Report

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

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

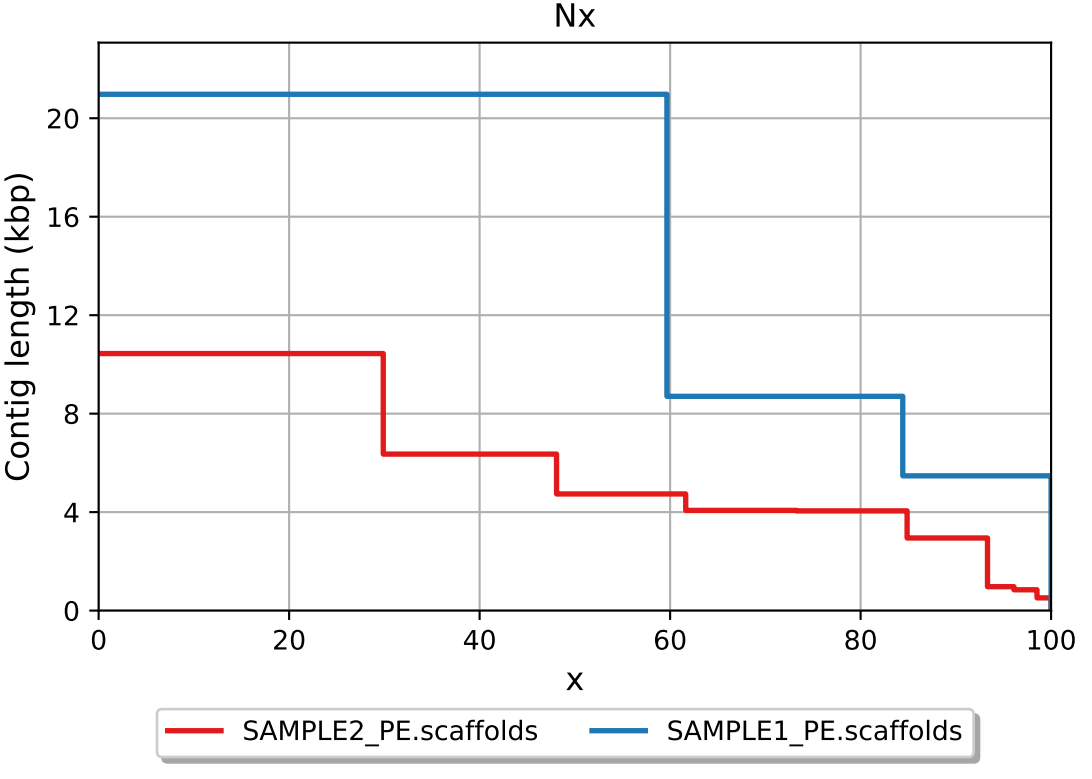
	SAMPLE2_PE.scaffolds	SAMPLE1_PE.scaffolds
# misassemblies	0	0
# contig misassemblies	0	0
# c. relocations	0	0
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	0	0
Misassembled contigs length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

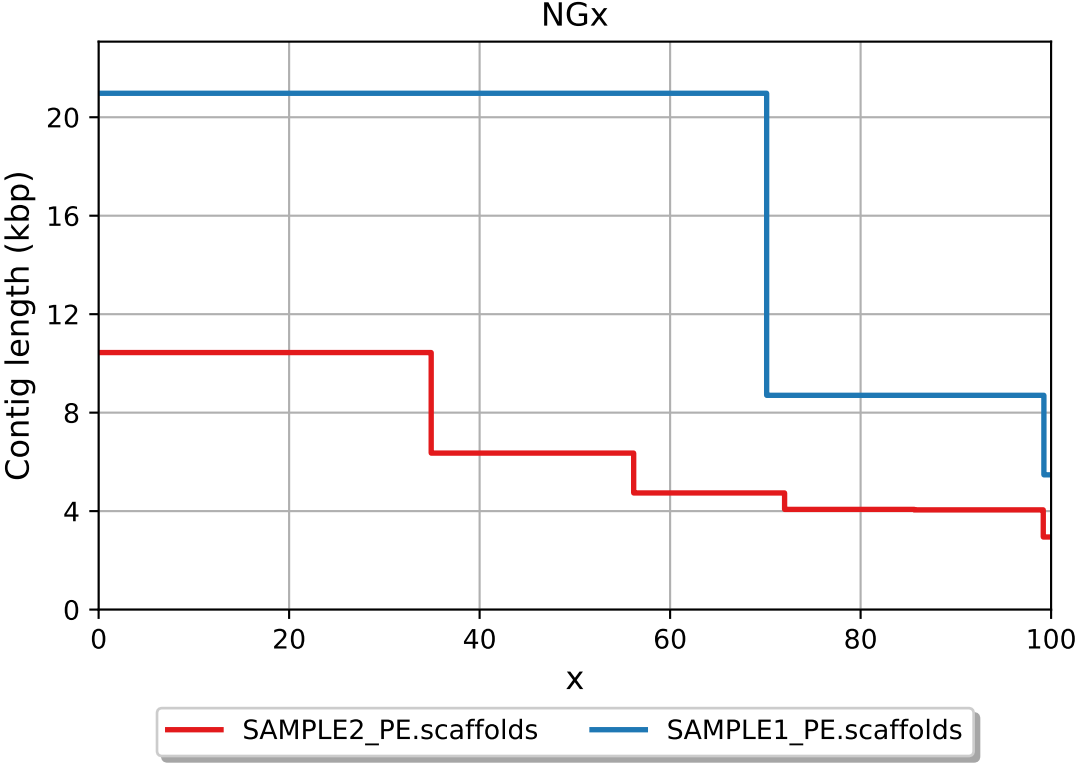
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

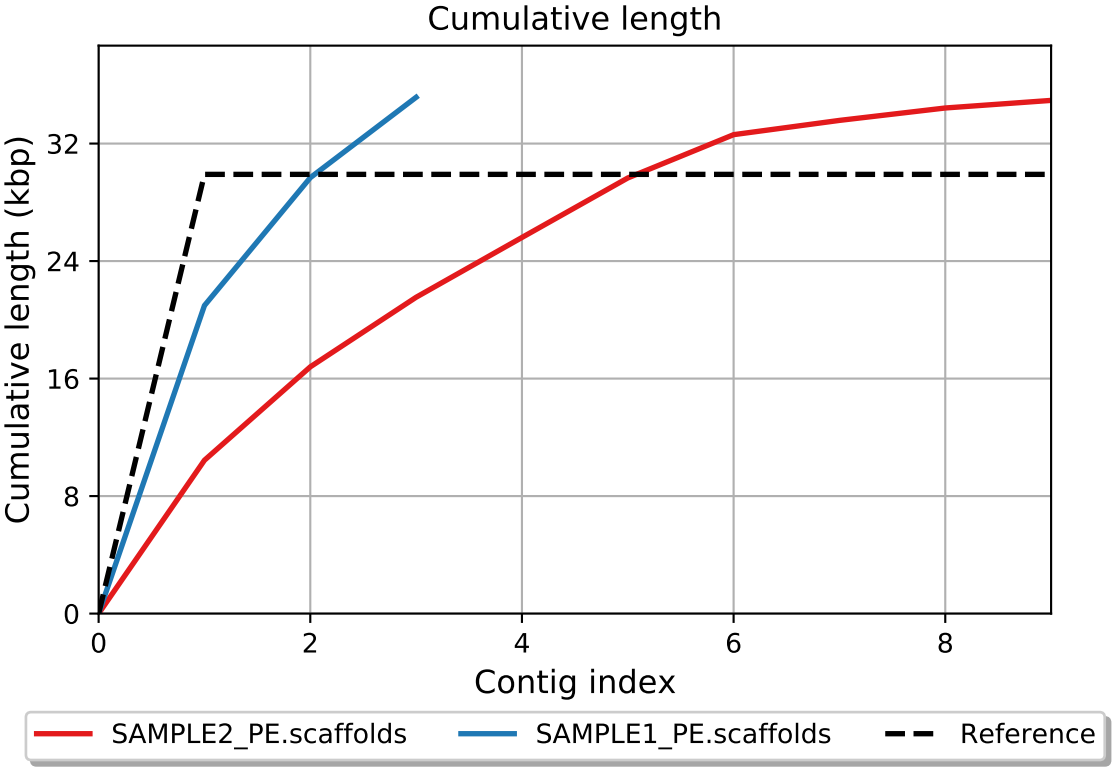
Unaligned report

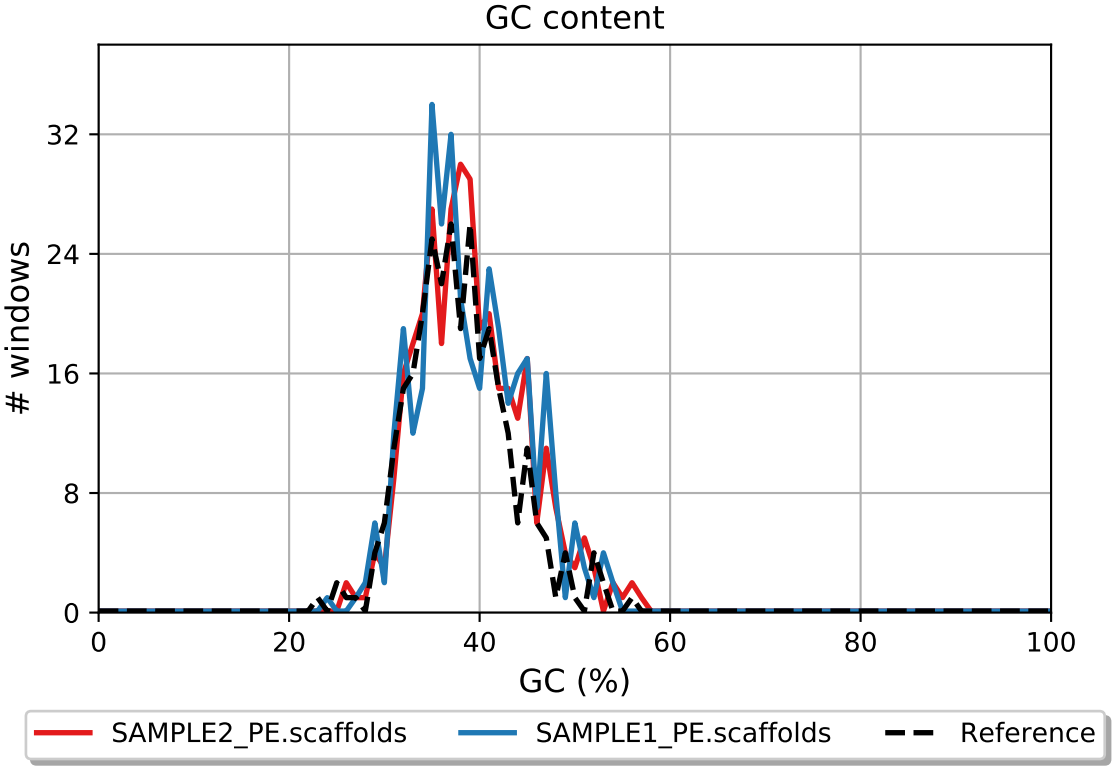
	SAMPLE2_PE.scaffolds	SAMPLE1_PE.scaffolds
# fully unaligned contigs	3	1
Fully unaligned length	5432	5474
# partially unaligned contigs	0	0
Partially unaligned length	0	0
# N's	0	0

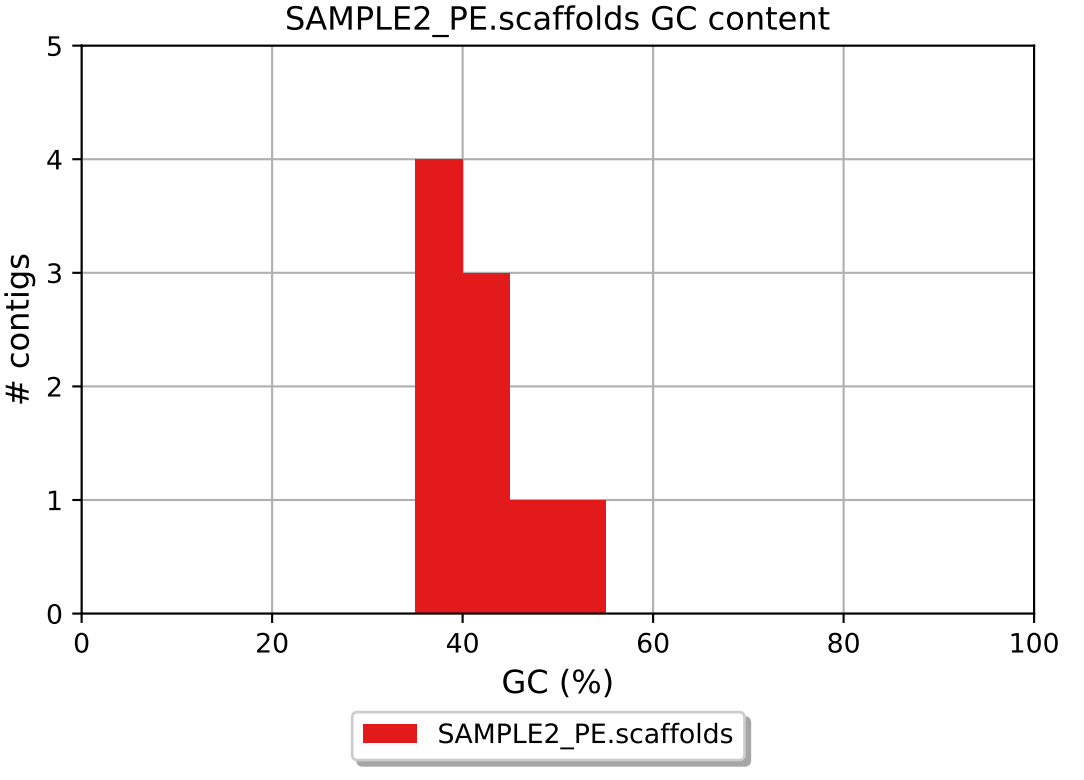
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

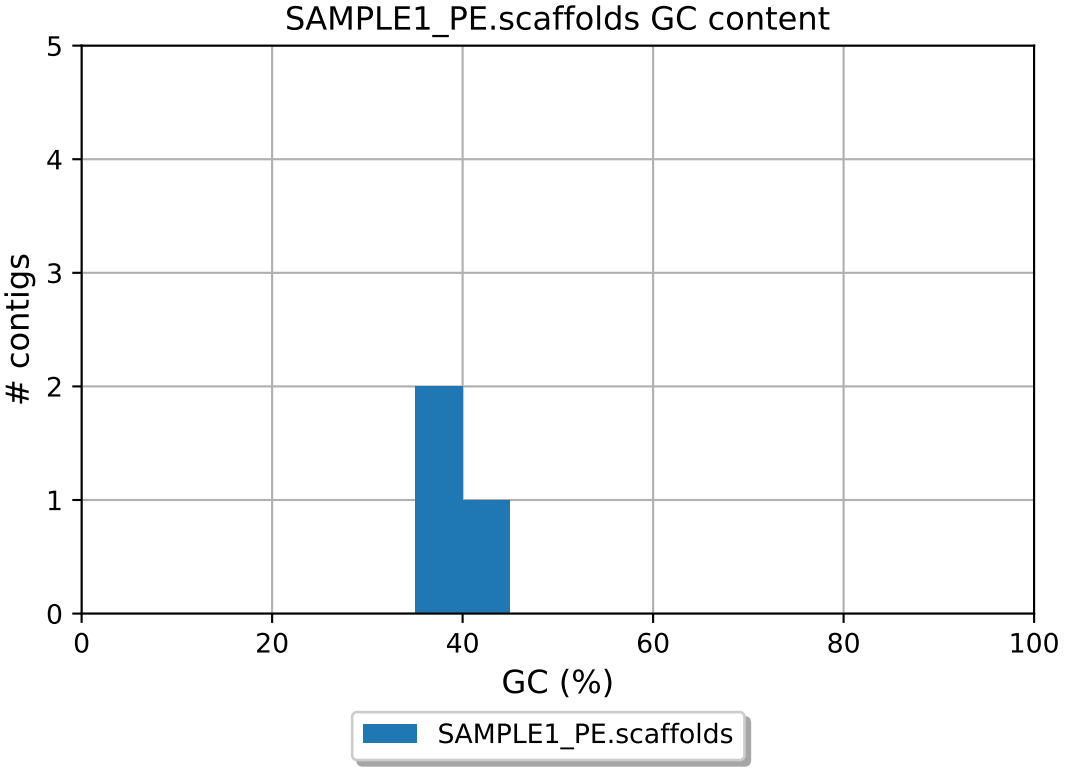

Nx
Contig length (kbp)
0
4
8
12
16
20
0
20
40
60
80
100
x
SAMPLE2_PE.scaffolds
SAMPLE1_PE.scaffolds

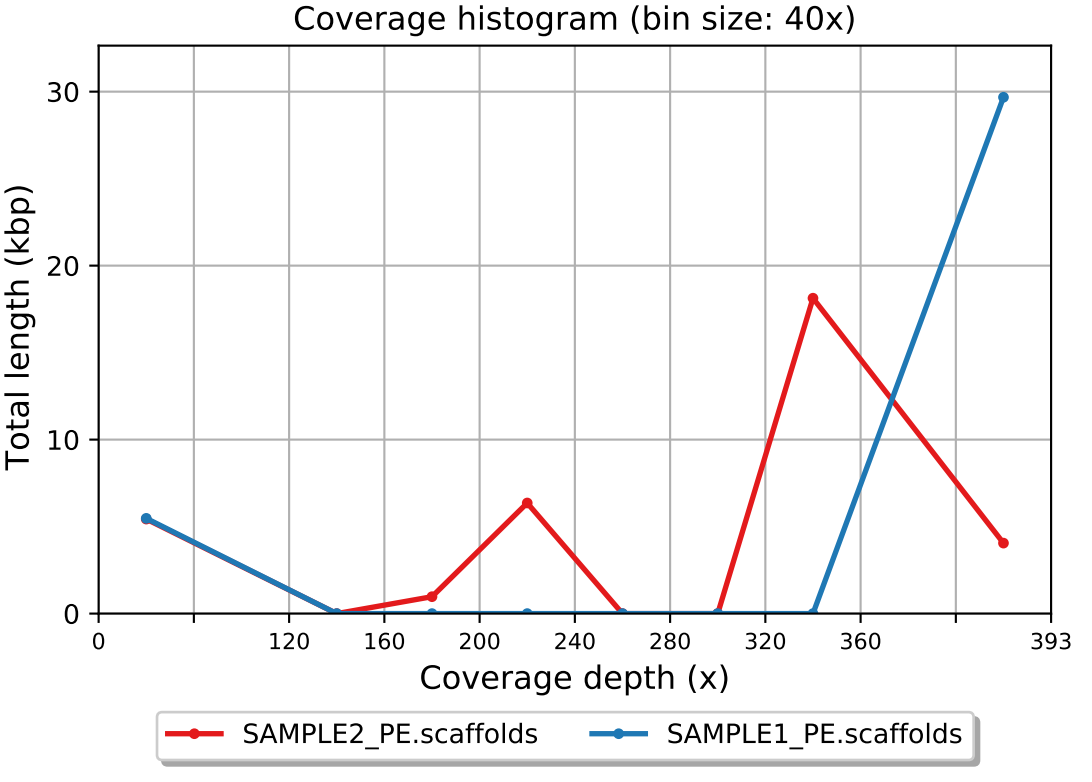

NGx
Contig length (kbp)
0
4
8
12
16
20
0
20
40
60
80
100
x
SAMPLE2_PE.scaffolds
SAMPLE1_PE.scaffolds

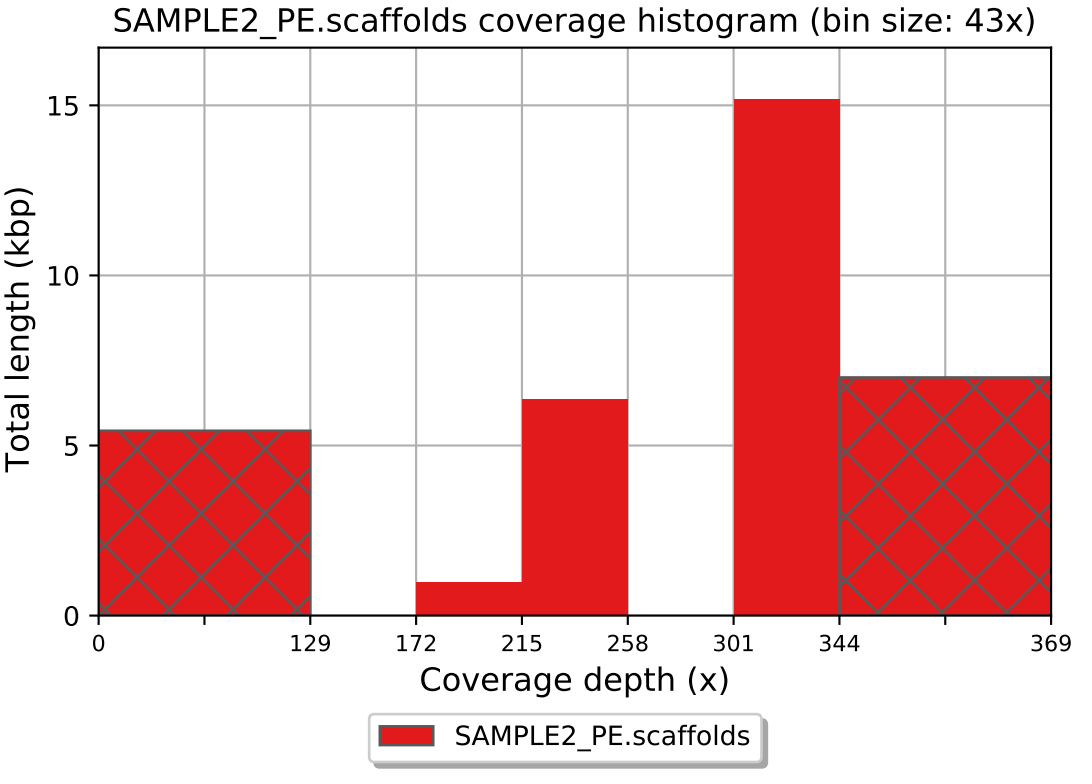

Cumulative length
Cumulative length (kbp)
0
8
16
24
32
0
2
4
6
8
Contig index
SAMPLE2_PE.scaffolds
SAMPLE1_PE.scaffolds
Reference

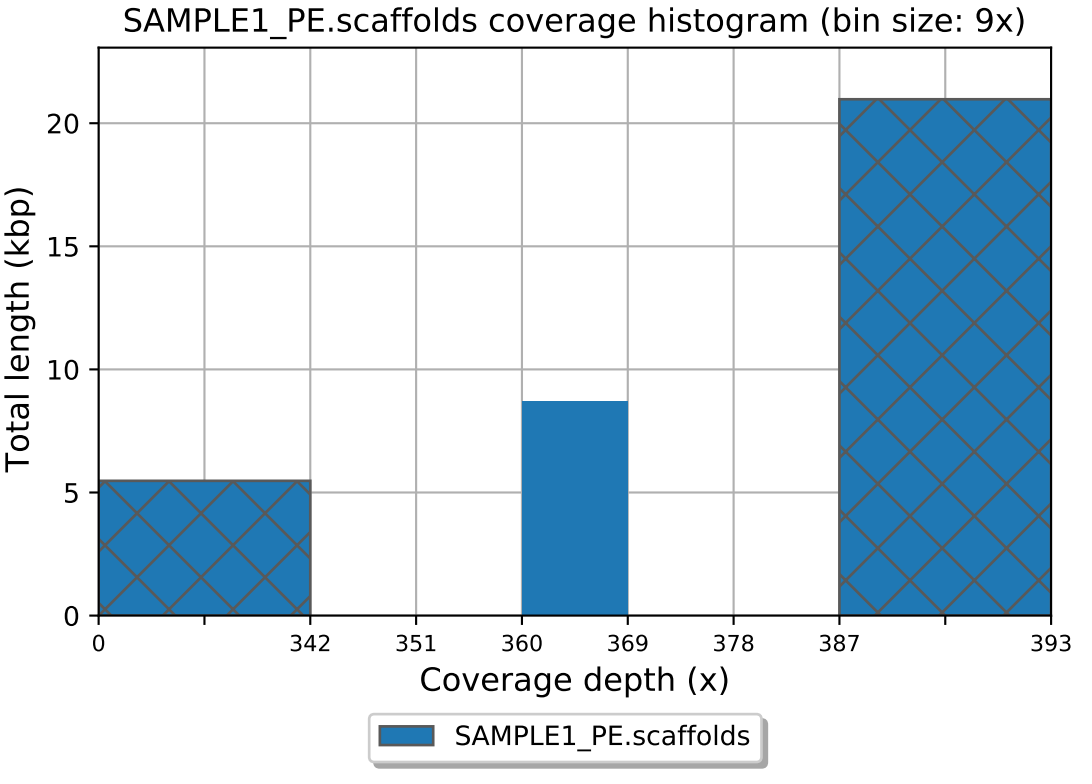

GC content
windows
0
8
16
24
32
0
20
40
60
80
100
GC (%)
SAMPLE2_PE.scaffolds
SAMPLE1_PE.scaffolds
Reference

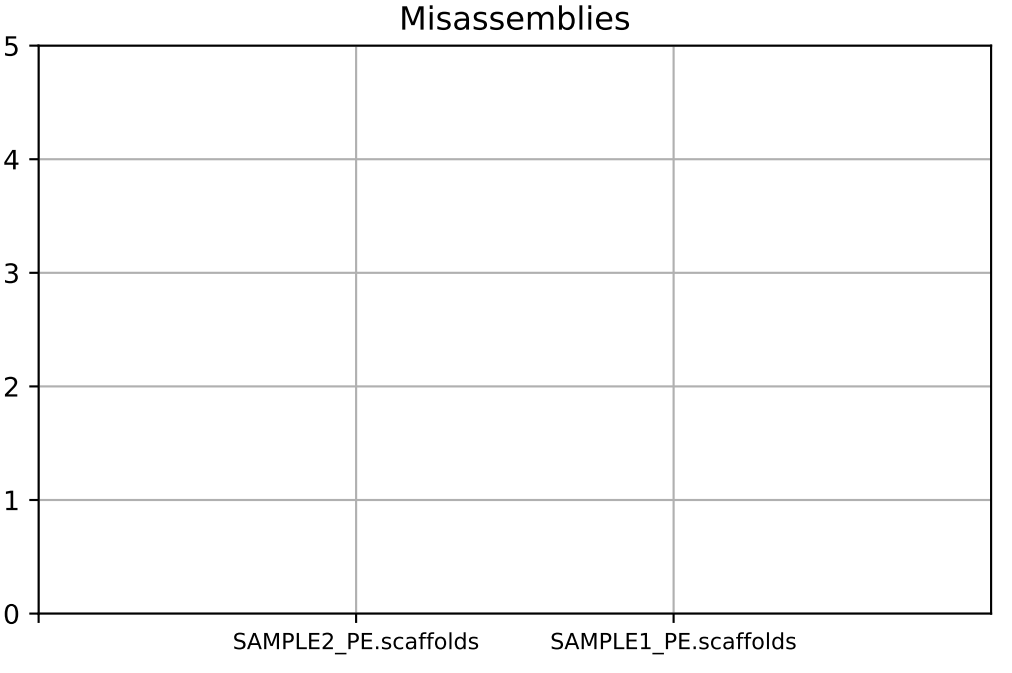

SAMPLE2_PE.scaffolds GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
SAMPLE2_PE.scaffolds

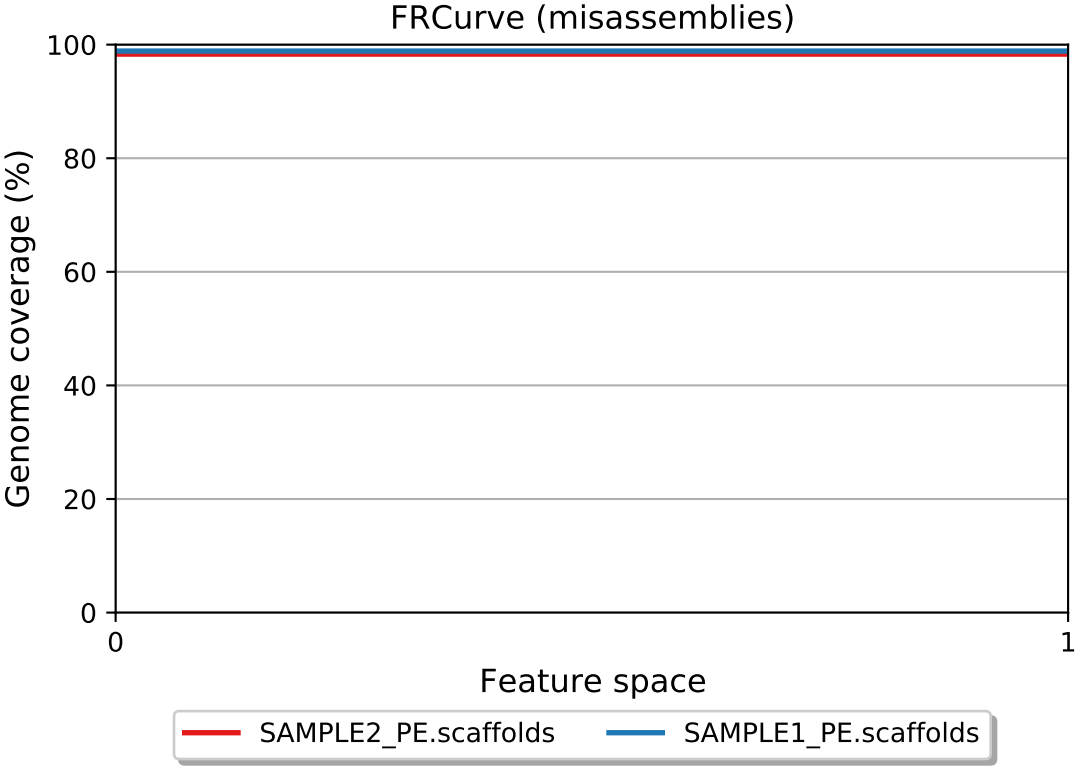

SAMPLE1_PE.scaffolds GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
SAMPLE1_PE.scaffolds

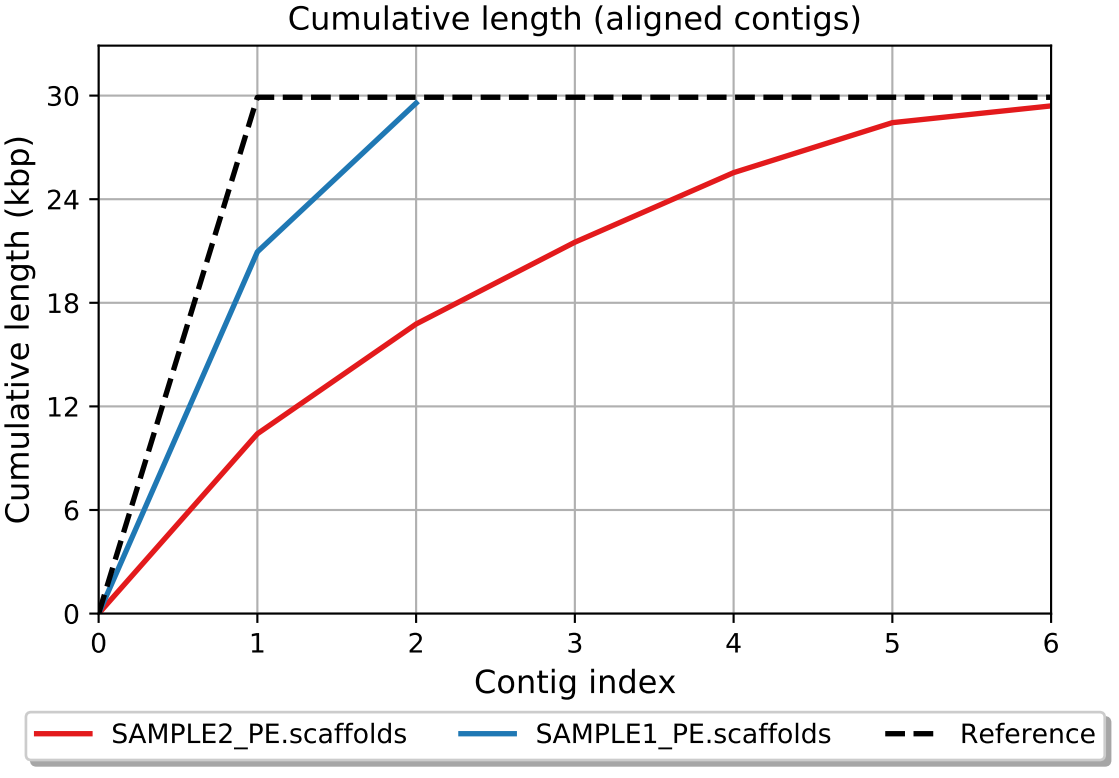

Coverage histogram (bin size: 40x)
Total length (kbp)
30
20
10
0
0
120
160
200
240
280
320
360
393
Coverage depth (x)
SAMPLE2_PE.scaffolds
SAMPLE1_PE.scaffolds

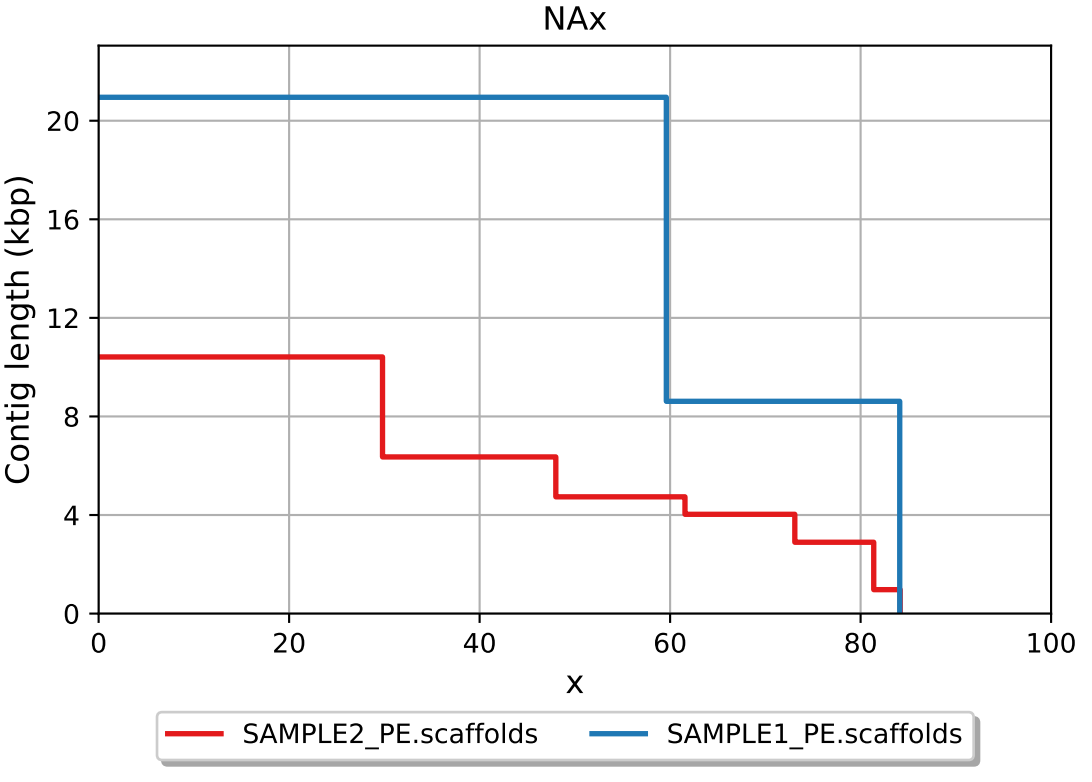

SAMPLE2_PE.scaffolds coverage histogram (bin size: 43x)
Total length (kbp)
0
5
10
15
0
129
172
215
258
301
344
369
Coverage depth (x)
SAMPLE2_PE.scaffolds

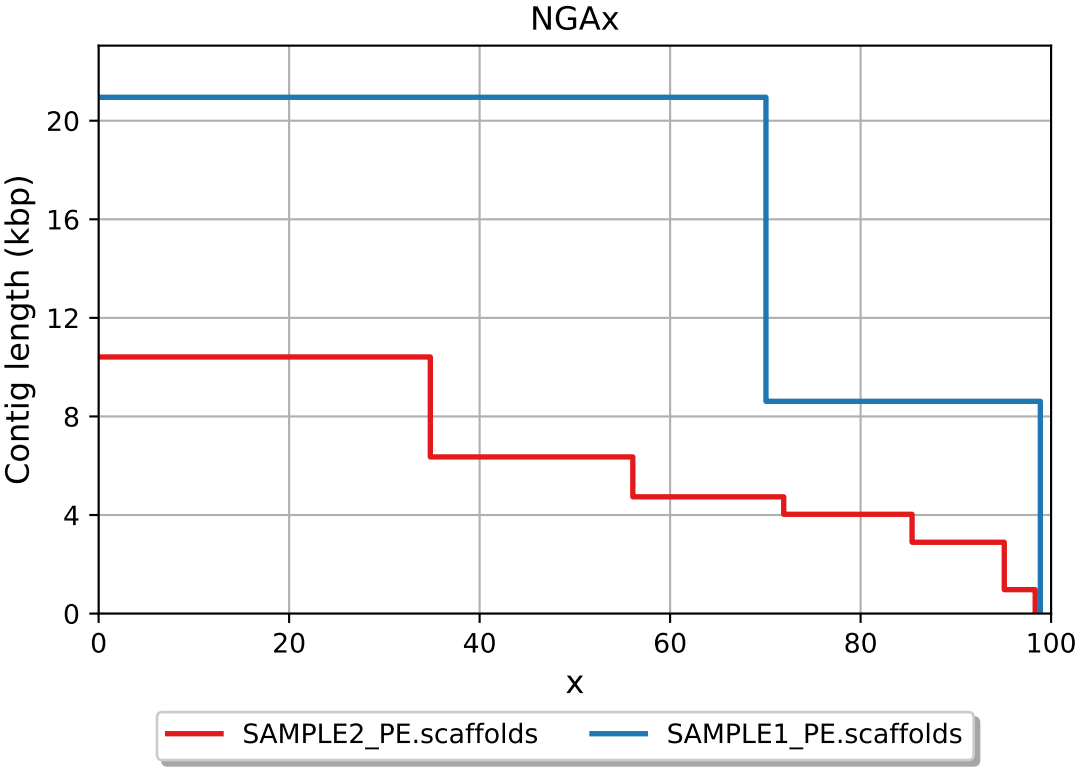

SAMPLE1_PE.scaffolds coverage histogram (bin size: 9x)
Total length (kbp)
0
5
10
15
20
0
342
351
360
369
378
387
393
Coverage depth (x)
SAMPLE1_PE.scaffolds

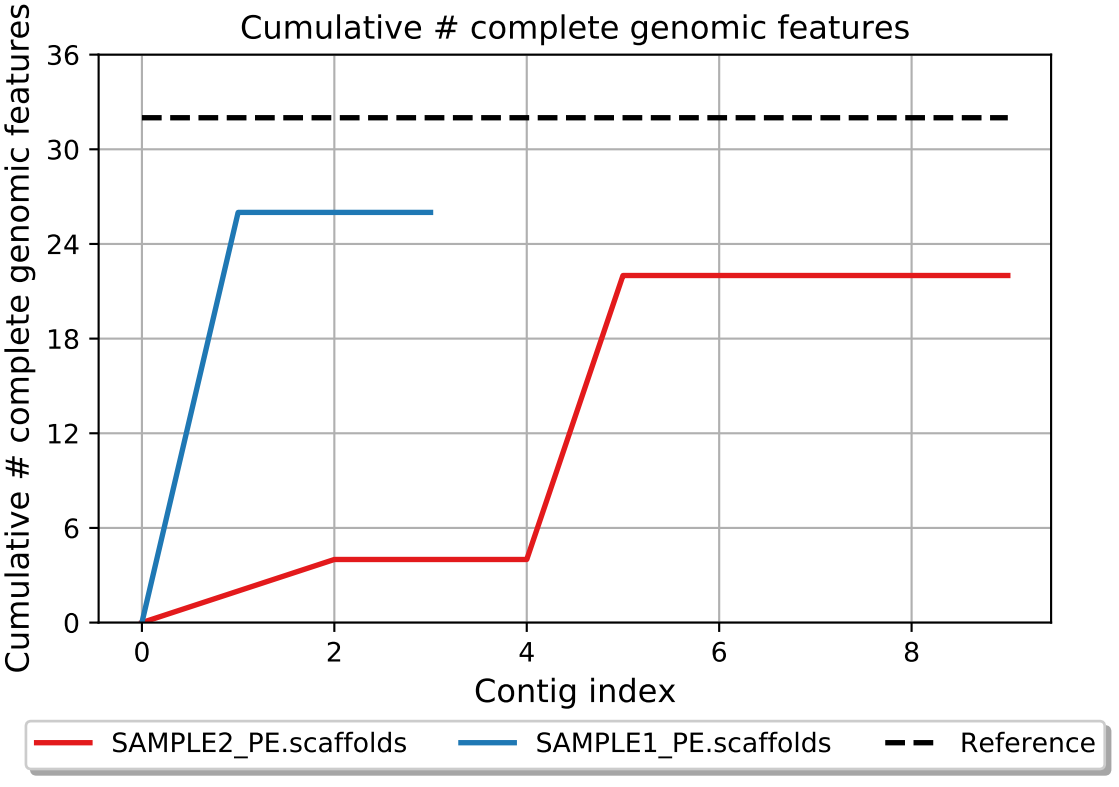

Misassemblies
5
4
3
2
1
0
SAMPLE2_PE.scaffolds
SAMPLE1_PE.scaffolds

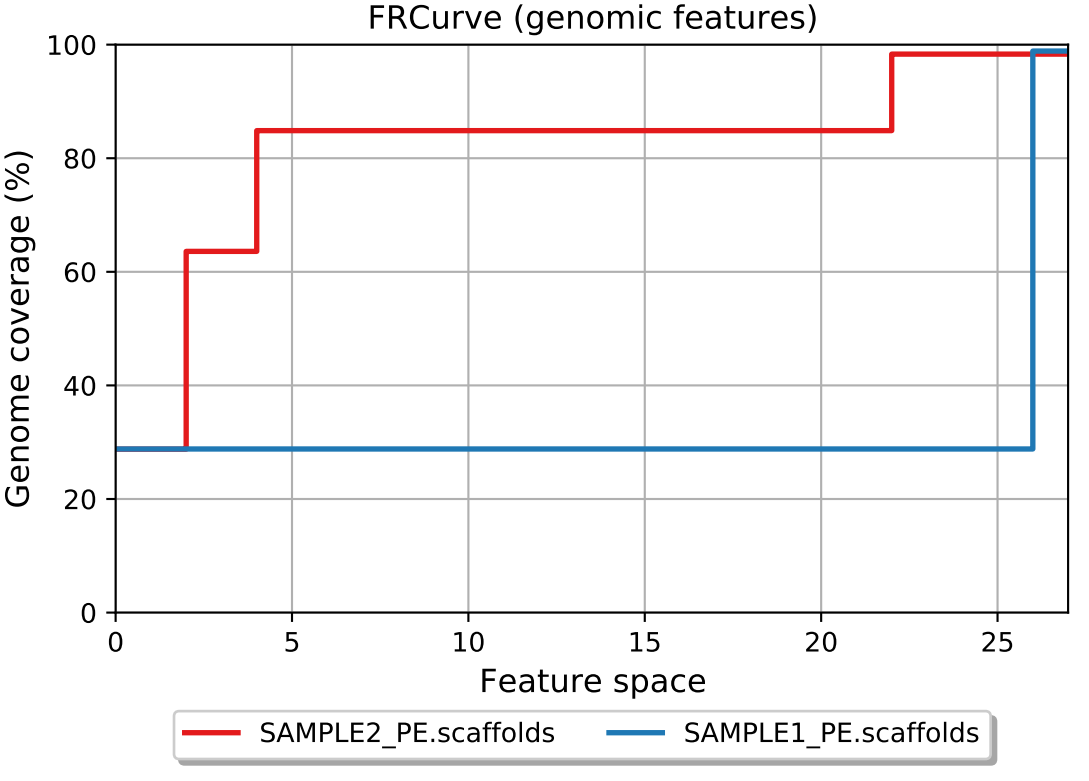

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
SAMPLE2_PE.scaffolds
SAMPLE1_PE.scaffolds

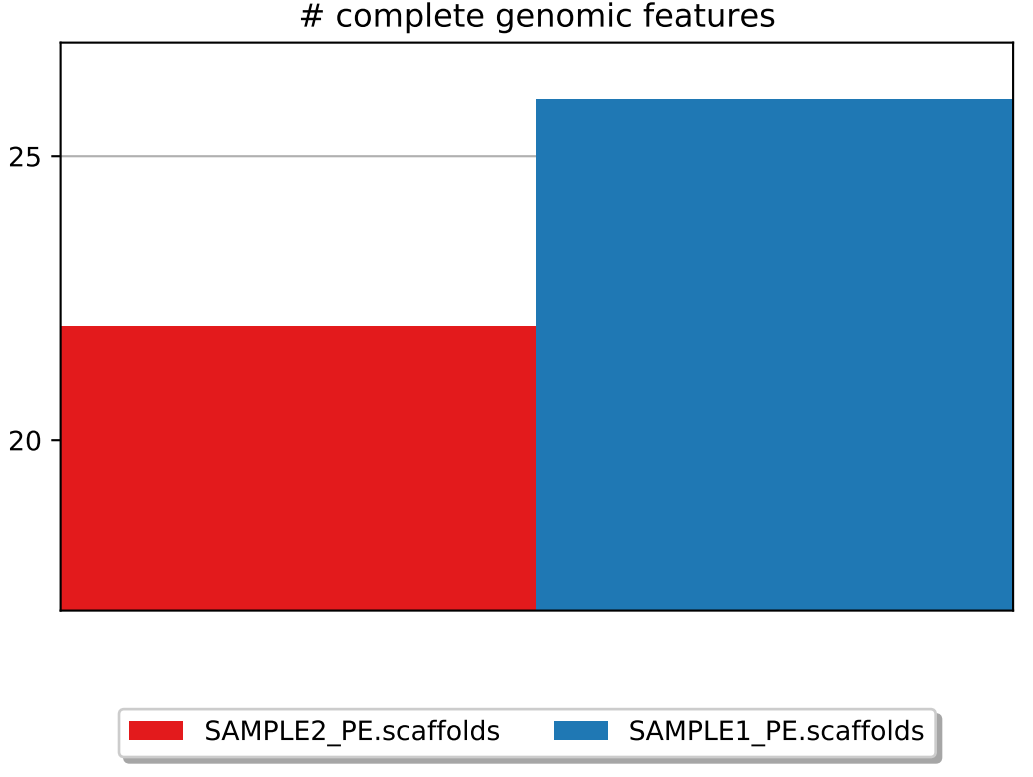

Cumulative length (aligned contigs)
Cumulative length (kbp)
30
24
18
12
6
0
0
1
2
3
4
5
6
Contig index
SAMPLE2_PE.scaffolds
SAMPLE1_PE.scaffolds
Reference

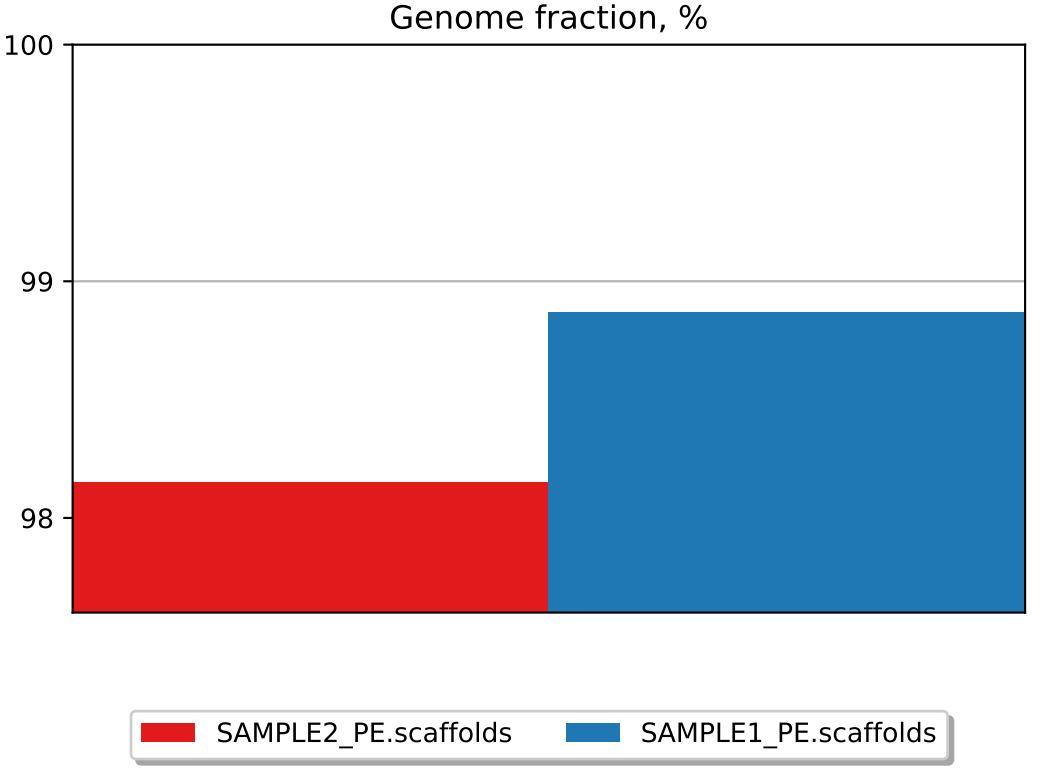

NAx
Contig length (kbp)
0
4
8
12
16
20
0
20
40
60
80
100
x
SAMPLE2_PE.scaffolds
SAMPLE1_PE.scaffolds


NGAx
Contig length (kbp)
0
4
8
12
16
20
0
20
40
60
80
100
x
SAMPLE2_PE.scaffolds
SAMPLE1_PE.scaffolds


Cumulative # complete genomic features
Cumulative # complete genomic features
36
30
24
18
12
6
0
0
2
4
6
8
Contig index
SAMPLE2_PE.scaffolds
SAMPLE1_PE.scaffolds
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
5
10
15
20
25
Feature space
SAMPLE2_PE.scaffolds
SAMPLE1_PE.scaffolds


complete genomic features
25
20
SAMPLE2_PE.scaffolds
SAMPLE1_PE.scaffolds


Genome fraction, %
100
99
98
SAMPLE2_PE.scaffolds
SAMPLE1_PE.scaffolds