

Report

	SAMPLE3_SE.k31.scaffolds	SAMPLE1_PE.k31.scaffolds	SAMPLE2_PE.k31.scaffolds
# contigs (>= 0 bp)	17	11	22
# contigs (>= 1000 bp)	8	7	10
# contigs (>= 5000 bp)	1	1	0
# contigs (>= 10000 bp)	0	1	0
# contigs (>= 25000 bp)	0	0	0
# contigs (>= 50000 bp)	0	0	0
Total length (>= 0 bp)	27908	28740	25497
Total length (>= 1000 bp)	24244	27715	19509
Total length (>= 5000 bp)	8200	10409	0
Total length (>= 10000 bp)	0	10409	0
Total length (>= 25000 bp)	0	0	0
Total length (>= 50000 bp)	0	0	0
# contigs	11	7	16
Largest contig	8200	10409	3319
Total length	26313	27715	23675
Reference length	29903	29903	29903
GC (%)	38.23	38.01	38.50
Reference GC (%)	37.97	37.97	37.97
N50	2997	3993	1631
NG50	2997	3807	1594
N75	1853	3317	1325
NG75	1687	2551	631
L50	3	2	5
LG50	3	3	7
L75	6	4	9
LG75	7	5	15
# 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	0 + 0 part	0 + 0 part	0 + 0 part
Unaligned length	0	0	0
Genome fraction (%)	87.814	92.676	79.092
Duplication ratio	1.002	1.000	1.001
# N's per 100 kbp	0.00	0.00	0.00
# mismatches per 100 kbp	11.42	21.65	25.37
# indels per 100 kbp	0.00	0.00	0.00
# genomic features	16 + 14 part	20 + 10 part	10 + 16 part
Largest alignment	8200	10409	3319
Total aligned length	26289	27715	23675
NA50	2997	3993	1631
NGA50	2997	3807	1594
NA75	1853	3317	1325
NGA75	1687	2551	631
LA50	3	2	5
LGA50	3	3	7
LA75	6	4	9
LGA75	7	5	15

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.k31.scaffolds	SAMPLE1_PE.k31.scaffolds	SAMPLE2_PE.k31.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	3	6	6
# indels	0	0	0
# indels (<= 5 bp)	0	0	0
# indels (> 5 bp)	0	0	0
Indels length	0	0	0

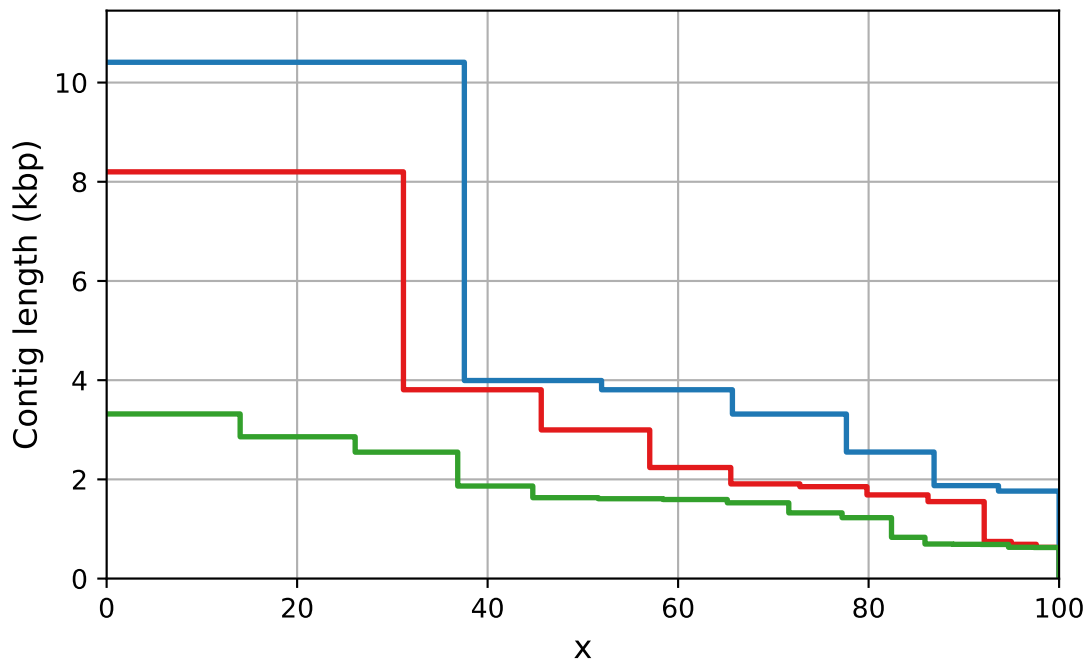
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	SAMPLE3_SE.k31.scaffolds	SAMPLE1_PE.k31.scaffolds	SAMPLE2_PE.k31.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 ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

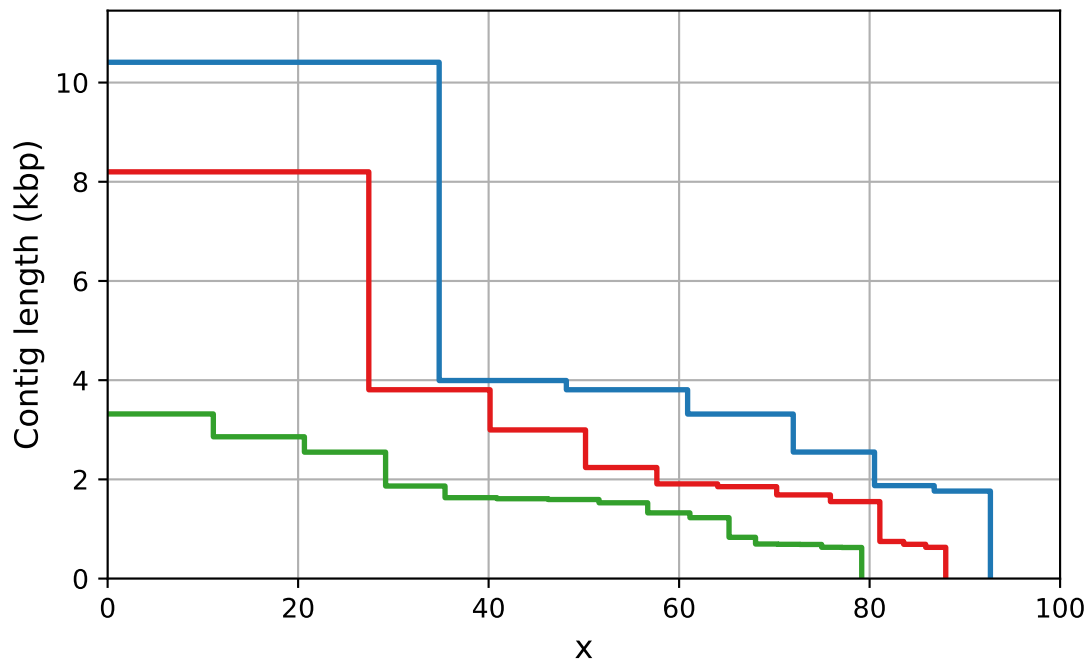


SAMPLE3_SE.k31.scaffolds

SAMPLE1_PE.k31.scaffolds

SAMPLE2_PE.k31.sc

NGx

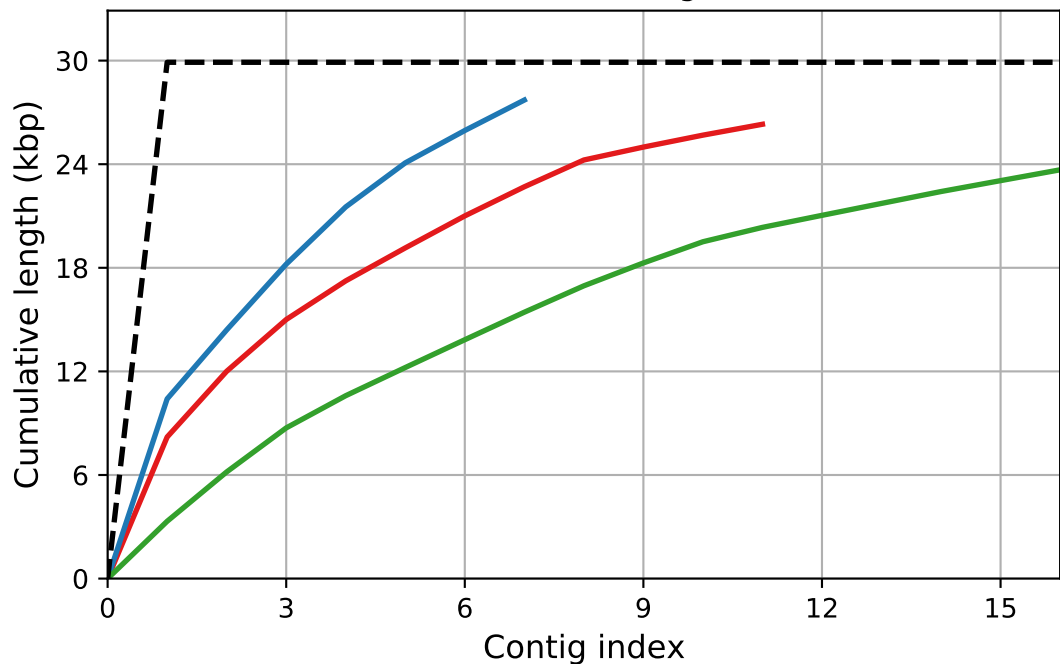


SAMPLE3_SE.k31.scaffolds

SAMPLE1_PE.k31.scaffolds

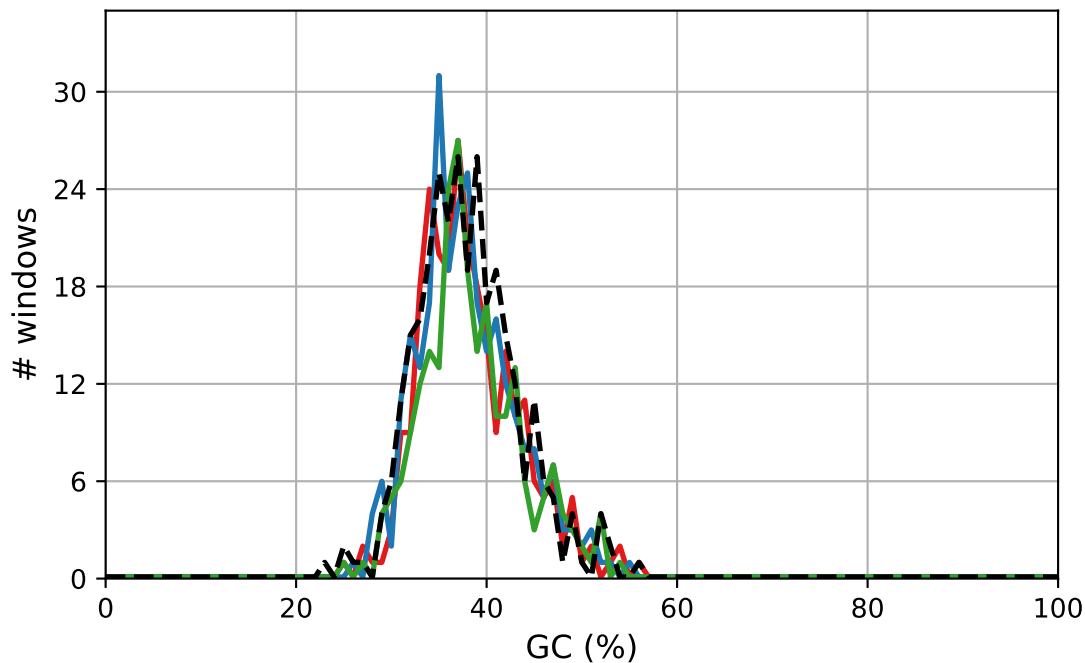
SAMPLE2_PE.k31.scaffolds

Cumulative length



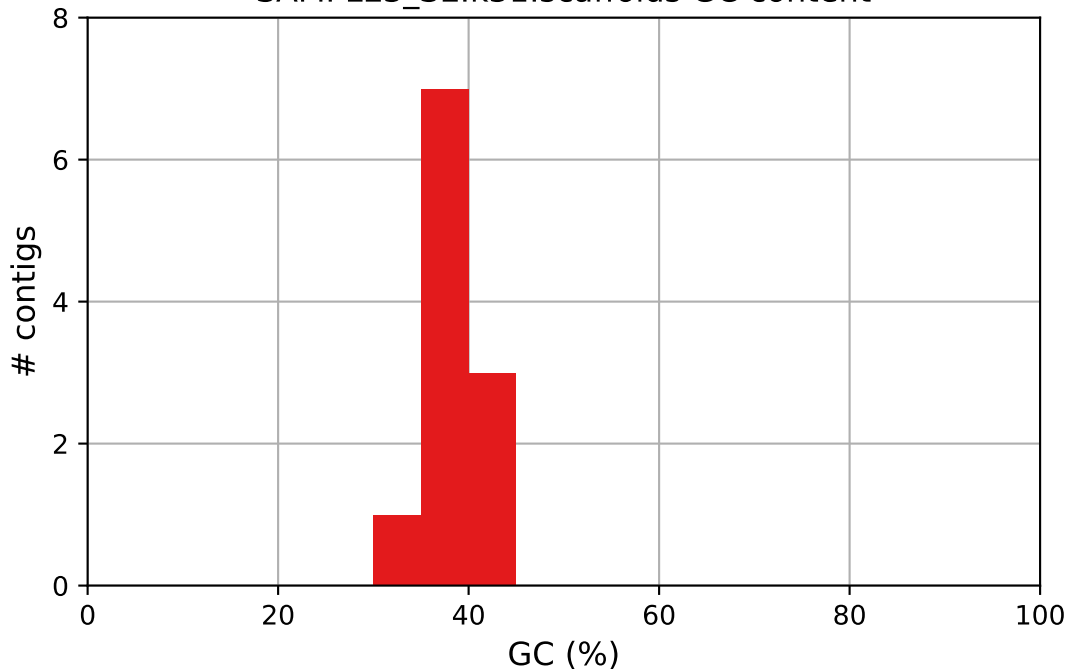
SAMPLE3_SE.k31.scaffolds SAMPLE2_PE.k31.scaffolds - - - Reference
SAMPLE1_PE.k31.scaffolds

GC content



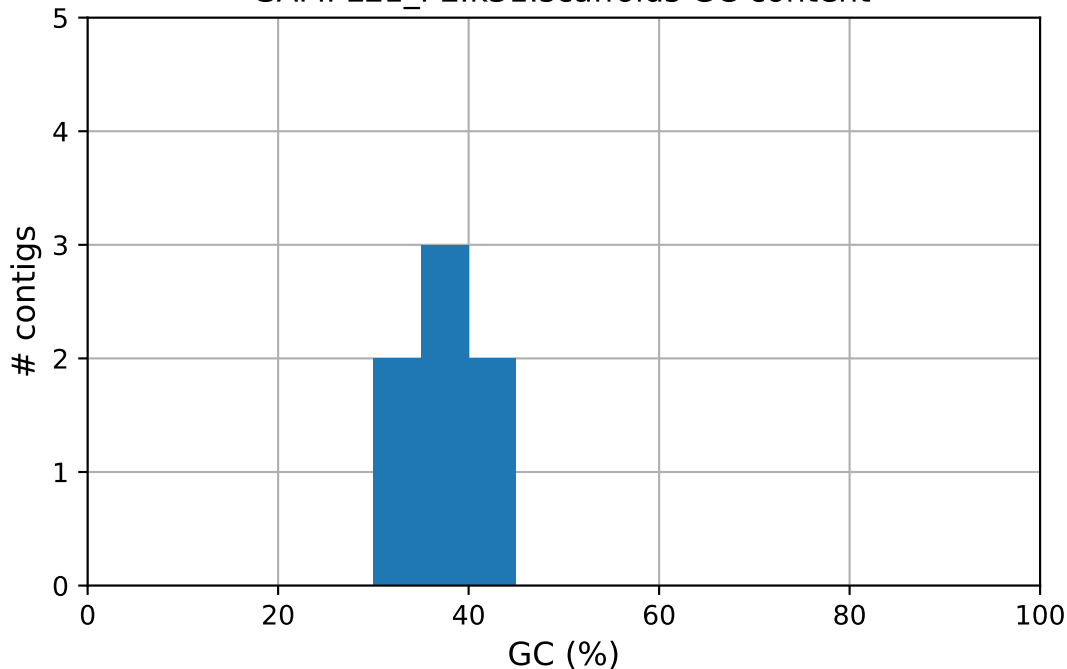
SAMPLE3_SE.k31.scaffolds SAMPLE2_PE.k31.scaffolds - - Reference
SAMPLE1_PE.k31.scaffolds

SAMPLE3_SE.k31.scaffolds GC content



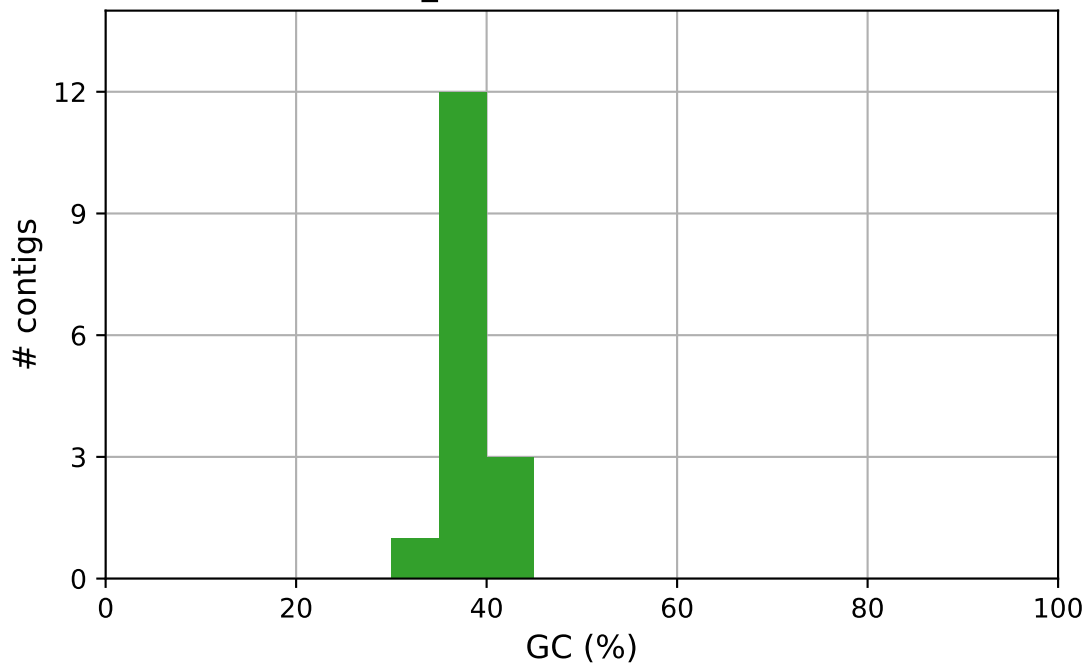
■ SAMPLE3_SE.k31.scaffolds

SAMPLE1_PE.k31.scaffolds GC content



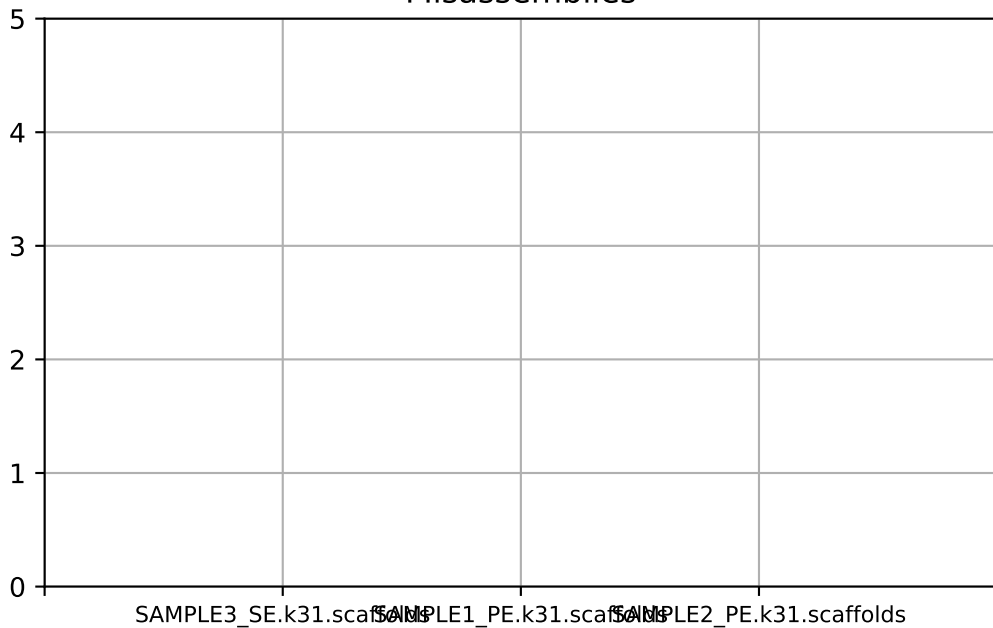
SAMPLE1_PE.k31.scaffolds

SAMPLE2_PE.k31.scaffolds GC content

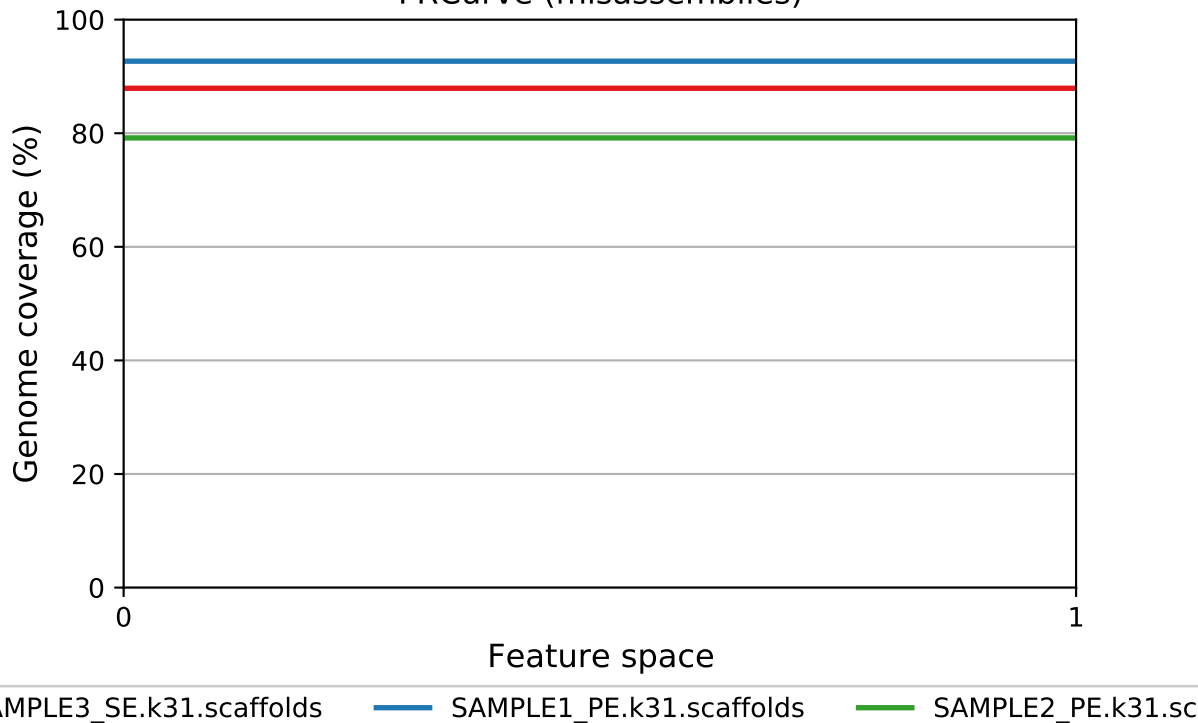


 SAMPLE2_PE.k31.scaffolds

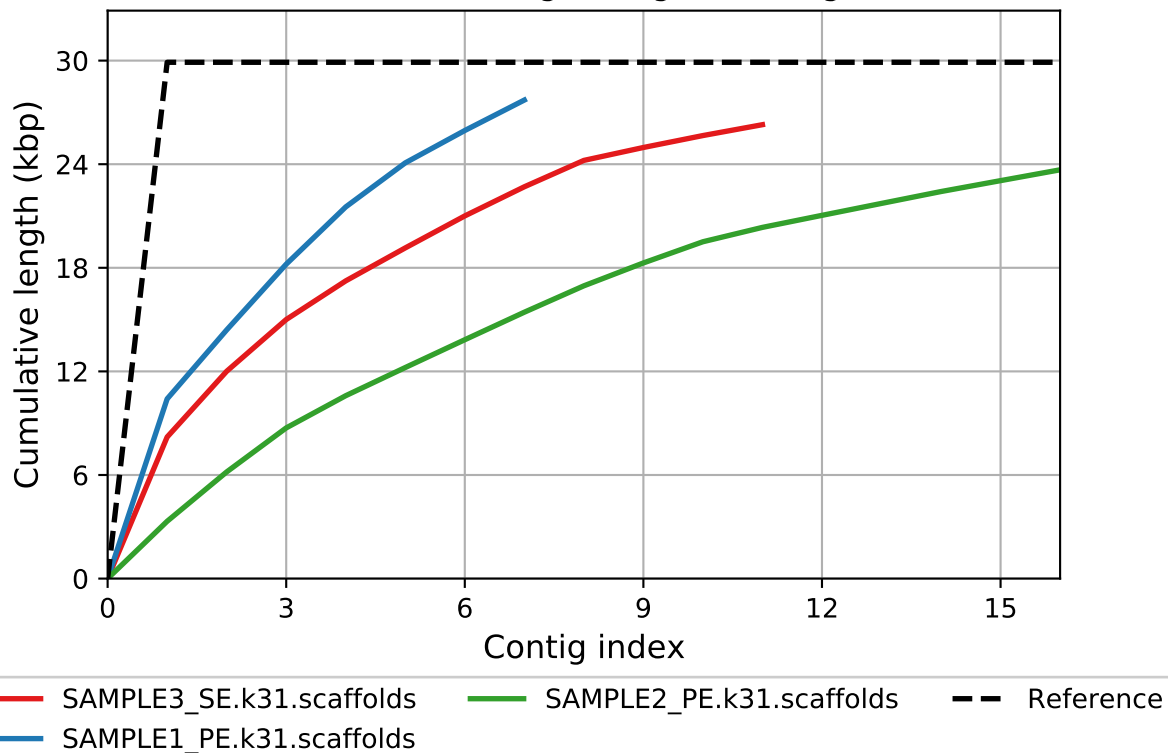
Misassemblies



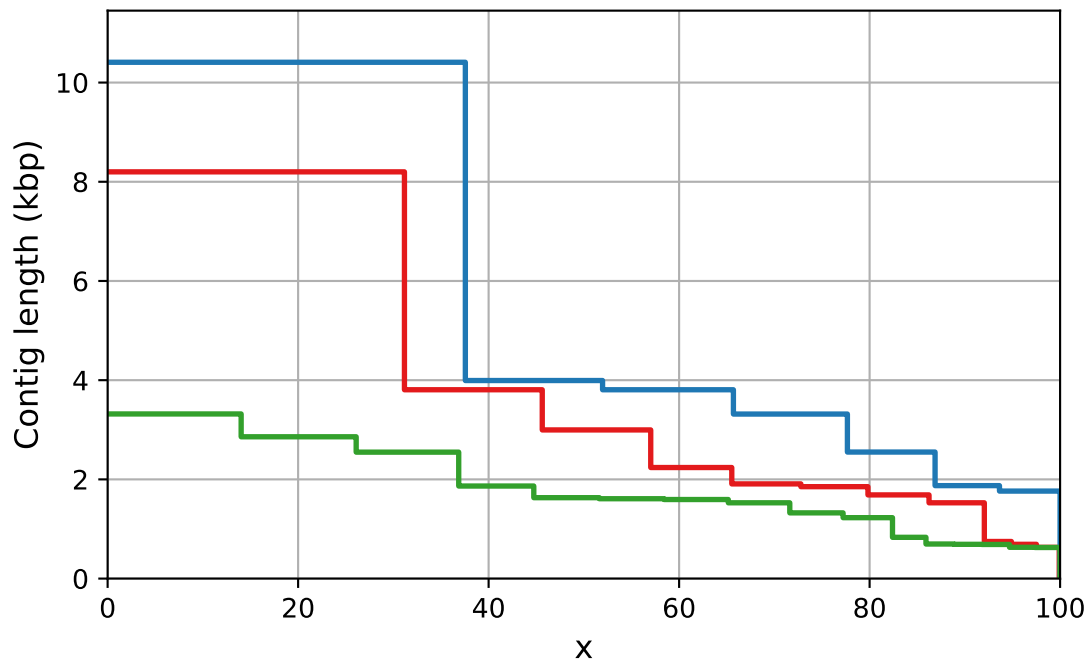
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx

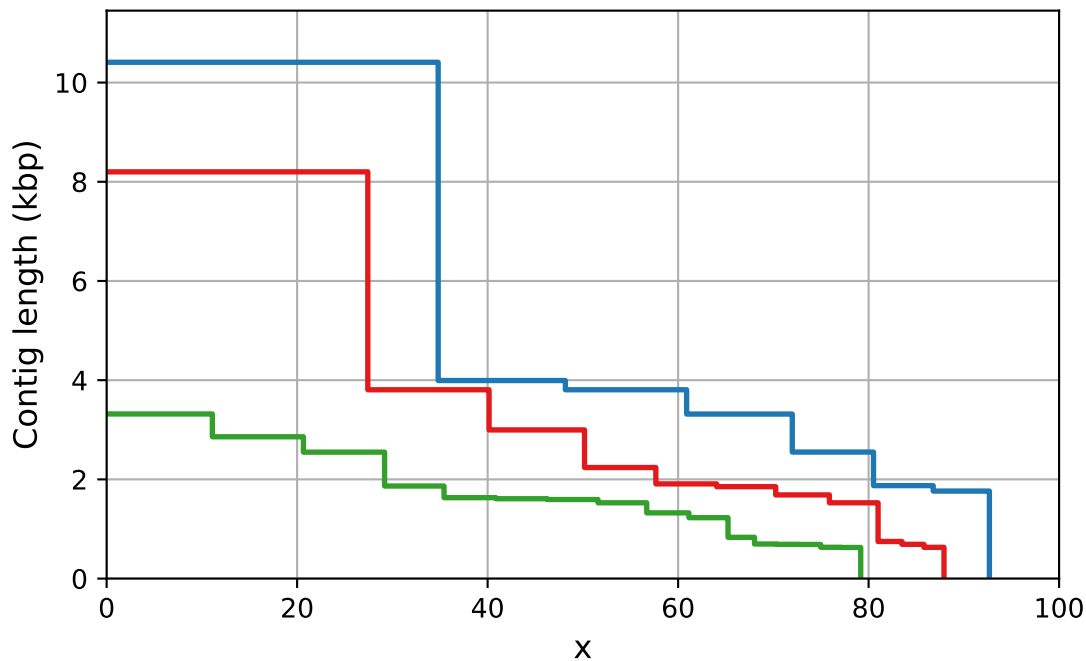


SAMPLE3_SE.k31.scaffolds

SAMPLE1_PE.k31.scaffolds

SAMPLE2_PE.k31.sc

NGAx

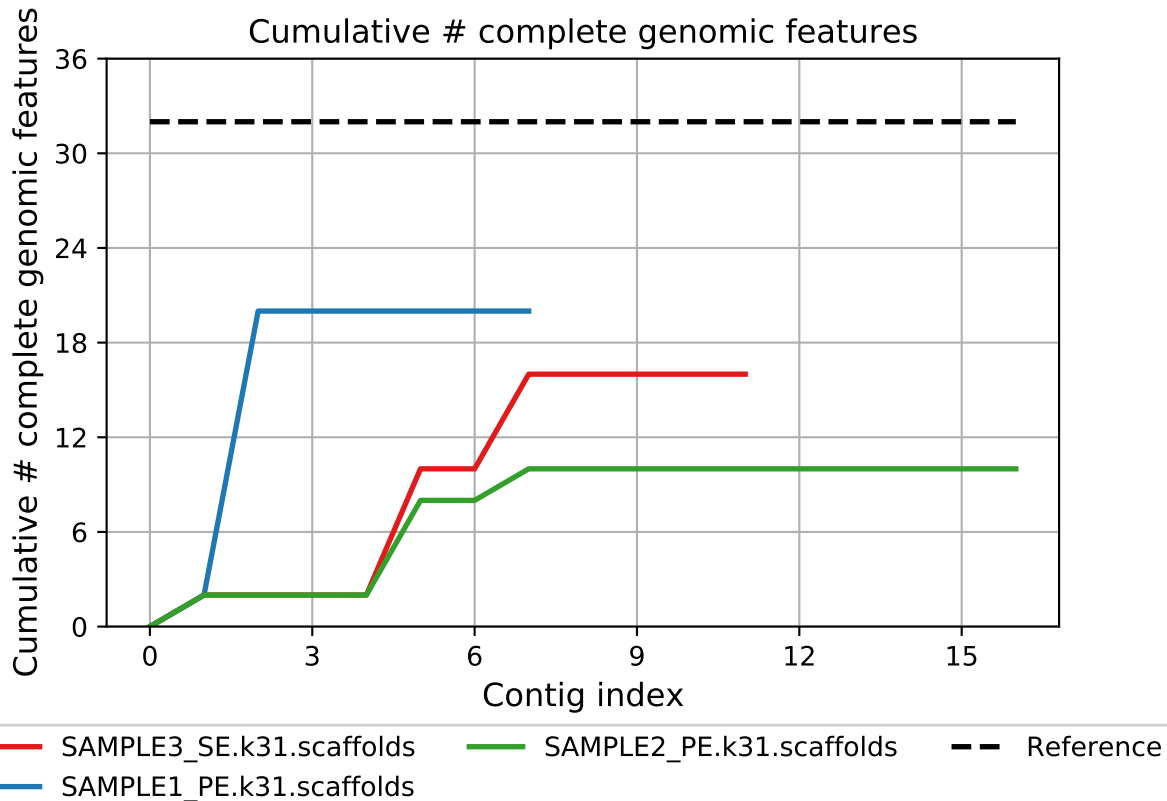


SAMPLE3_SE.k31.scaffolds

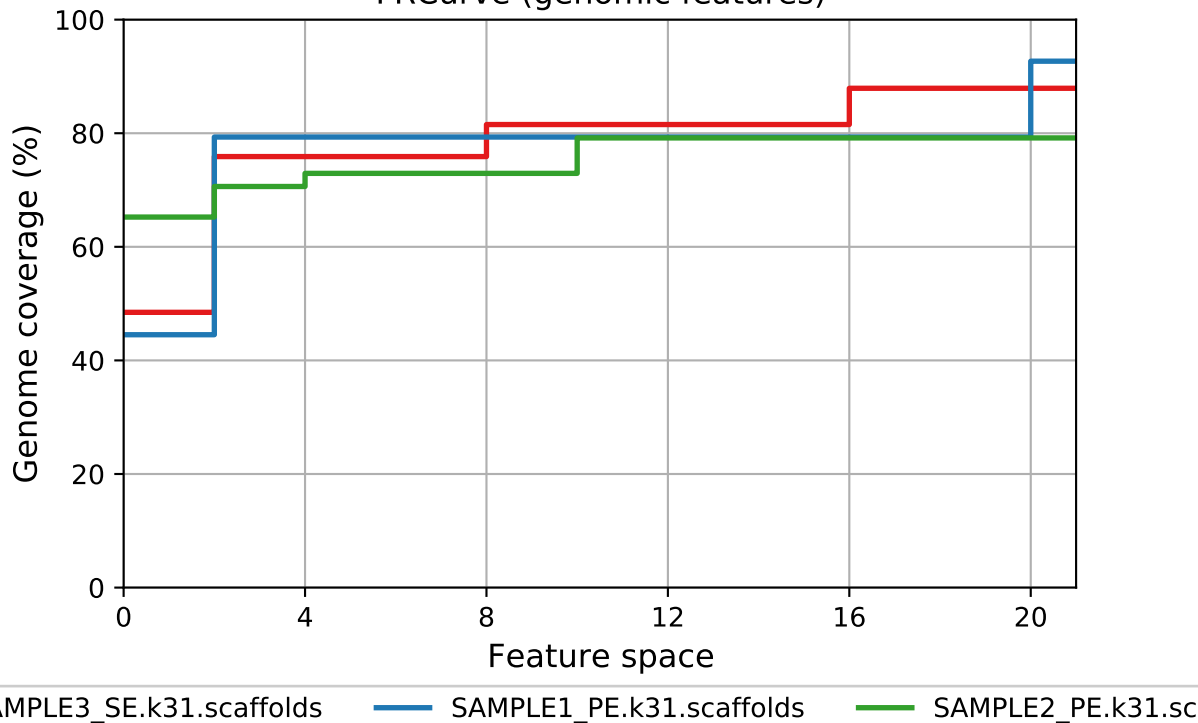
SAMPLE1_PE.k31.scaffolds

SAMPLE2_PE.k31.sc

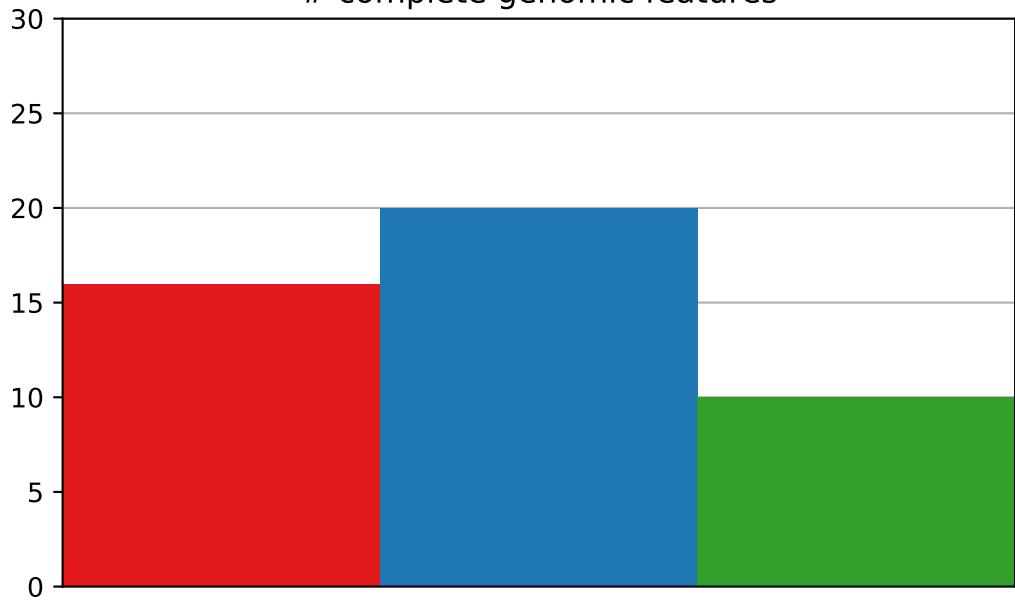
Cumulative # complete genomic features



FRCurve (genomic features)



complete genomic features



SAMPLE3_SE.k31.scaffolds

SAMPLE1_PE.k31.scaffolds

SAMPLE2_PE.k31.scaffolds

Genome fraction, %

100

50

SAMPLE3_SE.k31.scaffolds



SAMPLE1_PE.k31.scaffolds



SAMPLE2_PE.k31.sc

