

Report

	salmonella-8_fa	salmonella-8_fa_broken
# contigs (>= 0 bp)	150	-
# contigs (>= 1000 bp)	44	50
Total length (>= 0 bp)	4871123	-
Total length (>= 1000 bp)	4851345	4849767
# contigs	48	58
Largest contig	537866	537866
Total length	4853853	4853353
Reference length	4951383	4951383
GC (%)	52.19	52.19
Reference GC (%)	52.24	52.24
N50	272520	223891
NG50	272520	220071
N90	59728	54580
NG90	54580	52399
auN	301881.7	245920.8
auNG	295935.4	241051.9
L50	6	7
LG50	6	8
L90	21	26
LG90	22	27
# misassemblies	10	10
# misassembled contigs	9	9
Misassembled contigs length	2096548	1436747
# local misassemblies	6	6
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 5 part	0 + 5 part
Unaligned length	81853	81853
Genome fraction (%)	95.870	95.891
Duplication ratio	1.009	1.008
# N's per 100 kbp	10.34	0.04
# mismatches per 100 kbp	35.18	35.33
# indels per 100 kbp	3.63	3.46
Complete BUSCO (%)	98.65	98.65
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	2 + 4 part	2 + 4 part
Largest alignment	537775	537775
Total aligned length	4769483	4769491
NA50	232147	205673
NGA50	232147	159815
NA90	46041	41640
NGA90	37078	33346
auNA	246636.6	211985.8
auNGA	241778.5	207788.8
LA50	7	8
LGA50	7	9
LA90	26	31
LGA90	28	34

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

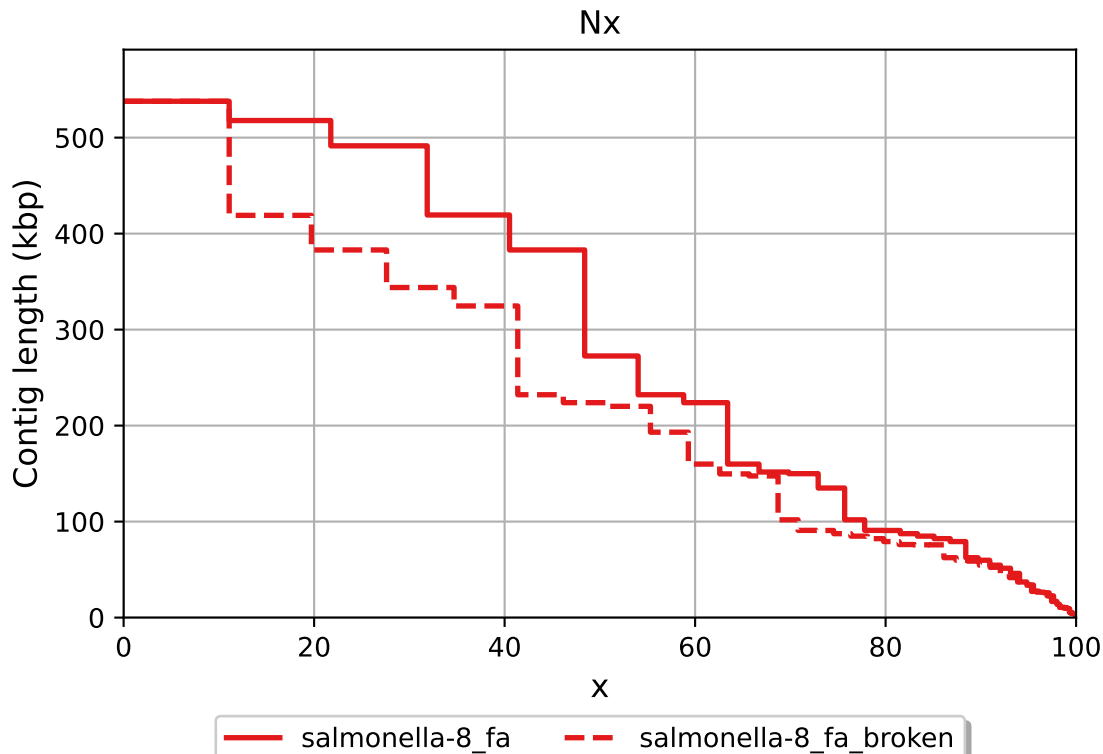
	salmonella-8_fa	salmonella-8_fa_broken
# misassemblies	10	10
# contig misassemblies	10	10
# c. relocations	10	10
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	9	9
Misassembled contigs length	2096548	1436747
# local misassemblies	6	6
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	0	0
# mismatches	1678	1685
# indels	173	165
# indels (<= 5 bp)	131	131
# indels (> 5 bp)	42	34
Indels length	3542	3048

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).

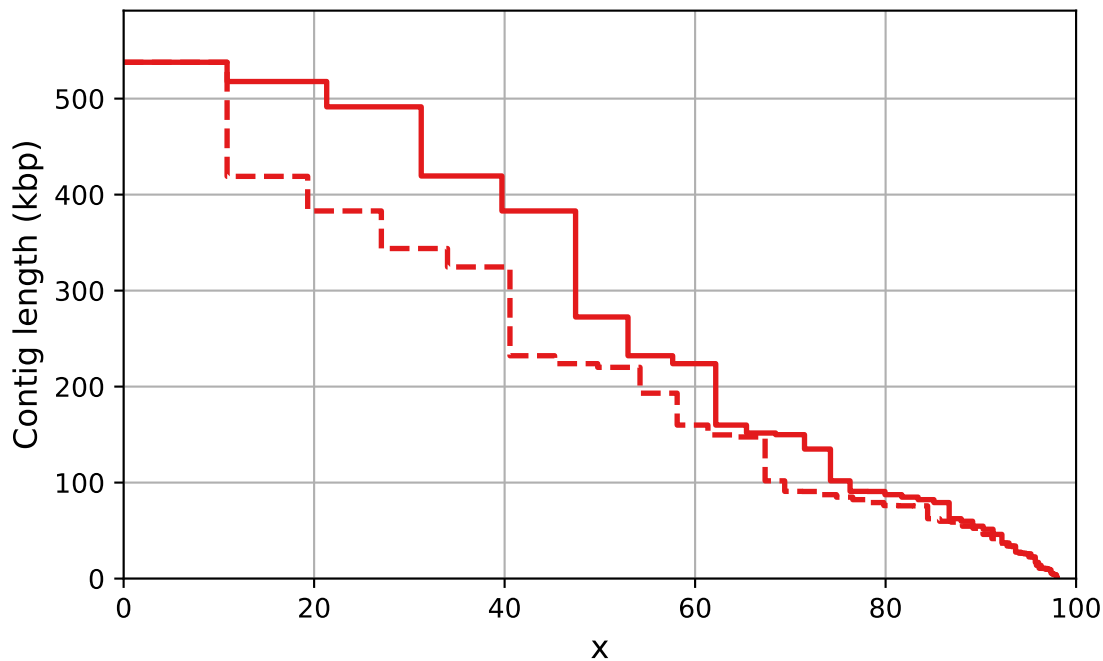
Unaligned report

	salmonella-8_fa	salmonella-8_fa_broken
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	5	5
Partially unaligned length	81853	81853
# N's	502	2

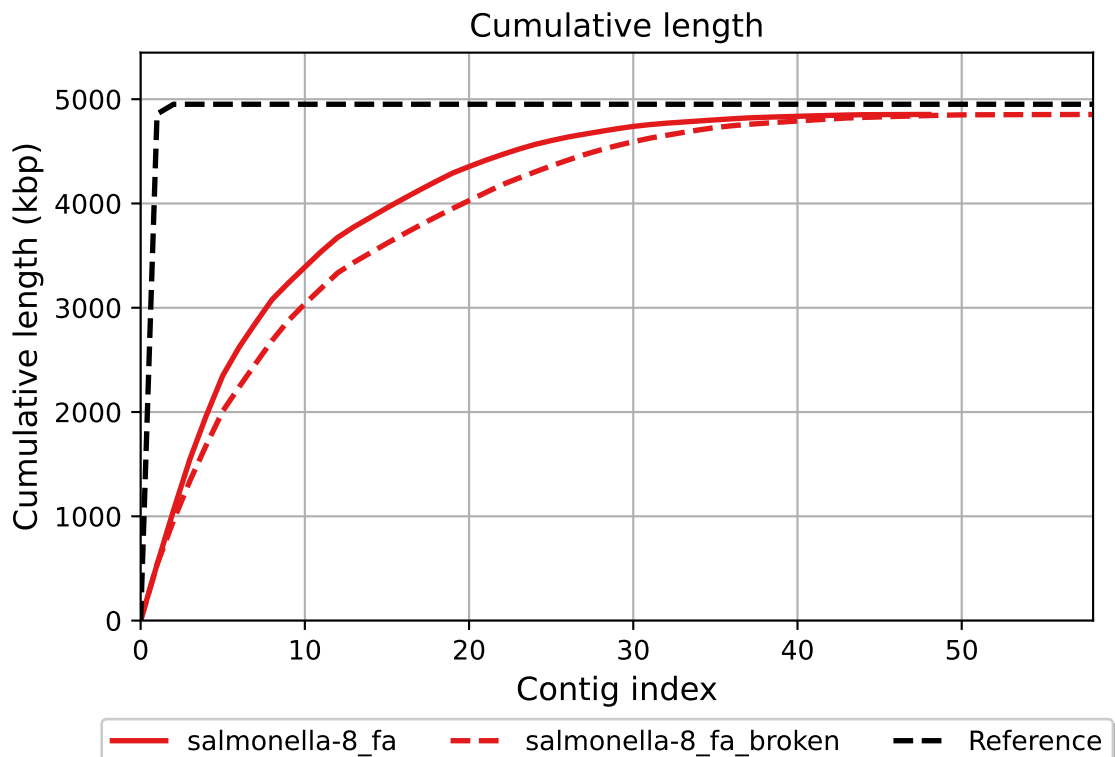
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



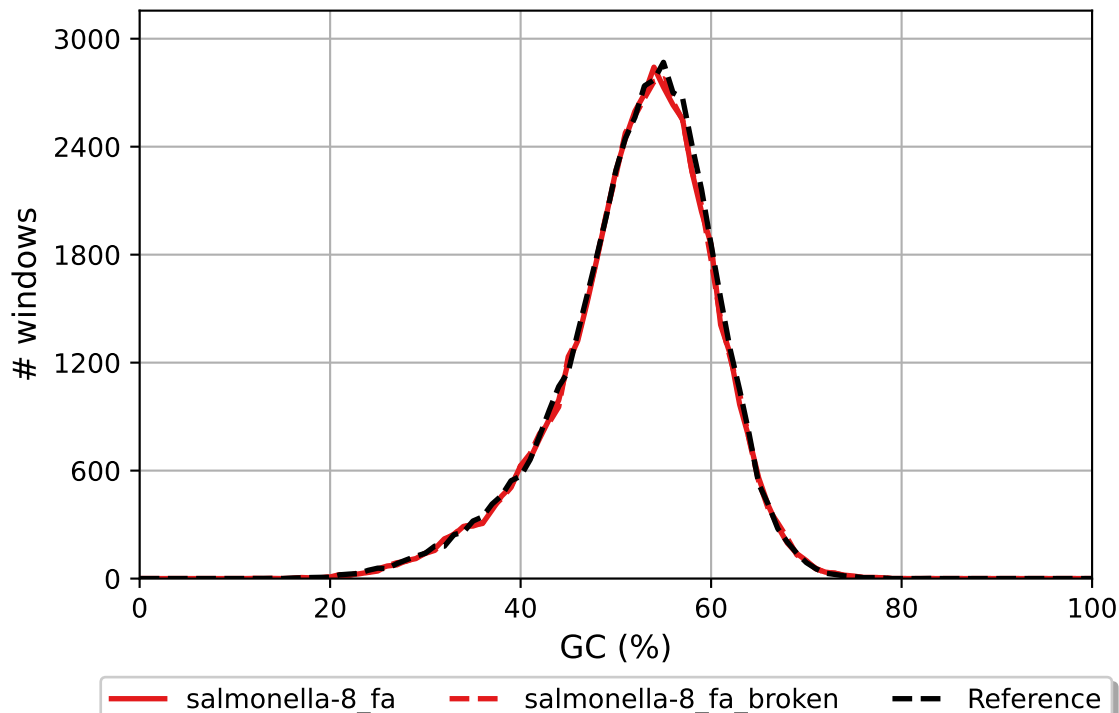
NGx



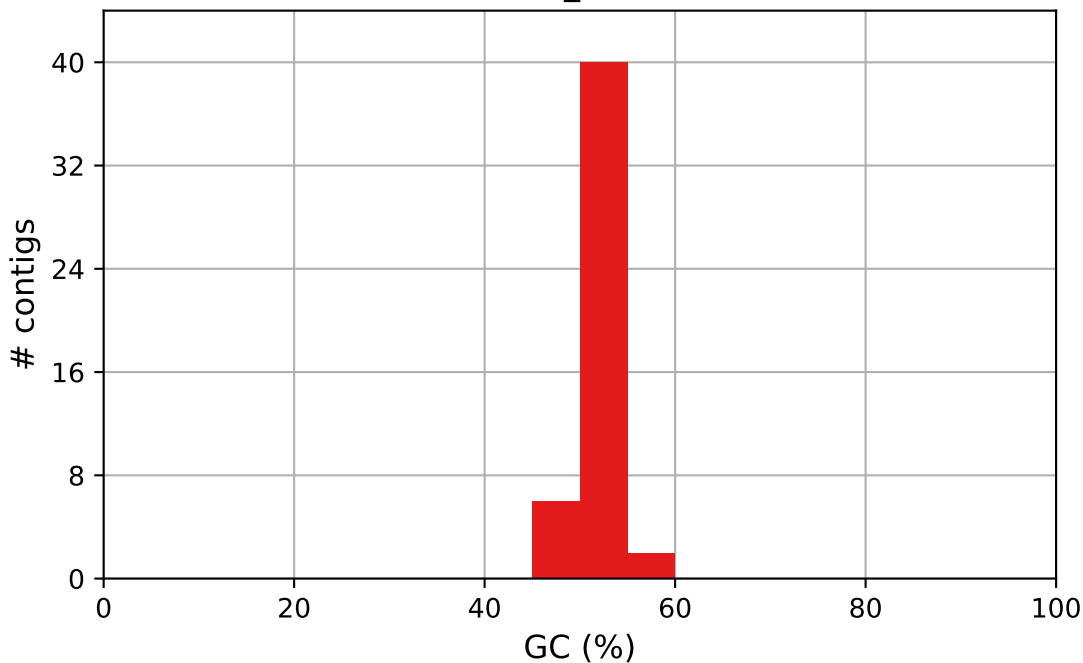
— salmonella-8_fa - - - salmonella-8_fa_broken



GC content

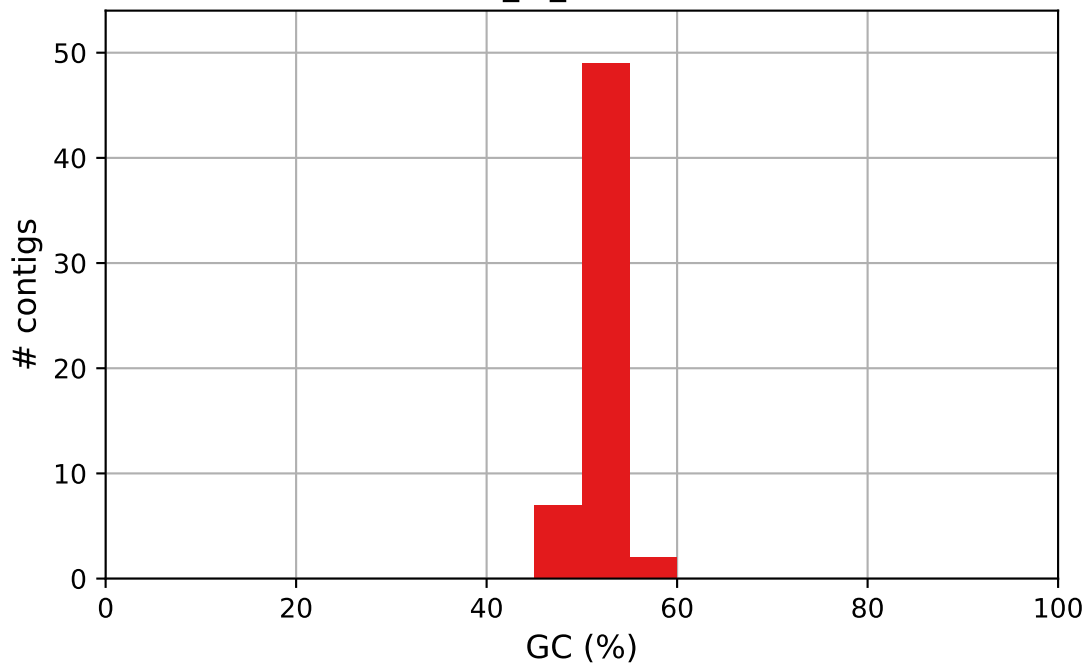


salmonella-8_fa GC content



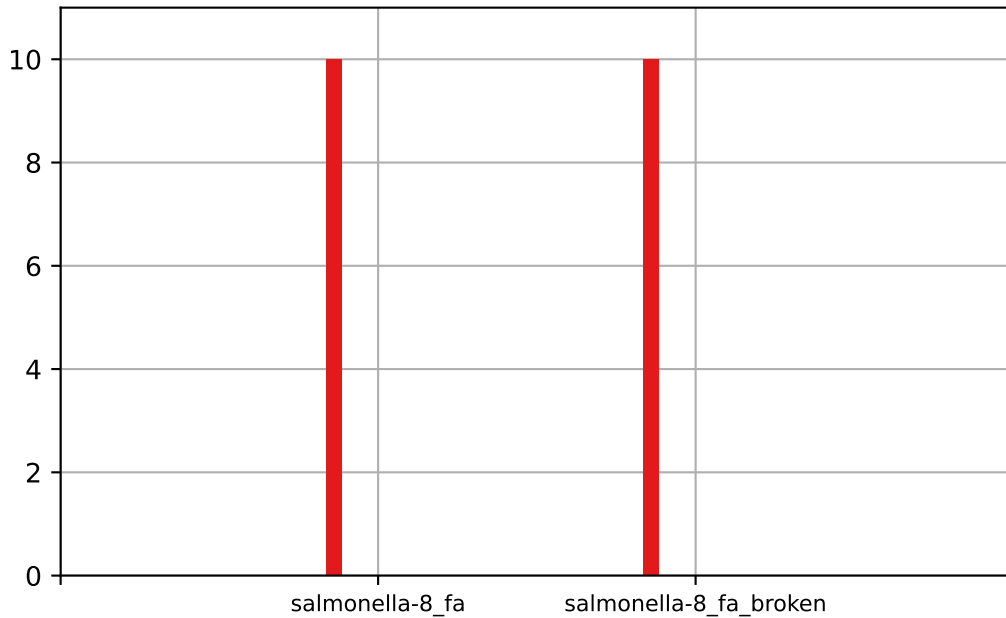
salmonella-8_fa

salmonella-8_fa_broken GC content



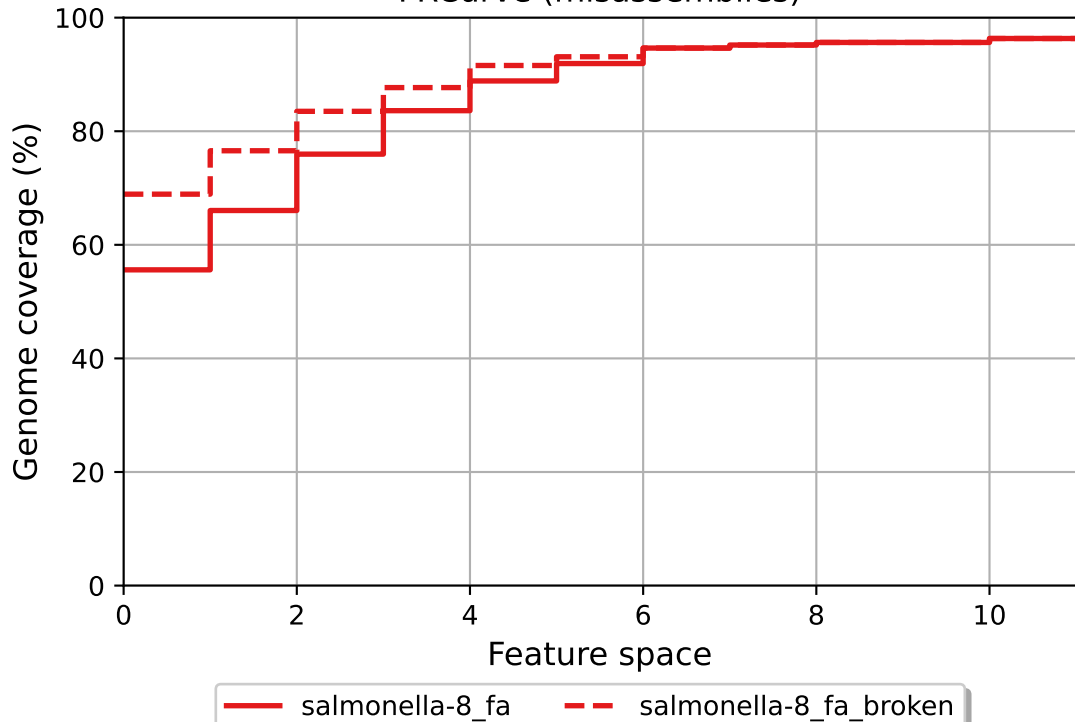
salmonella-8_fa_broken

Misassemblies

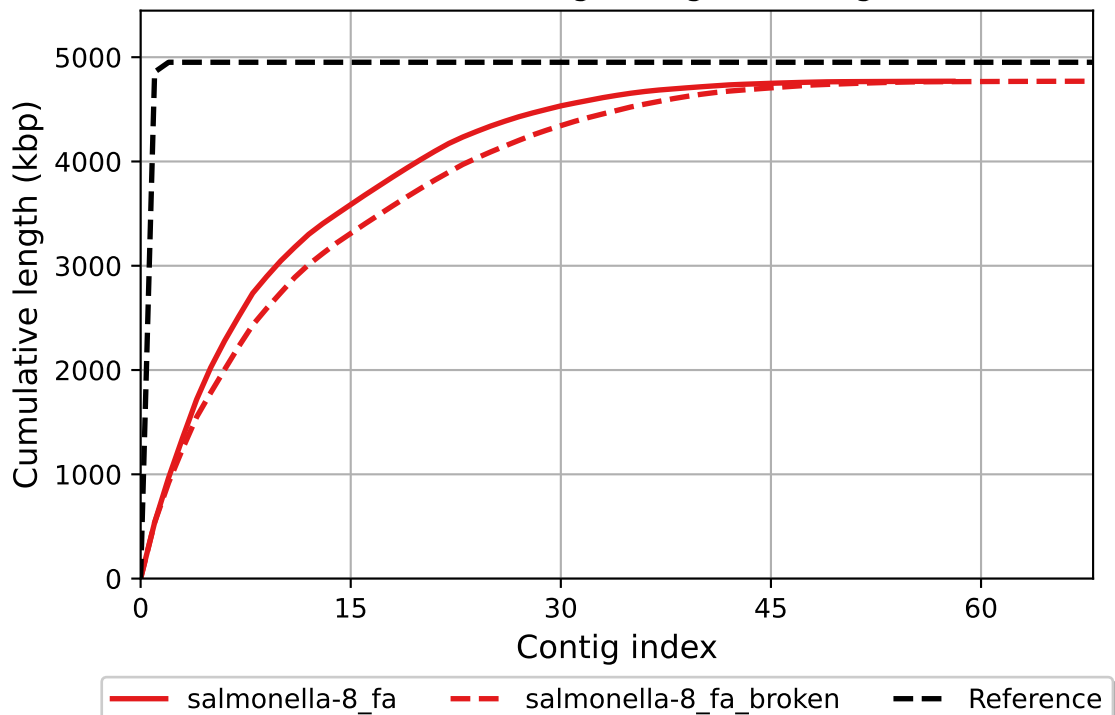


 # relocations

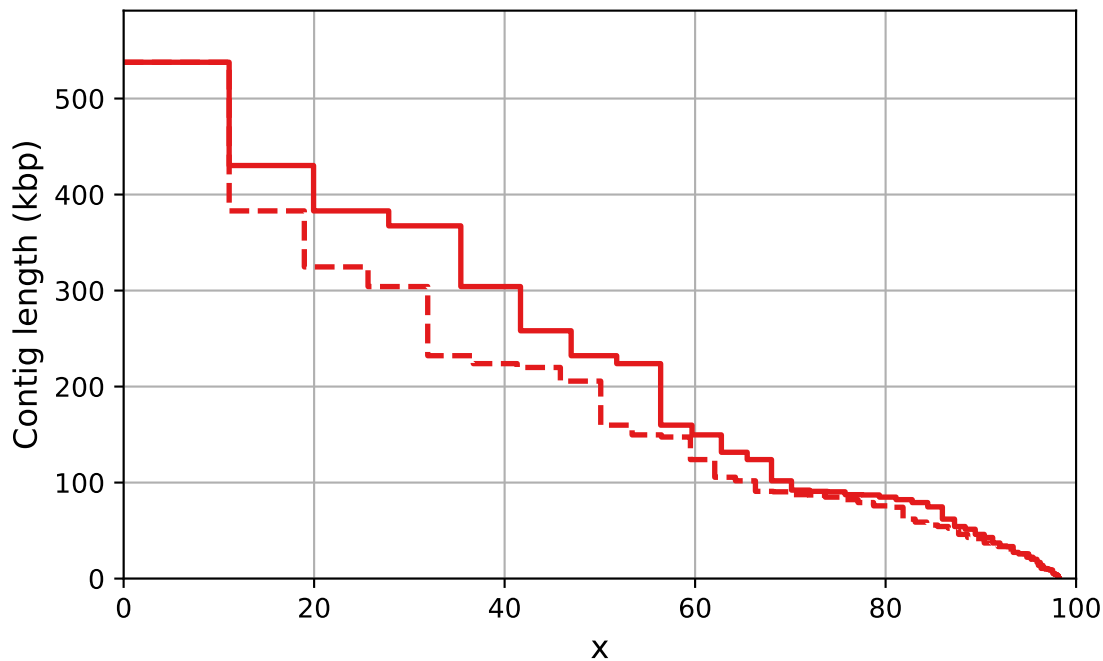
FRCurve (misassemblies)



Cumulative length (aligned contigs)

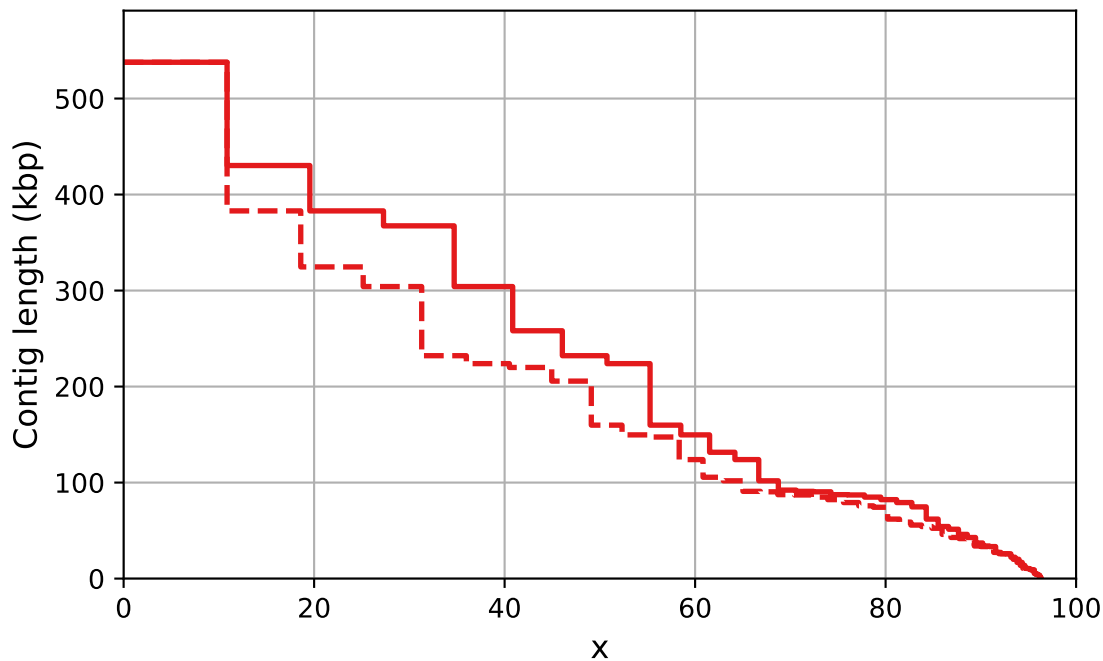


NAx



— salmonella-8_fa - - - salmonella-8_fa_broken

NGAx



— salmonella-8_fa - - - salmonella-8_fa_broken

Genome fraction, %



salmonella-8_fa



salmonella-8_fa_broken

Report

	SPAdes_on_data_2_and_data_1__Scaffolds	SPAdes_on_data_2_and_data_1__Scaffolds_broken
# contigs (>= 0 bp)	191	-
# contigs (>= 1000 bp)	63	71
Total length (>= 0 bp)	4813654	-
Total length (>= 1000 bp)	4788123	4786289
# contigs	72	82
Largest contig	549770	322638
Total length	4794213	4792805
Reference length	4951383	4951383
GC (%)	52.13	52.13
Reference GC (%)	52.24	52.24
N50	193475	168456
NG50	178662	149367
N90	53847	51504
NG90	44707	44707
auN	224465.2	166813.7
auNG	217340.1	161471.2
L50	8	10
LG50	9	11
L90	27	32
LG90	30	35
# misassemblies	7	7
# misassembled contigs	7	7
Misassembled contigs length	1416504	1035190
# local misassemblies	5	5
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	3	-
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 5 part	0 + 5 part
Unaligned length	81933	81933
Genome fraction (%)	96.032	96.017
Duplication ratio	1.001	1.001
# N's per 100 kbp	22.94	0.00
# mismatches per 100 kbp	28.13	28.20
# indels per 100 kbp	3.65	3.46
# genomic features	13701 + 108 part	13685 + 112 part
Complete BUSCO (%)	98.65	98.65
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	2 + 0 part	2 + 0 part
Largest alignment	376430	322563
Total aligned length	4710913	4709961
NA50	178662	129564
NGA50	152567	123652
NA90	35969	35969
NGA90	30214	26152
auNA	187266.9	155275.2
auNGA	181322.6	150302.2
LA50	9	11
LGA50	10	12
LA90	32	37
LGA90	36	42

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

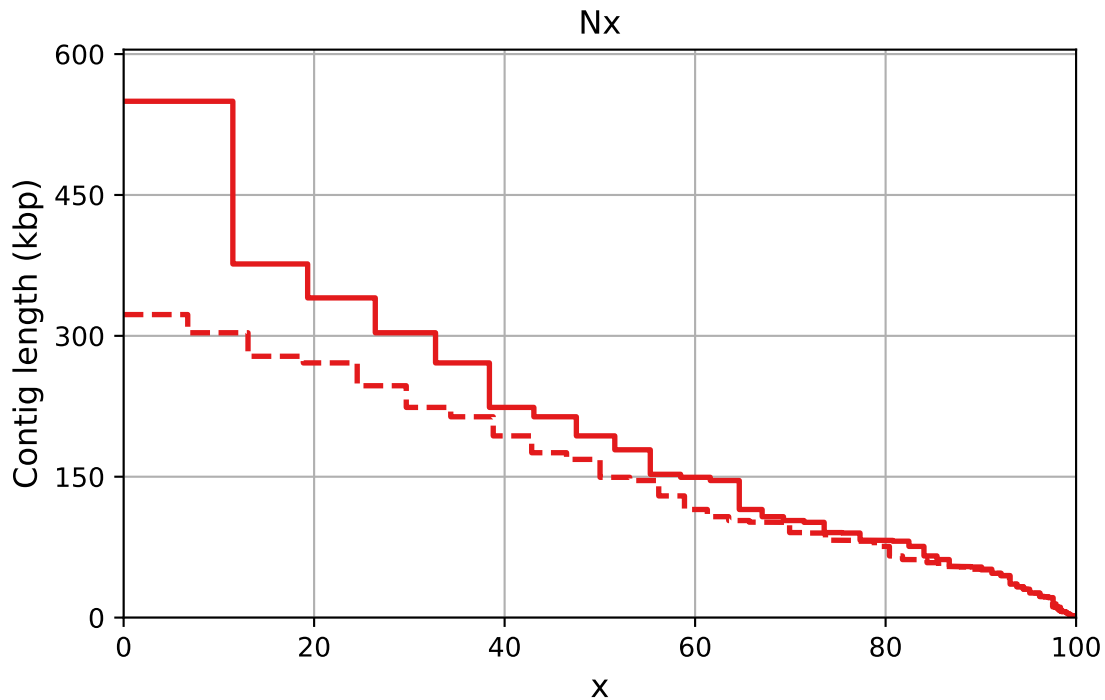
	SPAdes_on_data_2_and_data_1_Scaffolds	SPAdes_on_data_2_and_data_1_Scaffolds_broken
# misassemblies	7	7
# contig misassemblies	7	7
# c. relocations	7	7
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	7	7
Misassembled contigs length	1416504	1035190
# local misassemblies	5	5
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	3	-
# unaligned mis. contigs	0	0
# mismatches	1325	1328
# indels	172	163
# indels (<= 5 bp)	137	136
# indels (> 5 bp)	35	27
Indels length	3722	2336

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

	SPAdes_on_data_2_and_data_1__Scaffolds	SPAdes_on_data_2_and_data_1__Scaffolds_broken
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	5	5
Partially unaligned length	81933	81933
# N's	1100	0

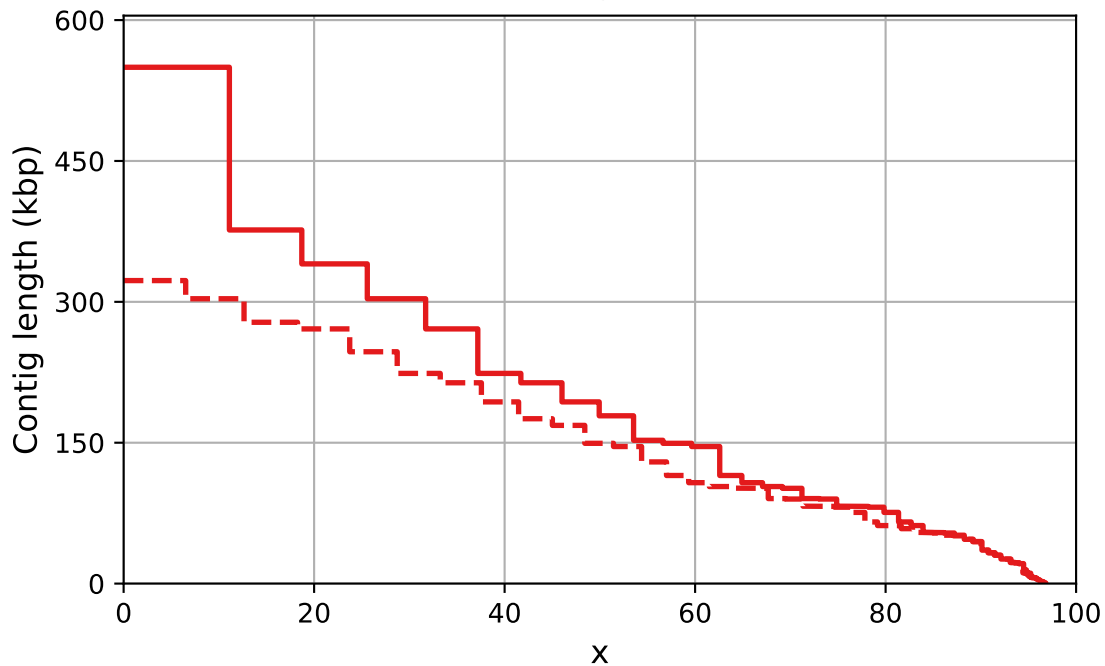
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



PAdes_on_data_2_and_data_1_Scaffolds

SPAdes_on_data_2_and_data_1_Scaffolds

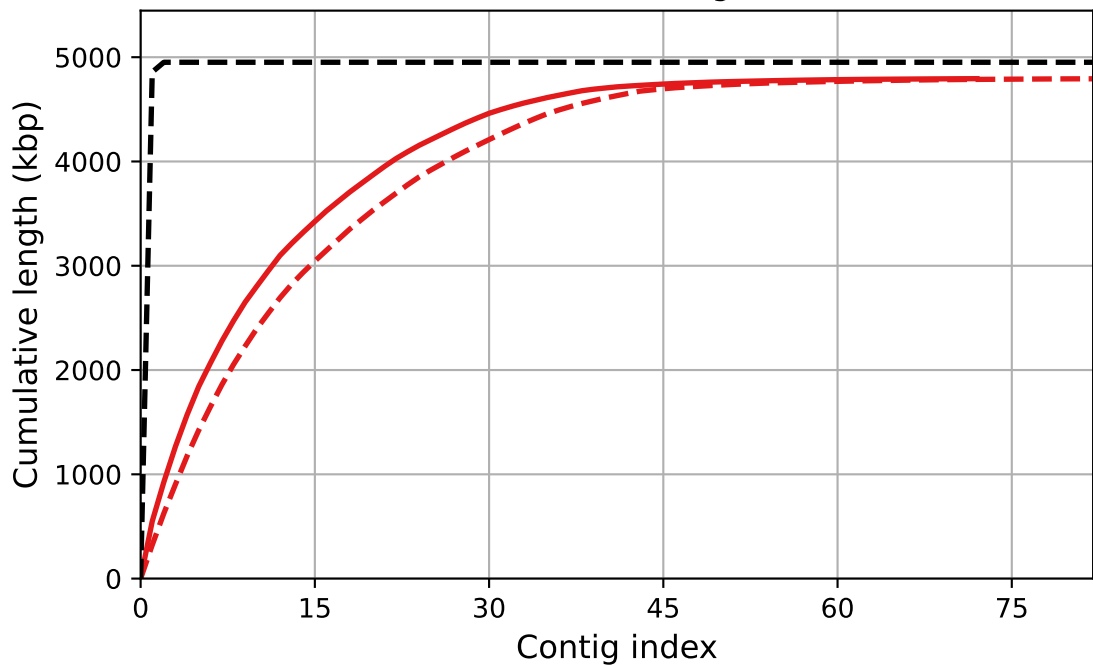
NGx



PAdes_on_data_2_and_data_1_Scaffolds

SPAdes_on_data_2_and_data_1_Scaffolds

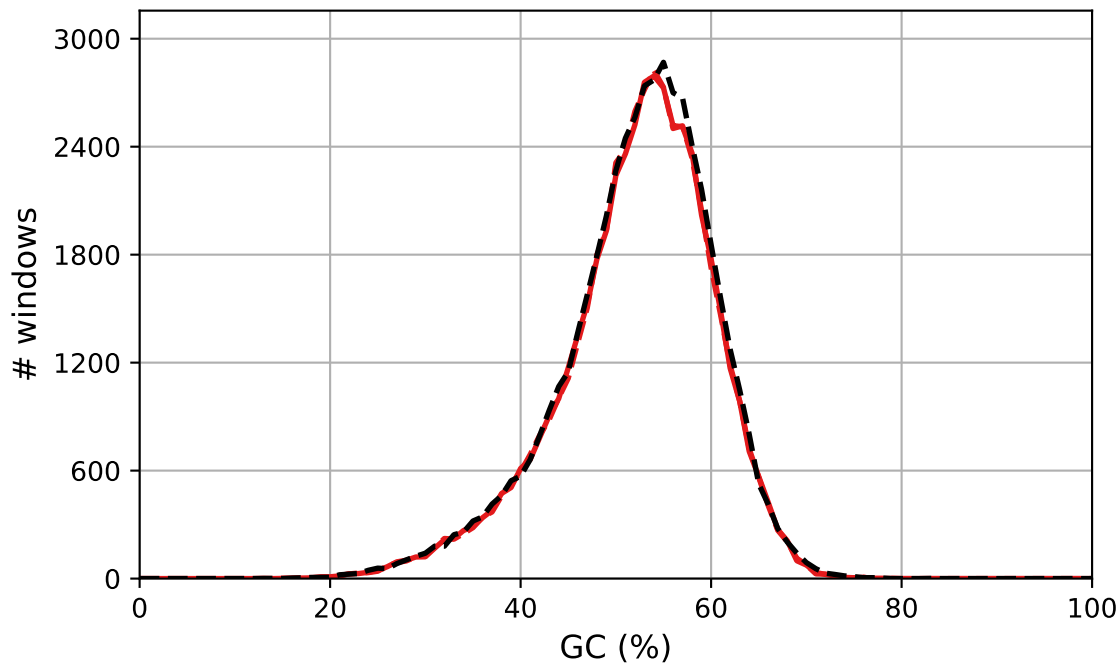
Cumulative length



_data_2_and_data_1__Scaffolds

-- SPAdes_on_data_2_and_data_1__Scaffolds_broken

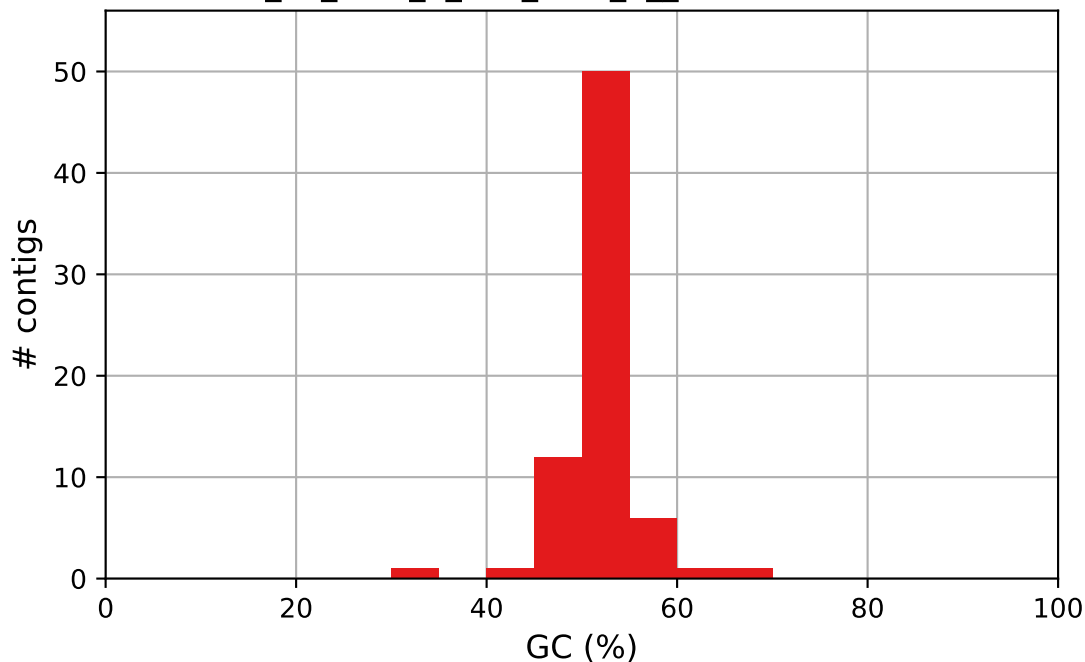
GC content



_data_2_and_data_1__Scaffolds

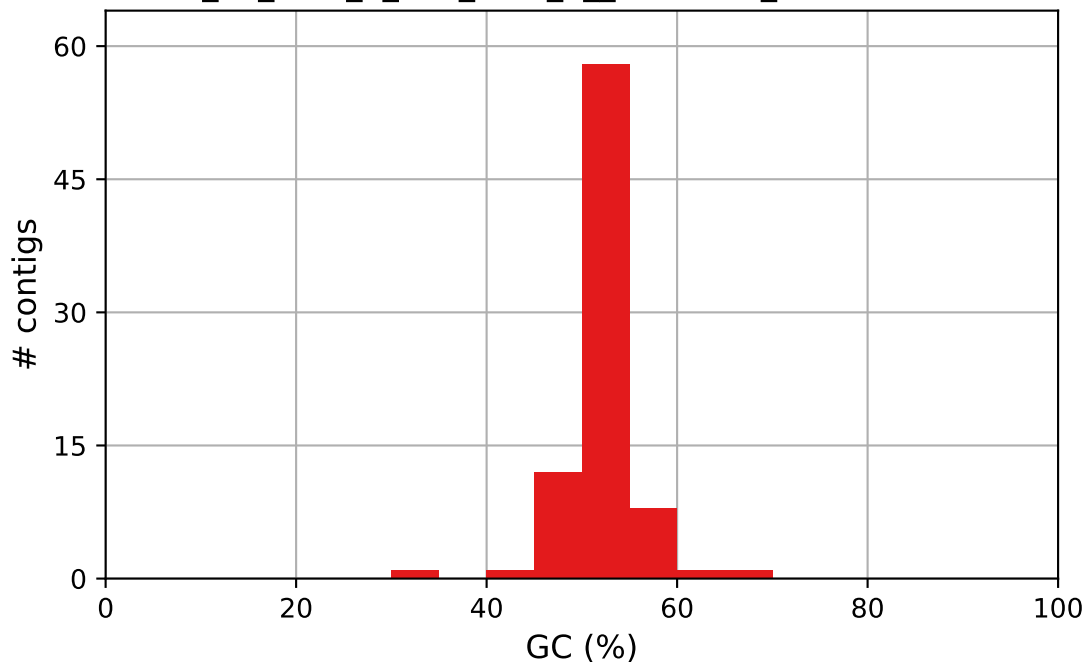
-- SPAdes_on_data_2_and_data_1__Scaffolds_broken

SPAdes_on_data_2_and_data_1__Scaffolds GC content



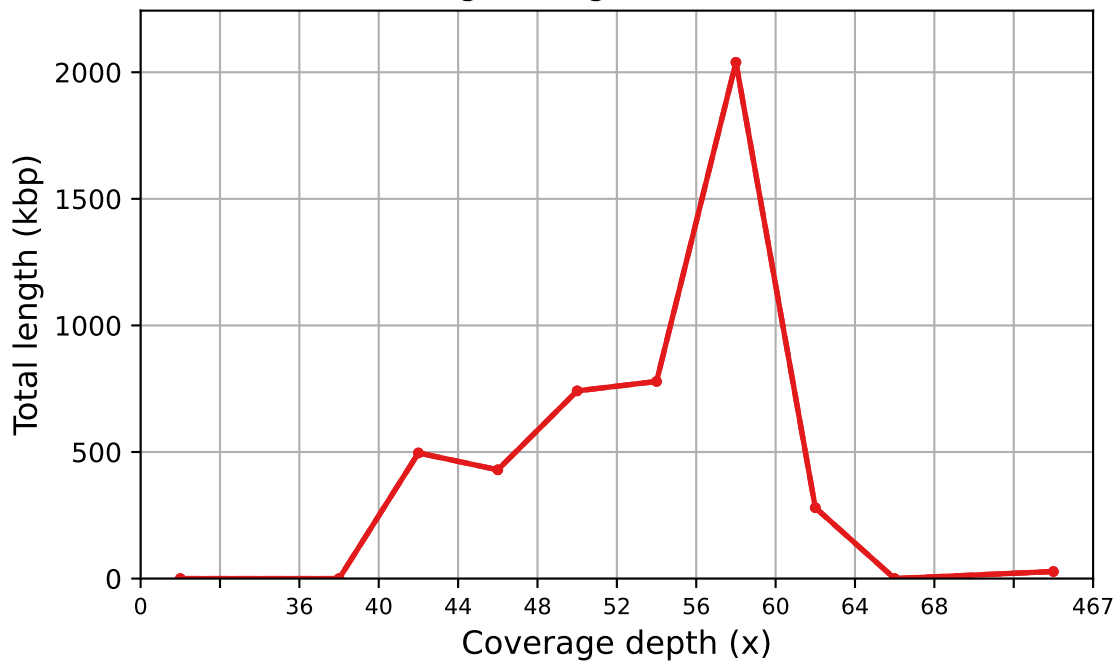
SPAdes_on_data_2_and_data_1__Scaffolds

SPAdes_on_data_2_and_data_1__Scaffolds_broken GC content



SPAdes_on_data_2_and_data_1__Scaffolds_broken

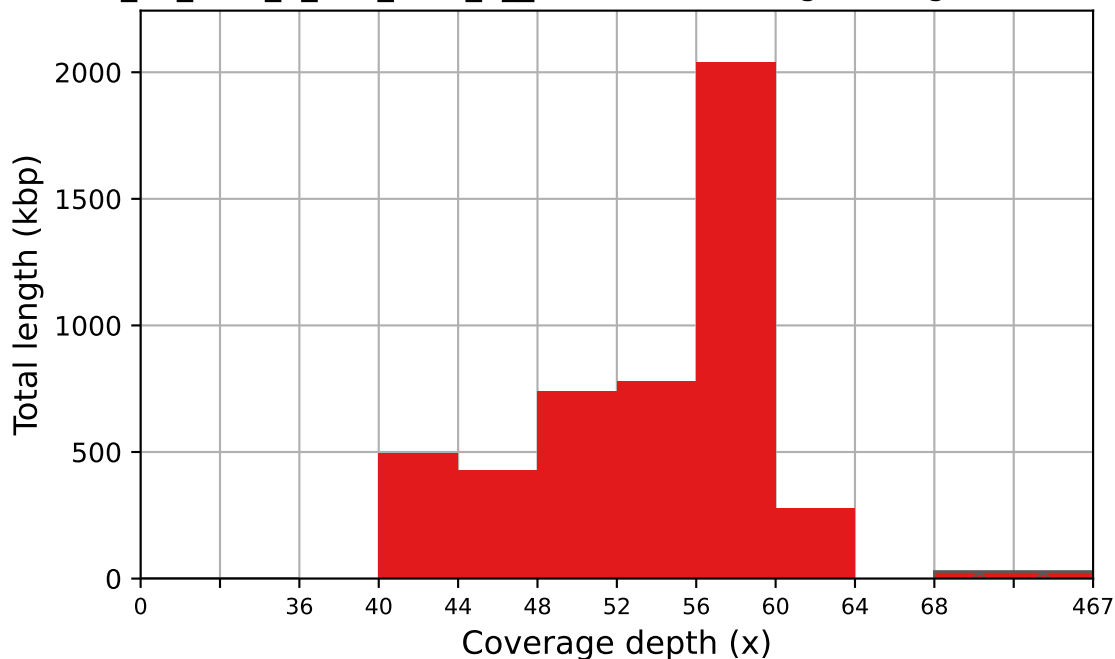
Coverage histogram (bin size: 4x)



PAdes_on_data_2_and_data_1_Scaffolds

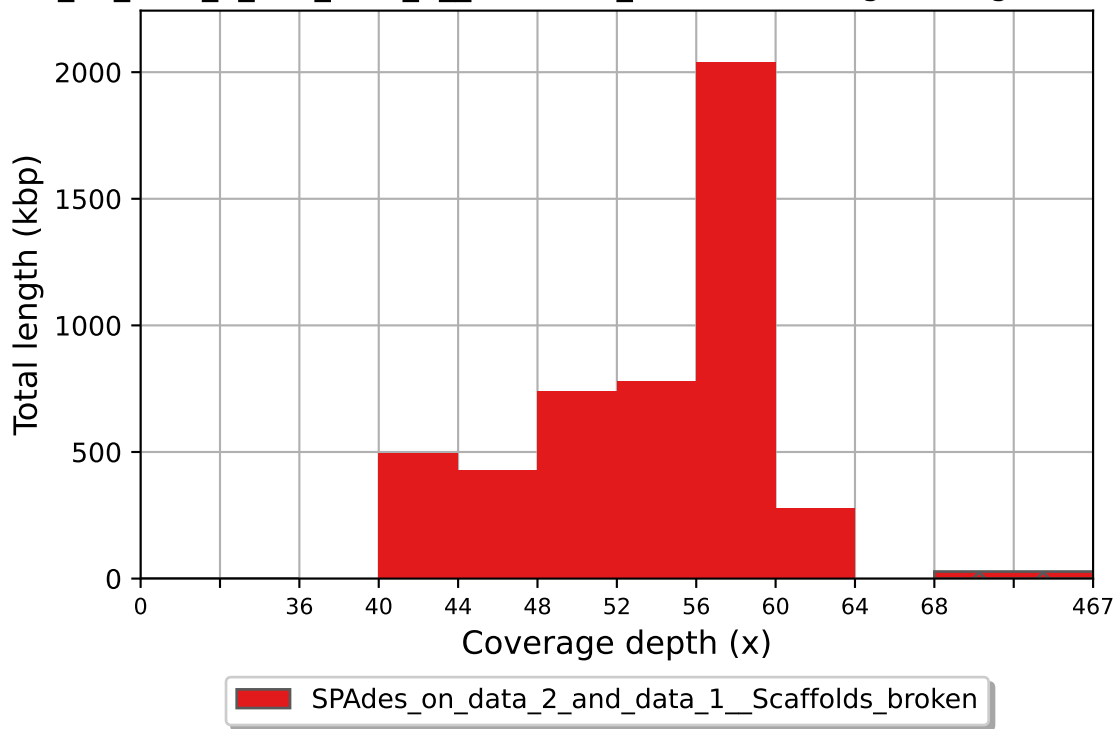
—●— SPAdes_on_data_2_and_data_1_Scaffolds

SPAdes_on_data_2_and_data_1__Scaffolds coverage histogram (bin size: 4x)

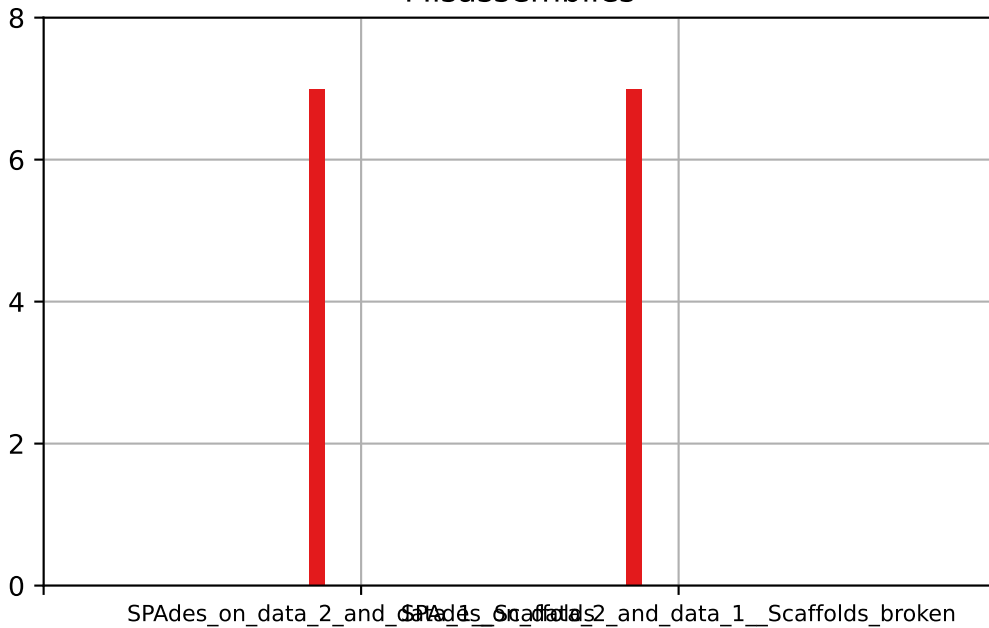


SPAdes_on_data_2_and_data_1__Scaffolds

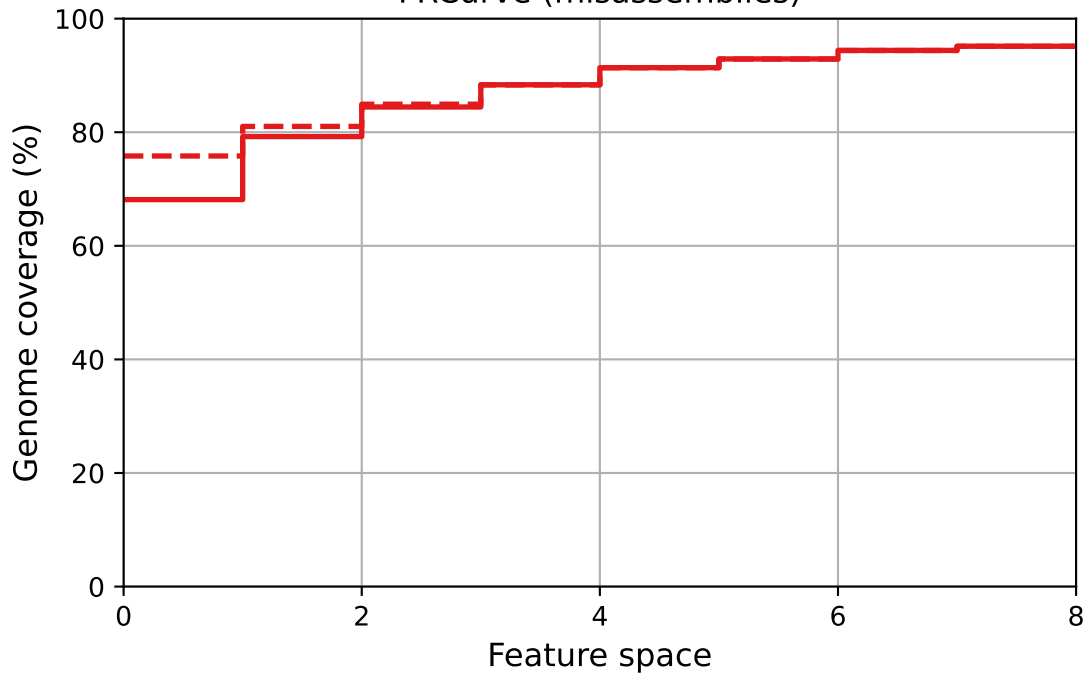
Ades_on_data_2_and_data_1__Scaffolds_broken coverage histogram (bin size



Misassemblies



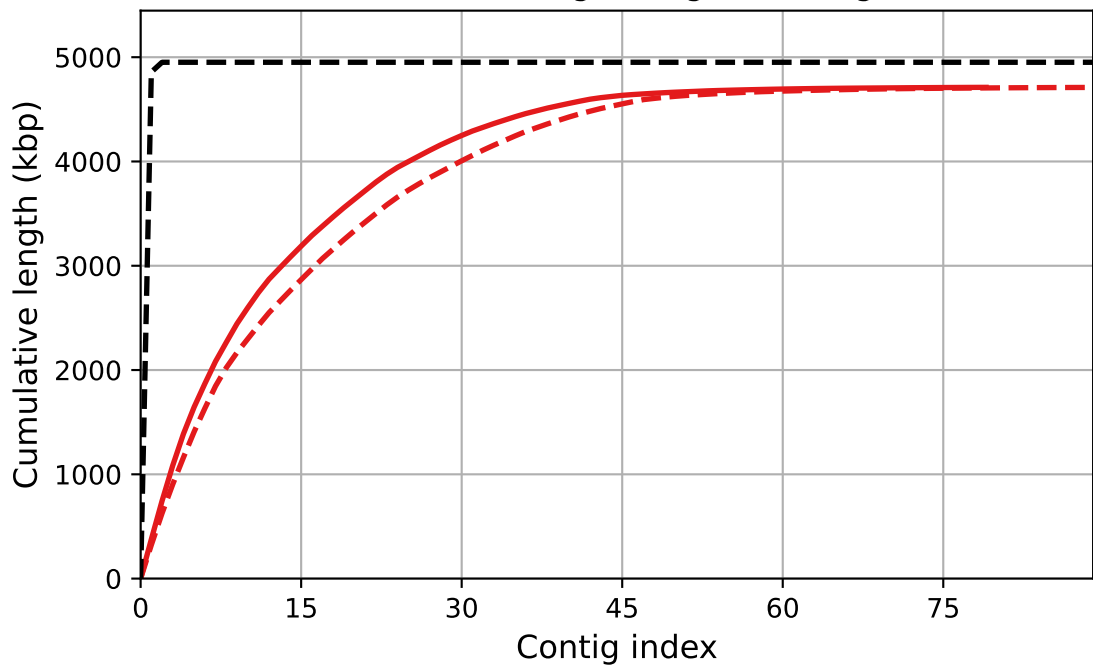
FRCurve (misassemblies)



PAdes_on_data_2_and_data_1_Scaffolds

-- SPAdes_on_data_2_and_data_1_Scaffolds

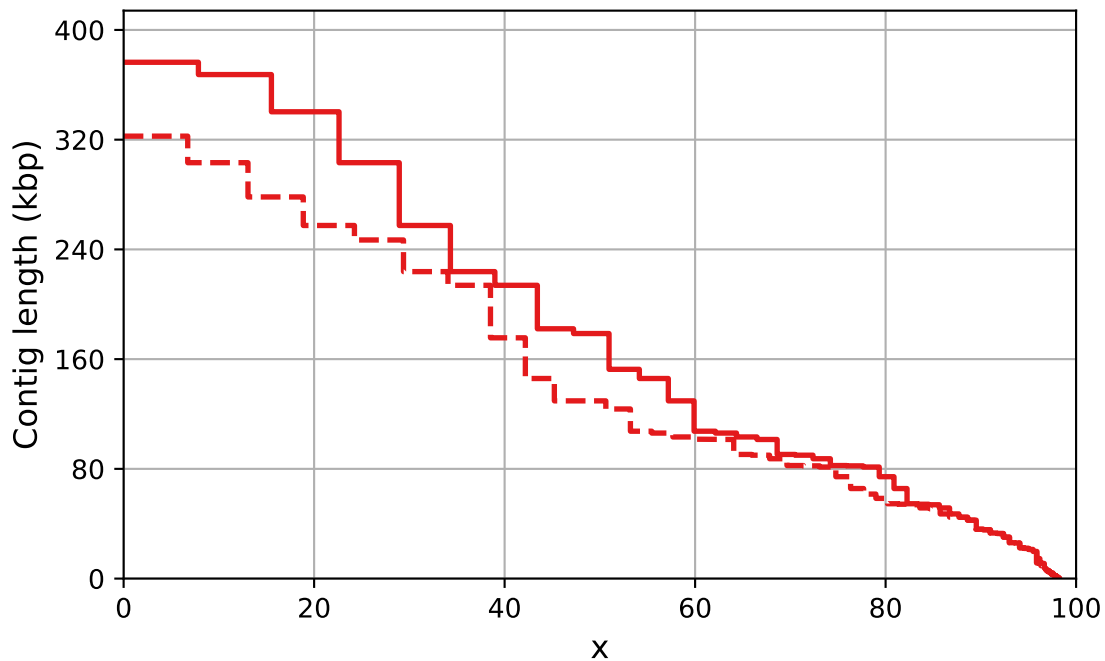
Cumulative length (aligned contigs)



_data_2_and_data_1__Scaffolds

-- SPAdes_on_data_2_and_data_1__Scaffolds_broken

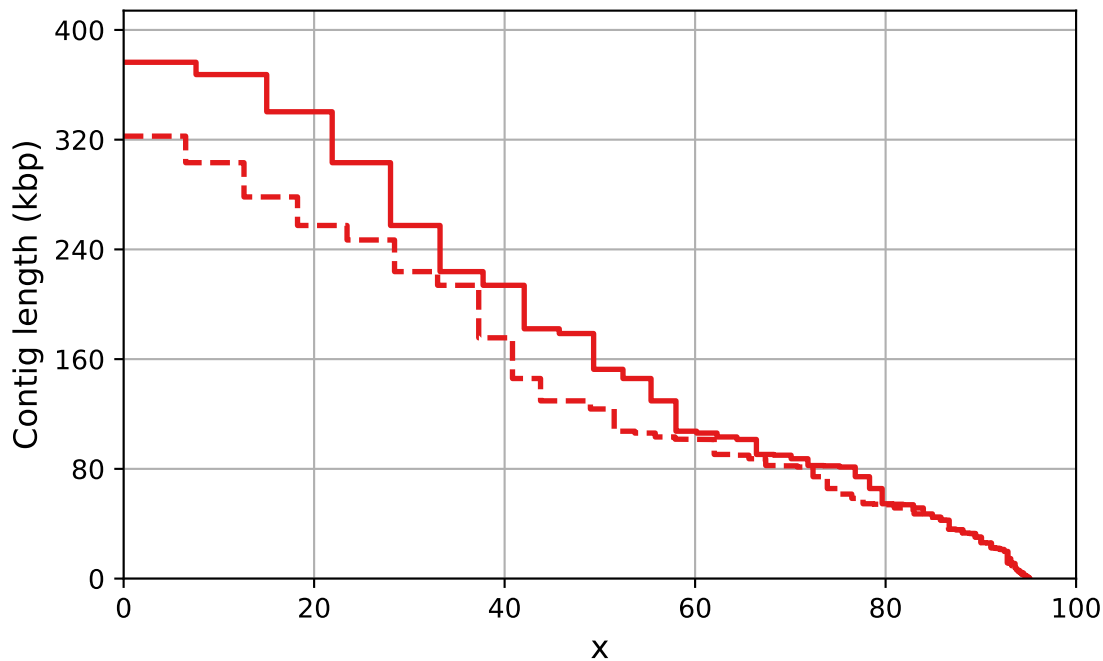
NAx



PADES_on_data_2_and_data_1_Scaffolds

SPADES_on_data_2_and_data_1_Scaffolds

NGAx

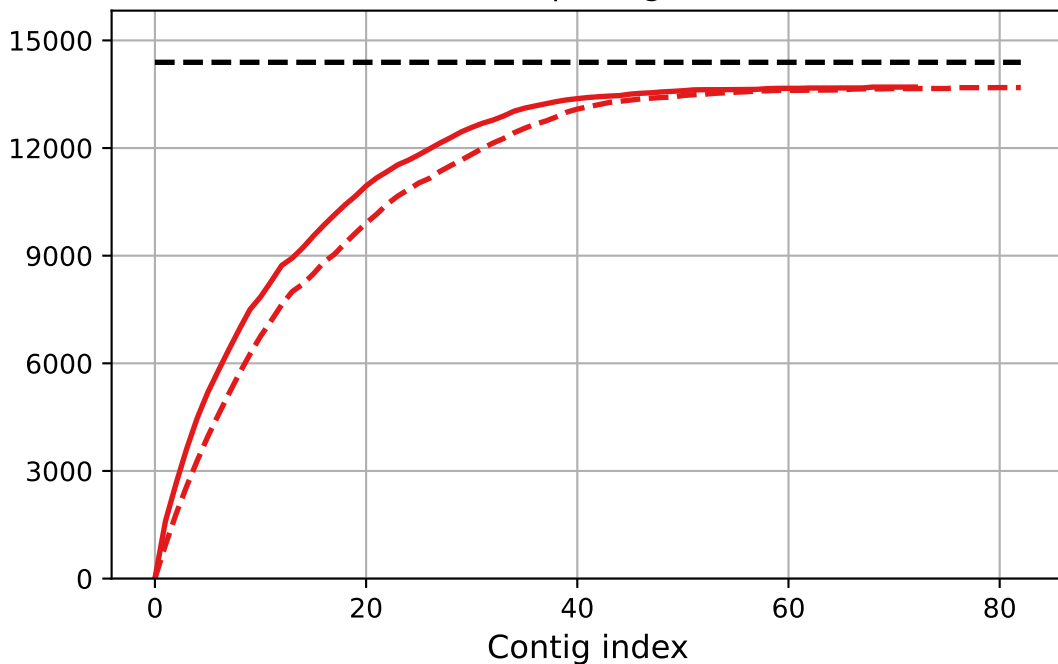


PAdes_on_data_2_and_data_1__Scaffolds

SPAdes_on_data_2_and_data_1__Scaffolds

Cumulative # complete genomic features

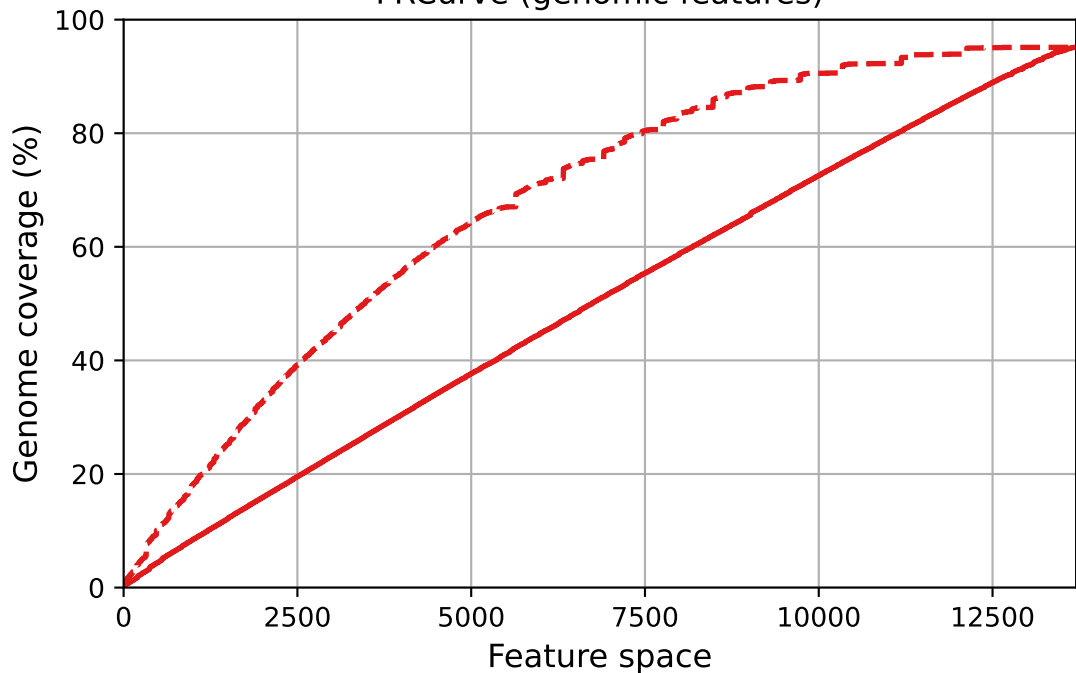
Cumulative # complete genomic features



SPAdes_on_data_2_and_data_1_Scaffolds

SPAdes_on_data_2_and_data_1_Scaffolds_broken

FRCurve (genomic features)



PAdes_on_data_2_and_data_1__Scaffolds

-- SPAdes_on_data_2_and_data_1__Scaffolds

complete genomic features



PAdes_on_data_2_and_data_1__Scaffolds



SPAdes_on_data_2_and_data_1__Scaffolds

Genome fraction, %



PAdes_on_data_2_and_data_1__Scaffolds



SPAdes_on_data_2_and_data_1__Scaffolds