

## 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	4871123	4871123
GC (%)	52.19	52.19
Reference GC (%)	52.23	52.23
N50	272520	223891
NG50	272520	223891
N90	59728	54580
NG90	59728	54580
auN	301881.7	245920.8
auNG	300811.4	245023.7
L50	6	7
LG50	6	7
L90	21	26
LG90	21	26
# misassemblies	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 0 part	0 + 0 part
Unaligned length	0	0
Genome fraction (%)	99.645	99.645
Duplication ratio	1.000	1.000
# N's per 100 kbp	10.34	0.04
# mismatches per 100 kbp	0.00	0.02
# indels per 100 kbp	0.00	0.00
Complete BUSCO (%)	98.65	98.65
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	2 + 4 part	2 + 4 part
Largest alignment	537866	537866
Total aligned length	4853853	4853353
NA50	272520	223891
NGA50	272520	223891
NA90	59728	54580
NGA90	59728	54580
auNA	301881.7	245920.8
auNGA	300811.4	245023.7
LA50	6	7
LGA50	6	7
LA90	21	26
LGA90	21	26

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

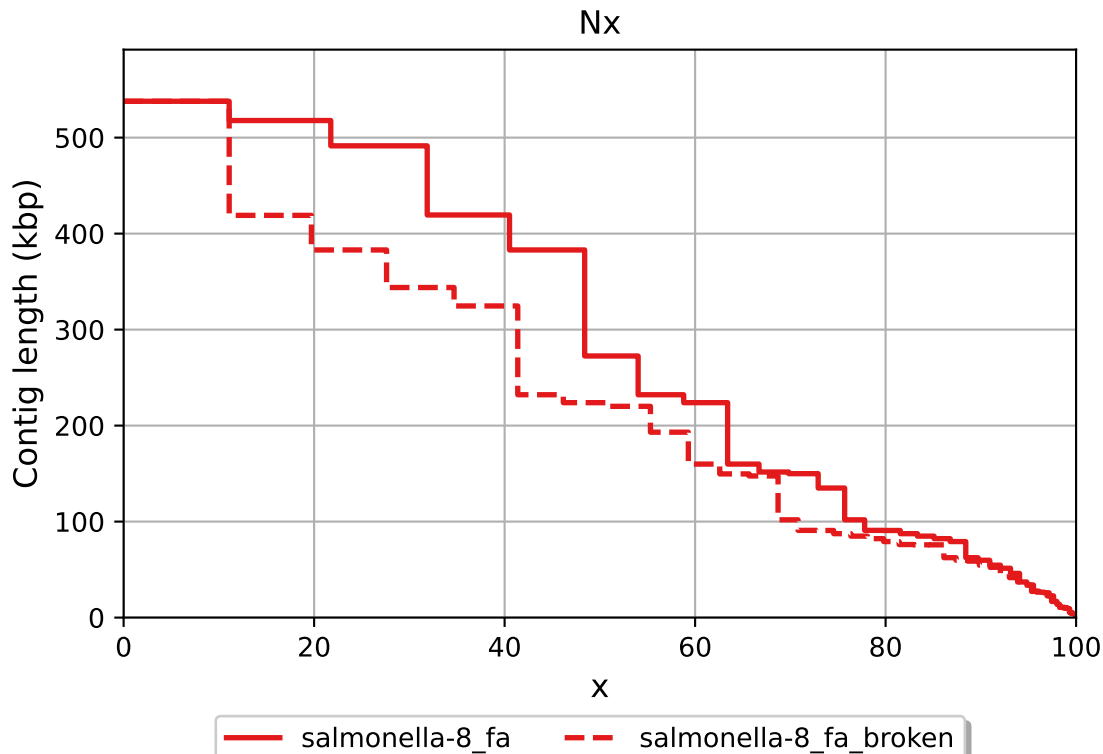
	salmonella-8_fa	salmonella-8_fa_broken
# misassemblies	0	0
# contig misassemblies	0	0
# c. relocations	0	0
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	0	0
# mismatches	0	1
# indels	0	0
# indels (<= 5 bp)	0	0
# indels (> 5 bp)	0	0
Indels length	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).

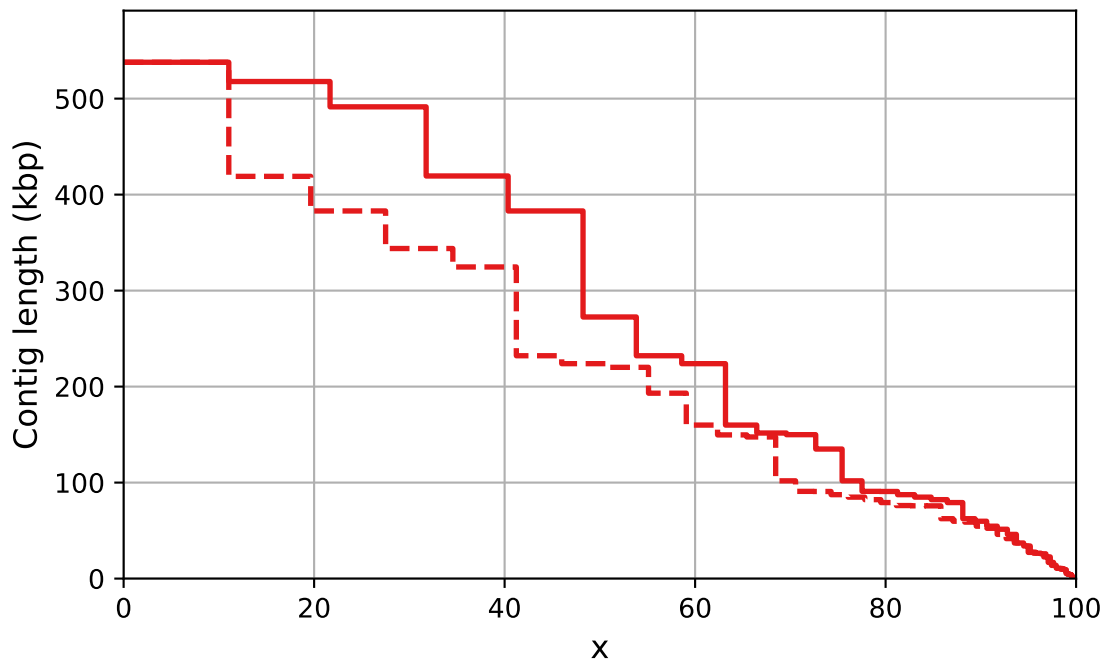
## Unaligned report

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

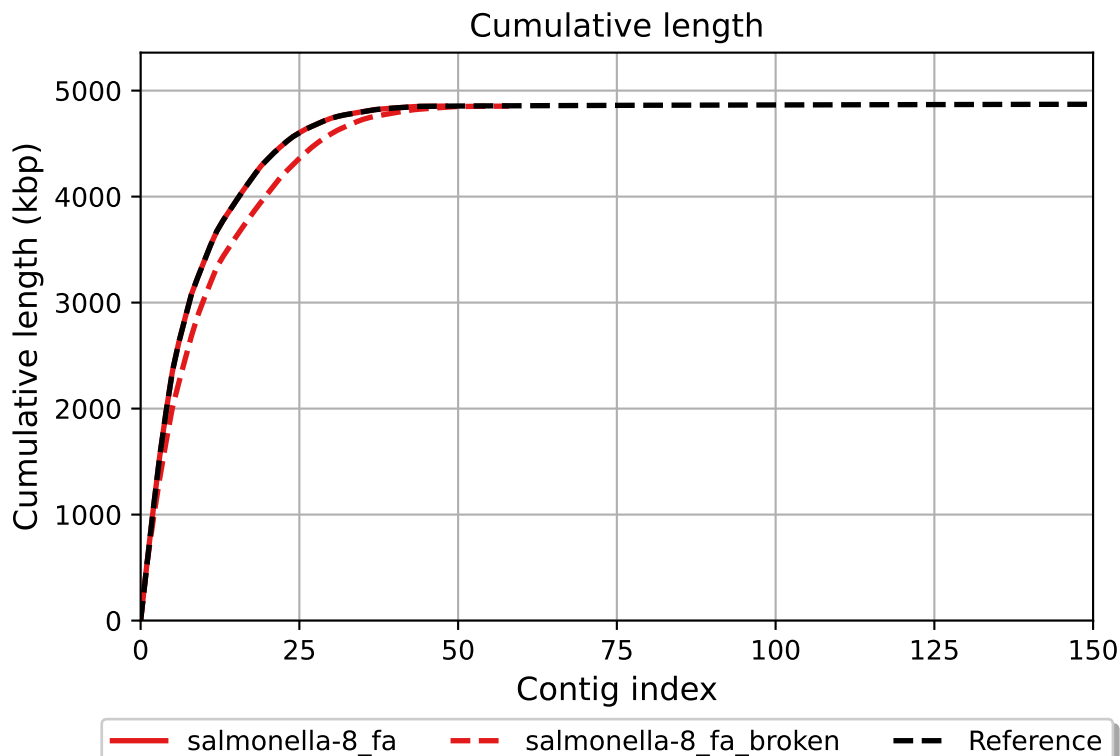
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



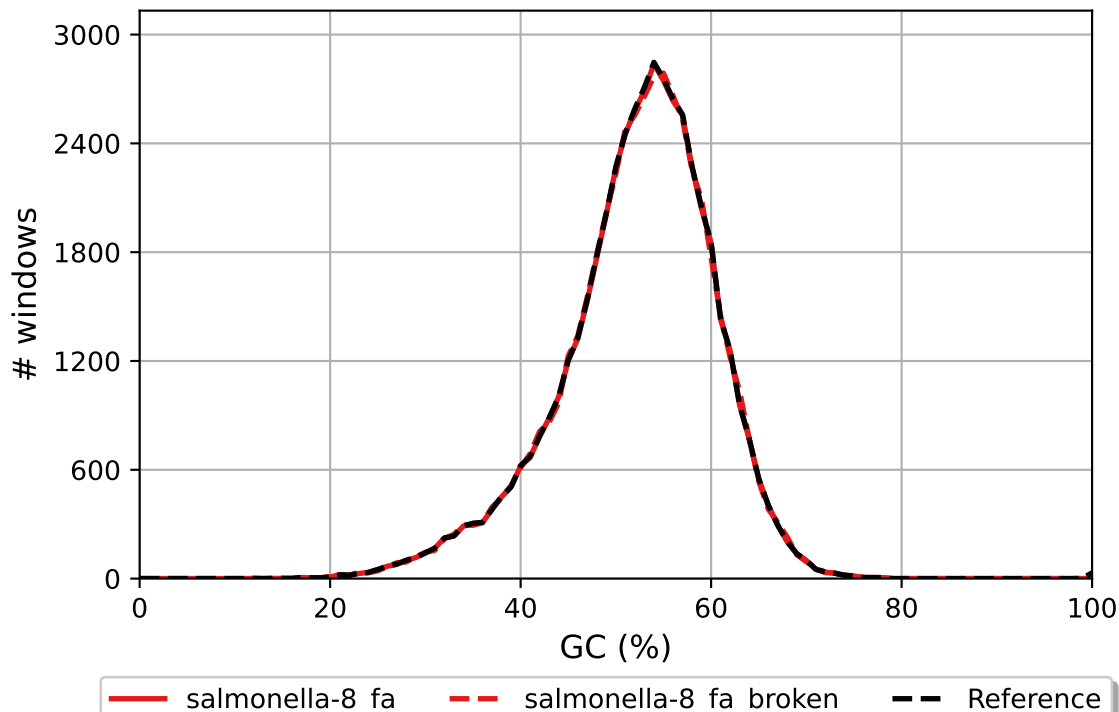
NGx



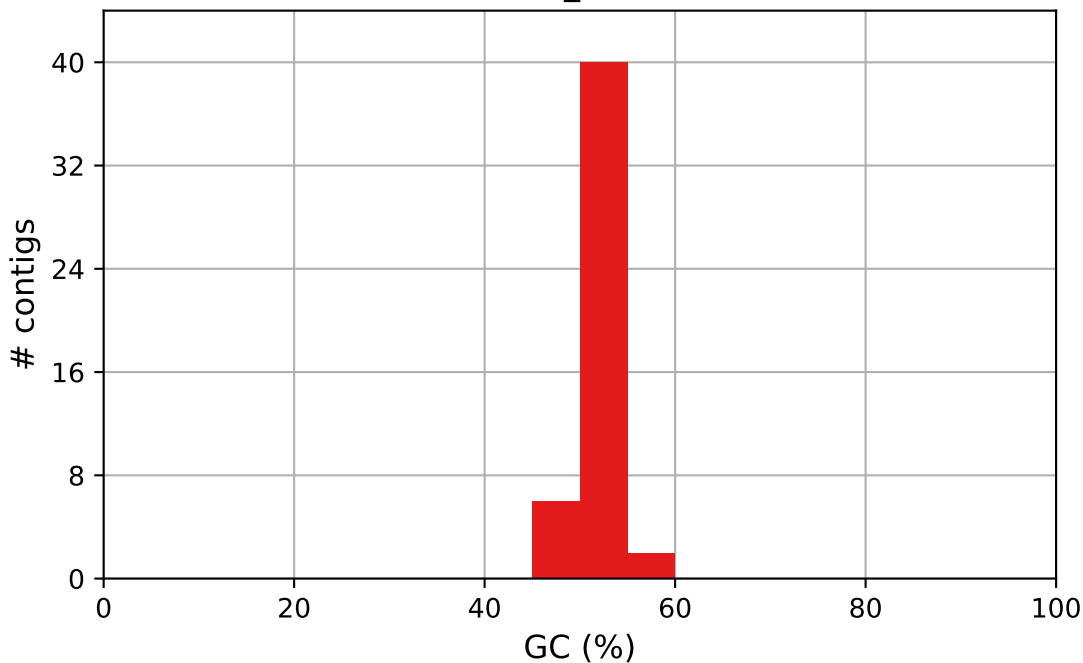
— salmonella-8\_fa    - - - salmonella-8\_fa\_broken



## GC content



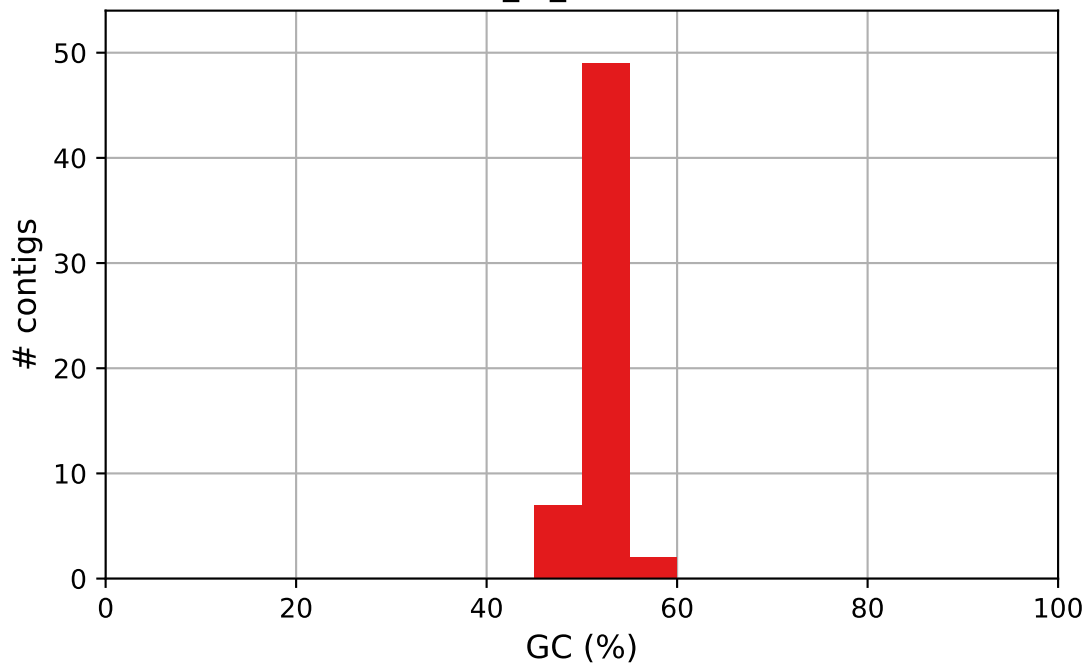
salmonella-8\_fa GC content



salmonella-8\_fa

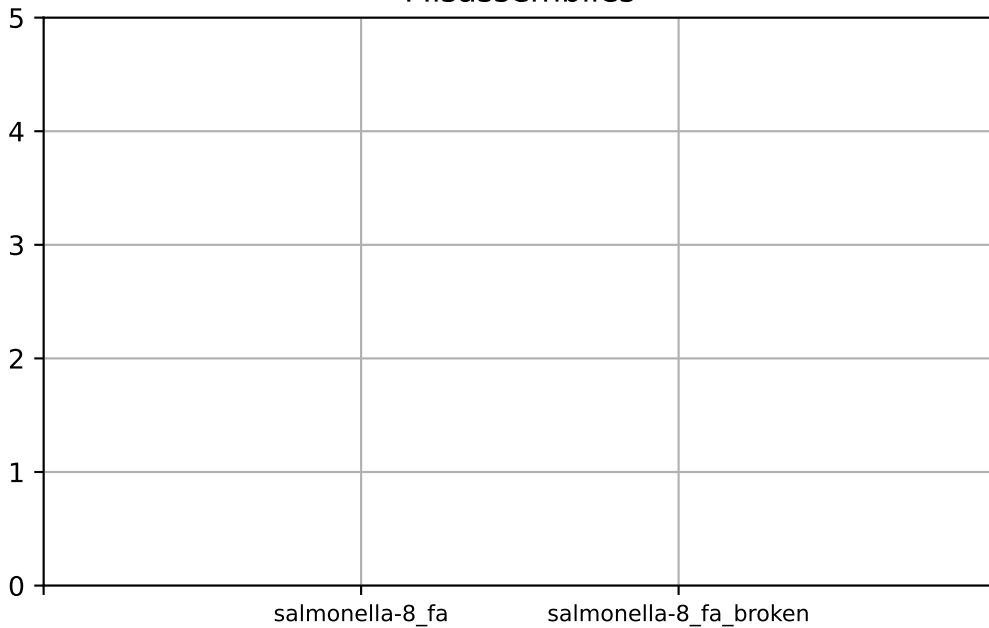


salmonella-8\_fa\_broken GC content

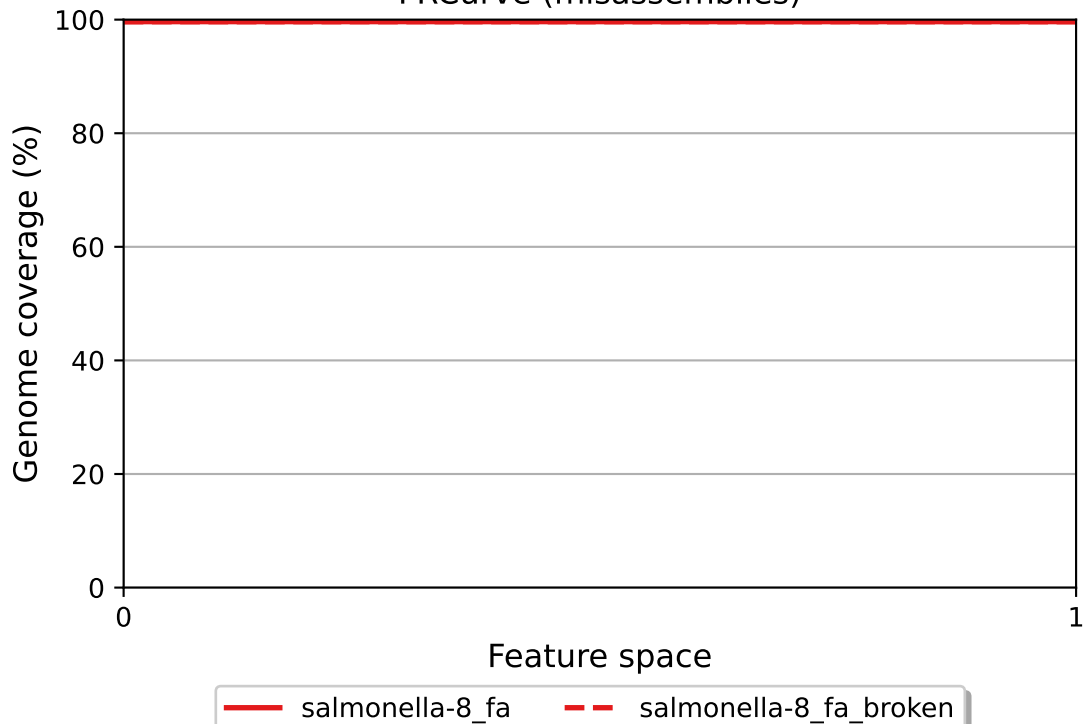


salmonella-8\_fa\_broken

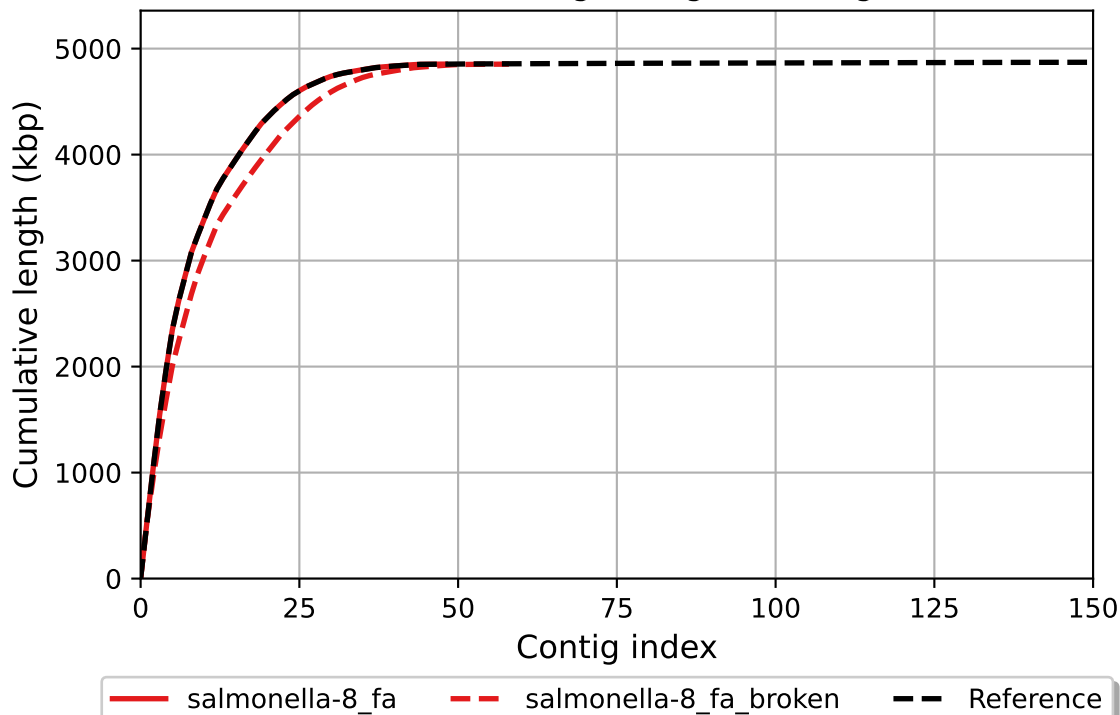
## Misassemblies



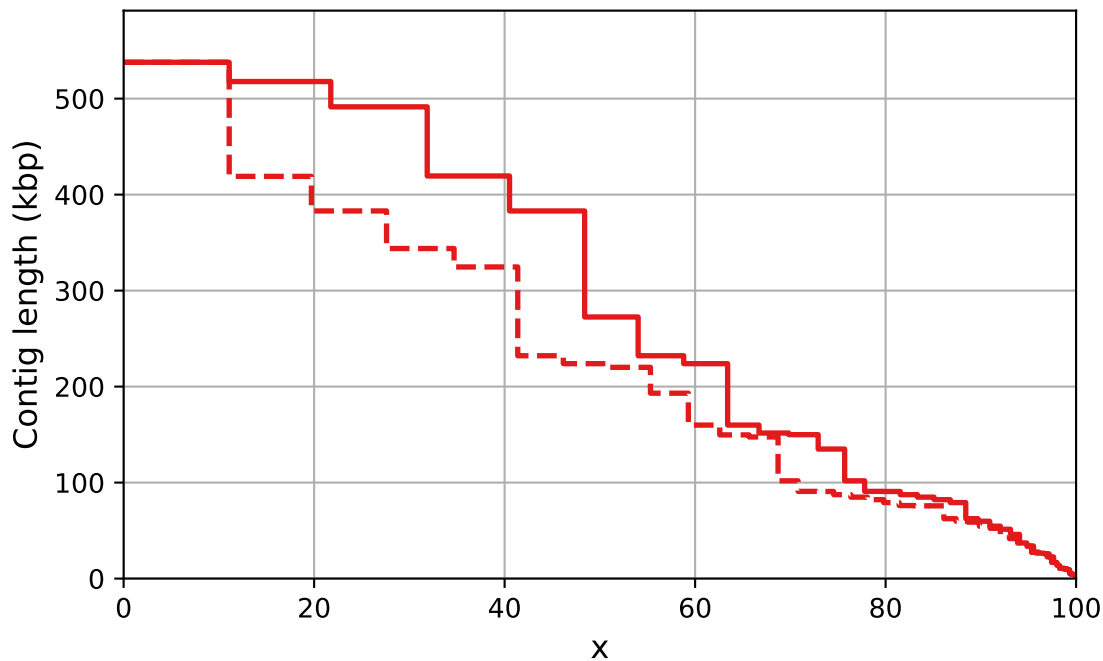
FRCurve (misassemblies)



Cumulative length (aligned contigs)

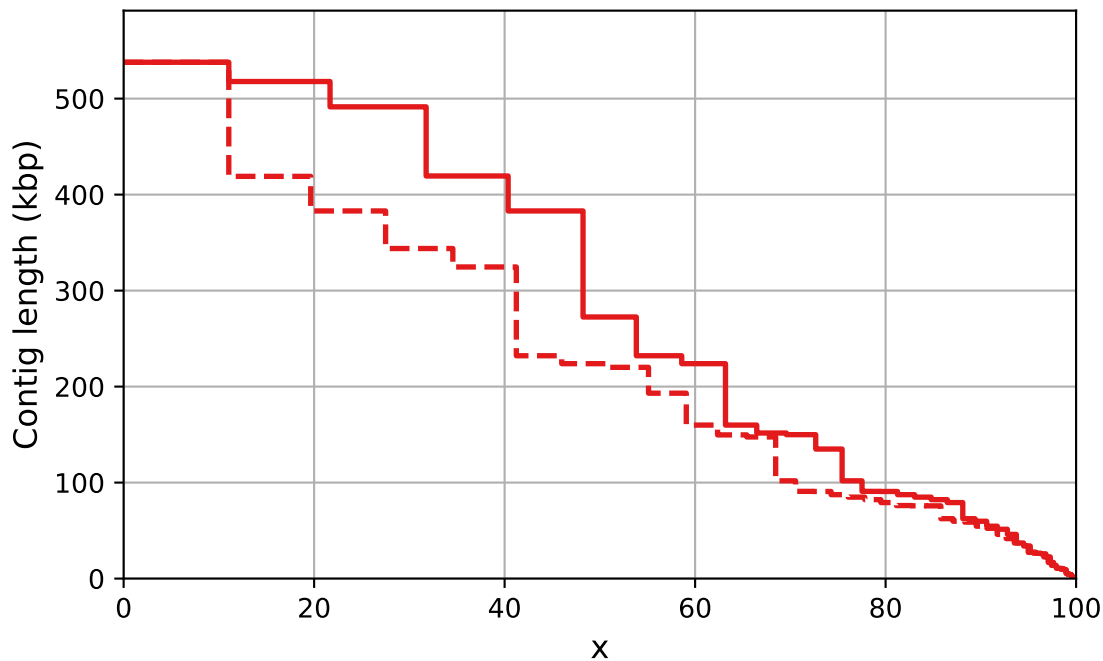


NAx



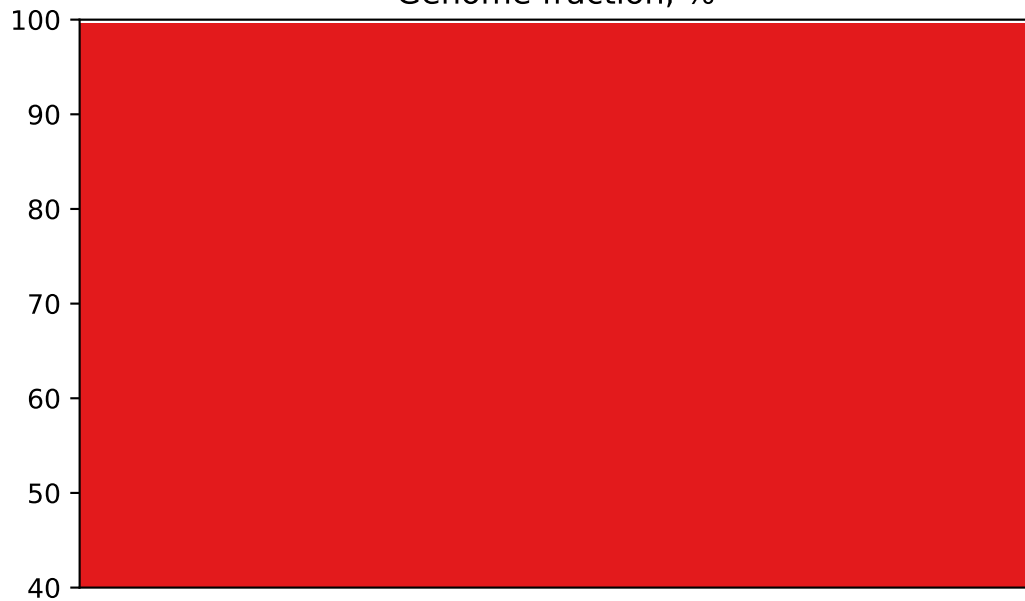
— salmonella-8\_fa    - - - salmonella-8\_fa\_broken

# NGAx



— salmonella-8\_fa    - - - salmonella-8\_fa\_broken

Genome fraction, %



salmonella-8\_fa



salmonella-8\_fa\_broken