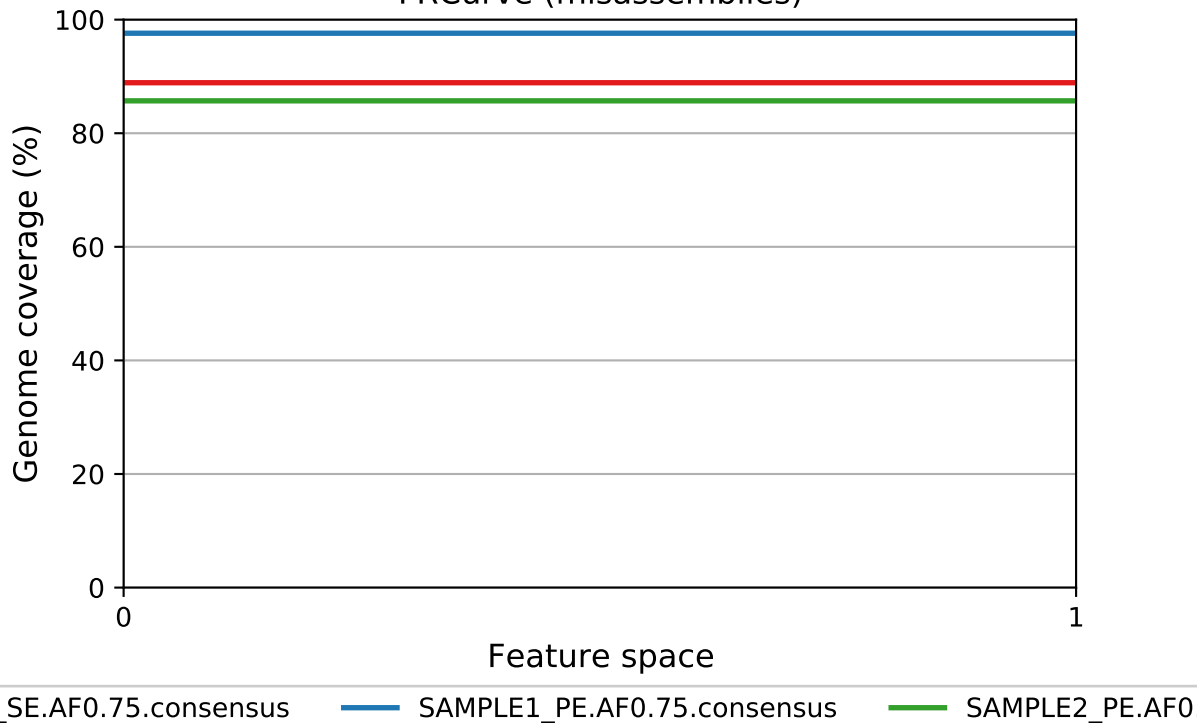


 SAMPLE2\_PE.AF0.75.consensus

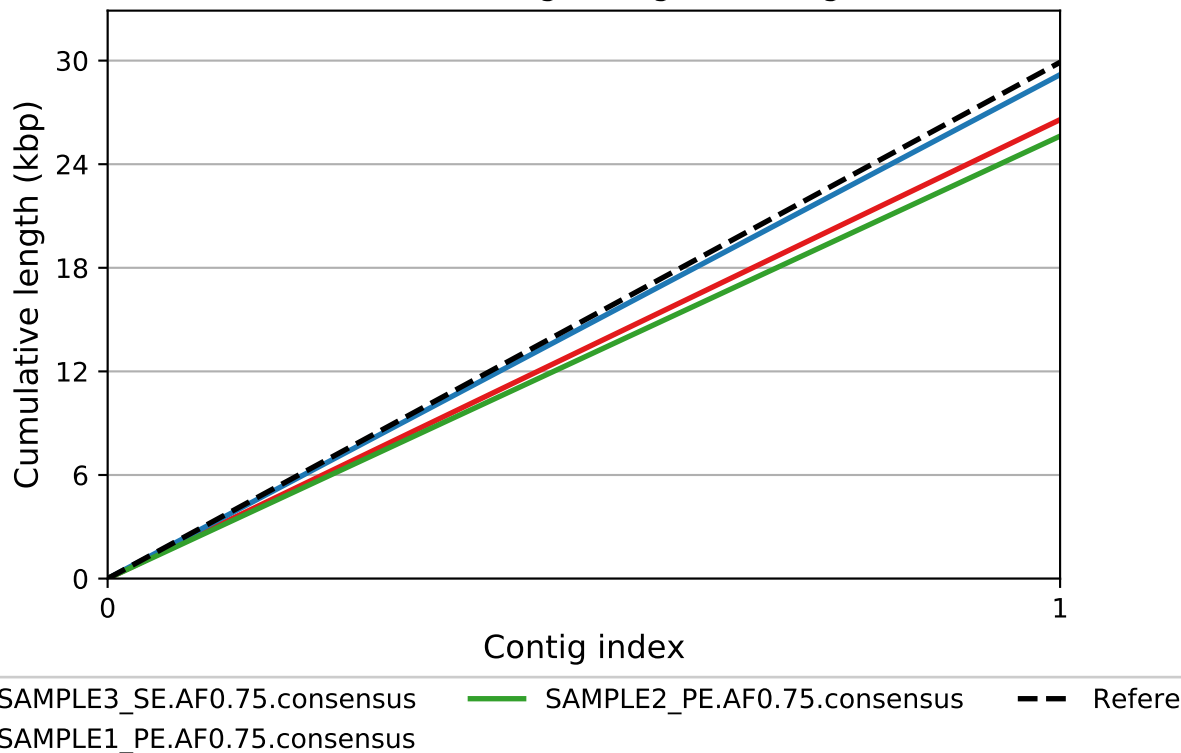
## Misassemblies



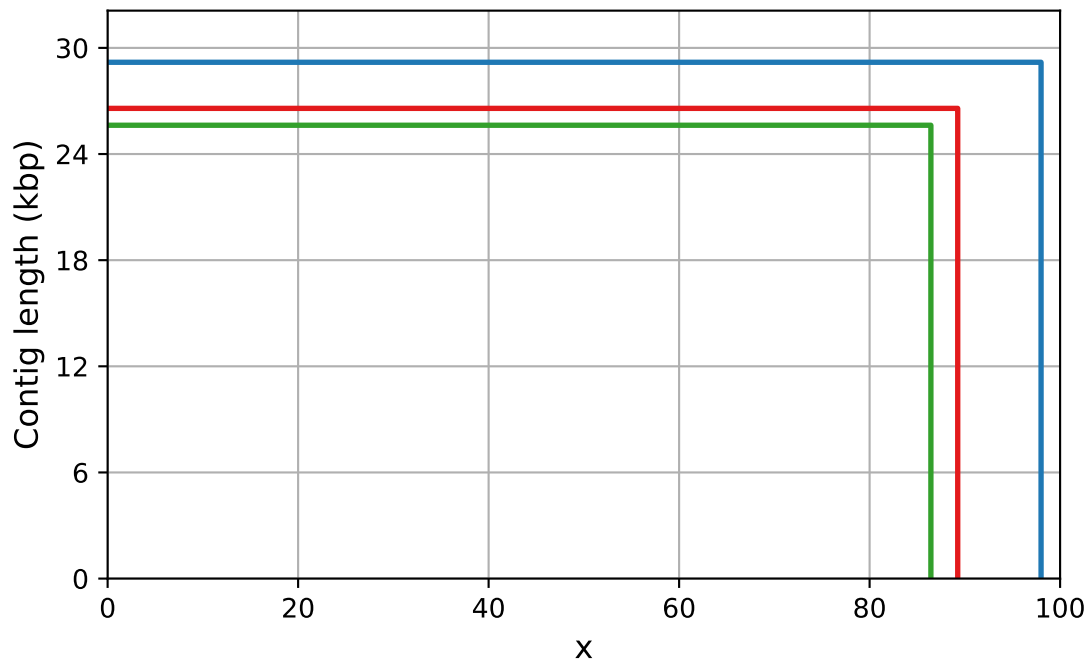
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx

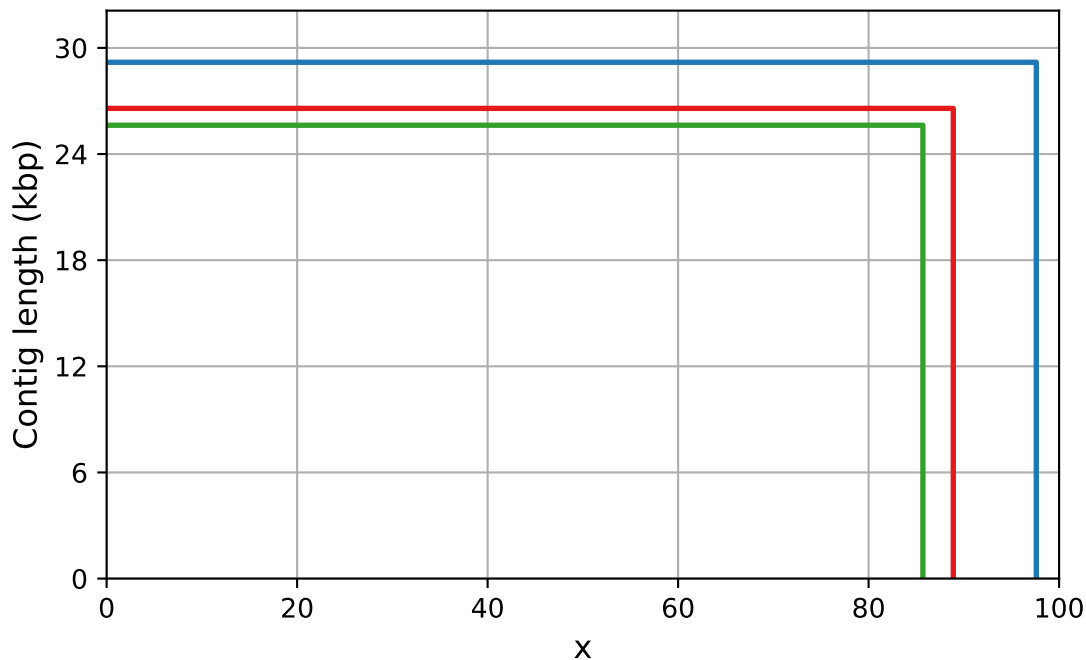


SAMPLE3\_SE.AF0.75.consensus

SAMPLE1\_PE.AF0.75.consensus

SAMPLE2\_PE.AF0.75.consensus

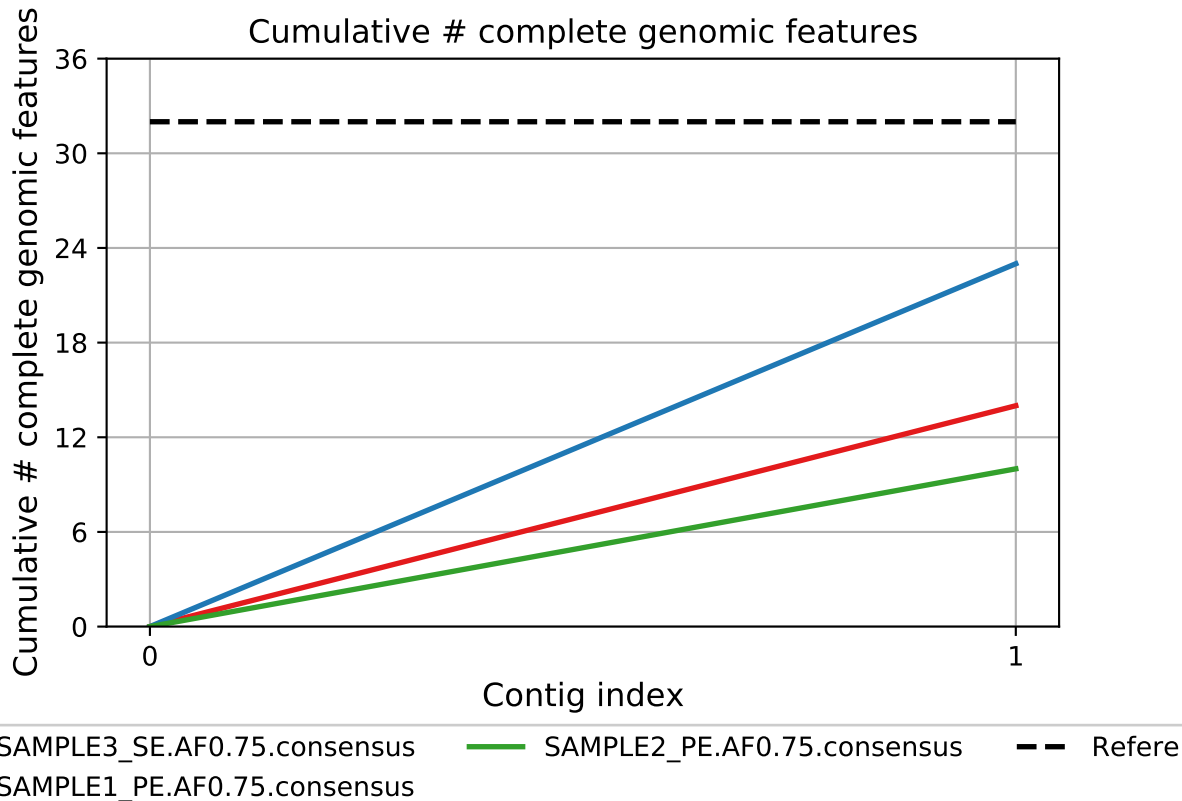
# NGAx



SAMPLE3\_SE.AF0.75.consensus

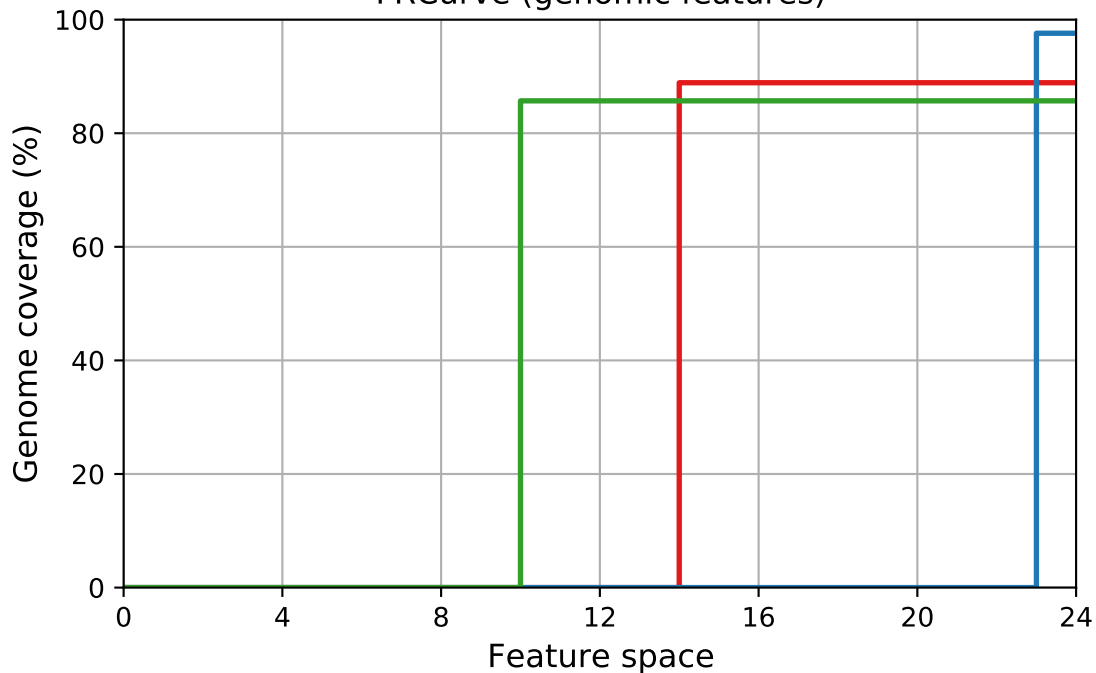
SAMPLE1\_PE.AF0.75.consensus

SAMPLE2\_PE.AF0.75.consensus





FRCurve (genomic features)

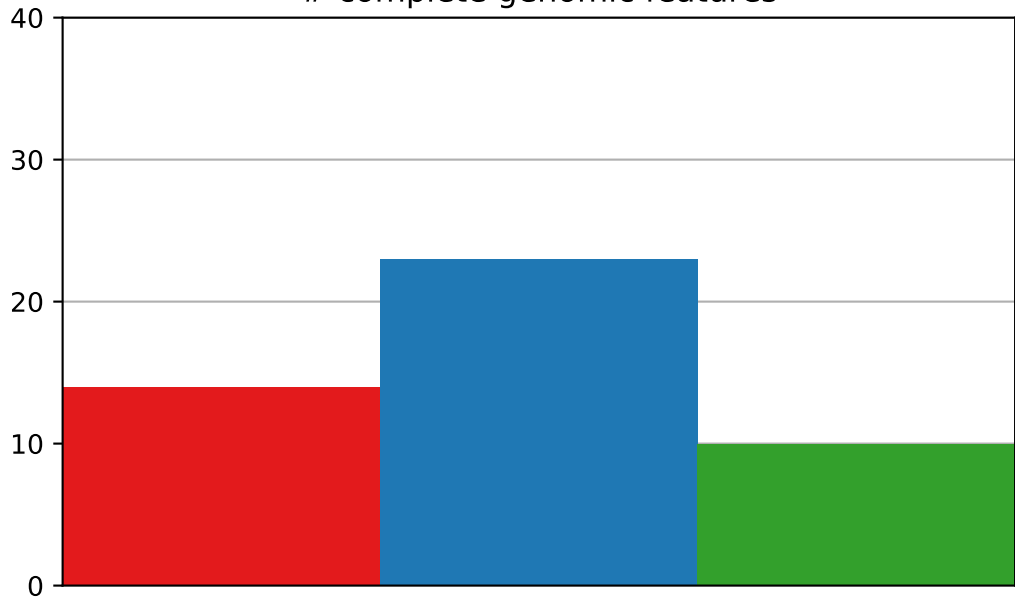


SAMPLE3\_PE.AF0.75.consensus

SAMPLE1\_PE.AF0.75.consensus

SAMPLE2\_PE.AF0.75.consensus

# complete genomic features



E3\_SE.AF0.75.consensus

SAMPLE1\_PE.AF0.75.consensus

SAMPLE2\_PE.AF0.75.consensus

Genome fraction, %

100

50

E3\_SE.AF0.75.consensus

SAMPLE1\_PE.AF0.75.consensus

SAMPLE2\_PE.AF0.75.consensus

