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
# genomic features	13759 + 92 part	13748 + 106 part
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).
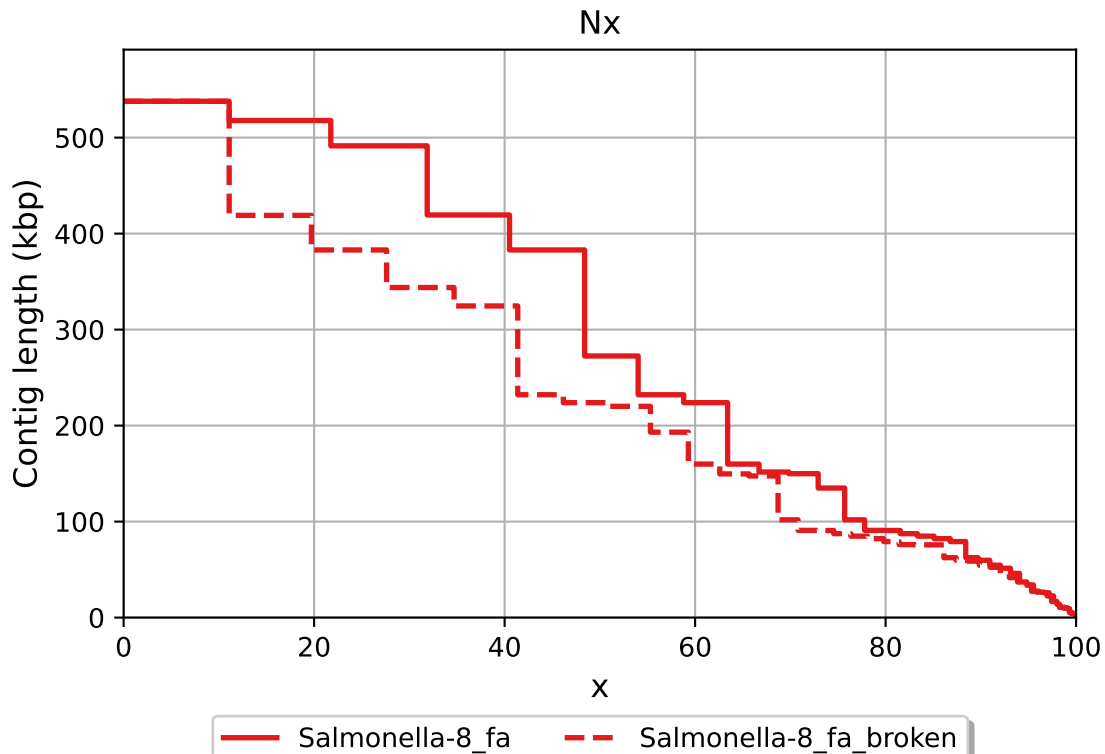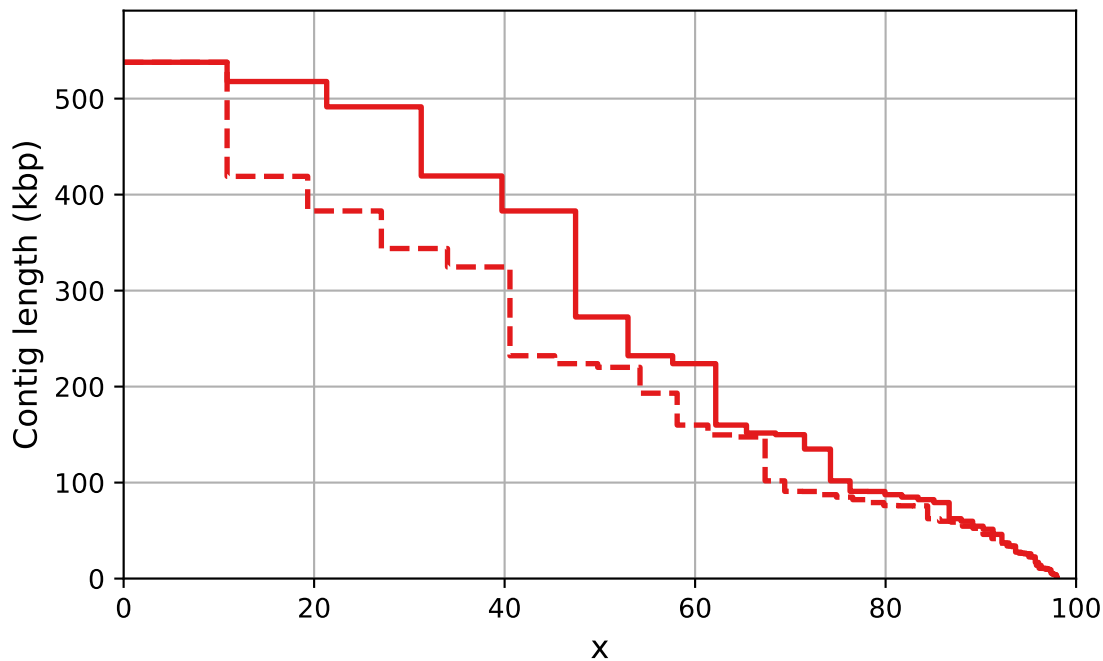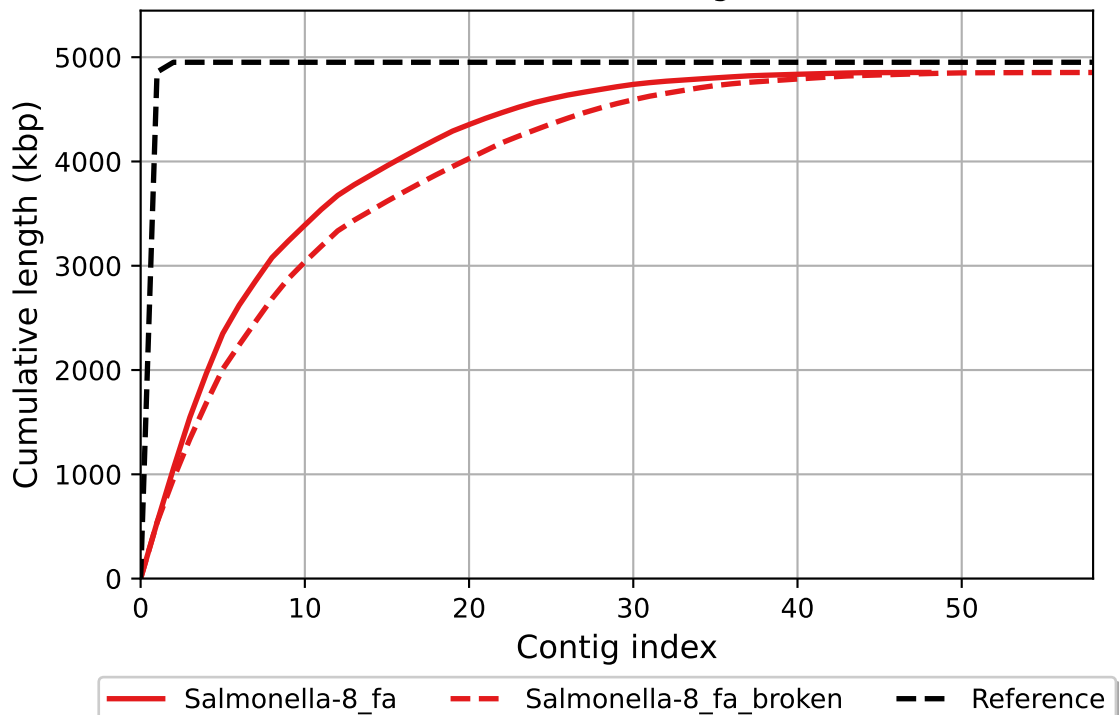
Misassemblies report

	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
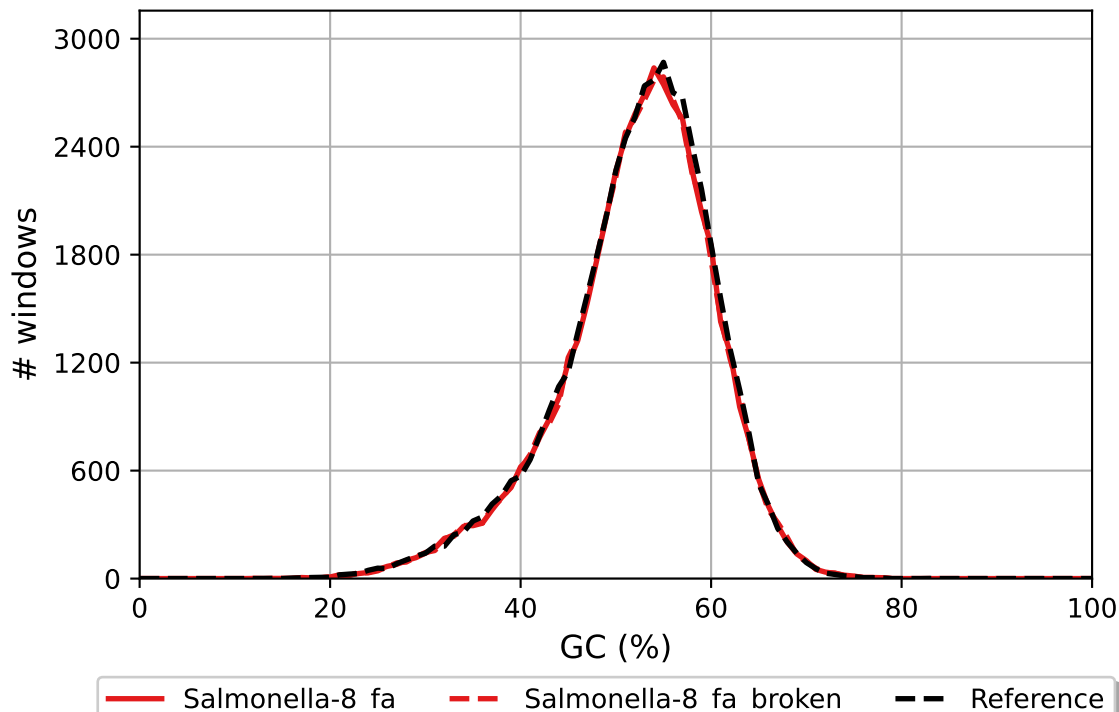(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

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).

Nx

Contig length (kbp) vs x

- Salmonella-8_fa
- - - Salmonella-8_fa_broken

NGx

Cumulative length

Contig index (x-axis), **Cumulative length (kbp)** (y-axis)

Legend:
- Salmonella-8_fa
- Salmonella-8_fa_broken
- Reference

GC content

Legend: Salmonella-8_fa, Salmonella-8_fa_broken, Reference
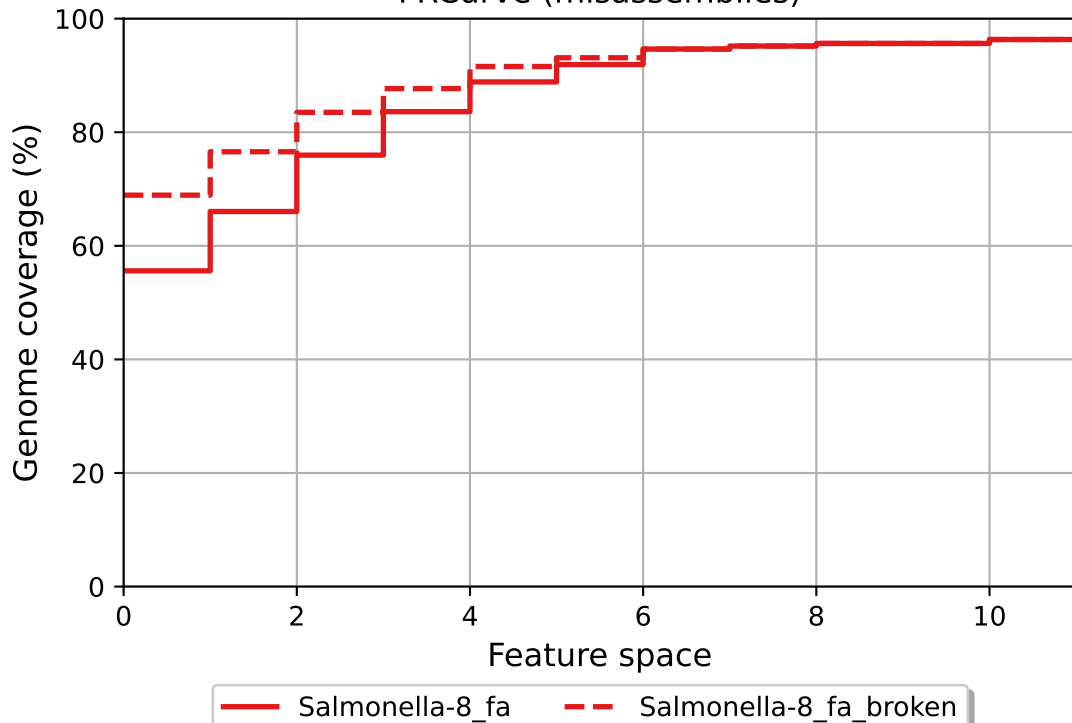
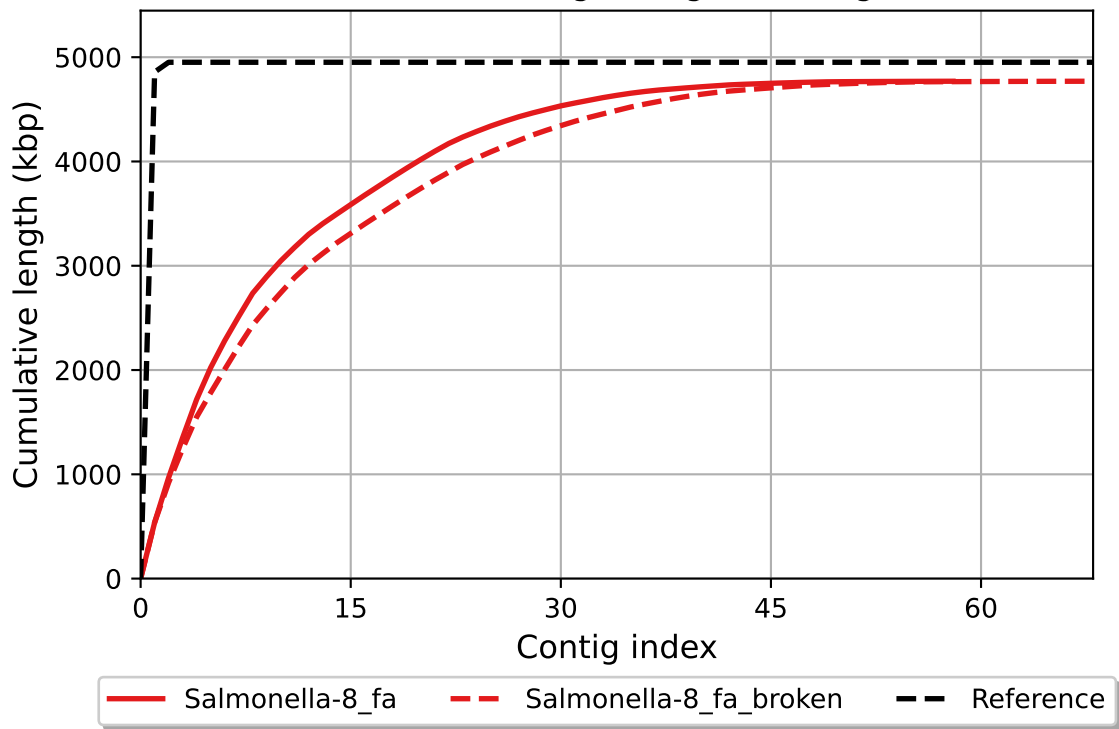Salmonella-8_fa GC content
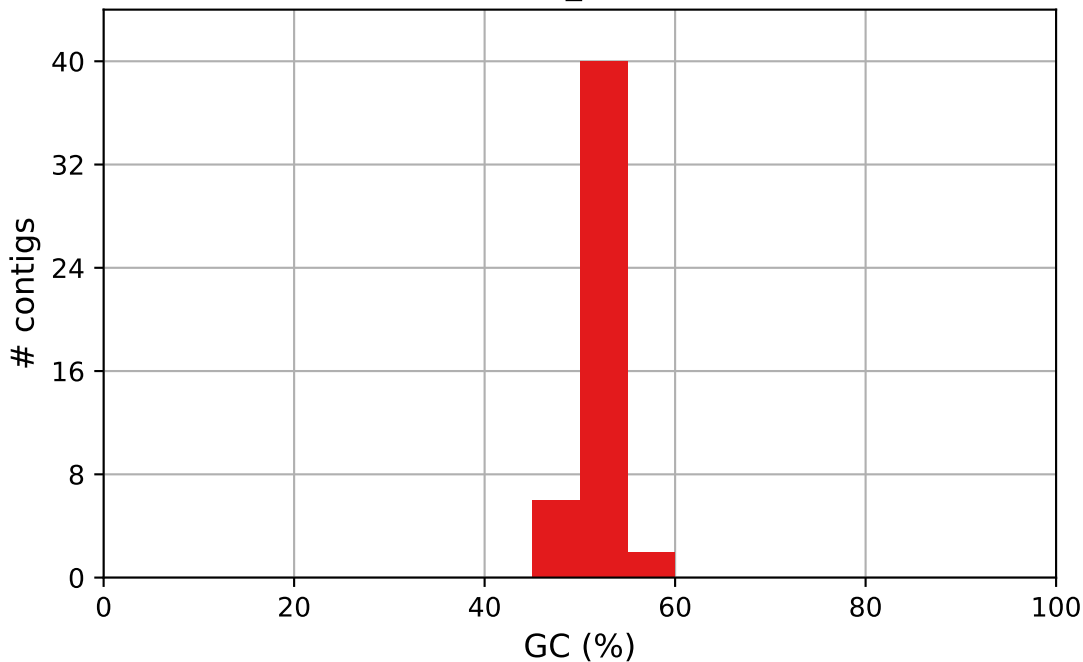
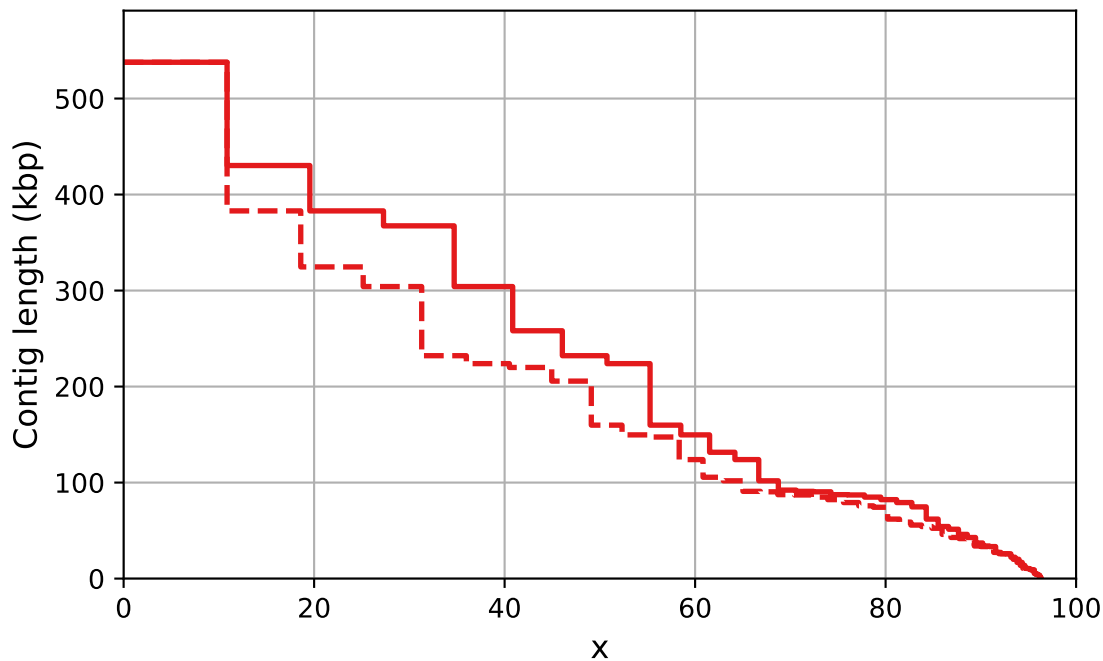Salmonella-8_fa_broken GC content

Misassemblies

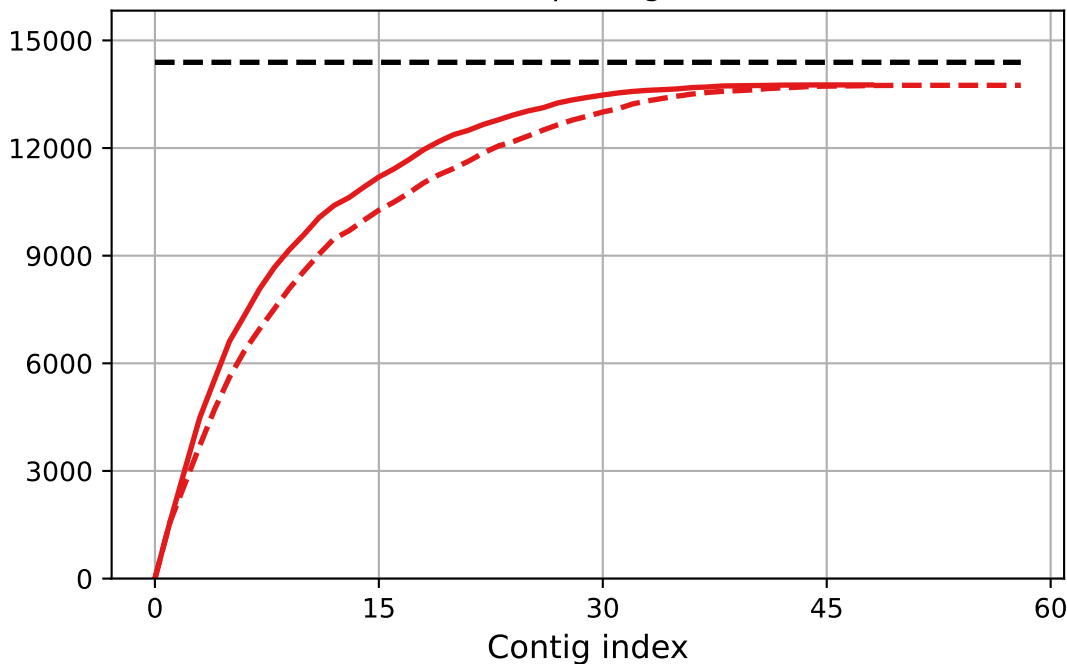FRCurve (misassemblies)

Cumulative length (aligned contigs)

NAx

Contig length (kbp) vs x
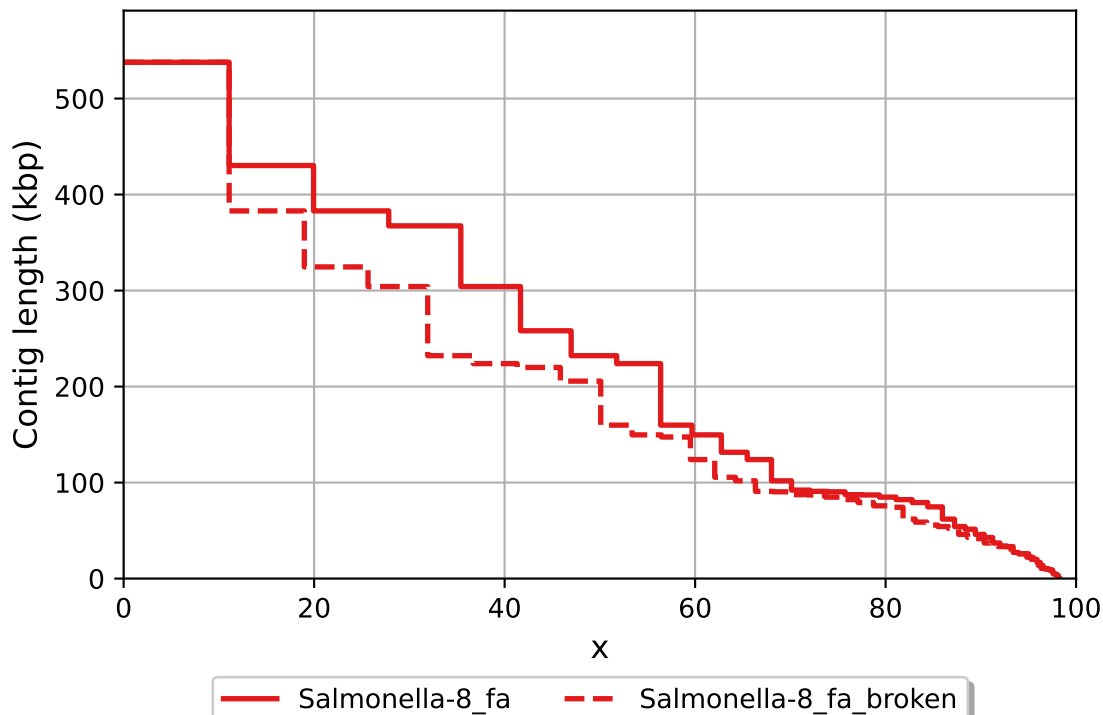
Salmonella-8_fa — Salmonella-8_fa_broken

NGAx

Cumulative # complete genomic features

FRCurve (genomic features)
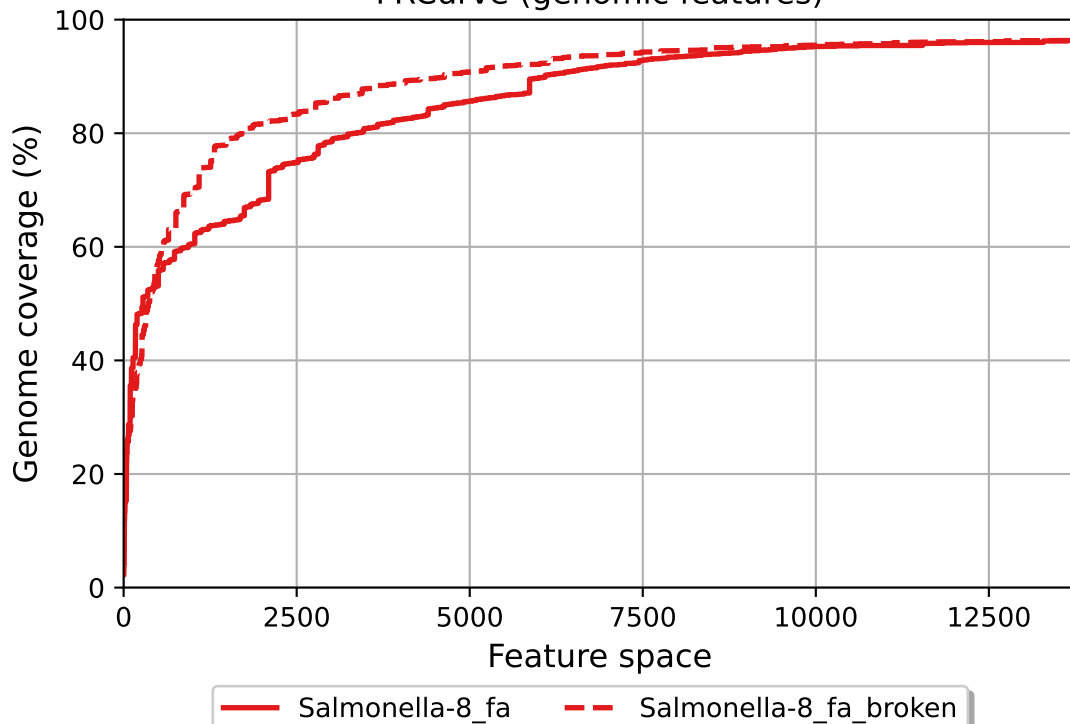
complete genomic features

Salmonella-8_fa   Salmonella-8_fa_broken

Genome fraction, %

Salmonella-8_fa   Salmonella-8_fa_broken